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Full Length Article

Alpha Taxonomic Study of Macrofungi at Marinduque Wildlife Sanctuary

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Abstract

Research on the species listing of macrofungi in Marinduque Wildlife Sanctuary in the Philippines was conducted from November 2022 to January 2023. The macrofungi were documented across habitats of primary and secondary forests, riparian areas, agricultural land, and grassland. A line transect of 1000 m was established at each study site where macrofungi were collected using opportunistic sampling. The collected species were identified based on the macrofungi's morphological attributes. A total of 149 morphospecies, belonging to 87 genera and 45 families, were documented, with the family Polyporaceae and the genus *Mycena* identified as the most dominant. Macrofungi species were also found to be most prevalent in forested areas. Each habitat also showed more unique species than shared species across habitats. This study was the first to unveil rich fungal flora in the province of Marinduque.

Keywords: Ascomycota; Basidiomycota; Fungal flora; Habitat; Morphospecies; Taxonomy

Introduction

Macrofungi are eukaryotic organisms characterized by their remarkable fruiting bodies (Cao *et al.* 2021). They play an essential role in the environment as saprophytes, parasites, and mycorrhizal (Li *et al.* 2018). Saprotrophs break down organic matter, while parasites serve as the parasitic pathogens. On the other hand, mycorrhizal fungi establish symbiotic relationships with living plant roots. These organisms are also considered valuable resources for industry, providing food, medicine, and raw materials used to produce dyes and cosmetics (Toma *et al*. 2023). They have also been proven to possess therapeutic and nutraceutical values (Anusiya *et al.* 2021; Mwangi *et al.* 2022). These exhibit antioxidant, antimicrobial, and antidiabetic properties (Dulay *et al.* 2014; Rangel-Vargas *et al.* 2021). Macrofungi are also ubiquitous or can be found in a wide range of habitats. However, despite the full potential of these organisms, mycoflora resource has not been well explored.

The Philippines possesses one of the world's most diverse ecosystems (Myers *et al.* 2000), providing a range of habitats for plants, animals, and other organisms. Given the country's archipelagic nature and rich natural environment, it is suitable for the growth and proliferation of macrofungi. Several reviews have yielded a comprehensive list of macrofungi, providing an overview of the Philippines' mycoflora. For instance, Luzon has the highest number of taxonomic studies (Jacob *et al*. 2022; Dulay *et al*. 2023). The studies of Dulay *et al.* (2020), Paguirigan *et al.* (2020), Tadiosa *et al.* (2021) and Bustillos *et al.* (2024) focused on systematic inventories and species diversity assessments. While Soriano *et al.* (2021) studied ecology and distribution patterns. However, other researchers focused on ethnomycological and indigenous knowledge (Tantengco and Ragrario 2018; Leon *et al.* 2019; Torres *et al.* 2020). Meanwhile, Torres *et al.* (2020) documented crucial macrofungi across various tribes, while Jusayan and Vicencio (2019) identified new species. Tadiosa and

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Briones (2013), Arenas *et al.* (2015), Liwanag *et al.* (2017) and Kim *et al.* (2021) have also delved into the exploration of macrofungi in protected areas. The findings from these studies provided compelling evidence of the abundant macrofungal diversity in the country.

According to the study of Jacob *et al.* (2022), the rate of mycological studies in the Philippines is slower. The review of this study revealed that only 220 species were added to the 156 recorded in 1906. This resulted in 376 validated species between 1906 to present. This shows that the country has a slow pace of documentation of macrofungi. Given the numerous islands of the Philippines, only a small fraction of the country's actual diversity is reported or investigated. Moreover, the country's low record of these species (Jacob *et al.* 2022) and the lack of conservation efforts hinder the possibility of setting the total significance of macrofungi (Kinge *et al*. 2020; Torres *et al.* 2020).

Despite previous explorations, only 19.88% of research efforts in the country focus on the ethnomycology and biodiversity of these organisms (Dulay *et al.* 2023). Thus, significant knowledge still requires more discoveries about macrofungi across the different islands of the Philippines (Leon *et al.* 2021). Moreover, the fungal flora of the Philippines is threatened by forest overexploitation, climate change (Parlucha *et al.* 2021) and other environmental factors. This underscores the urgent need for documentation to support the conservation and protection the environment.

Macrofungal surveys concentrated in Luzon, however several areas are still unexplored. One of these areas is the province of Marinduque. Marinduque lies in the Southwestern Tagalog Region (MIMAROPA). It houses the protected area, the Marinduque Wildlife Sanctuary, which covers 9,759 ha. This sanctuary is home to a diverse range of flora and fauna. The province also has a Type III climate, without very pronounced maximum rain period. Provinces with Type III climate are frequently affected by typhoons that hit the Philippines. On one hand, dry season in Marinduque is either from December to April or from March to May. To date, despite the sanctuary's rich biodiversity, macrofungal communities in these areas have not been explored or documented. Given this gap, this study was conducted to document and identify the taxonomic composition and habitat distribution of macrofungi in the Marinduque Wildlife Sanctuary.

Materials and Methods

Study sites

This study was conducted in the five habitats, *i.e*., primary forest (PF), secondary forest (SF), grassland (GL), riparian area (RP), and agricultural land (AG) which were found within the Marinduque Wildlife Sanctuary. This is a protected area situated in the municipalities of Buenavista and Torrijos in the province of Marinduque, Philippines. The sanctuary covers an area of 9,759 ha, located at 13°21'44.9"N 121°58'35.8"E (Fig. 1). It was established in 2004 under the Republic Act 7586 or the National Integrated Protected Areas System Act of 1992. Geographical and physical characteristics of the study sites are provided in Table 1.

