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Identification and comparison of the diversity of xylophagous fungi in forests and sawmills in the central jungle, Peru

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ABSTRACT

Xylophagous fungi have economic implications because they cause wood losses in commercial woodlands (CW) and sawmills, as they cause diseases in standing trees and decompose roundwood and sawnwood, respectively. The objective of the study was to identify and compare the diversity of xylophagous fungi in commercial woodlands (CW) and sawmills in the districts of San Martín de Pangoa, Río Negro, Mazamari, and Satipo (Satipo province, central jungle), Peru. Identification was based on the macroscopic and microscopic characteristics of the fungi; in addition, the Simpson (λ), Gini-Simpson (H_{GS}), Shannon-Wiener (H'), Pielou (J), Margalef (DMg) diversity indices and Sorenson's similarity coefficient (Cs) were used. The results show that 29 species of xylophagous fungi were identified, covering 11 family groups and 17 different genera, with Auricularia fuscosuccinea and Schizophyllum commune standing out in the two types of environments analyzed. The wooded areas used for timber production showed greater abundance and variety (Shannon-Wiener: 1.86–2.39; Margalef: 2.43–3.11) when compared to the sawmill sites, where variety was more limited, with a few resistant species dominating. However, the similarity between communities was high (Cs = 0.95), indicating that sawmills maintain a significant fraction of the fungal reservoir of forests, favoring the persistence of species with a high degradative impact on wood. These results show that, even though diversity is reduced in sawmills, the fungi that persist pose a considerable economic threat and highlight the importance of taking their lifestyle into account when managing forests and implementing methods to protect wood.

Keywords: diversity indices, xylophagous fungi, sawmill.

INTRODUCTION

Environmentalists have long sought to understand patterns of biodiversity, and changes along altitudinal gradients play a key role in the debate on this topic. (Deng et al., 2020). The study of biodiversity along altitudinal gradients is a key aspect of ecological research, as it allows us to capture the complex interaction between abiotic and biotic factors that determine the distribution and abundance of species. (Rahbek, 1995; Whittaker et al., 2001). Numerous studies have demonstrated how altitude affects various plant and animal species. (Costa et al., 2023; Dong et al., 2017), and the biodiversity of these groups tends to follow one of these three general altitudinal patterns: a hump-shaped distribution with a peak of diversity at mid-altitudes (Guo et al., 2013; Werenkraut and Ruggiero, 2011); a steady decline in diversity as altitude increases (Castro et al., 2020; Rahbek, 2005); or a continuous increase in diversity at higher altitudes (Kessler et al., 2011; McCain, 2005; Sanders et al., 2003), which makes it important to study them in all environments in order to find patterns of biodiversity for any species, one of which is fungi, due to their relevance in ecosystems (Zhang et al., 2025).

For their part, fungi play a crucial role in forest ecosystems, acting both as symbionts and decomposers (Dighton, 2018; Li et al., 2022), which makes them valuable indicators of environmental processes (Heilmann-Clausen et al., 2015). Soil fungi support nearly all higher life forms and contribute significantly to the biogeochemical cycle within ecosystems (Bowd et al., 2022). In this way, they play a fundamental role in soil microbial communities and are key factors in essential ecological processes, such as leaf litter decomposition, nutrient cycling, and plant growth regulation. (Chen et al., 2017). Their presence and activity are fundamental to the stability and health of ecosystems, as they directly influence biodiversity both above and below ground (Ni et al., 2018; Yang et al., 2021; Zhou et al., 2021). Recent research has revealed a series of distribution patterns for fungi in terrestrial ecosystems (Ogwu et al., 2019; Shen et al., 2020; Sui et al., 2023; Yang et al., 2017). Fungal communities are commonly classified into distinct taxonomic groups and functional guilds (Guerrero-Galán et al., 2019).

However, they also cause economic losses associated with the decomposition and degeneration of wood quality (Yalçın et al., 2019). After trees are felled in the forest, they are transported to sawmills for processing and sale, but they are usually stored outdoors for a considerable amount of time, which exposes them to weather conditions and contact with the ground, exposing them to fungi (Ador et al., 2024). In addition, fungal spores spread to freshly cut trees, causing even more losses (Sioma and Lenty, 2023). This generates economic losses and increased pressure on forests due to the demand for high-quality wood, affecting their sustainability (Arač et al., 2021; Jerusik, 2010).

Xylophagous fungi, also known as wood-decaying fungi, are organisms that break down lignin, cellulose, and hemicellulose through the production of hydrolytic enzymes (Iannaccone et al., 2024; Li et al., 2019), which is fundamentally important in forest ecosystems (Lonsdale et al., 2008; Yu-Lian, 2021), can cause significant damage to logs, creating economic problems for sawmills (Ador et al., 2024; Kumar and Gupta, 2006) and cause disease in trees in their natural state, affecting forest management (Lonsdale et al., 2008; Zhang and Wei, 2016), mainly in commercial woodlands (CW), understood as forests intended for the extraction of timber (wood) and non-timber products (resins, tannins, gums, medicinal plants, etc.) (Dourojeanni, 2022).

Using wood as a building material is a sustainable way to achieve the Paris Agreement goals, since, compared to cement or steel, it has a low environmental impact and greenhouse gas (GHG) emissions (Di Ruocco and Gaita, 2023; Dodoo et al., 2014; Hafner and Schäfer, 2017). Despite this, wood's susceptibility to decay due to microorganisms, which are affected by the microclimate, poses a challenge to its sustainable use (Olou et al., 2019).

Therefore, it is necessary to conduct exhaustive research on the diversity and importance of these organisms, especially fungi, and identify problematic species, thereby providing information that can be used to develop proposals to improve wood protection (Schrader et al., 2025). Understanding the diversity of organisms can provide information about a community and how it influences ecosystems (Perreault et al., 2023). The environmental conditions that favor sawmills can affect fungal diversity, and this approach makes it possible to identify the specific fungi that decompose wood in that environment (Ador et al., 2023), furthermore, comparing it with forests for forestry use can aid in forest management and help us understand the dynamics of decomposing fungi in the nutrient and carbon cycle. (Kouki and Salo, 2020).

It is estimated that there are between 0.7 and 5.1 million species of fungi (Blackwell, 2011; Hawksworth and Lücking, 2017), with a description of only 1.9% (97.330 species) to date (Abrahão et al., 2019). Therefore, the objective of this study is to identify and compare the diversity of xylophagous fungi in CW and sawmills (located in urban areas) in the central jungle of Peru. In addition, to examine the composition and structure of fungal populations.

MATERIALS AND METHODS

Study area

The study was conducted in the province of Satipo (central jungle) in the department of Junín, Peru, with a total of eight sampling sites for forests (four) and sawmills (four, located in urban areas) in the districts of San Martín de Pangoa, Río Negro, Mazamari, and Satipo, all located in the central jungle of Peru (Figure 1). In the case of the "San Martín de Pangoa" district, sampling was carried out at the "Forestales San Agustín" E.I.R.L. (FS) sawmill and the CW of the Cubantía native community (CNC); in the Mazamari district, the sawmill "Lumber Industry Los Ángeles S.A.C." (LILA) and the CW of the town of Shanqui (PCS); in the "Rio Negro" district, the sawmill "Export Wood – MADEXA" (EWM) and the CW of the native community "Puerto Ocopa" (CNPO); and in the Satipo district, the sawmill "Group ALMASA S.A.C" (GA) and the CW of the Satipo Agricultural Experimental Station of the National University of Central Peru (SAES) (Montano and Palomino, 2012).

The predominant habitat in the study area is the humid forest – tropical premontane (bh-PT), covering an area of 32.775 km² and distributed at altitudes between 500 and 2.000 m above sea level, typical of the high jungle. The average minimum annual biotemperature is 17.2 °C and the average maximum annual biotemperature is 24.9 °C. Average annual precipitation ranges from a minimum of 936 mm to a maximum of 1968 mm, with an average minimum relative humidity of 86.20% and a maximum of 92.20%. The climate is humid and warm, with maximum temperatures reaching 33.7 °C, an average of 24 °C, and a minimum of 12.9 °C. In terms of rainfall, there are three distinct periods throughout the year: heavy rains from January to April (1087.36 mm), moderate rains from October to December (642.44 mm), and light rains from May to September (487.26 mm) (Montano and Palomino, 2012).

Procedure and sampling

The materials used were: 80x stereoscopic microscope, 70% alcohol, Garmin e-Trex GPS, 14-megapixel Lumix camera, surgical gloves, field notebook, and sample collection bags.

