Oikos

OIK-04879

Pietsch, K. A., Eichenberg, D., Nadrowski, K., Bauhus, J., Buscot, F., Purahong, W., Wipfler, B., Wubet, T., Yu, M. and Wirth, C. 2018. Wood decomposition is more strongly controlled by temperature than by tree species and decomposer diversity in highly species rich subtropical forests. – Oikos doi: 10.1111/oik.04879

Appendix 1

Supplementary material to material and methods

Detailed description of fungal community composition analysis

For the analysis of fungal community composition we used wood samples harvested at the end of the experiment in 2012. For each species-by-treatment combination we analysed one out of four samples per plot. The samples used for this analysis have been frozen immediately after the harvest. For the analysis they were ground to fine powder. From this we extracted DNA using a ZR Soil Microbe DNA MiniPrep Kit (Zymo Research, Irvine, CA, USA) according to the manufacturer's protocol. We then checked the presence and quantity of genomic DNA using a NanoDrop ND-1000 spectrophotometer (Thermo Fisher Scientific, Dreieich, Germany). DNA extracts were then stored at –20°C for further analysis. We amplified fungal amplicon libraries for pyrosequencing using custom fusion primers.

We used 454 pyrotag sequencing for the analysis of the fungal community composition. We filtered for good quality sequences and used them for further analyses. Good quality sequences were characterised by holding one of the expected barcodes with at most one mismatch, a minimum length of 360 nt, a minimum average Phred score of 20, containing homopolymers with a maximum length of 15 nt and without ambiguous nucleotides. The quality-filtered reads were shortened to their first 360 bases and normalized to the smallest read per sample (3077). Potential chimeras were removed using UCHIME (Edgar et al. 2011) as implemented in MOTHUR. Unique sequences were sorted by decreasing abundances and were clustered into Operational Taxonomic Units (OTUs) using CD-HIT-EST (Fu et al. 2012) at a threshold of 97% pairwise similarity. Fungal ITS OTU representative sequences were first classified against the dynamic version of the UNITE fungal ITS sequence database (ver. 6, released 15.01.2014; Kõljalg et al. 2013). The sequences with fungi only identified were further classified against the full version of the UNITE database to improve their taxonomic annotation. Rare OTUs (singletons to tripletons) were removed from the dataset, as they could potentially originate from artificial sequencing errors (Kunin et al. 2010). Thus we used the abundant OTUs (OTUs with > 3 reads) for further statistical analysis. To assess the role of the omitted rare OTUs, a Mantel test based on a Bray–Curtis distance measure with 999 permutations was applied to both the full matrix and the one excluding the rare OTUs (Hammer et al. 2001, Hoppe et al. 2016, Purahong et al. 2017). The result indicated that the removal of rare OTUs from the fungal communities had no effect on community composition (RMantel = 0.999, p = 0.001). The raw sequence datasets are available in the European Nucleotide Archive under the study number PRJEB89781. Fungal biome OTU table, OTU representative sequences and the bioinformatics scripts are available at Dryad (<https://datadryad.org/resource/doi:10.5061/dryad.54qr4>).

Our bioinformatics analysis includes procedures to eliminate biases and errors for richness estimation. These procedures include, 1) the quality-filtering (only good quality sequences are further analysed), 2) the normalization (i.e. all samples were normalized to the smallest read per sample), 3) the removal of potential chimeras and 4) the removal of rare OTUs (i.e. singletons to tripletons; removing all sequences potentially originating from artificial sequencing errors). With the high number of sequencing reads per samples (3077), the sample-based rarefaction curves indicated a saturation of fungal richness at the analysed sequencing depth for most samples (Fig xx). This indicates that the observed OTU richness is a suitable measure for fungal diversity. We calculated fungal richness from high quality datasets with the normalization step to reduce the biases in richness estimates due to variation in the number of sequence reads per sample. An in-depth description of the methods that were used to extract DNA and determine the fungal community composition in our dead wood samples is given in Purahong et al. (2017).

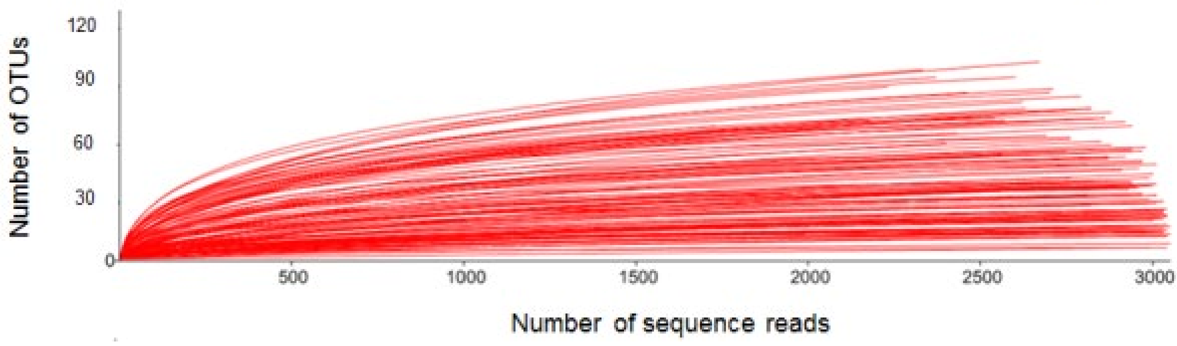

Figure A1. Individual rarefaction curves of wood-inhabiting fungi detected in each deadwood sample. The curves show a saturation of fungal richness at the analysed sequencing depth

Detailed description of invertebrate rearing

The chambers which we used to rear invertebrates were constructed of commercially available plastic boxes (~40 × 35 × 35 cm) with a lid. At the bottom in the middle close to one of the short sides we drilled a hole with 10 cm diameter to attach a funnel with a 100 ml plastic collection bottle. The bottle was filled with 50 ml of a glycol–water solution (1:1) as preservative. At the top of both short sides of the boxes we drilled three ventilation holes of 2 cm diameter. The holes were covered with a fine mesh to prevent invertebrates from escaping. During the rearing period, the microclimate should be similar to conditions in the forest. However we deliberately refrained from placing the emergence chambers directly in the forest because we could not insure their safety. Instead, the chambers were placed in a well ventilated barn room close to the study area in the forest. We used data loggers to constantly measure the temperature and humidity in the room and in randomly selected emergence chambers. Climatic conditions in the room were similar to the forest climate. Inside the chambers the humidity decreased slightly during the rearing. The chambers were installed for one year following each of the two wood retrievals. Reared invertebrates were collected from the catch bottles monthly and transferred to a solution of ethanol, acetic acid and water (7:1:2). The preservative solution was exchanged as required.

