**Supporting Information**

**Tree phylogenetic diversity structures multitrophic communities**

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**Detailed descriptions of sampling protocols**

We used a diverse set of complementary sampling methods across all 27 study plots (see also Binkenstein et al., 2018; Schuldt et al., 2015):

The identity and abundance of all plants in the herb layer, i.e. of non-woody plant individuals < 1 m in height, was assessed the central 10 m x 10 m area of each plot in 2008 (Both et al., 2011).

Arthropods were mostly collected with pitfall traps and flight interception traps. From March to September 2009, four standard pitfall traps (plastic drinking cups, diameter 8.5 cm, height 15 cm) were operated at the corners of the central 10 m x 10 m areas (Schuldt et al., 2011; Staab, Schuldt, Assmann, & Klein, 2014). Traps were emptied every fortnight by replacing the preservation fluid (40% ethanol, 30% water, 20% glycerol, 10% acetic acid, few drops of neutral dishwashing detergent to break surface tension). From the full pitfall catches, we sorted out all Araneae, Chilopoda, Curculionidae (excl. Scolytinae) and Formicidae for further identification.

At the same positions in each plot as the pitfall traps, four flight interception traps were operated in the understory (at about 2 m height) from May to August 2010 and also emptied fortnightly. Flight interception traps consisted of two crossed 50 cm x 30 cm rectangles that were covered by a roof (see also Knuff, Winiger, Klein, Segelbacher, & Staab, 2019). Below the rectangles, a funnel was connected to a 500 ml collection bottle filled with the above-mentioned preservation fluid. From the full flight interception trap catches, we sorted out all Cerambycidae, Formicidae and Scolytinae for further identification.

Furthermore, 25 understory trees and shrubs in each plot were sampled 3 times with beating (once in fall 2011, twice in spring 2012, 75 samples per plot in total). A circular beating sheet (diameter 72 cm) was placed under the tree or shrub individual that was hit seven times with a stick to dislodge arthropods, which were subsequently collected with aspirators or forceps (Schuldt, Bruelheide, Durka, Michalski, Purschke, & Assmann, 2014a). From all collected specimens, all Araneae, Formicidae and larval Lepidoptera were taken for further identification.

From September 2011 to October 2012, cavity-nesting predatory wasps (including their parasitoids) were collected with trap nests for cavity nesting Hymenoptera (Staab, Pufal, Tscharntke, & Klein, 2018). Trap nests were filled with reed (diameter 2 mm to 20 mm, length 20 cm), Monthly, occupied nests were collected and specimens reared.

In May 2012, ants were additionally collected with standardized protein (canned fish) and sugar (honey solution) baits. Per plot, nine bait pairs were placed at the ground and at breast height (i.e. 36 baits in total). Baits were left for three hours and all ants feeding on the baits were collected (Schuldt & Staab, 2015).

Arthropod specimens in each selected taxonomic group were pooled per plot as we were interested in the effects of woody phylogenetic diversity (i.e. woody plant PD) at the community level. Specimens were sorted to morphospecies and further identified to species whenever possible. For simplicity, use the term ‘species’ for both, species and morphospecies. Individual numbers of each species were counted to obtain a measure for species abundance. We are aware that pitfall traps and fight interception traps collect ‘activity abundance’. We are also aware that due to their colonial lifestyle, using individual numbers may be problematic for ants. An alternative for ants would be to use an abundance measure that is based on occurrence or incidence. However, using such occurrence-based abundances for ants would preclude merging the ant data with other predators. Because analysing trophic guilds is a central concept of our study, we decided to use ant individual counts as abundance measure.

The trophic guild ‘plants’ consisted of the herbaceous vegetation. As ‘herbivores’ we grouped Lepidoptera and Curculionidae (excl. Scolytinae), which are among the identified arthropods the taxa with almost exclusively herbivorous species. Arthropods feeding primarily on (dead)wood were grouped as ‘saproxylics’ (Cerambycidae, Scolytinae). Araneae, Chilopoda, Formicidae and predatory wasps (including their parasitoids) consume at least to a large extent other arthropods and were grouped as ‘predators’.

**Fungal DNA barcoding**

To quantify the diversity of fungi, DNA extracted from eight top soil samples (top 10 cm) collected in September 2012 was sequenced. Soil material was sieved to remove coarse material and the remaining fine soil was immediately freeze dried to halt degradation of DNA. The eight initial soil samples were combined to four composite samples per plot by merging two spatially proximate samples each, which makes the sampling scheme comparable to the four pitfall and four flight interception traps per plot. From each composite sample, 1 g (dry mass) was taken and microbial DNA was extracted with MoBio soil DNA extraction kits (Mo Bio Laboratories, Carlsbad, CA, USA). Fungal DNA was amplified with the primers ITS1F (Gardes & Bruns, 1993) and ITS4 (White, Burns, Lee, & Taylor, 1990) that target the fungal internal transcribed spacer (ITS) rRNA region. PCR conditions were as described by Wubet et al. (2012). QIAquick Gel Extraction Kits (QIAGEN, Venlo, Netherlands) were used to purify PCR products. We used equimolar mixtures of each amplicon library for sequencing. A 454 FLX + System Genome Sequencer (Roche Applied Biosystems, Basel, Switzerland) with 454 Titanium amplicon sequencing kits was used for unidirectional pyrosequencing from the 907R and ITS4 ends.

To allow comparison between plots, raw sequence reads were filtered and normalized to 10,000 fungal ITS reads per plot with ‘mothur’ (Schloss et al., 2009). Molecular operational taxonomic units (OTUs) were delineated based on a 97% sequence similarity criterion (Wubet et al., 2012). OTUs characterize distinct groups of organisms that can be treated equivalent to species in macroorganisms and we refer to fungal OTUs as species for simplicity. Because singleton, doubleton and tripleton OTUs are likely the result of sequencing errors (Kunin, Engelbrektson, Ochman, & Hugenholtz, 2010), they were removed from the data. OTUs were grouped into the trophic guilds ‘arbuscular mycorrhizae’, ‘ectomycorrhizae’, ‘pathogenic fungi’ and ‘saprophytic fungi’ on the basis of sequence similarity using the default parameters of the GAST algorithm (Huse et al., 2008) against the global functional reference dataset (Tedersoo et al., 2014).

**Detailed information on woody plant phylogenetic diversity**

During plot establishment in 2008, the species richness (i.e. woody plant SR) and species-specific individual number of all woody plants (i.e. trees and shrubs) taller than 1 m were inventoried (Bruelheide et al., 2011). In total, 147 woody species were found and species richness ranged from 25-69 species per plot (mean = 42 ± 10 SD). A full phylogeny of all 147 woody species was constructed by using sequences from the standard marker genes *mat*K and *rbc*L and the ITS region (including the *5.8s* gene). The exact procedure is described in detail by Baruffol et al. (2013) and Purschke, Michalski, Bruelheide, and Durka (2017). Sequences were either extracted from GenBank (Benson, Karsch-Mizrach, Lipman, Ostell, & Wheeler, 2007) or created anew with standard barcoding protocols (GenBank accession numbers: KF569888-KF569899). Tree inference based on maximum likelihood and the GTR+I+G model was calculated with PHYML (Guindon & Gascuel, 2003). Using 27 fossil calibration points (see electronic supplementary material of Baruffol et al., 2013 and references therein) and non-parametric rate smoothing in r8s (Sanderson, 1997) an ultrametric phylogenetic tree was created as illustrated in Purschke et al. (2017) and the electronic supplementary material of Schuldt et al. (2014b). Based on this ultrametric tree, phylogenetic diversity was calculated as abundance-weighted Rao’s Q with the R-package ‘picante’ (Kembel et al., 2010).

