Studies in Fungi 2 (1): 47–58 (2017) www.studiesinfungi.org ISSN 2465-4973
Article

Doi 10.5943/sif/2/1/6

Macro-fungal diversity in the Kilum-Ijim forest, Cameroon

Teke NA[1], Kinge TR[2*], Bechem E[1], Mih AM[1], Kyalo M[3] and Stomeo F[3]

[1]Department of Botany and Plant Physiology, Faculty of Science, University of Buea, P.O. Box 63, South West Region, Cameroon
[2]Department of Biological Sciences, Faculty of Science, The University of Bamenda, P.O. Box 39, Bambili, North West Region, Cameroon
[3]Bioscience eastern and central Africa-International Livestock Research Institute (BecA-ILRI) Hub, P.O Box 30709-00100, Nairobi, Kenya

Teke NA, Kinge TR, Bechem E, Mih AM, Kyalo M, Stomeo F 2017 – Macro-fungal diversity in the Kilum-Ijim forest, Cameroon. Studies in Fungi 2(1), 47–58, Doi 10.5943/sif/2/1/6

Abstract

Fungi are one of the most species-rich and diverse groups of organisms on Earth, with forests ecosystems being the main habitats for macro-fungi. The Kilum-Ijim forest in Cameroon is a community forest populated by several species of plant and animal life forms; although macro-fungi are exploited for food and medicine, their diversity has not been documented in this ecosystem. Since anthropogenic impact on this forest may cause decline of macro-fungal diversity or extinction of known and previously undiscovered species, it is imperative to generate a checklist of the existing macro-fungi for use in the implementation of sustainable conservation and management practices. This study was therefore carried out to generate information on macro-fungal diversity in this forest. During a field study carried out between 2013 and 2015, 206 macro-fungi samples were collected and molecularly identified using the ribosomal ITS1, 5.8S and ITS2 regions. Sequence data analysis revealed that majority of the fungal isolates (87.93%) belonged to phylum Basidiomycota while 12.07% belonged to Ascomycota. Among the fungal genera detected, 18 are new records for Cameroon. This work represents the first comprehensive record of macro-fungi in Kilum-Ijim forest in Cameroon.

Key words – Checklist – DNA barcoding – Kilum-Ijim – Mushrooms

Introduction

Macro-fungi include fungi distinguished by having fruiting bodies visible to the unaided eye commonly referred to as mushrooms (O'Dell et al. 2004). The majority of macro-fungi occurring in nature are members of Basidiomycota, while some others belong to Ascomycota. Macro-fungi like mushrooms, puffballs and bracket fungi, have several ecological functions in both natural and agro-ecosystems, and are widely exploited by humans for food and medicine (Boa 2004, Gates et al. 2011, Mueller et al. 2007, Osemwegie et al. 2006). Most terrestrial macro-fungi are saprobes and mycorrhizal symbionts; playing essential roles in decomposition and nutrient cycling, while a few are parasitic on woody substrata (Mueller et al. 2007). Mycorrhizal macro-fungi form symbiotic

Submitted 5 February 2017, Accepted 11 March 2017, Published 29 March 2017

Corresponding Author: Kinge, T. R. – e-mail – rosemary32us@yahoo.com

associations with roots of higher plants, facilitating uptake of phosphorus and nitrogen (Gates 2009). Macro-fungi also play vital roles in bio-degradation and bio-deterioration (Tibuhwa 2011) and are thus important ecosystem engineers. They are one of the richest and most diverse groups of organisms on earth (Seen-Irlet et al. 2007). Wild edible mushrooms are of high socio-economic importance in both developing and developed countries. In Cameroon, edible and medicinal mushrooms are ubiquitous and constitute a substantial volume of internal trade especially by women in rural areas (Kinge et al. 2014). Despite their importance, information on their diversity is scanty, especially in Africa (Xu & Cai 2015, Osarenkhoe et al. 2014). Only about 6.7% of the one million species of fungi estimated in the world are currently described and these are mostly in temperate regions. The tropical region with the highest fungal diversity has not been fully exploited (Hawksworth 2001). Although there are studies of macro-fungi in the domains of systematics, ecology, conservation, ethno-mycological surveys, nutritional studies and cultivation in Cameroon, just about 5% of the total tropical forest zone of 394.700km^2 has been studied (Kinge et al. 2014). Macro-fungi identification has in the past been based mainly on comparative morphology. In Cameroon, few studies on macro-fungal identification have been carried out and most of these studies have been based on the use of their macro- and micro-morphological and physiological characteristics (Douanla-Meli 2007, Kinge et al. 2013). Often, this is a tedious, ambiguous, and time consuming method as many diverse fungi may have similar characteristics (Lian et al. 2008). Information on macro-fungi identification using molecular tools in Cameroon is highly limited, with no published work on the macro-fungi of the Kilum-Ijim forest. Identification using molecular biology techniques provides quick and efficient methods (Fonseca et al. 2008) and is currently used in macro-fungi taxonomy. Many different gene sequences have been used as the basis for fungal molecular-based identification, including ribosomal RNA (rRNA). Internal Transcribed Spacer regions of rRNA genes are typically variable and as a result, useful for classification (Begerow et al. 2010). Recently, the ITS region was selected as the universal genetic barcode for fungi (Schoch et al. 2012). The main objective of this study was to identify macro-fungi using molecular techniques in order to produce a checklist of macro-fungi inhabiting the Kilum-Ijim forest. This is expected to provide information on edible and medicinal macro-fungi not yet adequately exploited, and may also provide direction towards domestication, conservation and commercialization of the wild species, for economic benefits, besides aiding molecular taxonomy. This is because the fungi are presently threatened by habitat degradation, climatic changes and anthropogenic activities.

