Fungal succession in decomposing woody debris across a tropical forest disturbance gradient: A field experiment

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Conflict of Interest

None

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Abstract

Background

Fungi are essential agents in decomposing woody debris (WD), an important carbon pool in forests. However, the ecology and dynamics of these fungal communities are poorly understood, especially in tropical forests. A better understanding of anthropogenic impacts, such as forest disturbances, on WD decomposition is also needed to appreciate their consequences on ecosystem functioning. Here, we examined the impacts of forest degradation and roles of fungal diversity and composition on WD decomposition rates across a disturbance gradient in a tropical montane rain forest in Xishuangbanna, SW China over three years. We measured wood specific gravity (WSG) loss from 280 logs from *Litsea cubeba* (low-WSG) and *Castanopsis mekongensis* (high-WSG). We concomitantly monitored fungal communities from 418 samples using next-generation sequencing after 0, 18 and 36 months field exposure.

Results

Incubation time, habitat and termite presence were key drivers of fungal community composition. Fungal community succession showed a priority effect of precedent communities. *C. mekongensis* WD consistently harbored ~1.4 times less fungal species than *L. cubeba*, but had ~1.4 times more unique operational taxonomic unit (OTU) at 18 mo. Shared OTUs between wood species increased with time up to ~63 % at 36 mo. Regardless of wood species, fungal diversity and both saprotrophs and white-rot abundances peaked at 18 months. However, fungal diversity was not a significant predictor of WSG loss. WSG loss did not vary among habitats. This may result from compensatory changes in dominant functional traits, such as decay mechanisms (e.g., proportion of white rot-fungi, soft-rot fungi). For example white- rot fungal proportions were double in open land compared to mature forest. Likewise, more saprothrophs colonized high-WSG wood. Finally, ascomycetes

(mainly Sordariomycetes and Dothiodeomycetes) and basidiomycetes (mostly Agaricomycetes) were dominant fungal groups. Open land was dominated by *Trichoderma*, regenerating forest by Herpothrichiellaceae and mature forest by *Penicillium*.

Conclusions

White- and soft-rot fungi co-dominated decomposition, with the later increasing through time. A succession of different fungal functional groups yielded similar decomposition rates across the disturbance gradient. Incorporating dominant fungal functional trait dynamics into biogeochemical models may improve predictions of carbon dynamics.

Key words: Bulong nature reserve, carbon cycle, coarse woody debris, decomposition, fungi, landscape, Mengsong, wood density.

Background

Organic matter decomposition represents an ecological process that redistributes nutrients produced by plants during their lifetime back into the atmosphere and soil. Woody debris (WD) comprises an important carbon pool [73 petagrams, [1]] with a relatively long residence time [2]. Moreover, WD is an important habitat for many microorganisms, animals and plants [3,4].

The abundance of WD and its relatively long residence time means that WD decomposition exerts a strong control on carbon cycling [5]. Factors affecting wood decomposition are diverse and generally classified into abiotic (e.g., temperature, moisture, soil parameters, etc.) and biotic factors (e.g., wood substrate quality, arthropods, microbial diversity, etc.) [6], although others suggested considering a third category of anthropogenic factors (e.g., prescribed fire, forest harvesting practices) [7]. Previous studies have largely dealt with abiotic factors and have found that wood biophysical traits along with climatic variables can only explain up to 56 % of the variation in WD decomposition at global scales [8]. Moreover, to obtain a more mechanistic understanding of the process of WD decomposition, it is vital to combine our understanding of the effects of abiotic factors with those of biotic factors. Such knowledge would greatly improve accuracy in predictive models of wood decomposition and therefore carbon cycling [9].

Fungi are commonly recognized as key biotic agents driving wood decomposition [9,10]. However, critical aspects of the role of fungal community ecology in the decay of WD remain to be explored [11]. For example, our understanding of the link between fungal richness and wood physio-chemical parameters is limited [12,13]. The roles of both the taxonomic and functional composition of the fungal community in determining wood decomposition rates is also not well understood [14]. Although it is generally accepted that white rot and brown rot basidiomycete

fungi play key roles in decay of lignocellulose [4,15,16], the role of "soft-rot" ascomycete fungi and the relative importance of each of these groups in tropical *versus* temperate forest ecosystems has not been well characterized. Moreover, studies that examined fungal community composition in temperate and boreal biomes have suggested that wood host species identity has the strongest effect on the composition of fruiting fungal species, followed by microclimatic factors (e.g., canopy openness) [17], as well as bark coverage [18].

Both negative and positive diversity-function relationships have been reported for wood decomposer fungal diversity and decomposition rates in microcosm experiments under controlled laboratory conditions [19–22], as well as in several field studies [9,12,13,17,23–25]. Recently, Maynard *et al.* suggested that the direction of the diversity-function relationship depends on the nature of the competitive network within fungal communities [21]. Maynard and colleagues also found that the importance of functional outcomes resulting from fungal species interactions and fungal community structure surpasse that of differences in environment conditions (i.e., abiotic factors).

Understanding how forest disturbance impacts WD decomposition is of critical importance [26–28], especially in tropical ecosystems. Tropical biomes are heavily affected by anthropogenic activities, such as deforestation and degradation, and have far higher woody plant and fungal diversity, as well as biomass. Moreover, there is a strong debate concerning whether tropical forests are carbon sinks or sources, and how this may be altered by climate change. Yet, across the globe, there is a marked geographical imbalance in studies on the role of microbes in wood decomposition, with far more studies in temperate and boreal biomes [7,9,29] than in the tropical biome [9,12,30]. Additionally, there is a paucity of studies characterizing the succession of fungal communities and decay type in WD over time. The few studies of WD decomposition

120 in the tropics have suggested that white rot dominates the early stages of decay [30], but how
121 fungal communities change in later stages of decay beyond two years and in response to
122 microclimatic variation or forest disturbance are poorly characterized [31,32].
123 In this study, our overarching goal was to investigate the role of abiotic and biotic factors
124 shaping the diversity and composition of fungal decomposers in decomposing logs and how
125 these change through time in a tropical montane rain forest in SW China across a disturbance
126 gradient from open land to mature forest. We aimed to address the following questions: (i) What
127 is the effect of wood species identity on the diversity and community structure of fungi? (ii) How
128 does the degree of forest disturbance affect fungal diversity and community structure? (iii) How
129 does fungal diversity and composition in woody debris change through time? And (iv) how do
130 these factors interact to influence the decomposition rate of WD?
131
132 **Results**
133 **Dynamics of WSG loss**
134 We previously examined the abiotic factors affecting wood decomposition in this landscape
135 (Dossa *et al.*, submitted). After 36 months of incubation, the WSG loss varied from 29.47 to
136 48.46 % (Fig. 1). The effect of habitat on WSG loss was not significant (Table S3), nor was the
137 main effect of tree species identity (Table S2). However, wood species identity interacted with
138 incubation time (Table S3), indicating a different temporal pattern of WSG loss in the two
139 species (Dossa *et al.* submitted).
140
141 **Taxonomic and functional classification of fungal community**

142 In total, after quality control steps, we obtained 9073 operational taxonomic units (OTUs).
143 Ascomycota was the dominant phylum followed by Basidiomycota throughout all sampling time
144 points (Fig. 2, S3). Sordariomycetes, Agaricomycetes, and Dothideomycetes were the most
145 abundant classes regardless of wood species, forest types and incubation time. Other moderately
146 abundant (>5% of total reads) classes included Leotiomycetes, Eurotiomycetes,
147 Saccharomycetes, and Tremellomycetes (Fig. S4).
148 Based on orders, Helotiales had the highest relative abundance regardless of wood
149 species except at 18 mo in open land and in mature forest. The relative abundance of other orders
150 varied with species, habitat and incubation time (Fig. S4). Those with greater than 5% relative
151 abundance included two basidiomycete orders, Agaricales and Polyporales, and various
152 ascomycete orders dominated by Xylariales, Hypocreales, Pleosporales, Chaetothyriales,
153 Coniochaetales, and Capnodiales (Fig. S4).
154 At the family level, the Xylarialeceae (Xylariales) and Sclerotiniaceae (Helotiales), which
155 was dominated by the genus *Botrytis*, were most abundant in the initial (0 mo) fungal community
156 in *L. cubeba* in all forest types, while Sclerotiniaceae and Cordycipitaceae (Hypocreales) were
157 most abundant at 0 mo in *C. mekongensis*. Across habitat types, Hypocreaceae (Hypocreales),
158 comprising primarily of fungi in the genus *Trichoderma*, was detected at >7% relative abundance
159 exclusively in open land at 18 mo for both tree species, while Herpotrichiellaceae
160 (Chaetothyriales) was abundant at 18 mo only in regenerating and mature forests. Genera
161 with >5% relative abundance included the ascomycetes *Penicillium* (Hepotrichiellaceae),
162 *Trichoderma* (Nectriaceae), *Beauveria* (Cordycipitaceae), *Hyaloscypha* and *Mollisia*
163 (Dermataceae; Helotiales), *Scytalidium* (family incertea sedis; Helotiales), and *Candida*

(Saccharomycetales), as well as the basidiomycete genus *Phlebia* (Meruliaceae; Polyporales) (Fig. S4).

At 18 mo the average proportions of pathotrophs, saprotrophs, and symbiotrophs across all habitat types and species were 11.5 %, 80.0 % and 8.5 %, respectively (Fig. 2 and S4). Regardless of habitat type or wood species, saprotroph abundance peaked at 18 mo. Pathotrophs also peaked at 18 mo, except for *L. cubeba* in mature forest. Within the saprotrophs, we were able to assign a small proportion ~30% to rot types (Fig. 2 B, C and Fig. S3). *C. mekongensis* harbored no brown rot initially, whereas *L. cubeba* had a relatively small proportion (< 1 %). As decomposition proceeded, the abundance of white rot fungi peaked at 18 mo, except for *L. cubeba* in mature forest (Fig. 2, Table S4) where there was a continuous increase in white rot fungi up to 36 mo. The proportion of all rot types out of the total fungal community increased from mature forest to open land. There was also a larger total abundance of fungi from all rot types in *C. mekongensis* than in *L. cubeba*, except in mature forest where the total proportion of rot types did not differ much between species.

Fungal alpha diversity in decomposing logs

L. cubeba harbored more fungal OTUs than *C. mekongensis* (Fig. 3, Table S5). In both species, fungal diversity peaked at 18 mo incubation. The best model for alpha diversity explained 23.3 % of the total variance including both fixed and random factors, while fixed factors explained 12.0 % of the variance. Incubation time and species identity had a significant effect on fungal diversity (Table S6), whereas habitat had no significant effect. However, fungal diversity explained only ~1 % of the variation in WSG loss, although this was still marginally significant. The presence of termites also significantly enhanced WSG loss (Table S5).

Fungal community structure

NMDS plots of fungal communities showed substantial overlap among species, but variation among samples increased through time ($F_{1, 382}$ = 6.694, P = 0.01, Fig. 4), and varied among habitat type ($F_{2, 381}$ = 6.775, P = 0.001, Fig. 4 and S6). Nevertheless, a multivariate analysis of factors influencing differences in fungal communities using *adonis* [33] found that time, habitat type and the interaction between time and presence of termites, but not species identity, had significant effects on community composition (Table 1). However, the model explained only ~ 3 % of the variance in fungal composition. Procrustes analysis showed a relationship between the position of the points in the first ordination (0 mo) and second ordination (18 mo) (For time 0 mo to 18 mo, Procrustes Sum of Squares (m12 squared) = 0.882, correlation in a symmetric procrustes rotation = 0.344, significance, P = 0.001, Figure S5A) and also between 18 mo and 36 mo (Procrustes Sum of Squares (m12 squared) = 0.884, correlation in a symmetric procrustes rotation = 0.340, significance, P = 0.001, Fig. S4B), indicating a priority effect of the initial community on the succession of fungal communities that developed at the early decay stage (0 mo to 18 mo) and in the transition from early to late decay stage (18 mo to 36 mo). A Venn diagram depicting number of unique or shared OTUs over time showed that regardless of wood species, there was a peak in number of unique OTUs at 18 mo, which declined afterwards. The percentage of unique OTUs at 18 mo was 1.44 times higher for *C. mekongensis* than for *L. cubeba* (Fig. 5), but the absolute number of unique OTUs was higher in *L. cubeba*. The shared OTUs between the two woody species increased through time and reached 63% after 36 mo of incubation (Fig. 5), at which time there were no unique OTUs in *C. mekongensis*.

Structural equation modeling

Our SEM revealed a best model that included all the direct effects and a few of our hypothesized indirect effects (Fig. 6). The final results showed a good fit (Chi square = 4.17, P-value = 0.53, degrees of freedom (DF) = 5, Comparative Fit Index (CFI) = 1, Fig. 6). Within this best model, the strongest path was from time with a standardized path coefficient = 0.97 ($P < 0.001$). The second strongest path was habitat with a path coefficient = -0.12 ($P < 0.001$). While the SEM showed that the effect of open land did not differ from that of mature forest, regenerating forest significantly reduced WSG loss compared to mature forest (Fig. 6, Table S7). Woody species identity and abundance of white rot fungi were also significant predictors of WSG loss. In addition, there was an indirect time effect mediated *via* white rot fungi abundance. Meanwhile woody species identity had a strong effect on fungal alpha diversity (Fig. 6, Table S7).

Discussion

Our current understanding of wood decomposition and fungal ecology relies heavily on patterns found in temperate and boreal ecosystems. Our study aimed to investigate successional changes in fungal diversity and composition in decomposing logs of two tree species across a disturbance gradient in a tropical forest, and their effects on WSG loss. We found that fungal diversity consistently peaked at 18 mo regardless of wood species and habitat. Fungal diversity was also significantly influenced by wood species identity, while fungal composition at the OTU level varied significantly with time, habitat type and the interaction between time and termite colonization. The peak of fungal species diversity at 18 mo coincided with a peak in both the relative abundance of saprotrophs and the number of unique OTUs. Within the saprotrophs, fungi assigned to the white rot type peaked at 18 mo, with the exception of *L. cubeba* in mature

forest which peaked at 36 mo. The abundance of soft rot fungi also peaked at 18 mo, except for *Castanopsis mekongensis* in open land and *L. cubeba* in mature forest, which both peaked at 36 mo. Overall, fungal diversity was not a significant factor determining WSG loss, but the abundance of white rot fungi explained a small but significant amount of the variation in WSG loss.