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**Table S1** Summary information of environmental variables and trophic guilds in 27 study plots in subtropical China. Given are range (min - max), mean (± SD), and median

|  |  |  |  |
| --- | --- | --- | --- |
| Variable | Range | Mean ± SD | Median |
| *Environment* |  |  |  |
| Aspect East [sine] | -1.00 - 1.00 | -0.18 ± 0.69 | -0.07 |
| Aspect North [cosine] | -1.00 - 1.00 | -0.08 ± 0.72 | -0.06 |
| Conifer basal area [%] | 0.00 - 0.87 | 0.30 ± 0.25 | 0.23 |
| Elevation [m] | 251 - 903 | 547 ± 168 | 569 |
| Slope [°] | 14 - 47 | 34 ± 8 | 35 |
| Stand age [years] | 22 - 116 | 67 ± 26 | 72 |
| Total basal area [m²] | 0.16 - 4.37 | 1.96 ± 1.21 | 1.71 |
| Woody plant density | 207 - 1233 | 597 ± 290 | 513 |
| Woody plant PD | 77 - 105 | 95 ± 7 | 96 |
| Woody plant SR | 25 - 69 | 42 ± 10 | 39 |
|  |  |  |  |
| *Trophic guilds* |  |  |  |
| Saproxylic abundance | 34 - 1956 | 564 ± 541 | 481 |
| Saproxylic richness | 14 - 49 | 29 ± 9 | 29 |
| Herbaceous plant abundance | 2 - 1972 | 441 ± 527 | 254 |
| Herbaceous plant richness | 2 - 29 | 7 ± 6 | 6 |
| Herbivore abundance | 15 - 186 | 55 ± 48 | 39 |
| Herbivore richness | 13 - 26 | 17 ± 4 | 17 |
| Predator abundance | 670 - 2341 | 1226 ± 398 | 1146 |
| Predator richness | 64 - 98 | 87 ± 8 | 87 |
| Arbuscular mycorrhiza fungi abundance | 5 - 123 | 37 ± 30 | 33 |
| Arbuscular mycorrhiza fungi richness | 3 - 18 | 9 ± 4 | 9 |
| Ectomycorrhiza fungi abundance | 1128 - 5913 | 3856 ± 1187 | 4238 |
| Ectomycorrhiza fungi richness | 76 - 117 | 98 ± 11 | 98 |
| Pathogenic fungi abundance | 42 - 1006 | 130 ± 179 | 99 |
| Pathogenic fungi richness | 11 - 27 | 20 ± 4 | 20 |
| Saprophytic fungi abundance | 1931 - 4999 | 3308 ± 823 | 3086 |
| Saprophytic fungi richness | 167 - 244 | 209 ± 22 | 205 |

**Table S2** Phylogenetic signal in the traits ‘leaf area’, ‘leaf nitrogen content’, ‘leaf phosphorous content’, ‘maximum tree height’, ‘specific leaf area’ and ‘wood density’ (Böhnke, Kreißig, Kröber, Fang, & Bruelheide, 2012; Kröber, Böhnke, Welk, Wirth, & Bruelheide, 2012). Values of Blomberg’s *K* (Blomberg, Garland, & Ives, 2003) and Pagel’s *λ* (Pagel, 1999) can range from 0 to 1 (calculated with the R-package ‘phytools’, Revell, 2012), with 0 indicating no phylogenetic signal (i.e. phylogenetic flexibility) and 1 indicating perfect phylogenetic conservatism. *P(K)* was obtained by permutating (n=999) the tips of the phylogenetic tree (n=999). *P(λ)* was obtained with likelihood-ratio tests. Significant values of *K* and *λ* indicate that closely related species are functionally more similar than based on a null model of no phylogenetic signal. Results are reproduced from Purschke et al. (2017), to whom we refer for further details.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Trait | Blomberg’s *K* | *P(K)* | Pagel’s *λ* | *P(λ)* |
| Leaf area | 0.902 | 0.001 | 0.991 | 0.001 |
| Leaf nitrogen content | 0.726 | 0.001 | 0.902 | 0.001 |
| Leaf phosphorous content | 0.576 | 0.001 | 0.596 | 0.001 |
| Maximum tree height | 0.460 | 0.005 | 0.479 | 0.001 |
| Specific leaf area | 0.385 | 0.023 | 0.450 | 0.001 |
| Wood density | 0.534 | 0.001 | 0.612 | 0.001 |

**Table S3** Spearman correlation coefficients (*ρ*) for all pairwise comparisons of environmental variables

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | Woody  plant  SR | Woody  plant  PD(p-a) | Woody  plant  PD | Woody  Plant  density | Total  basal  area | Stand  age | Slope | Elevation | Conifer  basal  area | Aspect  North | Aspect  East |
| Aspect East | 0.06 | -0.13 | -0.21 | 0.25 | -0.28 | -0.14 | 0.24 | -0.18 | 0.26 | 0.04 | 1 |
| Aspect North | 0.21 | 0.23 | 0.11 | 0.14 | -0.07 | -0.06 | 0.08 | 0.34 | -0.07 | 1 |  |
| Conifer basal area | -0.31 | -0.38 | -0.53 | 0.46 | -0.53 | -0.42 | -0.21 | 0.04 | 1 |  |  |
| Elevation | 0.04 | 0.01 | -0.27 | 0.13 | 0.22 | 0.22 | 0.06 | 1 |  |  |  |
| Slope | 0.16 | 0.26 | 0.08 | -0.12 | 0.19 | 0.22 | 1 |  |  |  |  |
| Stand age | 0.24 | 0.25 | 0.56 | -0.69 | 0.89 | 1 |  |  |  |  |  |
| Total basal area | 0.13 | 0.24 | 0.52 | -0.75 | 1 |  |  |  |  |  |  |
| Woody plant density | 0.05 | -0.19 | -0.64 | 1 |  |  |  |  |  |  |  |
| Woody plant PD | 0.47 | 0.53 | 1 |  |  |  |  |  |  |  |  |
| Woody plant PD(p-a) | 0.76 | 1 |  |  |  |  |  |  |  |  |  |
| Woody plant SR | 1 |  |  |  |  |  |  |  |  |  |  |

**Table S4** Results of a principal component analysis of standardized (mean = 0, SD = ±1) environmental covariates. Loadings of the first three principal components (PCs) selected for further analyses are given. The most influential variables for each PC (loadings > 0.50) are displayed in bold

|  |  |  |  |
| --- | --- | --- | --- |
| Variable | PC1 | PC2 | PC3 |
| Aspect East | -0.41 | **-0.81** | 0.49 |
| Aspect North | -0.27 | **0.71** | **0.84** |
| Elevation | 0.32 | **1.02** | 0.23 |
| Slope | 0.28 | -0.50 | **1.05** |
| Stand age | **1.28** | -0.01 | 0.15 |
| Total basal area | **1.32** | 0.10 | 0.08 |
| Woody plant density | **-1.14** | 0.40 | 0.21 |
|  |  |  |  |
| Eigenvalue | 2.64 | 1.36 | 1.13 |
| Cumulative proportion explained | 0.38 | 0.57 | 0.74 |

**Table S5** Results (standardized coefficients) of path models for trophic guilds. Significant paths (*P* < 0.05) are in bold. All variables are standardized residuals from *a priori* correlations with the abiotic environment. ΔAICc-values refer to comparisons (ΔAICc = AICc(SR + PD model) – AICc(PD model)) with the respective models that include paths from woody plant SR to abundance and species richness of trophic guilds. RMSEA = Root mean square error of approximation

