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Macroscopic Fungi at Southern Tagalog Region Protected Landscape: A Hidden Diversity

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ABSTRACT

Macroscopic fungi are found everywhere, mainly thriving in all kinds of ecosystems. A study was conducted at Southern Tagalog Region Protected Landscape, particularly in Quezon National Park found at Pagbilao and Atimonan, Quezon, one of the protected areas in Southern Luzon, to determine what kind of fungi thrive and grow in Karst and Lowland dipterocarp forests. The sampling used a transect line with quadrat and opportunistic sampling methods. One hundred forty-one morpho-species of macroscopic fungi belonging to 44 families in the

Quezon Protected Area were documented and collected. The most species-rich are the Family Polyporaceae (28 species), followed by the Family Agaricaceae (10 species) and Mycenaceae (6 species). The families Xylariaceae, Auriculariaceae, Hymenochaetaceae, Marasmiaceae, and Psathyrellaceae are represented by five species each, and four species represent the families Cantharellaceae, Fomitopsidaceae, Ganodermataceae, Stereaceae, and Tricholomataceae. The families Sarcoscyphaceae and Bolbitiaceae are represented by three species and families Pezizaceae, Auriscalpiaceae, Boletaceae, Clavariaceae, Corticiaceae, Crepidotaceae, Dacryomycetaceae, Geastraceae, Lyophyllaceae, Meruliaceae, Nidulariaceae, Physalacriaceae, Ramariaceae, Russulaceae, and Strophariaceae represented by two species. Only one species represents the rest of the families. Fungal research must be encouraged to evaluate the effects of anthropogenic activities in the area and use the data for forest management.

Keywords: Ecosystem, karst forest, macrofungi, morpho-species, protected landscape

INTRODUCTION

Macroscopic fungi are ubiquitous organisms thriving mainly in forest ecosystems. Like other organisms, fungi are heterotrophic and must consume preformed organic matter. They may live as saprophytes, which digest and consume dead plants. Alternatively, fungi may live as parasites and assimilate tissues of living plants. In all cases, digestive enzymes are liberated from the fungal cell and put into the immediate environment, where food molecules are simplified, and the nutrients pass into the fungal cell as a watery solution (Moore-Landecker, 1990).

The fungi are organisms that are grouped since they possess chitin in their cell walls, and they nourish themselves by digesting organic matter first and then ingesting it. Even though most fungi resemble plants, a distinct difference between the two groups is that the former nourish themselves by absorbing nutrients from dead or living organic matter, which are by-products of the enzymatic degradation process they initiate utilizing secreted exoenzymes. The following heterotrophy by absorption: fungal species cater to one of the most important ecological processes, nutrient recycling of organic matter (Taylor et al., 2006).

Macroscopic fungi such as basidiomycetes and ascomycetes can be easily recognized because these are visible to the naked eye and form above the ground.

Basidiomycota is a sister phylum to the monophyletic Ascomycota and is morphologically observed as filamentous fungi that can reproduce asexually via the production of specialized club-shaped basidia cells. These basidia typically contain four spores. Basidiomycota includes mushrooms, puffballs, earthstars, smuts, rusts, jelly fungi, and bracket fungi, among others (Swann & Hibbett, 2007). These fungi have gill-like, pore-like, and teeth-like structures under the cap where the spores are liberated. These spores develop into hyphae, threadlike cells. The hyphae usually contain chitin, a very resistant nitrogenous substance. These form tiny branching cells forming a tangled mass or a mycelium. This mycelium grows and becomes the fruiting body.

In the study of Sridhar and Desmukh, 2019, there were an estimated 53,000 to 110,000 species of macrofungi all over the world belonging to Basidiomycota and Ascomycota. According to de Leon et al., 2013, the number of macrofungi in our country is relatively high, though many species of macrofungi are still undiscovered. Many taxonomic studies have already been conducted in different parts of the country, particularly in Luzon, including Nueva Ecija (Sibounnavong et al., 2008; Lopez et al., 2016; Undan et al., 2016), Bulacan (Liwanag et al., 2017), Isabela (Jacob et al., 2017), Aurora (Tadiosa et al., 2011), Tarlac, Pampanga, Zambales (De Leon et al., 2013), Cavite (Arenas et al., 2015), Laguna (De Castro & Dulay, 2015; Tadiosa & Militante, 2006), La Union (Tadiosa & Arsenio, 2014; Tadiosa, 1998), Nueva Vizcaya (Torres et al., 2020) and Batangas (Tadiosa & Briones, 2013). These studies only indicate the richness of macrofungi species in the Philippines. However, many provinces remain unexplored, which further necessitates more taxonomic studies. Hence, the effort to consider this field of study demands the researchers as it can contribute to establishing a database of macrofungi throughout the country.

Currently, this group of organisms whose diversity in Southern Tagalog Region Protected Landscape (STRPL), particularly Quezon Protected Landscape, has not been thoroughly studied. In this study, fungal species belonging to Ascomycota and Basidiomycota were identified and characterized to provide baseline preliminary information regarding the diversity of this fungal group in STRPL. They are known to have a significant role in the nutrient cycling of the forest ecosystem (Klemm, 2005). Typically, they grow decaying plants, soil, leaf litter, rotting logs, or compost heaps or manure (Reyes et al., 2009).