References

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Appendix 2 Species list of reared invertebrates from decomposed dead wood samples

Class	Subclass/Order	Super-/Sub-/Family	Genus/Species	Occurance on Tree Species
Chelicerata	Acari		morpho species 05	*P. massoniana / S. superba*
Chelicerata	Araneae	Hahniidae	cf. Hahnia sp.	*S. superba*
Chelicerata	Araneae	Linyphiidae	Erigone cf. prominens	*P. massoniana*
Chelicerata	Araneae	Linyphiidae	morpho species 42	*S. superba*
Chelicerata	Araneae	Salticidae	cf. Plexippus sp.	*P. massoniana / S. superba*
Chelicerata	Araneae	Salticidae	morpho species 43	*P. massoniana*
Chelicerata	Araneae	Titanoecidae	morpho species 44	*S. superba*
Chelicerata	Araneae		morpho species 40	*P. massoniana / S. superba*
Chelicerata	Araneae		morpho species 41	*S. superba*
Chelicerata	Opiliones	cf. Phalangiidae	morpho species 45	*P. massoniana*
Chelicerata	Opiliones	cf. Phalangodidae	morpho species 46	*P. massoniana*
Chelicerata	Pseudoscorpiones	Atemnidae	morpho species 48	*P. massoniana*
Chelicerata	Pseudoscorpiones		morpho species 47	*P. massoniana*
Crustacea	Isopoda	Armadillidae	morpho species 49	*P. massoniana*
Crustacea	Isopoda	cf. Philosciidae	morpho species 06	*P. massoniana*
Insecta	Blattodea	Blattellidae	morpho species 07	*P. massoniana / S. superba*
Insecta	Blattodea	cf. Blattidae	morpho species 50	*P. massoniana*
Insecta	Coleoptera	Cantharidae/Cantharinae	cf. Rhagonycha sp.	*S. superba*
Insecta	Coleoptera	Carabidae/cf. Harpalinae	morpho species 08	*P. massoniana / S. superba*
Insecta	Coleoptera	Carabidae/Harpalinae/Pterostichini	morpho species 51	*S. superba*
Insecta	Coleoptera	Cerambycidae/Lamiinae	cf. Acalolepta sp.	*P. massoniana*
Insecta	Coleoptera	Cerambycidae/Lamiinae	morpho species 52	*S. superba*
Insecta	Coleoptera	cf. Tenebrionidae	morpho species 09	*S. superba*
Insecta	Coleoptera	cf. Trogossitidae/Carinotinae	morpho species 53	*P. massoniana*
Insecta	Coleoptera	Cleridae/Clerinae	Opilo sp.	*P. massoniana*
Insecta	Coleoptera	Corylophidae/Sericoderinae	cf. Sericoderus lateralis	*P. massoniana / S. superba*
Insecta	Coleoptera	Cryptophagidae	Henoticus sp.	*P. massoniana*
Insecta	Coleoptera	Curculionidae/Curculioninae	morpho species 10	*P. massoniana*
Insecta	Coleoptera	Curculionidae/Dryophthorinae	morpho species 11	*P. massoniana*
Insecta	Coleoptera	Curculionidae/Dryophthorinae	Sitophilus zeamais	*P. massoniana / S. superba*
Insecta	Coleoptera	Curculionidae/Scolytinae	morpho species 12	*P. massoniana*
Insecta	Coleoptera	Curculionidae/Scolytinae	morpho species 13	*P. massoniana*
Insecta	Coleoptera	Curculionidae/Scolytinae	Xyleborus species 1	*S. superba*
Insecta	Coleoptera	Elateridae/Agrypninae	morpho species 14	*S. superba*
Insecta	Coleoptera	Elateridae/Elaterinae/Ampedini	morpho species 15	*P. massoniana / S. superba*
Insecta	Coleoptera	Elateridae/Elaterinae/Melanotini	cf. Melanotus sp.	*P. massoniana*
Insecta	Coleoptera	Elateridae/Elaterinae/Physorhinini	morpho species 54	*P. massoniana*
Insecta	Coleoptera	Monotomidae	cf. Mimemodes sp.	*P. massoniana / S. superba*
Insecta	Coleoptera	Monotomidae	morpho species 16	*P. massoniana*
Insecta	Coleoptera	Ptiliidae	morpho species 55	*P. massoniana*
Insecta	Coleoptera	Scarabaeidae/Scarabaeinae	Haroldius cf. hwangi	*S. superba*
Insecta	Coleoptera	Scarabaeidae/Valginae	cf. Dasyvalgus sp.	*P. massoniana*
Insecta	Coleoptera	Scarabaeidae/Valginae	Hybovalgus sp.	*P. massoniana*
Insecta	Coleoptera	Silvanidae/Silvaninae	Silvanus lewisi	*S. superba*
Insecta	Coleoptera	Staphylinidae/Aleocharinae	morpho species 17	*P. massoniana*
Insecta	Coleoptera	Staphylinidae/Aleocharinae/ Callicerini	cf. Atheta Species 1	*P. massoniana*
Insecta	Coleoptera	Staphylinidae/Aleocharinae/cf. Homalotini	morpho species 56	*P. massoniana*
Insecta	Coleoptera	Staphylinidae/Aleocharinae/ Trichopseniini	morpho species 57	*P. massoniana*
Insecta	Coleoptera	Staphylinidae/cf. Aleocharinae	morpho species 58	*P. massoniana*
Insecta	Coleoptera	Staphylinidae/Euaesthetinae	cf. Edaphus species 1	*P. massoniana*
Insecta	Coleoptera	Staphylinidae/Pselaphinae	morpho species 18	*P. massoniana / S. superba*
Insecta	Coleoptera	Staphylinidae/Pselaphinae	morpho species 19	*P. massoniana*
Insecta	Coleoptera	Staphylinidae/Pselaphinae	morpho species 20	*P. massoniana*
Insecta	Coleoptera	Staphylinidae/Pselaphinae	morpho species 21	*P. massoniana*
Insecta	Coleoptera	Staphylinidae/Pselaphinae	morpho species 22	*S. superba*
Insecta	Coleoptera	Staphylinidae/Pselaphinae	morpho species 23	*S. superba*
Insecta	Coleoptera	Staphylinidae/Pselaphinae	morpho species 24	*P. massoniana*
Insecta	Coleoptera	Staphylinidae/Pselaphinae	morpho species 25	*S. superba*
Insecta	Coleoptera	Staphylinidae/Scydmaeninae	cf. Cephennodes	*P. massoniana*
Insecta	Coleoptera	Staphylinidae/Scydmaeninae	morpho species 26	*P. massoniana*
Insecta	Coleoptera	Staphylinidae/Scydmaeninae	morpho species 27	*P. massoniana*
Insecta	Coleoptera	Staphylinidae/Scydmaeninae	morpho species 28	*P. massoniana*
Insecta	Coleoptera	Tenebrionidae/Lagriinae	Laena cf. cooteri	*P. massoniana*
Insecta	Coleoptera	Tenebrionidae/Stenochiinae	morpho species 29	*P. massoniana*
Insecta	Coleoptera	Tenebrionidae/Stenochiinae	morpho species 30	*S. superba*
Insecta	Coleoptera	Tenebrionidae/Tenebrioninae	Uloma cf. polita	*P. massoniana*

