

PRELIMINARY SURVEY OF THE MACROFUNGI OF MARAI PARAI – GURKHA HUT, KOTA BELUD, SABAH

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ABSTRACT

Macrofungi represent a significant group of mycorrhizal species, many of which possess high nutritional and medicinal value. They are among the most promising mycorrhizal species for development and application. To improve the understanding of the biodiversity of Marai Parai a recent survey conducted by Sabah Parks in Marai Parai, and surrounding regions uncovered 50 fungal specimens. These specimens represent 31 different genera across 24 families, indicating a rich variety of fungal occurrence in the area. The dominant family during this survey was *Ganodermataceae* that contains 6 species and *Amanitaceae*, *Entolomaceae*, *Helotiaceae*, *Helvellaceae*, *Hericiaceae*, *Hydnaceae*, *Hymenochaetaceae*, *Aceraceae*, *Omphalotaceae*, *Thelephoraceae*, *Tricholomaceae*, and *Xylariaceae* was least observed with single species of each family. Macrofungi from this survey was categorized into saprophytic (52%), ectomycorrhizal (44%) and parasitic (4%). The results of this survey suggest that Marai Parai that is located on Mount Kinabalu along with its neighbouring regions on Mount Kinabalu, harbours a rich fungal ecosystem. Similarly, this site has a significant interest for early explorers and naturalists. Past expeditions have primarily focused on flora, leading to several important botanical findings. Despite this, the fungal biodiversity of this region has not been thoroughly examined. Continued and expanded research into the macrofungi of this area is encouraged, as it holds the potential for further significant biological discoveries.

Keywords: *macrofungi, diversity, Borneo, Sabah, Kinabalu*

INTRODUCTION

The diversity of macrofungi is a significant component of biodiversity. Macrofungi are a group of fungi known for their large and noticeable fruiting structures called sporocarps, which are responsible for spore production. These organisms belong to the phylum Basidiomycota and Ascomycota that exhibit various characteristics and uses. Some macrofungi are known because of their edible and healing properties (Dai & Yang, 2008), while others are known for being toxic effects (Corner & Bas, 1962), bioluminescent, or act as insect pathogens. In their natural habitats, fungi serve important functions, whether as decomposers, symbiotic partners, parasites, disease agents, or agents of nutrient distribution. They are key to the carbon cycle in forest ecosystems, supply plants with essential minerals, and help other soil organisms overcome carbon scarcity (Money, 2016). Despite over 14,000 mushroom species being identified worldwide (Borah et al., 2010; Thiribhuvanamala et al., 2011). It is estimated that there are about 1.5 million macrofungal species worldwide, but only approximately 120,000 of these species have been identified to date (Hawksworth & Lücking 2017). A comprehensive survey in Bukit Baka Bukit Raya National Park identified 32 genera spanning 20 families of Basidiomycota macrofungi distributed across various altitudinal gradients. This diversity underscores the significant influence of environmental variables such as elevation and forest composition on macrofungal communities (Harun et al., 2024). Similarly, an extensive inventory conducted in Perlis State Park, Malaysia, which is geographically proximate to Borneo, documented 69 macrofungi species. Of these, 59 species belonged to Basidiomycota, while 10 were from Ascomycota. This research emphasizes the crucial ecological roles played by macrofungi and underscores their potential importance in conservation strategies (Ahmadni et al., 2024)

Borneo, recognized as a biodiversity hotspot, is home to a broad range of macrofungal species that have yet to be discovered. It was believed that only 20% have been catalogued, indicating that Borneo's actual macrofungal variety far surpasses current records (Chang & Lee, 2004; Hyde, 2003). Research on macrofungi in Malaysia, particularly in Sabah, lags behind that of temperate zones of the world. This gap manifests insufficient data on the taxonomy and ecological contributions of these tropical fungi, as well as inadequate record-keeping and database practices. Recent fungal studies in Sabah have focused on the Polyporales order, encompassing families like Polyporaceae, Ganodermataceae, Fomitopsidaceae, Hymenochaetaceae, and Meripilaceae (Seelan et al., 2015; Foo et al., 2018; Paul et al., 2019; Paul et al., 2019c). The fungal diversity of tropical regions is fully unexplored. To explore the diversity of macrofungi in these regions, there is a need of

consistent surveys and fungal monitoring. Venturing into previously unexplored territories in Sabah could significantly enrich our understanding and inventory of the macrofungi in the region.

