# Decadal recovery of fungal but not termite deadwood decay in tropical rainforest

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**Abstract**

1. Deadwood represents ~11% of carbon stocks in tropical rainforest ecosystems and its decay is driven largely by fungi and termites which contribute to the cycling of carbon and nutrients. Due to land use change, such as forest clearing, secondary growth tropical rainforests are increasingly prevalent around the globe. In secondary growth rainforest, studies found lower decay rates of leaf litter; however, little is known about how secondary growth affects deadwood decay.
2. Here, we tested whether termite and fungal functions in deadwood decay were similar in secondary growth and old-growth tropical rainforests. We assessed termites' ability to discover and consume deadwood as well as fungi community composition and contributions to wood decay. We placed non-native pine blocks, half of which were accessible to termites, in an old-growth rainforest site as a reference and two secondary growth rainforest sites that were restored four and eight years before the start of the experiment. Blocks were harvested every 6 months for 4 years (8 harvests). Using fungal ITS amplicon sequencing of sawdust samples from the decaying deadwood blocks at the seventh harvest, we determined wood-dwelling fungal community composition.
3. We found that termites discovered similar proportions of deadwood across the secondary growth and old-growth rainforest sites, although the decay rates of the discovered deadwood were lower in the secondary growth rainforest.
4. Further, fungal decay was similar to old-growth rainforest levels in the older but not younger secondary growth rainforest where it was slower, although differences among sites were small. Wood-dwelling fungal communities were similar between secondary growth and the old-growth rainforest.

5. Contrary to common assumptions, microbial communities and their wood decay functions were resilient and recovered relatively quickly within secondary growth rainforests, however, those of termites did not, which could reduce carbon and nutrient cycling in secondary growth rainforests.

**Keywords**

Carbon cycling, deadwood decay, microbes, secondary growth, secondary forest, termites, tropical rainforest

## Introduction

Most carbon held in plant biomass is returned to the atmosphere (Falkowski et al., 2000) or soil (Chapin et al., 2002) through the action of decomposers including microbes, especially fungi, and macroinvertebrates, especially termites (Cornwell et al., 2009). Annually, tropical ecosystems account for up to 78% of global forest carbon emissions (Harris et al., 2021). At the same time, due to land use change, such as cultivated land abandonment and active regeneration strategies in degraded land, secondary regrowth is contributing an increasing proportion to total rainforest area (Chazdon et al., 2016). Although these areas of secondary growth likely act as net carbon sinks due to an increase in standing tree biomass (Pugh et al., 2019), it remains uncertain how key ecosystem functions such as vegetation decay differ between old- and secondary growth forested systems (Poorter et al., 2021). An understanding of such differences can help predict net carbon sequestration rates of secondary growth tropical rainforests and their response to future climate perturbations.

In tropical rainforests, deadwood represents ~11% of carbon stocks globally (Pan et al., 2024) and acts as an intermediate carbon pool between live vegetation, soils and the atmosphere as it is broken down by fungi and termites. While fungi are important as decomposers of

deadwood globally, termites are especially important macroinvertebrates because they consume ~50% of woody debris in some systems (Griffiths et al., 2019; Wu et al., 2021; Zanne et al., 2022). As fungi and termites consume deadwood, carbon is mineralized and released to the atmosphere as $CO_2$ and $CH_4$ through respiration or to the soil as dissolved and particulate organic matter (Wijas, Allison, et al., 2024).

Wood-dwelling fungi and wood-feeding termites differ in how they consume deadwood. Decay fungi may already be present in living wood and can colonise deadwood via spores in the air, and hyphae in the soil, quickly beginning the decay process as wood senesces. Fungal communities go through a succession as different species have adapted to consume deadwood under a variety of conditions. General trends in fungal succession include an increase in the abundance of Basidiomycota relative to Ascomycota fungi. Most clades of fungi specialised on deadwood decay are found within the Basidiomycota and more specifically within the Agaricomycetes (Dossa et al., 2021; Lepinay et al., 2021; Purahong et al., 2024). Through priority effects, the initial colonisers of deadwood can alter the communities at later stages of decay, leading to variations in decay rates of deadwood (Fukami et al., 2010; van der Wal et al., 2015). As fungi live within deadwood and depend on extracellular enzymes, which require moist warm conditions to function, deadwood decay rates are highly dependent on moisture availability (A'Bear et al., 2014). On the other hand, termites consume deadwood in a two-step process. First, individual workers actively search for deadwood. Upon discovery, they recruit more workers to return and consume deadwood (Almeida et al., 2018). Compared to fungi, wood-feeding termites are less dependent on wood microclimate given their ability to move away from the deadwood they consume. This digestion typically occurs in termite nests and mounds under consistent moisture and temperature conditions (Singh et al., 2019). In fact, the proportion of deadwood consumed by termites relative to fungi can increase under dry conditions (Bunney et al., 2023; Wijas, Flores-Moreno, et al., 2024).

The recovery of fungal decay and community composition in tropical rainforests has mainly been studied in leaf litter. These studies found that fungal decay decreased in secondary compared with old-growth rainforests (da Silva et al., 2018; He et al., 2009; Lohbeck et al., 2015; Martius et al., 2004; Parsons & Congdon, 2008; Stone et al., 2020). Fungal community composition partly determines deadwood decay, with certain taxa promoting faster decay (Gora et al., 2019), yet we have little knowledge of fungal recovery during regeneration. In the one published study to date from China, deadwood decay rates were similar in 25-year-old secondary growth compared with old-growth rainforests (Dossa et al., 2020). In addition, no differences in fungal community composition were found between 25-year secondary and old-growth rainforest (Dossa et al., 2021).

