Responses to #Reviewer 2

This manuscript presented a study on mapping eight key plant traits at 1 km spatial resolution across China using field measurements, environmental variables and vegetation indices. Two machine learning methods were used to develop the trait prediction models. This study is well written and is interesting to the community. The trait dataset of this study has great potential to advance trait-based ecology. However, the methods are not clearly described. Also, it is recommended to perform a quantitative comparison between the trait maps of this study with those from previous studies. I hope that the following comments are helpful to improve the quality of the manuscript.

[Response]: Thanks for your positive comments and constructive suggestions for our manuscript. We have carefully addressed the suggestions and comments on the method description and added a quantitative comparison between the trait maps of this study with those from previous studies. And detailed revisions and responses are listed below. In addition, we have used tracks to highlight the revisions in the revised manuscript.

Specific comments:

1. Line 67: “PROPECT model” should be “PROSPECT model”.

[Response]: We have corrected this word in the revised manuscript (see Line 70).

2. Line 125: It is interesting to know the proportion of data excluded by criteria #3. Since the trait values of individual plant were aggregated to community-weighted trait values within 1km, including these data can be helpful to increase the number of measurements.

[Response]: Thanks for your comment. The description was misleading on the criteria #3 in the old version of the manuscript. The aim of criteria #3 was to consider the intraspecific trait variation within the same species. When the same species occurred in the same sampling site from different studies, we included all original observed data from different studies rather than averaging the values at the species level. This criterion can contribute substantially to the trait variation within and between communities, and it also can be helpful to increase the number of trait measurements in subsequent analysis. We have corrected the relevant description about criteria #3 as “*In order to consider the intraspecific trait variation, when the same species occurred in the same sampling site from different studies, we included all original observed data from different studies rather than averaging the values at the species level*” in the section 2.2 in Materials and Methods (see Lines 153–156 in the revised manuscript).

3. Line 135: SLA of sun and shade leaves can be quite different, which may lead to uncertainties

for later analysis.

[Response]: Thanks. We have checked the literature that these literatures of SLA data that introduced the sampling and measurement methods all sampled the sun leaves according to according to standardized measurement procedures, which require sampling sun leaves during field sampling for trait studies (Perez-Harguindeguy et al., 2013). We have corrected this sentence as "*we included SLA measurements on sun-leaves*" in the section 2.2 in Materials and Methods (see Line 168 in the revised manuscript).

4. Line 159: Specify the full name of AI.

[Response]: We have added the full name of AI (i.e., aridity index) in the section 2.3 in Materials and Methods (see Line 197 in the revised manuscript).

5. Line 167: The soil data was from Shangguan et al., 2013. Please justify that soil properties are time invariant, or their variation across time has little influence on the plant traits.

[Response]: Soil properties are influenced by climate, vegetation, land use and management and human activities over a long period, and to some extent, soil properties may have temporal variability. However, due to the limitation of current technology and the availability of field survey data, a temporal dynamic dataset for multiple soil properties at a large scale is lacking, which is an inadequacy that cannot be resolved in current studies. The soil data that we use is the national-scale dataset that was surveyed based on multiple years during the Second National Soil Survey (1979–1985) and included 2444 counties, 312 national farms, and 44 forest farms in China, which is also a common and widely accepted practice in large-scale spatial mapping and biogeographical studies (Maire et al., 2015; Besnard et al., 2021; Huang et al., 2021; Ma et al., 2021). Soil properties are regarded to be more stable than that of plant traits. A current study has reported that soil organic carbon in most regions in China showed insignificant trend from 1980s to 2010s and slightly inter-decadal declines in North China and Northeast China (Zhang et al., 2023). At the time scale of decades, it is reasonable for being used for large-spatial scale studies.

Reference

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Huang, Y. Y., Ciais, P., Santoro, M., Makowski, D., Chave, J., Schepaschenko, D., Abramoff, R. Z., Goll, D. S., Yang, H., Chen, Y., Wei, W., and Piao, S. L.: A global map of root biomass across the world's forests. Earth Syst. Sci. Data, 13, 4263–4274, https://doi.org/10.5194/essd-13-4263-2021, 2021.

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Zhang, Z. P., Ding, J. L., Zhu, C. M., Wang, J. J., Li, X., Ge, X. Y., Han, L. J., Chen, X. Y., and Wang, J. Z.: Exploring the inter-decadal variability of soil organic carbon in China, Catena, 230, https://doi.org/10.1016/j.catena.2023.107242, 2023.

6. Lines 167-169: Were the soil properties of eight layers averaged? If the topsoil properties are important, it would be good to simply use the soil properties of the first layer (0-45cm).

