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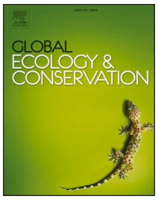

Latitudinal gradients of angiosperm plant diversity and phylogenetic structure in China's nature reserves

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ABSTRACT

The mechanisms underlying latitudinal and longitudinal patterns in species diversity remain a central issue in ecology and are vital for effective biodiversity conservation. Few studies have been conducted to synthesize the latitudinal patterns and the underlying mechanisms of multi-dimensional biodiversity in Chinese Nature Reserves, and we will provide comprehensive patterns of species and phylogenetic diversity for plant species along the latitudinal patterns. In this study, we selected 10,458 angiosperm species from 157 China's nature reserves along the latitudinal gradients to explore the geographical distribution patterns of species richness (SR), phylogenetic diversity (PD), phylogenetic endemism (PE), net relatedness index (NRI) and phylogenetic structure. The results indicated that the angiosperm's SR, PD, PE and NRI increased along the latitudinal gradients in China. Species diversity was significantly correlated with phylogenetic diversity and phylogenetic endemism. Our findings suggested that the species in the higher latitude regions were significantly phylogenetically clustered, whereas the species in the lower latitude regions indicated phylogenetic overdispersion. Temperature strongly correlated with species diversity, phylogenetic diversity, phylogenetic endemism, and phylogenetic structure for all plants. Our results showed that the determinants of diversity patterns and phylogenetic structure were different among herbs and woody plants. For herbs, the reserve area had the highest explanatory power for phylogenetic endemism. For woody plants, temperatures determine their diversity patterns and phylogenetic structure. This study improves our understanding of the latitudinal and longitudinal gradients of species diversity, and phylogenetic structure and provides support for the improvement of biodiversity conservation in China.

1. Introduction

Geographic patterns and the determinants of plant diversity at the species level are largely central to ecology, and they are remain one of the major challenges for effective biodiversity conservation (Kier et al., 2005). There are approximately 35,000 vascular plants

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and 10 % of world's flowering plants in China, making it as one of the most diverse countries in the northern hemisphere (Leighton, 2005; Wandesforde-Smith et al., 2014). Biological diversity is the foundation for human well-being, while currently climate change and the explosion of socio-economic development, making biodiversity losses a formidable challenge for China (Zheng and Cao, 2015). The loss of biodiversity profoundly affects the function of ecosystems and their services to humans (Weiser et al., 2017). Consequently, understanding the latitudinal gradient in plant species' multi-dimensional diversity in China's nature reserves can provide important insights into how to effectively conserve the biodiversity (Cardinale et al., 2012).

Currently, most researchers consider species richness (SR) along latitudinal gradients and biodiversity conservation (Willig and Presley, 2013). The species richness, however, does not capture the conservation value of individual species based on rarity or their unique evolutionary history (Brooks et al., 2006). The phylogenetic diversity (PD) method quantifies the combined phenotypic or genetic diversity across species and enhances our understanding of how the evolutionary history affects biodiversity conservation (Aguilar-Tomasini et al., 2021; Tucker et al., 2017). Phylogenetic information has been used in ecology that a region with high phylogenetic diversity has a higher chance of containing species with greater evolutionary potential (Winter et al., 2013). Thus, there should be more focus on preserving biodiversity in the high phylogenetic diversity regions. But the latitudinal patterns and determinants of PD of angiosperm plants are still not available on larger scale, which limit the identification of prioritized regions for the conservation of plant biodiversity. In addition, phylogenetic endemism (PE) combines the phylogenies and geographical distribution feathers of species and has been proposed as a new biodiversity index (Guerin and Lowe, 2015; Rosauer et al., 2009). The above biodiversity maintenance has drawn strong attention from ecologists and comparing the patterns of species and phylogenetic diversity has becoming one of the central topics in ecological research (Qian et al., 2013; Wang et al., 2011).

There are large-scale studies on the biodiversity patterns along elevational or latitudinal gradients (Kevin, 2000; Tang et al., 2012; Willig et al., 2003), but less attention has been given to understand angiosperm's phylogenetic structure along latitudinal gradients. The phylogenetic structure indicates the relatedness of co-occurring species in one community or region with different evolutionary and biogeographic histories (Qian, 2019). Specifically, in terms of phylogenetic clustering, environmental filtering dominates in the community, and species with similar ecological requirements may occupy more similar niches (Wiens and Graham, 2005). Phylogenetic overdispersion indicates that competitive exclusion dominates, and phylogenetically related species compete for limiting resources (Webb et al., 2002). Phylogenetic niche conservatism (PNC) is the tendency of lineages to retain their niche related traits through speciation events and over macro-evolutionary time (Cooper et al., 2010). The phylogenetic niche conservatism hypothesis suggests that species that are related to one another tend to live for longer time in tropical regions (Hawkins et al., 2014), and closely related species are more ecologically similar that would be expected due to their phylogenetic relationships (Losos, 2008). Dispersal limitation and habitat specialization through niche evolution may affect phylogenetic structure and its relation with the major gradients (Crisp and Cook, 2012).

