



Article Community Assembly of Forest Vegetation along Compound Habitat Gradients across Different Climatic Regions in China

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Abstract: Community assembly research has mostly focused on areas with single vegetation types; however, the abiotic and biotic factors affecting community assembly act across regions. Integrating biotic and abiotic factors into "compound" habitats has gained attention as an emerging strategy to analyze spatial and temporal patterns of biodiversity. We used a compound habitat approach to explore the relative roles of habitat filtering, biotic competition, and stochastic processes in the forest community assembly of four climatic zones (tropical, subtropical, temperate, and cold temperate forests). Specifically, we combined biotic and abiotic factors in four compound ecological gradients by principal component analysis (PCA), which we used to assess the geographic and phylogenetic distribution of multiple woody plant functional traits. We found that forest functional and phylogenetic diversity shifted from clustered to overdispersed along the first compound habitat gradient (PC1) across climate zones. This finding indicates that competitive exclusion strongly affected the community assembly in tropical and subtropical forests, while habitat filtering played a key role in cold temperate forests; these mechanisms may both exist and interact in temperate forests. We also found that both habitat filtering and biotic competition affected forest community assembly across climatic regions in China. Our results elucidate the underlying mechanisms driving geographical differentiation of forest vegetation across climatic zones, and bolster empirical evidence for the conservation of forest biodiversity in China. Further research is also needed to explore whether the patterns found in this paper are prevalent in different locations in different climatic zones in China.

Keywords: phylogenetic signal; community assembly; habitat filtering; intra- and interspecific interactions

1. Introduction

A major focus of ecology is to understand community assembly and maintenance across geographic scales [1]. Two main theories have been used to explain community assembly: the deterministic processes of niche theory and the stochastic processes of neutral theory [2,3]. Niche theory holds that each species has unique space and resource demands in an ecosystem; therefore, niche differentiation and resource allocation allow stable species coexistence in a community, with habitat filtering and interspecific competition shaping community composition [3–5]. The neutral theory posits that all species in a community have equal ecological opportunities, and emphasizes the importance of stochastic processes such as colonization opportunities, genetic variation, random extinction, and ecological drift [2]. Both theories are needed to describe community assembly, as niche and neutral processes are not mutually exclusive, and similar communities may arise under various combinations of underlying mechanisms [2]. Some studies suggest that competition and



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Copyright: © 2022 by the authors. Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (https:// creativecommons.org/licenses/by/ 4.0/). diffusion affect community assembly simultaneously [6–8], and that forest community assembly at a regional scale is a continuous dynamic process from niche- to neutral-driven. Therefore, the integration of niche and neutral theories, and their compound implications for community assembly, may continue to drive ecological research [9–11].

Combining ecological and evolutionary information has facilitated the understanding of biodiversity patterns and species assembly processes [6–9,11]. Specifically, the incorporation of a phylogenetic signal—a measurement of the tendency for closely related species to resemble each other more than they resemble species drawn at random—in functional traits and ecological factors has become a popular approach [12]. The phylogenetic signal (or lack thereof) in functional traits can be used to assess the degree to which traits are evolutionarily conserved or driven by habitat factors [13,14]. However, ecological and phylogenetic similarities often are not correlated, and therefore, phylogenetic signals alone should not be used to conclude ecological phenomena, such as niche conservatism [12]. Null-model-based approaches using functional and/or phylogenetic diversity have been used to quantify the relative importance of community assembly processes, including neutral effects, habitat filtering, and biotic competition [7,8,15,16]. Recent studies have linked patterns of phylogenetic clustering (i.e., co-occurring species more closely related than expected) to habitat filtering and phylogenetic divergence (i.e., sympatric species less closely related than expected) to competitive exclusion [7,14,17]. Mori et al. [18] compared the observed patterns of functional diversity of soil faunal communities with patterns expected from a given regional species pool, and found that species in harsh environments (e.g., little rain and high altitude) showed trait convergence due to habitat filtering, while the strong interaction between species resulted in different functional traits and different strategies to obtain resources and growth space in superior habitats. Both habitat filtering and intra- and interspecific interactions can result in convergent or divergent community functional and phylogenetic diversity structures [19–24].

