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Diversity of macro fungus across three altitudinal ranges in Lore Lindu National Park, Central Sulawesi, Indonesia and their utilization by local residents

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Abstract. *Yusran Y, Erniwati E, Wahyuni D, Ramadhanil R, Khumaidi A. 2021. Diversity of macro fungus across three altitudinal ranges in Lore Lindu National Park, Central Sulawesi, Indonesia and their utilization by local residents. Biodiversitas 22: 199-210.* A large amount of biodiversity research has been carried out in Lore Lindu National Park, a major biodiversity center in Central Sulawesi, Indonesia, but none have investigated the biodiversity of macrofungi and their traditional utilization. Therefore, this study aimed to explore the diversity of macro fungus in Lore Lindu National Park, and to identify their potential uses as food sources and medicinal uses by the local residents living around Lore Lindu National Park. Exploration of macrofungus species in Lore Lindu National Park was done at three locations representing three altitudinal ranges: (i) <500 m above sea level (asl); (ii) 500–1500 m asl; and >1500 m asl. Ten plots were placed in two major lines with a 100 m distance between plots in each sampling location. All macrofungi within the observation plots were then documented and identified. Ethnomycological studies were done by asking questionnaire to selective respondents, group discussion, and pictorial presentation studies to random respondents in five villages located in the buffer zone of the national park area. This study found 172 species (including unidentified species/sp.) from 33 families of macro fungus in Lore Lindu National Park in which 159 of them belong to the Basidiomycota division, while 13 of them were of the Ascomycota division. Our results also showed varying diversity of macrofungus at different altitudes. At the elevation of <500 m asl, as many 77 species were found, while 117 and 142 species were found at the elevation of 500-1500 and >1500 m asl, respectively. Marasmius spp and Hygrocybe spp were the most abundant genera, and nine species (i.e. *Schizophyllum commune*, *Termytomyces* sp, *Auricularia auricular-judge*, *Auricularia* sp., *Pleurotus ostreatus*, *Ganoderma lucidum*, *Xylaria* sp., *Agaricus* sp. dan *Lentinus sajor-caju*) were utilized as a food source and in traditional medicine by the residents around the national park area.

Keywords: Ethnomycology, Lore Lindu National Park, macro-fungi diversity, traditional knowledge

INTRODUCTION

Indonesia is a tropical country with rich natural resources, including high diversity of flora, fauna and microorganisms. Sulawesi is an island in Indonesia that biogeographically is located within the Wallace lines, a region between Asia and Australasia lines (Wallace 1869) and between the Laurasian and Gondwanan plates (Corlett and Primack 2006). This unique biogeographical position along with suitable environmental conditions make Sulawesi have enormous abundance of species diversity, including numerous endemic species. About 15% of flowering plant species from Sulawesi have been identified and categorized as endemic species (Whitten et al. 1987). Van Balgooy et al. (Van Balgooy et al. 1996) recognized that 933 new plant species originated from Sulawesi, and found that 112 species were endemic. A plant group with high diversity and endemism in Sulawesi is fungi.

Fungi is categorized as the second-largest biotic community after insects (Sarbhoy et al. 1996). Hawksworth & Lűcking (2017) estimated that fungi emerged around 2,2-3,8 million species in the world. Macrofungus is a major component of the fungal kingdom. This group of fungi plays important roles in the wider natural ecosystem, including as decomposers and food sources for animals (Tan et al. 2015). Ecologically, macrofungus can be classified into three major groups: saprophytes, parasites, and symbiotic species. Almost all terrestrial macrofungus are saprophytes or mycorrhizal symbionts, but some of them are plant pathogens. Taxonomically, most of them belong to Basidiomycota or Ascomycota, with a few being a member of Zygomycota (Mueller et al. 2007). Based on habitat characteristics, the known macrofungus are classified into three, whether they are terricolous saprophytic, wood-inhabiting, or ectomycorrhizal (Kutszegi et al. 2015).

Some wild macrofungus species are edible and considered as important food sources of communities in many countries due to their nutrient contents. An estimated 1069 species of macrofungus have been used as sources of food worldwide (Boa 2004). In some Asian countries, macrofungus is also traditionally used for medicinal purposes (Manzi et al. 1999). Ethnomycological research was done by Rosemary-Kinge et al. (2017) and Nema et al. (2014) revealed the uses of macrofungus from a variety of perspectives, such as for consumption, nutrients, and medicines. This research studied the potential utilizations of macrofungus in agro-industry sector and its commercial benefits in medical applications in developed countries. In line with these studies, Okhuoya et al. (2010), Herawati et al. (2016), and Hussein et al. (2016) summarized that macrofungus need to be successfully domesticated to unlock their commercialization potential. Once domesticated, they can become economically important commodities as food sources, medicines, biological control agents, and raw sources of chemical substances in pharmaceutical industry (Duarte et al. 2006). Kim & Song (2014) stated that many macrofungus show important commercial characteristics, such as high protein, fiber, vitamin, and mineral contents, with low-fat levels, and produce medical compounds known to treat cancer and diabetes. For example, the macro fungus *Trametes versicolor* is known as decomposer of resistant organic pollutants (Tran et al. 2010; Tran et al. 2013), and is used as bioremediation agent for industrial waste and heavy metals (Demirbas 2000; Kalac et al. 2004). It has also been reported that macrofungus in the ectomycorrhizal group is one of the most important non-wood forest products in international trade, especially from the genera of *Amanita, Boletus, Tuber, Tricholoma, Cantharellus,* and *Lactarius*, along with and saprophytic fungi from the genera of *Morchella, Pleurotus,* and *Agaricus*.

While Indonesia ranks second in term biodiversity richness after Brazil (Muchlisin and Azizah 2009), yet information on the diversity of macrofungus and their uses local communities are scarce. There are still abundant tropical fungal species that are yet to be identified, described, and documented. This lack of work is primarily caused by minimal research effort and the limited number of fungal taxonomists in Indonesia that can carry out rigorous identification, especially of medicinal and edible fungi. Recently, research done by several groups worldwide were not able to provide sufficient data on the biodiversity of fungi and their applications (Chang and lee 2004; Retnowati 2007; Haryati and Azrianingsih 2012; Enas et al. 2016; Herawati et al. 2016; Arko et al. 2017; Marzuki et al. 2017; Foo et al. 2018; Kang et al. 2013; Khastini et al. 2018).