Latitudinal species diversity gradients have received much more attention from ecologists, but there is little consensus on the mechanism underlying causes. The mechanism underlying the patterns of species diversity is one of the major challenges of biogeographical research (Kreft and Jetz, 2007). Many hypotheses have been proposed to explain the latitudinal gradients in species diversity in terms of water-energy dynamics hypothesis (Porter, 2003), and historical/evolutionary hypotheses (Ricklefs, 2005). Ample evidence have confirmed that climate-diversity relationship is critical for understanding the mechanisms of species diversity patterns, and contemporary climates, including temperature and precipitation, have considerable explanatory power for latitudinal patterns of species diversity (Gheyret et al., 2020; Harrison et al., 2020; McFadden et al., 2019). For instance, species diversity patterns of liana along a latitudinal gradient in the southern temperate rainforest had strong associations with the temperature (Lobos-Catalán and Jiménez-Castillo, 2019). Similarly, temperature is also an important driver of the composition and change of plant communities in

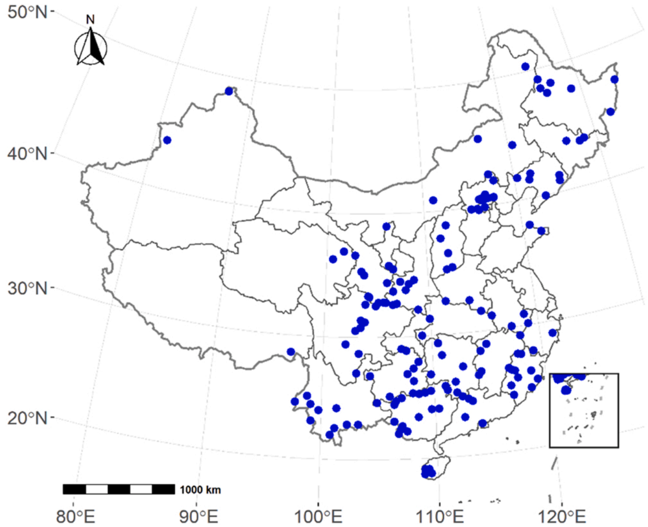

Fig. 1. The 157 China's nature reserves in this study. The blue circles represent the center point coordinates of each nature reserves.

North America (McFadden et al., 2019). Compared with the elevational patterns in species diversity, the effects of these factors in phylogenetic diversity and phylogenetic endemism have been much less studied along the latitudinal gradients.

Previous researches paid more attention on terrestrial vertebrates in China's nature reserves (Zhao et al., 2006), the species diversity of woody plants along latitudinal gradients (Cai et al., 2020) or woody angiosperm assemblages along the elevational gradients (Yue and Li, 2021). Few studies have been conducted to synthesize the latitudinal patterns and the underlying mechanisms of multi-dimensional biodiversity in Chinese Nature Reserves. In this study, 10,458 angiosperm species from 157 China's nature reserves along the latitude gradients were selected to explore the geographical patterns of SR, PD, PE, and phylogenetic structure. This study filled a knowledge gap of the angiosperm's SR, PD, PE and NRI increased along the latitudinal gradients in China. The main aims of this study are: (1) to characterize the patterns of plant species and phylogenetic diversity along latitudinal gradient; (2) to explore the patterns of phylogenetic structure of angiosperm along latitudinal gradient; (3) and to explore the underlying drivers of these patterns.

2. Material and methods

2.1. Data sources of plant species

The 157 China's nature reserves in this study covered a total area of 220490 km^2, with a latitudinal range of 18.71–50.39° N and a longitudinal range of 81.39–134.15° E (Fig. 1, Table S1). The study area covers different vegetation types from temperate to tropical, including coniferous forest, deciduous broad-leaved forest, evergreen broad-leaved forest and tropical rainforest. The 157 protected areas we selected cover different latitudes and longitudes in China, and the survey of plant resources is relatively complete. Angiosperm plants' distribution data were obtained from the published and unpublished scientific surveys on the nature reserves that were carried out to obtain complete species lists. We also obtained the data from China Nature Reserve Specimen data platform (http://www.papc.cn/). These data including the angiosperm plants list for the China's nature reserves. In order to reduce the inadequate sampling effort on the species richness, the largest value of species richness for each reserve were used in this study. We excluded the introduced and cultivated species from the database to minimize the effects of the possible errors. The introduced and cultivated species were refer to a list of cultivated plants in China (Lin, 2018). The species names were standardized using Taxonomic Name Resolution Service (tnrs.iplantcollaborative.org/TNRSapp.html) and Asian Plant Synonym Lookup (phylodiversity.net/fslik/synonym_lookup.htm). In total, there were 10,458 angiosperm species from 1904 genera and 227 families encountered in this study. Reserve area also was obtained from the above sources.

We also compiled information on growth forms of the all studied species that references to the Flora of China (http://www.efloras.org/) and the Database of China's Woody Plants (http://www.ecology.pku.edu.cn/plants/woody/index.asp) (Wang et al., 2009, 2011). Woody plant species included trees, shrubs and woody lianas, and herbaceous species included herbs, herbaceous lianas and subshrubs. We obtained 3689 woody plant species and 6769 herbaceous plant species.

2.2. Data sources of climate variables

To test how the species and phylogenetic diversity change with climate changes, we used the climate variables that were assigned to each reserve based on its location. The climate data were extracted from the *WorldClim* database (WorldClim 2.0, http://www.worldclim.org) at the spatial resolution of 30-arc-second (c. 1 km^2). We selected the climate factors according to eliminate the collinearity between climatic variables, the correlation coefficient of each variable pair was screened. Finally, six major bioclimatic variables with correlation coefficients < 0.75 were finally selected. The extracted climate data included temperature and precipitation, such as annual mean temperature (AMT), Temperature Seasonality (TS); Mean Temperature of Coldest Quarter (MTCQ); Annual precipitation (AP), Precipitation Seasonality (PS); Precipitation of Warmest Quarter (PWQ). ArcGis 10.2 software is used to extract the climate information above for each site.