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Response ~ Predictor | Estimate ± SE | *z* | *P(z)* | *R²* |
| *Saproxylics* | | | | |
| *χ²* = 0.394, *P(χ²)* = 0.821, ΔAICc = 19.2, RMSEA = 0.00 (90% CI = 0.00 - 0.23), *P(RMSEA)* = 0.832 | | | | |
| Covariance (Conifer basal area ~~ Woody plant SR) | -0.298 ± 0.194 | -1.537 | 0.124 |  |
| Woody plant PD |  |  |  | 0.295 |
| Conifer basal area | -0.193 ± 0.170 | -1.135 | 0.256 |  |
| Woody plant SR | **0.452 ± 0.170** | **2.658** | **0.008** |  |
| Abundance |  |  |  | 0.078 |
| Conifer basal area | -0.198 ± 0.196 | -1.009 | 0.313 |  |
| Woody plant PD | 0.143 ± 0.196 | 0.732 | 0.464 |  |
| Species richness |  |  |  | 0.563 |
| Abundance | **0.712 ± 0.132** | **5.377** | **<0.001** |  |
| Conifer basal area | -0.184 ± 0.137 | -1.339 | 0.181 |  |
| Woody plant PD | -0.162 ± 0.136 | -1.192 | 0.233 |  |
|  |  |  |  |  |
| *Herbivores* | | | | |
| *χ²* = 3.886, *P(χ²)* = 0.143, ΔAICc = 15.8, RMSEA = 0.18 (90% CI = 0.00 - 0.47), *P(RMSEA)* = 0.162 | | | | |
| Covariance (Conifer basal area ~~ Woody plant SR) | -0.298 ± 0.194 | -1.537 | 0.124 |  |
| Woody plant PD |  |  |  | 0.295 |
| Conifer basal area | -0.193 ± 0.170 | -1.135 | 0.256 |  |
| Woody plant SR | **0.452 ± 0.170** | **2.658** | **0.008** |  |
| Abundance |  |  |  | 0.425 |
| Conifer basal area | **0.691 ± 0.155** | **4.468** | **<0.001** |  |
| Woody plant PD | 0.203 ± 0.155 | 1.310 | 0.190 |  |
| Species richness |  |  |  | 0.150 |
| Abundance | 0.130 ± 0.234 | 0.554 | 0.580 |  |
| Conifer basal area | -0.086 ± 0.248 | -0.348 | 0.728 |  |
| Woody plant PD | **-0.400 ± 0.194** | **-2.064** | **0.039** |  |
|  |  |  |  |  |
| *Predators* | | | | |
| *χ²* = 0.329, *P(χ²)* = 0.848, ΔAICc = 19.3, RMSEA = 0.00 (90% CI = 0.00 - 0.21), *P(RMSEA)* = 0.857 | | | | |
| Covariance (Conifer basal area ~~ Woody plant SR) | -0.298 ± 0.194 | -1.537 | 0.124 |  |
| Woody plant PD |  |  |  | 0.295 |
| Conifer basal area | -0.193 ± 0.170 | -1.135 | 0.256 |  |
| Woody plant SR | **0.452 ± 0.170** | **2.658** | **0.008** |  |
| Abundance |  |  |  | 0.011 |
| Conifer basal area | -0.079 ± 0.203 | -0.392 | 0.695 |  |
| Woody plant PD | 0.047 ± 0.203 | 0.230 | 0.818 |  |
| Species richness |  |  |  | 0.419 |
| Abundance | **0.487 ± 0.148** | **3.302** | **0.001** |  |
| Conifer basal area | 0.070 ± 0.156 | 0.451 | 0.652 |  |
| Woody plant PD | **0.416 ± 0.156** | **2.672** | **0.008** |  |
|  |  |  |  |  |
| *Herbaceous plants* | | | | |
| *χ²* = 1.347, *P(χ²)* = 0.510, ΔAICc = 18.3, RMSEA = 0.00 (90% CI = 0.00 - 0.34), *P(RMSEA)* = 0.533 | | | | |
| Covariance (Conifer basal area ~~ Woody plant SR) | -0.298 ± 0.194 | -1.537 | 0.124 |  |
| Woody plant PD |  |  |  | 0.295 |
| Conifer basal area | -0.193 ± 0.170 | -1.135 | 0.256 |  |
| Woody plant SR | **0.452 ± 0.170** | **2.658** | **0.008** |  |
| Abundance |  |  |  | 0.293 |
| Conifer basal area | **0.564 ± 0.172** | **3.286** | **0.001** |  |
| Woody plant PD | 0.087 ± 0.172 | 0.508 | 0.611 |  |
| Species richness |  |  |  | 0.343 |
| Abundance | **0.401 ± 0.185** | **2.160** | **0.031** |  |
| Conifer basal area | 0.174 ± 0.196 | 0.889 | 0.374 |  |
| Woody plant PD | -0.197 ± 0.166 | -1.188 | 0.235 |  |
|  |  |  |  |  |
| *Arbuscular mycorrhiza fungi* | | | | |
| *χ²* = 5.114, *P(χ²)* = 0.078, ΔAICc = 14.5, RMSEA = 0.24 (90% CI = 0.00 - 0.51), *P(RMSEA)* = 0.091 | | | | |
| Covariance (Conifer basal area ~~ Woody plant SR) | -0.298 ± 0.194 | -1.537 | 0.124 |  |
| Woody plant PD |  |  |  | 0.295 |
| Conifer basal area | -0.193 ± 0.170 | -1.135 | 0.256 |  |
| Woody plant SR | **0.452 ± 0.170** | **2.658** | **0.008** |  |
| Abundance |  |  |  | 0.033 |
| Conifer basal area | -0.174 ± 0.201 | -0.867 | 0.386 |  |
| Woody plant PD | -0.134 ± 0.201 | -0.668 | 0.504 |  |
| Species richness |  |  |  | 0.672 |
| Abundance | **0.826 ± 0.112** | **7.368** | **<0.001** |  |
| Conifer basal area | 0.032 ± 0.119 | 0.273 | 0.785 |  |
| Woody plant PD | 0.049 ± 0.118 | 0.412 | 0.680 |  |
|  |  |  |  |  |
| *Ectomycorrhiza fungi* | | | | |
| *χ²* = 3.969, *P(χ²)* = 0.137, ΔAICc = 15.7, RMSEA = 0.19 (90% CI = 0.00 - 0.47), *P(RMSEA)* = 0.156 | | | | |
| Covariance (Conifer basal area ~~ Woody plant SR) | -0.298 ± 0.194 | -1.537 | 0.124 |  |
| Woody plant PD |  |  |  | 0.295 |
| Conifer basal area | -0.193 ± 0.170 | -1.135 | 0.256 |  |
| Woody plant SR | **0.452 ± 0.170** | **2.658** | **0.008** |  |
| Abundance |  |  |  | 0.027 |
| Conifer basal area | 0.037 ± 0.201 | 0.185 | 0.853 |  |
| Woody plant PD | 0.172 ± 0.201 | 0.853 | 0.394 |  |
| Species richness |  |  |  | 0.171 |
| Abundance | 0.285 ± 0.178 | 1.607 | 0.108 |  |
| Conifer basal area | -0.177 ± 0.186 | -0.952 | 0.341 |  |
| Woody plant PD | 0.154 ± 0.188 | 0.819 | 0.413 |  |
|  |  |  |  |  |
| *Pathogenic fungi* | | | | |
| *χ²* = 5.044, *P(χ²)* = 0.080, ΔAICc = 14.6, RMSEA = 0.24 (90% CI = 0.00 - 0.51), *P(RMSEA)* = 0.094 | | | | |
| Covariance (Conifer basal area ~~ Woody plant SR) | -0.298 ± 0.194 | -1.537 | 0.124 |  |
| Woody plant PD |  |  |  | 0.295 |
| Conifer basal area | -0.193 ± 0.170 | -1.135 | 0.256 |  |
| Woody plant SR | **0.452 ± 0.170** | **2.658** | **0.008** |  |
| Abundance |  |  |  | 0.019 |
| Conifer basal area | -0.057 ± 0.202 | -0.281 | 0.779 |  |
| Woody plant PD | -0.145 ± 0.202 | -0.718 | 0.473 |  |
| Species richness |  |  |  | 0.101 |
| Abundance | 0.215 ± 0.184 | 1.165 | 0.244 |  |
| Conifer basal area | 0.067 ± 0.194 | 0.348 | 0.728 |  |
| Woody plant PD | 0.281 ± 0.195 | 1.436 | 0.151 |  |
|  |  |  |  |  |
| *Saprophytic fungi* | | | | |
| *χ²* = 2.206, *P(χ²)* = 0.332, ΔAICc = 17.4, RMSEA = 0.06 (90% CI = 0.00 - 0.39), *P(RMSEA)* = 0.356 | | | | |
| Covariance (Conifer basal area ~~ Woody plant SR) | -0.298 ± 0.194 | -1.537 | 0.124 |  |
| Woody plant PD |  |  |  | 0.295 |
| Conifer basal area | -0.193 ± 0.170 | -1.135 | 0.256 |  |
| Woody plant SR | **0.452 ± 0.170** | **2.658** | **0.008** |  |
| Abundance |  |  |  | 0.050 |
| Conifer basal area | 0.048 ± 0.199 | 0.244 | 0.807 |  |
| Woody plant PD | -0.203 ± 0.199 | -1.018 | 0.309 |  |
| Species richness |  |  |  | 0.355 |
| Abundance | **0.607 ± 0.159** | **3.826** | **<0.001** |  |
| Conifer basal area | -0.101 ± 0.164 | -0.617 | 0.537 |  |
| Woody plant PD | 0.075 ± 0.167 | 0.451 | 0.652 |  |

**Table S6** Results (standardized coefficients) of path models in which either woody plant PD or woody plant SR were included. Significant paths (*P* < 0.05) are in bold. ΔAICc-values refer to the comparison between SR and PD model per trophic guild. Path coefficients for PD models were qualitatively and quantitatively similar to models including both plant diversity variables. Note that goodness of fit statistics (RMSEA and Chi-square) cannot be calculated for this fully saturated path models containing all possible path combinations