A stratified master sample (Ozturk and Kavlak, 2019) of four 10 × 100 m transects was used,

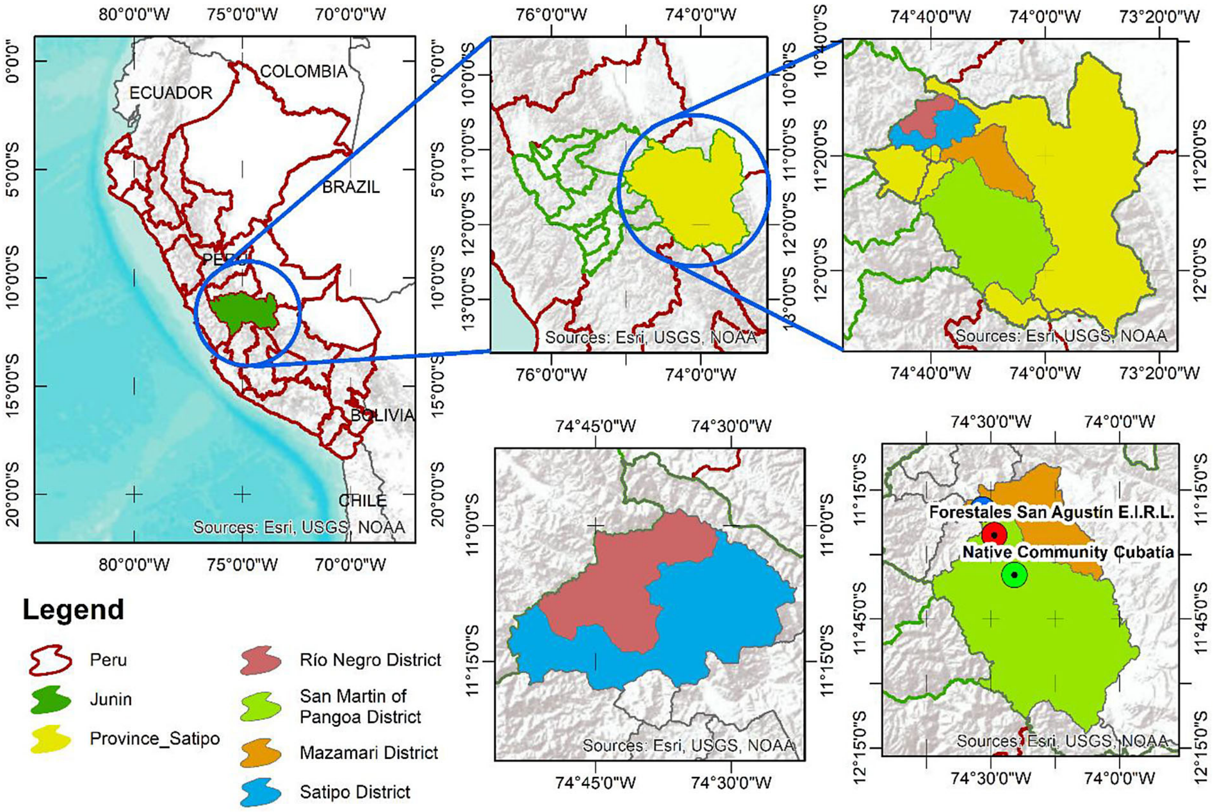

Figure 1. Location of the study area. Adapted from Montano and Palomino (2012)

established at a distance of 250 m between them in each CW; in each transect, 10 sampling units were established 10 m apart, and finally, in each sampling unit, samples of xylophagous fungi were collected in an area of 4 m². On the other hand, 10% of the total storage yard for round and sawn timber was evaluated, which was considered a very adequate sample size.

After establishing the sampling units, xylophagous fungi were collected from standing trees, fallen trees, and stumps within the CW, and in the case of the sawmill, from stored round and sawn wood. All fungi with complete carpophores were collected and placed in cardboard boxes, divided with Styrofoam and secured with pins and labels, taking into account the following characteristics: location, date, habitat, and in some cases the host. Finally, to preserve the samples, they were placed in a ventilation chamber at 40 °C for 1 to 2 hours to avoid the presence of contaminants such as bacteria and imperfect fungi. After that, they were refrigerated at 4 °C for 7 days and the specimen was removed on paper. °C for 1 to 2 hours to prevent the presence of contaminants, such as bacteria and imperfect fungi. They were then refrigerated at 4 °C for 7 days and removed from the Kraft paper for analysis at the Mycology Laboratory of the Plant Health Diagnostic Center (PHDC) of the National Agricultural Health Service (SENASA) – Lima.

Species identification

To identify xylophagous fungi, three processes were carried out to identify the fungi (Figures 2a and 2b) from the CWs in the Central Forest (Figure 2c) and the sawmill (Figure 2d). The collected fungi were identified by their macroscopic morphological characteristics (shape, size, color, texture, tube layer, hymenium, abhymenium, zoning, and pores per mm) with the aid of a stereoscope and millimeter ruler. and, on the other hand, for the microscopic characteristics (hyphal system, cystidia, asci, basidia, and spores), a longitudinal cut was made of the fruiting body to expose the tube layer, from which a sample of approximately 100 to 150 µm was extracted and placed on a slide, and potassium hydroxide (KOH) to hydrate and loosen the hyphae, then Melzer's reagent was added (if reddish, it is dextrinoid; blue is amyloid; and if there is no reaction, it is negative) or lactophenol blue (if it stains blue, it is cyanophilic).

Figure 2. Procedure and mushroom sampling: a) Ascomycetes in the Shanqui Water Conservancy – Río Negro, b) Schizophyllum commune in the Water Conservancy – Satipo, c) CW of the Cubantía native community – San Martín de Pangoa, and d) San Agustín E.I.R.L. Sawmill – San Martín de Pangoa

Finally, to determine the genus and species, the macroscopic and microscopic characteristics were noted and compared with identification keys. For ascomycetes, the authors Pavlich (1976), Pacioni (1980), and Guzmán (1979) were used; and for basidiomycetes, the authors were Ryvarde and Gilbertson (1994), Pavlich (1976) and Guzmán (1979).

Diversity indices

Diversity indices, represented by *H*(*p*), serve as a way to quantify biodiversity using mathematical functions to compare spatial regions and functional groups. They are an essential tool for ecological monitoring and conservation, and an effort to study and understand the biodiversity crisis (Daly et al., 2018). Therefore, the following indices will be used for the analysis of xylophagous fungus diversity.

The simplest index often used is species richness itself, which is simply the absolute number of species (S) found in the population of interest (Daly et al., 2018), being this way $H_{SR}(p)$.

The Simpson diversity index quantifies the probability that two individuals from the community chosen at random represent the same species, thus taking values in a unit interval. (Keylock, 2005) and is expressed according to Simpson (1949) as:

$$\lambda = \sum_{i=1}^{S} p_i^2 \tag{1}$$

where: p_i – proportional abundance of species *i*; *i* – total number of individuals in the sample.

However, other formulations to explain this phenomenon include the Gini-Simpson index (interspecific encounter), which is the probability that two species are different and is calculated as $H_{GS} = 1$.

The Shannon-Wiener index measures the uncertainty of a sample (Shannon, 1948), that is, it measures the average degree of uncertainty when predicting which species, a randomly selected individual from a community will belong to, and is expressed as:

$$H' = -\sum_{i=1}^{S} p_i \, ln\,(p_i) \tag{2}$$

The Shannon-Wiener index is the basis for another index, called the Pielou index (Pielou, 1969), which measures the uniformity of species within a population, being the ratio of observed diversity to maximum expected diversity (Hernández et al., 2018), and is expressed as $J = H'/H_{max}$, where H_{max} is the maximum value of H' and is calculated as ln(S), widely used in ecological literature (Borcard et al., 2018).

The Margalef index measures the diversity or richness of species in a given location, taking into account the number of individuals found of each species. It is therefore useful for comparing abundance in cases where the samples are different (Ulanowicz, 2001). Its original formula (Margalef, 1957) is expressed as:

$$D_{Mg} = \frac{S - 1}{lnN} \tag{3}$$

where: *S* – number of species and *N* – total number of individuals.

In addition, Sorenson's similarity coefficient (Cs) was determined to compare the similarity of fungal communities among the eight sampling sites (Kent, 2011), ranging from 0 to 1, where values close to 0 indicate less similarity between fungal communities and values equal to 0 indicate completely different communities (Daly et al., 2018), it was determined using the following formula:

$$Cs = \frac{2j}{a + b} \tag{4}$$

where: *j* – the number of fungal species between different sites; *a* and *b* – the number of species at each site, respectively.