2.3. Constructing phylogenetic diversity

A phylogenetic tree was constructed using the R package 'V.PhyloMaker2', 'picante' and 'ape', and the phylo.maker function under scenarios 1 was used in this study (Jin and Qian, 2019, 2022). The phylogenetic tree includes all families of extant vascular plants, which is the largest dated phylogeny for vascular plants (Jin and Qian, 2022). We used three diversity indices: Species diversity (SR), phylogenetic diversity (PD) and phylogenetic endemism (PE). Species diversity is the universal index generally employed in large-scale patterns and biodiversity studies (Wang et al., 2011). In the present study, the total count of angiosperm plants within per nature reserve was defined as species diversity. Species are not all equal and more evolutionarily distinct species and the species' phylogenetic information should be more considerable. Phylogenetic diversity (Faith's PD) can comprehensively use to estimate the phylogenetic diversity of angiosperm plants within each sites (Faith and Baker, 2006). Because species diversity is general strongly positively related to phylogenetic diversity, and PD measurements should be standardize to the observed species diversity to evaluate the contribution of evolutionary history to phylogenetic diversity after species diversity was accounted for Zu et al. (2019). We calculated the standard effect size of phylogenetic diversity (PD_{SES}) by dividing the difference between the observed and expected PD by the standard deviation of the null distribution. Phylogenetic endemism (PE) is another new index combining both evolutionary and spatial features(Rosauer et al., 2009). PE measures relative changes in the distribution range of plants and range-restricted phylogenetic diversity (Xu et al., 2017). We calculated the three diversity indices for each nature reserve using "Ape", "Picante" and "phyloregion" three R packages, in R 3.3.3 (R Core Team; available at http://www.r-project.org/).

2.4. Phylogenetic structure

The phylogenetic structure of each reserve was calculated using the net relatedness index (NRI), which is based on the mean phylogenetic distance (MPD). MPD indicates the average phylogenetic relatedness between all possible pairs of species (Webb et al., 2002). We calculated NRI index as follows: $\text{NRI} = -1 \times (\text{MPD}_{\text{observed}} - \text{MPD}_{\text{randomized}})/\text{sdMPD}_{\text{randomized}}$. $\text{MPD}_{\text{randomized}}$ and $\text{sdMPD}_{\text{randomized}}$ respectively represented the mean and standard deviation of MPD estimated using 999 randomly sampled communities with given species diversity. NRI values > 0 reflect significant phylogenetic clustering, while NRI values < 0 reflect significant phylogenetic overdispersion (Webb et al., 2002). We calculated the NRI values for each nature reserve using “Ape” and “Picante” R packages, in R 3.3.3 (R Core Team; available at http://www.r-project.org/).

2.5. Data analysis

In this study, the generalized linear models (GLMs) was used to test the relationships between the three diversity indices (species diversity, phylogenetic diversity and phylogenetic endemism) and different climatic factors (temperature, precipitation, climate seasonality). We tested the significance of the regression models of the relationship between the phylogenetic metrics and explanatory variables by modified t-test to account for the effect of spatial autocorrelation on model significance. In addition, we separately assessed the influence of climate factors on the species diversity patterns of the two growth forms (woody versus herbaceous plants). The proportion of deviance (R^2) in species diversity, phylogenetic diversity and phylogenetic endemism explained by each climate factor was estimated. We then compared the R^2 of different climatic variables on diversity patterns for the two growth forms, respectively. Further, we conducted hierarchical partitioning using the R package “hier.par” in order to compare the independent effects of different factors (Heikkinen, 2004).

3. Results

3.1. Distribution patterns in plant diversity and phylogenetic diversity

Species richness ranged from 720 to 3117 species per nature reserve, and the Jinfo nature reserve had the most species diversity. Phylogenetic diversity ranged from 21,722.94 to 65,445.97 and phylogenetic endemism from 223.56 to 4823.01 per nature reserve across China. Species diversity was strongly positively correlated with phylogenetic diversity and phylogenetic endemism, respectively (Fig. S1). For all plants, species diversity, phylogenetic diversity and phylogenetic endemism had similar latitude and longitude patterns (Fig. 2b, Fig. 3): both showed negatively correlated with latitude. PD_{SES} showed a significantly negative correlation with latitude, while non-significantly negative correlation with longitude (Fig. 2b). The patterns of woody plants and herbs showed similar trends, while the woody plants have more explanatory power than herbs (Table 1).

3.2. Latitudinal patterns of phylogenetic structure

Similar to the latitudinal gradient in species diversity, NRI showed an increasing pattern along the latitudinal gradients. However, it showed no significantly correlation with the longitude. The positive NRI values in the higher latitude regions (e.g. temperate regions) indicate phylogenetic clustering, but the negative NRI values in the latitude regions (e.g. subtropical and tropical regions) indicate phylogenetic overdispersion. For herbs plants, NRI also showed an increasing pattern along the latitudinal gradient, and a decreasing pattern along the longitudinal gradient. For woody plants, NRI also showed an increasing pattern along the latitudinal gradient, but no significant correlation with the longitude (Fig. 4).