Functional and phylogenetic diversity in forest communities with different environmental factors and disturbance levels can jointly explain community assembly mechanisms [7]. Ryo et al. [25] found a shift from phylogenetic overdispersion to clustering with the increase in slope and decrease in soil depth in a forest community; they interpreted this as evidence for non-random community assembly [7,23]. Plant diversity along environmental gradients is determined by both abiotic factors and biotic interactions, such as competition, at the local scale [26]. Swenson [7] demonstrated the importance of biotic interactions on phylogenetic or functional aggregation [16,27,28]. Community assembly research has mostly focused on coexistence and community assembly mechanisms along habitat gradients in forests of different climatic zones [29–32]. However, studies across climatic zones or at regional scales generally focus on latitudinal gradients associated with changes in climate, soil, and anthropogenic disturbances [33].

In this study, we bridge this gap in scales of community ecology to understand how abiotic and biotic factors influence community assembly at regional scales. We combined forest survey and plant functional trait data from different climatic regions in China to quantify functional and phylogenetic diversity across broad geographic and habitat gradients, and to assess the relative importance of niche and neutral processes in community assembly. We focused on the following questions: (1) Is there a phylogenetic signal in the functional traits of forest vegetation in China? (2) What is the geographical pattern of functional and phylogenetic diversity of forest vegetation in China? (3) What roles do habitat filtering and species interactions play in forest community assembly across climatic regions in China?

2. Materials and Methods

2.1. Study Site

We investigated seven forest communities of four typical forest types in different climatic regions of China (Table 1), including three tropical rainforests (Jianfengling, Bawangling, Xishuangbanna), two subtropical evergreen deciduous broad-leaved mixed forests

(Mulinzi, Xingdoushan), one warm temperate mixed coniferous and broad-leaved forest (Xiaolongshan), and one temperate coniferous forest (Kanasi) (Table 1). All sites were well-preserved old-growth forests that had not been disturbed by human activity for at least 100 years.

Table 1. Geographic, sampling, biodiversity, climate, and tree size information of forest plots across four climatic zones in China.