The functional recovery of termites for deadwood decay is also uncertain. However, a review by Wijas & Atkinson (2021) suggested that wood-feeding termite abundance tends to recover relatively quickly during tropical rainforest regeneration. Most studies of termite community recovery in tropical rainforests to date were carried out in South America and found that species richness and abundance of wood feeding termites recovered within a year of regeneration initiation (de Paula et al., 2016; Duran-Bautista et al., 2020; Vitorio et al., 2019). Whether these results translate to other locations is unclear, although termite species and their contribution to deadwood decay vary across continents (Jones & Eggleton, 2011; Zanne et al., 2022).

To better understand the recovery of decay agent communities and their contributions to carbon cycling in secondary growth rainforests of different ages, we set up a 4-yr deadwood decay experiment. The experiment took place in lowland tropical rainforests in Australia; previous work in old-growth rainforests at this location found that termites accelerate decay (Cheesman et al., 2018; S. Law et al., 2023; B. J. Wijas, Flores-Moreno, et al., 2024). We started our experiment in tropical rainforests after 8 and 4 years of secondary growth and

targeted early to mid-stages of deadwood decay by termites and fungi through time. Our expectations were as follows:

1) As previous studies found that wood-feeding termite abundances recover relatively rapidly in secondary growth rainforests, we expected that termite discovery and decay of deadwood would be similar to old-growth rainforest levels within the secondary growth rainforests.

2) Given the relatively young state of the secondary growth rainforest and previous evidence from leaf litter studies showing lower levels of decay in secondary growth rainforests, we expected fungal decay rates of deadwood to be lower in the secondary compared to the old-growth forest. Additionally, we expected fungal communities to be different compared with old-growth rainforests. For instance, we expected lower relative abundances of fungi within the phylum Basidiomycota and within the class Agaricomycetes in secondary growth rainforests. Within the Agaricomycetes, we also expected communities to be composed of more wood feeding specialists such as Phaenerochaetes or Sistotrema in the old compared with the secondary growth rainforest.

3) Finally, we expected decay rates driven by termites and fungi in the older secondary growth to be more similar to decay rates in old compared to younger secondary growth rainforest.

## Methods

*Study sites*

We carried out our study in lowland tropical rainforests close to the Daintree National Park in the Australia Wet Tropics World Heritage Area in far North Queensland, specifically at an old-growth rainforest at James Cook University's Daintree Rainforest Observatory (DRO, 16°06′S, 145°26′E) and two secondary growth rainforest sites (16°10'S, 145°24'E) managed by Rainforest Rescue. The old-growth rainforest site (0.5 ha), which we considered as a control with no history of clearing, was dominated by *Carnarvonia araliifolia* (Proteaceae), *Flindersia bourjotiana* (Rutaceae) and *Acacia celsa* (Fabaceae) with subcanopy tree species including *Macaranga subdentata* (Euphorbiaceae), *Licuala ramsayi* (Arecaceae) and *Brombya platynema* (Rutaceae), (Flores-Moreno et al., 2024). The secondary growth rainforest sites were 8.8 km away from the old-growth rainforest and were replanted in 2010 (hereafter 2010 secondary growth, 0.1 ha) and in 2014 (hereafter 2014 secondary growth, 0.1 ha), respectively. The secondary growth rainforest was originally lowland rainforest before conversion to agriculture including pineapple, banana, and oil palm plantations around 1900. The secondary growth rainforest sites were abandoned in the 2000's before being actively replanted. The 2010 secondary growth rainforest was planted with 207 stems from 55 native tree species and the 2014 secondary growth rainforest was planted with 390 stems from 72 native tree species. At the time of replanting and again in 2018, metrics of forest structure were assessed (R. Kooyman, pers. comm). By 2018, canopy cover increased from 45.5% to 70.5% in the 2010 secondary growth rainforest and from 13% to 75% in the 2014 secondary growth rainforest. Litter cover decreased from 58% to 47% in the 2010 secondary growth rainforest while increasing from 30.6% to 67% in the 2014 secondary growth rainforest. Log and branch cover increased from 5% to 6.5% in the 2010 secondary growth rainforest and from 3% to 6.4% in the 2014 secondary growth rainforest. Additionally, naturally recruiting trees successfully established from the surrounding rainforest into the planted matrix for both secondary growth rainforest sites (R. Kooyman, pers. comm).

172

173 *Deadwood decay experiment*

174 To examine recovery of decay processes, we used wood blocks (9 cm x 5 cm x 5 cm) from a
175 non-native indicator species, *Pinus radiata*, which has been commonly used to assess the role
176 of fungi and termites in the decay of deadwood in global studies (Zanne et al., 2022). Blocks
177 were dried at 105°C for 48 h, weighed, and wrapped in Lumite mesh (280 um). The mesh
178 was sewn shut, making the blocks accessible to fungi but inaccessible to most
179 macroinvertebrates, following protocols from Cheesman et al. (2018); Law et al. (2023);
180 Wijas, Flores-Moreno, et al. (2024) and Zanne et al. (2022). In half the bags, mesh was
181 perforated with ten 5 mm holes on the bottom to allow access by macroinvertebrates, which
182 we expected would largely be termites. In total 240 wood blocks were placed across the three
183 sites (i.e., 40 accessible and 40 inaccessible to termites at each site), with blocks at each site
184 spread across five stations each separated by 5 m. Every 6 months, at the end of each dry and
185 wet season across four years (December 2018 – June 2022), we randomly collected one wood
186 block from each treatment at each station.