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Response ~ Predictor | Estimate ± SE | *z* | *P(z)* | *R²* |
| *Saproxylics (~ SR)* AICc = 309.7 | | | | |
| Covariance (Conifer basal area ~~ Woody plant SR) | -0.298 ± 0.194 | -1.537 | 0.124 |  |
| Abundance |  |  |  | 0.087 |
| Conifer basal area | -0.192 ± 0.193 | -0.992 | 0.321 |  |
| Woody plant SR | 0.173 ± 0.193 | 0.893 | 0.372 |  |
| Species richness |  |  |  | 0.546 |
| Abundance | **0.703 ± 0.136** | **5.176** | **<0.001** |  |
| Conifer basal area | -0.156 ± 0.139 | -1.120 | 0.263 |  |
| Woody plant SR | -0.076 ± 0.138 | -0.547 | 0.585 |  |
|  |  |  |  |  |
| *Saproxylics (~ PD)* AICc = 307.4 |  |  |  |  |
| Covariance (Conifer basal area ~~ Woody plant PD) | -0.320 ± 0.195 | -1.640 | 0.101 |  |
| Abundance |  |  |  | 0.078 |
| Conifer basal area | -0.198 ± 0.196 | -1.009 | 0.313 |  |
| Woody plant PD | 0.143 ± 0.196 | 0.732 | 0.464 |  |
| Species richness |  |  |  | 0.563 |
| Abundance | **0.712 ± 0.132** | **5.377** | **<0.001** |  |
| Conifer basal area | -0.184 ± 0.137 | -1.339 | 0.181 |  |
| Woody plant PD | -0.162 ± 0.136 | -1.192 | 0.233 |  |
| ΔAICc(SR model – PD model) = 2.3 | | | | |
|  |  |  |  |  |
| *Herbivores (~ SR)* AICc = 318.6 |  |  |  |  |
| Covariance (Conifer basal area ~~ Woody plant SR) | -0.298 ± 0.194 | -1.537 | 0.124 |  |
| Abundance |  |  |  | 0.409 |
| Conifer basal area | **0.577 ± 0.156** | **3.711** | **<0.001** |  |
| Woody plant SR | -0.150 ± 0.156 | -0.963 | 0.336 |  |
| Species richness |  |  |  | 0.023 |
| Abundance | -0.007 ± 0.248 | -0.029 | 0.977 |  |
| Conifer basal area | 0.106 ± 0.246 | 0.431 | 0.666 |  |
| Woody plant SR | -0.084 ± 0.204 | -0.414 | 0.679 |  |
|  |  |  |  |  |
| *Herbivores (~ PD)* AICc = 313.6 |  |  |  |  |
| Covariance (Conifer basal area ~~ Woody plant PD) | -0.320 ± 0.195 | -1.640 | 0.101 |  |
| Abundance |  |  |  | 0.425 |
| Conifer basal area | **0.691 ± 0.155** | **4.468** | **<0.001** |  |
| Woody plant PD | 0.203 ± 0.155 | 1.310 | 0.190 |  |
| Species richness |  |  |  | 0.150 |
| Abundance | 0.130 ± 0.234 | 0.554 | 0.580 |  |
| Conifer basal area | -0.086 ± 0.248 | -0.348 | 0.728 |  |
| Woody plant PD | **-0.400 ± 0.194** | **-2.064** | **0.039** |  |
| ΔAICc(SR model – PD model) = 5.0 | | | | |
|  |  |  |  |  |
| *Predators (~ SR)* AICc = 323.4 |  |  |  |  |
| Covariance (Conifer basal area ~~ Woody plant SR) | -0.298 ± 0.194 | -1.537 | 0.124 |  |
| Abundance |  |  |  | 0.015 |
| Conifer basal area | -0.120 ± 0.201 | -0.598 | 0.550 |  |
| Woody plant SR | -0.081 ± 0.201 | -0.405 | 0.686 |  |
| Species richness |  |  |  | 0.299 |
| Abundance | **0.519 ± 0.162** | **3.197** | **0.001** |  |
| Conifer basal area | -0.005 ± 0.171 | -0.028 | 0.978 |  |
| Woody plant SR | 0.195 ± 0.170 | 1.146 | 0.252 |  |
|  |  |  |  |  |
| *Predators (~ PD)* AICc = 318.0 |  |  |  |  |
| Covariance (Conifer basal area ~~ Woody plant PD) | -0.320 ± 0.195 | -1.640 | 0.101 |  |
| Abundance |  |  |  | 0.011 |
| Conifer basal area | -0.079 ± 0.203 | -0.392 | 0.695 |  |
| Woody plant PD | 0.047 ± 0.203 | 0.230 | 0.818 |  |
| Species richness |  |  |  | 0.419 |
| Abundance | **0.487 ± 0.148** | **3.302** | **0.001** |  |
| Conifer basal area | 0.070 ± 0.156 | 0.451 | 0.652 |  |
| Woody plant PD | **0.416 ± 0.156** | **2.672** | **0.008** |  |
| ΔAICc(SR model – PD model) = 5.4 | | | | |
|  |  |  |  |  |
| *Herbaceous plants (~ SR)* AICc = 315.1 |  |  |  |  |
| Covariance (Conifer basal area ~~ Woody plant SR) | -0.298 ± 0.194 | -1.537 | 0.124 |  |
| Abundance |  |  |  | 0.288 |
| Conifer basal area | **0.522 ± 0.171** | **3.054** | **0.002** |  |
| Woody plant SR | -0.043 ± 0.171 | -0.249 | 0.803 |  |
| Species richness |  |  |  | 0.312 |
| Abundance | **0.382 ± 0.189** | **2.021** | **0.043** |  |
| Conifer basal area | 0.267 ± 0.195 | 1.372 | 0.170 |  |
| Woody plant SR | 0.058 ± 0.168 | 0.343 | 0.732 |  |
|  |  |  |  |  |
| *Herbaceous plants (~ PD)* AICc = 312.2 | -0.320 ± 0.195 | -1.640 | 0.101 |  |
| Covariance (Conifer basal area ~~ Woody plant PD) |  |  |  |  |
| Abundance |  |  |  | 0.293 |
| Conifer basal area | **0.564 ± 0.172** | **3.286** | **0.001** |  |
| Woody plant PD | 0.087 ± 0.172 | 0.508 | 0.611 |  |
| Species richness |  |  |  | 0.343 |
| Abundance | **0.401 ± 0.185** | **2.160** | **0.031** |  |
| Conifer basal area | 0.174 ± 0.196 | 0.889 | 0.374 |  |
| Woody plant PD | -0.197 ± 0.166 | -1.188 | 0.235 |  |
| ΔAICc(SR model – PD model) = 2.9 | | | | |
|  |  |  |  |  |
| *Arbuscular mycorrhiza fungi (~ SR)* AICc = 301.2 |  |  |  |  |
| Covariance (Conifer basal area ~~ Woody plant SR) | -0.298 ± 0.194 | -1.537 | 0.124 |  |
| Abundance |  |  |  | 0.108 |
| Conifer basal area | -0.031 ± 0.191 | -0.163 | 0.871 |  |
| Woody plant SR | 0.317 ± 0.191 | 1.658 | 0.097 |  |
| Species richness |  |  |  | 0.673 |
| Abundance | **0.801 ± 0.116** | **6.878** | **<0.001** |  |
| Conifer basal area | 0.033 ± 0.116 | 0.287 | 0.774 |  |
| Woody plant SR | 0.066 ± 0.121 | 0.541 | 0.589 |  |
|  |  |  |  |  |
| *Arbuscular mycorrhiza fungi (~ PD)* AICc = 302.0 |  |  |  |  |
| Covariance (Conifer basal area ~~ Woody plant PD) | -0.320 ± 0.195 | -1.640 | 0.101 |  |
| Abundance |  |  |  | 0.033 |
| Conifer basal area | -0.174 ± 0.201 | -0.867 | 0.386 |  |
| Woody plant PD | -0.134 ± 0.201 | -0.668 | 0.504 |  |
| Species richness |  |  |  | 0.672 |
| Abundance | **0.826 ± 0.112** | **7.368** | **<0.001** |  |
| Conifer basal area | 0.032 ± 0.119 | 0.273 | 0.785 |  |
| Woody plant PD | 0.049 ± 0.118 | 0.412 | 0.680 |  |
| ΔAICc(SR model – PD model) = -0.8 | | | | |
|  |  |  |  |  |
| *Ectomycorrhiza fungi (~ SR)* AICc = 324.7 |  |  |  |  |
| Covariance (Conifer basal area ~~ Woody plant SR) | -0.298 ± 0.194 | -1.537 | 0.124 |  |
| Abundance |  |  |  | 0.113 |
| Conifer basal area | 0.090 ± 0.191 | 0.470 | 0.638 |  |
| Woody plant SR | 0.354 ± 0.191 | 1.855 | 0.064 |  |
| Species richness |  |  |  | 0.212 |
| Abundance | 0.220 ± 0.181 | 1.212 | 0.225 |  |
| Conifer basal area | -0.143 ± 0.180 | -0.795 | 0.427 |  |
| Woody plant SR | 0.279 ± 0.191 | 1.461 | 0.144 |  |
|  |  |  |  |  |
| *Ectomycorrhiza fungi (~ PD)* AICc = 327.2 |  |  |  |  |
| Covariance (Conifer basal area ~~ Woody plant PD) | -0.320 ± 0.195 | -1.640 | 0.101 |  |
| Abundance |  |  |  | 0.027 |
| Conifer basal area | 0.037 ± 0.201 | 0.185 | 0.853 |  |
| Woody plant PD | 0.172 ± 0.201 | 0.853 | 0.394 |  |
| Species richness |  |  |  | 0.171 |
| Abundance | 0.285 ± 0.178 | 1.607 | 0.108 |  |
| Conifer basal area | -0.177 ± 0.186 | -0.952 | 0.341 |  |
| Woody plant PD | 0.154 ± 0.188 | 0.819 | 0.413 |  |
| ΔAICc(SR model – PD model) = -2.5 | | | | |
|  |  |  |  |  |
| *Pathogenic fungi (~ SR)* AICc = 327.9 |  |  |  |  |
| Covariance (Conifer basal area ~~ Woody plant SR) | -0.298 ± 0.194 | -1.537 | 0.124 |  |
| Abundance |  |  |  | 0.067 |
| Conifer basal area | 0.076 ± 0.195 | 0.389 | 0.697 |  |
| Woody plant SR | 0.273 ± 0.195 | 1.395 | 0.163 |  |
| Species richness |  |  |  | 0.125 |
| Abundance | 0.097 ± 0.186 | 0.520 | 0.603 |  |
| Conifer basal area | 0.075 ± 0.190 | 0.398 | 0.691 |  |
| Woody plant SR | 0.331 ± 0.196 | 1.686 | 0.092 |  |
|  |  |  |  |  |
| *Pathogenic fungi (~ PD)* AICc = 328.6 | -0.320 ± 0.195 | -1.640 | 0.101 |  |
| Covariance (Conifer basal area ~~ Woody plant PD) |  |  |  |  |
| Abundance |  |  |  | 0.019 |
| Conifer basal area | -0.057 ± 0.202 | -0.281 | 0.779 |  |
| Woody plant PD | -0.145 ± 0.202 | -0.718 | 0.473 |  |
| Species richness |  |  |  | 0.101 |
| Abundance | 0.215 ± 0.184 | 1.165 | 0.244 |  |
| Conifer basal area | 0.067 ± 0.194 | 0.348 | 0.728 |  |
| Woody plant PD | 0.281 ± 0.195 | 1.436 | 0.151 |  |
| ΔAICc(SR model – PD model) = -0.7 | | | | |
|  |  |  |  |  |
| *Saprophytic fungi (~ SR)* AICc = 318.1 |  |  |  |  |
| Covariance (Conifer basal area ~~ Woody plant SR) | -0.298 ± 0.194 | -1.537 | 0.124 |  |
| Abundance |  |  |  | 0.106 |
| Conifer basal area | 0.017 ± 0.191 | 0.086 | 0.931 |  |
| Woody plant SR | -0.321 ± 0.191 | -1.677 | 0.094 |  |
| Species richness |  |  |  | 0.365 |
| Abundance | **0.633 ± 0.162** | **3.901** | **<0.001** |  |
| Conifer basal area | -0.087 ± 0.161 | -0.542 | 0.588 |  |
| Woody plant SR | 0.136 ± 0.169 | 0.800 | 0.424 |  |
|  |  |  |  |  |
| *Saprophytic fungi (~ PD)* AICc = 319.4 |  |  |  |  |
| Covariance (Conifer basal area ~~ Woody plant PD) | -0.320 ± 0.195 | -1.640 | 0.101 |  |
| Abundance |  |  |  | 0.050 |
| Conifer basal area | 0.048 ± 0.199 | 0.244 | 0.807 |  |
| Woody plant PD | -0.203 ± 0.199 | -1.018 | 0.309 |  |
| Species richness |  |  |  | 0.355 |
| Abundance | **0.607 ± 0.159** | **3.826** | **<0.001** |  |
| Conifer basal area | -0.101 ± 0.164 | -0.617 | 0.537 |  |
| Woody plant PD | 0.075 ± 0.167 | 0.451 | 0.652 |  |
| ΔAICc(SR model – PD model) = -1.3 | | | | |

