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Ectomycorrhizal tree dominance drives species diversity and aboveground biomass by modulating stand structural heterogeneity in temperate-subtropical transition forests

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Abstract

Ectomycorrhizal (EcM) tree species often dominate temperate and warm-temperate forests, yet how their mycorrhizal dominance reshapes the species diversity–aboveground biomass relationship (DBR) remains unclear. In this study, we examined 6-ha permanent monitoring forest plots across the temperate–subtropical transition zone of China. Based on bivariate regression, generalized linear mixed models (GLMM), and structural equation modeling (SEM), we quantified the contribution and mechanistic pathways of the mycorrhizal dominance to aboveground biomass (AGB) accumulation. Our findings reveal that i) Ectomycorrhizal tree dominance is the key determinant of AGB accumulation in temperate-subtropical transition forests; ii) EcM tree dominance enhances AGB by reducing stand structural heterogeneity rather than increasing it. iii) Although EcM tree dominance reduces arbuscular mycorrhizal (AM) tree abundance and species richness through competitive exclusion, the positive biodiversity–ecosystem function (BEF) relationship persists. These results elucidate the interplay between selection and complementarity effects, offering new

insights into the ecological drivers of DBR and providing a scientific foundation for the sustainable management of temperate forests.

Keywords: Ectomycorrhizal dominance; Aboveground biomass; Species diversity; Stand structural heterogeneity

1. Introduction

Trees control the carbon sequestration and biomass development of forest ecosystems, which impact the global carbon cycle [1–3]. In the majority of temperate forests with a few or a single species dominating the overstorey, reduced diversity leads to increased aboveground biomass (AGB) because of large trees [4–6]. This is why these giants become the main agents of carbon storage in mature forests because carbon gain increases rapidly with tree size [7, 8]. As a result, under low diversity, AGB is more sensitive to large tree dominance than to the classical biodiversity ecosystem functioning (BEF) relationship [9, 6, 10]. This effect is amplified by ectomycorrhizal (EcM) tree dominance in nutrient-poor temperate forests. The dominant large trees in such forests are almost invariably EcM species [11–13]. Their fungal partners confer a competitive advantage, thereby reshaping the diversity – biomass relationship (DBR). [14, 15].

In temperate and warm-temperate forests, most tree species form symbiotic relationships with mycorrhizal fungi [16, 13]. These relationships fall into two functional groups: EcM tree species exhibit low species richness but high individual abundance, and arbuscular mycorrhizal (AM) tree species display high species richness yet rarely dominate temperate forest [17]. EcM and AM tree species differ significantly in nutrient acquisition strategies, nutrient foraging capabilities, and physiological and morphological traits [18]. EcM fungi decompose soil organic matter to acquire nitrogen and form dense hyphal sheaths around roots, enhancing host resistance to pathogens [19]. In contrast, AM fungi are more efficient at absorbing low-mobility inorganic nutrients, such as phosphorus, but offer less physical protection [20]. Given these functional differences, EcM tree species may leverage their competitive advantage in nutrient-limited forests to drive community biomass accumulation. This effect is particularly pronounced in nitrogen-constrained systems [21]. The competitive dominance of EcM species potentially reduces the direct contribution of species

diversity to aboveground biomass. [8, 22, 23].

The relationship between species diversity and AGB remains highly debated in forest ecosystems [24–26]. On the one hand, based on the niche complementarity and selection effect hypotheses, many studies have demonstrated that species diversity enhances resource use efficiency and significantly increases forest AGB [27–29, 26]. Conversely, some studies report non-significant or even negative relationships between diversity and productivity [27]. In diversity-manipulation experiments, DBR often exhibits a saturating curve, suggesting functional redundancy as species richness increases [30]. The DBR can even shift after controlling for community structural factors, indicating that AGB patterns are shaped by the combined influence of species diversity and stand structure rather than species diversity alone [31]. During succession in most temperate and warm-temperate forests, early stages dominated by AM trees typically exhibit high species diversity [32]. As succession progresses, highly competitive EcM trees (e.g., Pinaceae, Fagaceae) become dominant in late-successional or climax communities, potentially leading to reduced species richness but increased AGB [33, 34]. Global tree diversity studies show that the structural complexity of trees with different mycorrhizal types enhances forest productivity [35]. EcM dominance maximizes AGB not by increasing stand structural complexity but by stabilizing or homogenizing stand structure [36]. However, traditional ecological perspectives suggest that greater structural heterogeneity, (e.g., in DBH distribution and vertical stratification) optimizes resource acquisition (especially light) thereby promoting AGB accumulation [37]. Nonetheless, the specific mechanisms through which the EcM tree dominance regulates the DBR via community composition and structural attributes remain unclear [38].