187 After collection, wood blocks were transported at ambient temperatures and processed in the
188 laboratory within 24h. Mesh was removed and any fungal fruiting bodies, termites, soil and
189 termite castings inside mesh bags were noted and separated from the wood block. The block
190 was then placed in an oven at 105°C until constant mass was reached. If the wood block
191 showed termite activity through imported soil, carton or termite galleries or if termites were
192 collected within the mesh bag, the block was considered to be discovered by termites. With
193 all blocks, the proportion of mass remaining was calculated as in Equation 1.

194 $$Proportional\ mass\ remaining\ =\ 1\ -\frac{(Initial\ dry\ mass)-(Harvest\ dry\ mass)}{(Initial\ dry\ mass)}$$ Equation 1

To assess differences in the micro-climate found within wood blocks, we also calculated their moisture content as is found in Equation 2.

$$Moisture\ content\ = \frac{(Harvest\ wet\ mass) - (Harvest\ dry\ mass)}{(Harvest\ wet\ mass)} * 100 \qquad \text{Equation 2}$$

*Fungal community*

To determine fungal community composition, we collected sawdust from each wood block following standard procedures (Powell et al., 2021). The wood blocks were surface sterilised by submerging and rotating them first in 95% ethanol for 5 seconds, then in 0.5% sodium hypochlorite for 2 minutes and finally in 70% ethanol for 2 minutes after which they were air dried for >2 hours. Sawdust was obtained from >10 holes using a sterilised 3mm drill bit to a depth of 2.5 cm across all the surfaces of each wood block. Sawdust was collected in tubes containing sterilised CTAB buffer. The tubes were stored at -80°C before further processing.

DNA was extracted from 60 mg of sawdust using a modified CTAB DNA extraction protocol (Doyle and Doyle 1987, Soltis et al. 1991), as described in Powell et al. (2021). DNA samples were submitted to the Ramaciotti Centre for Genomics (University of New South Wales, Sydney, NSW, Australia). Fungal amplicons were generated using fITS7 (50-GTGARTCATCGAATCTTTG-30; (Ihrmark et al., 2012) and ITS4 (50-TCCTCCGCTTATT GATATGC-30; (White et al., 1990), purified using the Agencourt AMpure XP system (Beckman Coulter, Lane Cove, NSW, Australia), and genomic libraries were prepared with the use of the Nextera XT Index Kit (Illumina, San Diego, California, USA). Paired-end (2 x 251 bases) sequencing was performed on the Illumina MiSeq platform. To process the DNA sequencing data, we used the approach described by Bissett et al. (2016) with a few modifications, as described in Nielsen et al., (2024). Putative taxonomic identities for fungal

OTUs were generated using BLAST (v.2.6.0, Altschul et al. (1990)) to compare representative sequences for each OTU to a reference database of gene sequences and taxonomic annotations (UNITE version 8.3, sh_general_release_dynamic_s_10.05.2021; Abarenkov et al. (2021)). Fungal ITS2 sequences were extracted using ITSx (Bengtsson-Palme et al. (2013), v1.1.3) for use during BLAST.

*Analysis*

Termite deadwood decay functions

First, we examined differences in the discovery rate of wood blocks by termites across sites and through time using a generalised linear model with a binomial distribution. The proportion of wood blocks discovered by termites within accessible bags was used as a response variable with site and time since deployment as explanatory variables. We compared the odds ratios by computing their 95% confidence intervals and checking for overlap.

Second, we examined differences in the decay rate of wood blocks discovered by termites at each site across the secondary growth gradient through time using the package *'litterfitter'* (Cornwell & Weedon, 2014) in R (v 4.1.2) and following methods used in Wijas, Flores-Moreno, et al. (2024). We considered that blocks discovered by termites were consumed by both termites and fungi. We used a Weibull function to model decay through time at each site and chose time to 50% mass remaining ($T_{50}$) as a proxy for decay rates. For the curve with the best fit, we used a bootstrapping method with 1000 repetitions to generate 95% confidence intervals for $T_{50}$ at each site across the secondary growth gradient. We compared $T_{50}$ of each site to assess differences depending on time since secondary growth started. We considered that differences were significant if 95% confidence intervals did not overlap.

Fungal deadwood decay functions and community composition

To assess fungal deadwood decay, we generated $T_{50}$ for blocks undiscovered by termites at each site across the secondary growth gradient using the same analyses we carried out for termite discovered blocks. We considered that blocks undiscovered by termites were mainly consumed by fungi.

For fungal community composition, first, we compared differences in OTU richness among sites across the secondary growth gradient with Analysis of Variance (ANOVA). Second, we examined differences in relative abundances of Basidiomycota, Ascomycota and Agaricomycetes across the sites. For this, we calculated the proportion of OTU reads belonging to each phylum or to the class Agaricomycetes for each wood block. We used generalised linear mixed effects models with proportion of reads as an explanatory variable against site as a response variable and applied a quasibinomial distribution given the proportional nature of the response variable. Finally, to visually represent differences in fungal communities among sites across the secondary growth gradient, we used non-metric multidimensional scaling (NMDS) with Sorensen distance based metrics in *'vegan'* (Oksanen et al., 2001). We calculated the Sorensen distance based on the presence or absence of Agaricomycete fungal OTUs in each wood block and excluded OTUs which were found in <3 wood blocks. To examine the differences in the community composition of fungi, we ran a PERMANOVA (>9999 permutations) with site as the response variable.