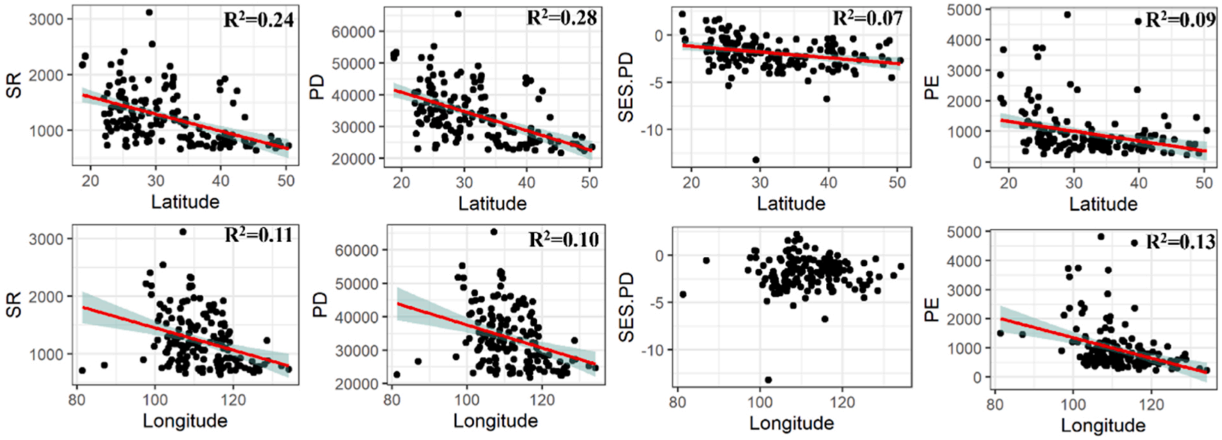

Fig. 2. The latitude and longitude patterns in Species richness (SR), phylogenetic diversity (PD), PD_{SES} and phylogenetic endemism (PE).

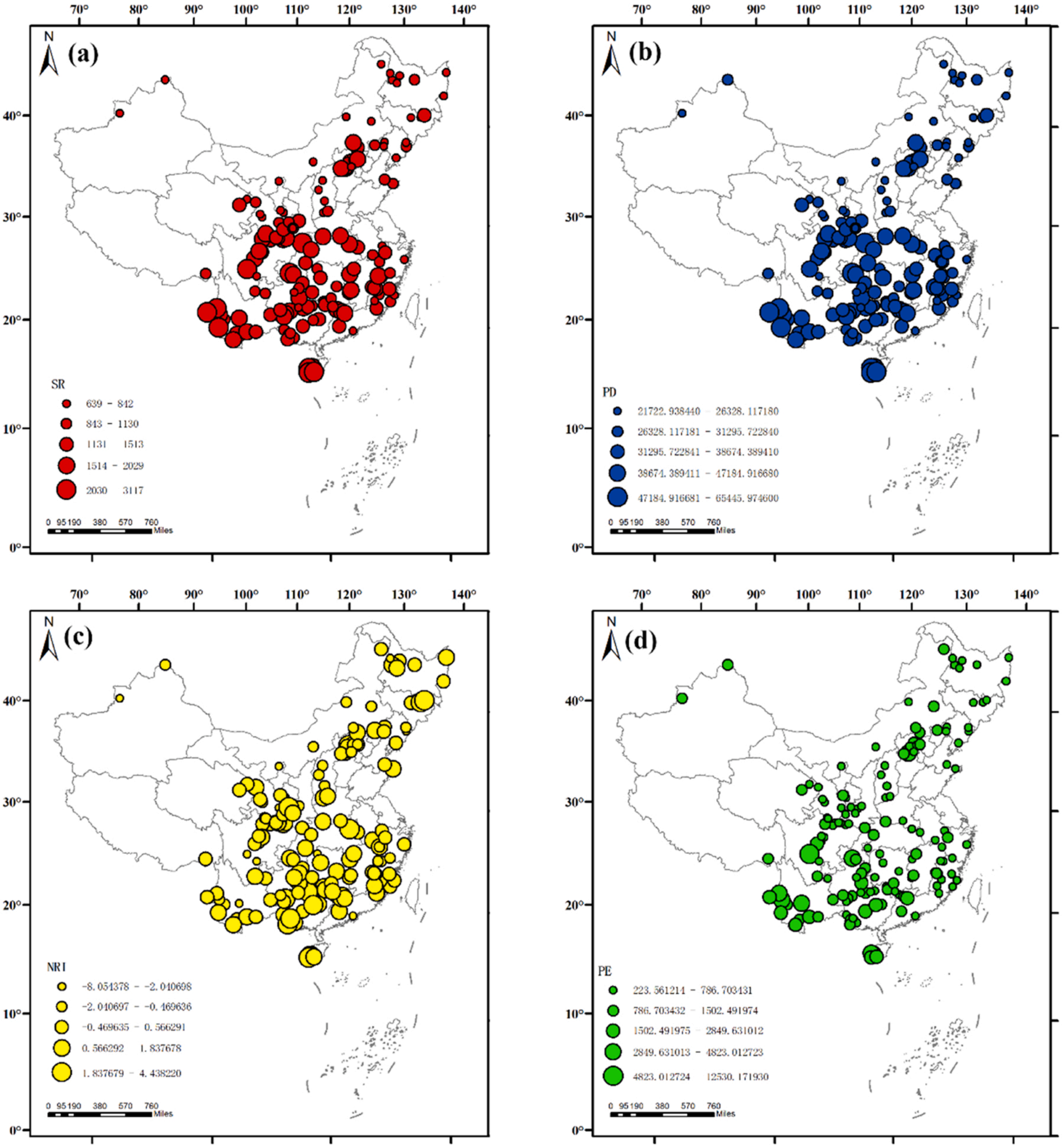

Fig. 3. The species richness (a), phylogenetic diversity (b), NRI (c) and phylogenetic endemism (d) patterns in China' reserves. The size of the circle represents the size of three diversity indices.