Sites		Jianfengling (JFL)	Bawangling (BWL)	Xishuangbanna (XSBN)	Mulinzi (MLZ)	Xingdoushan (XDS)	Xiaolongshan (XLS)	Kanasi (KNS)	
Clin	Climatic zone		Tropical			opical	Temperate	Cold temperate	
Num	Number of plots		50	40	44	25	50	50	
numb	er of species	247	236	208	130	94	111	7	
E	levation	726–937	865-1023	715-864	1368-1652	1521-1627	1853-1867	1624-1810	
L	Latitude		19.02-19.16	21.58-21.63	29.89-30.10	30.00-30.07	34.29-34.43	48.69-48.70	
Lo	ongitude	108.84-108.92	109.07-109.17	101.56-101.60	109.22-110.12	100.21-110.20	106.08-106.10	86.94-86.95	
pН	Soil pH	4.81 ± 0.29	4.37 ± 0.35	4.91 ± 0.56	4.41 ± 0.25	4.49 ± 0.31	5.70 ± 0.53	5.54 ± 0.20	
SOM	Soil organic matter (g/kg)	15.62 ± 5.62	6.39 ± 1.83	3.19 ± 0.76	8.40 ± 2.05	9.21 ± 2.20	9.69 ± 2.92	3.38 ± 1.03	
TN	Soil total N content (g/kg)	1.32 ± 0.43	2.11 ± 0.81	1.34 ± 0.44	5.90 ± 1.72	6.54 ± 1.51	3.58 ± 1.17	1.06 ± 0.34	
TP	Soil total P content (g/kg)	0.14 ± 0.08	0.33 ± 0.19	0.31 ± 0.07	0.50 ± 0.16	0.68 ± 0.33	0.38 ± 0.11	0.64 ± 0.13	
AN	Soil available K (mg/kg)	183.22 ± 54.10	193.00 ± 46.70	156.69 ± 27.93	299.38 ± 73.7	355.99 ± 102.1	266.03 ± 82.37	64.29 ± 19.53	
AP	Soil available N (mg/kg)	192.14 ± 136.72	179.90 ± 123.20	84.49 ± 28.69	34.59 ± 11.99	23.25 ± 12.47	60.37 ± 27.78	37.50 ± 16.61	
AK	Soil available P (mg/kg)	125.54 ± 53.66	150.18 ± 43.78	130.60 ± 58.25	142.84 ± 34.04	134.00 ± 33.78	186.19 ± 53.12	227.84 ± 58.83	
MAT	Annual mean temperature (°C)	205.18 ± 5.42	211.52 ± 15.59	217.40 ± 3.88	96.52 ± 54.39	95.20 ± 34.91	81.18 ± 2.79	-9.90 ± 2.83	
MAP	Mean annual precipitation (mm)	$\begin{array}{c} 1633.00 \pm \\ 49.81 \end{array}$	${\begin{array}{r} 1579.08 \pm \\ 145.0 \end{array}}$	1584.43 ± 27.00	${}^{1213.91\pm}_{363.3}$	13,854.00 ± 301.50	671.60 ± 5.16	316.34 ± 4.77	
CVPS	Precipitation seasonality (coefficient of variation) (%) Diameter at	79.80 ± 0.45	80.44 ± 0.50	$\textbf{72.93} \pm \textbf{0.47}$	71.91 ± 23.45	63.44 ± 18.53	78.62 ± 0.49	56.28 ± 0.81	
DBH	breast height (DBH, cm)	6.34 ± 1.38	5.62 ± 0.84	6.98 ± 2.94	11.06 ± 3.79	10.68 ± 1.21	7.03 ± 1.91	15.39 ± 2.87	
TH	Tree height (m)	18.43 ± 4.65	25.90 ± 5.34	37.25 ± 14.14	20.00 ± 3.19	18.46 ± 3.14	15.72 ± 1.58	23.76 ± 1.8	
BA	Basal area (≥ 1 cm DBH) (m ² /ha)	34.93 ± 11.94	45.77 ± 14.90	51.75 ± 20.03	35.14 ± 10.09	28.88 ± 9.53	33.86 ± 6.60	46.84 ± 10.66	
CVDBH	Coefficient of variation of DBH (%)	125.55 ± 24.39	158.26 ± 23.22	164.40 ± 51.23	87.15 ± 28.56	54.74 ± 12.23	110.48 ± 20.22	88.43 ± 15.24	
CVH	variation of tree height (%)	59.91 ± 12.14	$\textbf{79.96} \pm \textbf{8.36}$	95.37 ± 28.94	50.65 ± 15.42	32.69 ± 9.33	62.70 ± 11.10	67.10 ± 9.03	

2.2. Vegetation Survey and Functional Trait Sampling

At each of the seven forest communities, we selected 25–50 plots, each with an area of 20 m × 20 m, for a total of 309 dynamic monitoring plots (Table 1). In each old-growth forest type, we ensured that the distance among each of the 20 m × 20 m plot was more than 100 m. Thus, each of the plots in each forest type were randomly distributed, and they had no spatial autocorrelation. In addition, we conducted an autocorrelation analysis for each plots in each of the four forest types, the results of which showed that there were no spatial autocorrelations among the plots within each forest type (the distribution of sample sites is shown in Figure A1). In an initial vegetation survey, we identified all individual woody plants with a diameter at breast height (DBH, cm) of \geq 1 cm. Species names, DBH, tree height (TH, m), and relative coordinates of individual trees in the plot were recorded. We measured six key functional traits that represent major axes of resource use and allocation strategies [34]: specific leaf area (SLA, mm²/mg), leaf dry matter content (LDMC, mm²/mg²), leaf nitrogen content (LNC, mg/g), leaf phosphorus content (LPC, mg/g), wood density (WD, g/cm³), and leaf nitrogen/phosphorus ratio (N:P, %). We