The lack of biodiversity data on macrofungus is also a specific problem for Sulawesi, especially in Central Sulawesi Province. Although this province has a vast-range of forests in comparison to the other five provinces, no work has been done on macrofungus diversity or their ethnomycological uses. This work aimed to explore fungal diversity in Lore Lindu National Park, a major biodiversity center in Central Sulawesi, and to identify their potential uses as food sources and natural bioactive products. This aim was achieved by carried out sampling and species identification of macrofungus in the Lore Lindu National Park area, and complemented with surveying residents on their level of knowledge and uses of macrofungus.

MATERIALS AND METHODS

Study period and area

This study was conducted from January to August 2017 in Lore Lindu National Park. The park is located between Sigi District and Poso District, Central Sulawesi Province, Indonesia. This area lies between 119º 90’ - 120º 16’ E and 1º 8’ - 1º 3’ S with elevation from 200 to 2610 m above the sea level. The park has precipitation of 1200-2200 mm per year with average temperatures of 26°C (TNC/BTNLL 2002). Lore Lindu National Park has legal status as a National Park based on the Decree of the Minister of Forestry, Republic of Indonesia, No. 593/Kpts-II/93. Lore Lindu National Park has an area of ± 229,177.5 ha. This area has its own uniqueness because most of its constituent components are representative of the flora and fauna of the Sulawesi mountain forests, where 90% of the total area is at an altitude above 1000 m above sea level (Pitopang 2006). In this area, there are also several types of ecosystems such as lowland rain forest (200-1000 m asl), montane rain forest (1000-2500 m asl), grasslands, and highland swamp forests (TNC 2001).

Exploration of macrofungus species in Lore Lindu National Park was done at three altitudinal ranges. First site had elevation range of <500 m above sea level (asl), and was administratively part of Bora Village, Sigi Biromaru Sub-district, Sigi District. The other two sites had elevation range of 500–1500 m asl (part of the Nokilalaki Trekking line), and >1500 m asl (part of Sedoa Village), both were administratively in Lore Utara Sub-district, Poso District. The sampling area was located around ± 30-80 km southwest of Palu City, the capital of Central Sulawesi Province (Figure 1).

Survey, collection, and identification of macrofungus

Sampling locations were chosen based on the accessibility of the area and macro fungus occurrence (Rosemary-Kinge et al. 2011). Observation plots were deployed at each different altitudinal range, according to Engola et al. (2007). Ten observation plots with size of 5x200 m (0.1 Ha) were placed in two major lines, with 100 m distance between plots in primary forest in each location, resulting in 10 replicates. The observation was complete after 8 months starting from January 2017. Macro fungus observation was done by whole body collection of fungi that appeared in logs, rooted wood, leaf litter, animal waste, or soil. The detail on the morphological characteristics and the native condition of the environment were documented using a digital camera. Fruit body collections were maintained carefully to prevent sporocarp damage. Excess soil that stuck to the sporocarp was removed, the fruit body carefully dried using a tissue, and then transferred to an envelope, which was labeled to prevent spore contamination from different fungal species.