Materials & Methods

Study site, sample collection and preparation

The Kilum-Ijim forest is located between latitudes 6°07′ N and 6°17′ N and longitudes 10°20′ E and 10°35′ E, covering an area of about 20,000 ha in the Northwest Region of Cameroon (Fig. 1).

Sample collection and preparation

Five field surveys were conducted in the Kilum-Ijim forest from November 2013 to October 2015 during the beginning, middle and end of fructification time of different morphological types of macrofungi. A total of 206 samples of macrofungi were collected from their natural habitat. The fungi were labeled and immediately preserved after collection in aluminum foil and later dried in an open oven at 45–55ºC for 2–3 days. The dried samples were preserved using Silica gel in zip-lock bags pending molecular identification while duplicates were deposited at the University of Buea herbarium.

DNA Extraction and PCR amplification

Total DNA was extracted from powdered samples using the DNeasy® Plant Mini Kit (QIAGEN® Group) as per the manufacturer's protocol with minor modifications. The samples were ground in a geno-grinder at 1X rate (500strokes/minute) for 4 minutes using liquid nitrogen and glass beads to

obtain a powder. Hard samples were ground manually with a mortar and pestle in liquid nitrogen. 400µL of buffer AP1 and 4µL of RNase were added into each tube, vortexed and incubated for 15 mins at 65ºC. Tubes were inverted 2–3 times during incubation. 130µL of buffer P3 was added and incubated on ice for 5 mins. Samples were subsequently centrifuged for 5mins at 20,000 × g. The lysate was pipetted into QIA shredder spin column placed in 2mL collection tube and centrifuged for 2mins at 20,000 × g. The flow through was transferred into new collection tubes without disturbing any pellet present. 1.5 volumes of buffer AW1 was added into each tube and mixed by pipetting. The mixture was then transferred into DNeasy Mini spin column placed in 2ml tube and centrifuged for 1min at 20,000 × g. Spin columns were removed and placed into new 2mL collection tubes. 750µL of AW2 buffer was added into the tubes and centrifuged for 1min at 20,000 × g. The flow through was discarded. The spin columns were again centrifuged for 1min at 20,000 × g to remove any residual ethanol from the column. The spin column was then transferred into 1.5 eppendorf tube. 50µL of pre-warmed distilled water was pipetted into the spin column, incubated for 2mins at room temperature and centrifuged for 1min at 20,000 × g to elute DNA. DNA concentration and purity were determined by NanoDrop spectrophotometer (Thermo Scientific NanoDrop 2000) at absorbance (A260/280). The quality of DNA was visualized on a 0.8% agarose gel run at 7 V/cm for 45 mins.

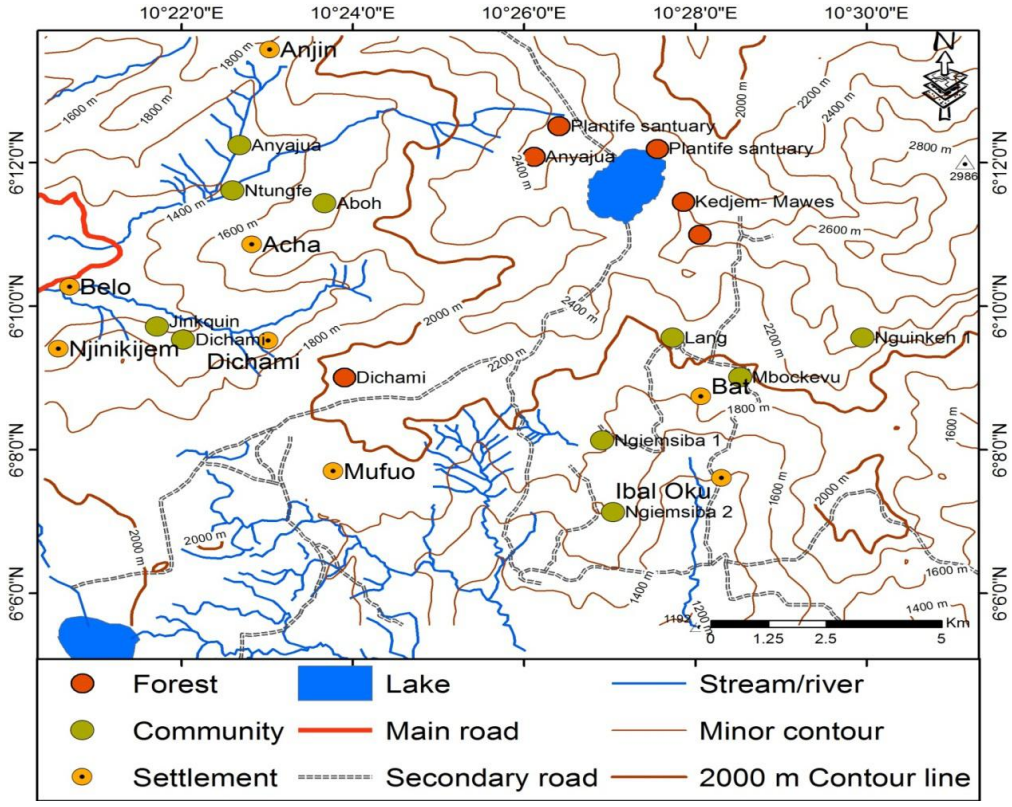

Fig. 1 – Location of Kilum-Ijim forest in north western Cameroon (Courtesy: Che Vivian, University of Buea). It is found on Mount Oku with Lake Oku lying in a crater in its center (Fomété et al. 2001).