Data analysis

Based on species identification, the number of individuals per species (absolute abundance) was obtained in accordance with the sampling described in section 2.2. These values represent the fungal communities at the eight sampling sites (CW and sawmill), which were used for further analysis.

Descriptive and comparative statistics were calculated for the absolute abundance of the eight sampling sites, and diversity indices were calculated for Richness ($H_{SR}(p)$, Shannon-Wiener (H'), Simpson (λ), Gini-Simpson (H_{GS}), Pielou (J), and Margalef (D_{Mg}) indexes were calculated using RStudio software. In addition, data normality was assessed using the Shapiro–Wilk test and homogeneity of variances ($p > 0.05$) using the Levene test. If the data met the above assumptions, one-way ANOVA was applied to compare the fungal communities at the sampling sites; and if the assumptions were not met ($p < 0.05$), the Kruskal-Wallis test was applied as an alternative, followed by multiple comparisons using the Wilcoxon paired test, adjusted with the Bonferroni method to control for type I error (Freund et al., 2010). The significance value was $\alpha = 0.05$, interpreting the results based on the p-values.

Relative abundance (percentage proportion of the number of individuals of a particular fungus to the total number of individuals) was determined using a stacked bar chart. In the case of community composition (Hou et al., 2025), Venn diagrams (Sun et al., 2021) and Heatmap graphs (Cao et al., 2022) were used.

RESULTS

Descriptive and comparative analysis of xylophagous fungal communities

Table 1 shows the descriptive statistics of the xylophagous fungal communities from eight sampling sites that are part of two different environments. The mean and standard deviation show variability among individuals, and the asymmetry values indicate a distribution biased toward dominant species, while the kurtosis shows a leptokurtic distribution, indicating that there are dominant species that account for a large proportion of the total number of individuals recorded.

On the other hand, not all sites represent a normal distribution, despite the fact that Levene's test indicates that homoscedasticity exists ($p = 0.617$). According to the Kruskal-Wallis test, there are differences ($p < 0.05$) between sampling sites ($p = 0.0468$), and using the Wilcoxon paired test, it was determined that the EWM groups between SAES ($p = 0.014$), FS between SAES ($p = 0.017$), GA between SAES ($p = 0.028$), LILA between SAES ($p = 0.016$), and PCS between SAES ($p = 0.026$) are different ($p < 0.05$), while the other groups are similar ($p > 0.05$). It should be noted that when applying the Bonferroni adjustment, all groups are statistically similar ($p > 0.05$).

Comparison of the structure and diversity of xylophagous fungi in two different environments

A total of 16 906 individuals were found in both locations, representing a heterogeneous composition (Table 2). In terms of the xylophagous fungi identified, the community is composed as follows: 2 classes, 7 orders, 11 families, and 17 genera. In addition, three species belonging to the Ascomycota class have been found that have not been identified: 1B 103–115467, 2B 106–115479, and 1A 107–115481. It should be noted that the species *P. sanguineus*, *Xilaria* sp. and 1A 107 – 115481 were exclusive to CW. The genera with the most individuals shared both spaces were Auricularia, Pleurotus and Schizophyllum, and also included the other genera, but with fewer individuals.

The abundance and structure of xylophagous fungi show significant differences, with the genus Schizophyllum having the highest number of individuals and Cookeina having the lowest (Figure 3A). A total of 10,149 individuals belonging to 29 species were found in CW, and 6,757 belonging to 26 species were found in sawmills.

Table 1. Descriptive statistics of xylophagous fungal communities

Site	$\bar{x}$	Median	Q3	Q5	σ	Standard error	Skewness	Kurtosis	Shapiro-Wilk
CNC	141.448	19	50	785	299.006	55.524	2.424	5.200	1.99e-08
CNPO	76.483	17	50	363.8	152.343	28.289	2.658	6.870	3.26e-08
EWM	61.379	8	13	409.8	151.153	28.068	2.660	6.015	2.61e-09
FS	52.276	5	31	309.6	127.742	23.721	2.896	7.884	3.25e-09
GA	68.414	5	22	250.2	198.745	36.906	4.035	16.591	5.26e-10
LILA	50.931	2	35	203	145.358	26.992	3.978	16.023	6.11e-10
PCS	56.586	10	35	182	150.664	27.978	4.002	16.415	8.18e-10
SAES	102.276	35	68	437	178.146	33.081	2.337	5.123	1.26e-07

Note: $\bar{x}$ is mean, "Q3" is quartile 3, "Q5" is quartile 5, 'IQR' is interquartile range, and "σ" is standard deviation. Furthermore, the Shapiro-Wilk test has a significance level of $\alpha = 0.05$.

Table 2. Xylophagous fungi identified in CW and sawmills in the central jungle of Peru

Class	Order	Family	Genus	Species
Basidiomycete	Agaricales	Pleurotaceae	Pleurotus	*Pleurotus ostreatus*
				Pleurotus sp.
		Schizophyllaceae	Schizophyllum	*Schizophyllum commune*
	Auriculariales	Auriculariaceae	Auricularia	*Auricularia fuscosuccinea*
	Hymenochaetales	Hymenochaetaceae	Inonotus	*Inonotus* sp.
		Fomitopsidaceae	Phellinus	*Phellinus* sp.
			Daedalea	*Daedalea* sp.
		Meripilaceae	Rigidoporus	*Rigidoporus* sp.
	Polyporales	Polyporaceae	Trametes	*Trametes elegans*
				Trametes sp.
				Trametes ochracea
				Trametes sclerodepsis
			Coriolopsis	*Coriolopsis floccosa*
				Coriolopsis rigida
			Fomes	*Fomes fasciatus*
				Fomes sp.
			Lenzites	*Lenzites elegans*
			Perenniporia	*Perenniporia* sp.
			Pycnoporus	*Pycnoporus sanguineus*
		Ganodermataceae	Ganoderma	*Ganoderma applanatum*
				Ganoderma australe
				Ganoderma ocellatum (≃ *G. orbiforme*)
Ascomycete	Russulales	Stereaceae	Stereum	*Stereum ostrea*
	Pezizales	Sarcoscyphaceae	Cookeina	*Cookeina sulcipes*
				Cookeina tricholoma
	Xylariales	Xylariaceae	Xylaria	*Xylaria* sp.

The composition of the taxa was almost similar in both spaces, as they shared 26 species, with the species *P. sanguineus*, *Xilaria* sp. and 1A 107 - 115481 (Figure 3D), resulting in a Cs similarity of 0.95, with the species with the highest number of individuals being *A. fuscosuccinea, S. commune*, and *Pleorotus* sp.

Likewise, statistical analysis of the abundance and diversity of xylophagous fungi at the eight sampling sites revealed that there is greater abundance and diversity in CW because the forest structure provides better climatic conditions for the growth of xylophagous fungi. However, despite the high level of richness, the average values of the Shannon-Wiener index, Simpson index, and Gini-Simpson index at the sawmill indicate that the transport of wood has maintained the xylophagous fungus community, posing a threat to commercial wood. The Pielou index and Margalef index indicate that some species are more abundant and greater care must be taken in this regard (Figure 3B).

On the other hand, the Venn diagram of the xylophagous fungi community in two different spaces revealed the different compositions of fungi at each sampling site. The species *P. ostreatus* was exclusive to SAES. Twelve species were common to all eight sampling sites, including *A. fuscosuccinea, C. rigida*, *Fomes* sp., *G. applanatum*, *G. australe*, *G. ocellatum*, *Inonotus* sp., *Pleorotus* sp., *S. commune*, *S. ostrea*, *Trametes* sp., and *T. ochracea* (Figura 3C).

