

***Mallocybe africana* (Inocybaceae), the first species of *Mallocybe* described from Africa**

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Abstract

The genus *Mallocybe* has been poorly studied in Africa. Here we describe the first species of *Mallocybe* from West African and Zambian woodlands dominated by ectomycorrhizal trees of Fabaceae and Phyllanthaceae. The new species *M. africana* is characterized by orange-brown fruiting bodies, a fibrillose pileus, a clavately bulbous stipe and large ellipsoid basidiospores. It resembles many north and south temperate species of *Mallocybe*, and is most closely related to the southeast Asian tropical species, *M. errata*, but is best distinguished from these by ecological association with tropical ectomycorrhizal Fabaceae and Phyllanthaceae and geographic distribution. Phylogenetic analyses based on ITS, nLSU and RPB2 sequence data confirm that *M. africana* is nested within *Mallocybe*. A complete description and illustrations, including photographs and line drawings, are presented.

Key words: African woodland, Agaricales, morphology, systematics, taxonomy.

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Introduction

Systematic studies of macrofungi in West Africa are nascent. Despite taxonomic progress in some groups documented from West Africa during the last twenty years (Rooij and Verbeken 2003; Yorou 2008; Yorou and Agerer 2008; Yorou et al. 2011; Bâ et al. 2013; Maba et al. 2014, 2015), tropical African ecozones and particularly West Africa, remain poorly explored. In Soudano-Guinean forest ecosystems, the family Inocybaceae Jülich, is among the least studied ectomycorrhizal fungi.

Aside from some recent studies conducted in Africa (Matheny and Watling, 2004; Matheny et al., 2017; Matheny and Bougher, 2006), most identifications of African species of Inocybaceae (Buyck and Eyssartier 1999; Watling 2001; Mouchacca 2013; Gardens 2017) were made with morphological or anatomical observations and using literature from other continents, such as Europe. As Inocybaceae species differ between these areas, many taxa could be misidentified (Cripps et al. 2010) and due to the lack of taxonomic studies the diversity in Africa has probably been underestimated (Hennings 1892, 1901; Buyck and Eyssartier 1999; Watling 2001; Mouchacca 2013) It is therefore essential to increase sampling efforts in order to identify and describe species of Inocybaceae hidden in African ecosystems.

Mallocybe was first described as a subgenus of *Inocybe* (Kuyper 1986) but recently Matheny et al. (2020) elevated *Mallocybe* to one of seven genera in Inocybaceae. The genus is a monophyletic group of some 55 species distributed over much of the globe but predominantly occurs in north and south temperate regions (Matheny et al. 2009, 2020). *Mallocybe* is not well known outside Europe, parts of North America, and Australia. Novel species have been documented and described only recently from localities such as Australia (Matheny and Bougher 2006) and southeast Asia (Horak et al. 2015). Only one species of *Mallocybe* has been recorded from Sub-Saharan Africa, but it remains undescribed (Matheny et al. 2009, 2020). Species of *Mallocybe* are generally characterized by coarsely fibrillose, tomentose, or squamulose basidiomata, dark reaction to weak alkali solutions like 5% potassium hydroxide, presence of necropigmented basidia, absence of pleurocystidia, and cheilocystidia present as terminal elements of hyphae of the hymenophoral trama that are often short (<50 µm long) (Kuyper 1986; Jacobsson 2008; Cripps et al. 2010; Matheny et al. 2020). Here we

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describe a new species of *Mallocybe*, *M. africana*, based on morphological and multigene molecular analysis of ITS, nLSU, and *RPB2* sequence data.

Material and methods

Study area and specimen sampling

Specimens were collected between 2013 and 2017 in Benin, Burkina Faso, Ivory Coast and Togo in woodland dominated by ectomycorrhizal tree such as *Isoberlinia doka* Craib, *I. tomentosa* (Harms) Craib et Stapf, *Uapaca togoensis* Pax, and *Berlinia grandiflora* (Vahl) Hutch (Fig. 1). Specimens were preserved by drying on an electric dryer (type Stöckli Dörrex) for 24 hours at 45°C. All studied materials, including the holotype, are deposited at the Mycological herbarium of Parakou University (UNIPAR).