The temperate-subtropical transition zone forests are characterized by diverse climatic and topographic conditions, which facilitates the admixture of northern and southern Chinese flora [39]. In our study area, the nature reserve harbors a large number of structurally complex and species-rich conifer–broadleaf mixed forests, where most plant species form mycorrhizal symbioses (predominantly with AM or EcM fungi). To assess the role of the mycorrhizal tree dominance in aboveground biomass (AGB) accumulation in temperate and warm-temperate forests, we established 6 ha long-term monitoring plots to address two questions: i) Does mycorrhizal tree dominance drive aboveground biomass accumulation in these forests? ii) What mechanisms

underlie the influence of mycorrhizal dominance on the diversity – biomass relationship? This study aims to investigate the mechanisms underlying the positive effects of species diversity on AGB in temperate-subtropical montane forests.

2. Materials and methods

2.1. Study area and vegetation survey

Our study site is located in the Baotianman National Nature Reserve (111°53′–112°04′E, 33°25′–33°33′N) in Henan Province, China [40]. This nature reserve is situated in the temperate and subtropical translation zone, with an elevation ranging from 1300 to 1830 m. It experiences a subtropical continental monsoon climate with cold winters, hot summers, and distinct seasonal variations [41]. Annual precipitation averages 886 mm, mostly occurring in summer, and the mean annual temperature is 15.1°C (Wang *et al.*, 2025). The nature reserve is primarily characterized by deciduous broadleaf forests and mixed coniferous-broadleaf forests, with dominant canopy tree species including *Quercus acutissima* var. *acutissima*, *Quercus serrata* var. *brevipetiolata*, *Carpinus turczaninowii*, *Pinus armandii*, and *Pinus tabulaeformis* [40].

Based on the 6 ha Baotianman forest dynamics plot (hereafter BTM) in Baotianman National Nature Reserve, which is a late-successional deciduous coniferous-broadleaf mixed forest dynamic plot (100 m × 100 m). All woody plants with a diameter at breast height (DBH) ≥ 1 cm were tagged, measured, and identified to species.In total, 7905 individuals belonging to 39 families, 65 genera, and 140 species were recorded. The same standardized procedures were applied across all subplots for tagging, identification, measurement, and mapping.

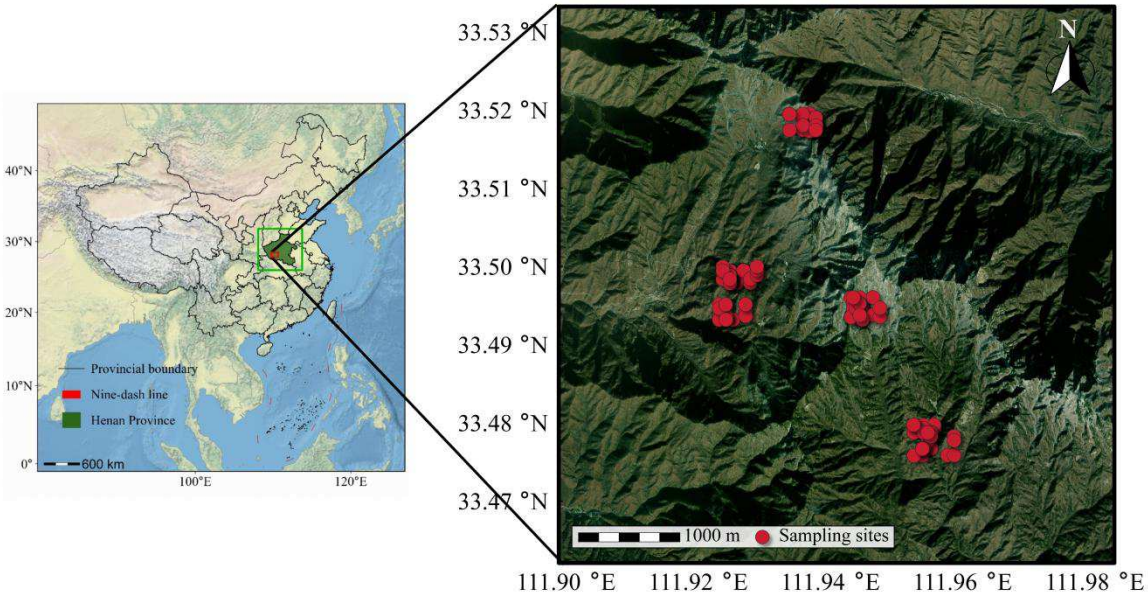


Figure. 1. Location of the study sites in the Baotianman National Nature Reserve, central China. Points show sampling sites.

2.2. Mycorrhizal association types

Mycorrhizal traits exhibit strong phylogenetic conservatism [43–45]. Accordingly, we classified the mycorrhizal types for each plant species based on two global comprehensive mycorrhizal databases (FungalRoot v.2.0 and FRED 3.0; [46–48] and existing literature (17 references; Supplementary Tables S1). Using taxonomic informatics (mostly based on species or genera classification), species were primarily categorized into ectomycorrhizal (EcM), arbuscular mycorrhizal (AM), ericoid mycorrhizal (ERM), dual association (EcM-AM), and Other. For most species, our classifications were consistent with the global mycorrhizal database. Within the subplots, we identified 24 EcM tree species (comprising 43.6% of total abundance) and 103 AM species (comprising 46.0% of total abundance). Some studies reported dual EcM and AM associations for certain species [45, 49], while for species without clear mycorrhizal information in the literature, we categorized them as 'Other.' We focused our analysis on dominant EcM and AM associated tree species.