sampled at least 10 individuals of each species for functional traits; for species with more than 10 individuals, samples were taken from 10 random trees. Five healthy and intact mature sun leaves were collected from every individual, weighed fresh, and then dried in an oven at 60 °C for 72 h. SLA was calculated as the ratio of fresh leaf area to leaf dry mass, and LDMC was the leaf dry mass divided by leaf fresh mass. The collected leaves were brought back to the laboratory to measure LNC and LPC. To avoid harming trees, WD was calculated based on measurements of branches with diameters between 1 cm and 2 cm, rather than from tree cores. The bark was removed from branches before measuring the fresh volume, and branches were dried in an oven at 105 °C for 72 h to measure the dry mass. WD was calculated as the ratio of dry mass to fresh branch volume. The same methods were used to collect and measure functional traits of forest communities in all climatic regions.

2.3. Data Collection of Biotic and Abiotic Factors

We measured five tree size metrics to represent overall productivity and canopy density in each plot: average DBH (DBH), average tree height (TH), basal area (BA), coefficient of variation of DBH (CVDBH), and coefficient of variation of tree height (CVTH).

The longitude and latitude coordinates were recorded for each plot during the survey, and were used to extract the 19 WorldClim2 bioclimatic variables for each plot using climate raster layers with a resolution of 30" (https://www.worldclim.org/, founded on 24 June 2005). Removing highly correlated predictor variables can increase model performance; therefore, we calculated pairwise Pearson correlation coefficients for each pair of variables. We removed those variables with a high load (correlation greater than 0.8) for two or more factors. Finally, three climatic variables (MAP, MAT, and CVPS) were selected. These climatic factors have been shown to significantly influence plant diversity and help verify ecological hypotheses in other ecosystems [4].

In each plot, measurements were taken at the center point of the quadrat and along two diagonals 14.14 m away from the center (0–20 cm depth). Subsequently, we thoroughly mixed the samples to create one bulk sample per plot for analysis. The samples were analyzed for pH, soil organic matter (SOM), total nitrogen (TN), total phosphorus (TP), available nitrogen (AN), available phosphorus (AP), and available potassium (AK) (Table 1).

2.4. Construction of a Compound Habitat Gradient of Biotic and Abiotic Factors

Principal component analysis (PCA) was performed on the 15 climatic, soil, and biotic factors to reduce the redundancy of the variables using the "factoextra" package in the software R [35]. We took the first four principal components (PC1–PC4) as compound habitat gradients, which explained 73.1% of the variation of the 15 variables (Figure 1). The first axis (PCA1) explained 31.8% of the variation, and climate variables (MAP and MAT) and CVDBH were significantly positively correlated with PCA1, while DBH was significantly negatively correlated with PCA1. The second axis (PCA2) explained 22.0% of the variation, and the biotic variables (CVH, BA, and TH) were significantly positively correlated with PCA2, while TN and AN were significantly negatively correlated with PCA2. The overall contributions of the third (PCA3) and fourth (PCA4) axes to the explanatory variation of all variables were relatively low, and mainly related to biotic and soil variables (Figure 1).



Figure 1. Loadings of biotic and abiotic factors of all forest plots on the first four principal components. The variable abbreviations are listed in Table 1. Note: (**A**) PC1 and PC2 of the compound habitat gradient axis; (**B**) PC3 and PC4 of the compound habitat gradient axis.

2.5. Phylogenetic Signal in Functional Traits

We identified a total of 46,280 woody plants (788 species) in our survey. We used the AWK version of Phylomatic to generate a phylogenetic tree for all species. To reduce redundant information and excessive fitting, we used the first three principal components as comprehensive functional trait factors. Then the trait matrix was transformed into a distance matrix by calculating Euclidean distance. Finally, hierarchical aggregation was used to construct trait trees.

We used Blomberg's K [36] to assess the phylogenetic signal. Values of K close to 1 indicate that species' traits are distributed as expected under a model of Brownian evolution and K > 1 implies strong phylogenetic conservatism; K values near 0 imply that traits are phylogenetically independent.