Gratuitous permit and entry protocol at the protected area

Approval of any activities inside the declared protected areas was necessary. Thus, before the sampling activities, the proposal was presented to the Marinduque Wildlife Sanctuary - Protected Area Management Board. Subsequently, a wildlife gratuitous permit (MIMAROPA-2022-03) was obtained for the legal conduct of the study. Each sampling activity was meticulously documented by both the researcher and the Protected Area Management Office or PAMO, under the guidance of the Protected Area Superintendent (PASU). The PAMO office provided invaluable logistical support and assistance throughout the research endeavor.

Macrofungal photo-documentation and collection

The extensive field collection and photo-documentation of macrofungi were conducted between November 2022 to January 2023 across different habitats in the Marinduque Wildlife Sanctuary.

Line transects of 1000 m were laid at each study site under the guidance of the foresters based on their knowledge and assessment of potential safety risk. The fieldwork typically started in the morning until the afternoon.

The study employed opportunistic sampling methods. The macrofungi were photographed in their natural habitat using the Sony ZV-1compact camera to display the features of all the fruiting bodies, with appropriate tags and a coin for scale reference. Woody macrofungi were collected with a sharp knife, while fleshy samples were collected with a trowel. Physical characteristics, substrate type, and precise location were recorded for each macrofungus.

Collected macrofungal species storage, preservation, and transport

The storage and preservation of collected samples followed the protocol of Tadiosa *et al.* (2011). Woody samples were dried using an improvised dryer to prevent decomposition and insect attack. Dried samples were placed inside paper packets with proper tagging.

Fleshy samples were submerged in a clean container with 70% ethanol. Upon reaching the laboratory, woody and fleshy samples were segregated and stored in a storage cabinet. Before transport from Marinduque to Cavite, all samples were presented and checked while travel permits were secured from DENR-PENRO PAMO Marinduque.

Table 1: Geographical and biophysical characteristics of study sites

Descriptions	Primary Forest	Secondary forest	Riparian	Agricultural land	Grassland
Barangay	Malbog, Buenavista	Malbog, Buenavista	Bagtingon, Buenavista	Malibago, Torrijos	Malibago, Torrijos
Geographical location	13°17'29.146"N 121°58'19.22"E	13°17'28.605"N 121°57'8.001"E	13°18'15.946'N 121°56'28.82"E	13°16'51.706"N 121°59'40.882"E	13°17'05.334"N 121°59'45.555"E
Elevation	786-1620 ft.	296-778 ft.	313-486 ft.	1241-1498 ft.	1035-1352 ft.
Zoning	Strict protection zone	Multiple use zone	Multiple use zone	Multiple use zone	Multiple use zone
Mean air temperature (°C)	28.07	28	29.19	28.07	30.93
Mean litter depth (cm)	2.8	1.11	2.18	1.17	0.4
Canopy cover (%)	89	83	78	0	0

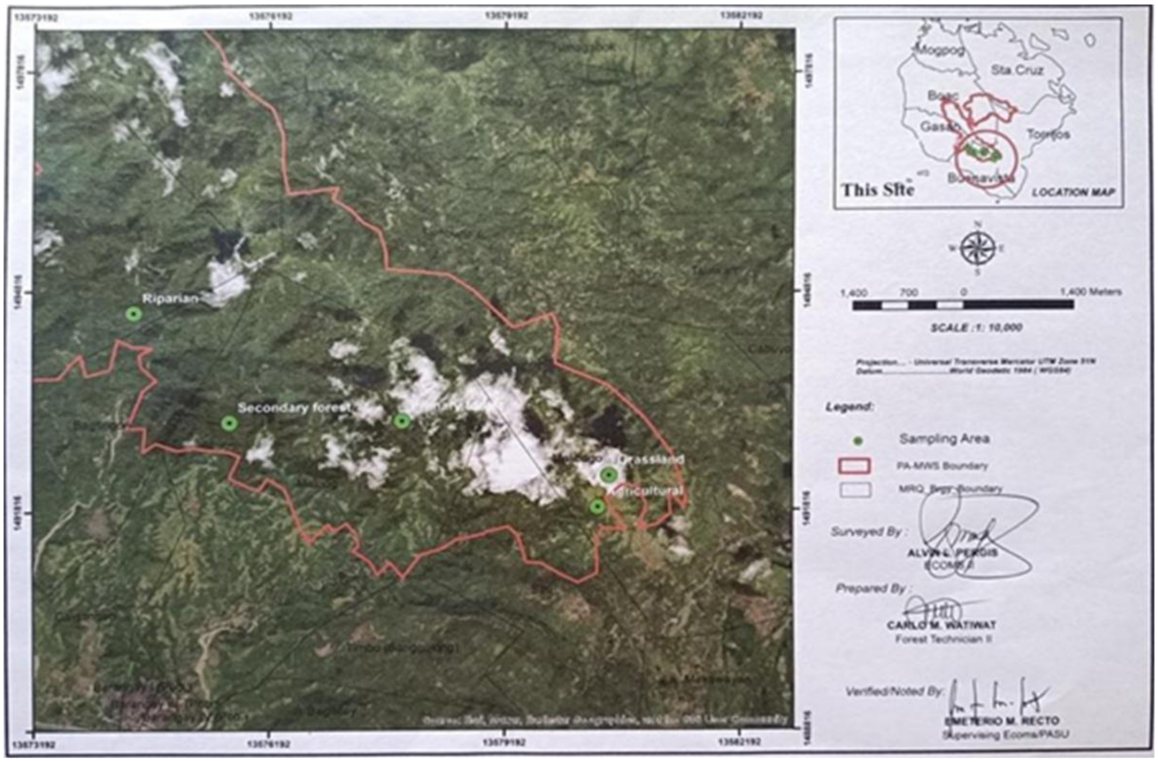

Fig. 1: Marinduque Wildlife Sanctuary showing the location of the sampling areas in green dots (Source: Provincial Environmental and Natural Resources Office-Marinduque)