Morpho-anatomical analyses

Specimens were photographed with a digital camera Sony FE. Color codes were described using Kornerup and Wanscher (1978). Samples of specimens were rehydrated and examined in 3% KOH and Congo red. Drawings of microscopic characters were made with the aid of a drawing tube attached to a Leica DM2700. Microscopic characters were drawn at magnification 100X. For each microscopic element observed, 40 measurements were made from three samples from three collections. We measured length (L) and width (l) of the basidiospores and calculated the ratio $Q = L / l$. Measurements of basidiospores and basidia excluded the apiculus and sterigmata respectively.

Molecular analyses

DNA extraction, PCR and sequencing

Genomic DNA was extracted from dried specimens by QIAGEN® plant mini kit. Three nuclear gene regions, internal transcribed spacer (ITS) and portions of the large subunit ribosomal RNA gene (nLSU) and RNA polymerase II subunit (RPB2), were amplified using the following primers: ITS1F and ITS4 for ITS (White et al. 1990; Gardes and Bruns 1993), LR0R, LR7 and LR5 and LR3R for nLSU b6F and b7.1R for the most variable region of RPB2 (Matheny 2005). PCR products were cleaned and sequenced

at? Macrogen Inc. (institute?, city?, Netherlands) using the same primers as those used for PCR.

Sequence alignment and phylogenetic analysis

We generated thirteen new sequences that have been submitted to GenBank (Tab.1). Obtained sequences were BLAST searched and retrieved from GenBank and UNITE (Benson et al. 2010). These sequences of ITS, LSU and RPB2 were aligned separately using MAFFT V7.464 (Katoh et al. 2019). For phylogenetic analysis, we used 5.8 region of ITS, LSU and RPB2

The 5.8 partition included 17 taxa with 156 sites, the LSU partition included 38 taxa with 1315 sites and RPB2 included 24 taxa with 772 sites. The final concatenated data set of 5.8, LSU and RPB2 was generated using Geneious 7.0.2 (Drummond et al. 2010) and included 49 taxa and 2243 sites

The dataset was partitioned in 5.8S, 28S, RPB2 codon position 1, RPB2 codon position 2, RPB2 codon position 3, and the intron in RPB2 separately. We tested for the best partitioning scheme, and best model for each partition. It was indicated that keeping all the partitions was the best. Maximum likelihood (ML) analysis was performed with IQTREE 1.6.12 (Nguyen et al. 2015). Branch support was assessed with 1000 replicates of ultrafast bootstrapping (Hoang et al. 2017). Sequences from *Tubariomyces* were used as outgroup taxa based on Matheny et al. (2020). Bootstrap values $\geq 70\%$ were considered significant.

Results

Phylogenetic analyses

The ML phylogeny shows the placement of the investigated specimens within *Mallocybe* (Fig 2). Six samples clustered together with 98% bootstrap support to form a unique lineage, which we recognize as a new species, *M. africana*. Three of these include sequences from two collections of Zambian populations. Within *Mallocybe*, the new species *M. africana* formed a subgroup with the southeast Asian tropical species, *M. errata*, with strong bootstrap support (100%).

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FIG 2. ML tree of ITS, LSU and RPB2 sequences showing the placement of *Mallocybe africana*. Values above or below branches indicate bootstrap proportions. BS values $\geq 70\%$ are shown. Origin of species are given after the name of each taxon.

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Taxonomy

***Mallocybe africana* sp. nov.** Aïgnon, Yorou & Ryberg

Figures 3, 4

MycoBank No: 835658

Diagnosis: *Mallocybe africana* is most closely related to *M. errata* from southeast Asia but differs from it by the smaller size of the basidiomata, larger basidiospores, and ecological association with Fabaceae and/or Phyllanthaceae. *Mallocybe errata* associated with Pinaceae and Dipterocarpaceae.

characterized by orange brown fruiting bodies, hemispherical to plano-convex, fibrillose pileus, clavate, bulbous stipe measuring 7-20 mm wide and has the basidiospores ellipsoid. It differs from *M. errata* by a large pileus and a longer stipe.