2.6. Phylogenetic Diversity of Communities

The net relatedness index (NRI) describes the phylogenetic clustering or dispersion in a community by quantifying the phylogenetic distance between all species in the community. The nearest taxon index (NTI) describes the degree of relatedness between the most similar species by quantifying the mean phylogenetic distance between pairs of the closest species in the community [19]. NTI and NRI values are calculated based on null models to assess whether communities are more clustered or dispersed than expected. NTI and NRI values greater than 0 indicate that species within a community are more closely related than expected, which provides evidence of community assembly by habitat filtering; negative values indicate that species are less closely related than expected, and suggest community assembly by competitive exclusion [23].

2.7. Functional Diversity Structure of Communities

We first tested for group differences in forest vegetation across different climatic regions in China. We then used all species from the 309 plots as the species pool in null models of functional diversity of a random community to assess the assembly processes of the observed communities. Specifically, we calculated the standardized effect size (SES) of

functional richness (FRic) and functional dispersion (FDis) to identify habitat filtering and interactions between species as follows:

$$SES.FRic = \frac{FRic_{obs} - FRic_{null}}{SD(FRic_{null})}$$
(1)

$$SES.FDis = \frac{FDis_{obs} - FDis_{null}}{SD(FDis_{null})}$$
(2)

where $FRic_{obs}$ and $FDis_{obs}$ are the observed FRis and FDis values of the communities, respectively; $FRic_{null}$ and $FDis_{null}$ are the mean FRis and FDis values calculated from 999 random communities, respectively; and $SD(FRic_{null})$ and $SD(FDis_{null})$ are the standard deviations of $FRic_{null}$ and $FDis_{null}$, respectively. We interpreted the resulting values as follows: SES.FRic values significantly less than 0 indicate that the observed community functional trait space is smaller than that of random communities, implying the niche processes of habitat filtering and interspecies interactions; SES.FDis values significantly greater than 0 indicate neutral processes of community assembly; and if there is no significant difference between ses.FDis and 0, community assembly was dominated by stochastic processes [37].

2.8. Statistical Testing and Data Analysis

We used linear regression to test the variation of functional and phylogenetic diversity with compound habitat gradients and chi-square tests to analyze the correlation between functional and phylogenetic diversity structure. All statistical analyses were performed in R 3.2.5 [35].

3. Results

3.1. Phylogenetic Signal in Functional Traits

Tests of the phylogenetic signal revealed that four functional traits (SLA, LDMC, LNC, and WD) had *K* values significantly (p < 0.05) less than 1 for all species across the 309 forest vegetation plots (Tables 2 and A1).

Table 2. Phylogenetic signal, as measured by Blomberg's *K*, in functional traits of forest vegetation across climatic regions in China. * p < 0.05; ** p < 0.01; NS, non-significant.

	SLA	LDMC	LNC	LPC	N:P	WD
K	0.09 **	0.07 **	0.08 **	0.04 (NS)	0.04 (NS)	0.05 *

3.2. Functional Diversity along Compound Habitat Gradients

Generally, SES.FRic and SES.FDis were significantly negatively correlated with PC1 and significantly positively correlated with PC2; however, values differed across forests after testing for group differences in forest vegetation across different climatic regions in China (Figure 1). In the cold temperate zone with low temperature and little rain, the SES.FRic and SES.FDis of the forest community was greater than 0, and the functional space of the community was larger than that of the random community. On the contrary, the SES.FRic and SES.FDis of tropical forest communities in China was less than 0, and the community structure was lower than stochastic (Figure 2). There were no significant relationships between SES.FRic or SES.FDis and PCA3 or PCA4 (Figure A2).



Figure 2. The relationships between functional diversity, SES.FRic (**A**,**C**) and SES.FDis (**B**,**D**), and compound habitat gradients, PC1 (**A**,**B**) and PC2 (**C**,**D**), of forest vegetation communities in China. Different color–marker combinations represent each forest plot. The abbreviations for each variable are listed in Table 1. Significance values: ***, p < 0.001.