2.3. Measuring aboveground biomass

In the plot census, we estimated the total aboveground biomass (AGB) of each tree based on the measured DBH using species-specific allometric equations. The calculation was referenced from the Carbon Storage of China's Forest Ecosystems—Biomass Equations manual (Zhou *et al.*, 2018), which integrates field-measured data from 7,800 typical forest ecosystem plots across China. This manual assigns values to previously published biomass equations and employs the least squares support vector machine (LSSVM) to iteratively optimize these equations. As a result, biomass equations applicable at both provincial (autonomous regions and municipalities) and national scales were established for dominant tree species. These equations were validated using field-measured data from standard trees within the plots, with an estimation error of within 10%.

2.4. Biodiversity measurements

2.4.1 Mycorrhizal dominance

To further elucidate the mycorrhizal tree dominance, we quantified the relative abundance of different mycorrhizal types. This index reflects the prominence of each mycorrhizal functional group within the forest stand and serves as a proxy for evaluating its contribution to community-level ecological processes [50, 51]. Given that the influence of mycorrhizal types on community function may vary with tree size, and MSE is often more evident in trees with larger diameters, we divided trees into large trees (DBH > 10 cm) and small trees (DBH ≤ 10 cm) for analysis [18, 22]. The abundance index is calculated as follows:(Equation (1); Supplementary Tables S2)

$$\text{Mycorrhizal dominance}=\frac{N_{myc}}{N_{total}} \quad (1)$$

where N_{myc} is the number of individuals of a certain mycorrhizal type, and N_{total} is the total number of individuals in the plot.

2.4.2 Species diversity

We used the Margalef Richness Index (species richness), the Shannon-Wiener Index (Shannon-Wiener index), the Simpson Index (simpson index) and Pielou Evenness Index (evenness index) to represent the level of species diversity within the community. The calculations were

146 performed using the 'vegan' package in R [52], which serves as a fundamental drivers of DBR under
147 MSE mediation [37].

148 **2.4.3 Stand structure diversity**

149 To identify the structural diversity index most representative of MSE, we used the coefficients
150 of variation (CV) of diameter at breast height (DBH) and tree height (H) to represent horizontal and
151 vertical stand heterogeneity, respectively [53, 54]. These metrics were calculated for large (DBH >
152 10 cm) and small (DBH ⩽ 10 cm) trees within each mycorrhizal type as follows: (Equation (2)
153 and (3); Supplementary Tables S3)

154 $$\text{DBH variation}=\frac{\sigma_{dbh}}{\mu_{dbh}} \quad (2)$$

155 $$\text{H variation}=\frac{\sigma_{h}}{\mu_{h}} \quad (3)$$

156 where σ_{dbh} and μ_{dbh} represent the standard deviation and mean of DBH measurements, σ_h and
157 μ_h represent the standard deviation and mean of H, respectively.

158 **2.5. Statistical Analyses**

159 Data analysis was conducted at the subplot level (20 m×20 m, n = 125). We first employed
160 Mantel tests to evaluate the relationships among mycorrhizal dominance, species diversity,
161 structural diversity, and AGB, followed by generalized linear mixed models (GLMM) to quantify
162 the relative importance of each predictor [55]. Structural equation models (SEM) were finally
163 performed to determine the direct and indirect effects of each variable on AGB [56]. As the
164 interaction effects among variables were not significant, we employed only main effects to fit the
165 model. All variables were standardized prior to analysis to facilitate comparable parameter
166 estimation.

167 **2.5.1 Multiple regression models**

168 In order to identify the optimal response variable for explaining AGB variation, we used the
169 'MuMIn' package to build generalized linear mixed models (GLMMs; Bartoń, 2010). These models
170 assessed the effect of the mycorrhizal dominance on the DBR. We calculated all the potential indices.
171 We then included all variables in a stepwise regression procedure to select the best-fitting model
172 based on Akaike's information criterion (AIC; Bates *et al*., 2015). Model averaging was

subsequently applied to the selected best model to determine parameter coefficients for the final set of predictors of AGB. We also calculated the relative importance of different predictor groups by comparing their effects against the overall parameter estimates in the model. The relative contributions (C%) of each variable were derived using the 'glmm.hp' R package [55]. Pairwise Spearman correlations among variables were calculated using the 'linkET' R package, and results were visualized as a heatmap. In addition, Mantel tests were employed to assess the association between AGB and other variables. All correlation visualizations were generated using 'ggplot2'. All statistical analyses were conducted in R (version 4.3.1).