Class	Subclass/Order	Super-/Sub-/Family	Genus/Species	Occurance on Tree Species
Insecta	Collembola		morpho species 59	*P. massoniana / S. superba*
Insecta	Diplura		morpho species 60	*P. massoniana*
Insecta	Diptera	"Nematocera"	morpho species 61	*P. massoniana / S. superba*
Insecta	Diptera	Brachycera	morpho species 62	*P. massoniana / S. superba*
Insecta	Diptera	Cecidomyiidae	aptere species	*P. massoniana*
Insecta	Diptera	Cecidomyiidae	morpho species 63	*P. massoniana / S. superba*
Insecta	Diptera	Ceratopogonidae	morpho species 64	*S. superba*
Insecta	Diptera	cf. Cecidomyiidae	morpho species 65	*P. massoniana*
Insecta	Diptera	cf. Diadociidae	cf. Diadocidia sinica	*P. massoniana*
Insecta	Diptera	cf. Drosophilidae	morpho species 66	*S. superba*
Insecta	Diptera	cf. Milichiidae	morpho species 67	*P. massoniana*
Insecta	Diptera	cf. Sciaridae	morpho species 68	*S. superba*
Insecta	Diptera	cf. Syrphidae	morpho species 69	*P. massoniana*
Insecta	Diptera	Phoridae	cf. Borophaga	*P. massoniana*
Insecta	Diptera	Phoridae	cf. Megaselia	*P. massoniana / S. superba*
Insecta	Diptera	Phoridae	morpho species 70	*P. massoniana / S. superba*
Insecta	Diptera	Psychodidae	morpho species 71	*P. massoniana*
Insecta	Diptera	Sciaridae	morpho species 72	*P. massoniana / S. superba*
Insecta	Heteroptera	Anthocoridae/Lyctocorinae	morpho species 73	*S. superba*
Insecta	Heteroptera	Coreidae/Coreinae	Hygia cf. opaca	*P. massoniana*
Insecta	Heteroptera	Pentatomidae/Pentatominae	Halyomorpha halys	*S. superba*
Insecta	Heteroptera	Pentatomidae/Pentatominae	Plaudia cf. crossota	*P. massoniana*
Insecta	Heteroptera	Reduviidae	morpho species 74	*S. superba*
Insecta	Homoptera/Aphidina		morpho species 75	*P. massoniana*
Insecta	Hymenoptera	cf. Apocrita	morpho species 76	*P. massoniana*
Insecta	Hymenoptera	Chalcidoidea/Chalcididae/ Chalcidinae	Brachymeria sp.	*P. massoniana*
Insecta	Hymenoptera	Chalcidoidea/Encyrtidae	morpho species 77	*P. massoniana*
Insecta	Hymenoptera	Cynipoidea/Eucoilidae	morpho species 78	*P. massoniana*
Insecta	Hymenoptera	Vespoidea/Formicidae/ Dolichoderinae	Tapinoma sp.	*P. massoniana / S. superba*
Insecta	Hymenoptera	Vespoidea/Formicidae/Formicinae	Camponotus cf. vitiosus	*P. massoniana*
Insecta	Hymenoptera	Vespoidea/Formicidae/Formicinae	Camponotus species 1	*P. massoniana*
Insecta	Hymenoptera	Vespoidea/Formicidae/Formicinae	Camponotus species 2	*P. massoniana*
Insecta	Hymenoptera	Vespoidea/Formicidae/Formicinae	morpho species 79	*S. superba*
Insecta	Hymenoptera	Vespoidea/Formicidae/Formicinae	Nylanderia sp.	*P. massoniana / S. superba*
Insecta	Hymenoptera	Vespoidea/Formicidae/Formicinae	Paratrechina longicornis	*P. massoniana*
Insecta	Hymenoptera	Vespoidea/Formicidae/Formicinae	Polyrhachis illaudata	*P. massoniana / S. superba*
Insecta	Hymenoptera	Vespoidea/Formicidae/Formicinae	Polyrhachis shixingensis	*P. massoniana*
Insecta	Hymenoptera	Vespoidea/Formicidae/Myrmicinae	Carebara sp.	*P. massoniana*
Insecta	Hymenoptera	Vespoidea/Formicidae/Myrmicinae	cf. Carebara sp.	*P. massoniana*
Insecta	Hymenoptera	Vespoidea/Formicidae/Myrmicinae	cf. Pheidole sp.	*P. massoniana / S. superba*
Insecta	Hymenoptera	Vespoidea/Formicidae/Myrmicinae	Crematogaster sp.	*P. massoniana / S. superba*
Insecta	Hymenoptera	Vespoidea/Formicidae/Myrmicinae	Monomorium sp.	*P. massoniana*
Insecta	Hymenoptera	Vespoidea/Formicidae/Myrmicinae	Strumigenys lewisi	*P. massoniana / S. superba*
Insecta	Hymenoptera	Vespoidea/Formicidae/Myrmicinae	Temnothorax (Leptothorax) cf. zhejiangensis	*P. massoniana*
Insecta	Hymenoptera	Vespoidea/Formicidae/Myrmicinae	Tetramorium cf. bicarinatum	*P. massoniana / S. superba*
Insecta	Hymenoptera	Vespoidea/Formicidae/Myrmicinae	Vollenhovia emeryi	*P. massoniana*
Insecta	Hymenoptera	Vespoidea/Formicidae/Ponerinae	cf. Ponera sp.	*P. massoniana / S. superba*
Insecta	Hymenoptera	Vespoidea/Formicidae/Ponerinae	Cryptopone sp.	*P. massoniana*
Insecta	Hymenoptera	Vespoidea/Formicidae/Ponerinae	Pachycondyla cf. luteipes	*P. massoniana / S. superba*
Insecta	Hymenoptera	Vespoidea/Vespidae/Vespinae	Vespa velutina	*S. superba*
Insecta	Isoptera	Rhinotermitidae/Heterotermitinae	Reticulitermes sp.	*P. massoniana / S. superba*
Insecta	Isoptera	Termitidae/cf. Macrotermitinae	cf. Macrotermes sp.	*P. massoniana / S. superba*
Insecta	Isoptera	Termitidae/cf. Nasutitermitinae	cf. Nasutitermes sp.	*P. massoniana*
Insecta	Lepidoptera	cf. Psychidae	morpho species 81	*P. massoniana / S. superba*
Insecta	Lepidoptera		morpho species 80	*P. massoniana / S. superba*
Insecta	Neuroptera	Berothidae/Berothinae	morpho species 82	*P. massoniana*
Insecta	Orthoptera/Ensifera	Grylloidea/Myrmecophilidae	Myrmecophilus cf. formosana	*P. massoniana*
Insecta	Psocoptera	cf. Liposcelididae	morpho species 84	*P. massoniana / S. superba*
Insecta	Psocoptera	cf. Peripsocidae	morpho species 31	*P. massoniana / S. superba*
Insecta	Psocoptera	cf. Psyllipsocidae	morpho species 85	*P. massoniana*
Insecta	Psocoptera	Hemipsocidae	(Meta-)Hemipsocus sp.	*S. superba*
Insecta	Psocoptera	Liposcelididae	Embidopsocus sp.	*S. superba*
Insecta	Psocoptera	Pachytroctidae	Tapinella sp.	*P. massoniana*
Insecta	Psocoptera		morpho species 83	*P. massoniana / S. superba*
Insecta	Thysanoptera	Phlaeothripidae	morpho species 32	*P. massoniana*
Insecta	Thysanoptera	Thripidae	morpho species 33	*P. massoniana*