On the other hand, when species are separated by each space, there are seventeen common species among CW sites, including *A. fuscosuccinea*, *C. rigida*, *F. fasciatus*, *Fomes* sp., *G. applanatu*, *G. austral*, *G. ocellatum*, *Inonotus* sp., *Perenniporia* sp., *Pleorotus* sp., *P. sanguineus*, *Rigidoporus* sp.,

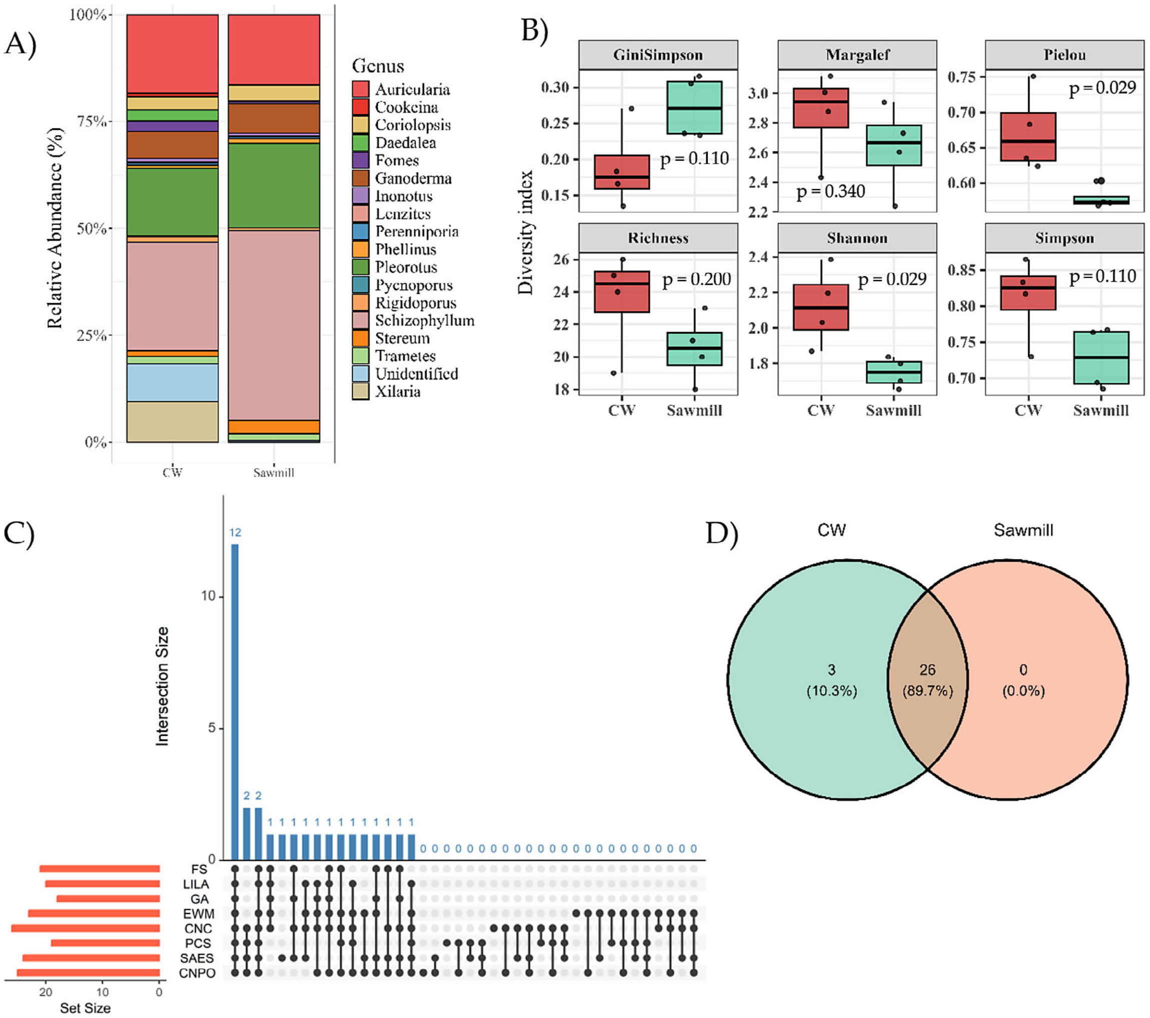

Figure 3. Comparison of xylophagous fungi communities between two areas (CW and sawmill): A) structure of fungal communities; B) comparison of diversity indices; C) Venn diagram of the different sampling sites, where CNC, PCS, SAES, and CNPO belong to CW and the sites FS, LILA, GA, and EWM belong to the sawmill; D) Venn diagram of the fungal community

S. commune, *S. Ostrea*, *Trametes* sp., *T. ochracea*, and *Xilaria* sp. (Figure 4A). Meanwhile, at the sawmill sites, there are fourteen common species, including *A. fuscosuccinea*, *C. rigida*, *Fomes* sp., *G. applanatum*, *G. australe*, *G. ocellatum*, *Inonotus* sp., *P. ostreatus*, *Pleorotus* sp., *S. commune*, *S. ostrea*, *Trametes* sp., *T. ochracea*, and 1B 103 – 115467 (Figure 4B).

Analysis of the diversity of the xylophagous fungi community at eight sampling sites

The composition of species at the sites is heterogeneous, with certain species dominating (Figure 5), mainly *A. fuscosuccinea*, *Pleorotus* sp., and *S. commune* at all sampling sites, with a difference at SAES, Where 1A 107–115481 dominates over the other species in the same group.

A total of 24, 24, 19, and 26 species were recorded at the CNPO, SAES, PCS, and CNC sites, respectively, while 23, 18, 20, and 21 species were recorded at the EWM, GA, LILA, and FS sites, respectively. The Sorenson coefficient indicates a high degree of similarity between fungal communities in most comparisons, as they are above 0.70, with the highest values being LILA and EWM (0.93) and CNC and CNPO (0.902). In contrast, PCS and GA (0.649) obtained the lowest value (Table 3). Taken together, these values show that CW fungal spores spread in sawmill environments, despite the limitations of conditions that can reduce their proliferation, posing a latent danger to commercial wood.

Diversity indices revealed marked contrasts between CW sites and sawmills (Table 4). CWs (CNC, CNPO, and SAES) recorded

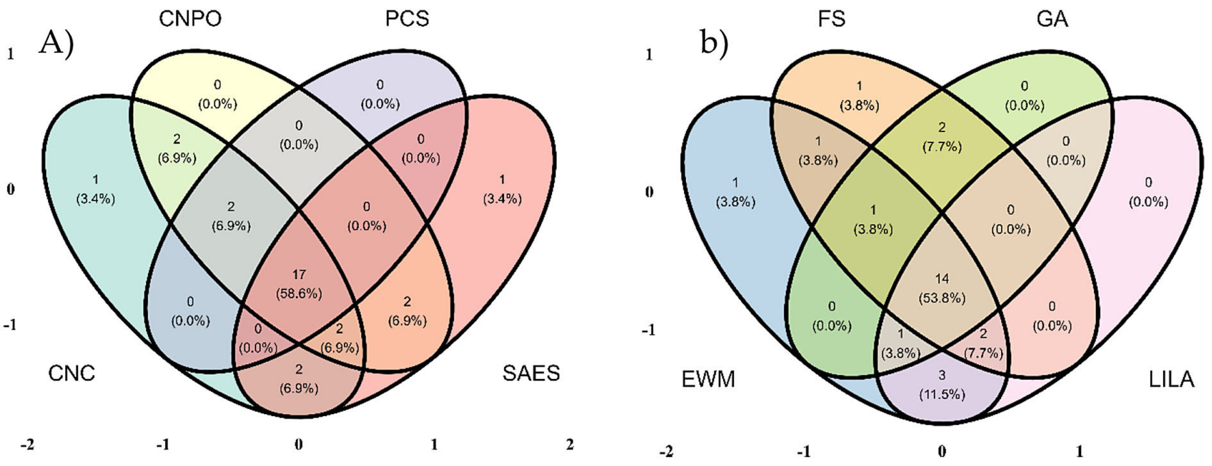

Figure 4. Venn diagram of the xylophagous fungi community by sampling site: A) CWs space, B) sawmill space