The Quezon Protected Landscape is a lowland rainforest with karst landscape and vegetation in the southern Sierra Madre Mountain range (Paclibar & Tadiosa, 2019). The park is situated north of the narrowest section of Luzon in Quezon province, located about 164 km southeast of Metro Manila, and

spans the municipalities of Pagbilao, Padre Burgos, and Atimonan in Quezon province—the highest point Mount Mirador (Mount Pinagbanderahan) of 366 meters (1,202 ft) elevation. The park was first established as a national park on October 25, 1934, with Proclamation No. 740. The park has 535.08 hectares (1,322.2 acres) and was named Quezon National Park. The park was enlarged to 983 hectares (2,430 acres) with Proclamation No. 594 on August 5, 1940. After implementing the National Integrated Protected Areas System (NIPAS) in 1992, the park was reclassified as a protected landscape. It was re-established as Quezon Protected Landscape on June 2, 2003, by Proclamation No. 394, with a smaller area of 938 hectares (2,320 acres).

Further field surveys of the Landscape are anticipated to uncover a rich and diverse fungal flora. The Landscape is experiencing anthropogenic disturbances, such as minor forest product gathering and kaingin making. Fungal diversity research efforts must be encouraged to evaluate these human disruptions' effects on the Landscape's ecology.

Figure 1

The views of Quezon Protected Landscape from the Pinagbanderahan and the dipterocarp forest

OBJECTIVES OF THE STUDY

This research study was done to account for the macroscopic fungi present in Southern Tagalog Protected Landscape, particularly in Quezon Protected Landscape (QPL). Specifically, this research aimed to (1) identify ascomycetes and basidiomycetes fungi based on external features, (2) provide a listing of this group of fungi present at QPL, and (3) determine the substrate, elevation, and growth habit of this group of organisms in QPL ecosystem.

Hypothesis

(a) Do protected areas have more macroscopic fungi to collect and document?

(b) Protecting the areas leads to better fungal collection and documentation.

H0: The areas the government protects do not affect the number of fungal species found in the landscape.

H1: The areas the government protects positively affect the number of fungal species found in the landscape.

MATERIALS AND METHODS

Description of Study Areas

The research study was carried out in Quezon Protected Landscape (QPL). The QPL is a 983.0765-hectare tropical rainforest (DENR CALABARZON, 2008) situated at 121046'30" and 1210 50'00" East longitude and 13058'30" and 14001'00" North latitude (Proclamation No. 394) within the southern Sierra Madre Mountain Range (Dagamac et al., 2014). It is classified as a protected landscape under the virtue of Proclamation No. 394 and considered a 'very high ' priority in biodiversity conservation based on the Department of Environment and Natural Resources – Protected Areas and Wildlife Bureau (DENR-PAWB), UP Center for Integrative and Development Studies, and Conservation International-Philippines (DENR CALABARZON, 2008). Few accounts are available about the studies conducted at QPL, which include plasmodial slime molds (Dagamac et al., 2014), vertebrate mega diversity and endemism (Brown et al., 2014), analysis in forest and grassland vegetation at the southwestern side (Tadiosa et al., 2016).

The mountain's forested areas boast many vegetation types ranging from sub-tropical to tropical. The study site is highly diverse because of its topography and climatic factors.

A sampling of Macroscopic Ascomycetes and Basidiomycetes

Field sampling was completed using four transect lines (TL) with ten quadrats each, 15m x 15m, with an interval of 250m on each quadrat. It is an essential method by which fungal organisms are counted directly in a particular habitat. It estimates population abundance (number), density, frequency, and distributions. The quadrat method has been widely used in fungal studies. A Transect line was laid starting at 100m above sea level and upward to the peak of 500 masl. A total of 40 quadrats were laid out in the study areas. The combination of the

quadrat and opportunistic or purposive sampling methods was employed in the study areas, and these biases were avoided. All macroscopic ascomycetous and basidiomycetous fungi inside and outside the quadrat were photographed in their natural habitat, collected, identified, and classified.

Fungal host, color, shape, the size of the fruiting bodies, prevailing temperature and humidity in the area at the time of collection, and Global Positioning System (GPS) coordinates were recorded during collection and documentation. Macroscopic fungi inhabiting the soil and ground litter were dug using a trowel, and those attached to tree branches or barks were gathered using a bolo and knife.

Macrofungal Species Collection

Specimens and data were collected during the rainy and summer seasons. Specimens were photographed in the field (as they occur in their natural habitats), and all essential morphological characters, including the substrata, were noted.

During collection, fragile and fleshy specimens were not mixed with woody ones. The woody specimens were removed using bolo and the wood tissues, while a shovel was used to collect the fleshy ones.