Previous research on the fungi of Mount Kinabalu lacks verification through local specimen collections. Additionally, the records of fungal presence in Kinabalu Park are outdated and need revision. Since 2019, initial explorations along Kinabalu Park's Summit Trail, Silau-Silau, Pandanus Trail, and the Mamut Copper Mining area have identified potential new fungal species (unpublished data, project is ongoing). These findings have not extended to the Marai Parai region, which might offer fresh insights or significant data regarding the spread of fungi within the park.

Marai Parai, located within Mount Kinabalu, is renowned for its wealth of unique and rare flora, which has been revealed through numerous botanical explorations over time (Van der Ent, 2013; Van der Ent et al., 2014). This site is renowned as the original habitat of the enigmatic *Nepenthes rajah*, a discovery attributed to Hugh Low. Marai Parai name derives from the local Dusun term for *Costularia pilisepala* grass, which is reminiscent of hill rice (Van der Ent, 2013; Van der Ent et al., 2014). The marshy zones are predominated by sedges like *Scirpus subcapitatus*, and the adjacent montane forest, characterized by its dwarfed stature, is primarily composed of species such as *Dacrydium beccarii*, *Syzygium* sp., and *Leptospermum recurvum* (Van der Ent et al., 2014). In this report, we present our findings on the fungal species around Marai Parai-Nunuk camp and its vicinity, following a recent scientific survey of the area.

METHODOLOGY

Field surveys and sporocarps collection

Field surveys were conducted during October 9th to 13th, 2023, in Kampung Kiau Nuluh (6.0430°N, 116.4959°E; 887m), Nunuk camp (6.0674°N, 116.507°E; 1178m), and Marai Parai camps (6.0819°N, 116.5204°E; 1675m). Figure 1 illustrates the specific zones within Mount Kinabalu that were explored during the scientific expedition, highlighting the Marai Parai-Gurkha Hut area and adjacent trails. Visual encounter surveys were conducted by a four-person team during daylight hours, from 8:30 a.m. to 12:00 p.m. Fruiting bodies were sampled opportunistically, with approximately 10-15 specimens per species collected along accessible trails within the Marai Parai forest. Fresh macrofungi were photographed in the field, including their growth substrates, and preliminary morphological identifications were made. Prior to

drying, fresh tissue samples were placed in the ionic detergent cetyltrimethylammonium bromide (CTAB), and tissue from selected mushrooms were taken for culture collections. Habitat variables, such as vegetation type and structure, were recorded. Dried voucher specimens were preserved and deposited at the Institute for Tropical Biology and Conservation Fungi Collection (BORNEENSIS), Universiti Malaysia Sabah, as well as the Sabah Parks (SP) collection for reference and potential future research.