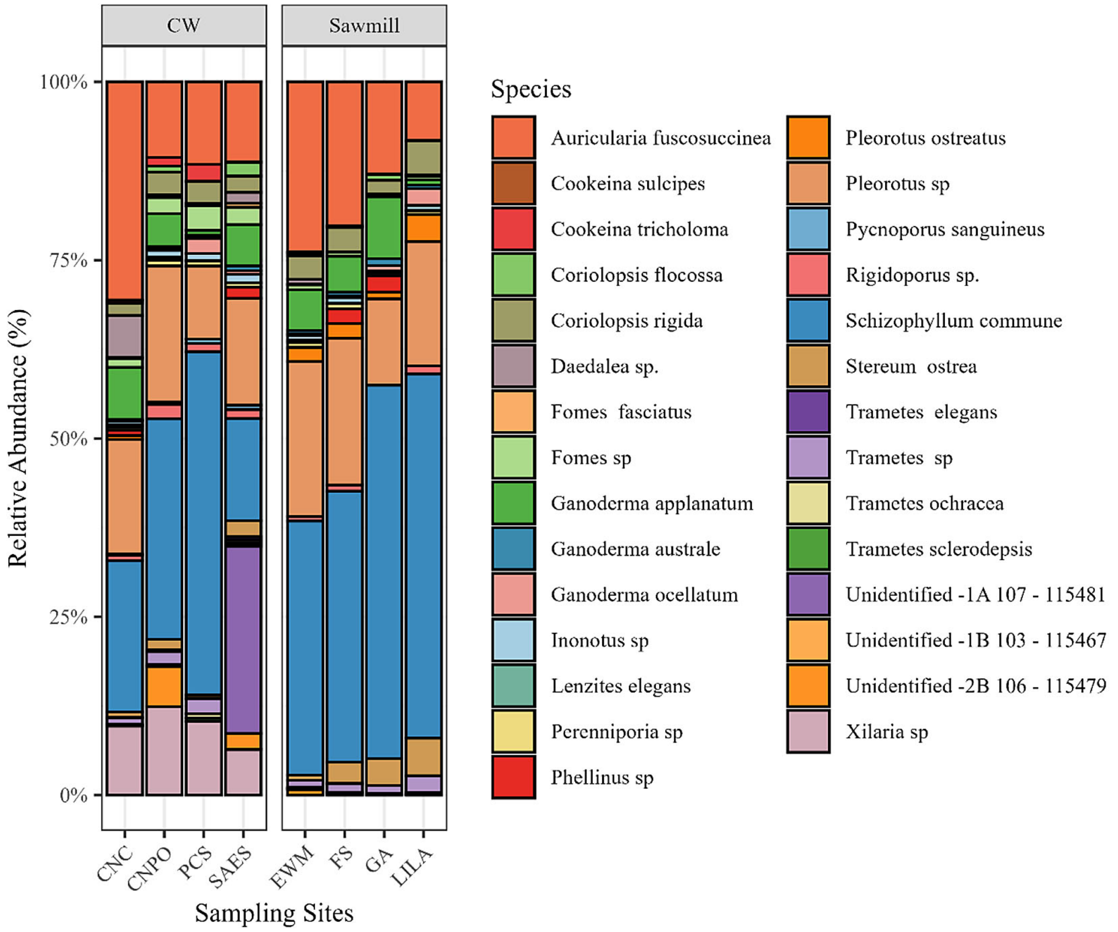

Figure 5. Distribution of the composition of xylophagous fungi from the different sampling sites, where CNC, PCS, SAES, and CNPO belong to CW and the sites FS, LILA, GA, and EWM belong to the sawmill

higher values for species richness, Shannon-Wiener diversity, and Pielou's evenness, indicating more diverse fungal communities and abundance with some species dominating. In contrast, sawmills (EWM, GA, LILA, and FS) showed lower values, evidencing the dominance of a few species in commercial wood processing and storage processes. In this sense, this trend suggests that environmental heterogeneity and resources in forests provide a better environment for the development of xylophagous fungi, and in the case of

Table 3. Sorenson similarity coefficient of wood-decaying fungal communities in CW and sawmills in the central jungle of Peru

Sample sites	CNPO	SAES	PCS	CNC	EWM	GA	LILA	FS
CNPO	1							
SAES	0.857	1						
PCS	0.864	0.791	1					
CNC	0.902	0.840	0.844	1				
EWM	0.875	0.766	0.810	0.857	1			
GA	0.744	0.714	0.649	0.773	0.780	1		
LILA	0.800	0.727	0.821	0.870	0.930	0.789	1	
FS	0.826	0.800	0.750	0.851	0.818	0.872	0.780	1

Table 4. Diversity indices of xylophagous fungi communities in CW and sawmills in the central jungle of Peru

Site	N	Richness	Shannon	Simpson	Gini-Simpson	Pielou	Margalef
CNPO	2,218	25	2.197	0.833	0.167	0.683	3.115
SAES	2,966	24	2.387	0.865	0.135	0.751	2.877
PCS	1,641	19	1.868	0.729	0.271	0.634	2.431
CNC	4,102	26	2.030	0.817	0.183	0.623	3.005
EWM	1,780	23	1.798	0.764	0.236	0.573	2.939
GA	1,984	18	1.653	0.685	0.315	0.572	2.239
LILA	1,477	20	1.700	0.694	0.306	0.567	2.604
FS	1,516	21	1.836	0.767	0.233	0.603	2.731

sawmills, they only benefit opportunistic and competitively dominant species.

The heatmap shows a pattern of differential distribution of xylophagous fungi between CW and sawmills, where greater diversity and evenness is observed in forests, associated with environmental heterogeneity and availability of microhabitats, while in sawmills, environmental filtering reduces richness and favors the dominance of opportunistic and resistant species such as *A. fuscosuccinea* and *S. commune* (Figure 6). Even so, the high similarity between fungal groups (Cs ≈ 0.95) indicates that sawmills act as a continuation of the natural place from which they originate, allowing species that cause wood decay to continue to exist. This pattern, which is consistent with the ideas of metacommunities and environmental selection, shows that, although variety is lost in man-made environments, the species that persist have a great capacity to move and adapt, which affects both the natural balance in the way wood decomposes and the economy, due to the decrease in the quality and durability of stored wood.

DISCUSSION

Common and different characteristics of the xylophagous fungi community in two areas

Xylophagous fungi are one of the main agents that cause biodeterioration, following the invasion and decomposition of living or dead wood (Deflorio et al., 2008). Research conducted by Ador et al. (2023), in sawmills with a tropical monsoon climate identified 23 species, 5 orders, 7 families, and 15 genera, with the Polyporaceae family being the most abundant with 17 species, but *S. commune* was the dominant species and *Microporus xanthopus*, *Daldinia concentrica*, *Trametes coccinea* y *Daedalea quercina* were co-dominant. However, the genus Ganoderma is dominant in mangrove forests, and Trametes and Inonotus were co-dominant (Das et al., 2017). Meanwhile, in tropical evergreen forests, the predominant species were *S. commune*, *Pleurotus ostreatus*, *Pleurotus populinus*, *Ganoderma tsugae*, *G. applanatum*, *Steccherinum ochraceum* y *Steccherinum ciliolatum*, but 25 species from 15 genera were identified (Tanjim et al., 2019). For example, *Trametes flavida*

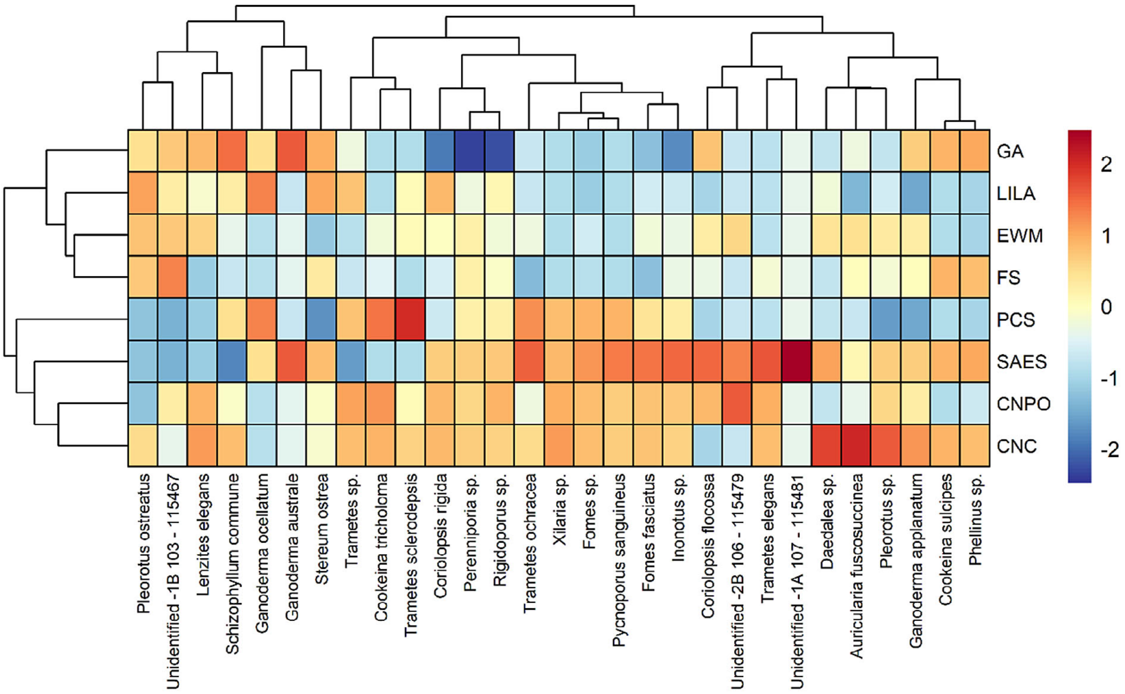

Figure 6. Heatmap distribution of xylophagous fungi species from different sampling sites, where CNC, PCS, SAES, and CNPO belong to CW, and FS, LILA, GA, and EWM belong to the sawmill

Note: The heatmap analysis was performed by transforming the data using the ln(x+1) method to reduce the heterogeneity of absolute abundance and highlight patterns.

causes greater loss of mass and density compared to *Daldinia eschscholtzii* in hardwoods, with *Gmelina arborea* being highly susceptible (Ador et al., 2024).

