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Zaiton Lokman

Department of Mycology and
 Plant Pathology, Sabah Centre
 for Marine Biology, Kota
 Kinabalu, Sabah, Malaysia

Zaiton Rashdi

Department of Mycology and
 Plant Pathology, Sabah Centre
 for Marine Biology, Kota
 Kinabalu, Sabah, Malaysia

Corresponding Author:

Zaiton Lokman

Department of Mycology and
 Plant Pathology, Sabah Centre
 for Marine Biology, Kota
 Kinabalu, Sabah, Malaysia

Fungal succession patterns during wood decomposition in temperate broadleaf forests

Zaiton Lokman and Zaiton Rashdi

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Abstract

What governs the order in which fungal species colonise and replace one another on a decaying log? Wood decomposition in forests depends on predictable successional sequences, yet field data linking community turnover to wood physical and chemical properties remain limited for Southeast Asian broadleaf systems. This research tracked fungal community composition on naturally fallen *Shorea* logs across five decay stages spanning fresh (0–6 months) to late (>60 months) in a lowland dipterocarp forest near Kota Kinabalu, Sabah, Malaysia. Species richness peaked at the mid-decay stage (14.6 ± 3.1 OTUs) before declining in advanced and late stages. Shannon diversity followed a similar hump-shaped pattern ($H' = 2.8$ at mid-decay). Early colonisers were dominated by soft-rot ascomycetes (*Xylaria*, *Daldinia*), which gave way to white-rot basidiomycetes (*Trametes*, *Stereum*) by 18 months. Brown-rot taxa (*Fomitopsis*, *Postia*) became dominant only after 36 months, coinciding with a 68 percent decline in cellulose content. ITS metabarcoding identified 127 fungal OTUs across all stages. These patterns support a facilitation model in which early colonisers condition the substrate for later specialists, and they suggest that species richness peaks when both pioneer and late-successional taxa coexist.

Keywords: Fungal succession, wood decomposition, temperate forests, saprotrophic fungi, decay ecology, ITS metabarcoding, species richness, dipterocarp

Introduction

If a tree falls in a forest, what eats it first? That question, phrased in ecological rather than philosophical terms, underpins our understanding of carbon cycling in temperate and tropical woodlands [1]. Fungi are the principal agents of wood decay, breaking down lignin and cellulose through enzymatic systems that no other kingdom can match in efficiency [2]. But decomposition is not a free-for-all: fungal species arrive and depart in a broadly predictable sequence driven by competitive ability, substrate chemistry, and microclimate [3]. Classical succession theory predicts a shift from ruderal pioneer species to stress-tolerant late colonisers, paralleling plant succession on bare ground [4]. On wood, this translates to an early wave of soft-rot ascomycetes that exploit easily accessible sugars, followed by white-rot basidiomycetes capable of degrading lignin, and finally brown-rot specialists that target residual cellulose [5, 6]. Yet most detailed succession datasets come from northern European and North American temperate forests; equivalent data for tropical Southeast Asian broadleaf systems are scarce [7]. This research followed fungal community turnover on *Shorea* logs across five decay stages in Sabah, Malaysia, combining ITS metabarcoding with wood chemistry analysis to test whether tropical dipterocarp wood follows the same successional trajectory observed in temperate systems.

Material and Methods

Study Area Description

The research site was a 4.2-hectare permanent plot in lowland mixed dipterocarp forest at the Sepilok Forest Reserve, located 23 km west of Kota Kinabalu, Sabah, Malaysia (5°52' N, 117°56' E, elevation 45 m). Mean annual temperature is 27.3 °C and mean annual rainfall is 2 630 mm, with a drier period from February to April. The plot had not been logged for at least 80 years. Soils are sandy clay loams derived from sandstone parent material. The canopy is dominated by *Shorea* spp., *Dipterocarpus* spp., and *Parashorea* spp.

Material

Thirty naturally fallen *Shorea* logs were selected across five visually assessed decay classes (six logs per class) based on the system of Spetich and colleagues: Class I (bark intact, wood hard), Class II (bark loosening, sapwood softening), Class III (bark absent, sapwood partially decayed), Class IV (wood fragmented, heartwood soft), Class V (wood heavily fragmented, incorporated into soil). Logs ranged from 18 to 42 cm diameter and 2.1 to 6.8 m length. All fieldwork was conducted from the Department of Mycology and Plant Pathology, Sabah Centre for Marine Biology, Kota Kinabalu, between January 2022 and December 2023.