**Table S7** Results (standardized coefficients) of path models for trophic guilds using raw instead of residual conifer basal area, woody plant PD and woody plant SR. Significant paths (*P* < 0.05) are in bold. ΔAICc-values refer to comparisons with the respective models (ΔAICc = AICc(SR + PD model) – AICc(PD model)) that include paths from woody plant SR to abundance and species richness of trophic guilds. RMSEA = Root mean square error of approximation

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Response ~ Predictor | Estimate ± SE | *z* | *P(z)* | *R²* |
| *Saproxylics* | | | | |
| *χ²* = 0.577, *P(χ²)* = 0.750, ΔAICc = 19.1, RMSEA = 0.00 (90% CI = 0.00 - 0.26), *P(RMSEA)* = 0.764 | | | | |
| Covariance (Conifer basal area ~~ Woody plant SR) | -0.309 ± 0.195 | -1.587 | 0.113 |  |
| Woody plant PD |  |  |  | 0.359 |
| Conifer basal area | **-0.376 ± 0.163** | **-2.312** | **0.021** |  |
| Woody plant SR | **0.361 ± 0.163** | **2.221** | **0.026** |  |
| Abundance |  |  |  | 0.053 |
| Conifer basal area | -0.162 ± 0.215 | -0.752 | 0.452 |  |
| Woody plant PD | 0.103 ± 0.215 | 0.479 | 0.632 |  |
| Species richness |  |  |  | 0.563 |
| Abundance | **0.714 ± 0.131** | **5.465** | **<0.001** |  |
| Conifer basal area | -0.205 ± 0.148 | -1.390 | 0.164 |  |
| Woody plant PD | -0.190 ± 0.147 | -1.292 | 0.196 |  |
|  |  |  |  |  |
| *Herbivores* | | | | |
| *χ²* = 4.062, *P(χ²)* = 0.131, ΔAICc = 15.6, RMSEA = 0.20 (90% CI = 0.00 - 0.47), *P(RMSEA)* = 0.149 | | | | |
| Covariance (Conifer basal area ~~ Woody plant SR) | -0.309 ± 0.195 | -1.587 | 0.113 |  |
| Woody plant PD |  |  |  | 0.359 |
| Conifer basal area | **-0.376 ± 0.163** | **-2.312** | **0.021** |  |
| Woody plant SR | **0.361 ± 0.163** | **2.221** | **0.026** |  |
| Abundance |  |  |  | 0.369 |
| Conifer basal area | **0.697 ± 0.176** | **3.967** | **<0.001** |  |
| Woody plant PD | 0.319 ± 0.176 | 1.816 | 0.069 |  |
| Species richness |  |  |  | 0.131 |
| Abundance | 0.181 ± 0.226 | 0.801 | 0.423 |  |
| Conifer basal area | -0.193 ± 0.259 | -0.743 | 0.457 |  |
| Woody plant PD | **-0.418 ± 0.218** | **-1.953** | **0.049** |  |
|  |  |  |  |  |
| *Predators* | | | | |
| *χ²* = 0.302, *P(χ²)* = 0.860, ΔAICc = 19.3, RMSEA = 0.00 (90% CI = 0.00 - 0.20), *P(RMSEA)* = 0.868 | | | | |
| Covariance (Conifer basal area ~~ Woody plant SR) | -0.309 ± 0.195 | -1.587 | 0.113 |  |
| Woody plant PD |  |  |  | 0.359 |
| Conifer basal area | **-0.376 ± 0.163** | **-2.312** | **0.021** |  |
| Woody plant SR | **0.361 ± 0.163** | **2.221** | **0.026** |  |
| Abundance |  |  |  | 0.007 |
| Conifer basal area | -0.067 ± 0.220 | -0.305 | 0.761 |  |
| Woody plant PD | 0.031 ± 0.220 | 0.140 | 0.889 |  |
| Species richness |  |  |  | 0.394 |
| Abundance | **0.496 ± 0.150** | **3.300** | **0.001** |  |
| Conifer basal area | 0.145 ± 0.172 | 0.842 | 0.400 |  |
| Woody plant PD | **0.413 ± 0.172** | **2.401** | **0.016** |  |
|  |  |  |  |  |
| *Herbaceous plants* | | | | |
| *χ²* = 1.131, *P(χ²)* = 0.568, ΔAICc = 18.5, RMSEA = 0.00 (90% CI = 0.00 - 0.32), *P(RMSEA)* = 0.589 | | | | |
| Covariance (Conifer basal area ~~ Woody plant SR) | -0.309 ± 0.195 | -1.587 | 0.113 |  |
| Woody plant PD |  |  |  | 0.359 |
| Conifer basal area | **-0.376 ± 0.163** | **-2.312** | **0.021** |  |
| Woody plant SR | **0.361 ± 0.163** | **2.221** | **0.026** |  |
| Abundance |  |  |  | 0.240 |
| Conifer basal area | **0.554 ± 0.193** | **2.875** | **0.004** |  |
| Woody plant PD | 0.185 ± 0.193 | 0.960 | 0.337 |  |
| Species richness |  |  |  | 0.315 |
| Abundance | **0.452 ± 0.183** | **2.475** | **0.013** |  |
| Conifer basal area | 0.101 ± 0.209 | 0.481 | 0.631 |  |
| Woody plant PD | -0.169 ± 0.186 | **-0.907** | **0.364** |  |
|  |  |  |  |  |
| *Arbuscular mycorrhiza fungi* | | | | |
| *χ²* = 4.532, *P(χ²)* = 0.104, ΔAICc = 15.1, RMSEA = 0.22 (90% CI = 0.00 - 0.49), *P(RMSEA)* = 0.120 | | | | |
| Covariance (Conifer basal area ~~ Woody plant SR) | -0.309 ± 0.195 | -1.587 | 0.113 |  |
| Woody plant PD |  |  |  | 0.359 |
| Conifer basal area | **-0.376 ± 0.163** | **-2.312** | **0.021** |  |
| Woody plant SR | **0.361 ± 0.163** | **2.221** | **0.026** |  |
| Abundance |  |  |  | 0.032 |
| Conifer basal area | -0.191 ± 0.217 | -0.878 | 0.380 |  |
| Woody plant PD | -0.160 ± 0.217 | -0.738 | 0.461 |  |
| Species richness |  |  |  | 0.672 |
| Abundance | **0.826 ± 0.112** | **7.371** | **<0.001** |  |
| Conifer basal area | 0.040 ± 0.128 | 0.310 | 0.756 |  |
| Woody plant PD | 0.053 ± 0.128 | 0.412 | 0.681 |  |
|  |  |  |  |  |
| *Ectomycorrhiza fungi* | | | | |
| *χ²* = 4.118, *P(χ²)* = 0.128, ΔAICc = 15.5, RMSEA = 0.20 (90% CI = 0.00 - 0.47), *P(RMSEA)* = 0.145 | | | | |
| Covariance (Conifer basal area ~~ Woody plant SR) | -0.309 ± 0.195 | -1.587 | 0.113 |  |
| Woody plant PD |  |  |  | 0.359 |
| Conifer basal area | **-0.376 ± 0.163** | **-2.312** | **0.021** |  |
| Woody plant SR | **0.361 ± 0.163** | **2.221** | **0.026** |  |
| Abundance |  |  |  | 0.023 |
| Conifer basal area | 0.068 ± 0.219 | 0.309 | 0.757 |  |
| Woody plant PD | 0.172 ± 0.219 | 0.789 | 0.430 |  |
| Species richness |  |  |  | 0.147 |
| Abundance | 0.295 ± 0.180 | 1.641 | 0.101 |  |
| Conifer basal area | -0.141 ± 0.205 | -0.688 | 0.492 |  |
| Woody plant PD | 0.116 ± 0.206 | 0.559 | 0.576 |  |
|  |  |  |  |  |
| *Pathogenic fungi* | | | | |
| *χ²* = 4.490, *P(χ²)* = 0.106, ΔAICc = 15.2, RMSEA = 0.22 (90% CI = 0.00 - 0.49), *P(RMSEA)* = 0.122 | | | | |
| Covariance (Conifer basal area ~~ Woody plant SR) | -0.309 ± 0.195 | -1.587 | 0.113 |  |
| Woody plant PD |  |  |  | 0.359 |
| Conifer basal area | **-0.376 ± 0.163** | **-2.312** | **0.021** |  |
| Woody plant SR | **0.361 ± 0.163** | **2.221** | **0.026** |  |
| Abundance |  |  |  | 0.017 |
| Conifer basal area | -0.081 ± 0.219 | -0.370 | 0.711 |  |
| Woody plant PD | -0.150 ± 0.219 | -0.685 | 0.493 |  |
| Species richness |  |  |  | 0.092 |
| Abundance | 0.211 ± 0.185 | 1.138 | 0.255 |  |
| Conifer basal area | 0.116 ± 0.211 | 0.551 | 0.582 |  |
| Woody plant PD | 0.282 ± 0.212 | 1.327 | 0.184 |  |
|  |  |  |  |  |
| *Saprophytic fungi* | | | | |
| *χ²* = 2.418, *P(χ²)* = 0.299, ΔAICc = 17.2, RMSEA = 0.09 (90% CI = 0.00 - 0.40), *P(RMSEA)* = 0.323 | | | | |
| Covariance (Conifer basal area ~~ Woody plant SR) | -0.309 ± 0.195 | -1.587 | 0.113 |  |
| Woody plant PD |  |  |  | 0.359 |
| Conifer basal area | **-0.376 ± 0.163** | **-2.312** | **0.021** |  |
| Woody plant SR | **0.361 ± 0.163** | **2.221** | **0.026** |  |
| Abundance |  |  |  | 0.036 |
| Conifer basal area | 0.008 ± 0.217 | 0.039 | 0.969 |  |
| Woody plant PD | -0.187 ± 0.217 | -0.860 | 0.390 |  |
| Species richness |  |  |  | 0.348 |
| Abundance | **0.597 ± 0.158** | **3.770** | **<0.001** |  |
| Conifer basal area | -0.082 ± 0.178 | -0.462 | 0.644 |  |
| Woody plant PD | 0.053 ± 0.181 | 0.292 | 0.771 |  |

**Table S8** Correlation coefficients, explained variance (*R²*), and probabilities *P* (based on n = 10000 permutations) for the relationship between the environmental PCs and plant diversity variables and the plot-based axes scores of 2-dimensional NMDS ordinations based on Bray-Curtis dissimilarity. PC-axes represent the abiotic environment (PC1: stand age, total basal area, woody plant density; PC2: aspect eastness, aspect northness, elevation; PC3: aspect northness, slope; see Table S4 for details). Significant *P*-values (at *P* < 0.05) are in bold. Increasing the number of dimensions in the ordination reduces stress but does not affect the configuration of the first two NMDS axes (procrustes rotation with 10,000 permutations, *R²* > 0.81, *P* < 0.001 in all cases)