[Response]: No, we averaged the first four layers. In Shangguan et al. (2013)'s study, the soil characteristics of soil profiles are divided into eight standard layers (i.e., 0–0.045, 0.045–0.091, 0.091–0.166, 0.166–0.289, 0.289–0.493, 0.493–0.829, 0.829–1.383, and 1.383–2.296 m). The first layer is 0-4.5 cm instead of 0-45cm. We averaged the soil data of the first four layers to represent the topsoil. We used the topsoil depth of about 30 cm, because we considered most relevant for community composition via plant establishment and by influencing plants in later life stages, for example, through the potentially high nutrient availability (Vitousek and Sanford, 1986; Boonman et al., 2020).

Reference

Shangguan, W., Dai, Y. J., Liu, B. Y., Zhu, A. X., Duan, Q. Y., Wu, L. Z., Ji, D. Y., Ye, A. Z., Yuan, H., Zhang, Q., Chen, D. D., Chen, M., Chu, J. T., Dou, Y. J., Guo, J. X., Li, H. Q., Li, J. J., Liang, L., Liang, X., Liu, H. P., Liu, S. Y., Miao, C. Y., and Zhang, Y. Z.: A China data set of soil properties for land surface modeling. J. Adv. Model. Earth Syst., 5, 212–224, https://doi.org/10.1002/jame.20026, 2013.

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7. Line 200: Please explain why the MTCT/MIR/etc. of January were used. They are not within the growing season.

[Response]: Thanks. Most selected variables were related to growing seasons because plant functional traits were measured during the growing season. Furthermore, based on the results of collinearity (r values), we found that MTCI, MIR, NIR, red and blue in January showed low correlations with those in other months, thus these variables were included to be used in the machine learning methods (see Lines 239–243 in the revised manuscript).

8. Lines 239-241: What is the difference between the 10-fold cross validation and 80%/20% data split?

[Response]: The description of this section was not clear in the old version. First, we spilt the data into two parts: 80% of the trait data was used to train the models, and the remaining 20% was used to assess model's performance. To obtain a stable and reliable model, this procedure was repeated 10 times, and the model performances (R^2, NRMSE and MAE) were calculated by the average values of these 10 results. We have corrected the description as "*we calibrated the models 10 times using randomly selected 80% of the data for training the models and validating against the remaining 20% based on cross-validation*." in the section 2.4 in Materials and Methods (See Lines 287–290 in the revised manuscript).

9. Line 252: Please describe the way of obtaining permuted values in more detail.

[Response]: Thanks. The relative importance of each variable is available from model prediction, but it may be model-specific. To overcome this limitation, Thuiller et al. (2009) used a randomisation procedure to estimate the importance of each variable that is independent of the modelling technique, thus enabling direct comparison across models. This method applies correlation between the standard predictions (i.e. fitted values) and predictions where the variable under investigation has been randomly permutated. If the correlation is high, i.e. it is showing little difference between the two predictions, the variable permutated is considered not important for the model. This is repeated multiple times for each variable, and the mean correlation coefficient over runs is recorded. Then the relative importance of each predictor was quantified as one minus the Spearman rank correlation coefficient (see Boonman et al. 2020). We have added more detailed description in the section 2.4 in Materials and Methods (see Lines 302–306 in the revised manuscript).

Reference

Thuiller, W., Lafourcade, B., Engler, R., and Araújo, M. B.: BIOMOD – A platform for ensemble forecasting of species distributions. Ecography, 32, 369–373, https://doi.org/10.1111/j.1600-0587.2008.05742.x, 2009.

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10. Line 259: It is not clear how the trait values of individual plant were aggregated with PFT to community-weighted trait values within 1km. Please describe the method in more detail.

[Response]: 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. 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 environmental variables and vegetation indices at a 1 km spatial resolution. Then, we obtained six prediction layers for single 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) and 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).

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

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

Reference

Garnier, E., Cortez, J., Billès, G., Navas, M.-L., Roumet, C., Debussche, M., Laurent, G., Blanchard, A., Aubry, D., Bellmann, A., Neill, C., and Toussaint, J. P.: Plant functional markers capture ecosystem properties during secondary succession. Ecology, 85, 2630–2637, https://doi.org/10.1890/03-0799, 2004.

11. Lines 263-264: It is not clear how the predictions of the two methods were merged. Did the authors set a threshold for the cross-validated R2? If the accuracies of predictions of one method were too low, it may not be necessary to include them.

[Response]: Thanks for your nice suggestion. In this manuscript, we did not set a threshold for the cross-validated R^2. We used Weighted Average methods based on the R^2 values of single-model to obtain the predictive performance of the ensemble models. Firstly, 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 merged predictive values (based on Eq. 5) against the observed trait values. In addition, the accuracies of these two models showed little variability for a given trait.