Initial wood quality and WSG loss

Given the differences in the tree species wood quality and density, we expected pronounced differences in the decomposition rates. Surprisingly, only the interactive effect between wood species identity with incubation time was significant. *C. mekongensis* logs had much higher initial WSG, slightly slower initial loss of WSG and consistently lower fungal diversity. The bark of *L. cubeba* had more labile carbon in the form of sugars that are easily accessible to microorganisms, which may explain the more rapid initial WSG loss and higher fungal alpha-diversity in this species [34]. Whether this is a general effect of bark chemistry on fungal diversity will require investigation over a more diverse selection of species. The lack of any significant effect of habitat on WSG loss was surprising. Rates of fungal decomposition were expected to be higher in forest habitats, where ambient moisture is higher. However, structural equation modelling showed a small but significant negative effect of regenerating forest on decomposition rates (Fig. 6).

Taxonomic and functional classification of fungal community

We found Ascomycota and Basidiomycota were the dominant phyla throughout the decomposition process regardless of woody species and forest type, with Ascomycetes being

more abundant than Basidiomycetes. These findings are in line with previous studies [27] and recent findings from researchers who monitored the decomposition of three tropical woody species and found Ascomycota and Basidiomycota to be the dominant phyla in all species at 3 and 11 mo after incubation [25]. This is not surprising given the fact that Basidiomycota contain the majority of white rot fungi, which are able to degrade both lignin and cellulose, and brown rot fungi, which modify lignin and degrade primarily cellulose [35,36]. Ascomycota, including many soft-rot fungi, have also been shown to play an underappreciated role in the early decay process, feeding on a diet of sugars to lignocellulose compounds [37–39]

The proportion of saprotrophs was greatest at 18 mo, which coincided with the peak in fungal diversity, and was ~2 times higher in *C. mekongensis* than in *L. cubeba.* This difference may explain why there was not more of a wood species effect on WSG loss. Although *C. mekongensis* had much higher initial wood density and lignin content, the higher proportion of saprotrophic fungi may have compensated to equalize decay rates over time. The higher initial rates of WSG loss in *L. cubeba* may be partially explained by a greater availability of sugars and hemicelluloses leading to a quick growth of decomposer fungi able to use these carbon sources (Figure 1). Notably, the proportion of saprotrophs in *L. cubeba* did not peak until 36 mo. In contrast, WSG loss in *C. mekongensis* was slow initially, presumably because of the relatively low proportion of easily digestible substrates and higher lignin content, but increased over time. Both this study and a previous study investigating aboveground decay of this species found the highest proportion of saprotrophs in *C. mekongensis* at 18 mo [40].

Our results also agree with previous studies [27,30,41] showing that white rot fungi dominate the early stage of decay in tropical forests. However, our study followed wood decay for a longer time period of 36 mo and found that after an initial peak of white rot fungi at 18 mo,

279 in some habitats, the proportion of brown and soft-rot fungi increased, especially in *C.*
280 *mekongensis*. This increase in brown rot and soft rot fungi in *C. mekongensis* in later stages of
281 decay, presumably after the early degradation of lignin by white rot fungi has freed cellulose and
282 sugars bound in lignin for degradation by these other decay mechanisms, may also partially
283 explain the lack of difference in final WSG loss of the two tree species. Both brown and soft rot
284 types can lead to substantial strength loss as quantified here by WSG loss [42]. In addition, there
285 is also a ~2 fold difference between the proportion of white rot in open versus mature forest,
286 which could also explain the lack of differences observed in WSG loss among habitats.
287 In terms of specific fungal taxa that may play roles in WD decay, the fungal communities
288 were dominated by Sordariomycetes and Dothideomycetes, both large and diverse classes of
289 ascomycetes found in many different habitats, as well as the basidiomycete class
290 Agaricomycetes, which contains a majority of both white rot and the brown rot fungi that
291 preferentially degrade lignin and cellulose, respectively [43]. In a previous study of early
292 decomposition (11 months) in five tropical species in Panama, researchers found an increase in
293 the abundance of Agariomycetes with time, which was not observed in our study, and the same
294 researcher also observed a decrease in Sordariomycetes over time [25]. In our study,
295 Sordariomycetes, including orders Xylariales and Hypocreales, were most abundant at the initial
296 sampling point and decreased slightly over time (Fig. S4). Some Xylariales are endophytes of
297 woody plants, including tropical trees [44], and many cause white rot [4]. The Sordariomycetes
298 genus *Beauveria* (Hypocreales), which was abundant at the initial sampling time point in *C.*
299 *mekongensis*, is also an endophyte of diverse grasses, angiosperms, and some woody plants
300 [45,46]. Surprisingly, Leotiomycetes, especially members of the family Sclerotiniaceae
301 (Helotiales), were also highly abundant at the initial time point in *L. cubeba*, comprising nearly

30% of all taxa at 0 mo, and also decreased over time. These patterns suggest the hypothesis that these Sordariomycetes and Leotiomycetes taxa may be endophytes that are highly abundant initially, but do not always persist in later fungal communities in WD. This is in contrast to other studies that have shown a strong priority effect for endophytic taxa or initial hyphal inoculum in dead wood in microcosm studies [47,48]. It is possible that competitive interactions among later colonizers in natural environments may lead to a decrease in initially abundant taxa during the succession of wood decay communities (Maynard et al. 2017). Nevertheless, we did observe large overlap between fungal community structure at different time points and evidence for priority effects in significant Procrustes results between initial (0 mo) and early decay (18 mo) and between early decay (18 mo) and later decay (36 mo). It is possible that endophytic taxa initially present in low abundance may increase in abundance in deadwood and contribute substantially to the decay processes over time [47]. In *C. mekongensis*, for example, Leotiomycetes as a whole showed an increase over time. While the family Sclerotiniaceae (Helotiales) was the most abundant at the initial sampling time point but decreased over time, other members of Helotiales (Dermateaceae and an unclassified family Incertae_sedis) increased at 18 or 36 mo. Similarly, the Eurotiomycete family Herpotrichiellaceae (Chaetothyriales) increased in abundance up to 18 mo for *C. mekongensis* in all habitats and for *L. cubeba* in regenerating and mature forest. Recent studies have shown that abundance of fungi within the ascomycete family Coniochaetaceae (Coniochatales), which were found in high abundance in the decaying wood of 13 temperate European tree species and were also detected in our study, correlated with abundance of laccases and different (hemi)cellulolytic enzymes, supporting a role in wood decay. The ecological and functional traits of these orders of ascomycete fungi have not

been well characterized, but our study and others suggests they warrant further attention for their role in wood decay in tropical systems.

Across habitats, the genus *Trichoderma*, which includes fungi known to degrade cellulose [50], was more abundant in open land, while Herpothrichiellaceae (Chaetothyriales) was more abundant in regenerating forest and mature forest. The higher abundance of *Penicillium* in logs in mature forest than in open land might reflect colonization from soil, as an earlier study at the same site found *Penicillium* was abundant in mature forest soils and declined in abundance in open land soils [51]. Many fungi involved in WD may colonise the substrate *via* the soil. Indeed, previous research suggests a dynamic interaction among soil and wood decomposing fungi in a temperate forest [52], as well as a homogenization of fungi involved in fungal necromass decomposition in both soil and wood media [53].

Fungal alpha diversity

We found that wood species identity and time were the main determinants of fungal alpha diversity during wood decomposition. This result corroborates recent findings in a subtropical forest in China, where Kahl and colleagues monitored the decomposition of *Pinus* sp. and *Schima* sp. over 2 years, and found species identity determined the composition of colonizing fungi. They also found that *Pinus* sp., which had higher C:N ratio and lower N content, harbored higher fungal diversity than *Schima sp.* [12,23]. In our study, *L. cubeba* had higher wood C:N ratio and lower N content and consistently higher fungal diversity through time.

Previous studies have reported both negative [12] and positive relationships [9,20,22,52] between fungal alpha diversity and incubation time but focused primarily on the early stages of decay during the first two years. A comparison of the results from these studies to ours should

347 also take into account the speed of decomposition in temperate *vs.* tropic environments. With this
348 in mind, we could say for early stage decomposition (18 mo in the tropical ecosystem and up to
349 36 mo elsewhere), we observed an increase in fungal diversity. However, after 18 mo, we
350 observed a decrease in diversity, with a continuous increase in WSG loss, suggesting a shift from
351 a positive to negative biodiversity – function relationship in later stage decomposition. These
352 results instead suggest a dynamic shift in the diversity and composition and the nature of
353 interactions among fungi that decompose wood through time, which may depend on various
354 factors, including wood properties. The first phase may reflect colonisation, when the log is still
355 relatively rich in easily decomposable components, and weak competitive interactions [9]. In
356 contrast, the next phase may reflect the exhaustion of easily decomposable components and
357 increasingly competitive interactions. Indeed, the sharp increase in the number of unique species
358 (Fig. 5) up to 18 mo may be explained by colonization of a newly available resource.
359 Increasingly strong competition through time for remaining resources may have led to a decline
360 of fungal richness thereafter. Moreover, the increase in white rot fungi up to 18 mo could have
361 enabled digestion of recalcitrant lignin, thereby exposing cellulose and hemicellulose, which are
362 then easily digestible by brown and soft rot fungi [30]. In most habitats in our study, the
363 proportion of brown and soft rot fungi increased from 18 mo to 36 mo. The magnitude of
364 increase was higher for *C. mekongensis*, which contained a higher initial lignin content (Table 1;
365 Fig. S2).
366
367 **Fungal community structure**
368 Fungal community composition at 0, 18 and 36 mo overlapped considerably, suggesting priority
369 effects were important [47,54]. However, both incubation time and habitat significantly affected

the fungal community composition as has been observed in other studies [55]. It is expected that fungal composition changes through time as the nature of the carbon substrates available are altered during the decay process, and similar results are reported from studies in temperate environments [9]. The microclimate within different habitats may not only affect which species of fungi colonize a log, but also may dictate the outcome of fungal interactions in decomposing logs. Hence, a significant effect of habitat on fungal composition is expected. However, our model only explained 3% of the variance in fungal composition. A large proportion of the variance in composition may arise from stochastic processes, such as dispersal-colonisation, which is supported by the fact that the variance in composition increased through time (Fig. 4). Termites also were found to alter indirectly wood decomposition through changes in the fungal composition [56], which is in line with our finding of a significant interactions between time and presence of termites. Termites may aid in dispersal-colonization for fungi by introducing fungal spores in holes or entry-points they created.

Caveats

Although, molecular methods are becoming popular and hold high potential of detecting species that would not otherwise being detected under traditional culture methods [11], these methods heavily rely on existing species sequences with taxonomic representation in public databases libraries. Moreover, the functional traits of many fungi have not been investigated thoroughly. The best available database to assign fungal sequences to trophic modes is the FunGuild database, yet a large proportion (70%) of OTUs could not be assigned to a rot type (see supplementary materials Fig. S3). This reflects both the lack of fungal DNA sequences for tropical fungi and the lack of knowledge of trophic modes and functions of many fungal taxa.

Conclusion

The effects of biotic factors on woody debris decomposition, including microbial diversity and functional composition, have been understudied in tropical ecosystems. In the present study, we employed next generation sequencing to investigate the succession of fungal communities in WD over time and their role in wood decomposition rates in a tropical mountainous forest subjected to anthropogenic disturbance. Over three years, habitat did not have a significant effect on WSG while the effect of wood species on fungal diversity and composition varied through time. The logs of the wood species with relatively low initial WSG harbored the highest diversity of fungi, perhaps due to the higher proportion of labile carbon in the form of sugars. In addition, fungal diversity and the proportion of saprotrophs and white-rot fungi peaked at 18 mo regardless of wood species and then declined, suggesting an initial period of colonisation and weak competitive interactions, followed by increasingly competitive interactions leading to decreased diversity. As anticipated, fungal community structure varied with time, wood species identity and habitat. However, fungal diversity was not a significant predictor of WSG loss. Our results suggest that changes in functional traits, such as mechanisms of rot type, rather than species diversity *per se* may better explain variation in WSG loss. Future studies should aim at investigating the role of fungal functional traits and rot types, particularly those of Ascomycete fungi whose roles in wood decay are less well characterized, as well as the effects of bark traits on the dynamics of fungal decomposers in tropical systems.

Materials & methods

Study site

Our study site was located in Mengsong a small township within Bulong Nature Reserve (Xishuangbanna, China, UTM/WGS84: 47 Q 656355 E, 2377646 N, 1100-1900 m above sea level, Figure S 1). The climate in Mengsong is seasonal and monsoonal. Mengsong receives 1600-1800 mm of rainfall annually [57] of which 80 % occurs within 6 months of the year from May to October. The vegetation found in Mengsong has been described by Zhu *et al.* [58]. Briefly, Mengsong is characterized by mountainous vegetation and shares many plant families with temperate Asian forests, with Fagaceae and Lauraceae as dominant canopy families.

Plot design to account for disturbance gradient

A stratified and systematic protocol [59,60] was used to select plots, based on both satellite imagery and ground truthing in 2009. The current landscape of Mengsong consists of a mosaic that includes open land such as barren fields, grassland and terraced tea fields, as well as regenerating forest and mature forest. In total, 28 one hectare plots were selected and established in 2010 to represent the disturbance gradient found in the landscape. Specifically, after classification 10, 12 and 6 plots classified as mature forests, regenerating forests and open land, respectively, were selected. Each plot was then subdivided into 9 subplots on a 3 x 3 grid with 50 m interval among subplots (Figure S1 Panel C). Only 5 of the 9 subplots per plot were used for the wood incubation experiment (subplots 1, 3, 5, 7, 9; Fig. S1).

Experimental set up and wood species selection

Based on a social survey conducted in September 2011 among farmers in Mengsong to assess local knowledge and understand how they classify woody trees in their landscape, we selected two native species contrasting in wood density: 1) *Litsea cubeba* (Lauraceae), which has

a relatively low wood specific gravity (0.42), and 2) *Castanopsis mekongensis* (Fagaceae), which has a relatively high wood specific gravity (0.75).

We purchased 29 living individual trees of *Litsea* and 32 of *Castanopsis* from local farmers' firewood plantations and harvested the main stem of these trees. The harvested stems were ~9 cm in diameter and were cut into logs 0.5 m in length using a handsaw. We sterilized the handsaw with ethanol and flamed it between cuts to prevent any microbial cross-contamination among samples. All the logs were transported to the field station for further preparation, such as fixing a unique tag number, and measurement of biometric variables (e.g., initial fresh weight, bark thickness, diameter, and total length). In order to establish initial wood functional traits, initial wood chemistry, and to examine initial fungal composition, a disk of 10 cm thickness was collected from the bottom of each individual tree and stored at -20 ^{o}C.