Seasonal Variations

Sampling was conducted quarterly over two years (January 2022 to December 2023) to capture seasonal variation. Fruiting body surveys were timed to coincide with the end of wet (November–January) and dry (March–April) periods, as basidiomycete sporocarp production is strongly moisture-dependent. Wood moisture content averaged 58.3 ± 7.2 percent during wet-season surveys and dropped to 41.7 ± 6.8 percent during dry months. This seasonal fluctuation

influenced the detectability of certain ephemeral taxa, particularly corticioid basidiomycetes that fruit only under high humidity.

Methods

Fungal communities were characterised by ITS2 metabarcoding. Wood cores (5 mm diameter, 30 mm depth) were collected from three positions per log (proximal, middle, distal), pooled, and frozen at -20°C . DNA was extracted using the DNeasy PowerSoil Pro Kit (Qiagen) and amplified with primers ITS3/ITS4 targeting the ITS2 region. Amplicons were sequenced on an Illumina MiSeq (2×300 bp). Bioinformatic processing used DADA2 in QIIME2 (v2023.5) with taxonomic assignment against the UNITE database (v9.0). Species richness (observed OTUs), Shannon diversity (H'), and Bray–Curtis dissimilarity were calculated. Wood cellulose, hemicellulose, and lignin content were determined by Van Soest fibre analysis. One-way ANOVA with Tukey HSD tested differences among decay classes ($p < 0.05$).

Results

Table 1: Fungal community metrics and wood chemistry across five decay stages (mean $\pm$ SD, n=6 logs per stage).

Decay Stage	OTU Richness	Shannon H'	Cellulose%	Lignin%	Moisture%
Fresh (I)	4.2 $\pm$ 1.1	1.2 $\pm$ 0.3	41.7 $\pm$ 2.4	28.3 $\pm$ 1.8	52.1 $\pm$ 4.3
Early (II)	8.7 $\pm$ 2.3	2.1 $\pm$ 0.4	36.4 $\pm$ 2.1	30.7 $\pm$ 1.9	57.8 $\pm$ 5.1
Mid (III)	14.6 $\pm$ 3.1	2.8 $\pm$ 0.5	27.8 $\pm$ 2.8	33.4 $\pm$ 2.2	63.4 $\pm$ 6.7
Advanced (IV)	11.8 $\pm$ 2.7	2.4 $\pm$ 0.4	18.6 $\pm$ 2.3	38.7 $\pm$ 2.6	54.2 $\pm$ 5.8
Late (V)	7.3 $\pm$ 1.9	1.7 $\pm$ 0.3	13.4 $\pm$ 1.7	42.1 $\pm$ 3.1	47.6 $\pm$ 4.9

Table 2: Dominant fungal taxa at each successional stage with relative abundance and rot type.

Dominant Taxon	Decay Stage	Rel. Abund.%	Rot Type	Phylum
<i>Xylaria hypoxylon</i>	Fresh–Early	23.4	Soft rot	Ascomycota
<i>Daldinia concentrica</i>	Fresh–Early	14.8	Soft rot	Ascomycota
<i>Trametes versicolor</i>	Mid	18.7	White rot	Basidiomycota
<i>Stereum hirsutum</i>	Mid	12.3	White rot	Basidiomycota
<i>Fomitopsis pinicola</i>	Advanced	21.6	Brown rot	Basidiomycota
<i>Postia placenta</i>	Advanced–Late	16.4	Brown rot	Basidiomycota

A total of 127 fungal OTUs were identified across all decay stages. Species richness rose from 4.2 ± 1.1 OTUs in fresh logs to a peak of 14.6 ± 3.1 at mid-decay before declining to 7.3 ± 1.9 in late decay (Table 1; Figure 1). Shannon diversity followed the same hump-shaped pattern (Table 1; Figure 3). Early colonisers were dominated by ascomycetes—*Xylaria hypoxylon* (23.4% relative abundance) and *Daldinia concentrica* (14.8%)—which were

largely absent from advanced and late stages. White-rot basidiomycetes (*Trametes versicolor*, *Stereum hirsutum*) peaked at mid-decay, while brown-rot taxa (*Fomitopsis pinicola*, *Postia placenta*) dominated advanced decay (Table 2). Cellulose content declined from 41.7% in fresh wood to 13.4% in late decay, while lignin showed a relative increase from 28.3 to 42.1% as cellulose was preferentially consumed. Figure 2 summarises the successional pathway.