Class	Subclass/Order	Super-/Sub-/Family	Genus/Species	Occurance on Tree Species
Insecta	Thysanoptera	Thripidae	morpho species 34	*P. massoniana*
Myriapoda	Chilopoda	Geophilomorpha/cf. Geophilidae	morpho species 35	*P. massoniana*
Myriapoda	Chilopoda	Geophilomorpha/cf. Geophilidae	morpho species 36	*P. massoniana*
Myriapoda	Chilopoda	Geophilomorpha/ cf. Mecistocephalidae	cf. Nodocephalus (Arrup) edentulus	*P. massoniana*
Myriapoda	Chilopoda	Geophilomorpha/ cf. Mecistocephalidae	cf. Nodocephalus (Arrup) species 1	*P. massoniana*
Myriapoda	Chilopoda	Geophilomorpha/ cf. Mecistocephalidae	cf. Nodocephalus species 2	*P. massoniana*
Myriapoda	Chilopoda	Geophilomorpha/Mecistocephalidae	cf. Mecistocephalus sp.	*P. massoniana / S. superba*
Myriapoda	Chilopoda	Lithobiomorpha/cf. Lithobiidae	morpho species 01	*P. massoniana / S. superba*
Myriapoda	Chilopoda	Lithobiomorpha/cf. Lithobiidae	morpho species 02	*P. massoniana / S. superba*
Myriapoda	Chilopoda	Lithobiomorpha/cf. Lithobiidae	morpho species 03	*P. massoniana / S. superba*
Myriapoda	Chilopoda	Lithobiomorpha/cf. Lithobiidae	morpho species 04	*P. massoniana*
Myriapoda	Chilopoda	Scolopendromorpha/ Scolopocryptopidae	Scolopocryptops sp.	*S. superba*
Myriapoda	Diplopoda	cf. Polydesmida	morpho species 38	*P. massoniana*
Myriapoda	Diplopoda	cf. Polydesmida	morpho species 39	*P. massoniana / S. superba*
Myriapoda	Diplopoda	Cryptodesmidae	cf. Trichopeltis sp.	*P. massoniana / S. superba*
Myriapoda	Diplopoda	Paradoxosomaidae	Oxidus gracilis	*P. massoniana / S. superba*
Myriapoda	Diplopoda		morpho species 37	*P. massoniana*
Myriapoda	Diplopoda		morpho species 86	*P. massoniana*
Myriapoda	Pauropoda	cf. Pauropodidae	morpho species 87	*P. massoniana*
Myriapoda	Pauropoda	Eurypauropodidae	morpho species 88	*P. massoniana*
Myriapoda	Symphyla	cf. Scolopendrellidae	morpho species 89	*P. massoniana / S. superba*