The logs used for the experiment had a mean diameter of 9.53 ± 1.11 cm (sd) and 9.58 ± 1.02 cm, mean initial weight of 2.3 ± 0.53 kg and 1.4 ± 0.36 kg, and mean bark thickness of 6.06 ± 2.83 mm and 2.82 ± 0.82 mm for *Castanopsis mekongensis* and *Litsea cubeba*, respectively. With respect to bark chemistry, *L. cubeba* had higher nitrogen (N), phosphorus (P), potassium (K), water soluble sugar, hemi-cellulose and tannin concentrations than *C. mekongnensis* and similar concentrations of carbon (C), cellulose and lignin. For wood chemistry, *L. cubeba* had higher concentrations of P, cellulose, hemi-celluloses and water soluble sugar, while *C. mekongensis* wood had higher concentrations of C, N, fiber and lignin (Table S1). Detailed chemical analysis protocols of the wood composition were reported in.[61]

At each of the five subplots within the established plots (see above), we set up a small decomposition plot 2 m x 2 m approximately 5 m north of the subplot center and incubated one

log of each species. In total, 280 logs (28 plots x 5 subplots x 2 species x 1 log) were incubated on the forest floor in 2011 and monitored for three years.

Sample collections

Wood cores were taken with a core borer (Forestry suppliers ®, Jackson, MS, USA). We calculated WSG using the following formula;

$$WSG = \frac{Ovendrymassofwoodcore}{Ovendryvolumeofwoodcore} * \rho_{water}$$

where: WSG is the wood specific gravity (unit less), oven dry mass (g), oven dry volume (cm^{-3}) and ρ_{water} is density of water (1.00 g cm^{-3}) [62].

At the same time, the presence/absence of termites was recorded and a cordless drill (Doug Jones, Doug Jones Jiwei company, Taiwan) was used to collect wood dust next to the core sample. Wood dust samples were placed directly in a tube (Corning tube Corning®) and immediately stored in -20 ^{o}C freezer for molecular analysis after being transported to the field laboratory on ice bags. Each log was divided longitudinally into 5 cm sections and on each sampling occasion one of these sections was randomly chosen for sampling. One core sample and one wood dust sample were collected from the bottom (surface in contact with the ground) of the selected section and one each from the top of the log. The sampling equipment was cleaned and flamed between samples to avoid cross-contamination, and the holes in the log were plugged with silicone (Tosseal® 381, Tokyo, Japan) to prevent inadvertent introduction of microbes. Samples were collected at 3, 6, 12, 18, 24 and 36 mo. However, to reduce costs, only wood dust samples collected at 18 mo and 36 mo, from four subplots (#1, 3, 7 and 9 each at the corner of the plot like number four on a dice) and from the bottom of the log were used for molecular analyses. Hence, we planned to do molecular analysis on a total of 432 field samples (27 plots x 4 subplots

481 x 2 species x 2 sample occasions), however only 384 field samples were conducted due to
482 missing samples and 34 samples from the initial wood discs. We elected to use the samples from
483 the bottom of the log to avoid interaction with photo-decomposition.
484
485 **Molecular analyses of fungal communities**
486 **DNA extraction**
487 Wood dust samples were homogenized to a fine powder with a mortar and a pestle in liquid
488 nitrogen. Subsequently, DNA was extracted from 150 to 250 mg of each homogenized wood
489 dust sample using the ZR Soil Microbe DNA MiniPrep kit (Zymo Research, Irvine, CA, USA)
490 according to the manufacturer's instructions. DNA quality was checked using a NanoDrop
491 ND1000 spectrophotometer (NanoDrop Technologies, Wilmington, DE, USA).
492 **DNA metabarcoding and next generation sequencing**
493 The DNA extracted from each sample was quantified using the Qubit fluorometer (Thermo-
494 Fischer) and approximately 10-25 ng of DNA for each sample were submitted to the University
495 of Minnesota Genomics Center (UMGC) for library amplification and sequencing. Additional
496 samples to assess the quality and accuracy of the amplification and sequencing steps included a
497 mock fungal community which contained equal quantities of 37 known fungal taxa (See
498 supplementary material Table S2 for the list of species in the mock community) and technical
499 replicates consisting of replicate libraries of the same DNA sample. A two-step dual-indexed
500 amplification method [63] was used for amplifying the fungal internal transcribed spacer 1 (ITS1)
501 barcode region. The universal fungal primers employed in this study are ITS1F
502 (CTTGGTCATTTAGAGGAAG*TAA) and ITS2R (GCTGCGTTCTTCATCGA*TGC) [64].
503 All the samples were amplified individually and the amplified PCR products were then barcoded

prior to pooling. The pooled sample was sequenced across two 300 base pair (bp) pair-end Illumina Miseq lanes to get sufficient coverage for each sample. The sequences from all Miseq lanes were aggregated together for the downstream quality control.

Data analysis

Bioinformatics

MOTHUR [65] was used to pair the sequences and make contigs, excluding sequences that had less than 100 bp overlap. The remaining sequences that had less than 2 bp mismatch to the fungal ITS1 region primer were retained for further filtering. The remaining sequences were filtered to remove those that had more than one ambiguous base, more than eight homopolymers, or were shorter than 150 bp or longer than 420 bp. The sequences that passed filtering in MOTHUR were transferred into the QIIME platform [66]. Chimeras were removed based on both the de novo and reference based chimera check algorithms of the USEARCH61 pipeline [67]. Representative OTUs were picked de novo at 97% similarity using USEARCH [68]. The taxonomy of OTUs was assigned using a 97 % similarity blast threshold. The UNITE database dynamic version 20.11.2016 [69] was used for the taxonomy assignment. The OTU table was transferred into R for subsequent statistical analyses.

FUNGuild was used to map OTUs to trophic modes and ecological guilds [70]. Our analyses first looked at the dynamics of the major trophic modes of fungi (e.g., pathotrophs, saprotrophs and symbiotrophs). Second we further explored the taxonomic diversity of saprotrophs, as these are the fungi that actively degrade wood constituents. Lastly, we focused on three functional traits/guilds relevant to wood decay, namely white, soft and brown rot fungi

526 which denote the decay rot type, while other guild categories were aggregated under the category
527 "other".
528
529 **Sequences**
530 All sequences are submitted to the NCBI database under the project bioproject accessible at
531 https://www.ncbi.nlm.nih.gov/bioproject/PRJNA503471. [Raw data file along with r script will
532 be uploaded upon acceptance of the MS]
533
534 **Statistical analyses**
535 **Wood specific gravity (WSG) dynamics**
536 WSG loss was reported in a previous study examining the habitat, species and abiotic effects on
537 wood decomposition (Dossa *et al.* submitted). Here our objective was to explain changes in the
538 diversity and composition of fungal decomposer communities and their effect on WSG loss.
539
540 **Fungal taxonomic diversity (Alpha diversity) and community structure (Beta-diversity)**
541 We used Chao 1 as an estimator of alpha diversity. The Chao 1 estimator was computed as
542 follows: $N + S^2 / (2\ D)$ where N is the number of OTUs, S is the number of singleton OTUs and
543 D is the number of doublet OTUs, (i.e. OTUs with abundance 2) [71]. We estimated alpha
544 diversity per sample and examined its change across time and the disturbance gradient. We then
545 modeled alpha diversity across time using all the variables including incubation time, habitat,
546 and species with all two way interactions. We used a linear mixed model implemented with the
547 function *lmer* from the package "lme4" [72]. We simplified the maximal model to the optimal
548 model by subtracting variables one at a time starting from the higher level (interactions),

549 respecting the principle of marginality. We used the likelihood ratio test to determine whether
550 there was a significant shift in the likelihood of the predecessor model while dropping a
551 particular variable. We also used variance partitioning through linear modeling to assess how
552 much of the variation in WSG was explained by alpha diversity at the mid time point, as the
553 alpha diversity temporal pattern was consistent across habitats and species. We used liner mixed
554 effects models function *lme* from "nlme" package [73] and considered plot as random factor.
555 To assess community structure and turn over (beta diversity) we generated a dissimilarity
556 distance matrix based on Bray-Curtis distance by using the function *vegdist* method "bray" from
557 the package "vegan" [33]. We also conducted a non-metric multidimensional scaling (NMDS)
558 based on this dissimilarity matrix using the function *metaMDS* from the "vegan" package. We
559 then assessed the effects of the factors tree species, forest disturbance, and time on the
560 dissimilarity between fungal communities by performing a constrained permutational
561 multivariate anova (PERMANOVA) with the function *adonis* from the "vegan" package. We
562 used the argument strata = Wood log ID to account for the random factor. Prior to modeling
563 fungal community structure, we checked for any time effect due to repeated measures. We then
564 examined any priority effects by conducting a procrustes analysis, using the function *protest*
565 from the "vegan" package on OTU matrixes from 0 mo, 18 mo and 36 mo of incubation time.
566 Procrustes analysis superimposes two matrices and asks whether the degree of superimposition is
567 likely to occur by chance. If not, this would suggest that the initial community composition
568 constrains the community assemblage that develops during the decay process. We further used
569 the traits obtained from FUNGuild to compute the percent of each ecological guild category
570 within each forest disturbance category (mature, regenerating forest and open land) and per
571 harvesting time (initial = time 0 mo, 18 mo and 36 mo after incubation). We plotted the

dynamics of the percentage of each guild category against time. We further assessed not only the dynamics of fungal guilds assigned to distinct rot types over time, but also examined how different rot type fungi contributed to WSG loss. Finally, we used structural equation modeling (SEM) to investigate both the direct and indirect effects of species, time, and habitat type on WSG loss via fungal alpha diversity and white rot fungi abundance (Figure S2 illustrates the initial SEM analysis model). We employed the package "lavaan" [74] to conduct SEM. For this analysis, we first converted the habitat variable, which is a categorical variable, to dummy variables using *dummy.code* function from the package "psych", and we included time in the modeling as an ordered categorical factor [75]. We examined the direct effects of main factors (time, woody species and habitat type) on the total response variable (loss of WSG). As we hypothesized that the fungal diversity and abundance of white-rot fungi would change over time, we subsequently tested the indirect effect of the main factors on WSG loss mediated *via* partial responses (fungal diversity and white rot abundance). We reduced the full model to best fit model using the likelihood ratio test, which compares nested models (full model against reduced model), using the function *LavTestLRT* within "lavaan" package. We removed non-significant variables one at a time and retained them in the best fit model only if they produced a reduced model that deviated significantly from the preceding more inclusive model by the likelihood ratio test. All analyses were performed in R version 3.5.2 [76].

Ethics approval and consent to participate

Not applicable

Consent for publication

Not applicable

Competing interests

The authors declare that they have no competing interest.

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Authors' contributions

G.G.O.D, E.P., D.S., K.F.C., and R.D.H. conceived the ideas and designed methodology; G.G.O.D. and E.P. collected field data; Y.Q.Y., W.H., and K.E.B. Conducted DNA extraction and molecular analyses; W.M. and KEB conducted bioinformatics analyses; G.G.O.D., W.H., K.E.B., and R.D.H. analyzed the data; G.G.O.D., R.D.H., and D.S. led the writing of the manuscript. All authors contributed critically to the drafts and gave final approval for publication.

Availability of data and materials

All sequences are submitted to the NCBI database under the project bioproject accessible at https://www.ncbi.nlm.nih.gov/bioproject/PRJNA503471.

[Raw data file along with r script are available from Harvard Dataverse (accession # upon acceptance of the MS)]

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Supplementary information

Supplementary information is available in separate file.

643 **References**

644 1. Pan Y, Birdsey RA, Fang J, Houghton R, Kauppi PE, Kurz WA, et al. A large and persistent
645 carbon sink in the world's forests. Science (80-) [Internet]. 2011 [cited 2013 Nov 7];333:988–93.
646 Available from: http://www.ncbi.nlm.nih.gov/pubmed/21764754
647 2. Dossa GGO, Paudel E, Wang H, Cao K, Schaefer D, Harrison RD. Correct calculation of
648 CO2efflux using a closed-chamber linked to a non-dispersive infrared gas analyzer. Methods
649 Ecol Evol. 2015;6:1435–42.
650 3. Harmon MEM, Franklin JFJ, Swanson FJ, Sollins P, Gregory SV, Lattin JD, et al. Ecology of
651 coarse woody debris in temperate ecosystems [Internet]. Adv. Ecol. Res. 1986. p. 133–302.
652 Available from:
653 http://books.google.de/books?hl=de&lr=&id=Lezo6XJVKloC&oi=fnd&pg=PA133&dq=Ecolog
654 y+of+coarse+woody+debris+in+temperate+ecosystems&ots=Au9sg7_ji-
655 &sig=_CxgdaRVt6l4dNuoeAFs_VdIjGo%5Cnhttp://www.sciencedirect.com/science/article/pii/
656 S006525040860121X
657 4. Stokland JN, Siitonen J, Jonsson BG. Biodiversity in dead wood. Cambridge, UK; 2012.
658 5. Law BE, Harmon ME. Forest sector carbon management , measurement and verification , and
659 discussion of policy related to climate change. Carbon Manag. 2011;2:73–84.
660 6. Cornelissen JHC, Sass-Klaassen U, Poorter L, van Geffen K, van Logtestijn RSP, van Hal J, et
661 al. Controls on coarse wood decay in temperate tree species: birth of the LOGLIFE experiment.
662 Ambio [Internet]. 2012 [cited 2012 Oct 23];41 Suppl 3:231–45. Available from:
663 http://www.ncbi.nlm.nih.gov/pubmed/22864697
664 7. Seibold S, Bässler C, Brandl R, Gossner MM, Thorn S, Ulyshen MD, et al. Experimental
665 studies of dead-wood biodiversity — A review identifying global gaps in knowledge. Biol

Conserv [Internet]. Elsevier B.V.; 2015;191:139–49. Available from: http://www.sciencedirect.com/science/article/pii/S0006320715002293

8. Hu Z, Michaletz ST, Johnson DJ, McDowell NG, Huang Z, Zhou X, et al. Traits drive global wood decomposition rates more than climate. Glob Chang Biol [Internet]. 2018;24:5259–69. Available from: http://doi.wiley.com/10.1111/gcb.14357

9. van Der Wal A, Ottosson E, De Boer W. Neglected role of fungal community composition in explaining variation in wood decay rates. Ecology. 2015;96:124–33.