In situations where wood is dead in temperate forests, certain fungi prefer coniferous trees, as they are more abundant than broadleaf trees (Purahong et al., 2018). The number of resources must also be considered, since dead wood is essential for xylophagous fungi and their community is influenced by the microclimate (Bässler et al., 2010). Despite the high diversity of wood-decaying fungi, the decomposition process can be slow when there are diverse communities in the same location, and those near forests can accelerate this process (Smith and Peay, 2021), due to competition and antagonistic interactions between organisms (Perreault et al., 2023). That is why the optimal temperature for the development of xylophagous fungi varies from 20 to 40 °C with a moisture content in the wood of 35% to 70% (Verbist et al., 2019). However, although wood is an important material in global demand, it should be noted that fungal communities in general may have greater diversity in logged areas (Bell-Doyon et al., 2022).

Effects of xylophagous fungi in sawmills

The vulnerability of wood to these decay agents is significantly related to storage conditions and duration, the condition of the storage yard, whether the wood is treated or not, and the use of shaded facilities (Ador et al., 2023). Exposure of commercial wood to these fungi can lead to loss of wood mass and density, causing it to lose its mechanical properties such as modulus of elasticity and breaking strength, resulting in economic losses (Yang et al., 2010), a decrease in energy content per unit volume (Gendek et al., 2023), a decrease in cellulose content and an increase in lignin due to the production of phenols during delignification (Rahniawati et al., 2020) and affecting pulp productivity and quality (Mafia et al., 2012); at the same time, some species such as *S. commune* can cause corrosion in metal screws embedded in wood (Suprapti et al., 2020). In addition, there may be health implications from exposure to these xylophagous fungi in sawmills (Straumfors and Afanou, 2021). Likewise, it can lead to a devaluation of the price of wood, since some fungi, such as *Meripilus giganteus*, cause heartwood rot and create false heartwood, reducing the usable volume and value of roundwood (Arač et al., 2021).

CONCLUSIONS

This research made it possible to identify and compare the variety of wood-decaying fungi in production forests (CW) and sawmills in the Peruvian central jungle. It was found that there is much more variety and types of fungi in CWs, compared to the low diversity observed in sawmills. Forests, with their more stable and heterogeneous environmental conditions, support complex and diverse fungal communities, while sawmills act as ecological filters that limit the proliferation of species, favoring only opportunistic and resistant taxa. Despite this, the remarkable similarity between the two locations suggests that sawmills do not form independent fungal communities, but rather preserve part of the natural fungal reserve, ensuring that species important for wood decomposition continue to exist.

The way in which fungal groups are organized and structured shows that, although variety decreases in storage areas, the most common types of fungi (e.g., *A. fuscosuccinea*, *S. commune*, and *Ganoderma* spp.) have a great ability to spread and adapt, which poses a significant economic threat to wood preservation. For all these reasons, the results highlight how crucial it is to take fungal diversity into account when caring for forests and storing wood. This allows for the creation of control and prevention plans aimed at minimizing economic losses while maintaining the good quality of the area's forest resources.

REFERENCES

1. Abrahão, M. C., Matheus Pires, R., De Mello Gugliotta, A., Pereira, E., Gomes, C., Ramos Bononi, V. L. (2019). Wood-decay fungi (Agaricomycetes, Basidiomycota) in three physiognomies in the Savannah region in Brazil. *Hoehnea*, *46*(1), e692018. https://doi.org/10.1590/2236-8906-69/2018
2. Ador, M. A. H., Ahmed, R., Dey, B., Haque, M. M. U. (2024). Assessment of decay caused by Trametes flavida and Daldinia eschscholtzii on several hardwood species. *Forest Pathology*, *54*(3). https://doi.org/10.1111/efp.12870
3. Ador, M. A. H., Ahmed, R., Khatun, R., Rahman, M. A., Haque, M. M. U. (2023). Identification, diversity and host specificity of the wood-decay fungi in major sawmill depots of north-eastern Bangladesh. *Forest Pathology*, *53*(1). https://doi.org/10.1111/efp.12792
4. Arač, K., Orlović, J. K., Diminić, D. (2021). Effect of fungus *meripilus giganteus* (Pers.) p. karst. on occurrence and development of false heartwood and rot in fagus sylvatica l. round wood. *Croatian Journal of Forest Engineering*, *42*(3), 529–542. https://doi.org/10.5552/crojfe.2021.885
5. Bässler, C., Müller, J., Dziock, F., Brandl, R. (2010). Effects of resource availability and climate on the diversity of wood-decaying fungi. *Journal of Ecology*, *98*(4), 822–832. https://doi.org/10.1111/J.1365-2745.2010.01669.X
6. Bell-Doyon, P., Bellavance, V., Bélanger, L., Mazerolle, M. J., Villarreal A., J. C. (2022). Bacterial, fungal, and mycorrhizal communities in the soil differ between clearcuts and insect outbreaks in the boreal forest 50 years after disturbance. *Forest Ecology and Management*, *523*, 120493. https://doi.org/10.1016/J.FORECO.2022.120493
7. Blackwell, M. (2011). The Fungi: 1, 2, 3 … 5.1 million species? *American Journal of Botany*, *98*(3), 426–438. https://doi.org/10.3732/AJB.1000298
8. Borcard, D., Gillet, F., Legendre, P. (2018). *Numerical Ecology with R*. https://doi.org/10.1007/978-3-319-71404-2
9. Bowd, E. J., Banks, S. C., Bissett, A., May, T. W., Lindenmayer, D. B. (2022). Disturbance alters the forest soil microbiome. *Molecular Ecology*, *31*(2). https://doi.org/10.1111/mec.16242
10. Cao, D., Lou, Y., Jiang, X., Zhang, D., Liu, J. (2022). Fungal diversity in barley under different storage conditions. *Frontiers in Microbiology*, *13*, 895975. https://doi.org/10.3389/FMICB.2022.895975/BIBTEX
11. Castro, F. S. de, Da Silva, P. G., Solar, R., Fernandes, G. W., Neves, F. de S. (2020). Environmental drivers of taxonomic and functional diversity of ant communities in a tropical mountain. *Insect Conservation and Diversity*, *13*(4). https://doi.org/10.1111/icad.12415
12. Chen, Y. L., Deng, Y., Ding, J. Z., Hu, H. W., Xu, T. Le, Li, F., Yang, G. B., Yang, Y. H. (2017). Distinct microbial communities in the active and permafrost layers on the Tibetan Plateau. *Molecular Ecology*, *26*(23). https://doi.org/10.1111/mec.14396
13. Costa, F. V. da, Viana-Júnior, A. B., Aguilar, R., Silveira, F. A. O., Cornelissen, T. G. (2023). Biodiversity and elevation gradients: Insights on sampling biases across worldwide mountains. *Journal of Biogeography*, *50*(11). https://doi.org/10.1111/jbi.14696
14. Daly, A. J., Baetens, J. M., De Baets, B. (2018). Ecological Diversity: Measuring the Unmeasurable. *Mathematics, 6*(7), 119. https://doi.org/10.3390/MATH6070119
15. Das, K., Aminuzzaman, F. M., Akhtar, N. (2017). Diversity of fleshy macro fungi in Mangrove forest regions of Bangladesh. *Journal of Biology and Nature*, 218–241. https://ikprress.org/index.php/JOBAN/article/view/1299