Amplification of the ITS1, 5.8S and ITS2 regions for assessing ITS length variation was done using primer ITS1F (5'-TCCGTAGGTGAACCTGCGG-3') (Gardes & Bruns 1993) and ITS4 (5'-TCCTCCGCTTATTGATATGC-3') (White et al. 1990). PCR amplification was done using AccuPower® Taq PCR premix (Bioneer, www.bioneer.com.) in a 20 µL reaction volume containing containing 50 ng template DNA, 0.18µM of each primer and 15.1µL Milli-Q water was added. The thermocycler settings were as follows: denaturation at 95ºC for 3 minutes; 35 cycles of denaturing at

94ºC for 30 seconds, annealing at 55ºC for 30 seconds, and extension at 72ºC for 1minute; and a final extension at 72ºC for 10 minutes. 2µL of each PCR product were electrophoretically separated on a 2% agarose gel prepared in 0.5X TAE to check the purity of the PCR product. The gel was run at 7 V/cm for 45 mins. DNA staining was done with 0.025X GelRed and photographed under UV exposure.

Sequence analysis

The PCR products were then purified using QIAGEN® purification kit following the manufacturer's instructions. The purified PCR products were sent to Macrogen (Netherlands) for Sanger sequencing. Related gene sequences for each of the macrofungal specimen were obtained from NCBI GenBank using UNITE ITS Database and then, automatically aligned using CLC Main Workbench. Multiple sequence alignments were then performed in MEGA6 (Tamura et al. 2013) to allow maximum sequence similarity.

Results

DNA was successfully extracted and the ITS region amplified for all 206 samples, using the ITS1F and ITS4 primer pair. The sizes of this region were between 600–800 bp, which corresponded to the expected rDNA target region.

After blast search using available sequences in the GenBank, it was observed that the identified species belonged to two main phyla; Basidiomycota (87.93%) and Ascomycota (12.07%). The macro-fungi were grouped into seven classes namely; Ascomycetes, Leotiomycetes, Pezizomycetes and Sordariomycetes for phylum Ascomycota and Agaricomycetes, Basidiomycetes and Dacrymycetes for phylum Basidiomycota. Of the 116 species (Table 1), 95 (82%) were Agaricomycetes, while the Ascomycetes, Pezizomycetes and Dacrymycetes were least represented with 1% each (Fig 2).

The identified species belonged to 15 orders, 36 families, 71 genera and 116 unique species. The Agaricales and Polyporales recorded the highest number of species representing 57% and 18%, respectively (Fig. 3).

The most frequent families were the Polyporaceae with 14 species, while Agaricaceae and Psathyrellaceae were represented with 13and 11 species respectively (Fig. 4).

There were a total of 71 genera (Table 1), with 18 of them being first records for Cameroon. These included *Abortiporus, Callistosporium, Coprinellus, Coprinopsis, Codyceps, Cystolepiota, Chlorociboria, Crinipellis, Clathrus, Galerina, Laetiporus, Melanoleuca, Panaeolus, Parasola, Podosordaria, Physisporinus, Skeletocutis* and *Tubaria*.

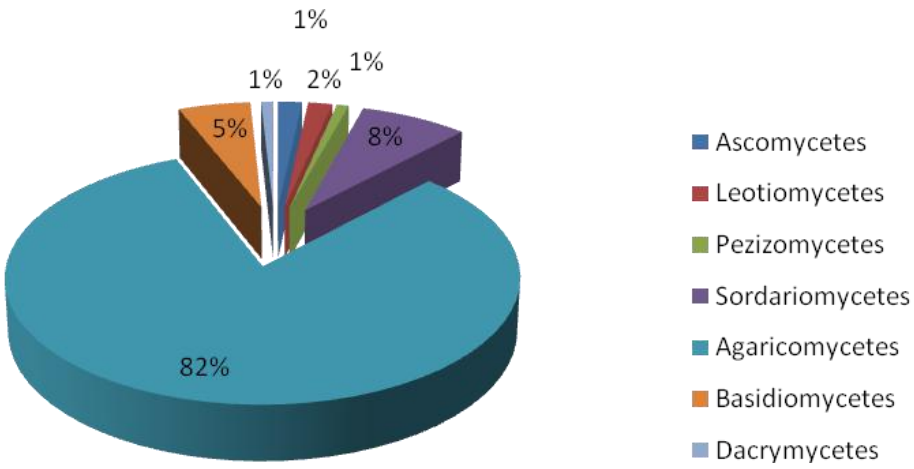

Fig. 2 – Distribution of macro-fungal classes in the Kilum-Ijim forest, north western Cameroon.