Collected macrofungal species identification and classification

The macroscopic characteristics of macrofungi, such as pileus (size and shape), underside features (pores, gill-like ridges, and teeth-like ridges), lamellae (attachment to the stipe), stipe (length and width), annulus (presence or absence), volva (presence or absence), and spore prints, were observed. Based on the recorded characteristics, dichotomous keys were created. The initial identification of the collected samples was cross-referenced with taxonomic works by Tadiosa *et al*. (2011), Arenas *et al.* (2018), Dulay *et al*. (2020) and the Pictorial Guide on Philippine Indigenous Mushrooms (2023). This was compared with herbarium specimens and further verified by a mycologist.

Data analysis

The taxonomic classification and habitat distribution of each identified macrofungal morphospecies were tabulated. The overall total top phylum, families, and genera in Marinduque Wildlife Sanctuary were presented using a bar graph. Moreover, the overall percentage composition of top families with ≥ 5 morphospecies and genera with ≥ 3 was computed using Microsoft Excel and presented in a table. The top genus across habitats was also identified and presented in a bar graph. Unique and shared species were analyzed on https://hiplot.com.cn/.

Results

Macrofungal taxa composition and their habitat distribution

A total of 149 macrofungi morphospecies belonging to 45 families and 87 genera were documented in the different habitats of the Marinduque Wildlife Sanctuary (Table 2).

Table 2: Taxonomic positions of the macrofungal morphospecies collected at Marinduque Wildlife Sanctuary

ASCOMYCOTA							
Family	Genus	Species	PF	SF	RP	AG	GL
Helotiaceae	*Bisporella*	*Bisporella* sp.			+		
Hypoxylaceae	*Daldinia*	*Daldinia concentrica* (Bolton) Ces. & de Not.		+	+		
		Daldinia sp.		+			
Lachnaceae	*Lachnum*	*Lachnum apalum* (Berk. & Broome) Nannf.				+	
Pezizaceae	*Peziza*	*Peziza repanda* Wahlenb.		+			
		Peziza succosa Berk.	+				
Pyronemataceae	*Octospora*	*Octospora humosa* (Fr.) Dennis	+	+	+		
	Tarzetta	*Tarzetta cupularis* (L.) Svrček	+				
Sarcoscyphaceae	*Cookeina*	*Cookeina sulcipes* (Berk.) Kuntze			+		
		Cookeina tricholoma (Mont.) Kuntze		+			
	Phillipsia	*Phillipsia domingensis* (Berk.) Berk. ex Denison	+	+	+		
	Sarcoscypha	*Sarcoscypha coccinea* (Jacq.) Lambotte			+		
Sarcosomataceae	*Galiella*	*Galiella rufa* (Schwein.) Nannf. & Korf		+			
Xylariaceae	*Xylaria*	*Xylaria filiformis* (Alb. & Schwein.) Fr.	+				
		Xylaria hypoxylon (L.) Grev.	+				
		Xylaria polymorpha (Pers.) Grev.		+			+
BASIDOMYCOTA							
Agaricaceae	*Agaricus*	*Agaricus crocopeplus* Berk. & Broome	+				
		Agaricus subrufescens Peck		+			
		Agaricus sp.	+				
	Bovista	*Bovista plumbea* Pers.					+
	Coprinus	*Coprinus comatus* (O.F.Müll.) Pers.	+	+	+		
		Coprinus sp.		+			
	Cyathus	*Cyathus striatus* (Hudds.) Willd.	+	+			
	Lycoperdon	*Lycoperdon* sp.		+			
Amylocorticiaceae	*Plicaturopsis*	*Plicaturopsis crispa* (Pers.) D.A.Reid		+			
Auriculariaceae	*Auricularia*	*Auricularia auricula-judae* (Bull.) Quél.		+			
		Auricularia cornea Ehrenb.			+		
		Auricularia mesenterica (Dicks.) Pers.		+			
		Auricularia nigricans (Sw.) Birkebak, Looney & Sánchez-García	+	+	+		
Bolbitaceae	*Bolbitius*	*Bolbitius coprophilus* (Peck) Hongo			+		
	Conocybe	*Conocybe apala* (Fr.) Arnolds	+				
	Panaeolina	*Panaeolina foenisecii* (Pers.) Maire			+		
	Panaeolus	*Panaeolus antillarum* (Fr.) Dennis		+		+	+
		Panaeolus cyanescens Sacc.					
Cantharellaceae	*Craterellus*	*Craterellus aureus* Berk. & M.A.Curtis	+				
Clavariaceae	*Clavaria*	*Clavaria zollingeri* Lév.	+				
		Clavaria sp.	+				
	Ramariopsis	*Ramariopsis subtilis* (Pers.) R.H.Petersen	+				
Coniophoraceae	*Gyrodontium*	*Gyrondotium sacchari* (Spreng.) Hjortstam		+			
Corticiaceae	*Corticium*	*Corticium* sp.		+			
	Erythricium	*Erythricium salmonicolor* (Berk. & Broome) Burds.	+				
Cortinariaceae	*Cortinarius*	*Cortinarius* sp.	+				
Dacrymycetaceae	*Dacryopinax*	*Dacryopinax spathularia* (Schwein.) G.W.Martin				+	
Entolomataceae	*Entoloma*	*Entoloma cetratum* (Fr.) M.M.Moser		+			
		Entoloma incanum (Fr.) Hesler			+		
		Entoloma umbiliciforme Hesler		+			
Fomitopsidaceae	*Rhodofomes*	*Rhodofomes roseus* (Alb. & Schwein.) Kolt. & Pouzar		+		+	
Ganodermataceae	*Ganoderma*	*Ganoderma applanatum* (Pers.) Pat.		+	+		
		Ganoderma lucidum (Curtis) P. Karst			+		
Geastraceae	*Geastrum*	*Geastrum saccatum* Fr.		+			
Gleophyllaceae	*Gleophyllum*	*Gloeophyllum striatum* (Sw.) Murrill		+			
		Gloeophyllum trabeum (Pers.) Murrill					+
Hygrophoraceae	*Hygrocybe*	*Hygrocybe coccinea* (Schaeff.) P.Kumm.			+		
		Hygrocybe sp.	+				
	Lichenomphalia	*Lichenomphalia umbellifera* (L.) Redhead, Lutzoni, Moncalvo & Vilgalys					+
Hymenochaetaceae	*Phellinus*	*Phellinus gilvus* (Schwein.) Pat.		+	+		
		Phellinus igniarius (L.) Quél.		+			
		Phellinus rimosus (Berk.) Pilát		+			
	Tropicoporus	*Tropicoporus linteus* (Berk. & M.A.Curtis) L.W.Zhou & Y.C.Dai		+			
Hymenogastraceae	*Galerina*	*Galerina calyptrata* P.D.Orton		+			
		Galerina sp.	+				
	Gymnopilus	*Gymnopilus* sp.		+			
	Psilocybe	*Psilocybe cubensis* (Earle) Singer	+				
		Psilocybe sp.	+				