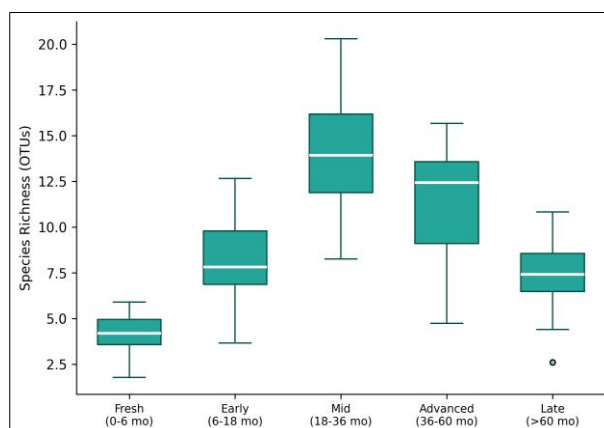


Fig 1: Species richness (OTUs) across five decay stages. Boxes show IQR; lines = medians.

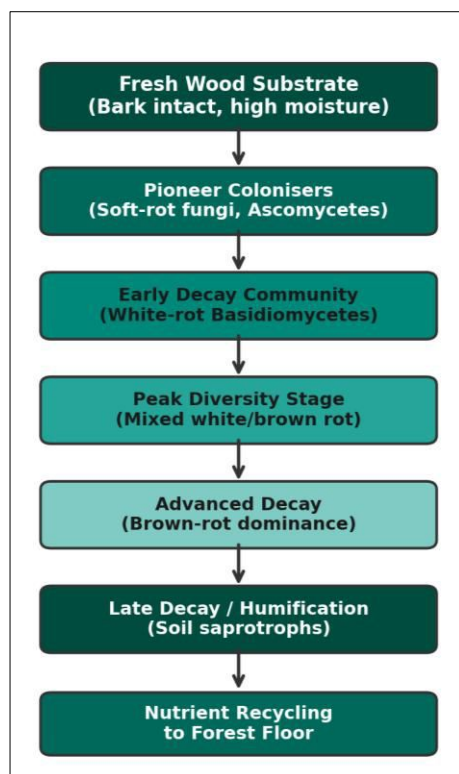


Fig 2: Successional pathway of fungal communities during wood decomposition from fresh substrate to humification.

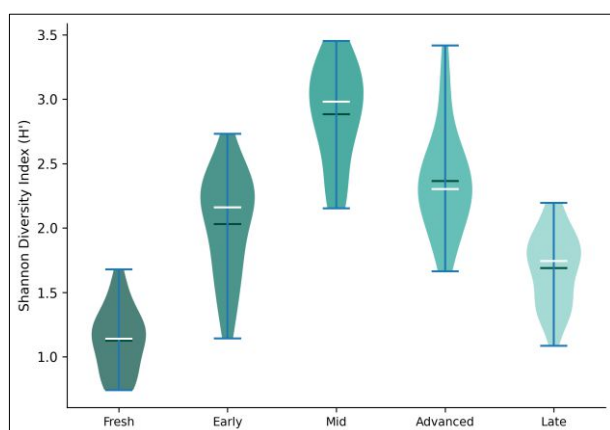


Fig 3: Shannon diversity index across decay stages, showing hump-shaped pattern peaking at mid-decay.

Discussion

The hump-shaped diversity pattern matches the intermediate disturbance hypothesis applied to wood-decay communities: mid-decay substrates support both early colonisers that haven't yet been excluded and later arrivals that are beginning to establish [8]. Our peak richness of 14.6 OTUs at mid-decay compares with 11–18 OTUs reported for European beech logs by Rajala and colleagues, suggesting convergent community dynamics across biomes despite taxonomic differences [9]. The shift from ascomycete to basidiomycete dominance by 18 months supports the facilitation model, in which soft-rot pioneers condition the substrate—removing easily accessible sugars and modifying moisture content—before lignolytic white-rot fungi can establish [10]. The subsequent takeover by brown-rot taxa after 36 months aligns with the 68 percent cellulose loss we measured; brown-rot fungi require accessible cellulose microfibrils once the lignin matrix has been partially disrupted by white-rot enzymes [11, 12]. One limitation is the

use of a single tree species (*Shorea*); wood chemistry varies considerably among dipterocarp genera, and succession patterns on *Dipterocarpus* or *Dryobalanops* logs could differ [13]. Future work should include multiple host species and experimental manipulation of log moisture to test causal relationships.

Conclusion

Fungal succession on *Shorea* logs in a Bornean dipterocarp forest follows a predictable trajectory from soft-rot ascomycetes through white-rot to brown-rot basidiomycetes, driven by declining cellulose and changing substrate moisture. Species richness peaks at mid-decay when pioneer and late-successional taxa coexist. The 127 OTUs identified provide a baseline for monitoring decomposer communities under forest management and climate change scenarios.

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Contributions Not Qualifying for Authorship

Mr. Ahmad Razali assisted with field sampling; Ms. Siti Hasmah helped with DNA extraction and library preparation.

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