Determining Fungal Diversity of the Study Area

Fungal diversity was measured by documenting species richness or the number of species in an area, the specific number of individuals or biomass, and the relative abundance of the species. One pronounced diversity index that includes the previous premise is Simpson's Index. This gives the probability of any individual drawn randomly from a community comprising different species.

$$D = 1 - \left(\frac{\Sigma\, n(n-1)}{N(N-1)} \right)$$

n = the total number of organisms of a particular species
N = the total number of organisms of all species

Macrofungal Species Preservation

Collected specimens were preserved by mechanical oven drying and alcohol. Field collection numbers were given to every specimen and stored in the Natural History Collections of the Biological Sciences Department of De La Salle University-Dasmariñas for future reference.

The woody and bracket specimens were wrapped in newspaper. In contrast, fragile and fleshy specimens were placed in wide-mouthed jars, with pertinent data and all other notes useful for taxonomic identification. They were dried and fumigated to kill insects, particularly the destructive larvae.

Upon reaching the laboratory, woody and fleshy specimens were segregated. After additional notes had been taken, the woody specimens underwent drying as preservation and fleshy ones were immersed in 70% denatured alcohol as a preservative. The length of the drying period of all specimens collected varied depending upon the nature of the specimens and the prevailing temperature and the relative humidity of the air during collection (Karun and Sridhar, 2013; Tadiosa et al., 2011).

Fungal Taxonomic Identification and Classification

The identification was facilitated using standard dichotomous keys such as those prepared by Arora (1986), and Hood (1992), together with colored and representative photographs from the books of Koon (1990), McKnight (1999), Quimio (1988 and 2001), and Læssøe (1998). After identification, collected specimens were listed according to their respective families.

RESULTS AND DISCUSSIONS

Taxonomy of Collected Basidiomycetous Fungi

Field sampling of Ascomycetous and Basidiomycetous fungi identified 44 families (Table 1) and 141 morpho-species with a total of 534 individuals. The dominant group is the Polyporaceae, with 28 out of 141 species identified, or 19% of the species collected. Agaricaceae, with ten species, is following in abundance, with roughly 7% of the species collected, and the third is Mycenaceae, having six species or 4% of the species collected. The rest of the families have less than six species each. Ascomycetous and Basidiomycetous fungi grew mostly on rotten trunks, branches, and stumps of dying and rotten trees.

Table 1

The taxa and its substrates where these fungi grow, including the elevation where these are found and growth habits.

TAXA	HOST/ SUBSTRATE	ELEVATION (masl)	GROWTH HABIT
ASCOMYCETES			
PEZIZACEAE			
Peziza repanda Pers.	rotten roots, along the trail	242	solitary
Sarcosphaera coronaria (Jacq.) J. Schrot.	forest litter, along the trail	246	solitary
PYRONEMATACEAE			
Octosphora humosa (Fr.) Dennis	soil, along the trail	272	solitary
SARCOSCYPHACEAE			
Cookeina sulcipes (Berk.) Kuntze	soil, along the trail	284	solitary

Table 1 continued

TAXA	HOST/ SUBSTRATE	ELEVATION (masl)	GROWTH HABIT
Cookeina tricholoma (Mont.) Kuntze	soil, along the trail	288	solitary
Phillipsia domengensis Berk.	soil, along the trail	302	solitary
SARCOSOMATACEAE			
Galiela rufa (Schwein.) Nannf. & Korf.	rotten roots, along the trail	262	solitary to gregarious (3-5 in a group)
XYLARIACEAE			
Daldinia concentrica (Bolt.) Ces. & de Not.	rotten branches, along the trail	284	solitary to gregarious (3-5 in a group)
Xylaria allantodea (Berk.) Fr.	rotten roots, along the trail	268	gregarious
Xylaria longipes Nitschke	rotten roots, along the trail	284	gregarious
Xylaria ridleyi Mass.	rotten roots, along the trail	266	gregarious
Xylaria polymorpha (Pers.) Grev.	rotten roots, along the trail	289	gregarious
BASIDIOMYCETES			
AGARICACEAE			
*Agaricus m*oelleri Wasser	soil, along the trail	263	gregarious
Agaricus campestris L.	soil, along the trail	274	gregarious
Agaricus perfuscus Copel.	soil, along the trail	282	gregarious
Agaricus arvensis Schaeff.	soil, along the trail	242	gregarious
Leucocoprinus luteus (Bolt.) Locq.	rotten branches, along the trail	268	gregarious
Lycoperdon echinatum Pers.	soil, along the trail	289	solitary
Lycoperdon pyriforme Schmach	soil, along the trail	272	solitary
Macrolepiota rhacodes (Vittadini) Singer	soil, along the trail	284	gregarious
Macrolepiota procera	soil, along the trail	296	gregarious
Omphalina sp.	soil, along the trail	270	gregarious
AURICULARIACEAE			
Auricularia auricula-judae (Hook.) Underw.	rotten branch, along the trail	262	gregarious
Auricularia delicata (Fr.) Henn.	rotten stump, along the trail	282	gregarious
Auricularia mesenterica (Dicks.) Pers.	rotten branch, along the trail	292	gregarious
Auricularia polytricha (Mont.) Sacc.	rotten branch, along the trail	266	gregarious
Exidia recisa (Ditman) Fr.	rotten stump, along the trail	274	gregarious