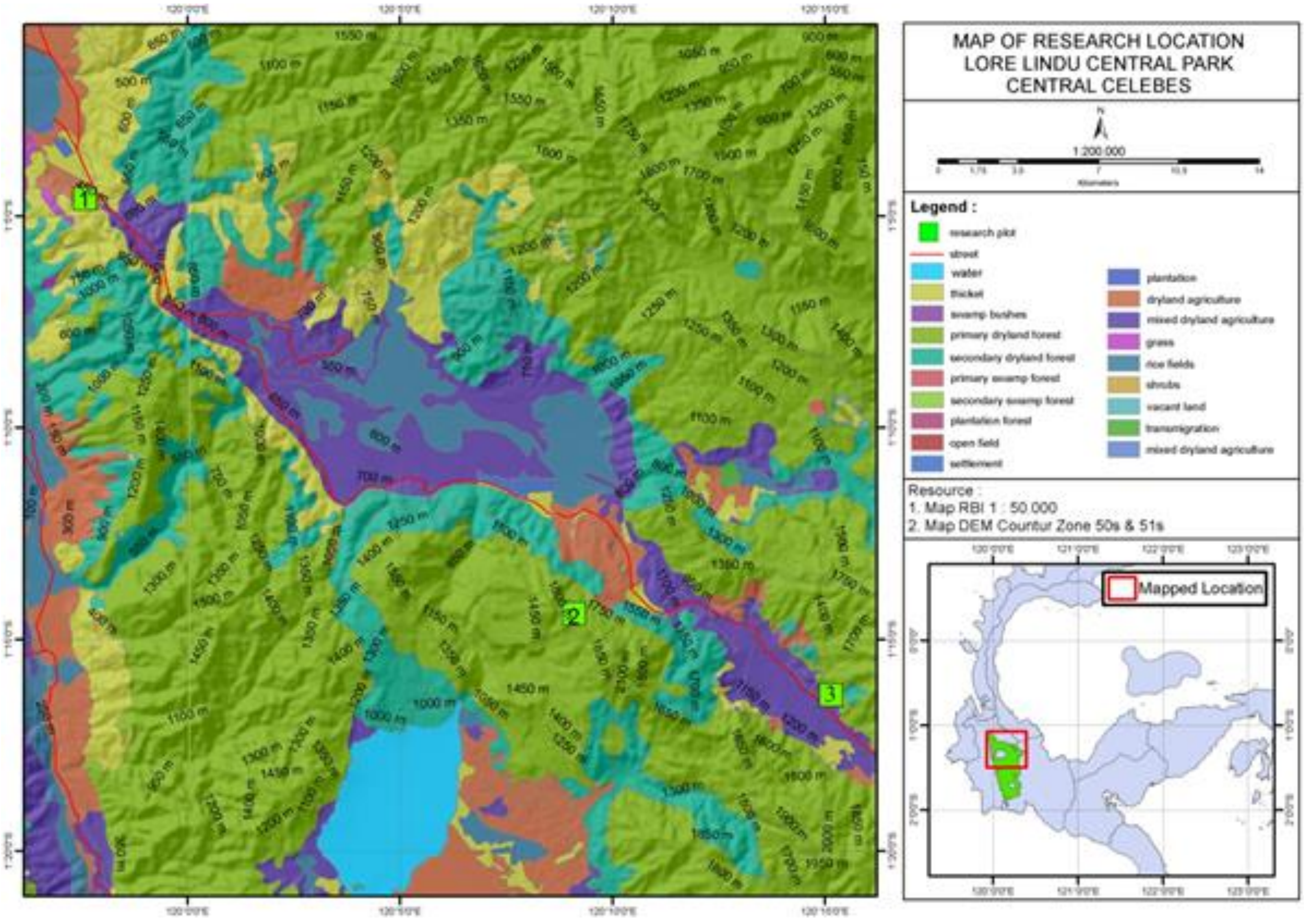

Figure 1. Map of sampling sites in Lore Lindu National Park, Central Sulawesi, Indonesia. Site 1: altitude <500 m asl; Site 2: >1500 m asl; and Site 3: 500–1500 m asl)

The fungi collection was then transferred to the laboratory for examination under a microscope and further identification. The sporocarp was dried using a drying machine with a maximum temperature of 35°C for 24 hours. Microscopy characteristics, such as form and color of the spore, were then identified. Fungal identification was carried out by macro and micro characteristics (Bates 2006; Desjardin et al. 2004; Desjardin et al. 2000; Hemmes and Desjardin 2002; Index Fungorum 2017; Mushroom Expert 2017; Stadler et al. 2014). Micro-features were observed using a standard microscope (Andrew et al. 2013). Samples were then stored in the Forest Science Laboratory, Faculty of Forestry, Universitas Tadulako, Palu, Indonesia. Data of macro fungus diversity was then analyzed using the descriptive statistics available in Microsoft Excel 2010.

Ethnomycology documentation

Interviews with residents living around Lore Lindu National Park were employed to complement the biodiversity information. Respondents of both genders were chosen in every village, mainly targeting respondents who served as village shaman (*dukun kampung=Sando),* traditional public figures, and fungus sellers in traditional markets that were located in the supporting zone of the national park. These respondents were targeted as they were assumed to be familiar with macrofungus that is edible and has medicinal purposes. Respondents were chosen in five main villages that were located in the supporting zone of the national park, which are Sedoa, Kamarora A, Kamarora B, Lembantongoa, and Tongoa. Residents of those villages are dominated by the Kaili – Da’a tribe, with a few from the Bugis, Bada, Seko, Behoa, and Toraja tribes, except in Sedoa Village that is occupied by the Lore tribe. Fifty questionnaires were given to the respondents in each village, followed by an interview and discussion. Questions on basic data (name, age, occupation, migration history, land ownership, and family members) were asked along with questions on the macrofungus known to grow around them (local name, description, time of emergence, growth place, how to use them as medicine or food, which part of the fungus residents prefer to use relating to the disease they are trying to cure, and how to use them). Furthermore, a group discussion and pictorial presentation were also conducted by showing photos of macro fungus that had already been collected in the national park area to the respondents. Statistical analysis was done to analyze ethnomycological data obtained from the interviews.

RESULTS AND DISCUSSION

Macro fungus diversity

This study found 172 species (including unidentified species/sp.) from 33 families of macro fungus in Lore Lindu National Park in which 159 of them belong to the Basidiomycota division, while 13 of them were of the Ascomycota division (Table 1). Around 24 species of macrofungus were identified as the members of the Polyporaceae family, 18 species the Russulaceae, 17 species the Marasmiaceae, 13 species the Hygrophoraceae, 10 species the Agaricaceae, 9 species the Auriculariaceae, 7 species the Ganodermataceae, 6 species for each family Phallaceae, Sarcoscyhaceae and Strophariaceae, 5 species the Amanitaceae, 4 species for each family Boletaceae, Mycenaceae, Pleurotaceae and Xylariaceae, 3 species for each family Entolomataceae, Geastraceae, Helotiaceae, Hymenogastraceae, Lyophyllaceae, and Scizophyllaceae, 2 species for each family Bolbitiaceae, Fumitopsidaceae, Gomphaceae and Gomphidiaceae, and 1 species of each belonged to the Clavulinaceae, Hymenochaeteceae, Inocybaceae, Niaceae, Psathyrellaceae, Stereaceae, Tricholomataceae and Tremelaceae families. Three families, i.e. Helotiaceae, Sarcoscyphaceae and Xylariaceae, belong to the Ascomycota division, while the others belong to the Basidiomycota. The family and the species of each family are presented in Figure 2.

Our results also showed varying diversity of macrofungus at different altitudes. At the elevation of <500 m asl, as many 77 species were found, while 117 and 142 species were found at the elevation of 500-1500 and >1500 m asl, respectively. This finding suggests that the diversity of macrofungus is positively correlated with increasing altitude (Figure 3). This result contradicts previous research, which reported the diversity of fungus decreased with increasing altitude (30, 37,48,). Our observations also indicate that 22 species of fungi were only found at the elevation of <500 m asl, four species at the elevation of 500–1500 m asl, and 31 species at the elevation of >1500 m asl. Further analysis revealed varying abundance across altitudes, with 48 species were found at all three altitudes, 53 species were found at both the altitudes of <500 m and 500-1500 m asl, 50 species were found at both the elevations of <500 m and >1500 m asl, and 109 were species found at both the elevations of 500–500 m and >1500 m asl (Figure 4).

The different abundances of macrofungus species found in the sampling locations could be caused by many factors, especially the altitude itself, which also relates to different plant composition in the area, then followed by the microclimate. Previous research reported that microclimatic environmental variables, such as temperature, humidity, soil humidity, rainfall intensity, organic composition, leaf litter quality, hummus, methods of collection, and the plant-soil condition shape the environment and determine the distribution and diversity of macrofungus (Baptista et al. 2010; Bergemann and Largent 2010; Conn and Dighton 2000; Engola et al. 2007; Ferris et al. 2000; Kutszegi et al. 2015; Lopez-Quintero et al. 2012; Luo et al. 2016; Packham et al. 2002; Pushpa and Purushothama 2012). These findings are also supported by Angelini et al. (2015), who suggested that macro fungus emergence is highly related to the plant type that dominates the forest.