We have added the relevant description on how the predictions of the two methods were merged in the section 2.5 in Materials and Methods (see Lines 326–336 in the revised manuscript).

12. Lines 403-417: It would be great to perform a quantitative comparison with previous trait maps, for instance, the differences between the trait maps from this study and those of previous studies can be calculated. From such maps, one can easily tell the main differences among the datasets.

[Response]: Thanks for your constructive suggestion. Previous studies mainly focused on the global scale (see Table F1 in Appendix F), we extracted the data of China from the global trait maps. Before the quantitative comparisons with previous studies, we performed two steps to make the products as comparable as possible and improve the consistency between different datasets. First, because the spatial resolution of most global trait maps is 0.5°, we resampled the data products of previous studies and our maps to 0.5° spatial resolution. In addition, Vallicrosa et al. (2022) generated the global maps of LNC and LPC with a 1 km spatial resolution, we also compared the frequency distribution of Vallicrosa et al. (2022) with that of our study at a 1 km spatial resolution. Second, our study focused on natural vegetation, so the global trait maps were used to filter out non-natural vegetation (e.g., croplands). For example, Madani et al. (2018) predicted the spatial distributions of key plant traits for SLA, canopy height and seed mass that include croplands. We quantitatively compared our maps with previous studies from two perspectives. The comparisons among trait maps were made using frequency plots and spatial correlations (Fig. 7 and Table 5, Fig. F1 in Appendix F) in the section 4.1 in

Discussion (see Lines 469–483 in the revised manuscript). And the maps of spatial differences between our study and previous studies were displayed as Figs. F2-F6 in Appendix F in the section 4.2 in Discussion (see Lines 513–542 in the revised manuscript).

Table F1 Summary table of related trait maps used in this study.

References	Related traits	Methods	Predictors	Consideration of PFT	Resolution
Dong et al. (2023)	SLA LNC	Optimality models	Climate	Yes	0.5°
Vallicrosa et al. (2022)	LNC LPC	Neural networks	Climate Soil N and P deposition	Yes	0.0083°
Schiller et al. (2021)	SLA LNC LA WD	Convolutional Neural Networks	Climate In-situ RGB images	No	0.5°
Boonman et al. (2020)	SLA LNC WD	Generalized linear model, Generalized additive model, Random forest, Boosted regression trees, Ensemble model	Climate Soil	No	0.5°
Moreno et al. (2018)	SLA LNC LPC LDMC	Regularized linear regression, Random forest, Neural networks, Kernel networks	Climate Elevation Reflectance	Yes	0.0045°
Madani et al. (2018)	SLA	Generalized additive model	Climate	No	0.5°
Butler et al. (2017)	SLA LNC LPC	Bayesian model	Climate Soil	Yes	0.5°
Bodegom et al. (2014)	SLA WD	Multiple regression analysis	Climate Soil	No	0.5°

The resolutions 0.5°, 0.0083°, and 0.0045° correspond to square grid cell sizes of about 50 km, 1 km and 500 m at the equator. SLA, specific leaf area; LDMC, leaf dry matter content; LNC, leaf N concentration; LPC, leaf P concentration; LA, leaf area; WD, wood density.

Table 5 Spatial correlations for SLA, LNC, LPC, LA and WD between this study and other previous trait maps, labelled by the first author of the corresponding publication (see Table F1 for citations).

Spatial correlation	Dong	Vallicrosa	Schiller	Boonman	Moreno	Madani	Butler	Bodegom
SLA	0.398		-0.082	0.327	0.242	0.136	-0.042	0.319
LNC	0.156	0.359	0.229	0.252			0.394	
LPC		0.136					0.057	
LA			0.514					
WD			0.647	0.107				

SLA, specific leaf area (m^2 kg^{-1}); LNC, leaf N concentration (mg g^{-1}); LPC, leaf P concentration (mg g^{-1}); LA, leaf area (cm^2); WD, wood density (g cm^{-3}).