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Holotype: - Benin, Borgou, North region, Village Gando.: 09°45'43.8"N, 002°19'56.2"E, on soil in woodland dominated by *Isoberlinia doka* and *I. tomentosa*, 2013-07-08, Leg. M. RYBERG, Specimen voucher (MR00358), deposited in Parakou University. GenBank accessions: ITS (MT476160), LSU (MT509360) and RPB2 (MT628398).

Commented [MPB8]: What???? Mallocybe errata has a pileus up to 40 mm wide. The stipe of *M. errata* is 10-35 x 4-8 mm wide, equal, not bulbous at the base. No odor.

Isotypes: Togo, Central region, prefecture of Assoli, on the road between Bafilo and Aledjo, reserve forest of Aledjo.: 09°20'25.1"N, 001°14'66.6"E, on soil in Woodland dominated by *Isoberlinia tomentosa*, 2013-07-17, leg. M. RYBERG, Specimen voucher (MR00385) deposited at Uppsala University. GenBank accessions: ITS (MN096194), LSU (MN097886) and RPB2 (MT465593).

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Etymology: *africana*, referring to the distribution in Africa.

Description. - Basidiomata (Fig. 3 A-D); Pileus 7–20 mm wide, hemispherical when young, expanding to convex or plane when mature; margin inflexed; surface dry, fibrillose to tomentose, at times diffracted scaly; disc occasionally with a grayish velipellis, otherwise orange-brown (5B4) to brown, sometimes yellowish (5B2) towards the margin

when young; flesh yellowish white (4A2), pale brown (4C4) to grayish white, 1–2 mm thick, **Lamellae** adnate, close, dark yellowish brown to dark brown (6B5), 2–4 mm deep, edges pallid-fimbriate. **Stipe** 1???? –25 × 2–4 mm wide at the apex?, clavate to slightly bulbous; surface dry, covered???, woolly or felty from veil remnants, becoming coarsely fibrillose or developing appressed fibrillose-scales; almost cinnamon to orange brown (5B4) or white yellowish pale brown, buff to brown, paler yellow at top; flesh pale yellow to white, becoming hollow.

Basidiospores (Fig. 4a): (9.5–)10–13.5(–14) × (4–)4.5–7.3(–8) µm, avl × avw = 11.5 × 5.6 µm Q: (1–)1.0–1.9(–2), avQ = 1.5, ellipsoid, smooth, thick walled, yellowish brown.

Basidia (Fig. 4 b): 20–47 × 5–14 µm, usually with 4 sterigmata, cylindric to slenderly clavate, hyaline becoming ochraceous (necropigmented). **Cheilocystidia** 25–42 × 10–25 µm, clavate, some almost pyriform or cylindrical and attenuated. **Pleurocystidia** absent.

Pileipellis (Fig. 4 e) a cutis of dense layers of hyphae, branched, with fusiform terminals, brown, 5–12 µm wide, parallel hyaline, terminal cells differentiated, hyphae incrustated???

Stipitipellis (Fig. 4f) a cutis made up of filamentous, branched, brown pale, septate hyphae 5–15 µm wide, thin- or thick-walled, terminal cells differentiated, hyaline, Clamp connections present. **Caulocystidia** (Fig. 4 d) 32–45 × 10–12 µm, scattered at stipe apex, infrequent.

Habit: Solitary, scattered or in small clusters on soil.

Habitat: Woodland dominated by one or association of either, *Isoblerlinia doka*, *I. tomentosa*, *Uapaca togoensis*, *Berlinia grandiflora* or *U. guineensis* (Fabaceae, Phyllanthaceae). Occurring during June to September.

Geographical distribution: West Africa - Benin, Togo, Burkina Faso, Ivory Coast, and in south-eastern Africa - Zambia.

Fig 3. A-D= Macromorphology of *Mallocybe africana* (HLA0462 and HLA0399). Bar = 1 cm

Fig. 4. Micromorphology of *Mallocybe africana*, A. Basidiospores. B. Basidia, C. Cheilocystidia, D. Caulocystidia, E. Pileipellis and F. Stipitipellis. Scale bars: A=3 µm, B=5 µm; C, D, E, F = 10 µm.