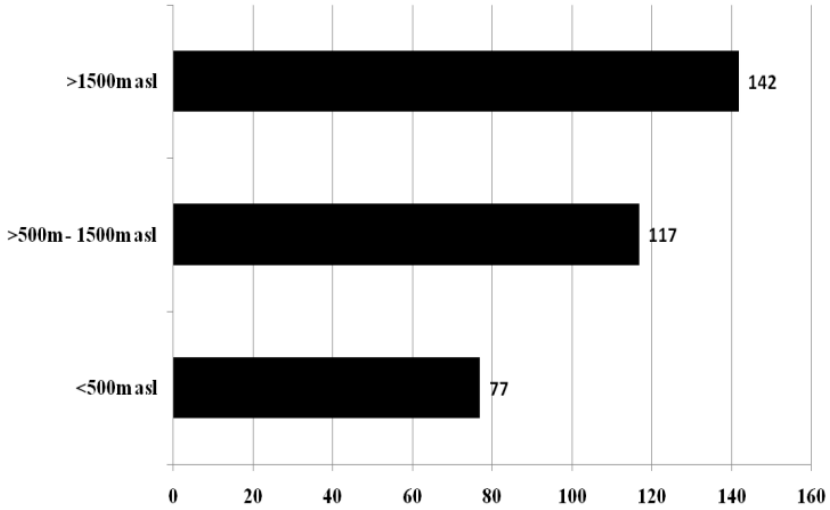

Figure 3. Number of species of macro fungus in the Lore Lindu National Park across altitudinal ranges. Note: asl: above sea level

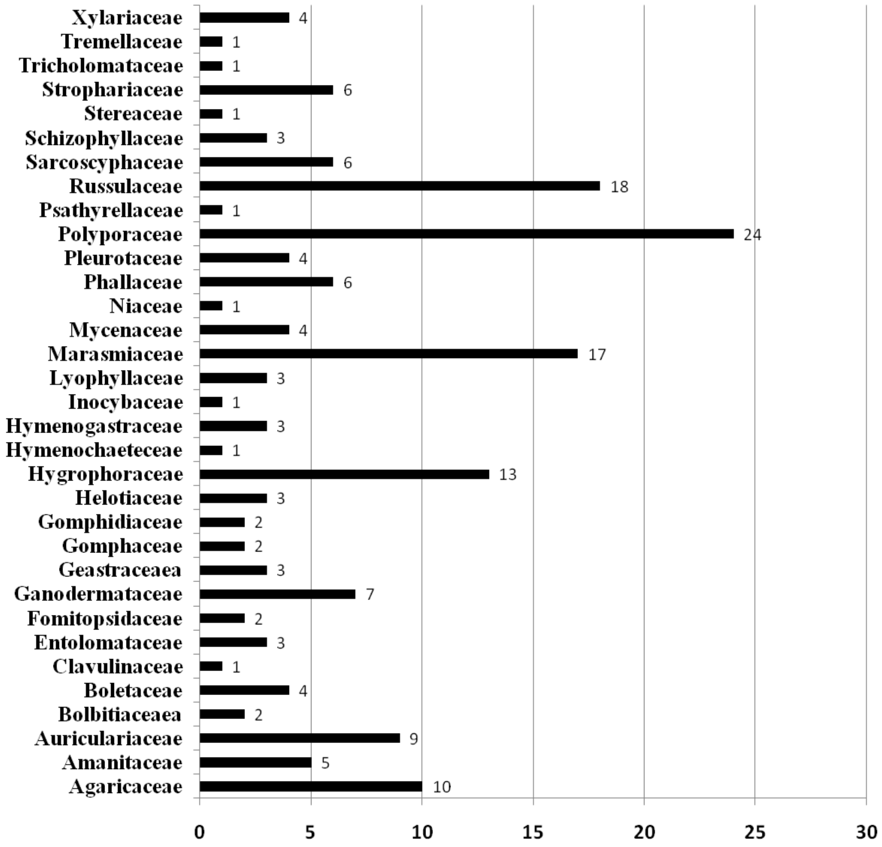

Figure 2. Family and the species of each family of macrofungus in Lore Lindu National Park, Central Sulawesi, Indonesia

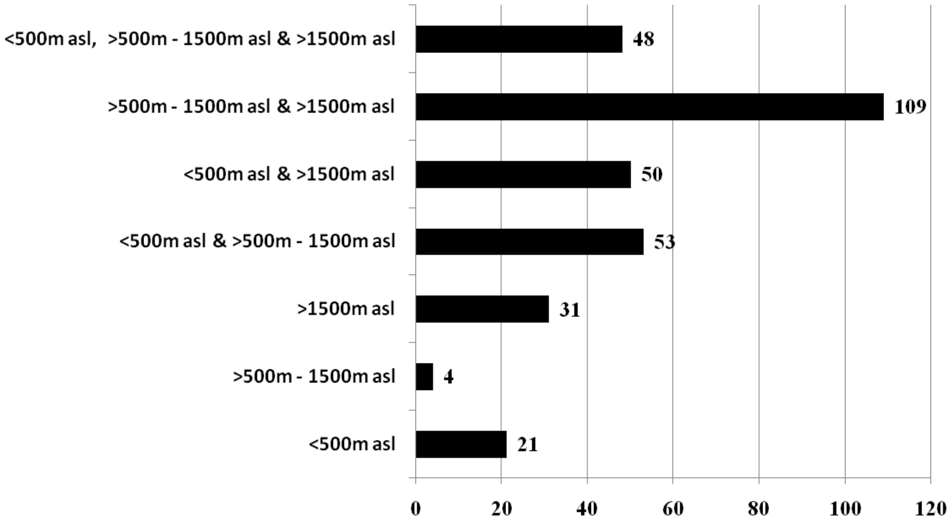

Figure 4. Number of species of macro fungus in the Lore Lindu National Park, Central Sulawesi, Indonesia that overlap across altitudinal ranges Note: asl = above sea level.