2.5.2 Structural equation models

We employed structural equation models (SEMs) to evaluate how mycorrhizal dominance shape the DBR pathways. We drew from the variable combinations identified in the GLMM analysis. We posit that high-biomass communities (climax communities) are shaped by EcM trees [59, 60], while low-biomass communities (seral communities) are largely composed of AM trees [61, 62]. During the selection of the best-fitting SEM, a series of tests was used to evaluate model fit [63], including the chi-square Chi-square (χ^2) test, goodness-of-fit index (GFI), comparative fit index (CFI), root mean square residual (RMR), standardized root mean square residual (SRMR), and root mean square error of approximation (RMSEA). From the final model, we identified the most influential predictors for AGB by examining the highest standardized effect size (β). The SEM analyses were implemented using the 'lavaan' R package [56].

3. Results

3.1. Correlation analysis between different variables and AGB

Circular stacked bars and boxplots (Figure. 2) illustrates the contrasting distributions of EcM and AM trees across aboveground biomass (AGB), abundance, and species richness. EcM trees comprised only 24 species yet accounted for 43.6% of total individual abundance. They contributed disproportionately to total AGB. In contrast, AM trees exhibited higher species richness (103 species, 73.6%) but contributed only 46.0% of total abundance. EcM large trees accumulated significantly more AGB per individual than AM large trees ($p < 0.05$; Figure. 2a). Among dominant species, *Quercus aliena* var. *acuteserrata*, *Pinus armandii* and *Pinus tabulaeformis* were the primary contributors to total AGB (Figure. 2a). AM species showed a more even distribution of

abundance across many species, whereas EcM abundance was concentrated in fewer species (Figure. 2b). Species richness was overwhelmingly dominated by AM-associated taxa (Figure. 2c). Together, these patterns confirm that EcM dominance in this forest is driven by the high individual abundance and large size of a few species, rather than by species diversity.

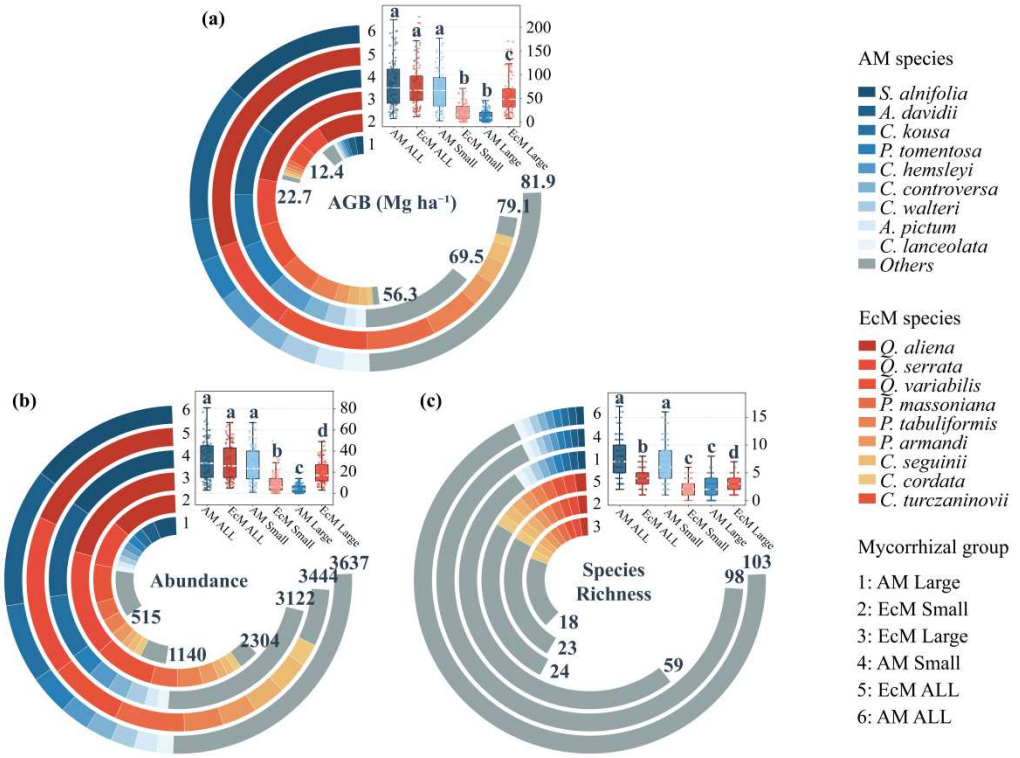


Figure. 2. Mycorrhizal differences in tree biomass, abundance and species richness. Circular stacked bars show EcM and AM tree distributions across all plots for (a) aboveground biomass (AGB), (b) abundance and (c) species richness. Inset boxplots show differences among mycorrhizal and size-class groups at the bigplot-level. Coloured arcs indicate dominant species, whereas grey arcs represent pooled "Others". Boxplots show medians, interquartile ranges and plot-level observations. Different lowercase letters denote significant differences from Dunn's post hoc tests with Bonferroni correction after Kruskal-Wallis tests ($p < 0.05$). EcM, ectomycorrhizal; AM, arbuscular mycorrhizal. Large trees were defined as DBH $\geqslant$ 10 cm, and small trees as DBH < 10 cm.

