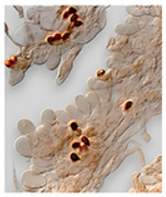
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Two new species of *Coltricia* (Hymenochaetales, Basidiomycota) from West Africa based on morphological and molecular phylogenetic evidence

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ABSTRACT

Coltricia (Hymenochaetales, Hymenochaetaceae) is a cosmopolitan group of wood-inhabiting fungi known for its ecological role in nutrient cycling and ectomycorrhizal associations, particularly in tropical ecosystems. Species diversity of *Coltricia* in tropical West Africa is poorly explored, with only four species previously documented from the region. Recent field surveys were conducted in Benin, Guinea, and Togo, leading to the collection of six *Coltricia* specimens. Through a combination of morphological and molecular analyses, two new species, *Coltricia langeri* and *Coltricia mosseboi*, were identified and described. Phylogenetic analyses based on sequence data of the internal transcribed spacer (ITS), large subunit ribosomal DNA (28S), and translation elongation factor 1-alpha (*EF1α*) regions confirmed the placement of these new species within *Coltricia*. Our results also revealed the polyphyletic nature of *Coltricia* and its close relationship with *Coltriciella*, challenging current generic boundaries. A dichotomous key to the six *Coltricia* species now known from tropical Africa is provided. This study expands the known diversity of *Coltricia* in Africa to six, contributing to the understanding of fungal diversity in tropical forests. The discovery of these new species highlights the need for further exploration and conservation of fungal species in West African ecosystems.

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Coltricia; ectomycorrhizal associations; fungal biodiversity; tropical West Africa; wood-decay fungi; 2 new taxa

INTRODUCTION

Coltricia Gray, typified by *Coltricia perennis* (L.) Murrill, is a cosmopolitan group of species within the order Hymenochaetales (Larsson et al. 2006; Zhao et al. 2024). Unlike several contentious genera in the family Hymenochaetaceae, such as *Fuscoporia* Murrill, *Fomitiporella* Murrill, *Fulvifomes* Murrill, and *Phylloporia* Murrill, *Coltricia* is consistently recognized as an independent and well-defined genus (Dai et al. 2009; Murrill 1904; Ryvarden 1972, 1991; Ryvarden and Johansen 1980). This genus is distinguished by its predominantly poroid and stipitate basidiocarps, a monomitic hyphal system lacking clamp connections, and colorful, ellipsoid to subglobose, smooth basidiospores (Dai et al. 2009). However, some species of *Coltricia* have lamellate hymenophore and resupinate to pileate basidiomata (Dai 2010). Species of *Coltricia* contribute to nutrient cycling through the decomposition of woody material and engaging in essential interactions with other organisms (Tedersoo et al. 2007). Understanding the diversity and taxonomy of *Coltricia* species, particularly in tropical regions, is therefore vital for effective forest management and conservation strategies.

Coltricia shares several morphological characteristics with the closely related genus *Coltriciella* Murrill (Dai and Li 2012; Zhou and Tedersoo 2012). However, *Coltriciella* can be distinguished from *Coltricia* by the presence of ornamented basidiospores as opposed to smooth basidiospores (Ryvarden 1991). The delineation between these two genera has been a topic of ongoing debate, with some taxonomists arguing that the presence of ornamented basidiospores as opposed to smooth basidiospores justifies maintaining them as separate genera (Murrill 1904; Ryvarden 1991; Susan et al. 2018; Zhou et al. 2024). Phylogenetic analyses revealed that *Coltricia*, as traditionally circumscribed, does not represent a monophyletic lineage but rather a continuum of morphological variation including species of *Coltriciella* (Wagner and Fischer 2002; Larsson et al. 2006; Tedersoo et al. 2007; Bian et al. 2022; Bian and Dai 2017; Wu et al. 2022). These findings have led to differing taxonomic treatments, with some mycologists treating *Coltriciella* as a synonym of *Coltricia*, thereby transferring species from the former into the latter (Wu et al. 2022), whereas others maintain the separation and describe new species under each genus

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(Zhou et al. 2024). In this study, we adopt a broad generic concept for *Coltricia*, which currently encompasses 86 globally recognized species (Dai et al. 2009; Baltazar et al. 2010; Baltazar and Da Silveira 2012; Dai and Li 2012; Valenzuela et al. 2012, 2020; Zhou and Tedersoo 2012; Decock 2013; Bian and Dai 2015, 2017, 2020; Bian et al. 2016; Ryvarden and Melo 2014; Susan et al. 2018; Wu et al. 2022; Zhou et al. 2024; Patil et al. 2024).