3.3. Phylogenetic Diversity along Compound Habitat Gradients

Generally, phylogenetic diversity was significantly negatively correlated with the first two compound habitat gradients (PC1 and PC2; Figure 3). In both cold and warm temperate climate zones, the NRI and NTI of forest vegetation were greater than 0, and the community structure was higher than stochastic. In tropical forest communities, the NRI and NTI were less than 0, and the community structure was lower than stochastic (Figure 2). There were no significant relationships between NRI or NTI and PCA3 or PCA4 (Figure A2).



Figure 3. The relationships between phylogenetic diversity, NRI (**A**,**C**) and NTI (**B**,**D**), and compound habitat gradients, PC1 (**A**,**B**) and PC2 (**C**,**D**), of forest vegetation communities in China. Different color–marker combinations represent each forest plot. The abbreviations for each variable are listed in Table 1. Significance values: ***, p < 0.001.

4. Discussion

4.1. Phylogenetic Signal in Functional Traits

We found that *K* values of functional traits across climate regions of China were all much lower than 1, and therefore showed phylogenetic independence (Table A1). Therefore, in this study, phylogeny was not a good predictor of functional diversity. Four functional traits (SLA, LDMC, LPC, and WD) had significant phylogenetic signals (p < 0.05); however, the lack of signal in LNC and N:P suggests that these two functional traits may be more affected by factors such as habitat [38]. Community phylogenies tend to exhibit stronger correlations with functional traits at larger taxonomic scales [39]. Secondly, the phylogenetic relationship cannot completely reflect all the information on functional traits of species in the community, and is a necessary but not sufficient condition required to study the similarity of functional traits of species in the community. The phylogenetic relationship can only be used as one of the indirect indicators, and cannot be substituted for functional traits in the study [7]. Finally, the factors and conditions that form the random phylogenetic relationship in the community are compound and diverse; some traits may show random divergence, while other traits show a non-random conserved state in the whole community [7,14].

4.2. Climate Influences Forest Community Construction across Climatic Regions

Habitat filtering, biotic competition, and interspecific interactions are three major ecological processes driving community assembly [40,41]. In this study, we show that functional diversity tended to converge along a compound habitat gradient composed of climate, soil, and biotic factors across multiple climatic regions of China (Figure 3). Our results provide evidence that niche processes (i.e., habitat filtering and interspecific interaction) had greater effects than neutral processes on the maintenance of forest vegetation diversity across climatic regions of China. This may be mainly because the species in these communities are not functionally equivalent, and therefore, random processes may play a role at the regional scale [42]. We found that the functional diversity of cold temperate forest vegetation was higher than that of random communities, and that the functional diversity of tropical and subtropical forest vegetation tended to be divergent. The high degree of functional dispersion in tropical forest communities confirms that interspecific interactions lead to higher functional differences [19]. In the cold temperate forest community, habitat filtering dominated the community assembly process due to the influence of extreme climates, such as low temperature and little rain, which improved species similarity and reduced the range of functional traits [4,19,43].

We also found that cold temperate forest vegetation tended to be phylogenetically clustered, while tropical and subtropical forest vegetation was overdispersed. Phylogenetic clustering may result from habitat filtering, which we interpret as niche conservatism. For example, closely related species may possess similar adaptions to environmentally challenging conditions [34]. Phylogenetic overdispersion in subtropical and tropical forest communities may indicate competitive exclusion of species with different survival strategies [5]. Competition for habitat resources, such as light, soil nutrients, and water, increases with species richness [44]. The limited similarity between species may lead to niche divergence and phylogenetic overdispersion. Therefore, it is possible that habitat filtering and biotic interactions (e.g., competition and exclusion) combined to affect phylogenetic patterns of trait values in forest vegetation in China across different climatic regions.