Table 1
Explanatory power (R^2) of Latitude and Longitude for the species patterns of herbs and woody plants evaluated by generalized linear models (GLM) (*p, 0.05; **p, 0.01; ***p, 0.001).

	Woody		Herbs	
	Latitude	Longitude	Latitude	Longitude
SR	31.1***	1.7***	19.2***	9.9***
PD	37.1***	9.7***	23.0***	9.2***
SES.PD	11.7***	0.2	3.2	2.9*
PE	21.2***	9.4***	1.8	6.7**

3.3. Determinants of species and phylogenetic diversity

Species diversity, phylogenetic diversity, PD_{SES}, and phylogenetic endemism had similar relationships with the climate factors. With the increase in AMT, MTCQ, AP, and PS, species diversity, phylogenetic diversity and phylogenetic endemism increased gradually. On the contrary, Species diversity, phylogenetic diversity, PD_{SES}, and phylogenetic endemism had significantly negative correlations with TS and PS. Both species diversity ($p < 0.1$) and phylogenetic endemism had positive correlations with reserve area, while phylogenetic diversity and PD_{SES} had no relationship with reserve area (Fig. 5). The explanatory power of climate factors for woody plants were higher than that for herbaceous plants (Table 2).

For all plants, temperature (including AMT, MTCQ and TS) had the high effect on the species diversity, phylogenetic diversity, PD_{SES}, phylogenetic endemism, and NRI. Among all the factors, TS had the highest explanatory power for species diversity, phylogenetic diversity, and phylogenetic endemism, while AMT had the highest explanatory power for PD_{SES} and NRI (Fig. 5). For herbs, TS had the highest explanatory power for species diversity and phylogenetic diversity, and MTCQ had the highest explanatory power for $PD_{SES.}$ Reserve area had the highest explanatory power for PE. AMT had the highest explanatory power for NRI (Fig. 6, Fig. S2). For woody plants, TS had the highest explanatory power for species diversity and PE, and MTCQ had the highest explanatory power for PD.