Table 2: Continued

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Inocybaceae	*Crepidotus*	*Crepidotus herbarum* Peck			+		
		Crepidotus mollis (Schaeff.) Staude	+		+		
Lyophyllaceae	*Termitomyces*	*Termitomyces eurrhizus* (Berk.) R.Heim		+			
Marasmiaceae	*Marasmius*	*Marasmius bulliardii* Quél.	+				
		Marasmius capillaris Morgan		+			
		Marasmius rotula (Scop.) Fr.		+			
	Pleurocybella	*Pleurocybella porrigens* (Pers.) Singer			+		
	Tetrapygros	*Tetrapyrgos alba* (Berk. & M.A.Curtis) E.Horak		+			
		Tetrapyrgos subdendrophora (Redhead) E.Horak			+		
		Tetrapyrgos sp.	+				
Meripilaceae	*Rigidoporus*	*Rigidoporus microporus* (Sw.) Overeem			+		
Meruliaceae	*Irpex*	*Irpex lacteus* (Fr.) Fr.				+	
	Podoscypha	*Podoscypha petalodes* (Berk.) Boidin		+			
Mycenaceae	*Favolaschia*	*Favolaschia manipularis* (Berk.) Teng		+			
	Mycena	*Mycena acicula* (Schaeff.) P.Kumm.		+			
		Mycena arcangeliana Bres.		+			
		Mycena capillaris (Schumach.) P.Kumm.		+			
		Mycena epipterygia (Scop.) Gray		+	+		
		Mycena galopus (Pers.) P. Kumm.		+			
		Mycena inclinata (Fr.) Quél.			+		
		Mycena pura (Pers.) P.Kumm.	+				
		Mycena singeri Lodge		+			
		Mycena sp.	+				
Omphalotaceae	*Gymnopus*	*Gymnopus androsaceus* (L.) Della Maggiora & Trassin.			+		
		Gymnopus foetidus (Sowerby) P.M.Kirk		+			
		Gymnopus peronatus (Bolton) Gray			+		
	Marasmiellus	*Marasmiellus affixus* (Berk.) Singer			+		
		Marasmiellus candidus (Fr.) Singer		+			
		Marasmiellus ramealis (Bull.) Singer		+			
	Mycetinis	*Mycetinis scorodonius* (Fr.) A.W.Wilson			+		
	Rhodocollybia	*Rhodocollybia maculata* (Alb. & Schwein.) Singer					+
Peniophoraceae	*Peniophora*	*Peniophora* sp.		+			
Physalacriaceae	*Oudemansiella*	*Oudemansiella canarii* (Jungh.) Höhn.		+			
Pleurotaceae	*Pleurotus*	*Pleurotus ostreatus* (Jacq.) P.Kumm.		+	+		
Pluteaceae	*Pluteus*	*Pluteus cervinus* (Schaeff.) P. Kumm.		+			
		Pluteus salicinus (Pers.) P.Kumm.		+			
		Pluteus sp.	+				
	Volvariella	*Volvariella volvacea* (Bull.) Singer		+			
Polyporaceae	*Daedaleopsis*	*Daedaleopsis confragosa* (Bolton) J. Schröt.		+			
		Daedaleopsis nitida (Durieu & Mont.) Zmitr. & Malysheva		+			
	Earliella	*Earliella scabrosa* (Pers.) Gilb. & Ryvarden	+	+	+		+
		Earliella sp.			+		
	Favolus	*Favolus tenuiculus* P.Beauv.			+		
	Fomes	*Fomes fomentarius* (L.) Fr.			+		
	Hexagonia	*Hexagonia hydnoides* (Sw.) M.Fidalgo	+				
		Hexagonia rigida Berk.		+			
		Hexagonia tenuis (Hook.) Fr.	+	+	+		
	Lentinus	*Lentinus squarrosulus* Mont.		+		+	
		Lentinus tigrinus (Bull.) Fr.	+				
		Lentinus velutinus Fr.	+				
	Microporus	*Microporus affinis* (Blume & T.Nees) Kuntze		+	+		
		Microporus xanthopus (Fr.) Kuntze	+	+			
	Panus	*Panus rudis* Fr.	+				
	Polyporus	*Polyporus picipes* Fr.	+				
		Polyporus squamosus Huds.			+		
		Polyporus sp.	+				
	Pycnoporus	*Pycnoporus sanguineus* (L.) Murrill		+	+		+
	Trametes	*Trametes gibbosa* (Pers.) Fr.		+			
		Trametes hirsuta (Wulfen) Lloyd		+	+		
		Trametes pubescens (Schumach.) Pilát			+		
		Trametes versicolor (L.) Lloyd		+			
		Trametes villosa (Sw.) Kreisel		+			
Psathyrellaceae	*Coprinellus*	*Coprinellus disseminatus* (Pers.) J. E. Lange		+			
		Coprinellus micaceus (Bull.) Vilgalys, Hopple & Jacq.Johnson		+			
	Coprinopsis	*Coprinopsis cinerea* (Schaeff.) Redhead, Vilgalys & Moncalvo		+			
		Coprinopsis lagopus (Fr.) Redhead, Vilgalys & Moncalvo		+	+		
	Psathyrella	*Psathyrella* sp.	+				