Table 1. Macro fungus species found in Lore Rindu National Park, Central Sulawesi, Indonesia (WD: Wood debris, W: Wood, DL: Decomposing Litter, S: Soil, D: Dung)

Species	Family	Division	Substrate
Agaricus sp.1	Agaricaceae	Basidiomycota	DL, S
Agaricus sp.2	Agaricaceae	Basidiomycota	DL, S
Agaricus sp.3	Agaricaceae	Basidiomycota	DL, S
Agaricus sp.4	Agaricaceae	Basidiomycota	DL, S
Agaricus lactifluus (L.) Pers	Agaricaceae	Basidiomycota	DL, S
Amanita sp.1	Amanitaceae	Basidiomycota	DL, S
Amanita sp.2	Amanitaceae	Basidiomycota	DL, S
Amanita craseoderma Bas	Amanitaceae	Basidiomycota	DL, S
Amanita pantherina (DC.) Krombh.	Amanitaceae	Basidiomycota	DL, S
Amanita phalloides (Vaill. ex Fr.) Link	Amanitaceae	Basidiomycota	DL, S
Amauroderma rugosum (Blume & T.Nees) Torrend	Ganodermataceae	Basidiomycota	DL, S
Agrocybe sp.1	Strophariaceae	Basidiomycota	DL
Agrocybe sp.2	Strophariaceae	Basidiomycota	DL
Agrocybe sp.3	Strophariaceae	Basidiomycota	DL
Agrocybe parasitica	Strophariaceae	Basidiomycota	W
Agrocybe pediades (Fr.) Fayod	Strophariaceae	Basidiomycota	DL, D
Agrocybe retigera (Speg.) Singer	Strophariaceae	Basidiomycota	DL
Auricularia sp.1	Auriculariaceae	Basidiomycota	WD,W
Auricularia sp.2	Auriculariaceae	Basidiomycota	WD,W
Auricularia sp.3	Auriculariaceae	Basidiomycota	WD, W
Auricularia asiatica	Auriculariaceae	Basidiomycota	WD, W
Auricularia auricula-judae (Bull.) Quél.	Auriculariaceae	Basidiomycota	WD, W
Auricularia delicata (Mont.) Henn.	Auriculariaceae	Basidiomycota	WD, W
Auricularia polytricha	Auriculariaceae	Basidiomycota	WD, W
Auricularia squamosa	Auriculariaceae	Basidiomycota	WD, W
Bisporella sp.	Helotiaceae	Ascomycota	WD
Bisporella citrina (Batsch) Korf & S.E.Carp.	Helotiaceae	Ascomycota	WD
Bisporella sulfurina	Helotiaceae	Ascomycota	WD
Boletus sp.1	Boletaceae	Basidiomycota	DL, S
Boletus sp.2	Boletaceae	Basidiomycota	DL, S
Boletus sp.3	Boletaceae	Basidiomycota	DL, S
Boletus sp.4	Boletaceae	Basidiomycota	DL, S
Clavulina cinereai (Bull.) J.Schröt.	Clavulinaceae	Basidiomycota	S
Conocybe sp.	Bolbitiaceae	Basidiomycota	DL, S
Cookeina sp.1	Sarcoscyphaceae	Ascomycota	WD
Cookeina sp.2	Sarcoscyphaceae	Ascomycota	WD
Cookeina sulcipes (Berk.) Kuntze	Sarcoscyphaceae	Ascomycota	WD
Cookeina tricholoma (Mont.) Kuntze	Sarcoscyphaceae	Ascomycota	WD
Copelandia sp.	Bolbitiaceaea	Basidiomycota	DL, S
Coprinellus disseminatus (Pers.) J.E.Lange	Psathyrellaceae	Basidiomycota	WD
Coprinus sp.	Agaricaceae	Basidiomycota	DL, S
Coprinus plicatilis (Curtis) Redhead et al.	Agaricaceae	Basidiomycota	DL, S
Crepidotus sp.	Inocybaceae	Basidiomycota	WD
Crinipellis sp.1	Marasmiaceae	Basidiomycota	WD
Crinipellis sp.2	Marasmiaceae	Basidiomycota	WD
Cyathus sp.	Agaricaceae	Basidiomycota	WD, DL
Cyathus striatus (Huds.) Willd.	Agaricaceae	Basidiomycota	WD, DL
Daedaleopsis sp.1	Polyporaceae	Basidiomycota	W
Daedaleopsis sp.1	Polyporaceae	Basidiomycota	W
Dendrothele sp.	Nicaea	Basidiomycota	WD, W
Dictyophora indusiata Vent.	Phallaceae	Basidiomycota	DL, S
Entoloma sp.	Entolomataceae	Basidiomycota	DL, S
Entoloma nitidum	Entolomataceae	Basidiomycota	DL, S
Entoloma pachypus	Entolomataceae	Basidiomycota	DL, S
Exidia recisa (Ditmar) Fr.	Auriculariaceae	Basidiomycota	WD
Galerina velutipes	Hymenogastraceaea	Basidiomycota	WD, W
Ganoderma sp.1	Ganodermataceae	Basidiomycota	WD, W
Ganoderma sp.2	Ganodermataceae	Basidiomycota	WD, W
Ganoderma sp.3	Ganodermataceae	Basidiomycota	WD, W
Ganoderma applanatum (Pers.) Pat.	Ganodermataceae	Basidiomycota	WD, W
Ganoderma lucidum Karst	Ganodermataceae	Basidiomycota	WD, W
Ganoderma nitidum	Ganodermataceae	Basidiomycota	WD, W