16. Deflorio, G., Johnson, C., Fink, S., Schwarze, F. W. M. R. (2008). Decay development in living sapwood of coniferous and deciduous trees inoculated with six wood decay fungi. *Forest Ecology and Management*, *255*(7), 2373–2383. https://doi.org/10.1016/J.FORECO.2007.12.040
17. Deng, W., Wang, J. L., Scott, M. B., Fang, Y. H., Liu, S. R., Yang, X. Y., Xiao, W. (2020). Sampling methods affect Nematode-Trapping Fungi biodiversity patterns across an elevational gradient. *BMC Microbiology*, *20*(1), 1–11. https://doi.org/10.1186/S12866-020-1696-Z/FIGURES/7
18. Di Ruocco, G., Gaita, A. (2023). Life cycle assessment from cradle-to-handover approach to greenhouse gas emissions mitigation: Carbon storage in timber buildings. *Buildings, 13*(7), 1722. https://doi.org/10.3390/BUILDINGS13071722
19. Dighton, J. (2018). Fungi in Ecosystem Processes. In *Fungi in Ecosystem Processes*. https://doi.org/10.1201/9781315371528
20. Dodoo, A., Gustavsson, L., Sathre, R. (2014). Lifecycle carbon implications of conventional and low-energy multi-storey timber building systems. *Energy and Buildings*, *82*, 194–210. https://doi.org/10.1016/J.ENBUILD.2014.06.034
21. Dong, K., Moroenyane, I., Tripathi, B., Kerfahi, D., Takahashi, K., Yamamoto, N., An, C., Cho, H., Adams, J. (2017). Soil nematodes show a midelevation diversity maximum and elevational zonation on Mt. Norikura, Japan. *Scientific Reports*, *7*(1). https://doi.org/10.1038/s41598-017-03655-3
22. Dourojeanni, M. (2022). Para democratizar y fortalecer el aprovechamiento forestal en el Perú. *Revista Kawsaypacha: Sociedad y Medio Ambiente*, *10*, A-010. https://doi.org/10.18800/kawsaypacha.202202.010
23. Freund, R. J., Wilson, W. J., Mohr, D. L. (2010). Inferences for Two or More Means. *Statistical Methods*, 245–320. https://doi.org/10.1016/B978-0-12-374970-3.00006-8
24. Gendek, A., Piętka, J., Aniszewska, M., Malaťák, J., Velebil, J., Tamelová, B., Krilek, J., Moskalik, T. (2023). Energy value of silver fir (Abies alba) and Norway spruce (Picea abies) wood depending on the degree of its decomposition by selected fungal species. *Renewable Energy*, *215*. https://doi.org/10.1016/j.renene.2023.118948
25. Guerrero-Galán, C., Calvo-Polanco, M., Zimmermann, S. D. (2019). Ectomycorrhizal symbiosis helps plants to challenge salt stress conditions. In *Mycorrhiza 29*(4). https://doi.org/10.1007/s00572-019-00894-2
26. Guo, Q., Kelt, D. A., Sun, Z., Liu, H., Hu, L., Ren, H., Wen, J. (2013). Global variation in elevational diversity patterns. *Scientific Reports*, *3*. https://doi.org/10.1038/srep03007
27. Guzmán, G. (1979). *Identificación de los hongos: comestibles, venenosos, alucinantes y destructores de la madera* (Primera reimpresión). Editorial Limusa.
28. Hafner, A., Schäfer, S. (2017). Comparative LCA study of different timber and mineral buildings and calculation method for substitution factors on building level. *Journal of Cleaner Production*, *167*, 630–642. https://doi.org/10.1016/J.JCLEPRO.2017.08.203
29. Hawksworth, D. L., Lücking, R. (2017). Fungal Diversity Revisited: 2.2 to 3.8 Million Species. *Microbiology Spectrum*, *5*(4). https://doi.org/10.1128/MICROBIOLSPEC.FUNK-0052-2016
30. Heilmann-Clausen, J., Barron, E. S., Boddy, L., Dahlberg, A., Griffith, G. W., Nordén, J., Ovaskainen, O., Perini, C., Senn-Irlet, B., Halme, P. (2015). A fungal perspective on conservation biology. *Conservation Biology*, *29*(1). https://doi.org/10.1111/cobi.12388
31. Hernández, G., Sáenz-Mata, J., Moreno-Reséndez, A., Castañeda-Gaytán, G., Ogaz, A., Carballar-Hernández, S., Hernández-Cuevas, L. (2018). Dinámica de la diversidad temporal de los hongos micorrícicos arbusculares de Larrea tridentata (Sesse & Mocino ex DC) Coville en un ecosistema semiárido. *Revista Argentina de Microbiología*, *50*(3), 301–310. https://doi.org/10.1016/J.RAM.2017.07.007
32. Hou, M., Zhu, J., Leng, C., Huang, X., Yang, M., Yin, Y., Xing, Y., Chen, J. (2025). Composition and Biodiversity of Culturable Endophytic Fungi in the Roots of Alpine Medicinal Plants in Xinjiang, China. *Journal of Fungi*, *11*(2), 113. https://doi.org/10.3390/JOF11020113/S1
33. Iannaccone, M., Amalfi, M., Buhagiar, J. A. (2024). Axenic Culture and DNA Barcode Identification of Wood Decay Fungi from the Maltese Islands. *Forests*, *15*(5). https://doi.org/10.3390/f15050850
34. Jerusik, R. J. (2010). Fungi and paper manufacture. *Fungal Biology Reviews*, *24*(1–2), 68–72. https://doi.org/10.1016/j.fbr.2010.04.003
35. Kent, M. (2011). *Vegetation Description and Data Analysis: A Practical Approach*. John Wiley & Sons: Hoboken, NJ, USA.
36. Kessler, M., Kluge, J., Hemp, A., Ohlemüller, R. (2011). A global comparative analysis of elevational species richness patterns of ferns. *Global Ecology and Biogeography*, *20*(6). https://doi.org/10.1111/j.1466-8238.2011.00653.x
37. Keylock, C. J. (2005). Simpson diversity and the Shannon–Wiener index as special cases of a generalized entropy. *Oikos*, *109*(1), 203–207. https://doi.org/10.1111/J.0030-1299.2005.13735.X
38. Kouki, J., Salo, K. (2020). Forest disturbances affect functional groups of macrofungi in young

successional forests – harvests and fire lead to different fungal assemblages. *Forest Ecology and Management*, *463*. https://doi.org/10.1016/j.foreco.2020.118039

39. Kumar, D., Gupta, R. K. (2006). Biocontrol of wood-rotting fungi. *Indian Journal of Biotechnology*. https://www.scopus.com/pages/publications/32044445049?origin=scopusAI
40. Li, T., Li, J., Wei, Y. (2019). Species diversity and distribution of wood-decaying fungi in Gutianshan national nature reserve. *Biodiversity Science*, *27*(1), 81–87. https://doi.org/10.17520/biods.2018156
41. Li, X., Qu, Z., Zhang, Y., Ge, Y., Sun, H. (2022). Soil fungal community and potential function in different forest ecosystems. In *Diversity* 14(7). https://doi.org/10.3390/d14070520
42. Lonsdale, D., Pautasso, M., Holdenrieder, O. (2008). Wood-decaying fungi in the forest: Conservation needs and management options. *European Journal of Forest Research*, *127*(1), 1–22. https://doi.org/10.1007/s10342-007-0182-6
43. Mafia, R. G., Santos, P. C., Demuner, B. J., Massoquete, A., Sartório, R. C. (2012). Eucalyptus wood decay: Effects on productivity and quality of cellulose. *Forest Pathology*, *42*(4), 321–329. https://doi.org/10.1111/j.1439-0329.2011.00757.x
44. Margalef, R. (1957). Information theory in ecology. *Annals of the Royal Academy of Arts and Sciences of Barcelona*, *32*(13), 373–449. https://digital.csic.es/handle/10261/284346
45. McCain, C. M. (2005). Elevational gradients in diversity of small mammals. *Ecology*, *86*(2). https://doi.org/10.1890/03-3147
46. Montano, R. del P., Palomino, E. R. (2012). *Diversidad de hongos e insectos xilófagos en bosque y aserraderos de selva central* [Thesis for a degree in Forestry and Environmental Engineering]. University (Peru: Universidad Nacional del Centro del Perú - Faculty of Forestry and Environmental Sciences).
47. Ni, Y., Tong, Z., Rong, D., Zhou, Z., Xu, X. (2018). Accurate thermal buckling analysis of functionally graded orthotropic cylindrical shells under the symplectic framework. *Thin-Walled Structures*, *129*. https://doi.org/10.1016/j.tws.2018.03.030
48. Ogwu, M. C., Takahashi, K., Dong, K., Song, H. K., Moroenyane, I., Waldman, B., Adams, J. M. (2019). Fungal elevational rapoport pattern from a high mountain in Japan. *Scientific Reports*, *9*(1). https://doi.org/10.1038/s41598-019-43025-9
49. Olou, B. A., Yorou, N. S., Striegel, M., Bässler, C., Krah, F. S. (2019). Effects of macroclimate and resource on the diversity of tropical wood-inhabiting fungi. *Forest Ecology and Management*, *436*, 79–87. https://doi.org/10.1016/J.FORECO.2019.01.016
50. Ozturk, O., Kavlak, K. B. (2019). Statistical inference using stratified ranked set samples from finite populations. *Ranked Set Sampling*, 157–170. https://doi.org/10.1016/B978-0-12-815044-3.00012-5
51. Pavlich, M. (1976). *Ascomycetes y Basidiomycetes del Perú: Con énfasis en especies de la Ceja de Montaña y Selva Tropical, 1*. Universidad Nacional Mayor de San Marcos. Dirección Universitaria de Biblioteca y Publicaciones.
52. Perreault, L., Forrester, J. A., Lindner, D. L., Jusino, M. A., Fraver, S., Banik, M. T., Mladenoff, D. J. (2023). Linking wood-decay fungal communities to decay rates: Using a long-term experimental manipulation of deadwood and canopy gaps. *Fungal Ecology*, *62*. https://doi.org/10.1016/j.funeco.2022.101220
53. Pielou, E. (1969). *An introduction to mathematical ecology*. Wiley Interscience. John Wiley & Sons, New York. VIII + 286 S., 32 Abb., Preis 140.
54. Purahong, W., Wubet, T., Krüger, D., Buscot, F. (2018). Molecular evidence strongly supports deadwood-inhabiting fungi exhibiting unexpected tree species preferences in temperate forests. *The ISME Journal*, *12*(1), 289–295. https://doi.org/10.1038/ISMEJ.2017.177
55. Rahbek, C. (1995). The elevational gradient of species richness: a uniform pattern? *Ecography*, *18*(2). https://doi.org/10.1111/j.1600-0587.1995.tb00341.x
56. Rahbek, C. (2005). The role of spatial scale and the perception of large-scale species-richness patterns. In *Ecology Letters* 8(2). https://doi.org/10.1111/j.1461-0248.2004.00701.x
57. Rahniawati, N., Sumardi, I., Dungani, R. (2020). Isolation and identification of fungi inhabiting rubber-impregnated wood, and their role of quality changing the impregnated wood. *BioResources*, *15*(2), 2839–2849. https://doi.org/10.15376/biores.15.2.2839-2849
58. Ryvarde, L., Gilbertson, R. L. (1994). *European polypores, Part 2*. Gronlands Grafiske A/S.
59. Sanders, N. J., Moss, J., Wagner, D. (2003). Patterns of ant species richness along elevational gradients in an arid ecosystem. *Global Ecology and Biogeography*, *12*(2). https://doi.org/10.1046/j.1466-822X.2003.00324.x
60. Schrader, L., Brischke, C., Trautner, J., Tebbe, C. C. (2025). Microbial decay of wooden structures: actors, activities and means of protection. *Applied Microbiology and Biotechnology*, *109*(1), 1–16. https://doi.org/10.1007/S00253-025-13443-Z/TABLES/1
61. Shannon, C. E. (1948). A Mathematical Theory of Communication. *Bell System Technical Journal*, *27*(3), 379–423. https://doi.org/10.1002/J.1538-7305.1948.TB01338.X