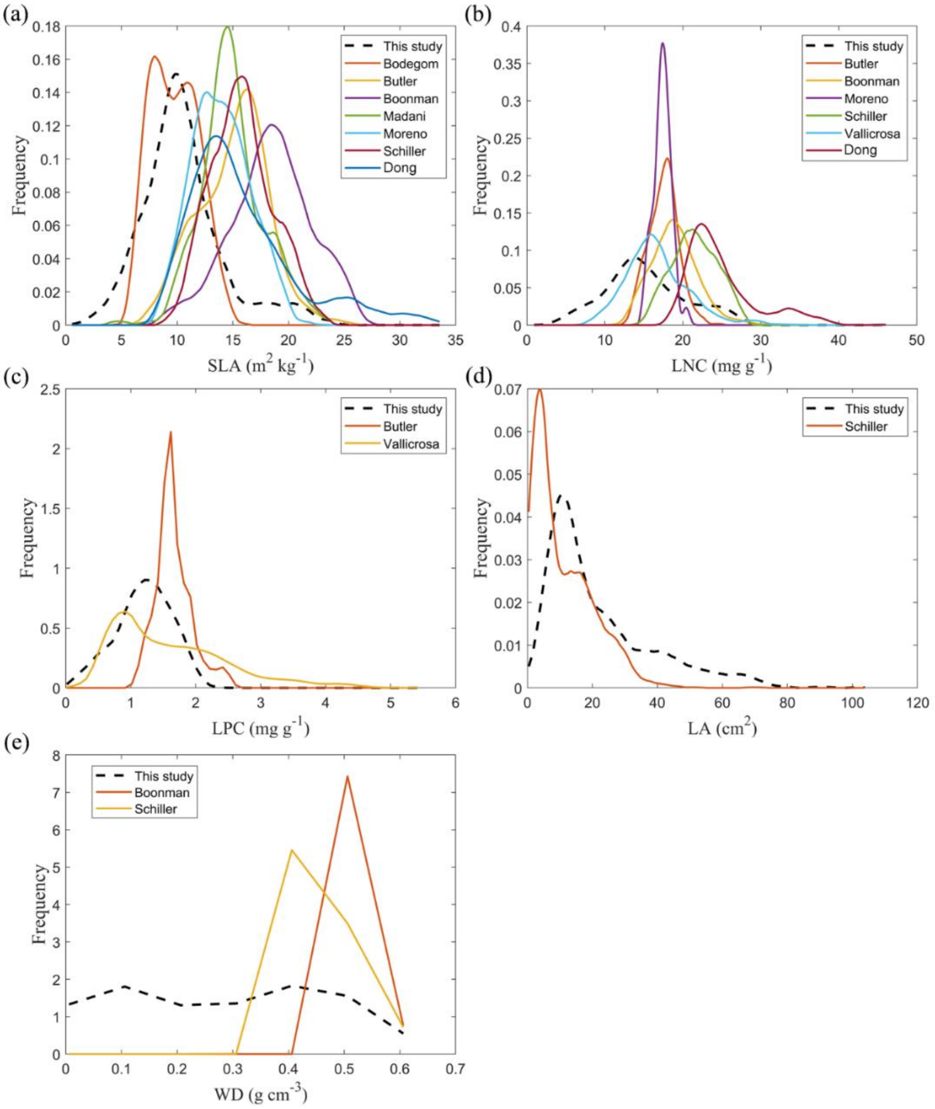

Figure 7. Frequency distributions of plant functional traits in our study ("This study", dashed black lines) and other trait maps, identified by the first author of the corresponding publication (see Table F1 for citations). SLA, specific leaf area (m^2 kg^{-1}); LNC, leaf N concentration (mg g^{-1}); LPC, leaf P concentration (mg g^{-1}); LA, leaf area (cm^2); WD, wood density (g cm^{-3}).

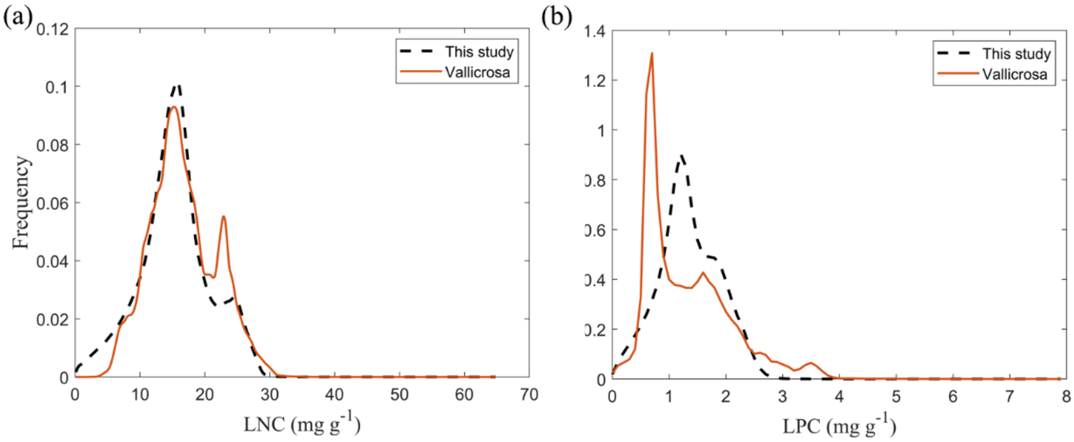

Figure F1. Frequency distributions of plant functional traits in our study ("This study", dashed black lines) and Vallicrosa et al. (2022) at 1 km spatial resolution. LNC, leaf N concentration (mg g^{-1}); LPC, leaf P concentration (mg g^{-1}).