Table 1 continued

TAXA	HOST/ SUBSTRATE	ELEVATION (masl)	GROWTH HABIT
AURISCALPIACEAE			
Artomyces sp.	soil, along the trail	266	solitary
Clavicorona javanica (Blume) DC.	soil, along the trail	270	gregarious
BOLBITIACEAE			
Conocyba tenera (Schaeff.) Fayod	soil, along the trail	267	gregarious
Panaeolus campanulatus (Bull.) Quel.	soil, along the trail	280	gregarious
Panaeolus papilionaceus (Bull. ex Fr.) Quel.	soil, along the trail	242	gregarious
BOLETACEAE			
Phylloporus bellus (Massee) Corner	soil, along the trail	268	gregarious
Strobilomyces strobilaceus (Step.) Berk.	soil, along the trail	270	gregarious
CANTHARELLACEAE			
Cantharellus aureus Berk.	rotten branch, along the trail	264	solitary
Cantharellus cibarius Fr.	rotten stump, along the trail	270	solitary
Cantharellus infundibuliformis (Scop.) Fr.	rotten branch, along the trail	282	solitary
CLAVARIACEAE			
Clavulinopsis miniata (Berk.) Corner	soil, along the trail	264	gregarious
Clavulinopsis vemicularis Fr.	soil, along the trail	284	gregarious
CONIOPHORACEAE			
Coniophora puteana (Schum.) Karst.	soil, along the trail	262	gregarious
CORTICIACEAE			
Corticium evolvens Fr.	rotten branch, along the trail	268	solitary
Corticium salmonicolor Berk. & Br.	rotten branch, along the trail	284	solitary
CREPIDOTACEAE			
Crepidotus herbarum (Peck.) Sacc.	rotten branch, along the trail	288	gregarious
Crepidotus mollis (Schaeff.) Quel.	rotten branch, along the trail	272	gregarious
DACRYOMYCETACEAE			
Dacrymyces palmatus (Schwein.) Bres.	rotten branch, along the trail	276	gregarious
Dacryopinax spathularia (Schw.) Mart.	rotten branch, along the trail	278	gregarious

Table 1 continued

TAXA	HOST/ SUBSTRATE	ELEVATION (masl)	GROWTH HABIT
DIPLOCYSTACEAE			
Astraeus hygrometricus (Pers.) Morgan	rotten roots, along the trail	264	solitary to gregarious (3-5 in a group)
ENTOLOMATACEAE			
Entoloma lividum (Bull.) Quelet	soil, along the trail	264	gregarious
FOMITOPSIDACEAE			
Daedalea ambigua Berk.	rotten branch, along the trail	266	solitary
Daedalea amanitoides Beauv.	rotten branch, along the trail	278	solitary
Daedalea quercina (L.) Pers.	rotten branch, along the trail	290	solitary
Daedaleopsis confragosa (Bolt.) J. Schrot.	rotten stump, along the trail	306	solitary
GANODERMATACEAE			
Amauroderma rude (Berk.) Torrend	rotten roots, along the trail	284	solitary to gregarious (3-5 in a group)
Amauroderma rugosum (Blume & T. Nees.) Torrenb.	rotten stump, along the trail	278	solitary to gregarious (3-5 in a group)
Ganoderma applanatum (Pers.) Pat.	rotten trunk, along the trail	304	solitary to gregarious (3-5 in a group)
Ganoderma lucidum (Leys.) Karst.	rotten roots, along the trail	274	solitary to gregarious (3-5 in a group)
GEASTRACEAE			
Geastrum saccatum Fr.	rotten roots, along the trail	264	gregarious
Geastrum triplex Jungh.	rotten roots, along the trail	274	gregarious
HYDNACEAE			
Hydnum sp.	rotten branch, along the trail	278	solitary
HYGROPHORACEAE			
Hygrocybe miniata (Fr.) P. Kumm.	soil, along the trail	270	gregarious
HYMENOCHAETACEAE			
Hymenochaete rubiginosa (Dicks)Lev.	rotten branch, along the trail	264	solitary
Phellinus caryophylli (Racib.) G. Cunn.	rotten branch, along the trail	266	solitary

Table 1 continued

TAXA	HOST/ SUBSTRATE	ELEVATION (masl)	GROWTH HABIT
Phellinus gilvus (Schw.) Fr.	rotten stump, along the trail	278	solitary
Phellinus rimosus (Berk.) Pilat	rotten roots, along the trail	274	solitary
INOCYBACEAE			
Inocybe peckii Atk.	soil, along the trail	264	gregarious
LYOPHYLLACEAE			
Termitomyces albuminosus (Berk. And Broome) Heim	soil, along the trail	266	gregarious
Termitomyces eurhizus (Berk.) Heinn.	soil, along the trail	274	gregarious
MARASMIACEAE			
Marasmius haematocephalus (Mont.) Fr.	rotten branch, along the trail	268	gregarious
Marasmius oreades (Bolt.) Fr.	soil, along the trail	278	gregarious
Marasmius pulcherripes Peck.	rotten branch, along the trail	268	gregarious
Marasmius rameales (Bolt.) Fr.	rotten branch, along the trail	288	gregarious
Marasmius rotula (Scop.) Fr.	rotten twigs, along the trail	284	gregarious
MERULIACEAE			
Cymatoderma elegans Jungh.	rotten stalk, along the trail	284	solitary to gregarious (3-5 in a group)
Podoscypha bolleana (Mont.) Boidin	rotten branch, along the trail	266	solitary
MYCENACEAE			
Mycena alcalina (Pers.) Gillet	soil, along the trail	260	gregarious
Mycena epipterygia (Scop.) Gray	soil, along the trail	274	gregarious
Mycena flavoalba (Fr.) Quel.	soil, along the trail	246	gregarious
Mycena galopus (Pers. ex Fr.) Kummer	soil, along the trail	242	gregarious
Mycena pura (Pers.) Kummer	soil, along the trail	266	gregarious
Mycena vulgaris (Pers.) Kumm.	soil, along the trail	270	gregarious
NIDULARIACEAE			
Cyathus rudis Pat.	rotten roots, along the trail	256	gregarious