The Mantel test results revealed significant correlations among the MSE, species diversity, structural diversity and AGB (Supplementary Figure S1). The Mantel test identified key predictor variables for further analysis, including EcM large trees dominance (EcM large trees_%), AM dominance (AM trees_%), species richness, EcM trees DBH variation, and EcM large trees H variation. Linear regression models further elucidated the effects of selected predictor variables on AGB (Figure 3). EcM large tree dominance exhibited a significant negative correlation with AM

dominance ($p < 0.001$; Figure 3a). Aboveground biomass was significantly positively correlated with EcM large trees dominance ($p < 0.05$; Figure 3b), but negative correlations with the EcM trees DBH variation($p < 0.01$; Figure 3e) and EcM large trees H variation($p < 0.05$; Figure 3f), suggesting that low structural heterogeneity EcM trees in communities may promote AGB accumulation.

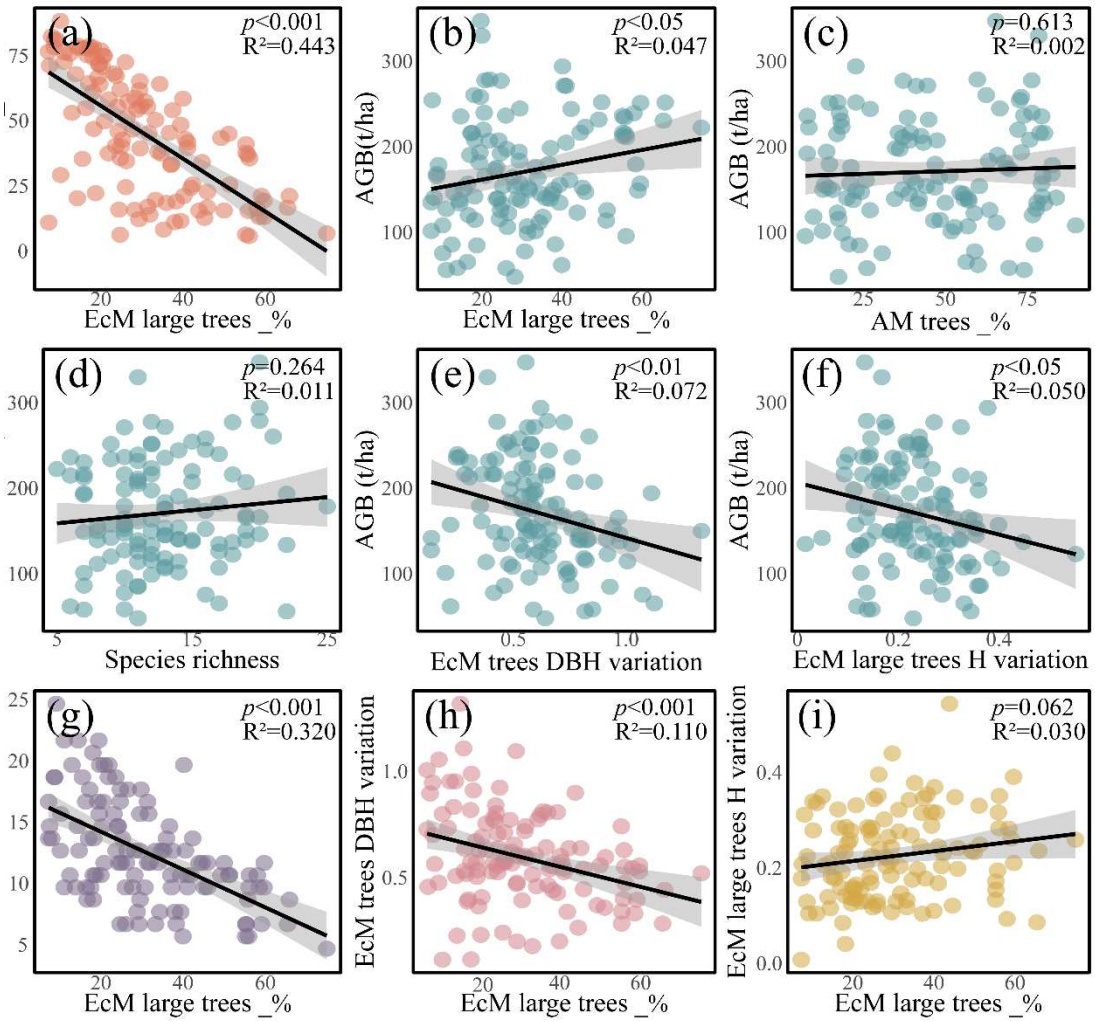


Figure. 3. Linear relationships between individual predictors and AGB. The shaded gray areas represent 95% confidence intervals.