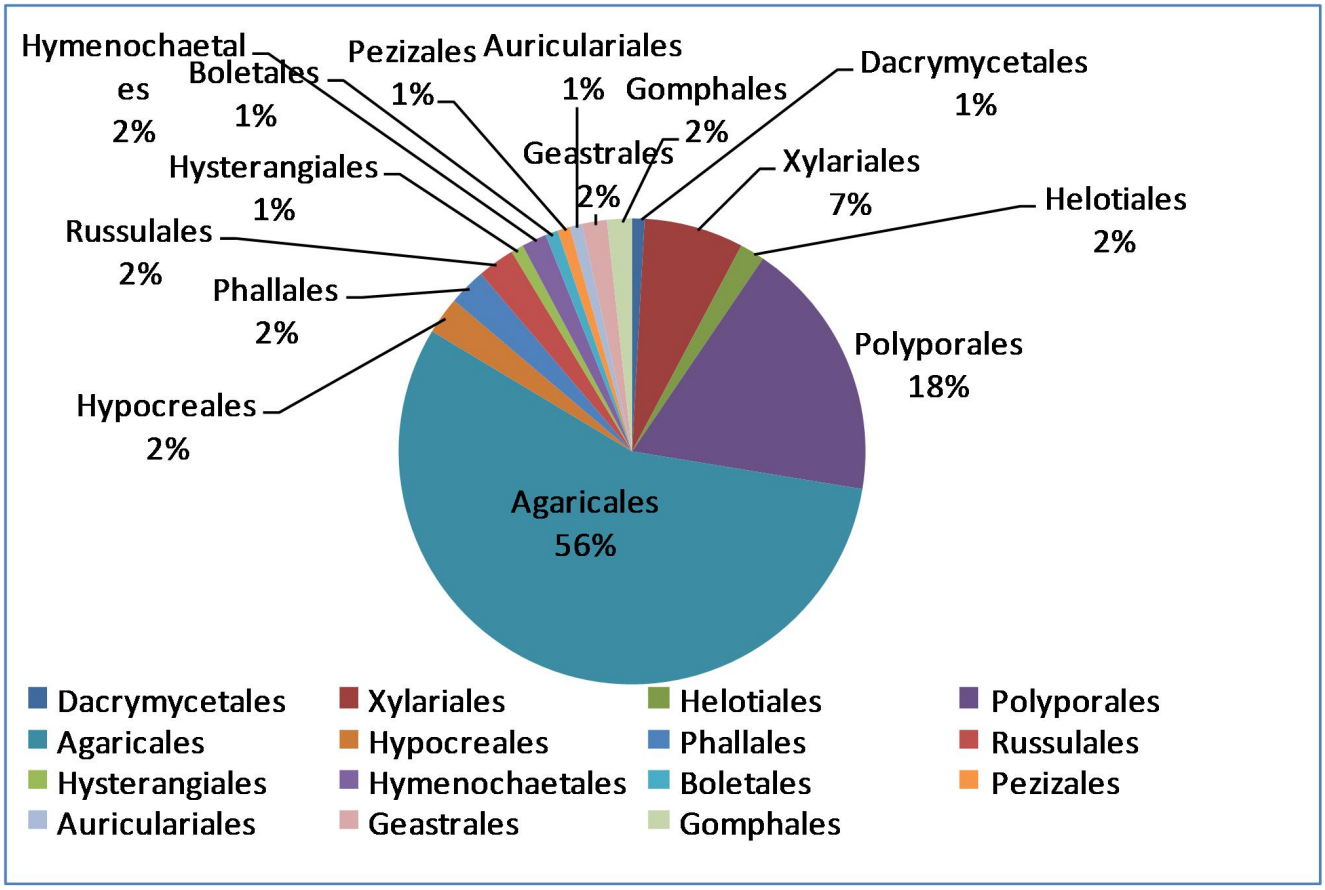

Fig. 3 – Orders of macro-fungi found at the Kilum-Ijim forest in north western Cameroon.

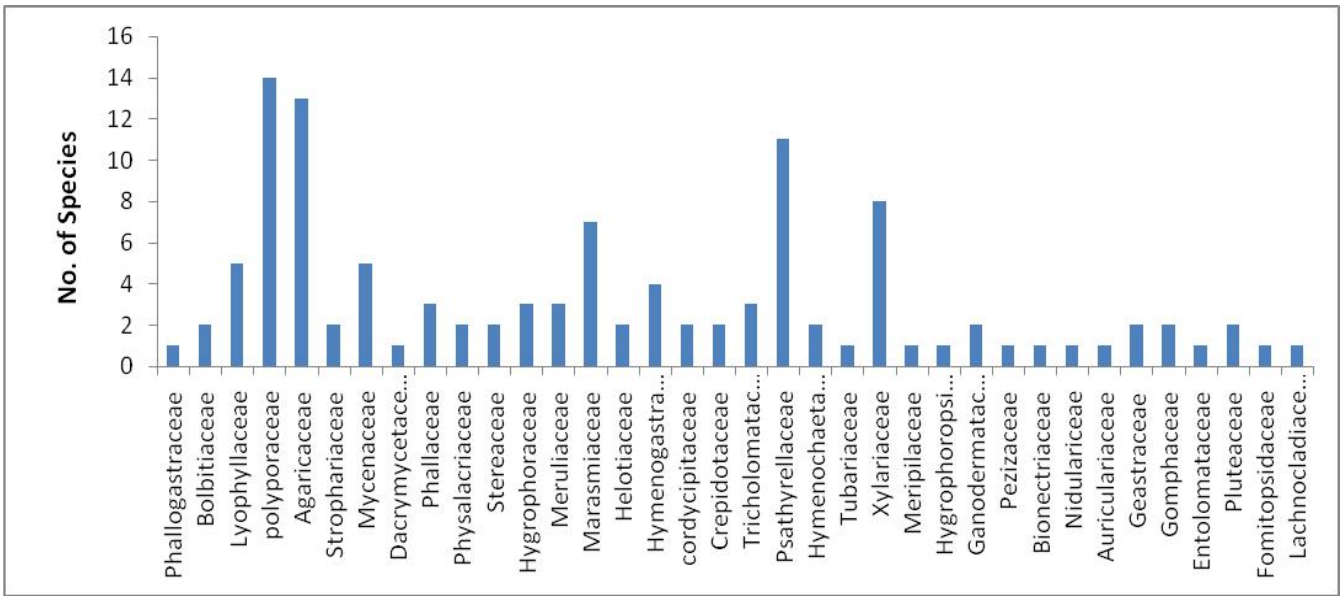

Fig. 4 – Number of species of different macro-fungal families in Kilum-Ijim forest north western Cameroon.