Table 2: Continued

Table 2: Continued

Russulaceae	*Lactarius*	*Lactarius pallidus* Pers.		+			
	Russula	*Russula queletii* Fr.			+		
		Russula virescens (Schaeff.) Fr.		+			
Schizophyllaceae	*Schizophyllum*	*Schizophyllum commune* Fr.	+	+	+	+	
Stereaceae	*Stereum*	*Stereum complicatum* (Fr.) Fr.			+		
		Stereum hirsutum (Willd.) Pers.			+		
		Stereum insignitum Quél.		+			
		Stereum ostrea (Blume & T.Nees) Fr.		+			
		Stereum subtomentosum Pouzar		+			
Strophoriaceae	*Protostropharia*	*Protostropharia semiglobata* (Batsch) Redhead, Moncalvo & Vilgalys					+
	Stropharia	*Stropharia* sp.	+				
Thelephoraceae	*Thelephora*	*Thelephora* sp.	+				
Tricholomataceae	*Clitocybe*	*Clitocybe* sp.	+				
	Collybia	*Collybia* sp.	+				
	Omphalina	*Omphalina* sp.		+			
	Tricholoma	*Tricholoma sulphureum* (Bull.) P.Kumm.			+		
		Tricholoma sp.		+			
	Tricholomopsis	*Tricholomopsis* sp.		+			

PF: Primary Forest, SF: Secondary Forest; GL: Grassland, RP: Riparian, AG: Agricultural land

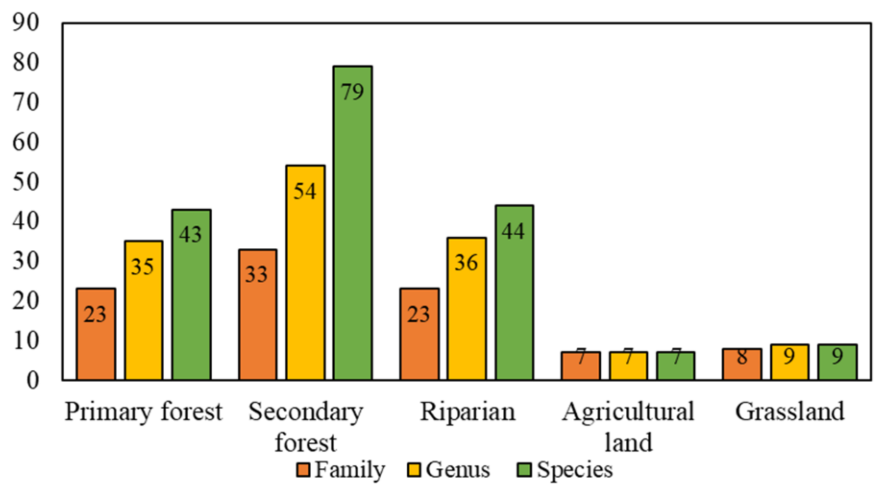

Fig. 2: Total number of families, genera, and morphospecies found in the habitats of the Marinduque Wildlife Sanctuary

Out of the 149 morphospecies recorded, 123 were identified up to the species level and 26 to the genus level. Among the explored habitats, the most species were found in the secondary forest with 79 morphospecies. This was followed by the riparian area with 44 and the primary forest with 43. On the other hand, agricultural land and grassland recorded 7 and 9 morphospecies, respectively (Fig. 2).

Top phyla

A high number of morphospecies were recorded under Phylum Basidiomycota with 37 families, 76 genera, and 133 morphospecies. In contrast, Phylum Ascomycota has 8 families, 11 genera and 16 morphospecies recorded (Fig. 3).

Top families

Analysis of the species richness of the 45 families revealed 10 families with ≥5 morphospecies (Table 3). The dominant families were Polyporaceae (24, 16.11%), followed by Mycenaceae (10, 6.71%), Agaricaceae (8, 5.37%), Omphalotaceae (8, 5.37%), Marasmiaceae (7, 4.70%), Tricholomataceae (6, 4.03%), Bolbitiaceae (5, 3.36%), Hymenogastraceae (5, 3.36%), Psathyrellaceae (5, 3.36%), and Stereaceae (5, 3.36%). In contrast, families with <5 morphospecies recorded 66 (44.27%) species.