4.3. Biotic Interactions and Soil Characteristics Affect Community Construction

We found that interspecific interactions gradually intensified from cold temperate to tropical forest communities, which may be due to the differentiation of functional traits in species during long-term evolution and phenotypic plasticity [34]. Functional trait divergence can reduce niche overlap, therefore allowing species to be more evenly distributed along resource axes [19] and improving resource utilization [42]. Our results show that the overall similarity of functional traits among all species in cold temperate forest communities was higher, which may be because the community structure of the cold temperate forest is single and the dominant species are obvious, while the functional traits in the community are determined by the species with greater abundance.

In contrast, the overall similarity of functional traits of all tropical forest species was higher, which may result from local habitat filtering and biotic competition [44,45]. In tropical and subtropical forest communities, limited similarity plays a more important role in increasing variability in community functional traits [34]. We confirmed that habitat modification only acted on the functional traits or relatedness of the species rather than the species itself [4,19,42].

In our study, compound habitat gradients acted as the abiotic and biotic filters, jointly influencing the phylogenetic diversity of forest communities. We found that niche processes based on habitat filtering and biotic competition played important roles in the formation of forest functional diversity across climatic regions in China, and in determining the mechanism of community assembly [29,46]. Furthermore, whether the patterns found in

this paper are prevalent in different locations in different climatic zones in China will be the focus of future research.

5. Conclusions

We found that phylogenetic and function diversity shifted from clustered to overdispersed temperate to tropical forest communities. Our results suggest that habitat filtering had greater effects in temperate forests, while competition had greater effects in tropical forests. Phylogenetic signal in functional traits was generally low across climatic regions. We further uncovered an interaction between habitat selection and biotic competition across climatic regions in China. Our results support the joint effects of habitat filtering and competition in community assemblies, and we often found more than one mechanism influencing community structure and function. In future studies, we need more plots and more accurate environmental data to verify whether the patterns found in this paper are prevalent in different locations in different climatic regions of China.

Author Contributions: R.Z. and C.W. designed this study and improved the English language and grammatical editing. L.Y. (Liangjin Yao) wrote the first draft of the manuscript and performed the data analysis. L.Y. (Lan Yao), F.D. and Y.X. did the fieldwork. X.A. gave guidance and methodological advice. All the coauthors contributed to the discussion, revision, and improvement of the manuscript. All authors have read and agreed to the published version of the manuscript.

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Conflicts of Interest: This is the first submission of this manuscript, and no parts of this manuscript are being considered for publication elsewhere. All authors have read and approved the content of the manuscript. No financial, contractual, or other interest conflicts exist for the study.

Appendix A Appendix

Table A1. The phylogenetic signal of functional traits in forest communities occupying different climatic zones in China.

Indexes-	Jianfengling		Bawangling		Xishuangbanna		Mulinzi		Xingdoushan		Xiaolongshan		Kanasi	
	К	Р	К	Р	К	Р	К	Р	К	Р	К	Р	К	Р
SLA	0.19	0.029	0.21	0.001	0.24	0.149	0.008	0.87	0.006	0.64	0.42	0.001	1.38	0.022
LDMC	0.2	0.001	0.25	0.001	0.25	0.069	0.04	0.696	0.047	0.66	0.27	0.001	0.68	0.035
LNC	0.07	0.25	0.15	0.095	0.17	0.329	0.02	0.816	0.033	0.78	0.19	0.011	0.89	0.049
LPC	0.09	0.054	0.14	0.069	0.18	0.263	0.04	0.286	0.038	0.32	0.12	0.079	1.01	0.082
N:P	0.05	0.786	0.12	0.426	0.18	0.27	0.008	0.906	0.008	0.71	0.17	0.07	0.57	0.686
WD	0.06	0.545	0.11	0.358	0.23	0.157	0.03	0.745	0.041	0.65	0.27	0.001	0.59	0.034



Figure A1. Geographical distribution of the 309 plots. Plots were taken from seven forest sites in China. At each site, plots with an area of 20 m \times 20 m were randomly established.



Figure A2. The relationships between functional and phylogenetic diversity and compound habitat gradients PC3 and PC4. Different color–marker combinations represent each forest plot. The abbreviations for each variable are listed in Table 1.

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