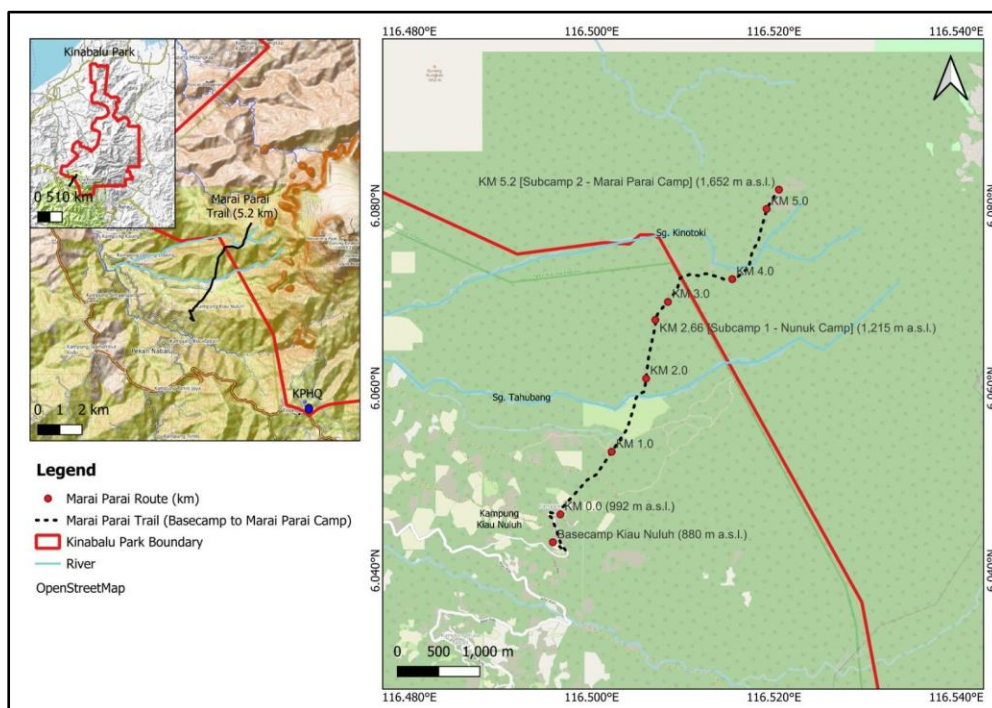


Figure 1. Locality map of Marai Parai trail.

Morphological examination and comparative analysis

Macro-morphological observations were based on fresh specimens according to Largent (1973). Colors were compared with the standard colors presented in the Methuen Handbook of Colour (Kornerup & Wanscher, 1978). Micro-morphological data from dried specimens were obtained using the methods described by Largent, Johnson, and Watling (1977) and were observed with an optical light microscope (LEICA DM2500 LED). The preparation of specimens for microscopic examination and the description of hyphal structures also adhered to the procedures outlined by Largent, Johnson, and Watling (1977). Measurements of the microscopic structures were taken using the MShot Image Analysis System 1.1.6 software. Scanning electron microscopy (SEM) analyses were conducted with a JEOL JSM-5610LV to

detail the hymenium surface topography and roughness, as documented by Choudhary & Ka (2017).

Species identification

Species identification was conducted using molecular techniques, selectively performed on specimens with cryptic morphology and to corroborate the morphological identification of highlighted species. The genomic DNA was isolated by using E.Z.N.A Fungal DNA Mini Kit (Omega Bio-Tek, USA). Primer pairs LROR/LR7 were used to amplify the LSU region. PCR reactions were performed in a total volume of 25 uL following Moncalvo et al., (2002). Sequences generated in this study and those downloaded from GenBank were combined and used for phylogenetic reconstruction. Sequences were aligned separately with software MAFFT v6.853. Maximum Likelihood (ML) analyses were inferred using RAxMLv7.2.6. Statistical support was obtained using rapid non-parametric bootstrapping with 1,000 replicates. Bayesian Inference (BI) phylogenies were inferred using MrBayes3.2.6. The phylogenetic trees were visualized using FigTree v1.4.23.