Appendix 3

Supporting figures and tables

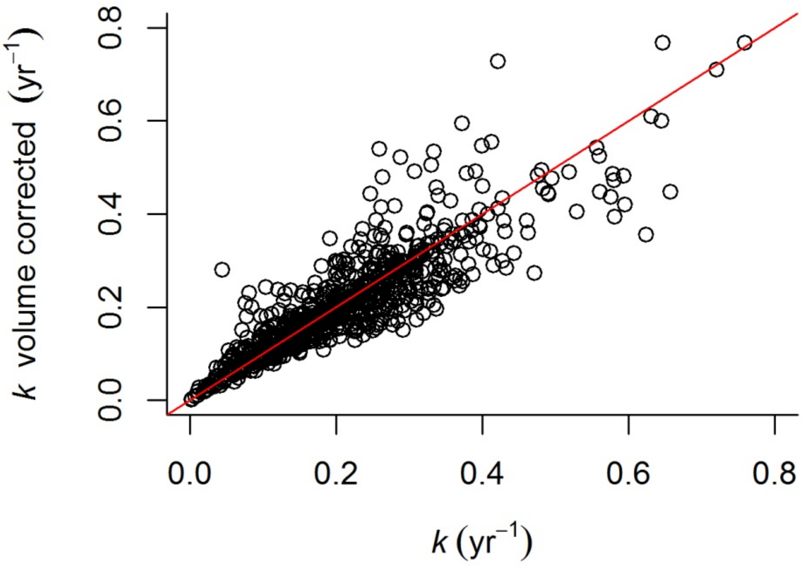


Figure A2. Observed versus volume corrected *k* rates ($r^2 = 0.77$, $p < 0.001$). Red line = 1:1 line.

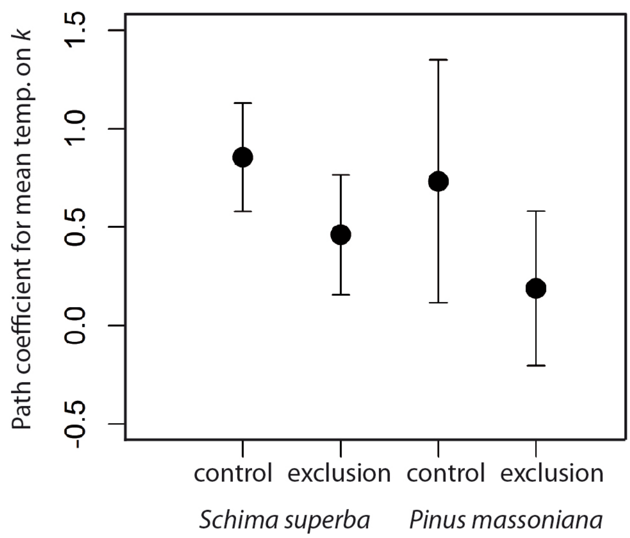


Figure A3. Standardized path coefficients between mean temperature and wood decay rate *k* of the four species by treatment combinations. Error bars represent 95% confidence intervals. Confidence intervals overlap, indicating that path coefficients are not significantly different from each other among species and treatments.

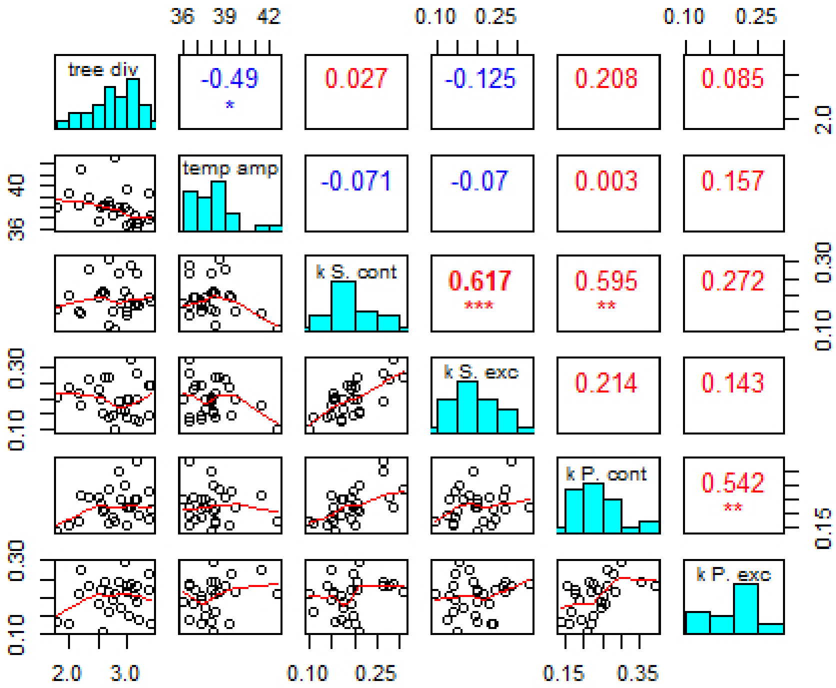
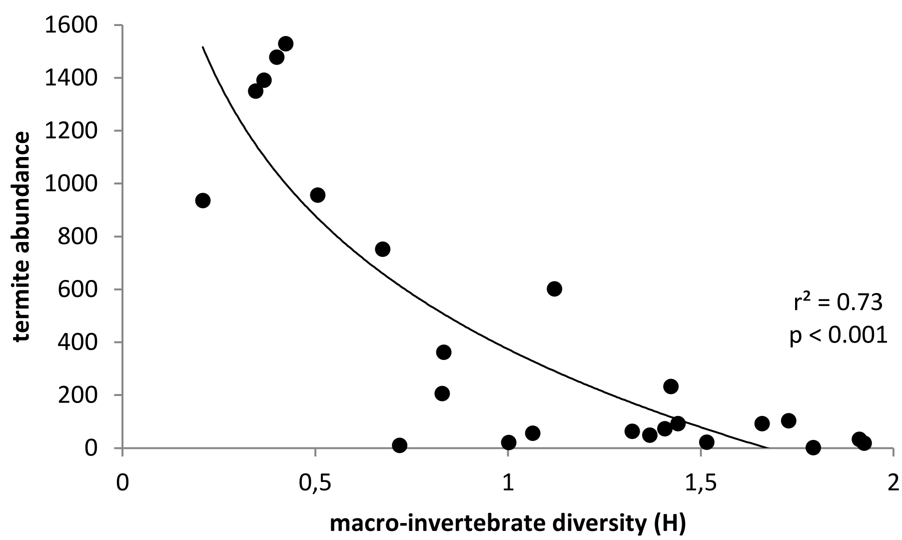