## Results

*Termite deadwood decay*

We did not observe a difference in termite discovery between the old-growth rainforest and the 2010 secondary growth rainforest (Table 1) or between the old-growth rainforest and the 2014 secondary growth rainforest (Table 1).

We observed that termite discovered deadwood decayed significantly faster compared with undiscovered deadwood in the old-growth rainforest as has been reported in Wijas et al. (2024b), but not in the secondary growth rainforests (Figure 1, Table S1). Decay rates for termite discovered deadwood were significantly lower in both secondary growth rainforests than in the old-growth rainforest (Figure 1, Table S1).

*Fungal deadwood decay and community composition*

In line with our predictions, we observed that undiscovered deadwood undergoing only a fungal decay pathway decayed slower in the 2014 secondary growth rainforest compared with the old-growth rainforest (Figure 1, Table S1). However, decay rates of undiscovered deadwood in the 2010 secondary growth rainforest did not differ from the old-growth rainforest (Figure 1, Table S1).

At the time of fungal community sampling (harvest 7 after 3.5 years of decay), we did not observe a difference in mass remaining (n = 22, F-value = 0.52, Df = 2, P-value = 0.6) or moisture content of deadwood undiscovered by termites among sites (n = 22, F-value = 0.84, Df = 2, P-value = 0.45), (Figure 2).

From our deadwood samples, we obtained 964 OTUs, of which 87.7% belonged to the phylum Basidiomycota and 11.5% belonged to the phylum Ascomycota. We did not observe a difference in the relative abundance of Basidiomycota (n = 22, F-value = 0.63925, Df = 2, P-value = 0.7264) or Ascomycota among sites (n = 22, F-value = 0.7207, Df = 2, P-value = 0.6974, Figure S1). At the class level, 74.9% of OTU reads belonged to the Agaricomycetes.

We did not observe a difference in the relative abundance of Agaricomycetes among sites (n = 22, F-value = 1.38, Df = 2, P-value = 0.5, Figure S2). We also did not observe a difference in OTU richness of Agaricomycetes among sites (n = 22, F-value = 1.68, Df = 2, P-value = 0.08, Figure 2c), and there were also no differences observed in community composition of Agaricomycetes within deadwood among sites (n = 22, F-value = 0.52, Df = 2, P-value = 0.97), (Figure 3).

## Discussion

In our study using a rainforest secondary growth gradient, the functional role of different biotic deadwood decay agents (fungi vs termites) differed in their rates of similarity to old-growth rainforest over 12 years of secondary growth in a tropical rainforest in Australia. Contrary to our first prediction, termite decay did not resemble old-growth rainforest levels even by 12 years of secondary growth, and contrary to our second prediction, fungal deadwood decay and community composition appeared similar to old-growth rainforest levels by at least 8 years of secondary growth. Our third prediction was partly supported, with fungal deadwood decay in the older secondary growth rainforest being closer to that of the old-growth rainforest than the younger secondary growth; however, there were no differences in termite decay among secondary growth sites. Given the dominant and interacting nature of fungi and termites in tropical rainforest ecosystems (Griffiths et al., 2019; Wijas, Flores-Moreno, et al., 2024), full recovery of the decay process will not happen until termite functions return. The uneven recovery of different biotic decomposers has consequences for the decay of deadwood, a key ecosystem process returning carbon and nutrients to the atmosphere and soil.

Termite decay function only partially resembled old-growth rainforest after 12 years of secondary growth. The first step of termite decay, discovery of deadwood, was similar in secondary growth rainforests compared with the old-growth rainforest, meaning termites are present in these different sites. However, once discovered by termites, the decay of deadwood in secondary growth remained lower than in the old-growth rainforest and did not exceed decay of undiscovered deadwood. These results suggest that termites were consuming less of the resources that they discovered in the secondary growth rainforests. The fact that termite discovery was similar but decay was lower is intriguing. This inability to boost decay rates may be due in part to a reduction in the size or number of the termite colonies or in the termites themselves in the secondary growth rainforests. While very little is known of the demography of termite populations in tropical Australian rainforests, species in Australian savanna ecosystems, colonies of some species can take up to 25 years to reach maturity and peak in biomass (Lee & Wood, 1971). Additionally, younger mounds tend to have smaller individuals (Lepage & Darlington, 2000). Taken together, it is plausible that the total termite biomass, and hence capacity to consume wood, was lower in the secondary growth forest. Studies from other tropical rainforests have shown that decreased termite abundances were linked to decreased decay rates of deadwood and a reduction in the contribution of termites to deadwood decay compared with fungi (Griffiths et al., 2019).

Similarly, deadwood decay driven by fungi was slower in the 2014 secondary growth rainforest than in the old-growth rainforest, but the 2010 secondary growth rainforest appeared to have comparable decay levels to old-growth rainforests. Notably, these differences in fungal decay among the sites were relatively small with time to 50% mass remaining just under 3 years for old-growth rainforest and just under 3 ½ years in the 2014 secondary growth rainforest. The rapid woody biomass recovery and closure of the canopy within the secondary growth sites may have allowed for improved moisture conditions to

increase enzyme efficiency for fungal activity (Bonner et al., 2020; Lohbeck et al., 2015). Quick recovery of fungal function likely has consequences for the soil, given the importance of decay for soil carbon and nutrient stores. For instance, work has shown quick recovery in soil carbon and nitrogen stocks in secondary growth rainforests (Poorter et al., 2021), which could be partly due to recovery of litter and deadwood decay.