For the African continent, only four species of *Coltricia* have been reported so far: *Coltricia africana* Masuka & Ryvarden, *Coltricia cinnamomea* (Jacq.) Murrill, *Coltricia grandispora* Ryvarden & Hauskn., and *Coltricia pyrophila* (Wakf.) Ryvarden (Ryvarden and Johansen 1980; Masuka and Ryvarden 1993; Ryvarden et al. 2006; Ryvarden et al. 2022). Given that *Coltricia* species are known to form ectomycorrhizal associations and that West Africa is home to unique vegetation with ectomycorrhizal tree species that maybe be distinct from other biogeographic regions (Bâ et al. 2012; Diedhiou et al. 2014; Corrales et al. 2018; Zhao et al. 2023), it is likely that many more species of *Coltricia* remain undiscovered in these ecosystems. Documenting these species is important for understanding their diversity and for the conservation of tropical forests in the region.

In this study, we conducted field works in diverse habitats across Benin, Guinea, and Togo (West Africa), leading to the collection of multiple specimens of *Coltricia*. By integrating morphological characteristics with molecular data, we were able to detect species delimitations, resulting in the recognition of two novel species of *Coltricia*.

MATERIALS AND METHODS

Field collections.—During mycological surveys in Benin, Guinea, and Togo, specimens belonging to *Coltricia* were collected. Small fragments of fresh basidiomata were placed in plastic bags partially filled with silica gel, whereas the remaining samples were air-dried or oven-dried at 45–50 C for 1–2 days, depending on the consistency of the basidiomata. The dried basidiomata were then preserved in plastic bags for morphological study and deposited at the mycological herbarium of the University of Parakou (UNIPAR) in Benin.

DNA extraction, amplification, and sequencing.—We extracted the DNA from dried fragments of the *Coltricia* spp. using the innuPREP Plant DNA Kit (Analytik Jena, Germany). Here, we amplified the internal transcribed spacer region of rDNA (ITS), the D1–D4 domains of the nuclear ribosomal large subunit of ribosomal DNA (28S), and the translation elongation factor 1-alpha (*EF1α*). The primer pairs ITS-1 F/ITS4 (White et al. 1990; Gardes and Bruns 1993), LR0R/LR5 (Vilgalys and Hester 1990), and EF1-983 F/2218R (Rehner and Buckley 2008) were used to amplify the target DNA regions. The polymerase chain reaction (PCR) procedure, the PCR products purification, and Sanger sequencing followed Olou et al. (2020). TABLE 1 presents the accession numbers for all the sequences obtained in the context of the present study and obtained from GenBank for the phylogenetic analysis.

Phylogenetic analyses.—To study phylogenetic relationships, newly generated sequences were aligned with sequences retrieved from GenBank and used in previous studies on *Coltricia* and related genera (Bian and Dai 2017; Bian et al. 2022; Wu et al. 2022; Patil et al. 2024; Zhou et al. 2024). Six ITS sequences generated in this study were aligned with 84 ITS sequences retrieved from GenBank. In addition, 76 28S sequences retrieved from GenBank were aligned together with six newly generated 28S sequences. Six *EF1α* newly generated sequences were aligned with 51 *EF1α* sequences retrieved from GenBank. Each region was aligned separately using the online mode of MAFFT 7 (Katoh et al. 2019). *Fomitiporella chinensis* (Pilát) Y.C. Dai, X.H. Ji &Vlasák and *Inonotus griseus* L.W. Zhou. were chosen as the outgroup taxa as used in previous molecular studies (Bian and Dai 2020; Bian et al. 2022). Multiple sequence alignments were inspected, and some bases were manually adjusted using AliView 1.28 (Larsson 2014). One data set of combined ITS-28S-*EF1α* data was assembled for the phylogenetic analysis (SUPPLEMENTARY FILE 1). The best-fit evolutionary model was estimated for each region using the standard model selection (Kalyaanamoorthy et al. 2017) implemented in IQ-TREE 1.6.12 (Minh et al. 2020, http://www.iqtree.org/) with the command line –m MFP. Following the substitution model of each region (ITS: TPM3u+F+R4, 28S: TIM3+F+R3, *EF1α*: SYM+I+G4), the phylogenetic tree estimation by maximum likelihood (ML) and Bayesian inference (BI) was performed to verify the phylogenetic position of the newly generated sequences. ML was run using IQ-TREE 1.6.12, and the branch support was evaluated using the Ultrafast Bootstrap (UFBoot) (Hoang et al. 2018) with 5000 replicates. BI was executed using MrBayes 3.2.7 in command line mode (https://github.com/NBISweden/MrBayes) for 5 million generations until the standard deviation of split frequencies reached 0.01. Chain convergence was determined using Tracer 1.7.1 (http://tree.bio.ed.