Geastrum sp.	Geastraceaea	Basidiomycota	DL, WD
Geastrum mirabile Mont.	Geastraceaea	Basidiomycota	DL, WD
Geastrum rufescens Pers.	Geastraceaea	Basidiomycota	DL, WD
Gerronema albidum	Marasmiaceae	Basidiomycota	WD
Gomphidius sp.1	Gomphidiaceae	Basidiomycota	DL. S
Gomphidius sp.2	Gomphidiaceae	Basidiomycota	DL, S
Gymnopilus sp.	Hymenogastraceae	Basidiomycota	W
Hexagonia apiaria (Pers.) Fr.	Polyporaceae	Basidiomycota	WD, W
Hydropus marginellus	Marasmiaceae	Basidiomycota	DL, WD
Hygrocybe sp.1	Hygrophoraceae	Basidiomycota	DL, S
Hygrocybe sp.2	Hygrophoraceae	Basidiomycota	DL, S
Hygrocybe sp.3	Hygrophoraceae	Basidiomycota	DL, S
Hygrocybe sp.4	Hygrophoraceae	Basidiomycota	DL, S
Hygrocybe sp.5	Hygrophoraceae	Basidiomycota	DL, S
Hygrocybe sp.6	Hygrophoraceae	Basidiomycota	DL, S
Hygrocybe sp.7	Hygrophoraceae	Basidiomycota	DL, S
Hygrocybe coccineocrenata (P.D. Orton) M.M. Moser	Hygrophoraceae	Basidiomycota	DL, S
Hygrocybe conicoides (P.D. Orton) P.D. Orton & Watling	Hygrophoraceae	Basidiomycota	DL, S
Hygrocybe constrictospora Arnolds	Hygrophoraceae	Basidiomycota	DL, S
Hygrocybe nitida (Berk. & M.A.Curtis) Murrill	Hygrophoraceae	Basidiomycota	DL, S
Hygrocybe psittacina (Schaeff.) P. Kumm.	Hygrophoraceae	Basidiomycota	DL, S
Hygrophorus sp.	Hygrophoraceae	Basidiomycota	DL, S
Hymenochaete tabacina (Sowerby) Lév.	Hymenochaeteceae	Basidiomycota	WD, W
Lactifluus sp.	Russulaceae	Basidiomycota	DL, S
Lactifluus acris (Bolton) Gray	Russulaceae	Basidiomycota	DL, S
Lactifluus aspideus (Fr.) Fr.	Russulaceae	Basidiomycota	DL, S
Lactifluus aquifluus (Peck) Kuntze	Russulaceae	Basidiomycota	DL, S
Lactifluus bicolor (Massee)	Russulaceae	Basidiomycota	DL, S
Lactifluus corrugis (Peck) Kuntze	Russulaceae	Basidiomycota	DL, S
Lactifluus curtus	Russulaceae	Basidiomycota	DL, S
Laetiporus sp.	Fomitopsidaceae	Basidiomycota	WD, W
Laetiporus discolor (Klotzsch) Corner	Fomitopsidaceae	Basidiomycota	WD, W
Lentinus sp.	Polyporaceae	Basidiomycota	DL, S
Lentinus ciliatus Lév.	Polyporaceae	Basidiomycota	DL, S
Lentinus sajor-caju (Fr.) Fr.	Polyporaceae	Basidiomycota	DL, S
Leucocoprinus fragilissimus (Berk. & M.A.Curtis) Pat.	Agaricaceae	Basidiomycota	DL
Marasmius sp.1	Marasmiaceae	Basidiomycota	DL, WD
Marasmius sp.2	Marasmiaceae	Basidiomycota	DL, WD
Marasmius sp.3	Marasmiaceae	Basidiomycota	DL, WD
Marasmius sp.4	Marasmiaceae	Basidiomycota	DL, WD
Marasmius androsaceus	Marasmiaceae	Basidiomycota	DL, WD
Marasmius botryoides	Marasmiaceae	Basidiomycota	DL, WD
Marasmius delectans	Marasmiaceae	Basidiomycota	DL, WD
Marasmius maximus Hongo	Marasmiaceae	Basidiomycota	DL, WD
Marasmius papyraceus	Marasmiaceae	Basidiomycota	DL, WD
Marasmius pellucidus	Marasmiaceae	Basidiomycota	DL, WD
Marasmius purpureostriatus	Marasmiaceae	Basidiomycota	DL, WD
Marasmius rotula (Scop.) Fr.	Marasmiaceae	Basidiomycota	DL, WD
Microporus xanthopus (Fr.) Kuntze	Polyporaceae	Basidiomycota	DL, WD
Mycena sp.1	Mycenaceae	Basidiomycota	DL, WD
Mycena sp.2	Mycenaceae	Basidiomycota	DL, WD
Mycena stylobates (Pers.) P.Kumm.	Mycenaceae	Basidiomycota	DL, WD
Phallus sp.1	Phallaceae	Basidiomycota	DL, WD, S
Phallus sp.2	Phallaceae	Basidiomycota	DL, WD, S
Phallus sp.3	Phallaceae	Basidiomycota	DL, WD, S
Phallus subtilis (Möller) Lloyd	Phallaceae	Basidiomycota	DL, WD, S
Phalus vulgaris Micheli	Phallaceae	Basidiomycota	DL, WD, S
Phillipsia domingensis Berk.	Sarcoscyphaceae	Ascomycota	WD
Phillipsia subpurpurea Berk. & Broome	Sarcoscyphaceae	Ascomycota	WD
Picnoporus sp.1	Polyporaceae	Basidiomycota	WD, W
Picnoporus sp.2	Polyporaceae	Basidiomycota	WD, W
Pycnoporus cinnabarinus (Jacq.) P.Karst.	Polyporaceae	Basidiomycota	WD, W
Pycnoporus sanguineus (L.) Murrill	Polyporaceae	Basidiomycota	WD, W
Pleurotus sp.1	Pleurotaceae	Basidiomycota	WD
Pleurotus sp.2	Pleurotaceae	Basidiomycota	WD
Pleurotus niger	Pleurotaceae	Basidiomycota	WD
Pleurotus ornatus (Fr.) Sacc.	Tricholomataceae	Basidiomycota	WD