62. Shen, C., Gunina, A., Luo, Y., Wang, J., He, J. Z., Kuzyakov, Y., Hemp, A., Classen, A. T., Ge, Y. (2020). Contrasting patterns and drivers of soil bacterial and fungal diversity across a mountain gradient. *Environmental Microbiology*, *22*(8). https://doi.org/10.1111/1462-2920.15090
63. Simpson, E. H. (1949). Measurement of diversity. *Nature*, *163*(4148), 688. https://doi.org/10.1038/163688A0;KWRD
64. Sioma, A., Lenty, B. (2023). Detection of Fungal Infections on the Wood Surface Using LTM Imaging. *Applied Sciences (Switzerland)*, *13*(1). https://doi.org/10.3390/app13010490
65. Smith, G. R., Peay, K. G. (2021). Multiple distinct, scale-dependent links between fungi and decomposition. *Ecology Letters*, *24*(7), 1352–1362. https://doi.org/10.1111/ELE.13749
66. Straumfors, A., Afanou, A. (2021). Fungal Contamination of Sawmills. *Encyclopedia of Mycology: 1,2*, *2*, 59–72. https://doi.org/10.1016/B978-0-12-809633-8.21044-3
67. Sui, X., Li, M., Frey, B., Dai, G., Yang, L., Li, M. H. (2023). Effect of elevation on composition and diversity of fungi in the rhizosphere of a population of Deyeuxia angustifolia on Changbai Mountain, northeastern China. *Frontiers in Microbiology*, *14*. https://doi.org/10.3389/fmicb.2023.1087475
68. Sun, D., Qu, J., Huang, Y., Lu, J., Yin, L. (2021). Analysis of microbial community diversity of muscadine grape skins. *Food Research International*, *145*, 110417. https://doi.org/10.1016/J.FOODRES.2021.110417
69. Suprapti, S., Djarwanto, Dewi, L. M. (2020). Determining the wood (*Parashorea* spp.) decaying and metal corroding abilities of Eight fungi. *Journal of the Korean Wood Science and Technology*, *48*(1), 50–60. https://doi.org/10.5658/WOOD.2020.48.1.50
70. Tanjim, A., Aminuzzaman, F. M., Rahaman, M., Tanni, J. F. (2019). Biodiversity, distribution and morphological characterization of macrofungi in Sylhet and Moulvibazar under tropical evergreen and semi - evergreen forest regions of Bangladesh. *International Journal of Advanced Research*, *7*(11), 567–589. https://doi.org/10.21474/IJAR01/10047
71. Ulanowicz, R. E. (2001). Information theory in ecology. *Computers & Chemistry*, *25*(4), 393–399. https://doi.org/10.1016/S0097-8485(01)00073-0
72. Verbist, M., Nunes, L., Jones, D., Branco, J. M. (2019). Service life design of timber structures. *Long-Term Performance and Durability of Masonry Structures: Degradation Mechanisms, Health Monitoring and Service Life Design*, 311–336. https://doi.org/10.1016/B978-0-08-102110-1.00011-X
73. Werenkraut, V., Ruggiero, A. (2011). Quality of basic data and method to identify shape affect richness-altitude relationships in meta-analysis. *Ecology*, *92*(1). https://doi.org/10.1890/09-2405.1
74. Whittaker, R. J., Willis, K. J., Field, R. (2001). Scale and species richness: Towards a general, hierarchical theory of species diversity. *Journal of Biogeography*, *28*(4). https://doi.org/10.1046/j.1365-2699.2001.00563.x
75. Yalçın, M., Doğan, H. H., Akçay, Ç. (2019). Identification of wood-decay fungi and assessment of damage in log depots of Western Black Sea Region (Turkey). *Forest Pathology*, *49*(2). https://doi.org/10.1111/EFP.12499
76. Yang, T., Adams, J. M., Shi, Y., He, J. S., Jing, X., Chen, L., Tedersoo, L., Chu, H. (2017). Soil fungal diversity in natural grasslands of the Tibetan Plateau: associations with plant diversity and productivity. *New Phytologist*, *215*(2). https://doi.org/10.1111/nph.14606
77. Yang, W., Li, S., Wang, X., Liu, F., Li, X., Zhu, X. (2021). Soil properties and geography shape arbuscular mycorrhizal fungal communities in black land of China. *Applied Soil Ecology*, *167*. https://doi.org/10.1016/j.apsoil.2021.104109
78. Yang, Z., Ren, H.-Q., Jiang, Z.-H. (2010). Effects of biological decay on mechanical properties of slash pine wood. *Beijing Linye Daxue Xuebao/Journal of Beijing Forestry University*. https://www.scopus.com/pages/publications/77954878486?origin=scopusAI
79. Yu-Lian, W. (2021). Forming mechanisms and ecological function of wood-decaying fungal community in forest ecosystem. *Chinese Journal of Ecology*, *40*(2), 534–543. https://doi.org/10.13292/j.1000-4890.202102.001
80. Zhang, L. Y., Wei, Y. L. (2016). Species diversity and distribution characters of wood-decaying fungi in fenglin nature reverse. *Chinese Journal of Ecology*, *35*(10), 2745–2751. https://doi.org/10.13292/j.1000-4890.201610.029
81. Zhang, S., Cao, Z., Fu, W., Shen, C., Hao, Z., Sun, G., Ge, Y., Zhang, L., Zhang, X., Chen, B. (2025). Distribution patterns and driving forces of soil fungal communities along elevational gradients on two snow mountains in the Hengduan Mountain Range. *Soil Ecology Letters*, *7*(3), 1–16. https://doi.org/10.1007/S42832-025-0323-1/METRICS
82. Zhou, Y., Jia, X., Han, L., Liu, Z., Kang, S., Zhao, Y. (2021). Fungal community diversity in soils along an elevation gradient in a *Quercus aliena* var. acuteserrata forest in Qinling Mountains, China. *Applied Soil Ecology*, *167*. https://doi.org/10.1016/j.apsoil.2021.104104