10. Rajala T, Peltoniemi M, Pennanen T, Mäkipää R. Fungal community dynamics in relation to substrate quality of decaying Norway spruce (Picea abies [L.] Karst.) logs in boreal forests. FEMS Microbiol Ecol [Internet]. 2012 [cited 2013 Aug 10];81:494–505. Available from: http://www.ncbi.nlm.nih.gov/pubmed/22458543

11. Zanne AE, Abarenkov K, Afkhami ME, Aguilar-trigueros CA, Bates S, Bhatnagar JM, et al. Fungal functional ecology : bringing a trait-based approach to plant-associated fungi. Biol Rev. 2019;

12. Purahong W, Pietsch KA, Lentendu G, Schöps R. Characterization of Unexplored Deadwood Mycobiome in Highly Diverse Subtropical Forests Using Culture-independent Molecular Technique. Front Microbiol. 2017;8:574.

13. Hoppe B, Purahong W, Wubet T, Kahl T, Bauhus J, Arnstadt T, et al. Linking molecular deadwood-inhabiting fungal diversity and community dynamics to ecosystem functions and processes in Central European forests. Fungal Divers. 2016;77:367–79.

14. Ottosson E, Kubartova A, Edman M, Jonsson M, Lindhe A, Stenlid J, et al. Diverse ecological roles within fungal communities in decomposing logs of Picea abies. FEMS

688 Microbiol Ecol [Internet]. 2015;91:fiv012. Available from:
689 http://femsec.oxfordjournals.org/cgi/doi/10.1093/femsec/fiv012
690 15. Cragg SM, Beckham GT, Bruce NC, Bugg TDH, Distel DL, Dupree P, et al. Lignocellulose
691 degradation mechanisms across the Tree of Life. Curr Opin Chem Biol [Internet]. Elsevier Ltd;
692 2015;29:108–19. Available from: http://dx.doi.org/10.1016/j.cbpa.2015.10.018
693 16. Janusz G, Pawlik A, Sulej J, Świderska-Burek U, Jarosz-Wilkołazka A, Paszczyński A.
694 Lignin degradation: microorganisms, enzymes involved, genomes analysis and evolution. FEMS
695 Microbiol Rev [Internet]. 2017;941–62. Available from:
696 http://academic.oup.com/femsre/article/doi/10.1093/femsre/fux049/4569254
697 17. Krah F-S, Seibold S, Brandl R, Baldrian P, Muller J, Bassler C. Independenteffects of host
698 and environment on the diversity of wood-inhabiting fungi. J Ecol. 2018;106.
699 18. Hagge J, Bässler C, Gruppe A, Hoppe B, Kellner H, Krah F, et al. Bark coverage shifts
700 assembly processes of microbial decomposer communities in dead wood. Proceeding R Soc B/
701 Biol Sci. 2019;286.
702 19. Fukami T, Dickie IA, Paula Wilkie J, Paulus BC, Park D, Roberts A, et al. Assembly history
703 dictates ecosystem functioning: evidence from wood decomposer communities. Ecol Lett
704 [Internet]. 2010 [cited 2011 Jul 28];13:675–84. Available from:
705 http://www.ncbi.nlm.nih.gov/pubmed/20412280
706 20. Valentín L, Rajala T, Peltoniemi M, Heinonsalo J, Pennanen T, Mäkipää R. Loss of diversity
707 in wood-inhabiting fungal communities affects decomposition activity in Norway spruce wood.
708 Front Microbiol. 2014;5.

709 21. Maynard DS, Crowther TW, Bradford MA. Competitive network determines the direction of
710 the diversity–function relationship. Proc Natl Acad Sci [Internet]. 2017;201712211. Available
711 from: http://www.pnas.org/lookup/doi/10.1073/pnas.1712211114
712 22. Rajala T, Tuomivirta T, Pennanen T, Makipaa R. Habitat models of wood-inhabiting fungi
713 along a decay gradient of Norway spruce logs. Fungal Ecol. 2015;18:48–55.
714 23. Kahl T, Arnstadt T, Baber K, Bässler C, Bauhus J, Borken W, et al. Wood decay rates of 13
715 temperate tree species in relation to wood properties, enzyme activities and organismic
716 diversities. For Ecol Manage [Internet]. Elsevier B.V.; 2017;391:86–95. Available from:
717 http://dx.doi.org/10.1016/j.foreco.2017.02.012
718 24. Maynard DS, Covey KR, Crowther TW, Sokol NW, Morrison EW, Frey SD, et al. Species
719 associations overwhelm abiotic conditions to dictate the structure and function of wood-decay
720 fungal communities. Ecology. 2018;99:801–11.
721 25. Jones JM, Heath KD, Ferrer A, Brown SP, Canam T, James W. Wood decomposition in
722 aquatic and terrestrial ecosystems in the tropics: contrasting biotic and abiotic processes. FEMS
723 Microbiol Ecol. 2019;95:fiy223.
724 26. Handa IT, Aerts R, Berendse F, Berg MP, Bruder A, Butenschoen O, et al. Consequences of
725 biodiversity loss for litter decomposition across biomes. Nature [Internet]. 2014;509:218–21.
726 Available from: http://www.ncbi.nlm.nih.gov/pubmed/24805346
727 27. Kubartova A, Ottosson E, Stenlid J. Linking fungal communities to wood density loss after
728 12 years of log decay. FEMS Microbiol Ecol [Internet]. 2015;91:fiv032–fiv032. Available from:
729 http://femsec.oxfordjournals.org/cgi/doi/10.1093/femsec/fiv032
730 28. Halme P, Ódor P, Christensen M, Piltaver A, Veerkamp M, Walleyn R, et al. The effects of
731 habitat degradation on metacommunity structure of wood-inhabiting fungi in European beech

732 forests. Biol Conserv [Internet]. Elsevier Ltd; 2013 [cited 2014 Jun 17];168:24–30. Available
733 from: http://linkinghub.elsevier.com/retrieve/pii/S000632071300308X
734 29. Parisi F, Pioli S, Lombardi F, Fravolini G, Marchetti M, Tognetti R. Linking deadwood traits
735 with saproxylic invertebrates and fungi in European forests - a review. IForest [Internet].
736 2018;11:423. Available from: http://www.sisef.it/iforest/contents/?id=ifor2670-011
737 30. Schilling JS, Ayres A, Kaffenberger JT, Powers JS. Initial white rot type dominance of wood
738 decomposition and its functional consequences in a regenerating tropical dry forest. Soil Biol
739 Biochem [Internet]. Elsevier Ltd; 2015;88:58–68. Available from:
740 http://linkinghub.elsevier.com/retrieve/pii/S0038071715001704
741 31. Fukasawa Y, Osono T, Takeda H. Wood decomposing abilities of diverse lignicolous fungi
742 on nondecayed and decayed beech wood. Mycologia. 2011;103:474–82.
743 32. Fukasawa Y, Osono T, Takeda H. Fungal decomposition of woody debris of Castanopsis
744 sieboldii in a subtropical old-growth forest. Ecol Res. 2012;27:211–8.
745 33. Oksanen J, Blanchet FG, Kindt R, Legendre P, Minchin PR, O'Hara RB, et al. vegan:
746 Community Ecology Package. R package version 2.0-5. [Internet]. 2012. Available from:
747 http://cran.r-project.org/package=vegan
748 34. Dossa GGO, Schaefer D, Zhang J-L, Tao J-P, Cao K-F, Corlett RT, et al. The cover
749 uncovered: Bark control over wood decomposition. J Ecol. 2018;106:2147–60.
750 35. Ohm RA, Riley R, Salamov A, Min B, Choi IG, Grigoriev I V. Genomics of wood-degrading
751 fungi. Fungal Genet Biol [Internet]. Elsevier Inc.; 2014;72:82–90. Available from:
752 http://dx.doi.org/10.1016/j.fgb.2014.05.001

753 36. Rytioja J, Hildén K, Yuzon J, Hatakka A, de Vries RP, Mäkelä MR. Plant-Polysaccharide-
754 Degrading Enzymes from Basidiomycetes. Microbiol Mol Biol Rev [Internet]. 2014;78:614–49.
755 Available from: http://mmbr.asm.org/lookup/doi/10.1128/MMBR.00035-14
756 37. van der Wal A, Geydan TD, Kuyper TW, de Boer W. A thready affair: linking fungal
757 diversity and community dynamics to terrestrial decomposition processes. FEMS Microbiol Rev
758 [Internet]. 2012 [cited 2012 Oct 29];1–18. Available from:
759 http://www.ncbi.nlm.nih.gov/pubmed/22978352
760 38. Boddy L, Owens EM, Chapela IH. Small scale variation in decay rate within logs one year
761 after felling: Effect of fungal community structure and moisture content. FEMS Microbiol Ecol.
762 1989;62:173–84.
763 39. Blanchette RA, Held BW, Jurgens JA, Mcnew DL, Harrington TC, Duncan SM, et al. Wood-
764 Destroying Soft Rot Fungi in the Historic Expedition Huts of Antarctica. Appl Environ
765 Microbiol. 2004;70:1328–35.
766 40. Gora EM, Lucas JM. Dispersal and nutrient limitations of decomposition above the forest
767 floor: evidence from experimental manipulations of epiphytes and macronutrients. Funct Ecol
768 [Internet]. 2019;33:2417–29. Available from:
769 https://onlinelibrary.wiley.com/doi/abs/10.1111/1365-2435.13440
770 41. Cline LC, Schilling JS, Menke J, Groenhof E, Kennedy PG. Ecological and functional effects
771 of fungal endophytes on wood decomposition. Funct Ecol. 2017;1–11.
772 42. Blanchette RA, Nilsson T, Daniel G, Abad A. Biological Degradation of Wood. In: Rowell R,
773 editor. Archaeol wood. 1989. p. 141–74.
774 43. Naranjo-ortiz MA, Gabald T. Fungal evolution : diversity , taxonomy and phylogeny of the
775 Fungi. Biol Rev. 2019;94:2101–37.

776 44. Bills GF, Gonzalez-Menendez V, Martin J, Platas G, Fournier J, Persoh D, et al. Hypoxylon
777 pulicicidum sp. nov. (Ascomycota, Xylariales), a Pantropical Insecticide-Producing Endophyte.
778 PLoS One. 2012;7:e46687.
779 45. Mckinnon AC, Saari S, Nicolai MEM, Meyling N V., Raad M, Glare TR. Beauveria bassiana
780 as an endophyte : a critical review on associated methodology and biocontrol potential. Biol
781 Control. Springer Netherlands; 2017;62:1–17.
782 46. Reay SD, Brownbridge M, Gicquel B, Cummings NJ, Nelson TL. Isolation and
783 characterization of endophytic Beauveria spp . (Ascomycota : Hypocreales) from Pinus radiata
784 in New Zealand forests. Biol Control. 2010;54:52–60.
785 47. Song Z, Kennedy PG, Liew FJ, Schilling JS. Fungal endophytes as priority colonizers
786 initiating wood decomposition. Funct Ecol. 2017;31:407–18.
787 48. Song Z, Vail A, Sadowsky MJ, Schilling JS. Influence of Hyphal Inoculum potential on the
788 Competitive Success of Fungi Colonizing Wood. Microb Ecol [Internet]. 2015;758–67.
789 Available from: http://link.springer.com/10.1007/s00248-015-0588-5
790 49. Lee MR, Powell JR, Oberle B, Cornwell WK, Lyons M, Rigg JL, et al. Good neighbors
791 aplenty: Fungal endophytes rarely exhibit competitive exclusion patterns across a span of woody
792 habitats. Ecology. 2019;
793 50. Martinez D, Berka RM, Henrissat B, Saloheimo M, Arvas M, Baker SE, et al. Genome
794 sequencing and analysis of the biomass-degrading fungus Trichoderma reesei (syn. Hypocrea
795 jecorina). Nat Biotechnol. 2008;26:553–60.
796 51. Shi L, Dossa GGO, Ekananda P, Huadong Z, Xu J, Harrison RD. Changes in fungal
797 communities across a forest disturbance gradient. Appl Environ Microbiolology.
798 2019;85:e00080-19.

52. Mäkipää R, Rajala T, Schigel D, Rinne KT, Pennanen T, Abrego N, et al. Interactions between soil- and dead wood-inhabiting fungal communities during the decay of Norway spruce logs. ISME J [Internet]. 2017;11:1964–74. Available from: http://www.nature.com/doifinder/10.1038/ismej.2017.57

53. Maillard F, Schilling J, Andrews E, Shreiner K, Kennedy P. Functional convergence in the decompositionof fungal necromass in soil and wood. FEMS Microbiol Ecol. 2019;

54. Hiscox J, Savoury M, Müller CT, Lindahl BD, Rogers HJ, Boddy L. Priority effects during fungal community establishment in beech wood. ISME J [Internet]. 2015;1–15. Available from: http://www.nature.com/doifinder/10.1038/ismej.2015.38

55. Hiscox J, Boddy L. Armed and dangerous – Chemical warfare in wood decay communities. Fungal Biol Rev [Internet]. Elsevier Ltd; 2017;31:169–84. Available from: http://dx.doi.org/10.1016/j.fbr.2017.07.001

56. Ulyshen MD, Diehl S V., Jeremic D. Termites and flooding affect microbial communities in decomposing wood. Int Biodeterior Biodegradation [Internet]. Elsevier Ltd; 2016;115:83–9. Available from: http://linkinghub.elsevier.com/retrieve/pii/S0964830516302499

57. Xu J, Lebel L, Sturgeon J. Functional links between biodiversity, livelihoods, and culture in a Hani swidden landscape in southwest China. Ecol Soc. 2009;14:20.

58. Zhu H, Yong C, Zhou S, Wang H, Yan L. Vegetation , floristic composition and species diversity in a tropical mountain nature reserve in southern Yunnan , SW China , with implications for conservation. Trop Conserv Sci. 2015;8:528–46.

59. Beckschäfer P, Fehrmann L, Harrison RD, Xu J, Kleinn C. Mapping leaf area index in subtropical upland ecosystems using RapidEye imagery and the randomForest algorithm. iForest. 2014;7:1–11.