Figure A4. Correlation matrix plots for the relationships between tree species diversity (tree div), temperature amplitude (temp amp) and the four decomposition rates (*Schima superba* control = k S. cont, *Schima superba* exclusion = k S. exc, *Pinus massoniana* control = k P. cont, *Pinus massoniana* exclusion = k P. exc). Tree species diversity is inversely correlated to temperature amplitude, but there is no relationship between temperature amplitude and any of the four decomposition rates. Numbers represent spearman rank correlations. Blue = negative relationship, red = positive relationship. Stars denote significance levels, p < 0.001 = ***, p < 0.01 = **, p < 0.05 = *.

(a)



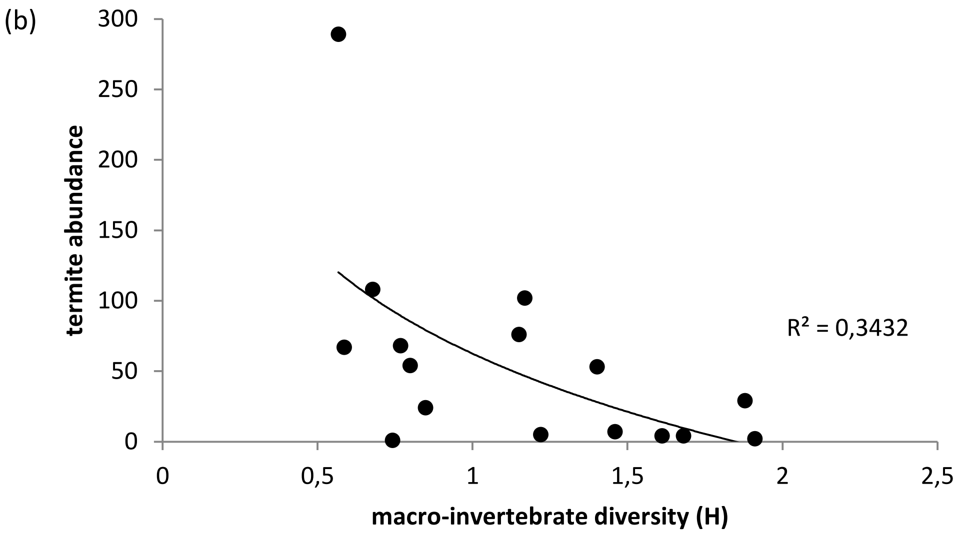


Figure A5. Log-linear relationship between macro-invertebrate diversity and termite abundance in *P. massoniana* samples (a) and *S. superba* samples (b). Termite abundance decreases with increasing macro-invertebrate diversity.

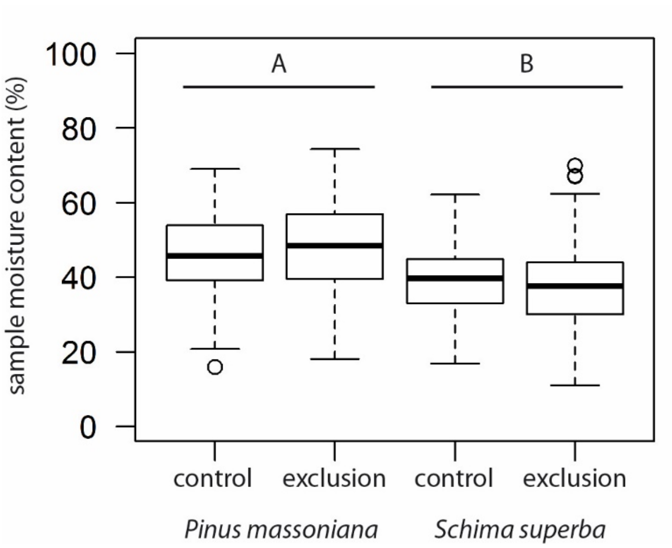


Figure A6. Variation of moisture content of decomposed samples between species and treatments across all 27 study plots. Letters represent significant differences between the two species. We detected no treatment effect on moisture contents in either of the species.