Table 1 continued

TAXA	HOST/ SUBSTRATE	ELEVATION (masl)	GROWTH HABIT
Cyathus striatus Willd.	rotten roots, along the trail	260	gregarious
PHANEROCHAETACEAE			
Byssomerulius corium (Pers.) Parmasto	soil, along the trail	268	gregarious
PHYSALACRIACEAE			
Armillaria sp.	soil, along the trail	242	gregarious
Oudemansiella canarii (Jungh.) Hohm.	rotten branch, along the trail	264	gregarious
PLEUROTACEAE			
Pleurotus ostreatus (Jacq. ex Fr.) Kummer	rotten stump, along the trail	268	gregarious
PLUTEACEAE			
Volvariella volvacea (Bull.) Sing.	rotten banana stalk, along the trail	256	gregarious
POLYPORACEAE			
Coriolopsis polyzona (Pers.) Ryvarden	rotten trunk, along the trail	254	solitary
Daedalea flavida Lev.	rotten branch, along the trail	242	solitary
Daedalea quercina (L.) Pers.	rotten stump, along the trail	266	solitary
Earliella scabrosa (Pers.) Gilb. & Ryvarden	rotten branch, along the trail	274	solitary to gregarious (3-5 in a group)
Favolus sp.	rotten stalk, along the trail	278	solitary
Fomes cinereus (Berk.) Sacc.	rotten trunk, along the trail	280	solitary
Hexagonia apiaria (Pers.) Fr.	rotten branch, along the trail	290	solitary to gregarious (3-5 in a group)
Hexagonia tenuis (Hook.) Fr.	rotten branch, along the trail	288	solitary to gregarious (3-5 in a group)
Lentinus velutinus Fr.	rotten branch, along the trail	286	solitary to gregarious (3-5 in a group)
Lentinus elegans (Spreng.) Pat.	rotten branch, along the trail	256	solitary to gregarious (3-5 in a group)
Lenzites elegans (Spreng.) Pat.	rotten stump, along the trail	242	solitary to gregarious (3-5 in a group)

Table 1 continued

TAXA	HOST/ SUBSTRATE	ELEVATION (masl)	GROWTH HABIT
Lenzites reparda (Pers.) Fr.	rotten twigs, along the trail	268	solitary to gregarious (3-5 in a group)
Microprus affinis (Blume & T. Nees.) Kuntze	rotten branch, along the trail	270	solitary to gregarious (3-5 in a group)
Microporus vermicipes (Berk.) Kuntze	rotten branch, along the trail	288	solitary to gregarious (3-5 in a group)
Microporus xanthopus (Fr.) Kuntze	rotten stump, along the trail	256	solitary to gregarious (3-5 in a group)
Microporus sp.	rotten twigs, along the trail	278	solitary to gregarious (3-5 in a group)
Polyporus arcularius (Batsch.) Fr.	rotten branch, along the trail	268	solitary to gregarious (3-5 in a group)
Polyporus grammocephalus Berk.	rotten stump, along the trail	276	solitary to gregarious (3-5 in a group)
Polyporus alveolaris (DC.) Bondartserv & Singer	rotten trunk, along the trail	306	solitary to gregarious (3-5 in a group)
Polyporus squamosus (Huds.) Fr.	rotten stump, along the trail	210	solitary to gregarious (3-5 in a group)
Polyporus adustus (Willd.) Fr.	rotten branch, along the trail	288	solitary to gregarious (3-5 in a group)
Polyporus cuticularis (Bull.) Fr.	rotten stump, along the trail	286	solitary to gregarious (3-5 in a group)
Polyporus durus Jungh.	rotten trunk, along the trail	280	solitary to gregarious (3-5 in a group)
Polyporus gilvus (Schw.) Fr.	rotten stump, along the trail	272	solitary to gregarious (3-5 in a group)
Polyporus hirsutus (Wulf.) Fr.	rotten branch, along the trail	258	solitary to gregarious (3-5 in a group)
Polyporus picipes Fr.	rotten branch, along the trail	266	solitary to gregarious (3-