Pleurotus ostreatus (Jacq. ex Fr.) P.Kumm.	Pleurotaceae	Basidiomycota	WD
Polyporus sp.1	Polyporaceae	Basidiomycota	WD, W
Polyporus sp.2	Polyporaceae	Basidiomycota	WD, W
Polyporus abietinus (Dicks.) Fr.	Polyporaceae	Basidiomycota	WD, W
Polyporus abruptus	Polyporaceae	Basidiomycota	WD, W
Polyporus acutus	Polyporaceae	Basidiomycota	WD, W
Polyporus angulatus Schumach.	Polyporaceae	Basidiomycota	WD, W
Polyporus squamosus	Polyporaceae	Basidiomycota	WD, W
Poromycena sp.	Mycenaceae	Basidiomycota	WD
Psilocybe coprophila (Bull.) P.Kumm.	Hymenogastraceae	Basidiomycota	D
Ramaria sp.1	Gomphaceae	Basidiomycota	DL, WD
Ramaria sp.2	Gomphaceae	Basidiomycota	DL, WD
Russula sp.1	Russulaceae	Basidiomycota	DL,S
Russula sp.2	Russulaceae	Basidiomycota	DL,S
Russula sp.3	Russulaceae	Basidiomycota	DL,S
Russula acris Steinhaus	Russulaceae	Basidiomycota	DL,S
Russula admirabilis Beardslee & Burl.	Russulaceae	Basidiomycota	DL,S
Russula aeruginosa	Russulaceae	Basidiomycota	DL,S
Russula albonigra (Krombh.) Fr.	Russulaceae	Basidiomycota	DL,S
Russula alutacea (Pers.) Fr.	Russulaceae	Basidiomycota	DL,S
Russula amoenicolor Romagn.	Russulaceae	Basidiomycota	DL,S
Russula annulata	Russulaceae	Basidiomycota	DL,S
Russula campinensis	Russulaceae	Basidiomycota	DL,S
Schizophyllum sp.1	Schizophyllaceae	Basidiomycota	WD
Schizophyllum sp.2	Schizophyllaceae	Basidiomycota	WD
Schizophyllum commune Fries	Schizophyllaceae	Basidiomycota	WD
Stereum ostrea (Blume & T. Nees ex Fr.	Stereaceae	Basidiomycota	WD,W
Termitomyces sp.	Lyophyllaceae	Basidiomycota	DL,S
Termitomyces clypeatus R.Heim	Lyophyllaceae	Basidiomycota	DL,S
Termitomyces eurrhizus (Berk.) R. Heim	Lyophyllaceae	Basidiomycota	DL,S
Trametes sp.1	Polyporaceae	Basidiomycota	WD,W
Trametes sp.2	Polyporaceae	Basidiomycota	WD,W
Trametes sp.3	Polyporaceae	Basidiomycota	WD,W
Trametes elegans (Spreng.:Fr.) Fr.	Polyporaceae	Basidiomycota	WD,W
Trametes gibbosa (Pers.) Fr.	Polyporaceae	Basidiomycota	WD,W
Trametes versicolor (L.) Lloyd	Polyporaceae	Basidiomycota	WD,W
Tremella mesenterica Retz.	Tremellaceae	Basidiomycota	WD
Trogia infundibuliformis	Marasmiaceae	Basidiomycota	WD
Vanromburghia silvetris Holterm.	Marasmiaceae	Basidiomycota	WD
Xylaria sp.1	Xylariaceae	Ascomycota	WD
Xylaria sp.2	Xylariaceae	Ascomycota	WD
Xylaria sp.3	Xylariaceae	Ascomycota	WD
Xylaria nigripes	Xylariaceae	Ascomycota	WD

Ethnomycology

The results of interview and discussion with the residents in the buffer zone of the national park showed that they were familiar with macrofungus that they used for food and medicinal purposes. They harvested fungal bodies that were found in the parking area or their yard. These were then sold to traditional markets to add cash incomes. Residents called small-sized fungi as “Tangidi” or “Tanggojo,” two names that appear popular among the ethnic Kaili-Da’a tribe or in the Lore tribe in the buffer zones of the national park. The macrofungus *Schyzophyllum commune* was known by the residents of Kaili as a food source because it has a good substrate to grow on, and is easier to collect and find, especially in the rainy season. These types of fungi have more diverse substrates to grow on, and frequently grow in rotten-wood of fallen trees, such as candlenut trunk (*Aleurites moluccana*), Pine (*Pinus merkusii*), Gamal (*Gliricidia sepium*), Bayan tree (*Ficus* sp), Mango (*Mangifera* spp), Java wood (*Lannea coromandelica*), Cassava (*Manihot esculenta*), River tamarind/Lamtoro (*Leucaena leucocephala*), Peacock plum/Sengon (*Paraserianthes falcataria* L. Nielsen), Milkwood-pine/Pulai (*Alstonia* sp), Siamese cassia/Johar (*Senna siamea*), Areng palm (*Arenga pinnata*), Teak (*Tectona grandis* L), Coconut (*Cocos nucifera*), Gebang palm (*Corypha* sp), *Macaranga* sp., etc. The macro fungus *Lentinus sajor-caju* was also found in some rotten-wood from the Burflower-tree/Jabon (*Anthocephalus cadamba*), Mango (*Mangifera* spp), Bayan tree (*Ficus* sp) and others. *Phallus* sp., which appears in the rainy season, is often believed by residents to be spiritual/ghost-related, representing a “male-ghost” because the trunk of the fungus is similar in shape to that of a human penis, and they strongly produce a bad-odor. Residents commonly called it “Lasu Mboa” (Lasu= penis, Mboa= ghost). The naming of macrofungus by residents is often influenced by the growth place of the fungi. Fungi found in rotten mango trunks, for example, are given the name “Tanggidi/Tanggojo Taipa” (Tanggidi/Tanggojo= fungus, Taipa= mango).