822 60. Paudel E, Dossa GGO, Blécourt M de, Beckschäfer P, Xu J, Harrison RD, et al. Quantifying
823 the factors affecting leaf litter decomposition across a tropical forest disturbance gradient.
824 Ecosphere. 2015;6:267.
825 61. Dossa GGO, Paudel E, Cao K, Schaefer D, Harrison RD. Factors controlling bark
826 decomposition and its role in wood decomposition in five tropical tree species. Sci Rep [Internet].
827 Nature Publishing Group; 2016 [cited 2016 Oct 7];6:34153. Available from:
828 http://www.nature.com/articles/srep34153
829 62. Williamson GB, Wiemann MC. Measuring wood specific gravity...Correctly. Am J Bot
830 [Internet]. 2010 [cited 2011 Sep 6];97:519–24. Available from:
831 http://www.ncbi.nlm.nih.gov/pubmed/21622413
832 63. Gohl DM, Vangay P, Garbe J, MacLean A, Hauge A, Becker A, et al. Systematic
833 improvement of amplicon marker gene methods for increased accuracy in microbiome studies.
834 Nat Biotechnol. 2016;34:942–8.
835 64. Hu W, Strom N, Haarith D, Chen S, Bushley KE. Mycobiome of cysts of the soybean cyst
836 nematode under long term crop rotation. Front Microbiol. 2018;9:Article 386.
837 65. Schloss PD, Westcott SL, Ryabin T, Hall JR, Hartmann M, Hollister EB, et al. Introducing
838 mothur: Open-source, platform-independent, community-supported software for describing and
839 comparing microbial communities. Appl Environ Microbiol. 2009;75:7537–41.
840 66. Caporaso JG, Kuczynski J, Stombaugh J, Bittinger K, Bushman FD, Costello EK, et al.
841 correspondence QIIME allows analysis of high- throughput community sequencing data
842 Intensity normalization improves color calling in SOLiD sequencing. Nat Publ Gr [Internet].
843 Nature Publishing Group; 2010;7:335–6. Available from: http://dx.doi.org/10.1038/nmeth0510-
844 335

67. Edgar RC, Haas BJ, Clemente JC, Quince C, Knight R. UCHIME improves sensitivity and speed of chimera detection. Bioinformatics. 2011;27:2194–200.

68. Edgar RC, Flyvbjerg H. Error filtering, pair assembly and error correction for next-generation sequencing reads. Bioinformatics. 2015;31:3476–82.

69. Koljalg U, Nilsson RH, Abarenkov K, Tedersoo L, Taylor AFS, Bahram M. Towards a unified paradigm for sequence-based identification of fungi. Mol Ecol. 2014;22:5271–7.

70. Nguyen NH, Song Z, Bates ST, Branco S, Tedersoo L, Menke J, et al. FUNGuild: An open annotation tool for parsing fungal community datasets by ecological guild. Fungal Ecol [Internet]. Elsevier Ltd; 2016;20:241–8. Available from: http://dx.doi.org/10.1016/j.funeco.2015.06.006

71. Chao A. Nonparametric Estimation of the Number of Classes in a Population Author. Scanadinavian J Stat. 1984;11:265–70.

72. Bates D, Maechler M, Bolker B, Walker S. lme4: linear mixed-effects models using eigen and S4. R package version 1.0-4. http://CRAN.R-project.org/package=lme4. 2013;

73. Pinheiro J, Bates D, Debroy S, Sarkar D, Team RDC. nlme: Linear and Nonlinear Mixed Effects Models. R package version 3.1-101. 2013.

74. Yves R, Oberski D, Byrnes J, Vanbrabant L, Savalei V, Merkle E, et al. Package ‘ lavaan ’ Latent variable analysis. 2018;

75. Revelle W. Package ‘ psych .’ 2019;

76. R Foundation for Statistical Computing. R: A language and environment for statistical computing. R Foundation for Statistical Computing. [Internet]. 2018. Available from: http://www.r-project.org/

869 **Figure legends**

870 **Fig. 1**: Percentage wood specific gravity (WSG) loss from logs installed across 28 plots in the
871 Mengsong landscape after 18 mo and 36 mo incubation. The experiment used two species, *Litsea*
872 *cubeba* and *Castanopsis mekongensis*. Points represent predicted mean values (±95% confidence
873 interval) for two species (*Litsea cubeba* and *Castanopsis mekongensis*) with respect to
874 disturbance category (mature forest, regenerating forest and open-land) and incubation time
875 during 36 month of wood decomposition in tropical montane forest, Mengsong, Xishuangbanna,
876 SW, China (Dossa *et al.* submitted).

877

878 **Fig. 2**: A) Average relative abundance of OTUs assigned to higher taxonomic units (Ascomycota,
879 Basidiomycota, Other), B) Average relative abundance of OTUs assigned by FUNGuild to
880 different tropic modes (Pathotroph, Saprotroph, Symotroph) and C) Average relative abundance
881 of OTUs assigned by FUNGuild to different rot types (white-rot, brown-rot, and soft-rot fungi).
882 In order to have comparable values, the relative abundance was calculated across all our samples
883 regardless of habitats and species. And this relative abundance represents the proportion of
884 OTUs assigned to each fungal guild identified *via* FUNGuild. Thus within each panel the total
885 percentage sums to 100.

886

887 **Fig. 3**: Change in fungal alpha diversity (Chao 1) across time and forest types for two wood
888 species (*Litsea cubeba* and *Castanopsis mekongensis*) across habitat (mature forest in red,
889 regenerating forest in blue and open forest in green) during 36 month of wood decomposition in
890 tropical montane forest, Mengsong, Xishuangbanna, SW, China. Points represent predicted
891 mean values (±95% confidence interval) for two wood species (*Litsea cubeba* and *Castanopsis*

892 *mekongensis*) with respect to disturbance category (mature forest, regenerating forest and open-
893 land) and incubation time during 36 month of wood decomposition in tropical montane forest,
894 Mengsong, Xishuangbanna, SW, China. Note that for 0 mo error bars represent standard error of
895 the mean (from pooled logs) while for the remainder time points the error bars are +/- 95 % from
896 the best predicted model.
897
898 **Fig. 4**: Change in fungal composition through time based on Bray-Curtis dissimilarity over 36
899 month of wood decomposition in tropical montane forest, Mengsong, Xishuangbanna, SW,
900 China (each point representing a sample; 95% confidence intervals around centroids are shown
901 (ellipses)). The upper two panels show ellipses (colored dashed lines) for incubation time. The
902 lower two panels show ellipses for forest disturbance categories. Initial in the lower two panels
903 represent the communities at 0 mo before incubation.
904
905 **Fig. 5**: Venn diagram for displaying the temporal dynamics of unique and shared fungal species
906 (OTUs) harbored by logs of A) *Castanopsis mekongensis*, B) *Litsea cubeba*, C) both species at
907 initial time 0 mo, D) both species at 18 mo, and E) both species at 36 mo after incubation during
908 36 month of wood decomposition in tropical montane forest, Mengsong, Xishuangbanna, SW,
909 China.
910
911 **Fig. 6:** Structural equation modeling summarizing the direct and indirect effects of time, fungal
912 alpha diversity, woody species, white rot abundance and forest type on wood specific gravity
913 (WSG) loss on logs of *Litsea cubeba* and *Castanopsis mekongensis* during 36 month of wood
914 decomposition in tropical montane forest, Mengsong, Xishuangbanna, SW, China. Thickness of

915 the path equates to the strength of path coefficient. Black and red arrows indicate positive and
916 negative paths respectively. For clarity we did not put the non-significant path coefficients in the
917 diagram (but see Table S5 for full SEM results). Chi square = 4.17, P-value = 0.53 , degrees of
918 freedom (DF) = 5, Comparative Fit Index (CFI) = 1. As habitat is a categorical variable with
919 three levels, we created dummy variables with mature forest as the baseline level so any path
920 regression coefficient for the other two levels represents the difference of that level from the
921 baseline. Time was included as ordered categorical variable with 18 mo < 36 mo.

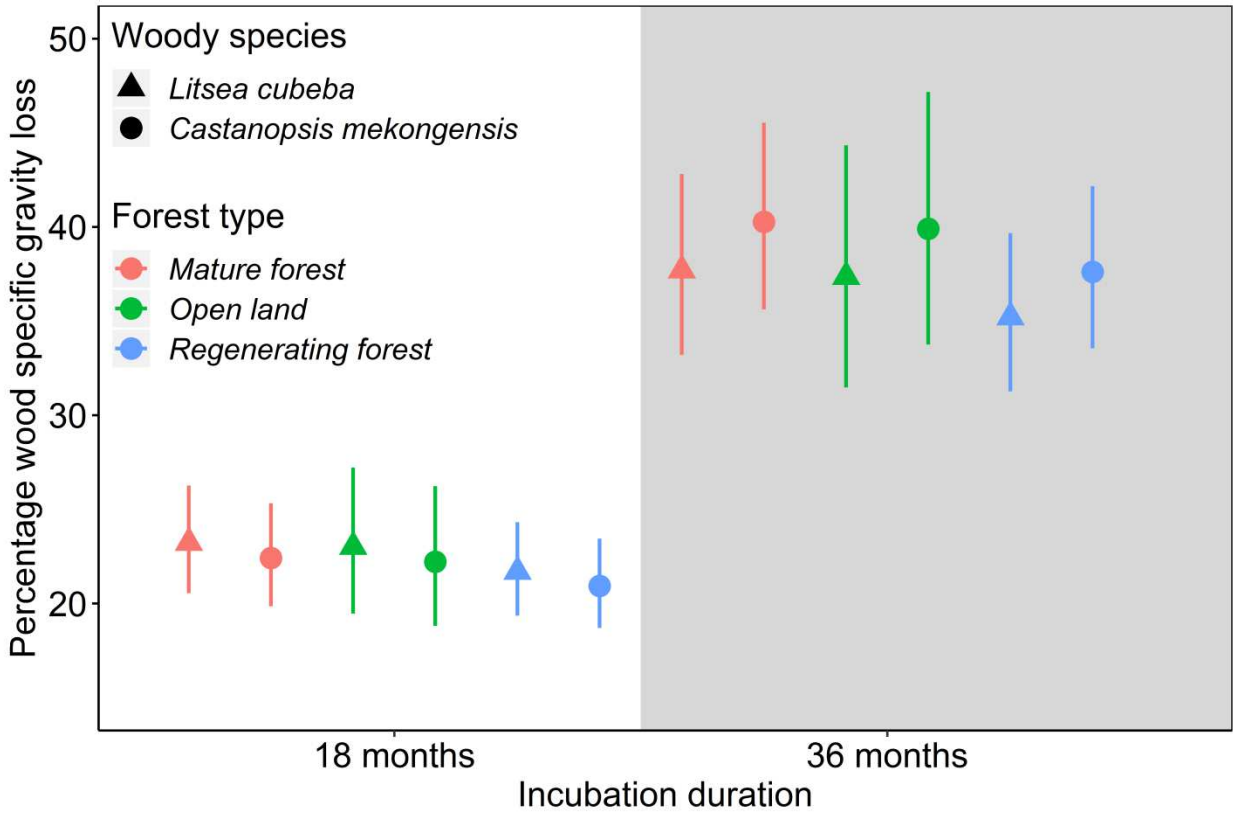
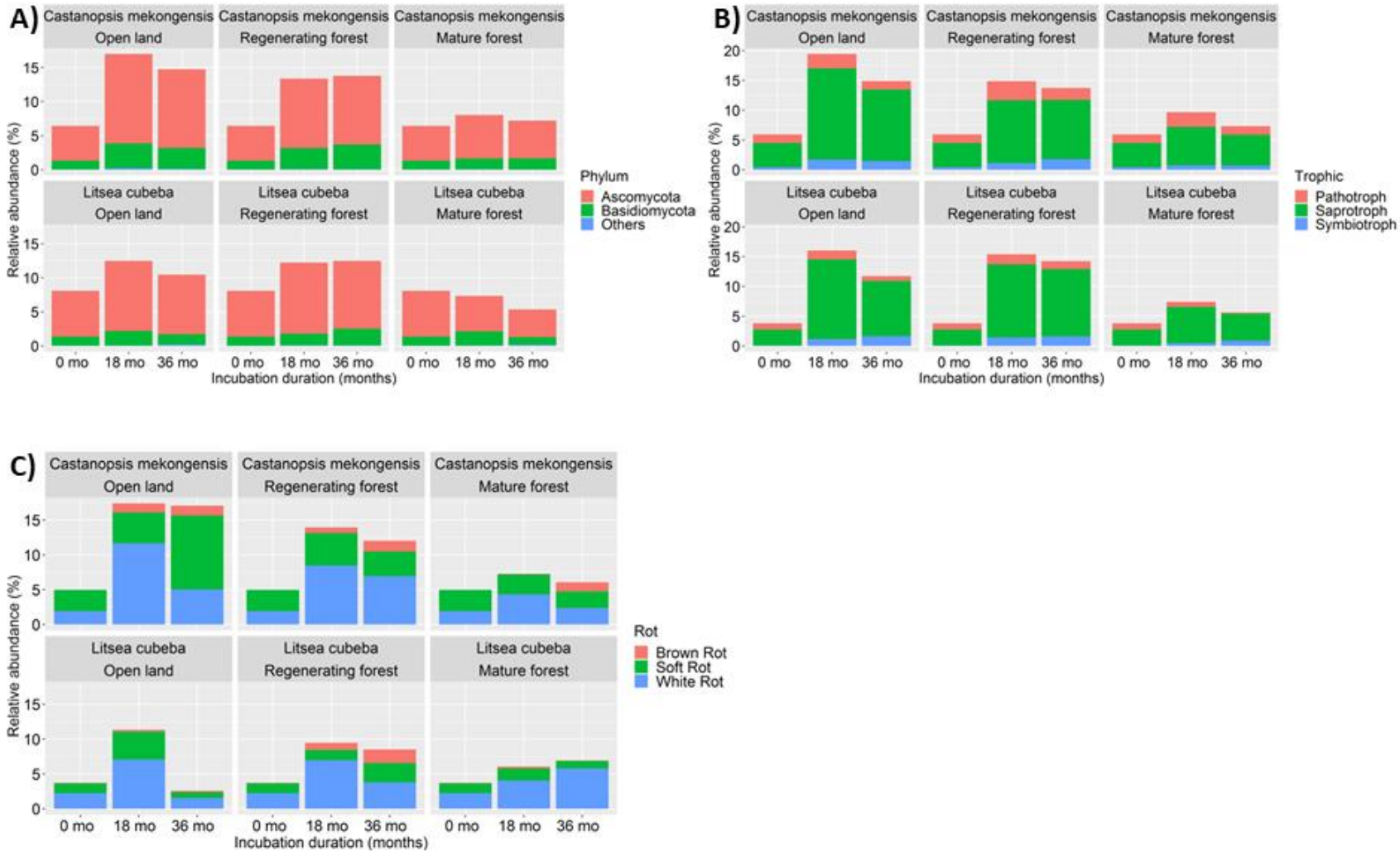
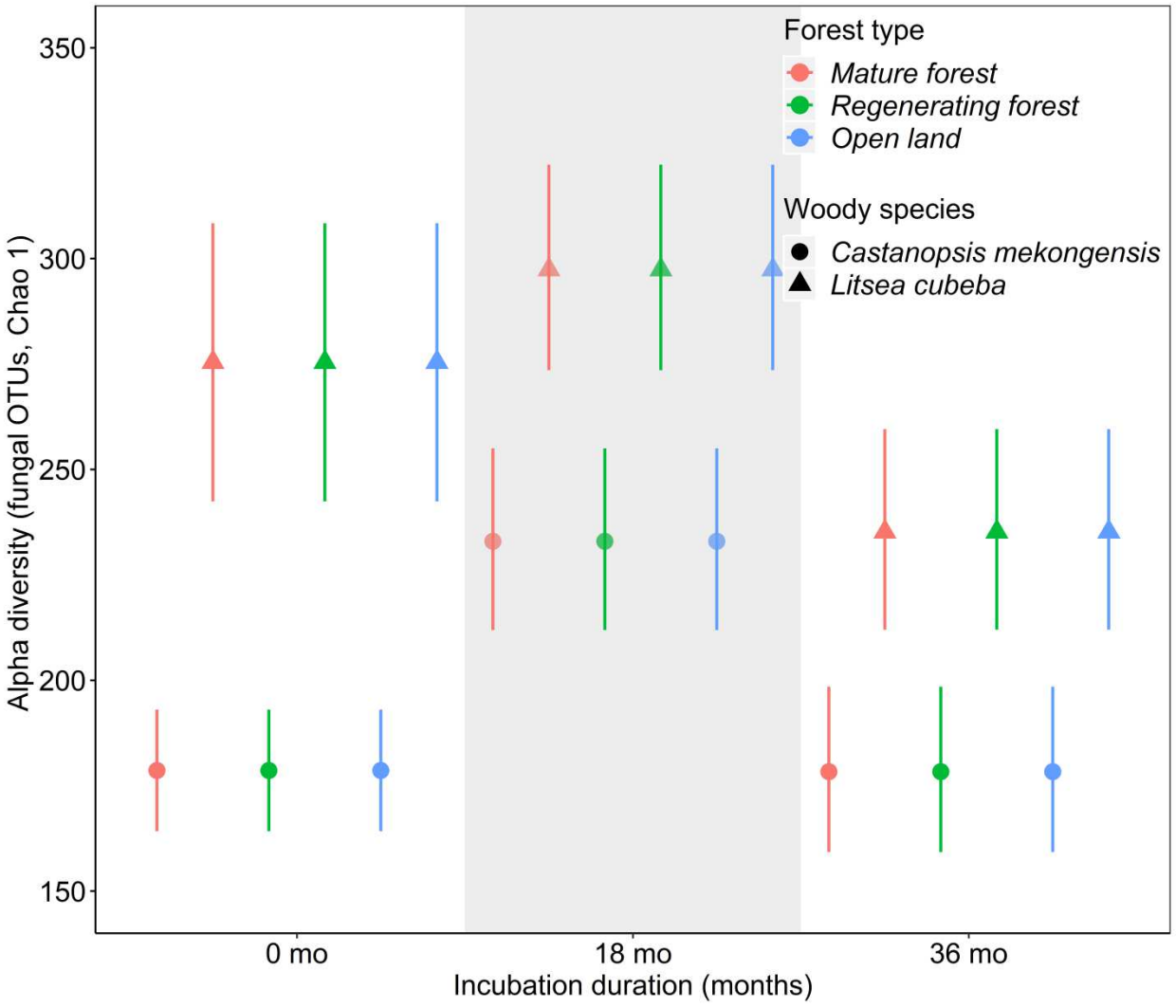