RESULTS

The recent expedition by Sabah Parks yielded a diverse collection of 50 fungal specimens, spanning 31 genera across 24 families, as detailed in Table 1. The taxonomic survey, illustrated in Figure 2, identified the family Ganodermataceae as the most prevalent (six specimens), followed by the families Corticiaceae and Russulaceae (four specimens each). Other families represented include Boletaceae, Cortinariaceae, Hygrophoraceae, Marasmiaceae, Mycenaceae, and Physalacriaceae (three specimens each), and Bondarzewiaceae, Polyporaceae, and Sclerodermataceae (two specimens each). The remaining families—Amanitaceae, Entolomataceae, Helotiaceae, Helvellaceae, Hericiaceae, Hydnaceae, Hymenochaetaceae, Laccariaceae, Omphalotaceae, Thelephoraceae, Tricholomataceae, and Xylariaceae—were represented by one specimen each. Ecologically, saprophytic fungi accounted for 64% of the findings, dominating ectomycorrhizal fungi, which constituted only 36%, as depicted in Figure 3. This distribution underscores the predominant ecological roles these fungi play within the ecosystem.

Table 1. Checklist of the macrofungi of Marai Parai and associated areas in Kota Belud, Sabah.

Family	Genus	No. of Individuals	Ecology
Amanitaceae	<i>Amanita</i> sp.	1	Ectomycorrhizal
Boletaceae	<i>Austroboletus</i> sp.	1	Ectomycorrhizal
	<i>Pulveroboletus</i> sp.	2	Ectomycorrhizal
Bondarzewiaceae	<i>Wrightoporia</i> sp.	2	Saprophytic
Corticaceae	<i>Corticoid</i> sp.	3	Saprophytic
	<i>Phlebia</i> sp.	1	Saprophytic
Cortinariaceae	<i>Cortinarius</i> cf. <i>iodes</i>	1	Ectomycorrhizal
	<i>Cortinarius</i> sp.	2	Ectomycorrhizal
Entolomataceae	<i>Entoloma</i> cf. <i>hochstetteri</i>	1	Ectomycorrhizal
Ganodermataceae	<i>Ganoderma</i> sp.	2	Parasitic
	<i>Sanguinoderma</i> sp.	4	Ectomycorrhizal
Helotiaceae	<i>Bisporella</i> cf. <i>citrina</i>	1	Saprophytic
Helvellaceae	<i>Helvella</i> sp.	1	Ectomycorrhizal
Hericiaceae	<i>Hericum coralloides</i>	1	Saprophytic
Hydnaceae	<i>Sarcodon</i> sp.	1	Ectomycorrhizal
Hygrophoraceae	<i>Hygrocybe</i> sp.	3	Ectomycorrhizal
Hymenochaetaceae	<i>Coltricia</i> sp.	1	Saprophytic
Laccariaceae	<i>Laccaria</i> sp.	1	Ectomycorrhizal
Marasmiaceae	<i>Marasmius</i> sp.	2	Saprophytic
	<i>Marasmiellus</i> sp.	1	Saprophytic
Mycenaceae	<i>Poromycena</i> sp.	1	Saprophytic
	<i>Mycena</i> sp.	2	Saprophytic
Omphalotaceae	<i>Lentinula</i> cf. <i>lateritia</i>	1	Saprophytic
Physalacriaceae	<i>Armilarria</i> sp.	3	Saprophytic
Polyporaceae	<i>Tyromyces</i> sp.	1	Saprophytic
	<i>Favolus</i> sp.	1	Saprophytic
Russulaceae	<i>Russula</i> sp.	3	Ectomycorrhizal
	<i>Lactarius</i> sp.	1	Ectomycorrhizal
Sclerodermataceae	<i>Calostoma retisporum</i>	2	Saprophytic
Thelephoraceae	<i>Thelephora</i> sp.	1	Ectomycorrhizal

Tricholomataceae	<i>Gymnopilus</i> sp.	1	Saprophytic
Xylariaceae	<i>Xylaria</i> sp.	1	Saprophytic