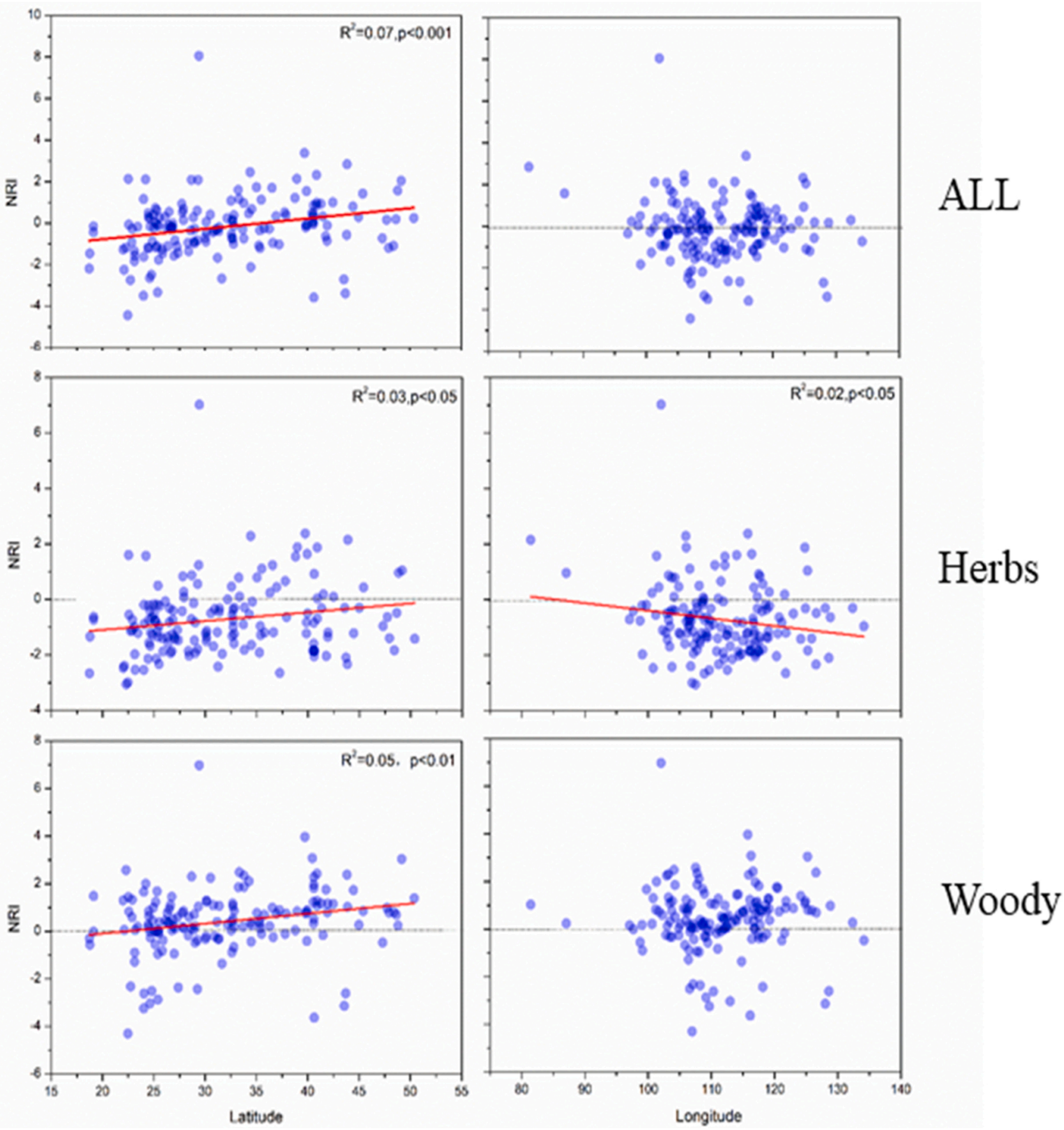

Fig. 4. The net relatedness index (NRI) of all plants, herbs and woody plants along the latitudinal and longitudinal gradient.

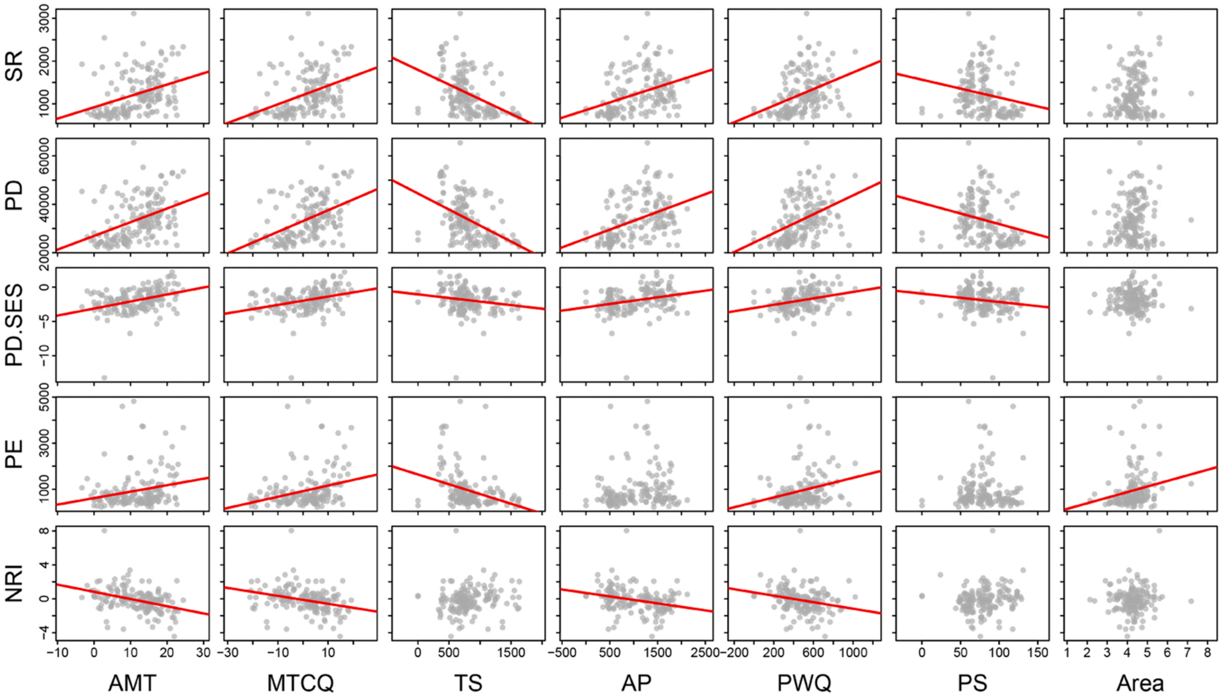

Fig. 5. Relationships between species diversity phylogenetic diversity, PD_{SES}, PE, NRI and the factors. AMT, annual mean temperature; TS: Temperature Seasonality; MTCQ, Mean Temperature of Coldest Quarter; AP, annual precipitation; PS: Precipitation Seasonality; PWQ: Precipitation of Warmest Quarter.

Table 2
Explanatory power (R^2) of the predictors for the species patterns of herbs and woody plants evaluated by generalized linear models (GLM) (*p, 0.05; **p, 0.01; ***p, 0.001).

	Woody					Herbs				
	SR	PD	SES.PD	PE	NRI	SR	PD	SES.PD	PE	NRI
AMT	18.3***	25.2***	13.9***	13.5***	8.1***	8.9***	13.2***	4.8*	0	11.4***
MTCQ	25.0***	31.8***	13.4***	18.2***	6.1***	14.1***	18.3***	1.9	0.5	7.1**
TS	24.6***	27.7***	7.4**	18.3***	1.7	16.4***	18.4***	0	3.1*	0.9
AP	19.9***	25.5***	10.6***	9.6**	6.2**	10.3***	13.6***	1.1	0	5.5**
PWQ	19.3***	21.4***	4.6**	14.3***	3.8**	9.9***	12.5***	0.9	0.4	3.5**
PS	6.7***	9.6***	7.5**	0.6	5.7**	3.0*	4.0*	0.1	0.5	0.6
Area	1.5	0.6	0.1	1.4	0.1	2.7*	2.2	0.9	5.9**	1.9

AMT had the highest explanatory power for PD_{SES} and NRI (Fig. 6; Fig. S3).