Woody species
Litsea cubeba
Castanopsis mekongensis
Forest type
Mature forest
Open land
Regenerating forest
Percentage wood specific gravity loss
50
40
30
20
18 months
36 months
Incubation duration

Fig. 1


A)
Castanopsis mekongensis
Open land
Regenerating forest
Mature forest
Litsea cubeba
Relative abundance (%)
0 mo
18 mo
36 mo
Incubation duration (months)
Phylum
Ascomycota
Basidiomycota
Others
B)
Trophic
Pathotroph
Saprotroph
Symbiotroph
C)
Rot
Brown Rot
Soft Rot
White Rot

925

926 **Fig. 2**

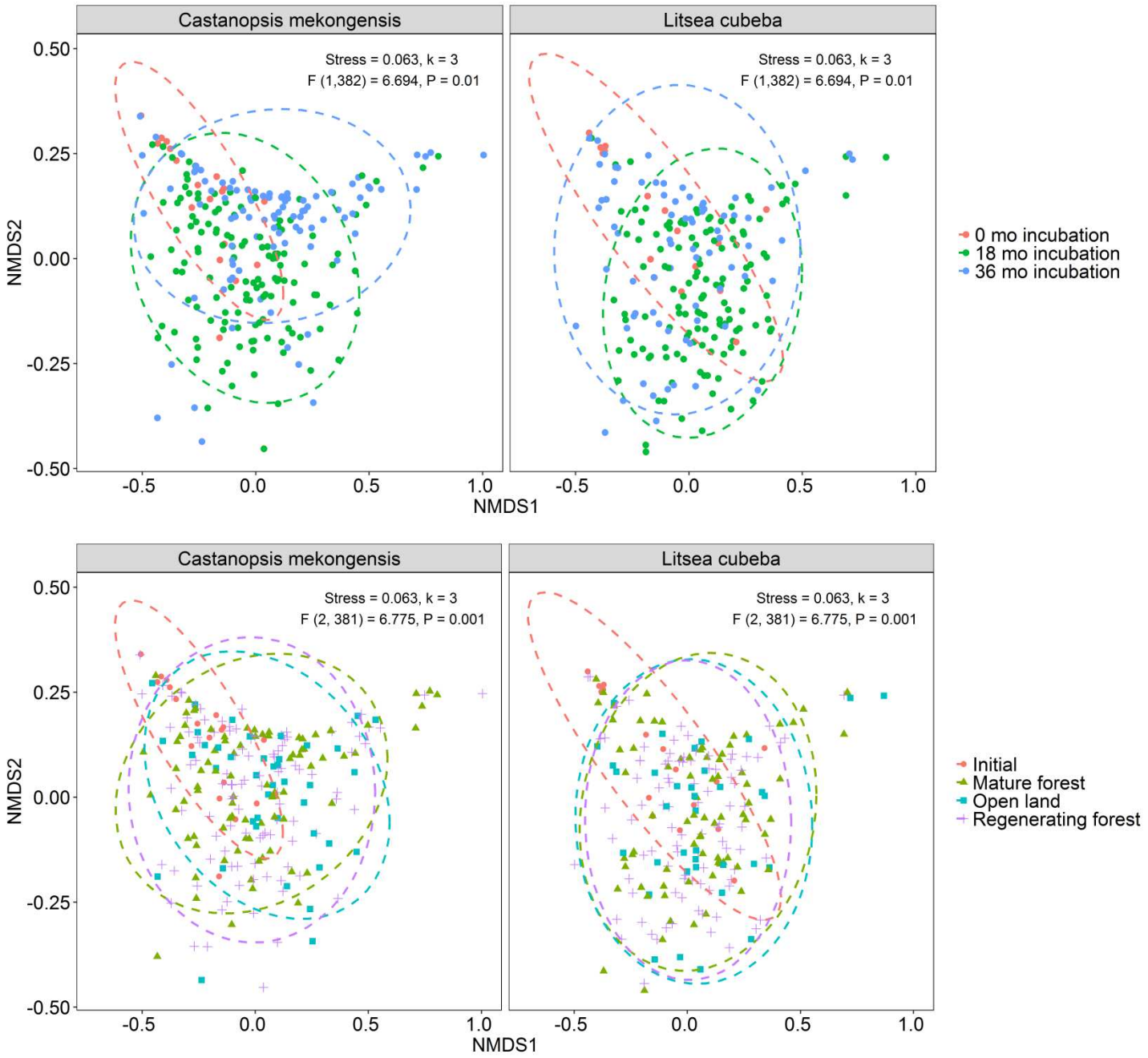

Forest type
Mature forest
Regenerating forest
Open land
Woody species
Castanopsis mekongensis
Litsea cubeba
Alpha diversity (fungal OTUs, Chao 1)
350
300
250
200
150
0 mo
18 mo
36 mo
Incubation duration (months)

927

928 **Fig. 2**

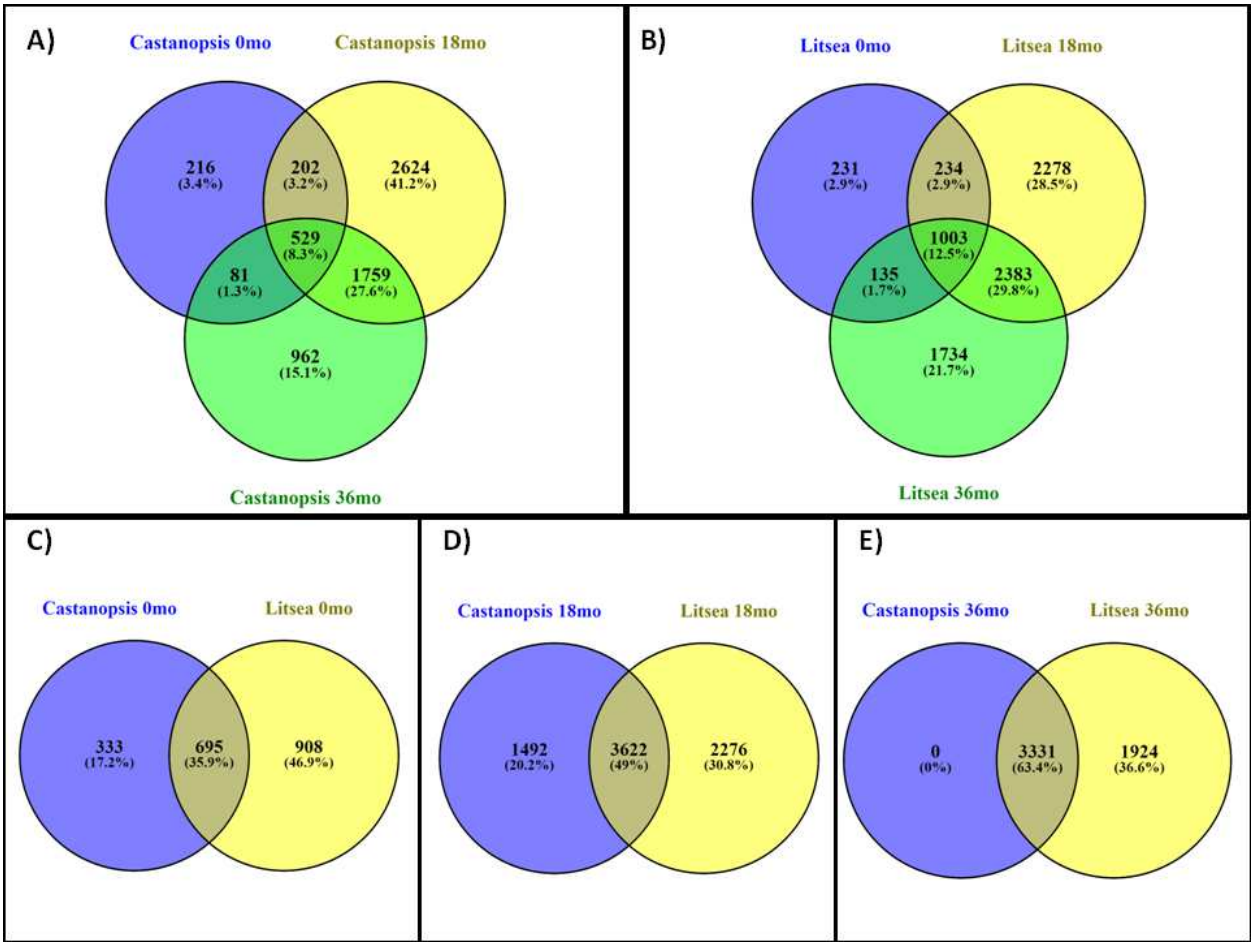
929

930


Castanopsis mekongensis
Litsea cubeba
Stress = 0.063, k = 3
F (1,382) = 6.694, P = 0.01
NMDS2
NMDS1
0.50
0.25
0.00
-0.25
-0.50
-0.5
0.0
0.5
1.0
0 mo incubation
18 mo incubation
36 mo incubation
Castanopsis mekongensis
Litsea cubeba
Stress = 0.063, k = 3
F (2, 381) = 6.775, P = 0.001
Initial
Mature forest
Open land
Regenerating forest

931

932 **Fig. 4**



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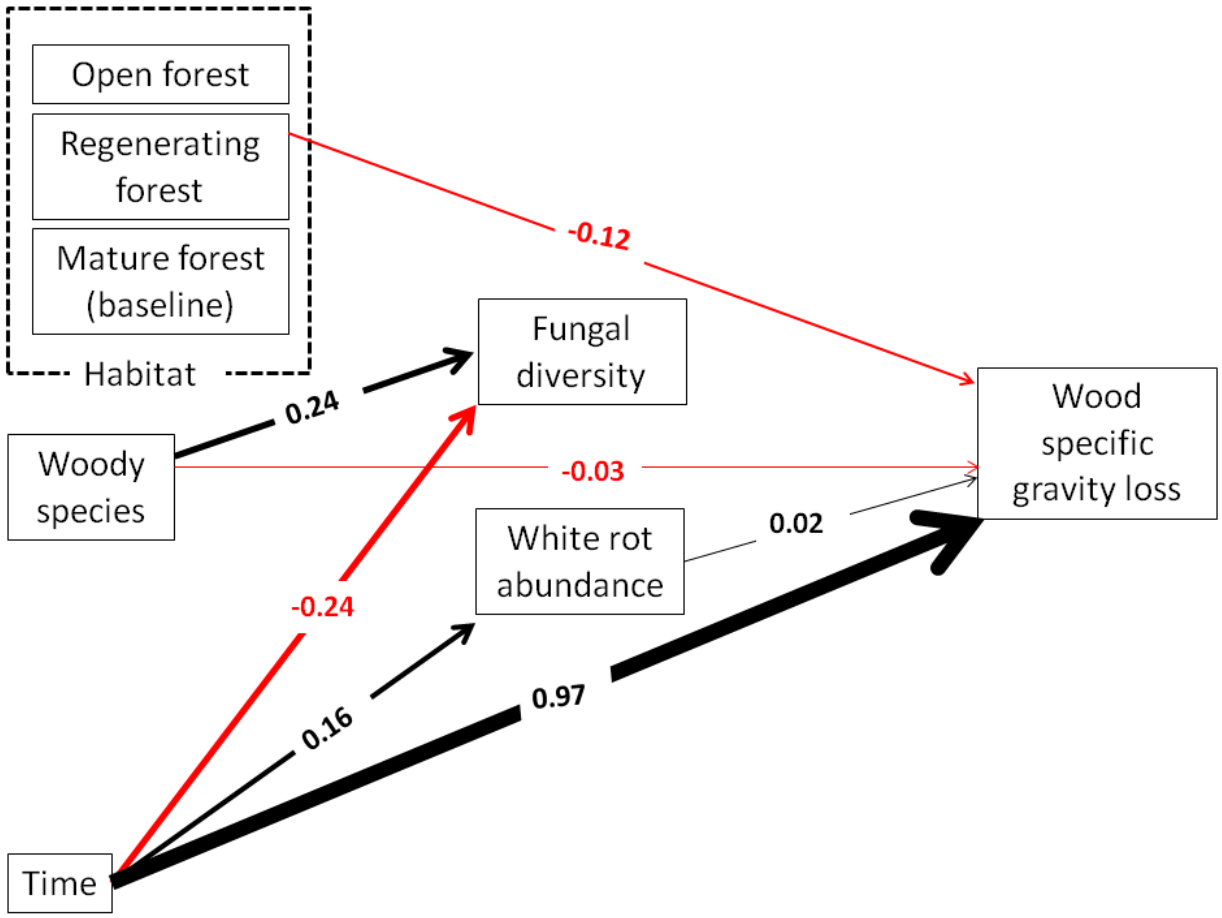
934

935 **Fig. 5**



936

937

938 **Fig. 6**

Tables

Table 1: Analysis of factors affecting Bray-Curtis dissimilarity between fungal communities using permutational multivariate analysis PERMANOVA with repeated measurement implemented in adonis for fungal communities found in log of *Litsea cubeba* and *Castanopsis mekongensis* during 36 month of wood decomposition in tropical montane forest, Mengsong, Xishuangbanna, SW, China. DF = Degree of freedom.