The resilience of fungal decay functions was underpinned by the similarity of the fungal communities between the two secondary growth rainforests and the old-growth rainforest. We further found similar proportions of Basidiomycota and Agaricomycetes in deadwood across the secondary growth gradient suggesting that their abundances and capability of colonising deadwood were not hindered even in secondary growth rainforests. Our results add to findings from (Dossa et al., 2021) and highlight that the functional role and composition of deadwood fungal communities in tropical rainforests may largely recover within a decade of secondary growth.

In conclusion, our results have implications for how we understand carbon cycling in secondary rainforest ecosystems. Differences in the strategies used by termites versus fungi to process carbon in deadwood may lead to different pathways of carbon cycling within secondary growth rainforests. For instance, most termite species contain methanogenic bacteria in their guts, producing methane while consuming deadwood (Law et al., 2024), while fungi decay deadwood with extracellular enzymes without methane production. Given the lower rates of termite-driven decay in secondary growth rainforests, we would expect to see lower rates of carbon cycling, as well as different forms of carbon release compared with old-growth rainforests. While our results provide initial insight into recovery of fungal and termite functioning in deadwood decay after rainforest regeneration in Australia, future research should address the consequences for transfer of carbon into soil and the atmosphere across global ecosystems.

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**Author contributions**

AEZ, SDA, PE and LAC designed the experiment. AEZ, SDA and PE obtained funding for the project. HF, AWC, and AEC led the data collection with help from all the other authors. JRP carried out the bioinformatics for metagenomics. BJW led the data analysis with help from AEZ, JRP and SDA. BJW wrote the manuscript with input from all of the other authors.

**Data availability**

The data will be made available on Dryad upon publication of the manuscript.

**Conflict of Interest Statement**

We declare no conflict of interests.

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611 **Tables and Figures**

612 Table 1 – Model output of termite discovery against time since deployment of wood block
613 and site. P-values in bold are significant.

| *Predictors* | *Odds Ratios* | *CI* | *p-value* |
|---|---|---|---|
| (Intercept) | 0.01 | 0.00 – 0.05 | **<0.001** |
| Time since deployment (in years) | 4.21 | 2.30 – 8.91 | **<0.001** |
| 2010 secondary growth | 0.30 | 0.07 – 1.11 | 0.081 |
| 2014 secondary growth | 0.49 | 0.13 – 1.72 | 0.269 |