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Additional specimens examined

Burkina Faso, Bobo-Dioulasso, Forest reserve of Dan.: 10°53'39.7"N, 004°50'17.6"W, on soil in woodlands and gallery forests dominated by *Berlinia grandiflora* and *Uapaca guineensis*, 2013-07-12, Leg. M. RYBERG, Specimen voucher (MR00369), GenBank accession: ITS (MT458691) and nLSU (MT509361).

Ivory coast, Bouake; Gbêkê region, District of Bandama Valley.: 7°40'31.4"N, 004°54'29.2"W, on soil in woodland dominated by *Berlinia grandifolia*, 2018-07-11, Leg. L.H. AIGNON, Specimen voucher (HLA0561), GenBank accession: ITS (MT476161).

Benin, Collines, central region, Forest reserve of Toui-Kilibo.: 8°33'38.15"N, 002°36'5.44"E, on soil in woodland dominated by *Isobertinia doka*, 2017-08-12, Leg. LH AIGNON, Specimen voucher (HLA0378), GenBank accession: ITS (MT458692).

Benin, Borgou, North region, Forest reserve of N'dali.: 09°44'55.73"N, 002°41'40.51"E, on soil in woodland dominated by *Isobertinia doka* and *I. tomentosa*, 2017-08-30, Leg. LH AIGNON, Specimen voucher (HLA0462), GenBank accession No.: ITS (MT458691) and nLSU (MT456364).

Zambia, 6 kilometers before the Gibbon's farmar, on soil in miombo woodland (Phyllanthaceae, Fabaceae), 1996-11-17 Leg. G. Eyssartier, specimen voucher EG96012.

Zambia, Luanshya-Ibenga road, on soil in miombo woodland (Phyllanthaceae, Fabaceae), 1996-02-03, Leg. G. Eyssartier, specimen voucher EG96012 bis.

Zambia, Lusaka, on soil in miombo woodland (Phyllanthaceae, Fabaceae), 1996-02-08, Leg. G. Eyssartier, specimen voucher EG96012 ter.

Discussion

This study describes the first species of *Mallocybe* from the African continent. Previously, *M. africana* was provisionally referred to as "*Inocybe microdulcamara*" in Matheny et al. (2009) based on collections made by Bart Buyck and Guillaume Eyssartier in Zambia. Here we have detected the species from other regions of tropical Africa, where

it is widely distributed in different habitats including woodlands dominated by Fabaceae (*Isobерlinia doka*, *I. tomentosa* and *Berlinia grandiflora*) and of Phyllanthaceae (*Uapaca togoensis* and *U. guineensis*).

On the basis of our multi-gene (ITS, LSU and RPB2) phylogenetic analyses (Fig. 2), *M. africana* is subdivided into two subclades, with separation of the samples from West Africa from those in Zambia. However, the low sequences divergence in ITS and LSU between the clades (1.1% and 0.3% respectively) make us conclude that they belong to the same species.

In the phylogenetic tree, *M. africana* is most closely related to *M. errata* with strong bootstrap support, a species from northwest Thailand and India (Kerala) found in tropical forests mainly dominated by *Pinus kesiya* Royle ex Gordon, *P. Jungh et de Vries*, and dipterocarp forest dominated by *Dipterocarpus obtusifolia* Teijsm ex Miq (Horak et al. 2015). The phylogenetic affinities of the Zambian collections of *M. africana* with *M. errata* has long been recognized, and, according to Matheny et al. (2009) and Horak et al. (2015), both were strongly supported as phylogenetically related to *M. heimii*. However, our phylogeny reveals that *M. africana* and *M. errata* may be more closely related to *M. unicolor* and *M. multispora*.

Mallocybe africana shares some morphological similarities with *M. errata* as both have a brown to orange-brown pileus with radially fibrous, fibrillose squamules or scales (Horak et al. 2015). However, *M. african* differs from *M. errata* by the larger basidiospores (10–14 x 4–8 µm), not to mention ecological plant associates and geographic distribution. During this study, *M africana* has been collected from tropical Africa and associated with Fabaceae and Phyllanthaceae species while *M. errata* is distributed in tropical Asia and associates with Dipterocarpaceae and *Pinus* (Horak et al. 2015).

Mallocybe has a widespread distribution across the globe (Matheny et al. 2020) but no species has previously been described from Africa. This study represents the first formal description of a species of *Mallocybe* from the African continent.

Acknowledgments

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