Parameters	DF	Sums of Squares	Mean Squares	F. Model	R^2	Pr(>F)
Time	1	1.565	1.565	3.560	0.009	0.001
Forest	2	1.166	0.583	1.327	0.007	0.001
Termites	1	0.409	0.409	0.930	0.004	0.176
Time:Termites	1	0.602	0.602	1.369	0.004	0.003
Residuals	377	165.726	0.440		0.976	

Figures

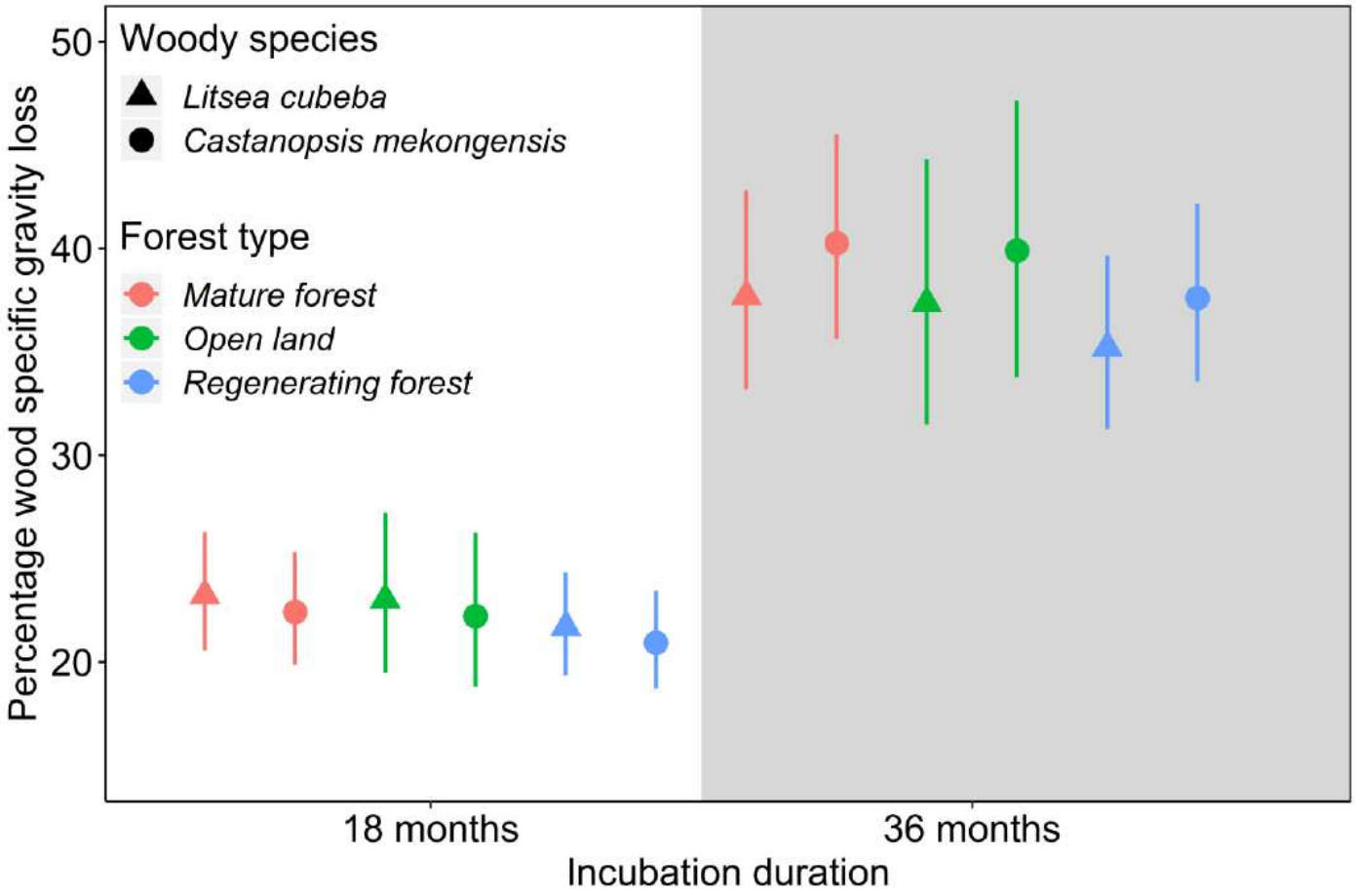


Figure 1

Percentage wood specific gravity (WSG) loss from logs installed across 28 plots in the Mengsong landscape after 18 mo and 36 mo incubation. The experiment used two species, Litsea cubeba and Castanopsis mekongensis. Points represent predicted mean values (±95% confidence interval) for two species (Litsea cubeba and Castanopsis mekongensis) with respect to disturbance category (mature forest, regenerating forest and open-land) and incubation time during 36 month of wood decomposition in tropical montane forest, Mengsong, Xishuangbanna, SW, China (Dossa et al. submitted).

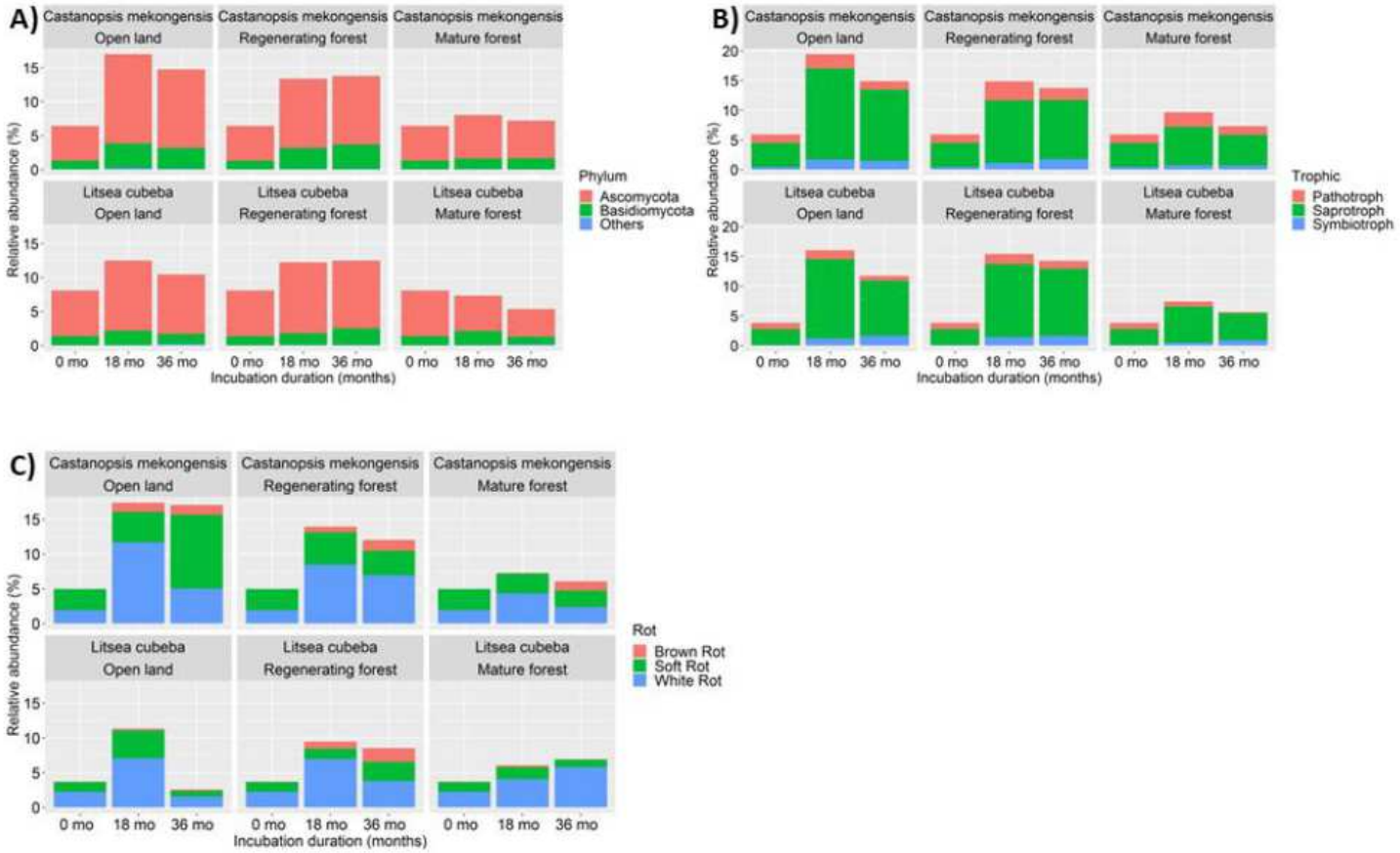


Figure 2

A) Average relative abundance of OTUs assigned to higher taxonomic units (Ascomycota, Basidiomycota, Other), B) Average relative abundance of OTUs assigned by FUNGuild to different tropic modes (Pathotroph, Saprotroph, Symotroph) and C) Average relative abundance of OTUs assigned by FUNGuild to different rot types (white-rot, brown-rot, and soft-rot fungi). In order to have comparable values, the relative abundance was calculated across all our samples regardless of habitats and species. And this relative abundance represents the proportion of OTUs assigned to each fungal guild identified via FUNGuild. Thus within each panel the total percentage sums to 100.

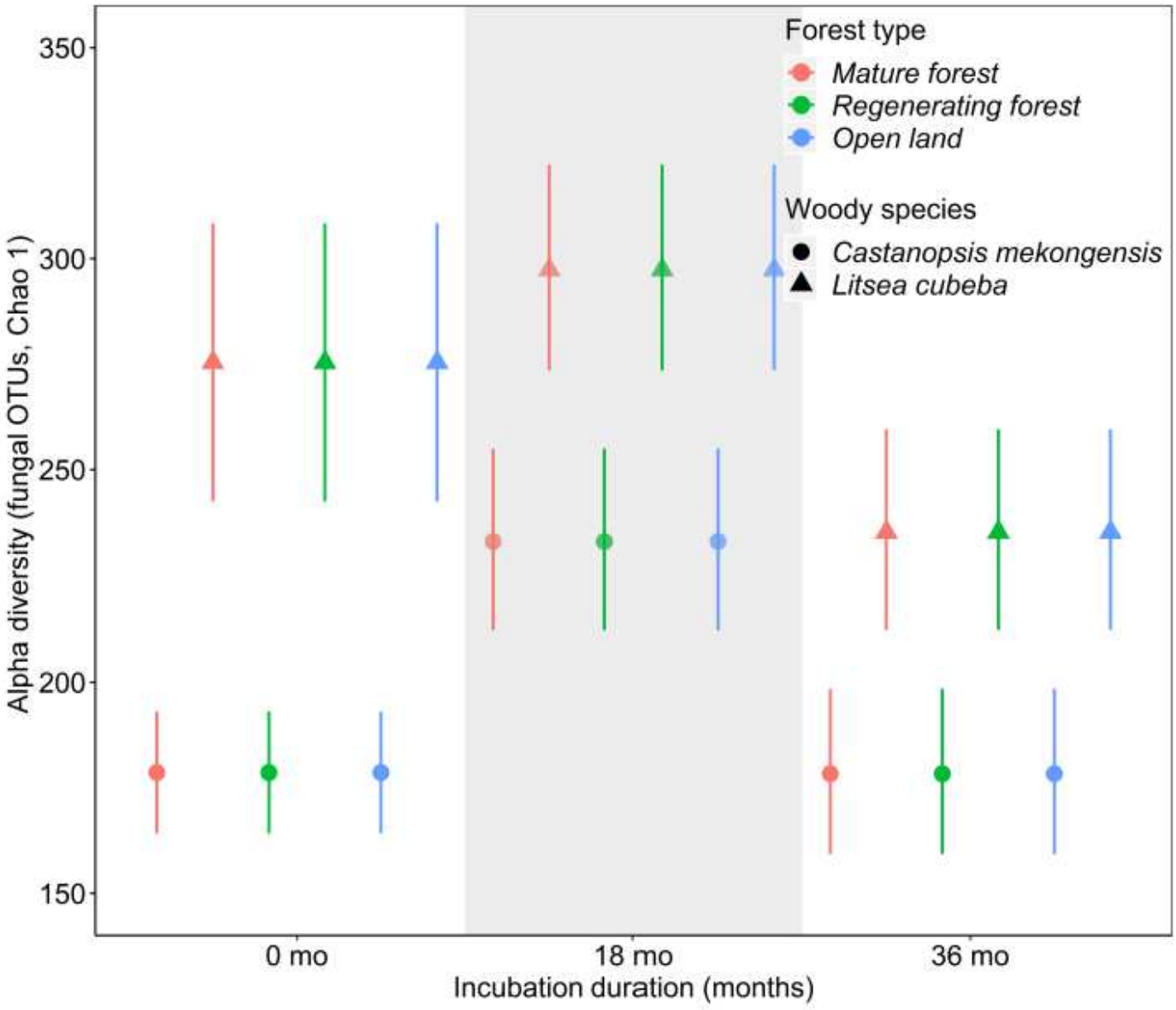


Figure 3

Change in fungal alpha diversity (Chao 1) across time and forest types for two wood species (Litsea cubeba and Castanopsis mekongensis) across habitat (mature forest in red,regenerating forest in blue and open forest in green) during 36 month of wood decomposition in tropical montane forest, Mengsong, Xishuangbanna, SW, China. Points represent predicted mean values (±95% confidence interval) for two wood species (Litsea cubeba and Castanopsis mekongensis) with respect to disturbance category (mature forest, regenerating forest and open-land) and incubation time during 36 month of wood decomposition in tropical montane forest, Mengsong, Xishuangbanna, SW, China. Note that for 0 mo error bars represent standard error of the mean (from pooled logs) while for the remainder time points the error bars are +/- 95 % from the best predicted model.