Table 1 continued

TAXA	HOST/ SUBSTRATE	ELEVATION (masl)	GROWTH HABIT
Poria sp.	rotten stump, along the trail	258	solitary to gregarious (3-5 in a group)
Pycnoporus sanguineus (Fr.) Murr.	rotten stump, along the trail	278	solitary to gregarious (3-5 in a group)
Trametes hirsuta (Wulf.) Lloyd.	rotten branch, along the trail	288	solitary to gregarious (3-5 in a group)
PSATHYRELLACEAE			
Coprinellus disseminatus (Pers.) J. E Lange	soil, along the trail	242	gregarious
Coprinellus micaceus (Bull.) Vilgalys, Hopple & Jacq.	soil, along the trail	278	gregarious
Coprinopsis atramentaria (Bull.) Redhead, Vilgalys & Moncalvo	soil, along the trail	258	gregarious
Coprinus plicatilis (Curt.) Fr.	soil, along the trail	280	gregarious
Psathyrella delineata (Fr.) Henn.	soil, along the trail	268	gregarious
RAMARIACEAE			
Ramaria gracilis (Pers.) Quel.	soil, along the trail	268	gregarious
Ramaria sp.	soil, along the trail	256	gregarious
RUSSULACEAE			
Lactarius piperatus (L.) Pers.	soil, along the trail	242	gregarious
Russula rosea Pers.	soil, along the trail	290	gregarious
SCHIZOPHYLLACEAE			
Schizophyllum commune Fr.	rotten branch, along the trail	288	gregarious
STEREACEAE			
Stereum complicatum (Fr.) Fr.	rotten twigs, along the trail	266	solitary
Stereum hirsutum (Willd.) Pers.	rotten branch, along the trail	280	solitary
Stereum insignatum (Blume) Fr.	rotten twigs, along the trail	284	solitary
Stereum ostrea (Bl.& Nees.) Fr.	rotten stump, along the trail	242	solitary
STROPHARIACEAE			
Hypholoma fasciculare (Huds.) Kummer	soil, along the trail	264	gregarious
Stropharia semiglobata (Batsch.) Quel.	soil, along the trail	288	gregarious

Table 1 continued

TAXA	HOST/ SUBSTRATE	ELEVATION (masl)	GROWTH HABIT
THELEPHORACEAE			
Thelephora terrestris (Ehrenb.) Fr.	soil, along the trail	290	gregarious
TREMELLACEAE			
Tremella fuciformis Berk.	rotten branch, along the trail	264	gregarious
TRICHOLOMATACEAE			
Collybia albuminosa (Berk.) Petch.	soil, along the trail	266	gregarious
Clitocybe dealbata (Sowerby) P. Kumm.	soil, along the trail	280	gregarious
Tricholoma lascivum (Fr.) Gillet	soil, along the trail	296	gregarious
Tricholoma saponaceum (Fr.) P. Kumm.	soil, along the trail	304	gregarious

Table 2

Ascomycetous and Basidiomycetous fungal families and their corresponding number of species collected at QPL

FUNGAL FAMILIES	NUMBER OF SPECIES
ASCOMYCETES	
Pezizaceae	2
Pyronemataceae	1
Sarcoscyphaceae	3
Sarcosomataceae	1
Xylariaceae	5
BASIDIOMYCETES	
Agaricaceae	10
Auriculariaceae	5
Auriscalpiaceae	2
Bolbitiaceae	3
Boletaceae	2
Cantharellaceae	4
Clavariaceae	2
Coniophoraceae	1
Corticiaceae	2
Crepidotaceae	2
Dacryomycetaceae	2
Diplocystaceae	1
Entolomataceae	1
Fomitopsidaceae	4
Ganodermataceae	4
Geastraceae	2
Hydnaceae	1

Table 2 continued

FUNGAL FAMILIES	NUMBER OF SPECIES
Hygrophoraceae	1
Hymenochaetaceae	5
Inocybaceae	1
Lyophyllaceae	2
Marasmiaceae	5
Meruliaceae	2
Mycenaceae	6
Nidulariaceae	2
Phanerochaetaceae	1
Physalacriaceae	2
Pleurotaceae	1
Pluteaceae	1
Polyporaceae	28
Psathyrellaceae	5
Ramariaceae	2
Russulaceae	2
Schizophyllaceae	1
Stereaceae	4
Strophariaceae	2
Thelephoraceae	1
Tremellaceae	1
Tricholomataceae	4
Number of Families = 44	**Number of Morpho-species = 141**

Figure 4

Represents the different morphological features of macrofungi collected at QPL

Schizophyllum commune Fr.

Cookeina tricholoma (Mont.) Kuntze

Ganoderma applanatum (Pers.) Pat.

Earliella scabrosa (Pers.) Gilb. & Ryvarden

Figure 4 continued

Tremella fuciformis Berk.

Hexagonia tenuis (Hook.)Fr.

Microporus xanthopus (Fr.) Kuntze

Daldinia concentrica (Bolt.) Ces. & de Not.