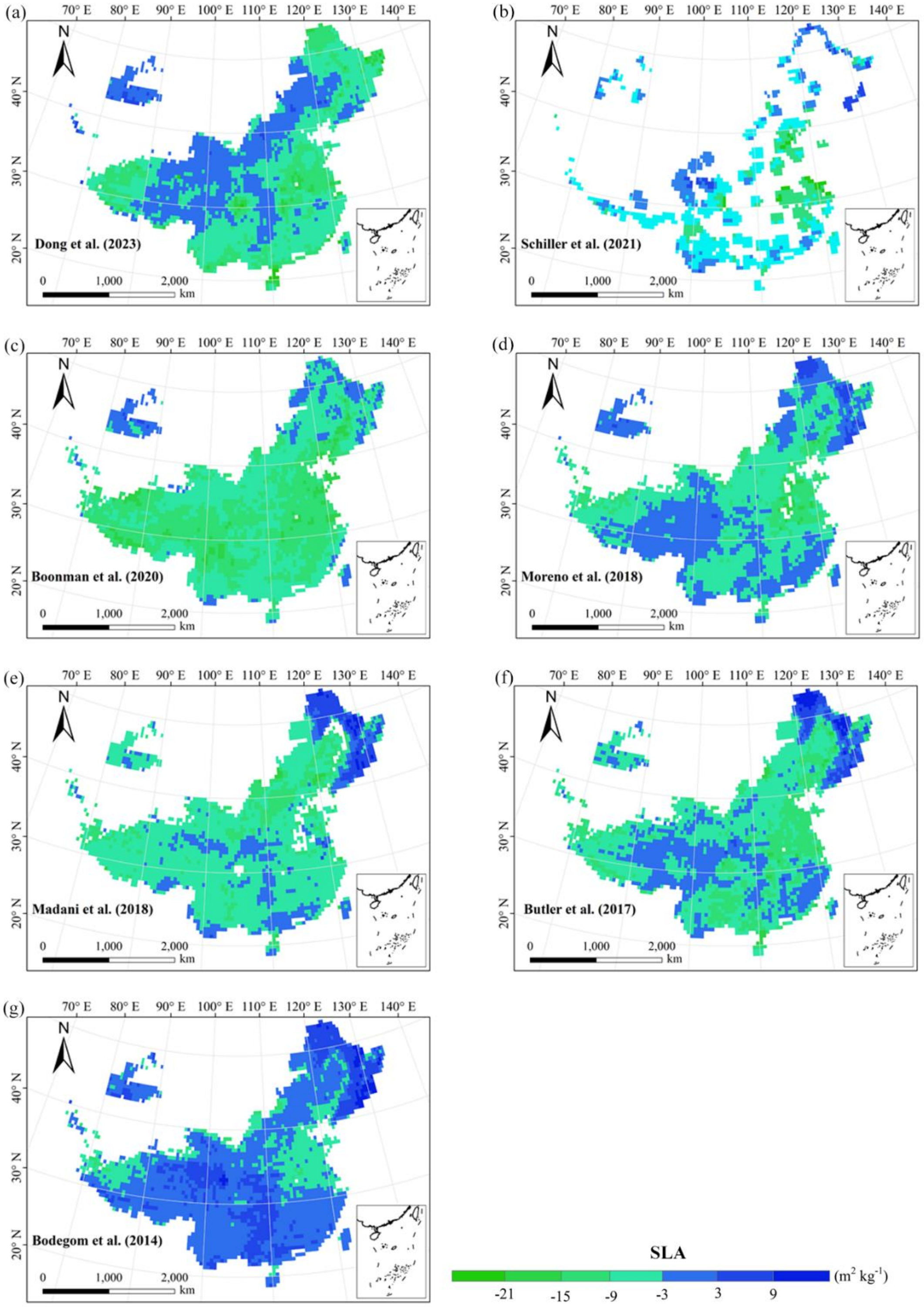

Figure F2. Spatial differences in SLA (specific leaf area, m^2 kg^{-1}) between our study and trait maps from previous studies (see Table F1 for citations).