Top genera

The collection of macrofungi in Marinduque Wildlife Sanctuary resulted in 87 genera, of which 16 genera recorded ≥3 morphospecies (Table 4). Meanwhile, *Mycena* had the highest number of morphospecies recorded (9, 6.04%). *Mycena* was primarily found in primary, secondary, and riparian areas, with no records from the agricultural and grassland areas of Marinduque Wildlife Sanctuary. This was followed by *Trametes* (5, 3.36%), *Stereum* (5, 3.36%) and *Auricularia* (4, 2.68%). Moreover, Xylaria, Agaricus, Entoloma, Phellinus, Marasmius, Tetrapygros, Gymnopus, Marasmiellus, Pluteus, Hexagonia, Lentinus, and Polyporus each had three species, with 2.01% each. The top genera, accounting for 39.56%, were commonly found in forested areas.

Table 3: Top families (≥ 5) with the most significant number of morphospecies in the Marinduque Wildlife Sanctuary (n = 149)

Family	No. of species	Percentage (%)
Polyporaceae	24	16.11
Mycenaceae	10	6.71
Agaricaceae	8	5.37
Omphalotaceae	8	5.37
Marasmiaceae	7	4.70
Tricholomataceae	6	4.03
Bolbitiaceae	5	3.36
Hymenogastraceae	5	3.36
Psathyrellaceae	5	3.36
Stereaceae	5	3.36
Other families (< 5 morphospecies)	66	44.27
Total	149	100.00

Table 4: Top genera (≥ 3) with the most significant number of morphospecies in the Marinduque Wildlife Sanctuary (n = 149)

Genus	No. of species	Percentage (%)
Mycena	9	6.04
Trametes	5	3.36
Stereum	5	3.36
Auricularia	4	2.68
Xylaria	3	2.01
Agaricus	3	2.01
Entoloma	3	2.01
Phellinus	3	2.01
Marasmius	3	2.01
Tetrapygros	3	2.01
Gymnopus	3	2.01
Marasmiellus	3	2.01
Pluteus	3	2.01
Hexagonia	3	2.01
Lentinus	3	2.01
Polyporus	3	2.01
Other genus (< 3 morphospecies)	90	60.40
Total	149	100.00

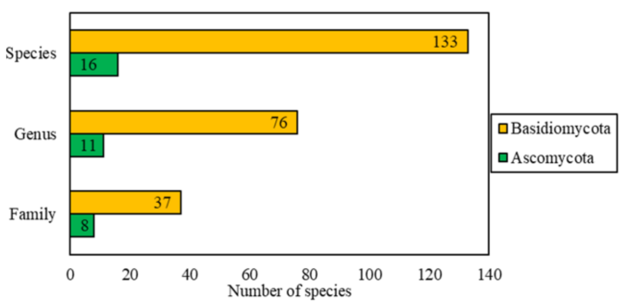

Fig. 3: Overall taxa composition of the collected macrofungal morphospecies at Marinduque Wildlife Sanctuary

Top genera across habitats

In the primary forest, two species from each of the following genera were collected, *i.e.*, *Agaricus*, *Clavaria*, *Hexagonia*, *Lentinus*, *Mycena*, *Polyporus*, *Psilocybe,* and *Xylaria*. This accounted for 40% of the collection. The remaining 60% belonged to other genera, with one collection each. In the secondary forest, *Mycena* (6, 8%) was the dominant genus, followed by Trametes (4, 5%), Auricularia (3, 4%), Phellinus (3, 4%) and Stereum (3, 4%), which collectively comprised 25% of the collection. The remaining 75% belonged to other genera, with fewer than three collections each. Regarding riparian areas, two species were collected from each genus: *Auricularia*, *Crepidotus*, *Earliella*, *Ganoderma*, *Gymnopus*, *Mycena*, *Stereum* and *Trametes.* This constituted 40% of the total collection, while the remaining 60% belonged to other genera with less than three morphospecies. On the other hand, agricultural land recorded only 7 morphospecies, which comprised *Dacryopinax*, *Irpex*, *Lachnum*, *Lentinus*, *Panaeolus*, *Rhodofomes* and *Schizophyllum*. Lastly, grassland harbored 9 morphospecies: *Bovista*, *Earliella*, *Gleophyllum*, *Lichenomphalia*, *Panaeolus*, *Protostropharia*, *Pycnoporus*, *Rhodocollybia* and *Xylaria*. Among all genera, *Mycena* consistently recorded a high number of morphospecies in primary, secondary and riparian areas (Fig. 4).

Shared and unique species across the habitats

Within the Marinduque Wildlife Sanctuary, each habitat type exhibited a greater number of unique macrofungal morphospecies than shared ones (Fig. 5). The secondary forest had the highest count of unique morphospecies (57), followed by the primary forest (33), riparian area (27), grassland (5) and agricultural land (3).

Most reported species across habitats

Nine macrofungi morphospecies were commonly shared across most of the studied habitats in Marinduque Wildlife Sanctuary (Table 5). The most reported macrofungi across habitats were Earliella scabrosa, present in all habitats except agricultural land, while, Schizophyllum commune was recorded at all sites except grassland. It can be noticed that *Octospora humosa*, *Phillipsia domingensis*, *Coprinus comatus*, *Auricularia nigricans*, *Hexagonia tenuis* and *Pycnoporus sanguineus* were commonly found in the forested areas. On the other hand, *Panaeolus antillarum* was found in secondary forest, agricultural land, and grassland, where cow dung substrates were common and favorable for its growth.

Discussion

This study provided valuable insights into the rich macrofungal diversity and the ecological value of macrofungi in the different habitats of Marinduque Wildlife Sanctuary. The presence of macrofungi across different habitats underscored the importance of microclimatic conditions, substrate availability and vegetation structure to these species (Chen *et al.* 2018).