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Variable | NMDS 1 | NMDS 2 | *R²* | *P* |
| *Saproxylics* (stress = 0.203) |  |  |  |  |
| PC1 | **0.714** | **0.701** | **0.659** | **<0.001** |
| PC2 | 0.902 | -0.432 | 0.089 | 0.323 |
| PC3 | **-0.704** | **0.710** | **0.263** | **0.025** |
| Conifer basal area | **0.283** | **0.959** | **0.215** | **0.048** |
| Woody plant SR | -0.617 | -0.781 | 0.101 | 0.275 |
| Woody plant PD | **0.080** | **-0.997** | **0.246** | **0.029** |
|  |  |  |  |  |
| *Herbivores* (stress = 0.245) |  |  |  |  |
| PC1 | -0.826 | 0.564 | 0.141 | 0.163 |
| PC2 | -0.288 | -0.958 | 0.209 | 0.065 |
| PC3 | 0.133 | 0.991 | 0.039 | 0.624 |
| Conifer basal area | **-0.380** | **0.925** | **0.442** | **0.001** |
| Woody plant SR | -0.318 | -0.948 | 0.186 | 0.083 |
| Woody plant PD | **-0.420** | **-0.908** | **0.380** | **0.004** |
|  |  |  |  |  |
| *Predators* (stress = 0.176) |  |  |  |  |
| PC1 | **-0.876** | **-0.482** | **0.546** | **<0.001** |
| PC2 | **-0.467** | **0.884** | **0.358** | **0.005** |
| PC3 | 0.560 | -0.829 | 0.083 | 0.350 |
| Conifer basal area | **-0.458** | **-0.889** | **0.507** | **<0.001** |
| Woody plant SR | 0.379 | 0.926 | 0.123 | 0.207 |
| Woody plant PD | **0.005** | **1.000** | **0.423** | **0.002** |
|  |  |  |  |  |
| *Herbaceous plants* (stress = 0.207) |  |  |  |  |
| PC1 | **-0.210** | **0.978** | **0.435** | **0.001** |
| PC2 | **-0.924** | **-0.383** | **0.329** | **0.008** |
| PC3 | 0.998 | -0.060 | 0.017 | 0.809 |
| Conifer basal area | **-0.188** | **0.982** | **0.640** | **<0.001** |
| Woody plant SR | **0.172** | **-0.985** | **0.222** | **0.048** |
| Woody plant PD | **-0.137** | **-0.991** | **0.487** | **<0.001** |
|  |  |  |  |  |
| *Arbuscular mycorrhiza fungi* (stress = 0.265) |  |  |  |  |
| PC1 | -0.422 | 0.906 | 0.163 | 0.117 |
| PC2 | 0.436 | -0.900 | 0.016 | 0.819 |
| PC3 | -0.153 | 0.988 | 0.091 | 0.320 |
| Conifer basal area | **-0.414** | **0.910** | **0.266** | **0.025** |
| Woody plant SR | 0.530 | -0.848 | 0.070 | 0.423 |
| Woody plant PD | **0.093** | **-0.996** | **0.473** | **<0.001** |
|  |  |  |  |  |
| *Ectomycorrhiza fungi* (stress = 0.216) |  |  |  |  |
| PC1 | **0.527** | **-0.850** | **0.655** | **<0.001** |
| PC2 | 0.999 | -0.032 | 0.046 | 0.570 |
| PC3 | **-0.970** | **-0.242** | **0.246** | **0.036** |
| Conifer basal area | **0.079** | **-0.997** | **0.383** | **0.003** |
| Woody plant SR | -0.996 | 0.093 | 0.082 | 0.358 |
| Woody plant PD | **0.268** | **0.963** | **0.231** | **0.042** |
|  |  |  |  |  |
| *Pathogenic fungi* (stress = 0.257) |  |  |  |  |
| PC1 | **-0.428** | **0.904** | **0.235** | **0.043** |
| PC2 | 0.559 | 0.829 | 0.183 | 0.087 |
| PC3 | -0.730 | -0.684 | 0.114 | 0.237 |
| Conifer basal area | -0.804 | 0.594 | 0.181 | 0.092 |
| Woody plant SR | -0.039 | -0.999 | 0.110 | 0.246 |
| Woody plant PD | **0.951** | **-0.309** | **0.232** | **0.042** |
|  |  |  |  |  |
| *Saprophytic fungi* (stress = 0.178) |  |  |  |  |
| PC1 | **0.287** | **0.958** | **0.612** | **<0.001** |
| PC2 | 0.964 | -0.266 | 0.106 | 0.253 |
| PC3 | -0.997 | -0.082 | 0.201 | 0.069 |
| Conifer basal area | **-0.089** | **0.996** | **0.357** | **0.005** |
| Woody plant SR | -0.759 | -0.651 | 0.153 | 0.140 |
| Woody plant PD | 0.476 | -0.880 | 0.205 | 0.065 |

**Table S9** Results (standardized coefficients) of path models for trophic guilds in which presence-absence PD (Woody plant PD(p-a)) instead of abundance-weighted PD was used. Significant paths (*P* < 0.05) are in bold. All variables are standardized residuals from *a priori* correlations with the abiotic environment. RMSEA = Root mean square error of approximation

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Response ~ Predictor | Estimate ± SE | *z* | *P(z)* | *R²* |
| *Saproxylics* | | | | |
| *χ²* = 1.258, *P(χ²)* = 0.533, RMSEA = 0.00 (90% CI = 0.00 - 0.33), *P(RMSEA)* = 0.555 | | | | |
| Covariance (Conifer basal area ~~ Woody plant SR) | -0.298 ± 0.194 | -1.537 | 0.124 |  |
| Woody plant PD(p-a) |  |  |  | 0.522 |
| Conifer basal area | **-0.380 ± 0.140** | **-2.714** | **0.007** |  |
| Woody plant SR | **0.508 ± 0.140** | **3.627** | **<0.001** |  |
| Abundance |  |  |  | 0.064 |
| Conifer basal area | -0.205 ± 0.221 | -0.930 | 0.352 |  |
| Woody plant PD(p-a) | 0.075 ± 0.221 | 0.338 | 0.735 |  |
| Species richness |  |  |  | 0.541 |
| Abundance | **0.689 ± 0.135** | **5.113** | **<0.001** |  |
| Conifer basal area | -0.127 ± 0.157 | -0.809 | 0.419 |  |
| Woody plant PD(p-a) | 0.016 ± 0.155 | 0.102 | 0.919 |  |
|  |  |  |  |  |
| *Herbivores* | | | | |
| *χ²* = 0.218, *P(χ²)* = 0.897, RMSEA = 0.00 (90% CI = 0.00 - 0.17), *P(RMSEA)* = 0.903 | | | | |
| Covariance (Conifer basal area ~~ Woody plant SR) | -0.298 ± 0.194 | -1.537 | 0.124 |  |
| Woody plant PD(p-a) |  |  |  | 0.522 |
| Conifer basal area | **-0.380 ± 0.140** | **-2.714** | **0.007** |  |
| Woody plant SR | **0.508 ± 0.140** | **3.627** | **<0.001** |  |
| Abundance |  |  |  | 0.412 |