3.2. The relative importance of different variables in affecting AGB

Generalized linear mixed models (GLMM) were used to evaluate the relative contributions and effect sizes of selected predictor variables on AGB variability (Figure 4). Predictors included EcM large tree dominance, AM dominance, species richness and structural heterogeneity metrics (EcM DBH variation and EcM large trees H variation). Results identified EcM large tree dominance as

the most influential variable (Supplementary Tables S4), with a significant positive effect on AGB ($p < 0.001$). Species richness was also significantly positively correlated with AGB ($p < 0.001$), whereas AM dominance, EcM DBH variation, and EcM large trees height variation exhibited negative parameter estimates. Hierarchical partitioning results highlighted the relative importance of each predictor (Figure 4). EcM large tree dominance, species richness, and AM dominance were the top three contributors to AGB variability. Although AM dominance showed no significant direct effect on AGB, its substantial explanatory power suggests an influence via indirect pathways, while EcM large tree dominance likely regulates AGB accumulation through direct pathways.

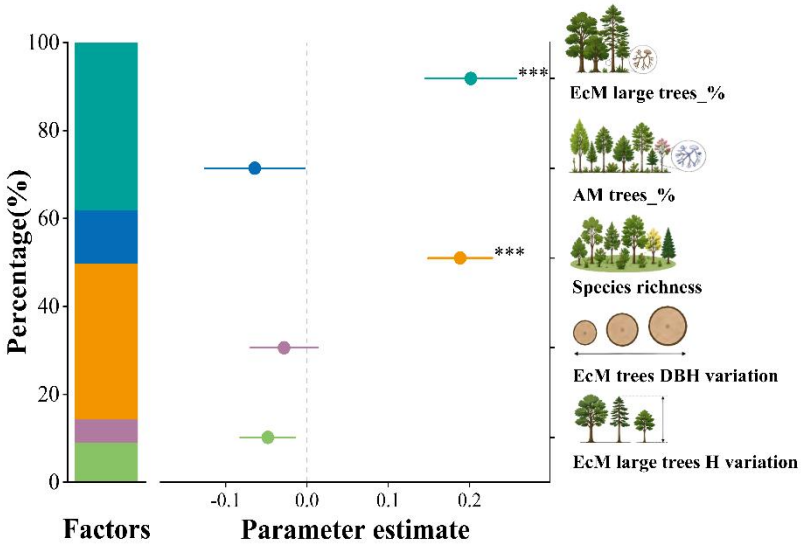


Figure. 4. Relative importance and effect sizes of key predictors of AGB based on GLMM analysis.The left panel shows the percentage contributions of each predictor to AGB variation. The right panel presents standardized regression coefficients for each variable. Variables include EcM large trees_%, AM trees_%, species richness, EcM trees DBH variation, and EcM large trees H variation. Asterisks indicate significance levels (*$p < 0.05$, **$p < 0.01$, ***$p < 0.001$).

3.3. The direct and indirect effects of different variables on AGB

Structural equation modeling (SEM) elucidated the interrelationships among EcM large tree dominance, AM dominance, species richness, structural diversity metrics and AGB (Figure 5). The model revealed that AGB is significantly influenced by multiple variables, acting through direct and indirect pathways to drive AGB accumulation. EcM large tree dominance emerged as the primary driver of AGB (Supplementary Table S5; path coefficient = 0.641, $p < 0.001$), strongly promoting AGB accumulation via direct pathways. EcM large tree significantly influenced the DBR by reducing structural heterogeneity, including vertical and horizontal structural diversity (path coefficient = -0.798, $p < 0.001$). EcM tree dominance reduced structural diversity and the abundance

of AM tree species, thus decreasing species diversity. But it promoted aboveground biomass (AGB) accumulation by altering stand structure.

EcM large-tree dominance reduced AM tree abundance and species diversity, but AM species in this EcM-dominated community still enhanced AGB substantially by increasing species richness (Figure 5). This positive effect suggests that the biodiversity–ecosystem function relationship persists even in EcM-dominated forests. AM-associated species therefore play a critical role in sustaining AGB in such ecosystems.