Among the habitats observed, the secondary forest, followed by the primary forest and riparian zones, had the highest recorded macrofungal morphospecies. This suggests that forest areas support higher species richness and that macrofungi thrive in shaded, humid, and decaying organic materials. Forested areas (Arenas *et al.* 2018) and protected

Table 5: Most reported species in the Marinduque Wildlife Sanctuary

Species	PF	SF	RP	AG	GL
Earliella scabrosa	+	+	+		+
Schizophyllum commune	+	+	+	+	
Octospora humosa	+	+	+		
Phillipsia domingensis	+	+	+		
Coprinus comatus	+	+	+		
Auricularia nigricans	+	+	+		
Panaeolus antillarum		+		+	+
Hexagonia tenuis	+	+	+		
Pycnoporus sanguineus		+	+		+

+ = present, blank=absent

PF (Primary forest)- ≥ 2 morphospecies, 43 morphospecies, SF (Secondary forest)- ≥ 3, 79 morphospecies, RP (Riparian area)- ≥ 2, 44 morphospecies, AG (Agricultural area)- =1, 7 morphospecies, GL (Grassland)- 1 = 9 morphospecies

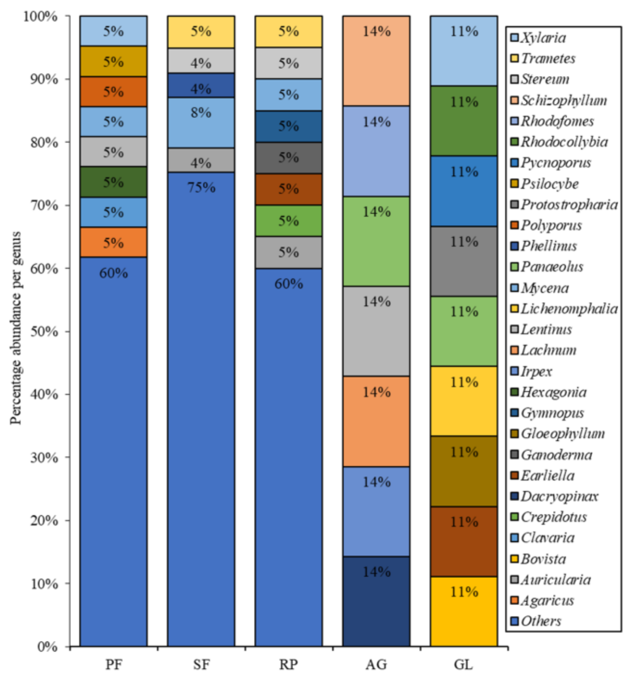

Fig. 4: Top genus across habitats at Marinduque Wildlife Sanctuary: PF (Primary forest)- ≥2 morphospecies, 43 morphospecies, SF (Secondary forest)- ≥ 3, 79 morphospecies, RP (Riparian area)- ≥2, 44 morphospecies, AG (Agricultural area)- =1, 7 morphospecies, GL(Grassland)- 1 = 9 morphospecies

landscapes (Parlucha *et al.* 2021) were ideal habitats for macrofungi due to thick litter depth, dense canopy cover, and abundant substrates. The variety of plants and which include trees, provided an ideal landscape for macrofungi to grow due to the abundance of substrates (Paquit and Pampolina 2017; Arenas *et al*. 2018; Izati *et al*. 2020) and moisture (Tadiosa and Briones 2013). Furthermore, the rainy season increased moisture and humidity in the environment (Tadiosa and Briones 2013), conditions suitable for these macrofungal species.

Intact forests supported high macrofungal diversity (Richard *et al.* 2004; Tuo *et al.* 2022). However, in this study, the primary forest was precipitous, and the 1000 m transect line was laid in the forest ridges, thus leading to less macrofungi found in the primary forest habitat. Moreover, agricultural and grassland areas had fewer recorded species due to their limited cover and substrates. While this study was conducted during the rainy season, sunlight exposure in these areas led to low moisture levels. Therefore, it was not beneficial for macrofungi growth. It is important to note that secondary forests are more accessible than other habitats, which explains the higher species record in these areas. Nevertheless, the study aimed to document the species present in the sanctuary and to obtain preliminary data on macrofungal species in each habitat.

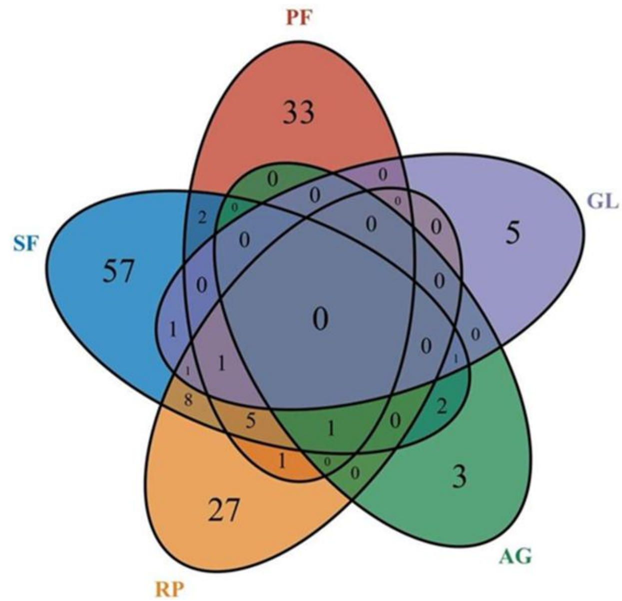

Fig. 5: The shared and unique morphospecies across the habitats

The rich collection of macrofungi in this study was mainly from the Phylum Basidiomycota, rather than Ascomycota (Izati *et al.* 2020). The dominance of basidiomycetes aligns with their ecological roles as wood-saprotrophic fungi (Riley *et al.* 2014) and ectomycorrhizal fungi. These fungi thrive on decaying matter and on host trees (He *et al.* 2022). The abundance of wood debris, fallen logs, and leaf litter at the investigated study sites supported the dominance of this phylum. Basidiomycetes produce specialized enzymes capable of degrading complex polymers such as cellulose, hemicellulose, and lignin in woods (Riley *et al.* 2014). The high reported basidiomycete counts aligned with macrofungal surveys conducted in the Philippines (Jacob *et al.* 2022; Dulay *et al.* 2023).