4. Discussion

4.1. Latitude patterns and determinants of plant diversity

Although more researchers focused on the species diversity along the latitudinal or elevational gradients (Cai et al., 2020; Yue and Li, 2021), Few studies had been conducted to synthesize the latitudinal patterns and the underlying mechanisms of plant diversity in different life forms across China. In this study, 10,458 angiosperm species from 157 China's nature reserves along the latitude gradients were selected to explore the geographical patterns of species diversity, phylogenetic diversity, phylogenetic endemism, and phylogenetic structure. Our results showed that angiosperm diversity decreased significantly along latitude gradients in China. Geographic patterns in the species diversity, phylogenetic diversity, and phylogenetic endemism showed striking consistency in their relationships with latitude and longitude. This result was consistent with the findings of previous studies on increasing trends of biological diversity from polar to equatorial regions (Willig et al., 2003), and the species diversity of woody plants along latitudinal gradients (Cai et al., 2020). The reason of the higher species diversity in tropical regions is that tropical environments have had a long and relatively undisturbed evolutionary history compared with temperate environments (Mittelbach et al., 2007), and the tropical community has no seasonality and the temperature remains relatively stable. On the contrary, temperate and polar regions have been

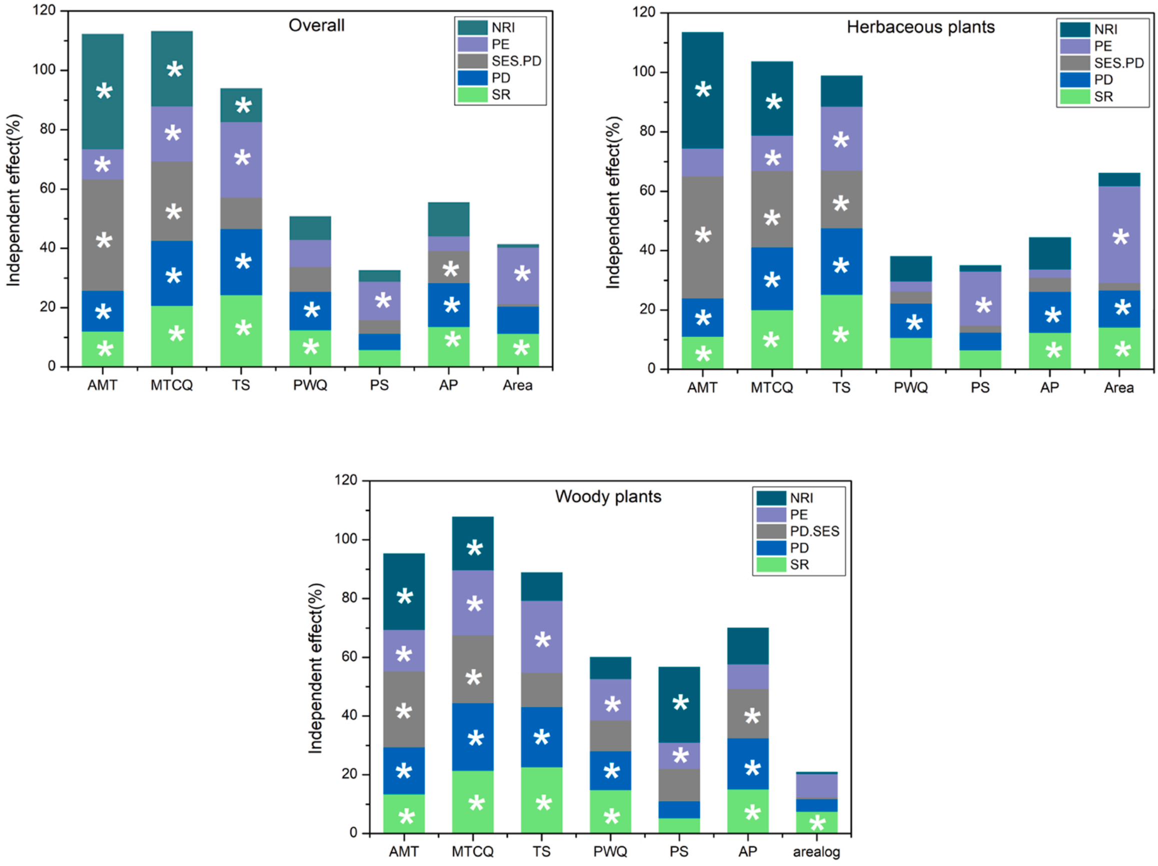

Fig. 6. Relative importance of different variables for species diversity of all plants, herbs and woody plants. The asterisks indicate significant independent effects ($P < 0.05$).

repeatedly disturbed by the advance and retreat of glaciers in the past, suffered more catastrophic climate changes, and are still in the recovery process since the Pleistocene ice age. As a result, they have relatively young and immature communities with low diversity (Kevin, 2000).

In addition, the mean abundance-weighted net relatedness index (NRI) increased with latitude but decreased with the mean temperature, the temperature of the coldest month, and precipitation in our study. These results indicated that environmental filtering at high latitudes is more common, and competition shapes communities at low latitudes. Our results are consistent with the previous studies that NRI increased with latitude for the forest trees, which suggested that species tend to be more phylogenetically related to each other in temperate environments than those in tropical environments (Gheyret et al., 2020). It is generally assumed that the cold and dry conditions increase along the latitudinal gradient (Wiens and Graham, 2005). Closely related plant species have similar traits to survive in the harsh climate prevailing at high latitudes, so that the species tend to be phylogenetic clustering in these regions (Qian et al., 2013; Zu et al., 2019).