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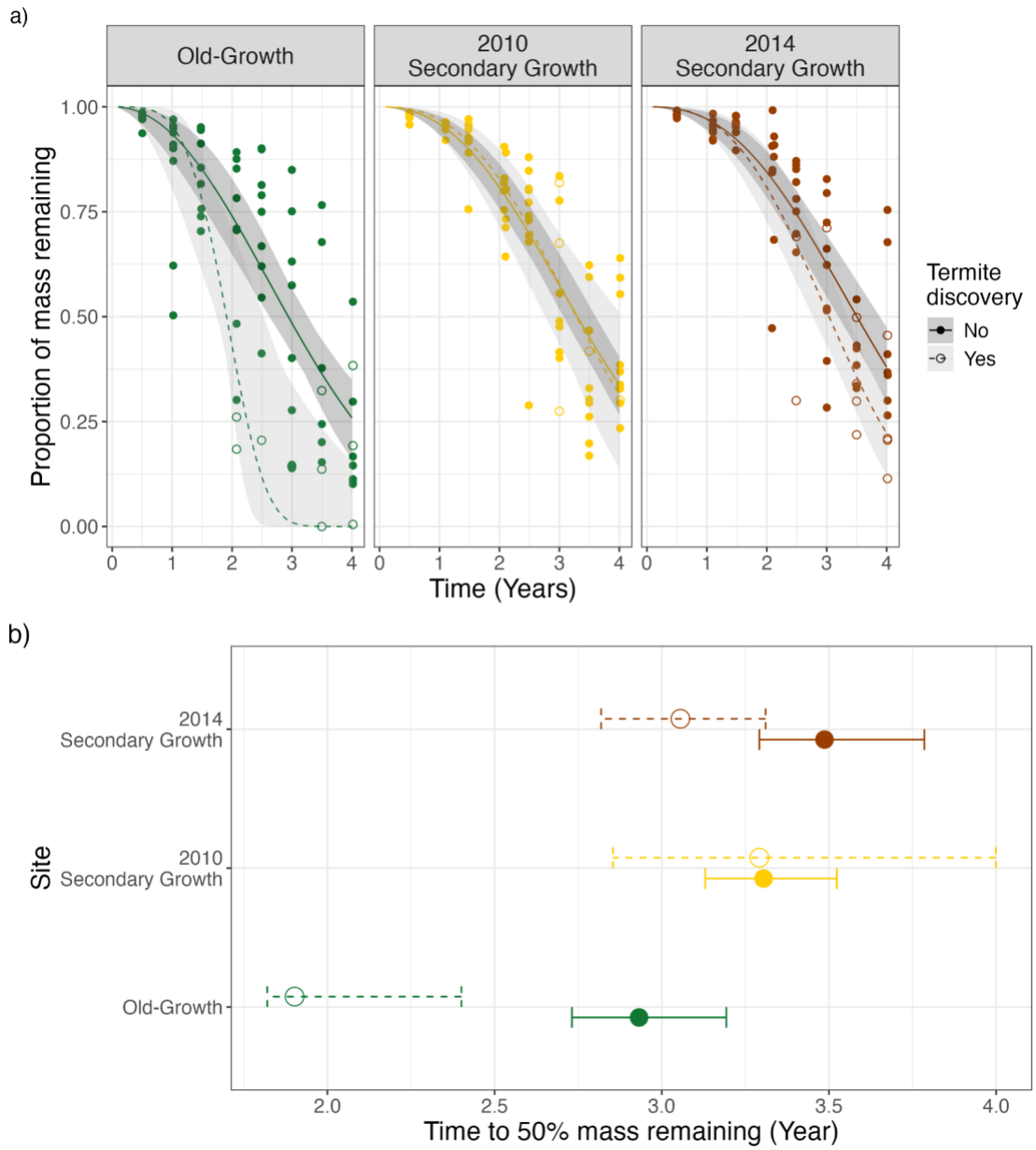
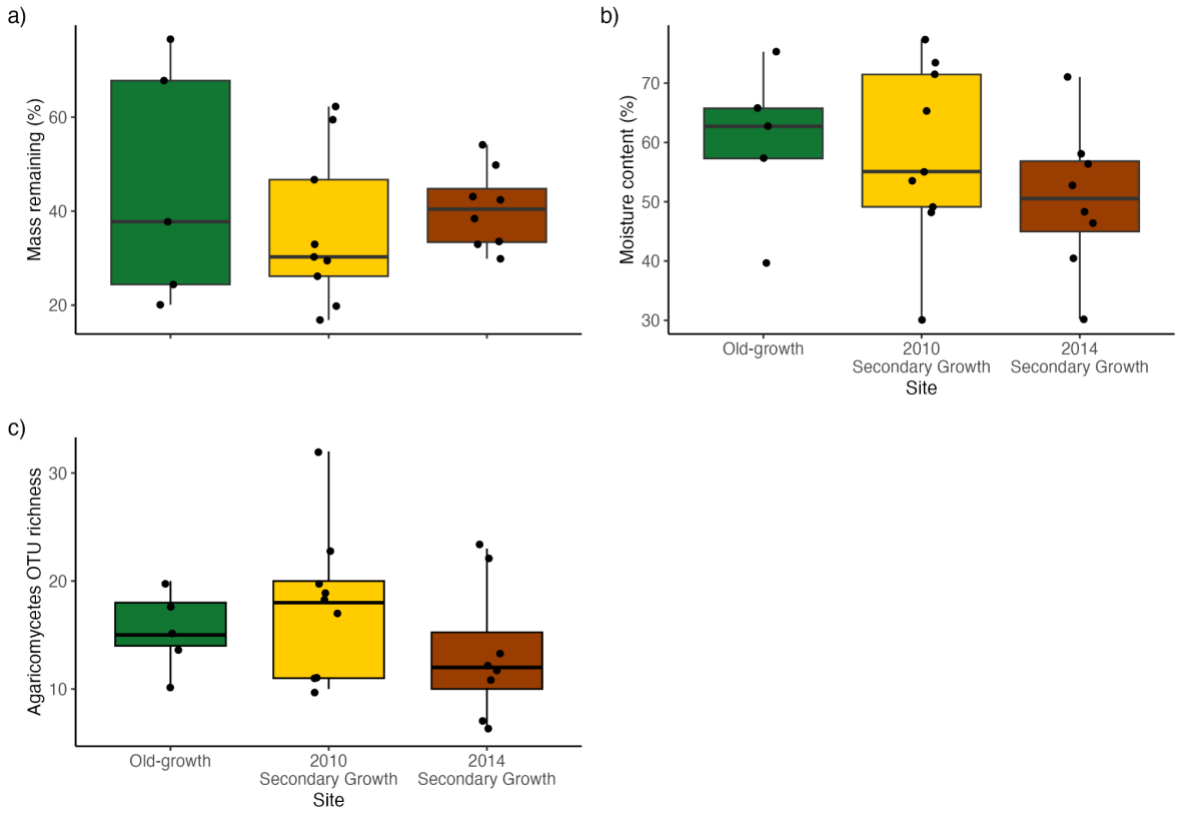



617

618 Figure 1 – a) Modelled proportion mass remaining through time (solid lines) of blocks
619 discovered (dashed lines) or undiscovered (solid lines) by termites, (± 95% CI) across sites
620 along the rainforest secondary growth gradient with each point representing an individual
621 wood block discovered (open circles) or undiscovered (solid circles) by termites. b) Time to
622 50% mass remaining (± 95% CI) for wood blocks discovered (open circles and dashed lines)
623 or undiscovered (solid circles and lines) by termite across sites along the rainforest secondary
624 growth gradient.

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626 Figure 2 – a) Mass remaining, b) moisture content and c) Agaricomycetes OTU richness in

627 deadwood across the secondary growth gradient.