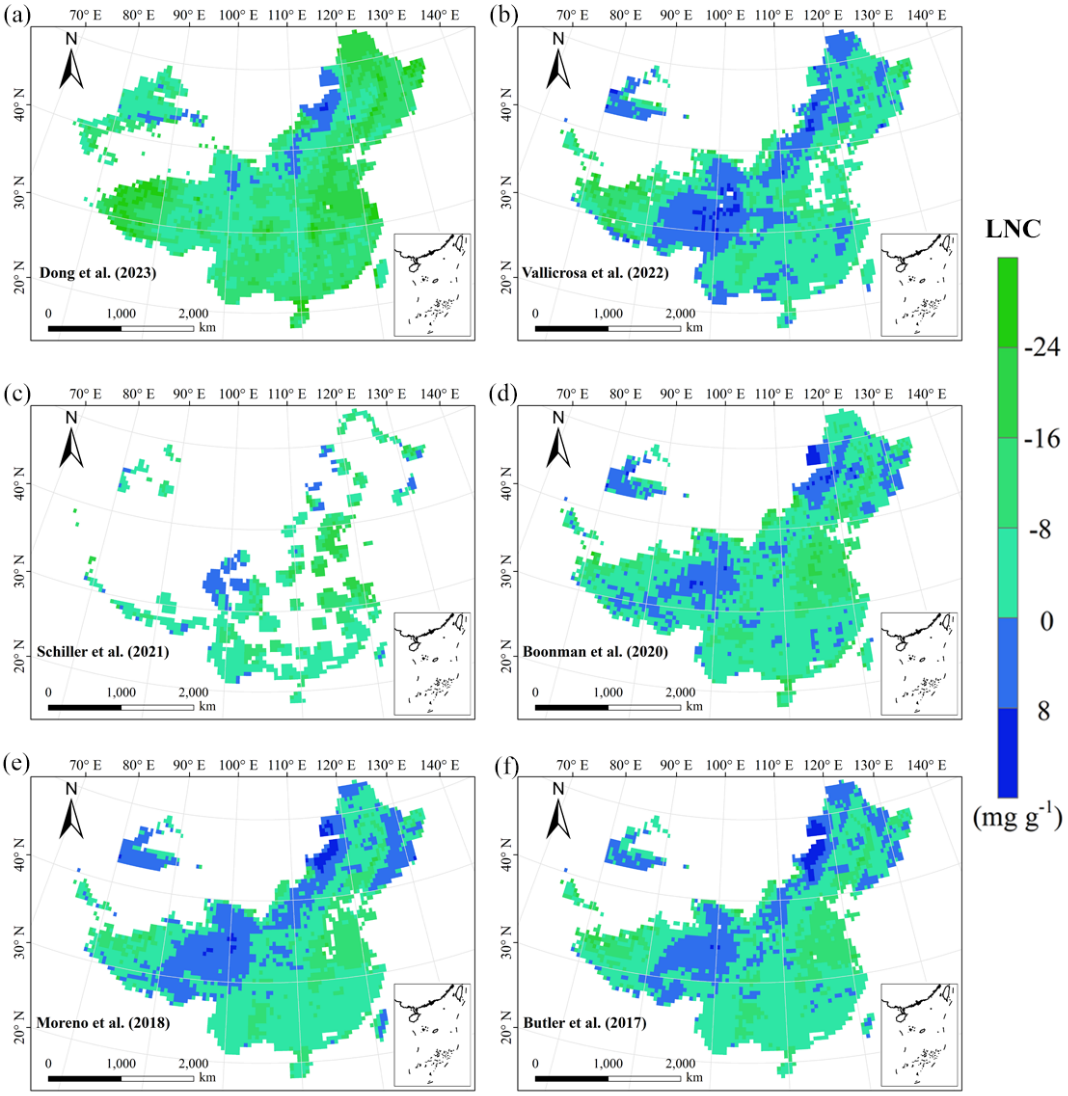

Figure F3. Spatial differences in LNC (leaf N concentration, mg g^{-1}) between our study and trait maps from previous studies (see Table F1 for citations).