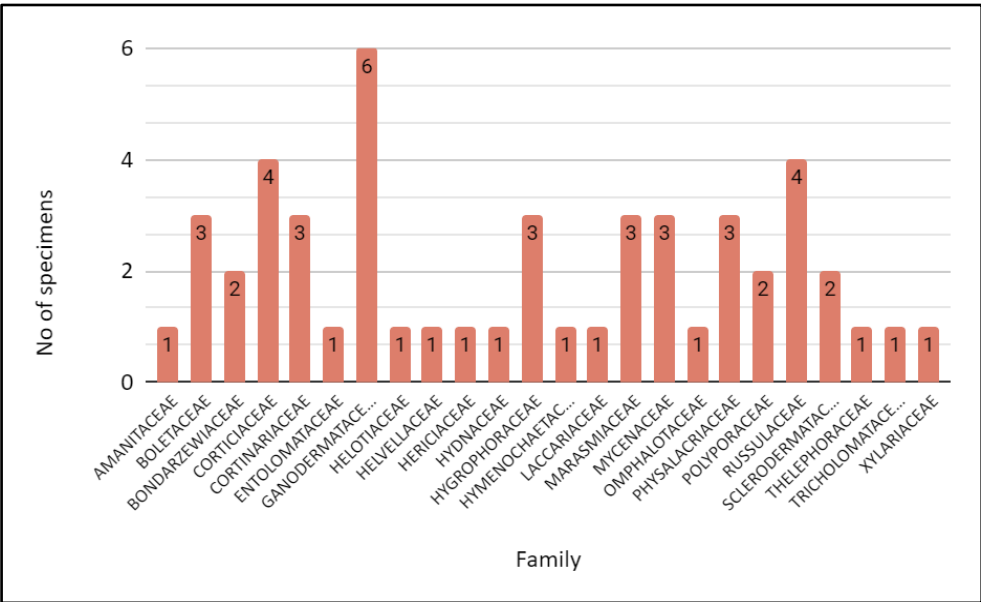


Figure 2. Number of specimens collected from each family.

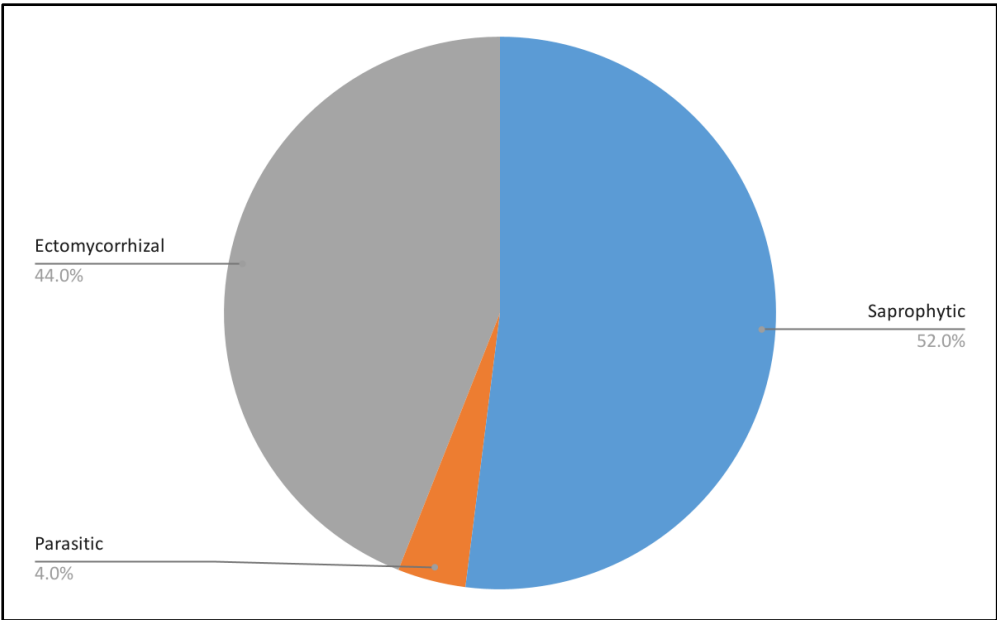


Figure 3. Ecological role of fungi in Marai Parai



Figure 4. Some fungi found at Marai Parai and adjacent areas: a. *Lentinula* cf. *lateritia*. b. *Hericium* *coralloides* c. *Boreostereum* sp. d. *Calostoma* sp. e. *Gymnopilus* sp. f. *Hygrocybe* cf. *firma*. g. *Russula* sp. h. *Marasmius* cf. *pelucidus*. i. *Amanita* cf. *pyramidifera*. Scale bars: 1 cm.
All photographs by Lim Jing Yi.