Among the identified families in the sanctuary, the most represented were Polyporaceae. This also aligned with the Philippines' record of dominant macrofungal families (Dulay *et al.* 2023). Members of these families were wood-saprophytes and were commonly seen growing on dead wood, twigs, bark, and leaf litter. Moreover, Polyporaceae are tough and large, surviving longer, thereby ensuring detection throughout the survey period and contributing to

Fig. 6: Common reported macrofungi across habitats: (**a**) *Earliella scabrosa,* (**b**) *Schizophyllum commune,* (**c**) *Octospora humosa,* (**d**) *Phillipsia domingensis,* (**e**) *Coprinus comatus,* (**f**) *Auricularia nigricans,* (**g**) *Panaeolus antillarum,* (**h**) *Hexagonia tenuis,* (**i**) *Pycnoporus sanguineus*

their persistent high abundance in species listings (Tibuhwa 2011). In terms of genera, *Mycena* was the most represented in primary and secondary forests and riparian areas. The investigation of agaricoid mushrooms in the study by Fungwa *et al.* (2021) yielded the same result that *Mycena* was the dominant genus in primary and secondary forests. *Mycena* species are small, delicate fungi that have a diverse range of substrates, including fallen leaves and twigs, in humid forests (Chang and Ju 2017). This indicates that the shaded, moist environments of primary and secondary forests and riparian areas favored the growth of the *Mycena* species and served as key decomposers in these habitats. Other top genera, such as *Trametes*, *Stereum* and *Auricularia*, were likewise distributed across primary and secondary forests and riparian areas.

Macrofungi in the sanctuary exhibited habitat-specific distributions (Fig. 6), suggesting that macrofungal species were adapted to specific microhabitats and substrates, and that only a few can thrive across a wide range of habitats. Similar findings were reported by Tuo *et al.* (2022) who noted that a small number of shared species were found compared to unique species. This depicts that habitats supported distinct macrofungi fitted to their environmental conditions (Chen *et al.* 2018). This also highlighted the importance of each habitat in supporting distinct macrofungal communities.

The most reported species across habitats were *Earliella scabro*sa and *Schizophyllum commune*. The rich organic nutrients in the substrate, such as decomposing wood, stumps, and twigs, supported the growth of *E. scabrosa* and *S. commune* in the study sites. The abundance of these substrates highlighted the importance of decomposition processes in maintaining biodiversity in these areas. Aside from these, other species such as *Octospora humosa*, *Phillipsia domingensis*, *Coprinus comatus*, *Auricularia nigricans*, *Hexagonia tenuis* and *Pycnoporus sanguineus* were noted in abundance in the habitats observed (Fig. 7).

The presence of macrofungi in the different habitats of Marinduque Wildlife Sanctuary underscored the ecological and conservation importance of these organisms in protected areas. Macrofungi supported the environment (Ye *et al.* 2019) through nutrient cycling (Caiafa *et al.* 2017) and helped with carbon storage and productivity (Koide *et al.* 2011). Since macrofungi are habitat-specific, their presence indicated environmental stability and served as a bioindicator of habitat quality. Moreover, the identified macrofungi and others that are not yet recorded, have potential ecological, medicinal, and economic value. This emphasizes the need for continued monitoring and protection to safeguard the integrity of the macrofungal communities.

Fig. 7: Some uncommon reported macrofungi across habitats: **(a)** *Agaricus crocopeplus,* (**b**) *Cookeina tricholoma,* (**c**) *Clavaria zollingeri,* (**d**) *Agaricus subrufescens,* (**e**) *Plicaturopsis crispa,* (**f**) *Gyrodontium sacchari,* (**g**) *Pluteus cervinus,* (**h**) *Peziza repanda,* (**i**) *Sarcoscypha coccinea,* (**j**) *Russula queletii,* (**k**) *Tricholoma sulphureum,* (**l**) *Coprinus* sp.

Conclusions

This study overall emphasized the critical role of Marinduque Wildlife Sanctuary as a reservoir for macrofungal species. Habitats such as primary and secondary forests and riparian areas had higher macrofungi diversity than agricultural and grassland areas. Overall, Polyporaceae and *Mycena* accounted for the majority of the collected macrofungi in Marinduque Wildlife Sanctuary. Each habitat type proved crucial for macrofungal diversity, since the number of unique morphospecies observed within each habitat surpassed the number of shared species. This study was the first to reveal macrofungi in the Marinduque Wildlife Sanctuary and highlighted the importance of habitat conservation. Further study is recommended to document macrofungi over a longer period and to explore adjacent areas not covered in this study.

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Author Contributions

AGD: Conceptualization, secured permits, field sampling, sample sorting, writing of the initial and final drafts. FMC: Field sampling, sample sorting. MCA: Field sampling, sample sorting, paper editing. LMC: Conceptualization, field sampling, sample sorting, language editing. ERT: Conceptualization, species identification, paper editing, supervision.

Conflict of Interest

All authors declare no conflict of interest.

Data Availability

Data presented in this study will be available on a fair request to the corresponding author.

Ethics Approval

A gratuitous wildlife permit from the Department of Environment and Natural Resources MIMAROPA Region was issued to the authors on August 1, 2022.

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