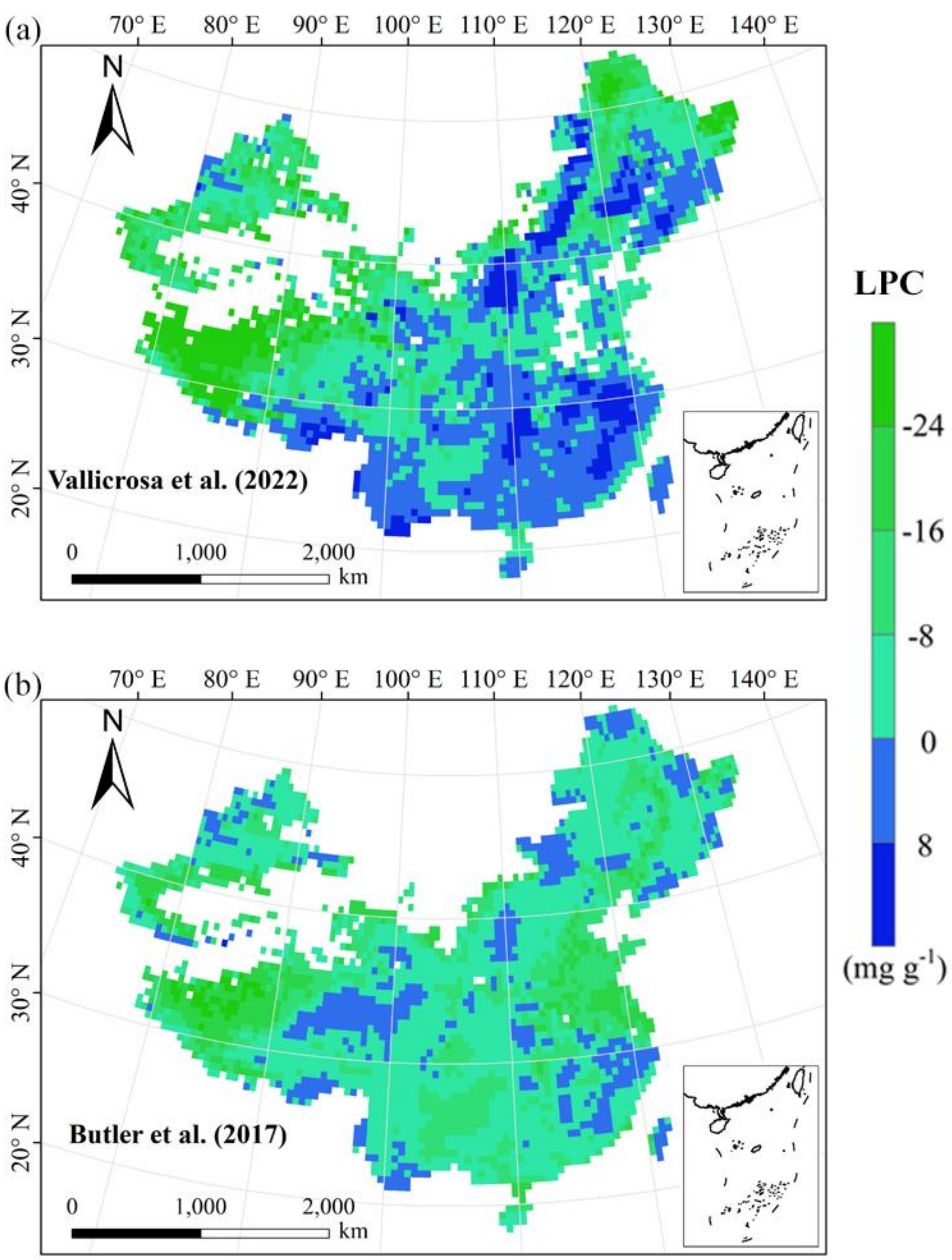

Figure F4. Spatial differences in LPC (leaf P concentration, mg g^{-1}) between our study and trait maps from previous studies (see Table F1 for citations).

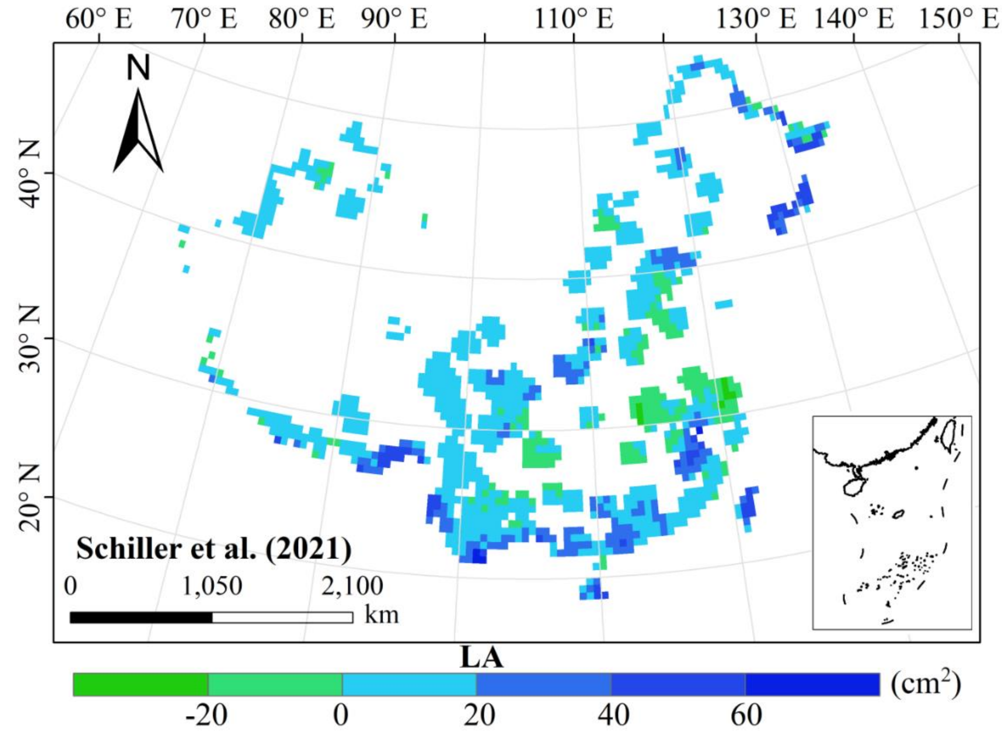

Figure F5. Spatial differences in LA (leaf area, cm^2) between our study and trait maps from previous studies (see Table F1 for citations).