Figure 5. Some fungi found at Marai Parai and adjacent areas: j. *Heimioporus* sp. k. *Entoloma* cf. *hochstetteri* l. *Cortinarius* sp. m. *Tyromyces* sp. n. *Cortinarius* cf. *iodes*. o. *Ganoderma* sp. p. *Poromyceia* sp. q. *Favolus* sp. r. *Wrigthoporia* sp. Scale bars: 1 cm. All photographs by Lim Jing Yi.



Figure 6. Some fungi found at Marai Parai and adjacent areas: s. *Sanguinoderma* sp. t. *Amouroderma rugosum*. u. *Thelephora* sp. v. *Helvella* sp. w. *Laccaria* sp. x. *Lactarius* sp. y. *Mycena* sp. z. *Pulveroboletus* sp. z1. *Sarcodon* sp. Scale bars: 1 cm. All photographs by Lim Jing Yi.

DISCUSSION

The comprehensive preliminary survey in the Marai Parai - Gurkha Hut area, Kota Belud, Sabah, represents a significant advancement in our understanding of macrofungi diversity within the Mount Kinabalu region, highlighting the ecological complexity and biodiversity richness of this montane forest ecosystem. By documenting 50 fungal specimens across 31 genera and 24 families, this research reveals the previously underexplored fungal components of the ecosystem, with a notable emphasis on the families Ganodermataceae, Corticiaceae, and Russulaceae. Particularly, the identification of *Ganoderma* and *Sanguinoderma* species, known for their medicinal properties, not only enriches the biological database but also hints at potential pharmacological applications.

The ecological roles identified predominantly saprophytic (52%) and ectomycorrhizal (44%) over parasitic fungi (4%) highlight the critical functions these organisms play in nutrient cycling and plant symbiosis, respectively, thereby emphasizing their importance in ecosystem processes and functions. The unexpected dominance of saprophytic fungi over ectomycorrhizal fungi in a pristine forest can be attributed to the large amounts of dead organic matter available as a result of tree deaths caused by parasitic fungi (genus *Ganoderma*). This creates a cycle where saprophytic fungi decompose the dead trees, releasing nutrients that support forest growth, while ectomycorrhizal fungi aid the living trees in nutrient uptake (Buckling et al., 2012), and parasitic fungi contribute to the cycle by causing tree mortality. Each group plays a distinct role that, together, contributes to the overall health and sustainability of forest ecosystems. The findings promote the conservation of these habitats, recognized as UNESCO World Heritage Sites, as they harbour crucial biodiversity components, including diverse fungal communities that are important for ecosystem stability and resilience.

This study underscores the critical need for further taxonomic, phylogenetic, and ecological research. Continued investigations are essential to uncover the complex evolutionary relationships, biogeographical patterns, and ecological interactions of macrofungi in the region. This deeper understanding will contribute to the development of more effective conservation strategies and management practices aimed at preserving the unique montane forest ecosystems of Sabah, which are of global ecological and conservation significance.

CONCLUSION

In total we explored 50 fungal specimens. These specimens represent 31 different genera across 24 families from Marai Parai survey. The presence of a diversity of macrofungi in Marai Parai is comparable with the biodiversity found in other Kinabalu regions at similar altitudes. This study highlights the continuous necessity for thorough investigations in even the most well-documented or frequently explored areas, as additional species are likely to be identified through ongoing research efforts.

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