| Conifer basal area | **0.526 ± 0.175** | **3.008** | **0.003** |  |
| Woody plant PD(p-a) | -0.182 ± 0.175 | -1.038 | 0.299 |  |
| Species richness |  |  |  | 0.028 |
| Abundance | -0.016 ± 0.247 | -0.067 | 0.947 |  |
| Conifer basal area | 0.067 ± 0.260 | 0.257 | 0.797 |  |
| Woody plant PD(p-a) | -0.133 ± 0.229 | -0.578 | 0.563 |  |
|  |  |  |  |  |
| *Predators* | | | | |
| *χ²* = 0.375, *P(χ²)* = 0.829, RMSEA = 0.00 (90% CI = 0.00 - 0.22), *P(RMSEA)* = 0.839 | | | | |
| Covariance (Conifer basal area ~~ Woody plant SR) | -0.298 ± 0.194 | -1.537 | 0.124 |  |
| Woody plant PD(p-a) |  |  |  | 0.522 |
| Conifer basal area | **-0.380 ± 0.140** | **-2.714** | **0.007** |  |
| Woody plant SR | **0.508 ± 0.140** | **3.627** | **<0.001** |  |
| Abundance |  |  |  | 0.009 |
| Conifer basal area | -0.083 ± 0.227 | -0.364 | 0.716 |  |
| Woody plant PD(p-a) | 0.023 ± 0.227 | 0.101 | 0.920 |  |
| Species richness |  |  |  | 0.337 |
| Abundance | **0.499 ± 0.157** | **3.171** | **0.002** |  |
| Conifer basal area | 0.104 ± 0.186 | 0.557 | 0.577 |  |
| Woody plant PD(p-a) | 0.318 ± 0.186 | 1.710 | 0.087 |  |
|  |  |  |  |  |
| *Herbaceous plants* | | | | |
| *χ²* = 0.937, *P(χ²)* = 0.626, RMSEA = 0.00 (90% CI = 0.00 - 0.31), *P(RMSEA)* = 0.645 | | | | |
| Covariance (Conifer basal area ~~ Woody plant SR) | -0.298 ± 0.194 | -1.537 | 0.124 |  |
| Woody plant PD(p-a) |  |  |  | 0.522 |
| Conifer basal area | **-0.380 ± 0.140** | **-2.714** | **0.007** |  |
| Woody plant SR | **0.508 ± 0.140** | **3.627** | **<0.001** |  |
| Abundance |  |  |  | 0.325 |
| Conifer basal area | **0.409 ± 0.187** | **2.181** | **0.029** |  |
| Woody plant PD | -0.235 ± 0.187 | -1.253 | 0.210 |  |
| Species richness |  |  |  | 0.378 |
| Abundance | 0.454 ± 0.185 | **2.457** | **0.014** |  |
| Conifer basal area | 0.383 ± 0.195 | 1.962 | 0.050 |  |
| Woody plant PD | 0.320 ± 0.185 | 1.729 | 0.084 |  |
|  |  |  |  |  |
| *Arbuscular mycorrhiza fungi* | | | | |
| *χ²* = 2.338, *P(χ²)* = 0.311, RMSEA = 0.79 (90% CI = 0.00 - 0.40), *P(RMSEA)* = 0.335 | | | | |
| Covariance (Conifer basal area ~~ Woody plant SR) | -0.298 ± 0.194 | -1.537 | 0.124 |  |
| Woody plant PD(p-a) |  |  |  | 0.522 |
| Conifer basal area | **-0.380 ± 0.140** | **-2.714** | **0.007** |  |
| Woody plant SR | **0.508 ± 0.140** | **3.627** | **<0.001** |  |
| Abundance |  |  |  | 0.035 |
| Conifer basal area | -0.043 ± 0.224 | -0.191 | 0.849 |  |
| Woody plant PD(p-a) | 0.161 ± 0.224 | 0.719 | 0.472 |  |
| Species richness |  |  |  | 0.699 |
| Abundance | **0.796 ± 0.108** | **7.405** | **<0.001** |  |
| Conifer basal area | 0.122 ± 0.125 | 0.971 | 0.331 |  |
| Woody plant PD(p-a) | 0.204 ± 0.126 | 1.611 | 0.107 |  |
|  |  |  |  |  |
| *Ectomycorrhiza fungi* | | | | |
| *χ²* = 1.374, *P(χ²)* = 0.503, RMSEA = 0.00 (90% CI = 0.00 - 0.34), *P(RMSEA)* = 0.526 | | | | |
| Covariance (Conifer basal area ~~ Woody plant SR) | -0.298 ± 0.194 | -1.537 | 0.124 |  |
| Woody plant PD(p-a) |  |  |  | 0.522 |
| Conifer basal area | **-0.380 ± 0.140** | **-2.714** | **0.007** |  |
| Woody plant SR | **0.508 ± 0.140** | **3.627** | **<0.001** |  |
| Abundance |  |  |  | 0.165 |
| Conifer basal area | 0.238 ± 0.209 | 1.143 | 0.253 |  |
| Woody plant PD(p-a) | **0.481 ± 0.209** | **2.305** | **0.021** |  |
| Species richness |  |  |  | 0.201 |
| Abundance | 0.209 ± 0.188 | 1.111 | 0.267 |  |
| Conifer basal area | -0.073 ± 0.209 | -0.350 | 0.726 |  |
| Woody plant PD(p-a) | 0.292 ± 0.223 | 1.308 | 0.191 |  |
|  |  |  |  |  |
| *Pathogenic fungi* | | | | |
| *χ²* = 9.300, *P(χ²)* = 0.010, RMSEA = 0.37 (90% CI = 0.15 - 0.620), *P(RMSEA)* = 0.013 | | | | |
| Covariance (Conifer basal area ~~ Woody plant SR) | -0.298 ± 0.194 | -1.537 | 0.124 |  |
| Woody plant PD(p-a) |  |  |  | 0.522 |
| Conifer basal area | **-0.380 ± 0.140** | **-2.714** | **0.007** |  |
| Woody plant SR | **0.508 ± 0.140** | **3.627** | **<0.001** |  |
| Abundance |  |  |  | 0.048 |
| Conifer basal area | -0.148 ± 0.223 | -0.663 | 0.508 |  |
| Woody plant PD(p-a) | -0.259 ± 0.223 | -1.163 | 0.245 |  |
| Species richness |  |  |  | 0.055 |
| Abundance | 0.212 ± 0.192 | 1.106 | 0.269 |  |
| Conifer basal area | 0.072 ± 0.224 | 0.322 | 0.748 |  |
| Woody plant PD(p-a) | 0.182 ± 0.227 | 0.801 | 0.423 |  |
|  |  |  |  |  |
| *Saprophytic fungi* | | | | |
| *χ²* = 1.260, *P(χ²)* = 0.533, RMSEA = 0.00 (90% CI = 0.00 - 0.33), *P(RMSEA)* = 0.555 | | | | |
| Covariance (Conifer basal area ~~ Woody plant SR) | -0.298 ± 0.194 | -1.537 | 0.124 |  |
| Woody plant PD(p-a) |  |  |  | 0.522 |
| Conifer basal area | **-0.380 ± 0.140** | **-2.714** | **0.007** |  |
| Woody plant SR | **0.508 ± 0.140** | **3.627** | **<0.001** |  |
| Abundance |  |  |  | 0.071 |
| Conifer basal area | -0.036 ± 0.220 | -0.165 | 0.869 |  |
| Woody plant PD(p-a) | -0.283 ± 0.220 | -1.288 | 0.198 |  |
| Species richness |  |  |  | 0.412 |
| Abundance | **0.655 ± 0.153** | **4.280** | **<0.001** |  |
| Conifer basal area | 0.032 ± 0.175 | 0.180 | 0.857 |  |
| Woody plant PD(p-a) | 0.304 ± 0.180 | 1.689 | 0.091 |  |