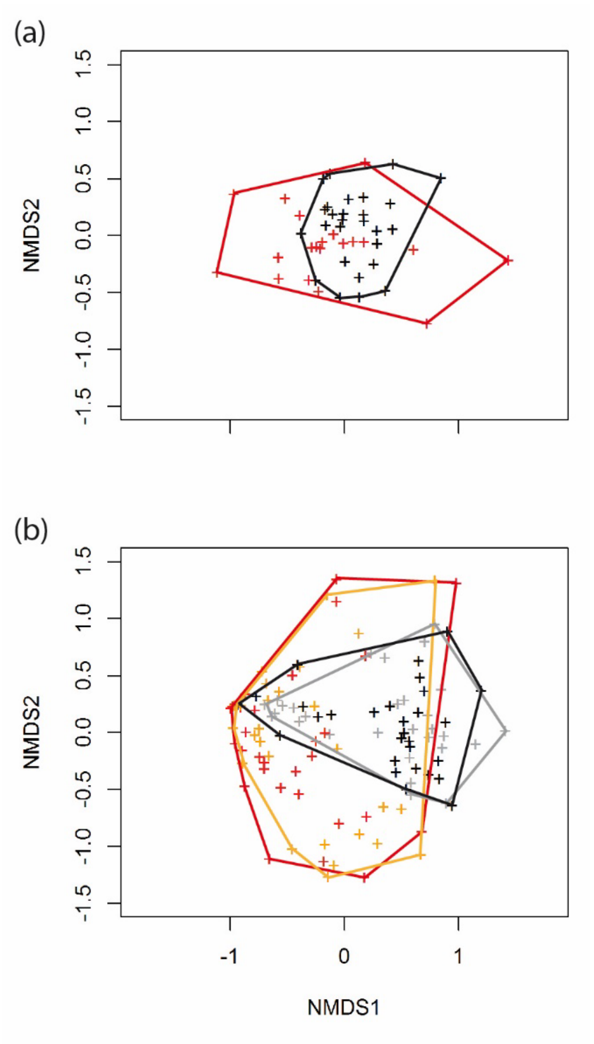


Figure A7. Nonmetric multidimensional scaling (NMDS) ordination of (a) macro-invertebrate community composition in *S. superba* (red) and *P. massoniana* (black) samples of the control treatments across all plots, and (b) fungal community composition in *S. superba* control treatment (red), *S. superba* exclusion treatment (orange), *P. massoniana* control treatment (black) and *P. massoniana* exclusion treatment (grey). The NMDS ordination was fitted to species and treatments. PERMANOVA revealed significant differences in macro-invertebrate and fungal communities between the two species ($r^2 = 0.06$, $p = 0.001$ and $r^2 = 0.05$, $p = 0.001$ for macro-invertebrates and fungi, respectively), but not between fungal communities in the control and exclusion treatment ($r^2 = 0.01$, $p > 0.05$).

Table A1. pSEM model fit. Supporting information to Fig. 3 in the main text. Significant relationships are printed in bold.

S. superba control treatment

Response variable	Predictor variable	Estimate	SE	p-value
tree species diversity	forest age	0.591	0.169	**0.002**
tree species diversity	elevation	-0.281	0.169	0.109
mean temp	elevation	-0.851	0.105	**0.000**
fungal OTU rich (*S. sup.* cont.)	mean temp	-0.771	0.352	**0.039**
fungal OTU rich (*S. sup.* cont.)	tree species diversity	0.284	0.187	0.142
fungal OTU rich (*S. sup.* cont.)	elevation	-0.498	0.349	0.167
invertebrate div (*S. sup*. cont.)	tree species diversity	-0.524	0.207	**0.019**
invertebrate div (*S. sup*. cont.)	mean temp	-0.676	0.321	**0.047**
invertebrate div (*S. sup*. cont.)	forest age	0.287	0.211	0.188
invertebrate div (*S. sup*. cont.)	elevation	-0.445	0.332	0.193
decay rate (*S. sup.* cont.)	mean temp	0.856	0.138	**0.000**
decay rate (*S. sup.* cont.)	invertebrate div (*S. sup*. cont.)	0.191	0.138	0.177

S. superba exclusion treatment

Response variable	Predictor variable	Estimate	SE	p-value
tree species diversity	forest age	0.591	0.169	**0.002**
tree species diversity	elevation	-0.281	0.169	0.109
mean temp	elevation	-0.851	0.105	**0.000**
fungal OTU rich (*S. sup.* excl.)	tree species diversity	-0.431	0.222	0.064
fungal OTU rich (*S. sup.* excl.)	forest age	0.333	0.222	0.147
decay rate (*S. sup*. excl.)	mean temp	0.461	0.152	**0.006**
decay rate (*S. sup.* excl.)	forest age	-0.365	0.148	**0.022**
decay rate (*S. sup.* excl.)	fungal OTU rich (*S. sup.* excl.)	-0.226	0.152	0.151

P. massoniana control treatment

Response variable	Predictor variable	Estimate	SE	p-value
tree species diversity	forest age	0.591	0.169	**0.002**
tree species diversity	elevation	-0.281	0.169	0.109
mean temp	elevation	-0.851	0.105	**0.000**
fungal OTU rich (*P. mas.* cont.)	mean temp	-0.546	0.170	**0.004**
fungal OTU rich (*P. mas.* cont.)	tree species diversity	0.311	0.170	0.080
invertebrate div (*P. mas*. cont.)	forest age	-0.407	0.175	**0.029**
invertebrate div (*P. mas*. cont.)	mean temp	-0.391	0.188	**0.049**
invertebrate div (*P. mas.* cont.)	fungal OTU rich (*P. mas.* cont.)	0.280	0.199	0.174
decay rate (*P. mas.* cont.)	mean temp	0.733	0.308	**0.026**
decay rate (*P. mas.* cont.)	invertebrate div (*P. mas.* cont.)	-0.386	0.185	**0.048**
decay rate (*P. mas.* cont.)	elevation	0.478	0.309	0.136

P. massoniana exclusion treatment

Response variable	Predictor variable	Estimate	SE	p-value
tree species diversity	forest age	0.591	0.169	**0.002**
tree species diversity	elevation	-0.281	0.169	0.109
mean temp	elevation	-0.851	0.105	**0.000**
fungal OTU rich (*P. mas.* excl.)	tree species diversity	0.351	0.191	0.078
fungal OTU rich (*P. mas.* excl.)	mean temp	-0.594	0.360	0.112
fungal OTU rich (*P. mas.* excl.)	elevation	-0.507	0.357	0.169
decay rate (*P. mas.* excl.)	mean temp	0.189	0.196	0.346

Table A2. pSEM model fit for models including plot mean values for relative humidity. Significant relationships are printed in bold.