In this study, species diversity was correlated with phylogenetic diversity and phylogenetic endemism, and this result suggested that nature reserves with high species diversity, their phylogenetic diversity and phylogenetic endemism are also higher. This is consistent with the previous studies in which strong correlations between the geographical patterns in SR, PD, and PE (Fritz and Rahbek, 2012; Mishler et al., 2014). The recent study of national park planning in China also suggested that the high consistency among hotspots of the different diversity measures for flowering plants in China (Lu et al., 2022). The result that both species and phylogenetic diversity correlated well with climate factors along the latitudinal gradients is consistent with previous findings on terrestrial vertebrates in China's nature reserves (Zhao et al., 2006), woody plant species in China (Wang et al., 2011) and liana diversity in South America (Lobos-Catalán and Jiménez-Castillo, 2019). In particular, both temperature and precipitation play an important role in determining diverse latitudinal patterns. Similar with the present research that the standardized effect size of mean phylogenetic distance was positively correlated with temperature and precipitation for both natives and aliens (Qian et al., 2022b). In contrast to previous studies, our analyses indicate that temperature seasonality accounted for much more variation in species diversity. This suggests that temperature is the predominant environmental factor than precipitation in China. Similar results have been observed in alpine grasslands that average temperature and temperature seasonality are major climatic predictors of plant community composition and change in the America's (McFadden et al., 2019).

We did find that the reserve area has a power explanation for the species richness and phylogenetic diversity, while reserve area also has an effect on the phylogenetic endemism. This finding indicates that the climatic variation across China is likely sufficient to mask the reserve area effect for species richness and phylogenetic diversity. Furthermore, the phylogenetic endemism has area effect for plants. Therefore, in future conservation planning, the impact of reserve area on plants should be fully considered when the phylogenetic endemism of species is protected.

4.2. Conservation planning for the species diversity

Our results also provide strong evidence that the species diversity patterns of woody plants are more influenced by the climate factors than those of herbaceous plants. For instance, AMT, MTCQ, TS, AP, and PWQ all has a higher rate of explanation for woody plants than herbs. The reason might be that herbaceous plants can better survive in the cold temperature, and woody plants are more sensitive to winter temperature (Qian et al., 2022a; Wang et al., 2011). Another reason is the evolutionary differences between herbaceous and woody species, and previous research have indicated that eastern China represents a floristic museum and western China an evolutionary cradle for herbaceous plants, while eastern China has served as both a museum and a cradle for woody plants (Lu et al., 2018).

In addition, we found that the reserve area was a significant predictor for herbs, while it had no effect on the species diversity, phylogenetic diversity, and phylogenetic endemism for the woody plants. This result suggested that reserve area may affect endemic herbaceous plants. Therefore, we need to expand the protected regions when we want to protect the regions with high phylogenetic endemism for herbs. For instance, Hainan Datian reserve with 1490 herbs plants, but its area is only 1314 hm^2. We should pay more attention to these regions when considering biodiversity conservation for the regions with more endemism species. Because the distributional regions of endemism are irreplaceable, and the regions with high phylogenetic endemism are likely to have a high degree of phylogenetic diversity (Rosauer et al., 2009). Therefore, we highlight the conservation priority should be given for the reserves with high phylogenetic endemism and phylogenetic diversity. In this study, the reserves with high phylogenetic endemism and phylogenetic diversity are mainly distributed in the Southwest mountain regions of China. For instance, Gongga Mountain has the high phylogenetic diversity of 47,184.9 and the highest phylogenetic endemism of 12,530.1, and Jinfo Mountain has the highest phylogenetic diversity of 65,445.9 and the high phylogenetic endemism 4823.1. So the future conservation plans should focus on the plant diversity of southwest mountain regions.

5. Conclusions

In this study, we used angiosperm species data from 157 nature reserves in China, together with climate variables and the reserve area information, to evaluate the patterns and the determinants of the angiosperm plant diversity. The result suggested that species in the higher latitude regions were significantly phylogenetically clustered, whereas the species in the lower latitude regions were phylogenetic overdispersion. Temperature has a high explanation on the latitude gradients of species diversity, phylogenetic diversity, phylogenetic endemism, and phylogenetic structure for all plants. However, the determinants of diversity patterns and phylogenetic structure were different among herbs and woody plants. The reserve area had the highest explanatory power for phylogenetic endemism of herbs. Temperature determines their diversity patterns and phylogenetic structure for woody plants. This study improves our understanding of the latitudinal gradients of species diversity and phylogenetic structure, and provides support for the improvement of biodiversity conservation in China. This study also fills a knowledge gap of the angiosperm's SR, PD, PE and NRI increased along the latitudinal gradients in China.

CRediT authorship contribution statement

Kuiling Zu collected the data, conceived the idea and wrote the manuscript. **Cancan Zhang**, **Fusheng Chen**, **Zhiyong Zhang**, **Shahid Ahmad**, and **Ghulam Nabi** provided ideas and suggestions. All authors contributed to the writing.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Data Availability

Data will be made available on request.

Acknowledgments

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Data accessibility

The data that supports the findings of this study are available in this article and the Supplementary material of this article.

Appendix A. Supporting information

Supplementary data associated with this article can be found in the online version at doi:10.1016/j.gecco.2023.e02403.

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