Table 1 Checklist of macro-fungi identified at Kilum-Ijim forest, north western Cameroon.

S/N	Species	Accession No.	Frequency
	AGARICALES		
	Agaricaceae		
1	*Agaricus litoralis* (Wakef. & A. Pearson) Pilat.	JN204436	1
2	*Agaricus xanthodermus* Genev. (1876)	EU326208	1
3	*Cystolepiota hetieri* (Boud.) Singer	AY176459	1
4	*Lepiota* sp PA620 (Pers.) Gray (1821)	EF527355	1
5	*Leucoagaricus cupresseus* (Burl.) Boisselet & Guinb.	GU139787	1
6	*Leucoagaricus flavovirens* J.F. Liang, Zhu L. Yang & J. Xu	EU416295	1
7	*Leucoagaricus gaillardii* Bon & Boiffard 1974	GQ329042	1
8	*Leucoagaricus littoralis* (Menier) Bon & Boiffard 1970	GQ329041	2
9	*Leucoagaricus rubrotinctus* (Peck) Singer (1948)	JN944081	1
10	*Leucoagaricus serenus* (Fr.) Bon & Boiffard 1974	AY176420	1
11	*Leucoagaricus viriditinctus* (Berk. & Broome) J.F.	EU419375	1
12	*Macrolepiota dolichaula* (Berk. & Broome) Pegler & R.W. Rayner	JQ683120	2
13	*Vascellum pretense* (Pers.) Kreise	FJ481033	3
	Bolbitiaceae		
14	*Panaeolus foenisecii* (Pers.) R.Maire (1933).	JF908520	2
15	*Panaeolus sphinctrinus* (Fr.) Quél.	JF908513	1
	Crepidotaceae		
16	*Crepidotus epibryus* (Fr.) Quél. 1888	HM240524	1
17	*Crepidotus mollis* (Schaeff.) Staude 1857	JF907959	1
	Entolomataceae		
18	*Entoloma araneosum* (Quél.) M.M. Moser.	EU784204	1
	Hygrophoraceae		
19	*Camarophyllus pratensis* (Pers.) P. Kumm.	FJ596880	1
20	*Hygrocybe helobia* (Arnolds) Bon	JF908056	1
21	*Hygrocybe persistens* (Britzelmayr) Singer	FM208893	1
	Hymenogastraceae		
22	*Galerina badipes*(Pers.) Kühner	JF908012	1
23	*Galerina hybrid* Kühner.	AJ585445	1
24	*Galerina marginata* (Batsch) Kühner (1935)	AF501564	1
25	*Psilocybe cubensis* (Earle) Singer	HM035082	2
	Lyophyllaceae		
26	*Lyophyllum connatum* P.Karst.	JF908332	1
27	*Termitomyces microcarpus* (Berk. & Broome) R.Heim	AF357023	1
28	*Termitomyces striatus* (Beeli) R.Heim	AF321367	4
29	*Termitomyces* sp V1P R.Heim	JF302830	2
30	*Termitomyces* sp Group8 R.Heim	AB073529	5
	Marasmiaceae		
31	*Clitocybula lacerata* (Scop.) Singer ex Métrod	FJ596916	2
32	*Clitocybula oculus* (Peck) Singer 1962	DQ192178	5
33	*Crinipellis scabella* (Alb. & Schwein.) Murrill	JF907969	2

Table 1 (Continued)

S/N	Species	Accession No.	Frequency
34	*Hydropus marginellus* (Pers. : Fr.) Singer 1948	EU669314	1
35	*Marasmius purpureostriatus* Hongo 1958	FJ904978	2
36	*Marasmiellus ramealis* (Bull.) Singer	JF313670	5
37	*Marasmius rotula* (Scop.) Fr.	JN714927	5
	Mycenaceae		
38	*Favolaschia calocera* R. Heim	EU489640	6
39	*Mycena acicula* (Schaeff.) P.Kumm. (1871)	JF908384	1
40	*Mycena laevigata* (Lasch) Gillet	JF908397	1
41	*Mycena pura* (Pers.) P. Kumm.	EU517506	3
42	*Panellus stipticus* (BµLl.) P.Karst. (1879)	FJ481038	1
	NidµLariaceae		
43	*Cyathus stercoreus* (Schwein.) De Toni (1888)	FJ478125	1
	Physalacriaceae		
44	*Flammulina mexicana* Redhead, Estrada & R.H. Petersen	AF032129	1
45	*Oudemansiella canarii* (Jungh.) Höhn. (1909)	AY216473	2
	Pluteaceae		
47	*Pluteus romellii* (Britzelm.) Sacc 1895.	HM562078	1
48	*Volvariella volvacea* (Bul. ex Fr.) Singer (1951)	HM246500	1
	Psathyrellaceae		
49	*Coprinus fissolanatus* Park,D.S., Shin,H.S. and Moncalvo,J.M.	AF345812	2
50	*Coprinellus hiascens* (Fr.) Redhead, Vilgalys & Moncalvo	JN159528	1
51	*Coprinellus micaceus* (Bull.:Fr.) Vilgalys, Hopple & Jacq. Johnson	JN943116	3
52	*Coprinus sterquilinus* (Fr.) Fr. 1838.	FJ501551	2
53	*Parasola auricoma* (Pat.) Redhead, Vilgalys & Hopple (2001).	JN943107	2
54	*Parasola conopila* (Fr.) Örstadius & E. Larss.	FJ770396	1
55	*Psathyrella bipellis* (Quél.) A.H.Sm. (1946)	FN430689	1
56	*Psathyrella candolleana* (Fr.) Maire (1937)	AB306311	1
57	*Psathyrella pyrotricha* (Holmsk.) M.M. Moser	FJ481046	1
58	*Psathyrella spadicea* (Schaeff.) Singer (1951)	FN396134	1
59	*Psathyrella vestita* (Peck) A.H. Smith	FN430693	1
	Strophariaceae		
60	*Hypholoma fasciculare* (Huds.:Fr.) P.Kumm. (1871).	FJ481034	3
61	*Pholiota* sp (Fr.) P.Kumm. (1871)	FJ596817	2
	Tricholomataceae		
62	*Callistosporium xanthophyllum* (Malençon & Bertault) Bon 1976.	JF907781	1
63	*Lepista irina* (Fr.) Bigelow 1959.	HM237136	2
64	*Melanoleuca pseudoluscina* (M. Bon) ex M. Bon 1980.	JN616457	2
	Tubariaceae		
65	*Tubaria serrulata* (Cleland) Bougher & Matheny	DQ182507	2
	AURICULARIALES		
	Auriculariaceae		