The suitability of growth and factors affecting the diversity of macroscopic fungi in the Quezon Protected Landscape area

The interplay between wind speed, temperature, humidity, and faunal statistics is responsible for the diversity of ascomycetous and basidiomycetous fungal specimens collected at the study site. As organisms that rely heavily on spore dispersal and high moisture content of the environment, it is logical to think that these species will thrive in areas that are always almost humid. Protected and forested areas in the Southern Tagalog Region, such as QPL, are suitable environments for the reproduction of these organisms.

The wind speed assists in the rapid dispersal of spores, bringing them to other places that can support their development into adulthood. Season of collection directly influences the number of fungal organisms that can be collected and observed. During the dry season (December to May), where humidity is low, and it is usually hot, the diversity of ascomycetous and basidiomycetous fungi tends to decrease as compared to the wet season, where substrate tree tissues and soil receive enough moisture to support the proliferation and development of varying ascomycetous and basidiomycetes and the plethora of fruiting bodies they have. The variety of insects feeding on fungal fruiting bodies also dictates the kinds of ascomycetes and basidiomycetes that can be surveyed for a particular period.

Functional diversity of macroscopic fungi

The functional diversity values of macroscopic fungi recorded in the study area showed prominence of decomposer groups and mycorrhizas. The proportion of functional diversity of macrofungi at STRPL was mycorrhizal (28%), pathogenic (20%), and saprophytic fungi (52%). Among the 141 morpho-species, 73 were saprophytic, mostly on woody substrates like Cymatoderma, Ganoderma, and Oudemansiella. The decomposition of organic matter by these macrofungal species releases key plant nutrients to the soil that allow the new plants to grow on the forest floor. Distinct mycorrhizal fungi were Phylloporus, Strobilomyces, and Thelophora, which were recorded also in STRPL. Sixty-two percent, for example, of all fungal species at STRPL were saprophytes mainly of wood and forest litter, while 24% were pathogenic fungi on standing trees. The remaining 14% of fungal taxa were soil-inhabiting genera that form ectomycorrhizal associations with fine roots of higher plants like dipterocarps.

Most saprophytes recorded among the groups of wood decay fungi were exemplified by Microporus, Polyporus, and Xylaria. These groups of wood decomposers occurred mostly on wood substrates such as branches, twigs, and stumps, which are important links to nutrient cycling by hastening the decomposition of substrates induced by enzymes that break down organic matter (Lapitan et al., 2018). These types of fungi are characteristically tough and leathery in texture and persist under limited moisture conditions during the dry season. Mycorrhizal species were found in the study area, where moisture could be influenced by thick canopy layers in the forest. Examples were Russula rosea found under canopies of Areca catechu and Lactarius piperatus associated with roots of P. malaanonan Merr. and Dipterocarpus grandiflorus Blanco.

In QPL, there was a defined distribution of saprophytic (52%) and mycorrhizal (28%) fungi represented by Agaricus and Strobilomyces in the forest. Aside from ecological functions, fungi have long been recognized as a source of food, medicine, and industrial applications. Lentinus reportedly contains active compounds against carcinoma cells (Sadi et al., 2015), exemplified by edible species of fungi. Lentinus elegans had antioxidant potential as an additive in ruminant feedstock (Reyes & Nair 2016; Hamchara et al., 2018), which was further reported to have mycoremediation potential in addressing uranium, chromium, and iron contamination (Bayramoglu et al., 2006).

RESULTS AND DISCUSSION

Fieldwork and studies provide recent documentation on the existence and distribution of the different species of ascomycetous and basidiomycetous macroscopic fungi in the Quezon Protected Landscape. The collection sites provide a wider range of fungal habitats and substrates, such as dead or rotten logs, living trees, leaf litter, fence posts, structural timbers, and soil. Thus, the area was a good fungal collection and documentation study site.

Transect, quadrat, and opportunistic sampling methods were employed, which resulted in collecting and identifying 141 taxa of macroscopic fungi belonging to 44 families and 81 genera. The most species-rich are the Family Polyporaceae (28 species), followed by the Family Agaricaceae (10 species) and Mycenaceae (6 species). The families Xylariaceae, Auriculariaceae, Hymenochaetaceae, Marasmiaceae, and Psathyrellaceae are represented by five species each, and four species represent the families Cantharellaceae, Fomitopsidaceae, Ganodermataceae, Stereaceae, and Tricholomataceae. The families Sarcoscyphaceae and Bolbitiaceae are represented by three species and families Pezizaceae, Auriscalpiaceae, Boletaceae, Clavariaceae, Corticiaceae, Crepidotaceae, Dacryomycetaceae, Geastraceae, Lyophyllaceae, Meruliaceae, Nidulariaceae, Physalacriaceae, Ramariaceae, Russulaceae, and Strophariaceae represented by two species. Only one species represents the rest of the families.

Among 141 different taxa, 129 taxa (91.48%) are basidiomycetous fungi, while 12 taxa (8.51%) are ascomycetous ones that accounted for the five families, namely, Pezizaceae, Pyronemataceae, Sarcoscyphaceae, Sarcosomataceae, and Xylariaceae. On the other hand, 39 families belong to the class Basidiomycetes. For Basidiomycetes, Table 1 shows that the family Polyporaceae is the most abundant in QPL with 13 genera and 28 species, ten of which belong to the Polyporus. The family Agaricaceae ranked second in high species count with ten different species. The Xylariaceae family has the highest species count for Ascomycetes, with five species seen and collected. Schizophyllum commune is the most abundant macroscopic fungi in the collection, comprising 302 individuals. A greater number of fungal species (84 species) were markedly observed in lower elevations (245-265 masl) than in higher elevations (285-300 masl) which documented only 57 species.