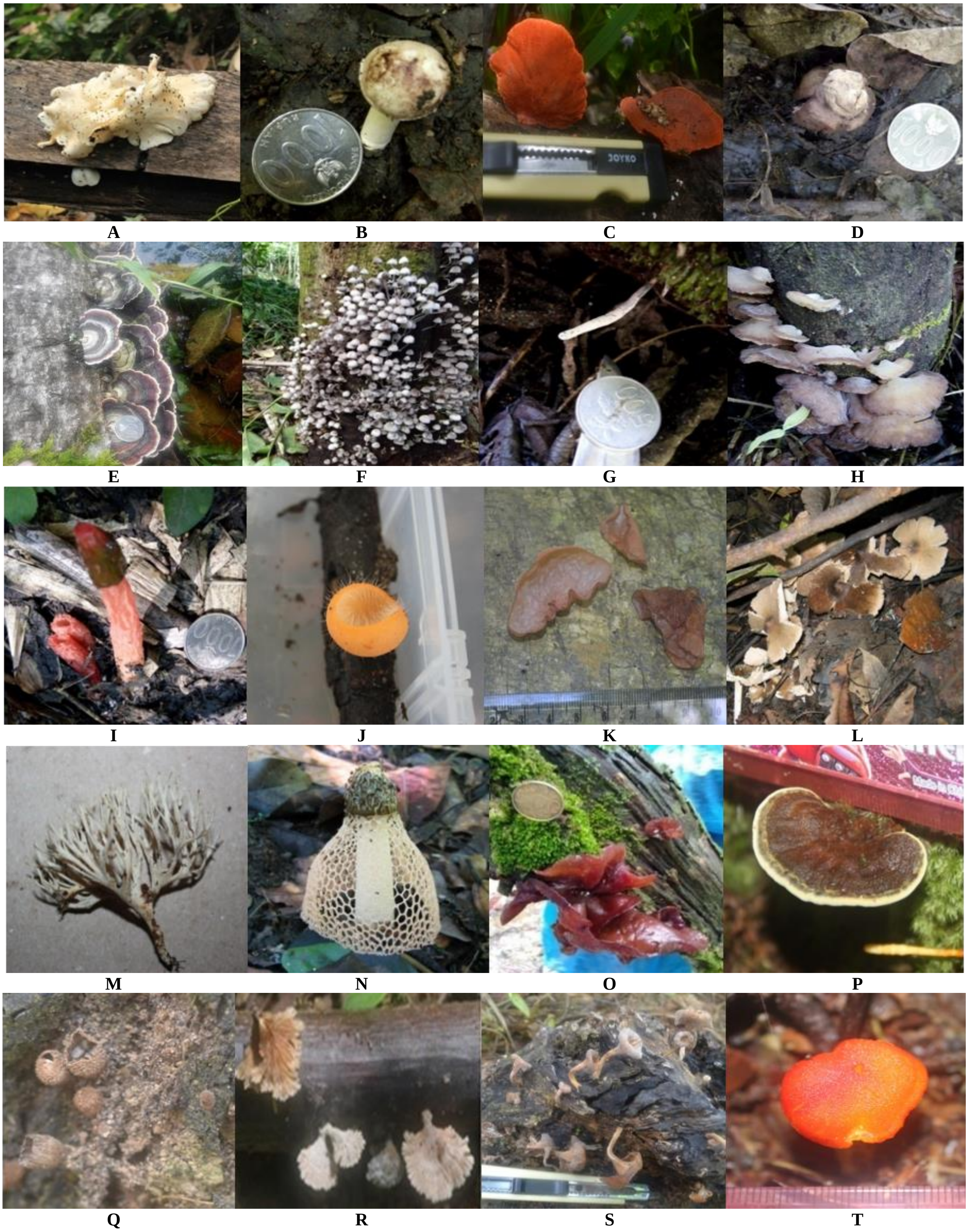

Figure 5. A. *Pleurotus ostreatus* (Jacq. ex Fr.) P.Kumm., B. *Lycoperdon* sp., C. *Picnoporus* sp., D. *Geastrum* sp., E. *Trametes versicolor* (L.) Lloyd, F. *Marasmius* sp., G. *Xylaria* sp., H. *Pleurotus* sp.1., I. *Phallus* sp., J. *Cookeina tricholoma* (Mont.) Kuntze., K. *Auricularia auricula-judae* (Bull.) Quél., L. *Termytomyces* sp., M. *Ramaria* sp., N. *Dictyophora indusiata* Vent., O. *Auricularia* sp.1, P. *Ganoderma lucidum* Kars, Q. *Cyathus* sp., R. *Schizophyllum commune* Fries., S. *Lentinus sajor-caju* (Fr.) Fr., T. *Hygrocybe* sp.

The common name of the large-sized macro fungus is “Tambata,” and has been given to members of the genera *Pleurotus* sp, *Lentinus sarjo-caju*, and *Auricularia* sp. These results show the same naming trends as found by Teke et al. (2018) in the Northeast Region of Cameroon, where the residents gave names to fungi based on their growth substrates.

The major reason why residents use these fungi was that the edible part of the fungus is highly palatable. They also believed that once they consumed the fungus, their digestive system is smoother than usual, and they simultaneously fulfill their nutrient needs. However, those statements still need further experimental analysis. Still, from the interviews, residents were also familiar with some toxic fungus types. According to the residents, the features of toxic fungus are a brightly colored trunk that is not predated by insects (such as ants, termites, grasshopper, and beetles) or rodents (such as mouse and squirrels). In contrast, if the fruit body of the fungus is a white color, or tends to dark, and is visited by sticks insects, or other animals, they believed that the fungus is safe to consume. Similar indicators were reported by Teke et al. (2018) who describe that the “Killum-Ijim,” in Northwest region of Cameroon, have different methods to determine whether the fungus could be eaten or not. Local knowledge that leads residents to distinguish the type of fungus is usually passed down between generations.

We found nine macrofungus species that are often used as source of food and medicine by the residents, such as *Schizophyllum commune, Termytomyces* sp, *Auricularia auricular-judae*, *Auricularia* sp, *Pleurotus ostreatus, Ganoderma lucidum, Xylaria* sp, *Lentinus sajor-caju,* and *Agaricus* sp. A similar exploration was done by Khastini et al. (2018), who found six species of macrofungus that were used as medicines by the Baduy tribe in Banten Province, Indonesia. Also, Rosemary-Kinge et al. (2017) found eight species of fungus that were also used as medicine and food sources by the residents of the Awing Wildlife Sanctuary in Cameroon. Another report found that 14 species of macrofungus were used as medicinal and food sources in Central Luzon, Philippines (De Leon et al. 2012), while 36 species were also used by the residents in Nueva Ecija, Philippines (De Leon et al. 2016). Traditional medicine plays an important role in the lives of the residents of the Kaili Tribe. They often use the macrofungus as a medicine source in first aid kits, and if the problem is still not solved, they prefer to go to a shaman (in Kaili language= Sando), who can usually be found in each village. Pictures of the documented macrofungus are shown in Figure 5.

In conclusion, we found 172 species (including unidentified species) of macrofungus in the Lore Lindu National Park area. Twenty-four species of the family Polyporaceae were found, making it the most abundant family. *Marasmius* spp. and *Hygrocybe* spp. were the most abundant genera. Species diversity of macrofungus increased alongside the increase in altitude of the sampling locations. Furthermore, we found nine species of macrofungus that were intensively used as food and medicinal sources by the local residents. The results of this study can serve as basic data of macrofungus diversity in the area to complement the existing biodiversity data. The information can be used as reference for the management of Lore Lindu National Park in the future. Nonetheless, future research on the topics of domestication of edible and medicinal fungus found in this study, especially regarding commercialization, are still required.

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