Table 1 (Continued)

S/N	Species	Accession No.	Frequency
66	*Auricularia polytricha* (Mont.) Sacc.	FJ792587	5
	BOLETALES		
	Hygrophoropsidaceae		
67	*Hygrophoropsis aurantiaca* (Wulfen) Maire	AJ419202	1
	DACRYMYCETALES		
	Dacrymycetaceae		
68	*Dacrymyces chrysospermus* Berk. & M.A. Curtis	AB712452	1
	GEASTRALES		
	Geastraceae		
69	*Geastrum minimum* Schwein	EU784238	1
70	*Geastrum triplex* Jungh.	JN942821	4
	GOMPHALES		
	Gomphaceae		
71	*Ramaria decurrens* (Pers.) R. H. Petersen	AJ408375	1
72	*Ramaria rubribrunnescens* Fr. ex Bonord.	EU652351	1
	HELOTIALES		
	Helotiaceae		
73	*Chlorociboria aeruginascens* (Nyl.) Kanouse	JN943460	2
74	*Chlorociboria awakinoana* P.R.Johnst.	JN943462	1
	HYMENOCHAETALES		
	Hymenochaetaceae		
75	*Phellinus repandus* Quél.	AF534076	1
76	*Fuscoporia gilva* (Schwein.) T. Wagner & M. Fisch.	AM269795	1
	HYPOCREALES		
	Bionectriaceae		
77	*Bionectria ochroleuca* (Schwein.) Schroers & Samuels	GU566253	1
	Cordycipitaceae		
78	*Cordyceps brongniartii* (Saccardo) Petch	AJ309349	1
79	*Cordyceps takaomontana* Fr. (1818)	AB189447	1
	HYSTERANGIALES		
	Phallogastraceae		
80	*Protubera canescens* G.W.Beaton & Malajczuk (1986)	GQ981520	1
	PEZIZALES		
	Pezizaceae		
81	*Peziza ostracoderma* Dill. ex Fries (1822)	JN002180	1
	PHALLALES		
	Phallaceae		
82	*Clathrus archeri* (Berk.) Dring 1980".	KP688386	1
83	*Clathrus ruber* P.Micheli ex Pers. (1801)	GQ981501	2
84	*Phallus impudicus* Linnaeus (1753)	AF324171	1
	POLYPORALES		
	Fomitopsidaceae		
85	*Fomitopsis cajanderi* (P.Karst.) Kotl. & Pouzar (1957)	JQ673050	1
	Ganodermataceae		
86	*Ganoderma applanatum* (Pers.) Pat.	AJ608709	1

Table 1 (Continued)

S/N	Species	Accession No.	Frequency
87	*Ganoderma pfeifferi* Bres.	AM906059	1
	Meripilaceae		
88	*Physisporinus vitreus* (Pers.) P.Karst. (1889)	JN182920	1
	Meruliaceae		
89	*Abortiporus biennis* (Schwein.) Murrill (1944)	FJ608589	1
90	*Panus* sp Fr. (1838)	HM245784	1
91	*Podoscypha petalodes* (Berk.) Boidin	AM773629	5
	Polyporaceae		
92	*Coriolopsis sanguinaria*(Klotzsch) Teng 1963	FJ627251	1
93	*Daedaleopsis confragosa* (Bolton) J.Schröt. (1888).	FJ810177	2
94	*Laetiporus sulphureus* (Bull.) Murrill (1920)	AY835667	1
95	*Lentinus squarrosulus* Mont. 1842.	GU001951	6
96	*Lenzites elegans*(Spreng.) Pat.	HQ248217	1
97	*Microporus subaffinis* (Lloyd) Imazeki 1943.	FJ627249	3
98	*Polyporus arcularius* (Batsch) Fr.	AB638344	3
99	*Polyporus dictyopus* Mont. 1835.	AF516561	9
100	*Polyporus tenuiculus* (Beauv.) Fr.	JQ409357	6
101	*Skeletocutis nivea* (Jungh.) Keller.	JQ673120	1
102	*Trametes hirsute* (Wulfen) Pilát	JN164952	2
103	*Trametes polyzona* (Pers.) Corner	JN164980	1
104	*Trametes sanguinea* (L.) Imazeki	JN164981	1
105	*Trametes versicolor* (L.) Lloyd (1920)	EU153514	1
	RUSSULALES		
	Lachnocladiaceae		
106	*Lachnocladium* sp Lév. (1846)	DQ192176	1
	Stereaceae		
107	*Stereum hirsutum* (Willd.) Pers. (1800).	AM269810	4
108	*Stereum sanguinolentum* (Alb. & Schwein.) Fr. (1838).	EU673084	1
	XYLARIALES		
	Xylariaceae		
109	*Daldinia concentrica* (Bolton) Cesati & de Notaris	AF163021	1
110	*Podosordaria muli* J.D. Rogers, Y.M. Ju & F. San Martín	GU324761	1
111	*Xylaria* sp MUCL 51605 Hill ex Schrank (1789)	FN689802	1
112	*Xylaria adscendens* (Fr.) Fr., 1851.	GU322432	1
113	*Xylaria bambusicola* Y.M. Ju & J.D. Rogers	GU300088	1
114	*Xylaria curta* Fries	GU322444	4
115	*Xylaria grammica* (Mont.) Mont.	AB524025	1
116	*Xylaria ianthinovelutina* (Mont.) Mont.	GU322441	1