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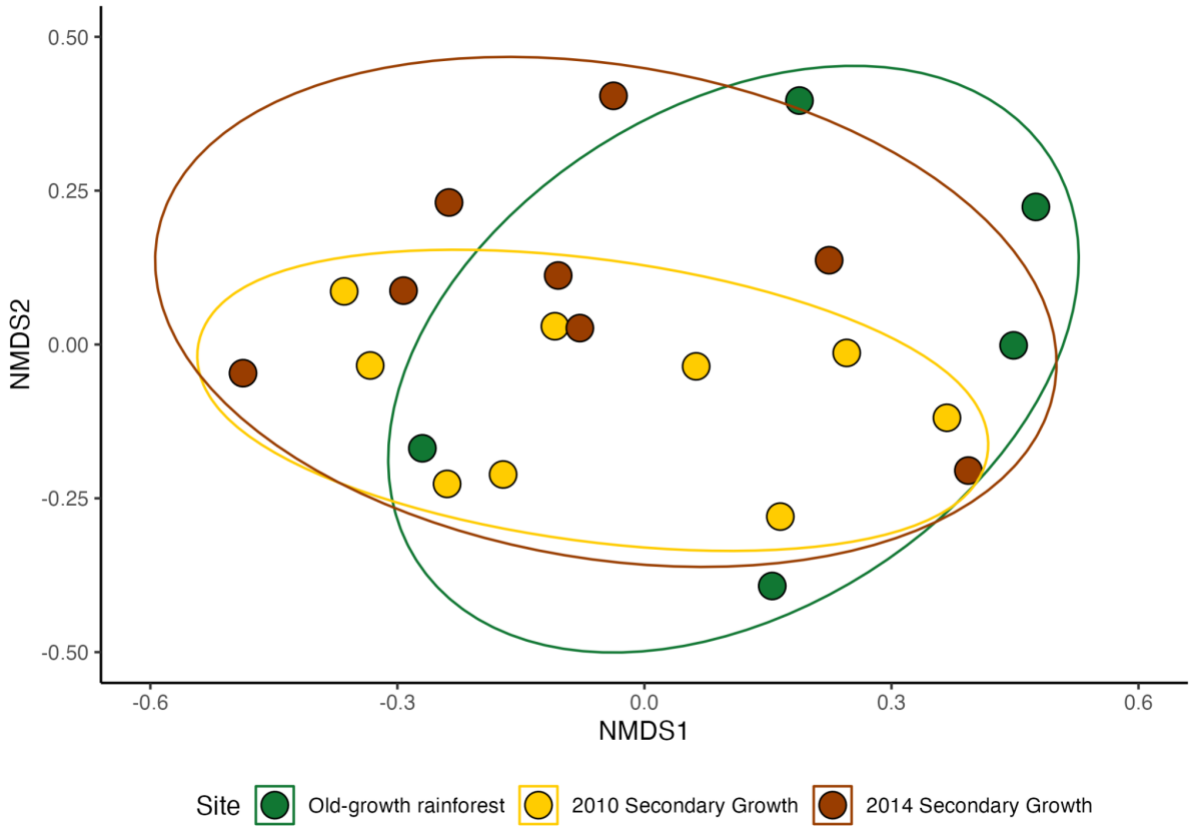


Figure 3 – Nonmetric multidimensional scaling (NMDS) plot of Agaricomycetes fungal community composition in deadwood (represented as the presence/absence of OTUs) using Sorensen distances in old-growth (green), 2010 secondary growth (yellow) and 2014 secondary growth (brown) rainforests. The ellipses were estimated using the Khachiyan algorithm and plotted with the package *'ggforce'* (Pedersen, 2024). The NMDS stress value was 0.19.

## Supplementary materials

Table S1 – Average time to 50% mass remaining ($T_{50}$, ± 95% CI) of wood blocks undiscovered versus discovered by termites across the secondary growth gradient. Superscript letters indicate whether the confidence intervals overlap with two observations with the same letters indicating an overlap.

| Site | Undiscovered by termites *$T_{50}$ (95% CI)* | Discovered by termites *$T_{50}$ (95% CI)* |
|---|---|---|
| Old-growth | 2.93 (2.71 - 3.20)$^{a}$ | 1.90 (1.81 - 2.39)$^{b}$ |
| 2010 secondary growth | 3.3 (3.13 – 3.55)$^{ac}$ | 3.29 (2.85 – 3.99)$^{ac}$ |
| 2014 secondary growth | 3.49 (3.28 – 3.79)$^{c}$ | 3.06 (2.79 – 3.31)$^{ac}$ |