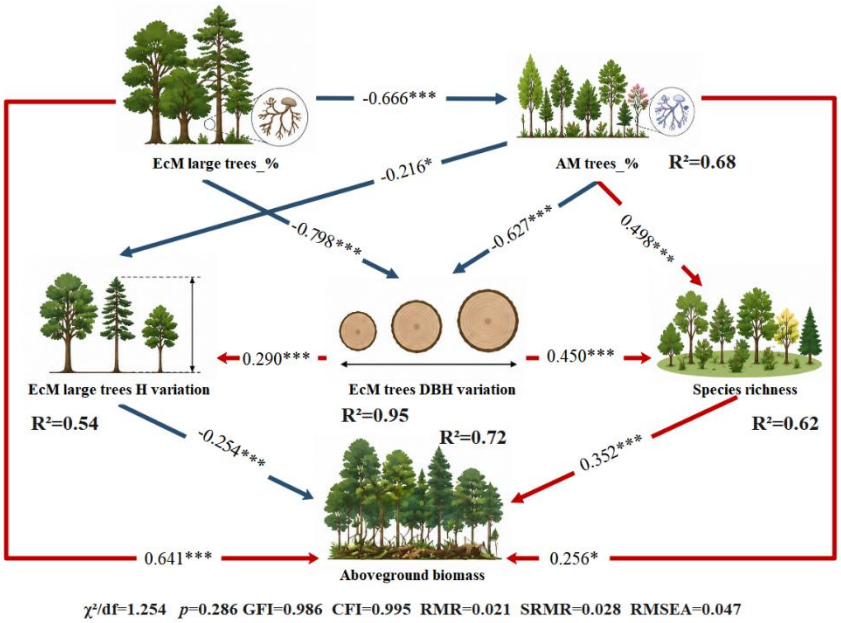


Figure. 5. Structural equation models (SEMs) illustrating the effects of mycorrhizal dominance, species diversity and structural diversity on AGB. Solid arrows indicate statistically significant paths (standardized path coefficients with p-values: *$p < 0.05$, **$p < 0.01$, ***$p < 0.001$). Red and blue arrows represent significant positive and negative effects, respectively.Conditional R2 values for each response variable are shown in corresponding boxes.

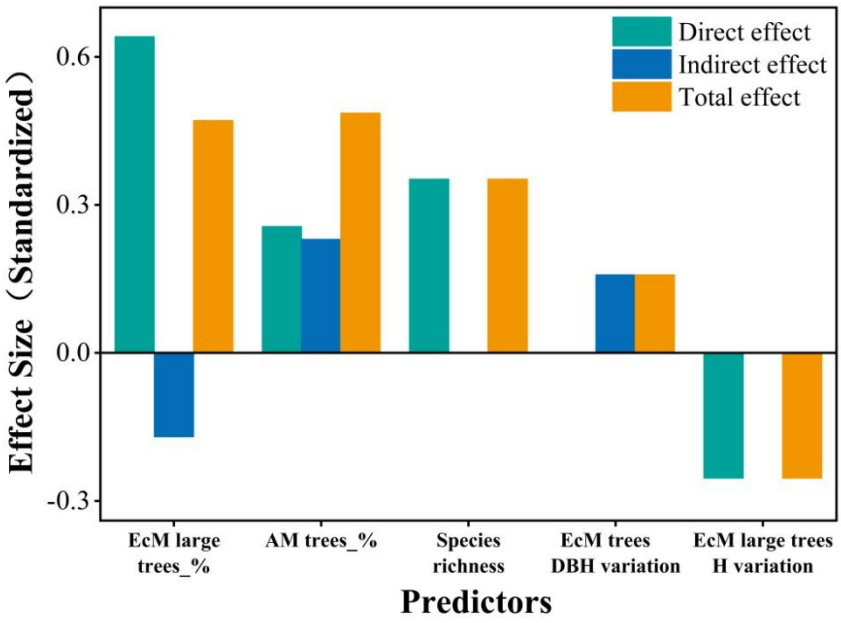


Figure. 6. Direct, indirect and total standardized effects on AGB. EcM large trees_%, AM trees_%, EcM large trees H variation, EcM trees DBH variation and species richness as predictors of AGB.

4. Discussion

4.1. The Dominant Role of the EcM Large Tree in Forest AGB Accumulation

Bivariate regressions (Figure. 3), GLMMs (Figure. 4), and SEMs (Figure. 5) show that AGB in temperate and warm-temperate forests is chiefly regulated by the EcM large-tree dominance. GLMM variable selection retained this metric as the leading explanatory factor for AGB variation, and subsequent analyses confirmed its direct positive effect on biomass. Our findings align with numerous studies in temperate and northern forests, where AGB accumulation is primarily driven by the selection effect of a few dominant species [64, 65], typically trees symbiotic with EcM fungi [66]. EcM trees exhibit a significant competitive advantage in nutrient-limited environments, particularly through their specialized ability to decompose soil organic matter via mycorrhizal networks to acquire nitrogen [67], which enables them to dominate communities and accumulate substantial biomass. Under strong environmental filtering, highly adaptive EcM species are selected and tend to grow into large individuals [68]. Their expansive crowns capture a disproportionate share of available light, while their extensive root systems and fungal networks afford them a dominant position in belowground nutrient competition [69]. This resource dominance establishes a positive feedback mechanism. The dominant status of EcM trees promotes their growth, and large EcM individuals reinforce their competitive advantage while suppressing neighbouring rivals. The

selection effect of EcM large tree dominance outweighs the niche complementarity driven by species coexistence in promoting AGB. This suggests that in EcM-dominated ecosystems, the contribution of species diversity to biomass may be of secondary importance, offering a potential explanation for ongoing debates about the diversity–biomass relationship (DBR).