Discussion

Fungi are diverse organisms playing essential roles in maintaining forest ecosystems and biodiversity (Hawksworth 1991, Molina et al. 2008). In Cameroon, mushrooms are one of the non-timber forest products which people in the rural areas depend on as their protein source and to improve on their livelihoods (Kinge et al. 2014). In spite of this, their diversity in most ecosystems is properly established. Studies in Cameroon by Kinge et al. (2013) and Douanla-Meli (2007) gave a checklist of

macro-fungi in Mount Cameroon region and Mbalmayo forest reserves, respectively. Identification of species was however mainly based on the use of macro and micro-morphological characters, which in most cases have their limitations in allowing a reliable distinction of intraspecific characteristics (Oyetayo 2014). This study made use of molecular techniques, which is the method of choice for fungal identification (Schoch 2012). The findings have revealed that majority of the species collected belong to the polyporaceae family, phylum Basidiomycota. This is in line with different studies carried out by Tadiosa et al. (2011), De Leon et al. (2013) and Rajput et al. (2015), who reported higher numbers of species belonging to Polyporaceae in the province of Aurora, Central Luzon, Philippines and Gujarat State India, respectively. These findings are probably justified by the fact that most wood inhabiting species are polypores. Results also show that the highest occurring and most frequent species belong to the genera *Favolaschia, Leucoagaricus, Marasmius, Polyporus, Lentinus, Podoscypha and Termitomyces.* Some genera like *Coprinus, Lepiota, Crepidotus, Ganoderma, Geastrum, Ramaria, Marasmius, Mycena, Polyporus, Trametes* and *Xylaria* have been reported in previous works in Cameroon by Kinge et al. (2013) and Douanla-Meli (2007). It is worth noting that genera like *Abortiporus, Callistosporium, Coprinellus, Coprinopsis, Cordyceps, Cystolepiota, Chlorociboria, Crinipellis, Clathrus, Galerina, Laetiporus, Melanoleuca, Panaeolus, Parasola, Podosordaria, Physisporinus, Skeletocutis* and *Tubaria* are all new records to the Cameroon macro-fungal literature. Continuous surveys of the fungal diversity in an area can provide valuable information on the effects of increased human activity and may be an adequate indicator of regional climate change, including global warming (Vitousek 1994, Frankland 1996). It is therefore imperative that the diversity of fungi in different ecosystems be documented so as to help in the development of better strategies for management and conservation of these ecosystems (Molina et al. 2008, Richard et al. 2004).

Acknowledgements

The authors gratefully acknowledge the Rufford Small Grant award and the BecA-ILRI Hub through the Africa Biosciences Challenge Fund (ABCF) program towards the realization of this work. The ABCF Program is funded by the Australian Department for Foreign Affairs and Trade (DFAT) through the BecA-CSIRO partnership; the Syngenta Foundation for Sustainable Agriculture (SFSA); the Bill & Melinda Gates Foundation (BMGF); the UK Department for International Development (DFID) and; the Swedish International Development Cooperation Agency (SIDA). Dr. Ndam Lawrence Monah is acknowledged for logistic and technical support during the field collection, and Dr. Che Vivian of the Remote Sensing Laboratory at the University of Buea for producing the map.

References

Begerow D, Nilsson H, Unterseher M, Maier W. 2010 – Current state and perspectives of fungal DNA barcoding and rapid identification procedures. Applied Microbiology and Biotechnology 87, 99–108.

Boa ER, 2004 – Wild edible Fungi: A Global perspective view of Their Use and Importance to People. FAO Publishing Management Services.

De Leon AM, Luangsa-ard JJD, Karunarathna SC, Hyde KD, Reyes RG, Dela Cruz TEE. 2013 – Species listing, distribution, and molecular identification of macrofungi in six Aeta tribal communities in Central Luzon, Philippines. Mycosphere 4, 478–494.

Douanla-Meli C. 2007 – Fungi of Cameroon: ecological diversity with emphasis on the taxonomy of non-gilled Hymenomycetes from the Mbalmayo Forest Reserves. Bibliotheca Mycologica 410.

Fomété T, Vermaat J, Gardner A, DeMarco J, Asanga C, Tekwe C, Percy F. 2001 – A Conservation Partnership: Community Forestry at Kilum-Ijim, Cameroon. Rural Development Forestry Network.

Fonseca GG, Gandra EA, Sclowitz LF, Correa APA, Costa JAV, Levy JA. 2008 – Oyster mushrooms species differentiation through molecular markers RAPD. International Journal of Plant Breeding and Genetics 2, 13–18.

Frankland JC, Magan N, Gadd GM. 1996 – Fungi and environmental change. (Symposium of the British Mycological Society held at Cranfield University, March 1994). Cambridge University.