The high number of species and quantities gathered can be accounted for during the rainy season during the field survey. Most fungi grow best when there is abundant moisture available. The study of Talley et al. (2002) reveals that measures of moisture availability, such as relative humidity and vapor pressure

deficit, explained more of the variance in fungal abundance and richness than temperature. Thus, the data indicate that the time of collection influences the abundance and diversity of macroscopic fungi in QPL.

The difference in the altitude where the fungi were collected provides varying results. Eighty-four species of macroscopic fungi were collected in the lowlands, while fifty-seven were in the highlands. This number shows that the number of species and individuals decreases as the altitude increases. For example, the number of individuals of Microporus xanthous counted in the lowlands is one hundred forty-three while four fifty-three in the highlands. Climatic factors such as humidity, temperature, and the presence of moisture played significant roles in the existence of numerous macroscopic fungi in the lowlands.

Ecological functions of forest fungi

The macroscopic fungi, ecologically can be categorized as saprotrophs, pathogens, or mutualists. With emphasis on the saprotrophic group, this obtains food by assimilating nutrients from organic matter on forest litter, soil, and wood debris through a decomposition process that facilitates nutrient cycling (Asiegbu & Kovalchuk, 2021). The forest litter trapped on canopies is also a potential substrate of a saprotrophic group of fungi and is eventually washed as throughfall (Dighton, 2007). The forest organic matter decomposition by specific groups of fungi is through enzymes, mineralizing lignocellulosic components into simple compounds absorbed through extensive hyphae (Kubartová et al., 2015; Osono, 2020).

The fungal hyphae of saprotrophic fungi (e.g., Collybia, Marasmiellus, Marasmius, and Mycena) act as the binder of forest litter in soil, preventing nutrient loss after soil erosion and leaching in tropical forests (Lodge & Asbury, 1988). Saprophytic basidiomycetes are the most common Philippine macroscopic fungi, dominated by Polyporaceae on many decaying woody forest substrates (Arenas et al., 2015; Parlucha et al., 2021). In marginal ecosystems, forest fungi are exemplified by Auricularia under rain tree (Samanea saman Jacq. Merr.), ipil-ipil (Leucaena leucocephala Lam. de Wit), mahogany (Swietenia macrophylla King), mango (Mangifera indica L.). Pathogenic fungi cause diseases to trees as hosts from natural or plantation forests. This happens when air or water-borne fungal spores colonize wounds on stumps, trunks, and roots, developing mycelial growth (Gonthier and Thor, 2013).

Potential Conservation and Sustainable Landscape

Our country faces rapid environmental changes, particularly the conversion of

forest land and other landscapes, threatening biodiversity, including macroscopic fungi. Forest and other ecosystem disturbances have been demonstrated to alter fungal composition and function (Robinson et al., 2020), with the possibility of dysbiosis that favors pathogenic fungi due to the loss of saprophytic competitors (Shi et al., 2019).

While efforts to improve forest cover have been implemented through policies and reforestation programs, satellite observations continue to track forest loss in the country (Perez et al., 2020), where observed deforestation hotspots brought about by unsustainable practices such as logging, kaingin making, and other anthropogenic activities often overlap with primary forests (Araza et al., 2021). Strengthening forest-protected areas, a holistic approach that integrates the sustainable use of forest resources, restoration of degraded forests, and climate change mitigation in the Philippines, is important for conserving forest fungal resources.

In-depth knowledge of the distribution and biological and ecological knowledge of forest macrofungi is important to inform forest managers and policymakers in formulating plans for priority forest areas that are critical fungal niches and identifying priority fungal species for conservation. While studies on macroscopic fungi in the Philippines remain fragmented and underfunded, different avenues for forest mycological research can provide new discoveries crucial to fungal conservation.

CONCLUSIONS

The diversity of macroscopic ascomycetous and basidiomycetous fungi in QPL was still observed and accounted for even though there was limited time and season during collection, which is not ideal for specimen collection. After identifying the collected specimens and providing a listing of them, the results of this study indicate that QPL is one of the species-rich areas of the country, teeming with many organisms. Based on our observation, these fungi are great decomposers in the forest ecosystem. These fungi are largely responsible for decay in living trees, rotten branches and trunks, other wood in service, and valuable standing timbers. Other species are known for their edibility and can be a source of food and medicine.

RECOMMENDATIONS

Hence, it is recommended that continuous research be done to acquire more data establishing the seasonal fungal biodiversity profile of the study site, which is very important in devising conservation measures to protect and preserve the richness of the landscape. Further, this study also considers it a long-term monitoring program (LTMP). Establishing an LTMP can track temporal changes in fungal communities over multiple years. This would enhance understanding seasonal variability, succession dynamics, and responses to environmental disturbances.

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