4.2. EcM Tree Dominance regulates the DBR by stabilizing structural heterogeneity

Structural equation modeling revealed that a higher proportion of large EcM trees exerted significant negative effects on both EcM trees DBH variation and EcM large trees height variation (Figure 5). These findings suggest that increasing EcM dominance promotes structural stabilization within forest stands, which in turn contributes to greater AGB. Our study highlights a novel mechanism whereby the dominance of EcM species indirectly regulates AGB not by enhancing, but by reducing, both horizontal and vertical structural heterogeneity, which contrasts sharply with traditional theories [70, 71]. Conventional perspectives suggest that greater structural heterogeneity, such as multi-layered canopies and diverse tree size distributions, enhances AGB accumulation by optimizing resource acquisition, thereby supporting a positive DBR [72]. However, this principle may not apply in temperate forest systems strongly dominated by the EcM large trees and may even be reversed. Recent studies in temperate forests report that stand structural uniformity supports AGB accumulation [8, 73]. When EcM trees dominate a stand, their expansive canopies capture the majority of available light, while their extensive mycorrhizal networks confer a competitive advantage in belowground nutrient acquisition, effectively monopolizing soil resources [74, 75]. This dual aboveground and belowground suppression significantly limits the growth and survival of understory tree species and smaller conspecific individuals, leading to the gradual elimination of weaker individuals (Yan *et al*., 2024; Zhang *et al*., 2024). In these communities, intense intraspecific competition and competitive thinning select for similarly sized individuals, resulting in a uniform stand structure. Although this reduces structural complexity, it maximizes the productivity of dominant EcM trees. Consequently, the surviving trees consist primarily of dominant EcM individuals of comparable size, reducing variability in stand diameter and height, thereby promoting AGB accumulation.

Notably, although dominance by large EcM trees reduces species richness via competitive exclusion, the positive BEF relationship is preserved. Species richness remains a significant driver

of AGB, even as its contribution is attenuated under EcM dominance. This provides further insight into the long-standing dichotomy between selection and complementarity effects, indicating that forest AGB emerges from the combined contribution of both mechanisms. [78, 79]. Our results demonstrate that in natural ecosystems, the selection effect driven by EcM dominance and the complementarity effect facilitated by AM tree species diversity can coexist. This coexistence stems from niche differentiation between mycorrhizal tree types, particularly their distinct nutrient acquisition strategies[80, 21]. EcM trees have a superior capability to decompose organic matter for nitrogen acquisition, establishing them as dominant competitors in temperate forests[61, 81]. In contrast, AM trees and their symbiotic fungi excel at absorbing low-mobility inorganic nutrients, such as phosphorus [82]. This resource use complementarity allows AM trees to establish and persist in nutrient-specific microhabitats within EcM-dominated stands. In the understory environment shaped by EcM trees, AM trees face intense interspecific and intraspecific competition, resulting in rapid growth and high mortality rates (Dolezal *et al*., 2024; Zhang *et al*., 2024). This rapid turnover of individuals prevents individual AM tree species from achieving dominance but fosters temporal and spatial species coexistence, maintaining high species richness within the forest community [85]. This dynamic contributes to AGB accumulation in temperate and warm-temperate forests.

5. Conclusions

This study shows that the dominance of large EcM tree species is a primary driver of AGB accumulation in temperate–subtropical forests, mainly by reducing stand structural heterogeneity. Although competitive exclusion by EcM species diminishes the abundance and diversity of AM trees, AM tree diversity still exerts a positive complementarity effect on AGB. These findings refine our understanding of the BEF relationship and may inform sustainable management strategies for temperate forests.

Declarations

Availability of data and materials

Data will be made available on request.

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Author Contribution

Guanjie Wang and Kun Shi conceived the ideas and designed the methodology; Guanjie Wang, Kun Shi, Tianai Zhang, Qin Huang, Chenyi Yu and Xiaonian Jin collected the data; Guanjie Wang and Kun Shi analyzed the data; Guanjie Wang, Kun Shi and Ting Wang wrote the manuscript; Bing Zhao, Zhicheng Chen, Jianqiang Qian, Deliang Kong, Liu Yang and Ting Wang modified the manuscript. All the authors contributed critically to the drafts and approved the final manuscript for

publication.

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Competing interests

The authors declare no competing interests.

Ethics approval and consent to participate

All field sampling in this study was conducted within the Baotianman National Nature Reserve, which is a publicly managed protected area. No privately owned land was accessed. Permission for field sampling was formally granted by the Baotianman Forest Ecosystem Research Station and the Forestry Bureau of Neixiang County, Henan Province, China (the local governing authority responsible for managing and regulating access to the reserve). All sampling activities complied with relevant local regulations and conservation management policies.

Consent to Participate declaration

Not applicable.

Consent to Publish declaration

Not applicable.

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