S. superba control treatment

Fisher C = 9.32; p = 0.997

Response variable	Predictor variable	Estimate	SE	p-value
tree species diversity	forest age	0.707	0.174	**0.001**
tree species diversity	mean temp	0.368	0.167	**0.038**
tree species diversity	mean humidity	0.367	0.180	0.053
mean temp	elevation	-0.874	0.083	**0.000**
mean temp	mean humidity	-0.333	0.083	**0.001**
mean humidity	mean temp	-1.137	0.275	**0.000**
mean humidity	elevation	-0.875	0.284	**0.005**
mean humidity	forest age	-0.485	0.181	**0.014**
mean humidity	tree species diversity	0.341	0.177	0.067
fungal OTU rich (*S. sup.* cont.)	mean temp	-0.771	0.352	**0.039**
fungal OTU rich (*S. sup.* cont.)	tree species diversity	0.284	0.187	0.142
fungal OTU rich (*S. sup.* cont.)	elevation	-0.498	0.349	0.167
invertebrate div (S. sup. cont.)	elevation	-0.826	0.350	**0.027**
invertebrate div (S. sup. cont.)	mean temp	-0.633	0.350	0.083
decay rate (*S. sup.* cont.)	mean temp	0.758	0.121	**0.000**
decay rate (*S. sup.* cont.)	invertebrate div (S. sup. cont.)	0.226	0.121	0.075

Variable	R^2
tree species diversity	0.44
mean temp	0.84
mean humidity	0.55
fungal OTU rich (*S. sup.* cont.)	0.23
invertebrate div (S. sup. cont.)	0.19
decay rate (*S. sup.* cont.)	0.65

S. superba exclusion treatment

Fisher C = 11.86, p = 0.75

Response variable	Predictor variable	Estimate	SE	p-value
tree species diversity	forest age	0.707	0.174	**0.001**
tree species diversity	mean temp	0.368	0.167	**0.038**
tree species diversity	mean humidity	0.367	0.180	0.053
mean temp	elevation	-0.874	0.083	**0.000**
mean temp	mean humidity	-0.333	0.083	**0.001**
mean humidity	mean temp	-1.137	0.275	**0.000**
mean humidity	elevation	-0.875	0.284	**0.005**
mean humidity	forest age	-0.485	0.181	**0.014**
mean humidity	tree species diversity	0.341	0.177	0.067
fungal OTU rich (*S. sup.* excl.)	mean temp	-0.324	0.198	0.115
fungal OTU rich (*S. sup.* excl.)	mean humidity	-0.271	0.198	0.184
decay rate (*S. sup*. excl.)	mean temp	0.461	0.152	**0.006**
decay rate (*S. sup*. excl.)	forest age	-0.365	0.148	**0.022**
decay rate (*S. sup*. excl.)	fungal OTU rich (s. sup excl.)	-0.226	0.152	0.151

Variable	R^2
tree species diversity	0.44
mean temp	0.84
mean humidity	0.55
fungal OTU rich (*S. sup.* excl.)	0.13
decay rate (*S. sup*. excl.)	0.51

P. massoniana control treatment

Fisher C = 5.62, p = 0.93

Response variable	Predictor variable	Estimate	SE	p-value
tree species diversity	forest age	0.707	0.174	**0.001**
tree species diversity	mean temp	0.368	0.167	**0.038**
tree species diversity	mean humidity	0.367	0.180	0.053
mean temp	elevation	-0.874	0.083	**0.000**
mean temp	mean humidity	-0.333	0.083	**0.001**
mean humidity	mean temp	-1.137	0.275	**0.000**
mean humidity	elevation	-0.875	0.284	**0.005**
mean humidity	forest age	-0.485	0.181	**0.014**
mean humidity	tree species diversity	0.341	0.177	0.067
fungal OTU rich (*P. mas.* cont.)	forest age	0.393	0.177	**0.037**
fungal OTU rich (*P. mas.* cont.)	mean temp	-0.307	0.195	0.129
fungal OTU rich (*P. mas.* cont.)	invertebrate div (*P. mas*. cont.)	0.282	0.201	0.174
invertebrate div (*P. mas*. cont.)	forest age	-0.407	0.175	**0.029**

invertebrate div (*P. mas*. cont.)	mean temp	-0.391	0.188	**0.049**
invertebrate div (*P. mas*. cont.)	fungal OTU rich (*P. mas.* cont.)	0.280	0.199	0.174
decay rate (*P. mas.* cont.)	mean temp	1.004	0.386	**0.017**
decay rate (*P. mas.* cont.)	elevation	0.789	0.394	0.059
decay rate (*P. mas.* cont.)	invertebrate div (*P. mas*. cont.)	-0.339	0.210	0.122
decay rate (*P. mas.* cont.)	mean humidity	0.343	0.220	0.135
decay rate (*P. mas.* cont.)	fungal OTU rich (*P. mas.* cont.)	-0.291	0.195	0.151
decay rate (*P. mas.* cont.)	forest age	0.282	0.197	0.167

Variable	R^2
tree species diversity	0.44
mean temp	0.84
mean humidity	0.55
fungal OTU rich (*P. mas.* cont.)	0.38
invertebrate div (*P. mas*. cont.)	0.39
decay rate (*P. mas.* cont.)	0.53

P. massoniana exclusion treatment

Fisher C = 9.91; p = 0.97

Response variable	Predictor variable	Estimate	SE	p-value
tree species diversity	forest age	0.707	0.174	**0.001**
tree species diversity	mean temp	0.368	0.167	**0.038**
tree species diversity	mean humidity	0.367	0.180	0.053
mean temp	elevation	-0.874	0.083	**0.000**
mean temp	mean humidity	-0.333	0.083	**0.001**
mean humidity	mean temp	-1.137	0.275	**0.000**
mean humidity	elevation	-0.875	0.284	**0.005**
mean humidity	forest age	-0.485	0.181	**0.014**
mean humidity	tree species diversity	0.341	0.177	0.067
fungal OTU rich (*P. mas.* excl.)	mean humidity	0.476	0.195	**0.022**
fungal OTU rich (*P. mas.* excl.)	forest age	0.348	0.195	0.087
decay rate (*P. mas.* excl.)				

Variable	R^2
tree species diversity	0.44
mean temp	0.84
mean humidity	0.55
fungal OTU rich (*P. mas.* excl.)	0.22
decay rate (*P. mas.* excl.)	0.04