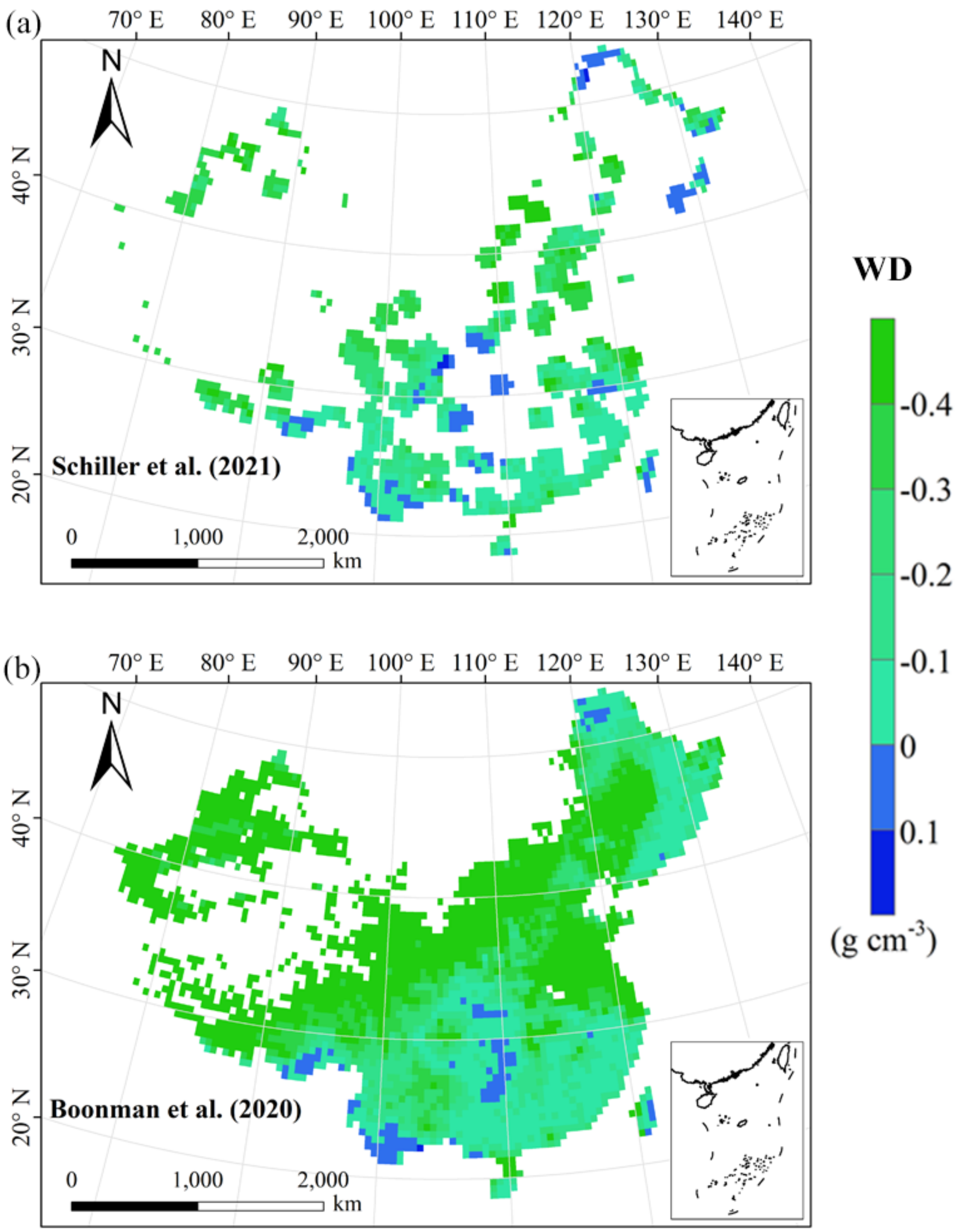

Figure F6. Spatial differences in WD (wood density, g cm^{-3}) between our study and trait maps from previous studies (see Table F1 for citations).

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