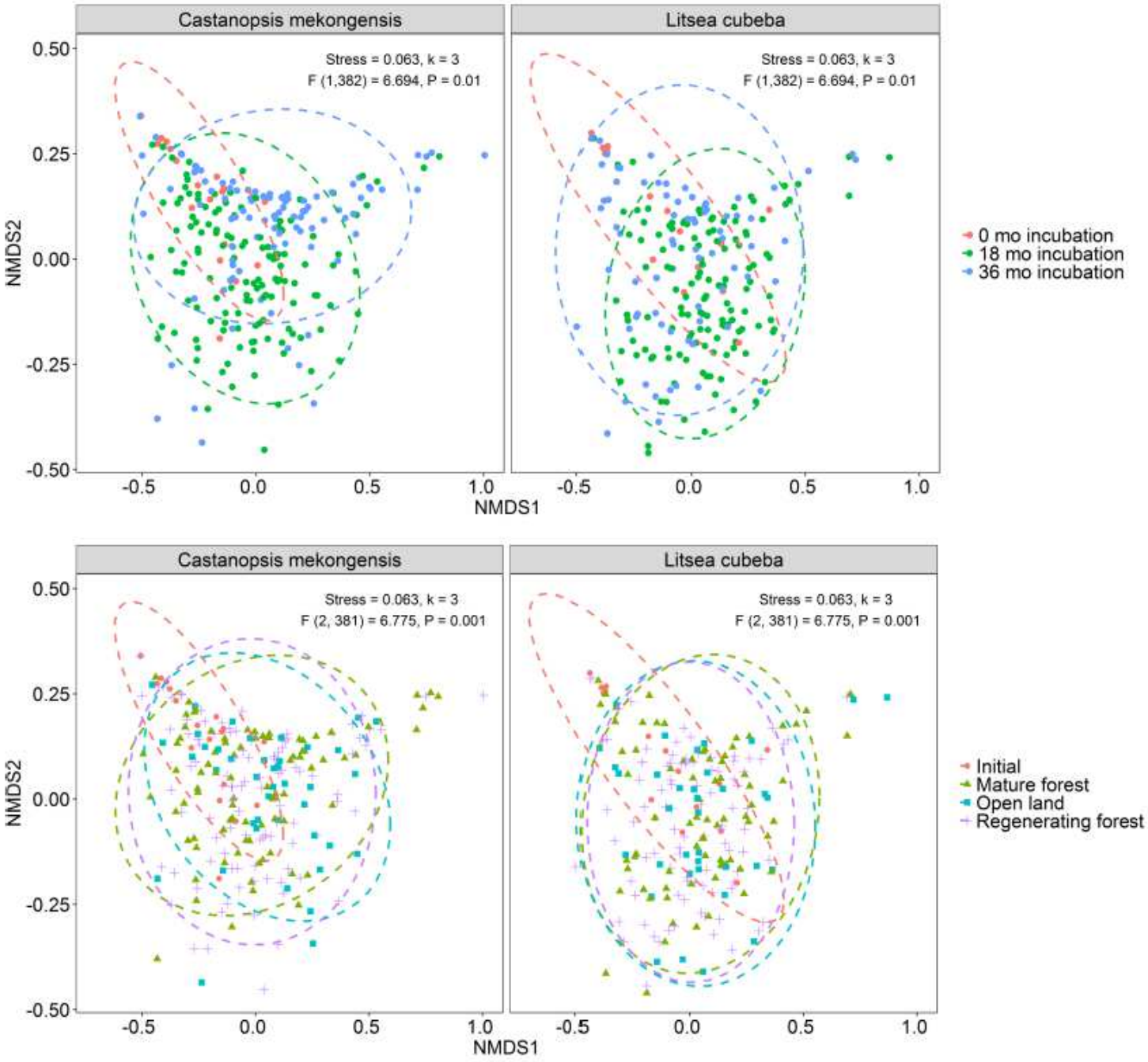


Figure 4

Change in fungal composition through time based on Bray-Curtis dissimilarity over 36 month of wood decomposition in tropical montane forest, Mengsong, Xishuangbanna, SW, China (each point representing a sample; 95% confidence intervals around centroids are shown (ellipses)). The upper two panels show ellipses (colored dashed lines) for incubation time. The lower two panels show ellipses for forest disturbance categories. Initial in the lower two panels represent the communities at 0 mo before incubation.

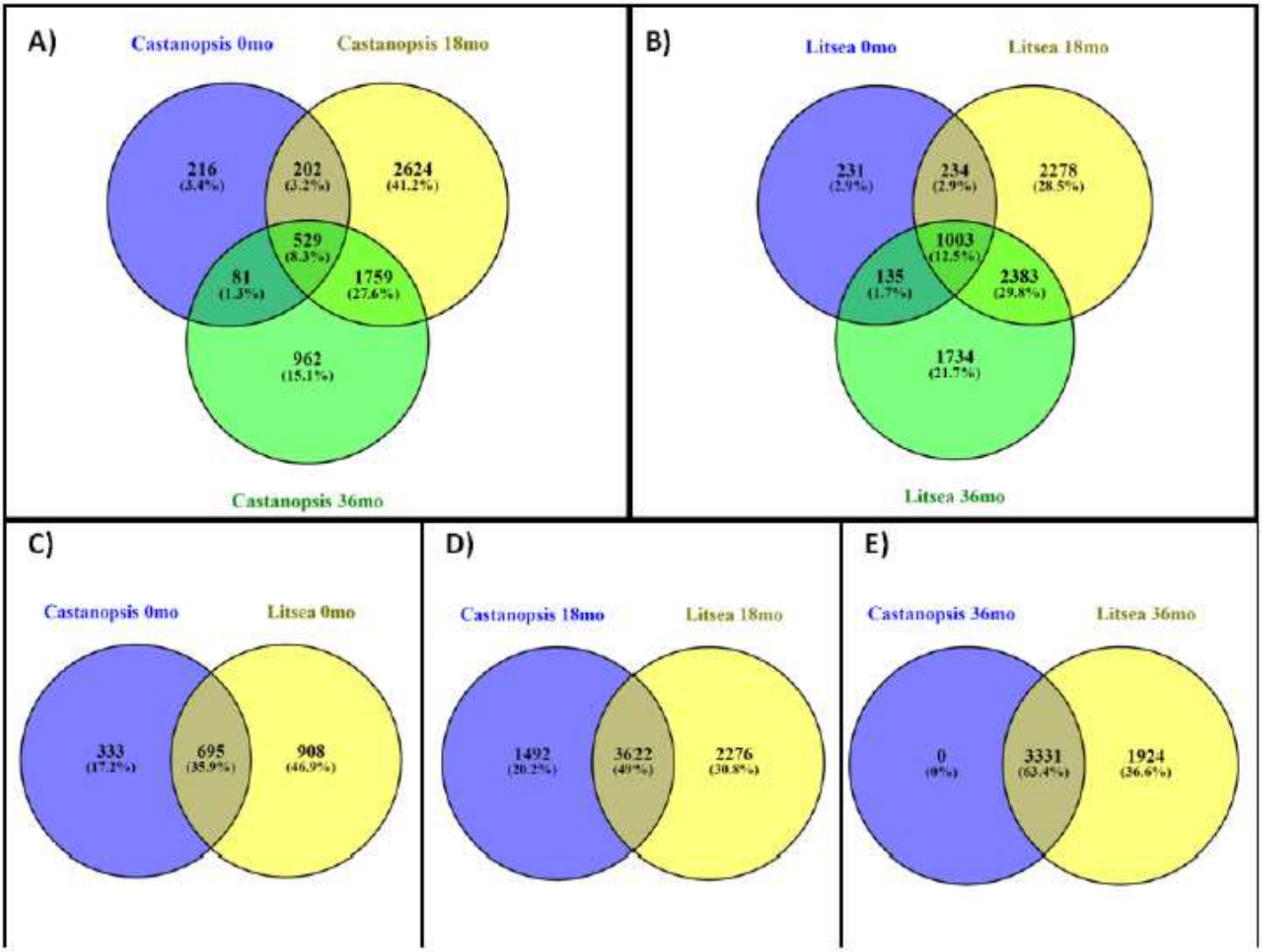


Figure 5

Venn diagram for displaying the temporal dynamics of unique and shared fungal species (OTUs) harbored by logs of A) Castanopsis mekongensis, B) Litsea cubeba, C) both species at initial time 0 mo, D) both species at 18 mo, and E) both species at 36 mo after incubation during 36 month of wood decomposition in tropical montane forest, Mengsong, Xishuangbanna, SW, China.

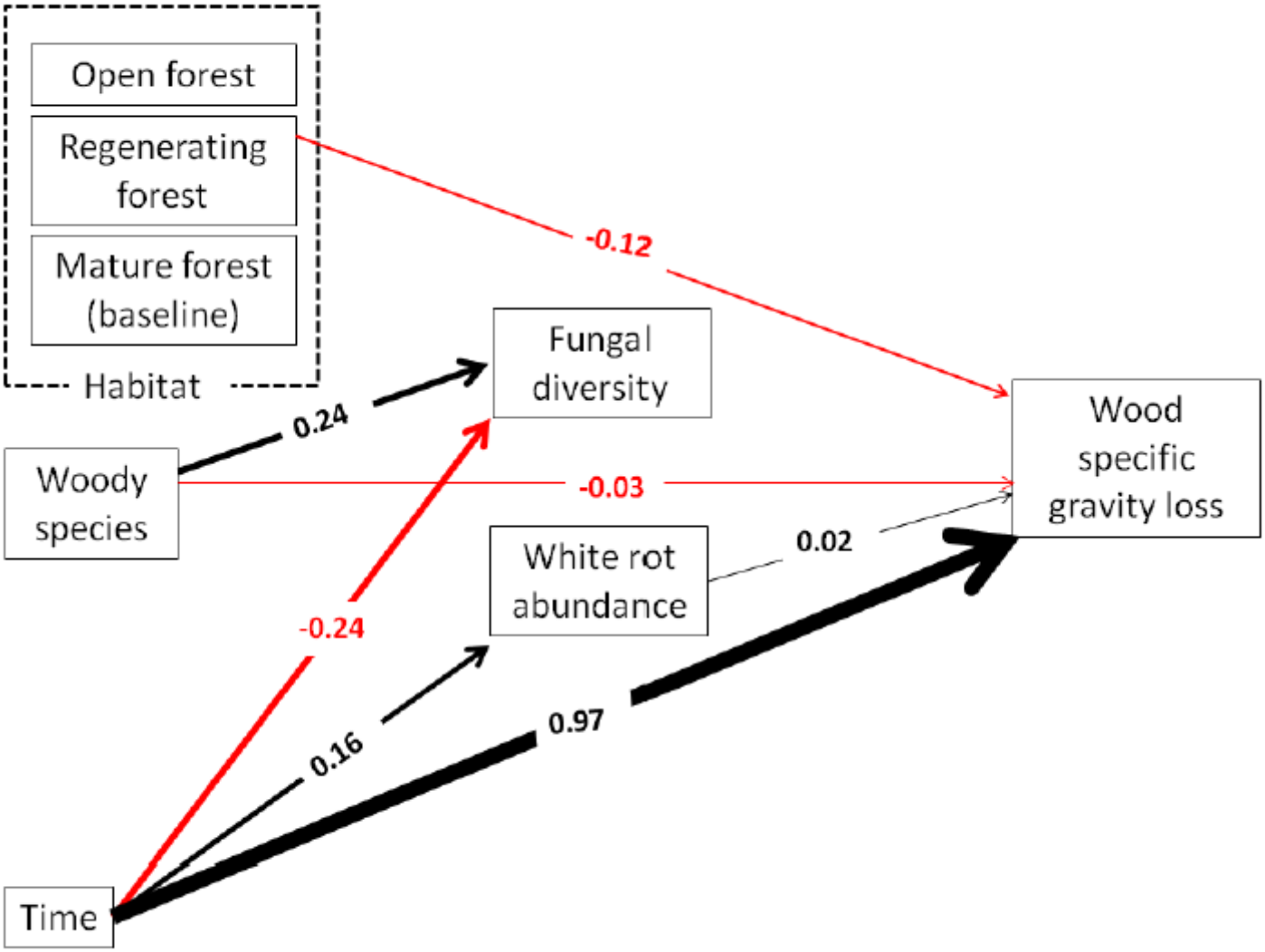


Figure 6

Structural equation modeling summarizing the direct and indirect effects of time, fungal alpha diversity, woody species, white rot abundance and forest type on wood specific gravity (WSG) loss on logs of Litsea cubeba and Castanopsis mekongensis during 36 month of wood decomposition in tropical montane forest, Mengsong, Xishuangbanna, SW, China. Thickness of the path equates to the strength of path coefficient. Black and red arrows indicate positive and negative paths respectively. For clarity we did not put the non-significant path coefficients in the diagram (but see Table S5 for full SEM results). Chi square = 4.17, P-value = 0.53 , degrees of freedom (DF) = 5, Comparative Fit Index (CFI) = 1. As habitat is a categorical variable with three levels, we created dummy variables with mature forest as the baseline level so any path regression coefficient for the other two levels represents the difference of that level from the baseline. Time was included as ordered categorical variable with 18 mo < 36 mo.

Supplementary Files

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