**Table S10** Correlation coefficients, explained variance (*R²*), and probabilities *P* (based on n = 10000 permutations) for the relationship between woody plant PD quantified as presence-absence based PD and the plot-based axes scores of 2-dimensional NMDS ordinations (identical to displays in Figure 3 and Table S8) based on Bray-Curtis dissimilarity. Correlation results for environmental PCs, conifer basal area and woody plant SR are equivalent to Table S8. Significant *P*-values (at *P* < 0.05) are in bold.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Trophic group | NMDS 1 | NMDS 2 | *R²* | *P* |
| Saproxylics | -0.800 | -0.607 | 0.044 | 0.582 |
| Herbivores | 0.115 | -0.993 | 0.173 | 0.099 |
| Predators | 0.334 | 0.943 | 0.111 | 0.240 |
| Herbaceous plants | **-0.093** | **-0.996** | **0.328** | **0.005** |
| Arbuscular mycorrhiza fungi | 0.182 | -0.983 | 0.082 | 0.362 |
| Ectomycorrhiza fungi | -0.796 | 0.605 | 0.071 | 0.423 |
| Pathogenic fungi | 0.235 | -0.972 | 0.084 | 0.348 |
| Saprophytic fungi | -0.669 | -0.743 | 0.114 | 0.236 |



**Figure S1** Woody plant PD is positively correlated with woody plant SR (Spearman’s *ρ* = 0.47). In our study plots, woody plant PD (quantified as abundance weighted Rao’s Q) increases when a community contains more woody species. This indicates that (see also Fig. 2) woody plant SR likely influences associated organisms via woody plant PD, even though Rao’s Q is not always mathematically related to wood plant SR



**Figure S2** Evolutionary distinct woody plants do not cluster in high PD plots. a) Occurrence (i.e. the number of plots a woody plant species is present in) is independent of a species evolutionary distinctness (Spearman’s *ρ* = -0.11). b) NMDS ordination (2-dimensional, stress=0.16) of woody plant species composition. Dots illustrate species scores and are scaled by evolutionary distinctness (range: 17.35 – 125.84). Contour lines delineate PD values per plot. Species scores are not related to species-specific evolutionary distinctness (*ρ*(NMDS1) = 0.04, *ρ*(NMDS2) = -0.01), indicating that high PD plots are not the outcome of co-occurring distinct species. Evolutionary distinctness was calculated with the R-package ‘picante’ (Kembel et al., 2010) following the approach of Redding and Mooers (2006)



**Figure S3** Path diagrams for a) arbuscular mycorrhiza (*χ²* = 5.114, *P* = 0.078, ΔAICc = 14.5), b) ectomycorrhiza (*χ²* = 3.397, *P* = 0.137, ΔAICc = 15.7), c) pathogenic fungi (*χ²* = 5.044, *P* = 0.0.80, ΔAICc = 14.6), and d) saprophytic fungi (*χ²* = 2.206, *P* = 0.332, ΔAICc = 17.4) illustrating direct and indirect relationships between woody plant SR, woody plant PD, conifer basal area and the abundance and species richness per trophic guild. All variables are standardized residuals from *a priori* correlations with the abiotic environment. ΔAICc-values (ΔAICc = AICc(SR + PD model) – AICc(PD model)) refer to comparisons with the respective models that include paths from woody plant SR to abundance and species richness. Numbers next to arrows give standardized path coefficients. Positive and negative relationships are, respectively, indicated by black and red arrows. Covariance is indicated by a curved double arrow. Significant relationships are \*\*\**P* < 0.001 and \**P* < 0.05 and indicated with full arrows. See Table S5 for statistical details



**Figure S4** Density plot of phylogenetic dispersion calculated with the ‘ses.mpd’ function in ‘picante’ (10,000 iterations, nullmodel ‘independentswap’). Values of observed and null PD broadly overlap. For each study plot, the observed PD value is not statistically different from PD obtained from a null community. Standardized effect sizes of PD vs. null communities range between -1.13 and 1.02 (mean = 0.34 ± 0.48 SD, median = 0.33). None of the corresponding p-values (range: 0.13 – 0.94, mean = 0.60 ± 0.23 SD, median = 0.59) are within the upper or lower 5% quantile. This suggests random phylogenetic community assembly as neither phylogenetic clustering nor phylogenetic overdispersion occurred