Gardes M, Bruns TD. 1993 – ITS primers with enhanced specificity for basidiomycetes-application to the identification of mycorrhizae and rusts. Molecular Ecology 2, 113–118.

Gates GM. 2009 – Coarse woody debris, macrofungal assemblages, and sustainable forest management in a Eucalyptus oblique forest of southern Tasmania. University of Tasmania, Hobart, Tasmania.

Gates GM, Mohammed C, Wardlaw T, Ratkowsky DA, Davidson NJ. 2011 – The ecology and diversity of wood-inhabiting macrofungi in a native Eucalyptus obliqua forest of southern Tasmania, Australia. Fungal Ecology 4, 56–67.

Hawksworth DL. 1991 – The fungal dimension of biodiversity: magnitude, significance, and conservation. Mycological Research 95, 641–655.

Hawksworth DL. 2001 – The magnitude of fungal diversity: the 1.5 million species estimate revisited. Mycological Research 105, 1422–1432.

Kinge TR, Egbe EA, Tabi EM, Nji TM, Mih AM. 2013 – The first checklists of macrofungi of mount Cameroon. Mycosphere 4, 694–699.

Kinge TR, Nji TM, Ndam LM, Mih AM. 2014 – Mushroom research, production and marketing in Cameroon: A review. Biological Sciences and Pharmaceutical Research 2, 069–074.

Lian B, Zang JP, Hou WG, Yuan S, Smith DL. 2008 – PCR-based sensitive detection of the edible fungus *Boletus edulis* from rDNA ITS sequences. Electronic Journal of Biotechnology 11, 102–109.

Molina R, Pilz D, Smith J, Dunham S, Dreisbach T, O'Dell T, Castellano M. 2008 – Conservation and management of forest fungi in the Pacific Northwestern United States: an integrated ecosystem approach. In: Moore D, Nauta MM, Evans SE, Rotheroe M, eds. Fungal conservation: issues and solutions. Cambridge University Press.

Mueller GM, Schmit JP, Leacock PR, Buyck B, Cifuentes J, Desjardin DE, Halling R, Hjortstam K, Iturriaga T, Larsson KH, Lodge DJ, May TW, Minter DW, Rajchenberg M, Redhead SA, Ryvarden L, Trappe JM, Watling R, Wu W. 2007 – Global diversity and distribution of macrofungi. Biodiversity Conservation 16, 37–48.

O'Dell TE, Lodge DJ, Mueller GM. 2004 – Biodiversity of Fungi: Inventory and Monitoring Methods. Mueller, G. M., Bills, G. & Foster, M. S. (eds.). San Diego, CA: Elsevier Academic Press.

Osarenkhoe O, John O, Theophilus D. 2014 – Ethnomycological Conspectus of West African Mushrooms: An Awareness Document. Advances in Microbiology 4, 39–54.

Osemwegie OO, Eriyaremu EG, Abdulmalik J. 2006 – A survey of macrofungi in Edo/Delta region of Nigeria, their morphology and uses. Global Journal of Pure and Applied Science 12, 149–157.

Oyetayo VO. 2014 – Molecular Identification of *Trametes* Species Collected from Ondo and Oyo States, Nigeria. Jordan Journal of Biological Sciences 7, 165–169.

Rajput KS, Koyani RD, Patel HP, Vasava AM, Patel RS, Patel AD, Singh AP. 2015 – Preliminary checklist of fungi of Gujarat State, India. Current Research in Environmental & Applied Mycology 5, 285–306.

Richard F, Moreau PA, Selosse MA, Gardes M. 2004 – Diversity and fruiting patterns of ectomycorrhizal and saprobic fungi in an old-growth Mediterranean forest dominated by Quercus ilex L. Canadian Journal of Botany 82, 1711–1729.

Seen-Irlet B, Heilmann-Clausen J, Genney D, Dahlberg A. 2007 – Guidance for the conservation of mushrooms in Europe. Convention on the conservation of European wildlife and natural habitats. 27th meeting, Strasbourg.

Schoch CL, Seifert KA, Huhndorf S, Robert V, Spouge JL, Levesque CA, Chen W, Consortium FB. 2012 – Nuclear ribosomal internal transcribed spacer (ITS) region as a universal DNA barcode marker for Fungi. Proceedings of the National Academy of Sciences 109, 6241–6246.

Tadiosa ER, Agbayani ES, Agustin NT. 2011 – Preliminary Study on the Macrofungi of BazalBaubo Watershed, Aurora Province, Central Luzon, Philippines. Asian Journal of Biodiversity 2,149–171.

Tamura K, Stecher G, Peterson D, Filipski A, Kumar S. 2013 – MEGA6: Molecular Evolutionary Genetics Analysis version 6.0. Molecular Biology and Evolution 30, 2725–2729.

Tibuhwa DD. 2011– Substrate specificity and phenology of macrofungi community at the University of Dar es Salaam main campus, Tanzania. Journal of Applied Biosciences 46, 3173–3184.

Vitousek PM. 1994 – Beyond global warming: ecology and global change. Ecology 75, 1861–1876.

White TJ, Bruns T, Lee S, Taylor J. 1990 – Analysis of phylogenetic relationships by amplification and direct sequencing of ribosomal RNA genes. In PCR Protocols: A Guide to Methods and Applications. Innis, MA, Gelfand DH, Sninsky JJ, White TJ, eds. New York: Academic Press.

Xu J, Cai L. 2015 – Diversity, population genetics, and phylogeography of selected wild mushrooms. Mycology 6, 77–77.