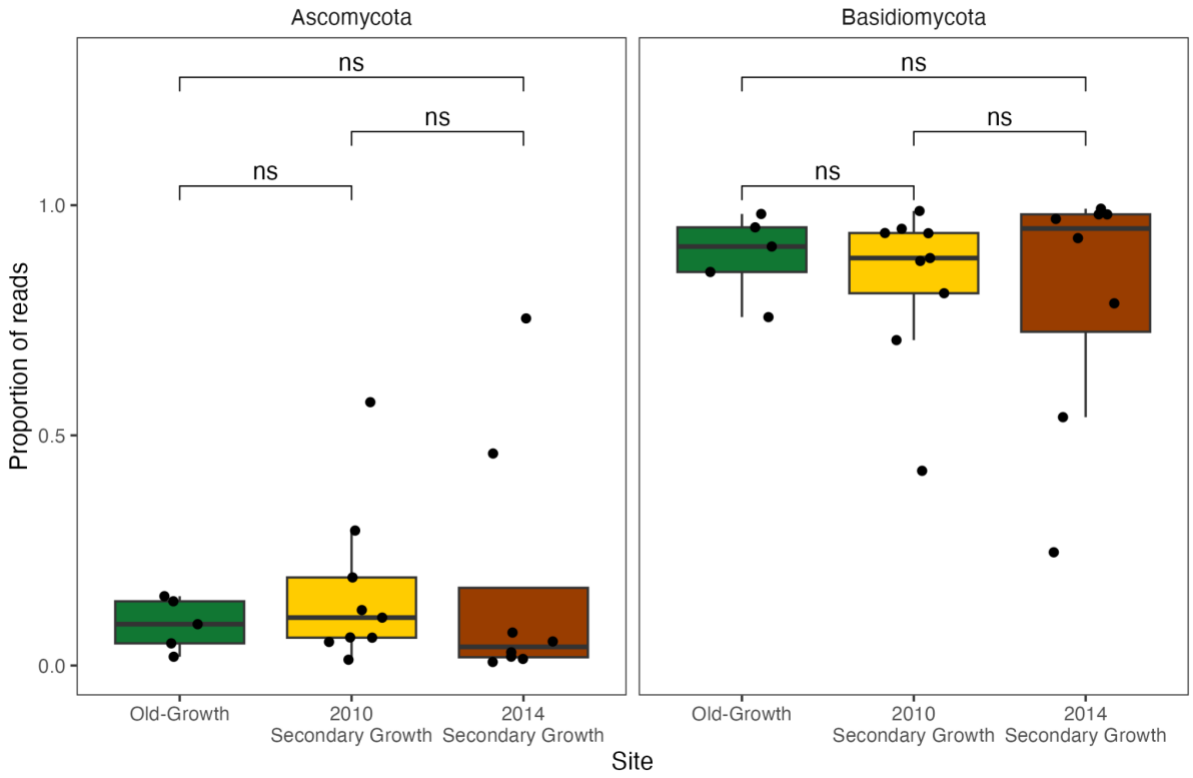


Figure S1 - Proportion of reads identified as Ascomycota or Basidiomycota in the deadwood across the secondary growth gradient. The bars above the plots indicate the statistical difference across mean plot comparisons using Wilcoxon test from the 'ggpubr' package (Kassambara, 2023), (ns = non-significant).

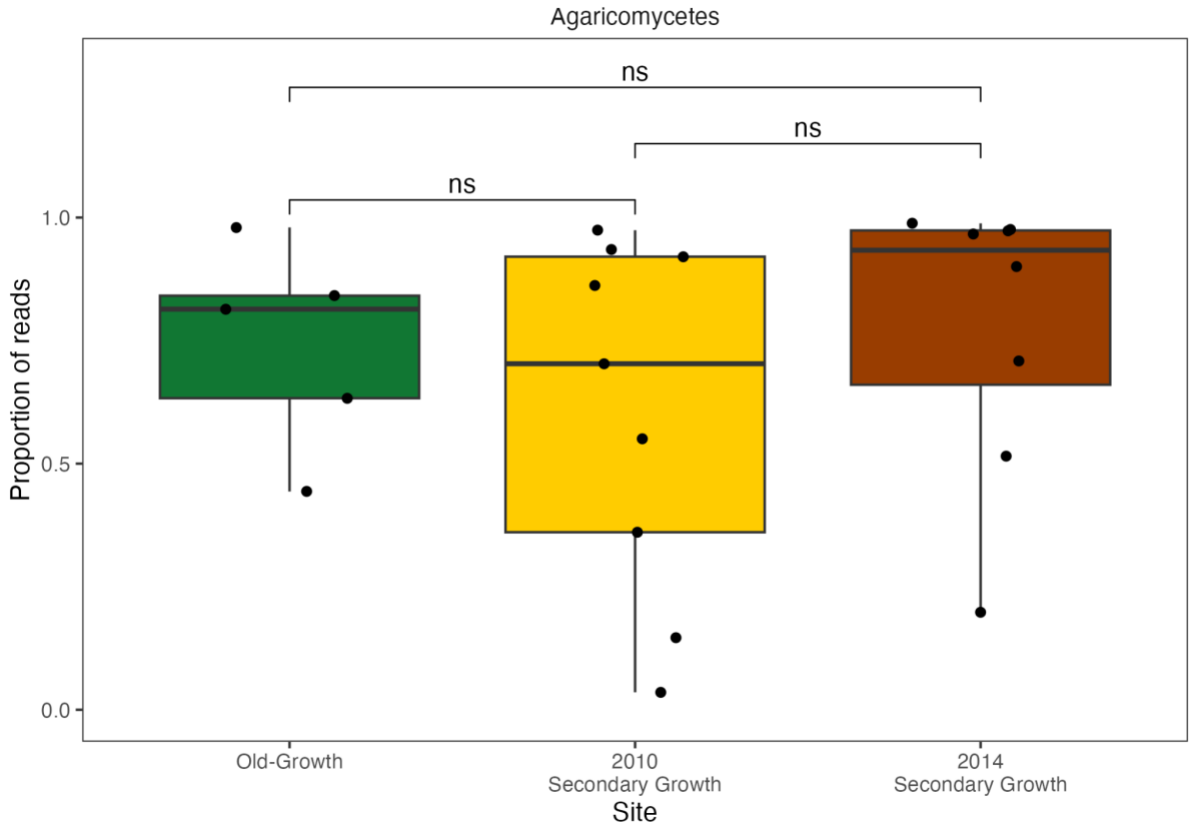


Figure S2 - Proportion of reads identified as Agaricomycetes in the deadwood across the secondary growth gradient. The bars above the plots indicate the statistical difference across mean plot comparisons using Wilcoxon test from the 'ggpubr' package (Kassambara, 2023), (ns = non-significant).