Table 1. Species names, sample data, and GenBank accession numbers of sequences of *Coltricia* spp. obtained in the context of the present study and retrieved from GenBank.

			GenBank accession numbers		
Species name	Origin	Voucher or strain	ITS	28S	*EF1a*
Coltricia abieticola	China	Cui 12276	KU360673	KU360643	KY693912
C. abieticola	China	Cui10321	KX364785	KX364804	KY693911
C. australica	Australia	TU 103694	—	AM412243	—
C. austrosinensis	China	Dai 13093	KU360670	KU360640	KY693913
C. austrosinensis	China	Dai 13098	KU360671	KU360640	—
C. austrosinensis	China	Dai 13823	KU360672	KU360642	KY693914
C. barbata	Colombia	AMV 1866	KT724137	—	—
C. barbata	Colombia	AMV 1925	KT724136	KT724149	—
C. cinnamomea	China	Cui 12549	KY693728	KY693742	KY693916
C. cinnamomea	China	Cui 10494	KU360675	KJ000217	—
C. cinnamomea	China	Cui 10505	KU36067	KU360645	KY693915
C. cinnamomea	China	Cui 14262	KY693731	KY693747	KY693919
C. confluens	China	Cui17791	ON567327	—	—
C. confluens	Czech Republic	JV 1708/69	ON567325	—	—
C. crassa	China	Cui 10255	KU360678	KU360647	KY693921
C. crassa	China	Cui 9211	KU360677	KU360646	KY693920
C. fimbriata	China	Dai 22300	OL691607	OL691616	OL689394
C. focicola	China	Dai 16090	KX364786	KX364805	KY693923
C. focicola	China	Dai 26383	OR964386	OR964380	—
C. fragilissima	Thailand	Dai 16636	KY693733	KY693749	—
C. hamata	Brazil	4054	MZ484546	—	—
C. hamata	Colombia	AMV 1897	KT724146	KT724150	—
C. hirtipes	Thailand	Dai 16647	KY693734	KY693750	—
C. kinabaluensis	Thailand	Dai 13957	KX364787	KX364806	KY693924
C. kinabaluensis	Thailand	Dai 13958	KX364788	KX364807	KY693925
C. langeri	**Benin**	**OAB1152**	**PV448891**	**PV383199**	**PV468593**
C. langeri	**Benin**	**OAB1153**	**PV448892**	**PV383200**	**PV468594**
C. langeri	**Togo**	**OAB1218**	**PV448893**	**PV383201**	—
C. langeri	**Togo**	**OAB1221**	**PV448894**	**PV383202**	—
C. lateralis	China	Cui 12553	KX364789	KX364808	KY693926
C. lateralis	China	Dai 13564	KX364790	KX364809	KY693927
C. lenis	China	Dai 22367	OL691608	OL691617	—
C. lenis	China	Dai 22373	—	OL691618	OL689395
C. lenis	China	Dai 22374	OL691609	OL691619	OL689396
C. macropora	China	Cui 9019	KU360680	KJ000220	—
C. macropora	China	Cui 9039	KU360681	KJ000221	KY693928
C. minima	China	Dai 15206	KU360682	KU360649	KY693929
C. minima	China	Dai 15222	KU360683	KU360650	KY693930
C. minor	China	Dai 16088	KU360684	KU360651	KY693931
C. montagnei	China	Cui 10169	KU360685	KU360652	KY693932
C. montagnei	China	Dai 12137	—	KX364810	KY693933
C. montagnei	China	MHHNU 31367	MK182316	—	—
C. mosseboi	**Guinea**	**OAB1033**	**PV448895**	**PV383203**	**PV468595**
C. mosseboi	**Guinea**	**OAB1085**	**PV448896**	**PV383204**	**PV468596**
C. perennis	China	Cui 10318	KU360686	KJ000224	KY693934
C. perennis	China	Cui 10319	KU360687	KU360653	KY693935
C. pyrophila	China	Cui 10314	KU360689	KU360655	KY693937
C. pyrophila	China	Cui 10411	KU360690	KU360656	KY693938
C. pyrophila	China	Cui 12553	KX364792	KX364812	KY693939
C. raigadensis	India	AMH-10511	OR072877	—	—
C. rigida	China	Dai 13622a	KX364793	KX364813	KY693940
C. rigida	China	Dai 16322	KX364794	KX364814	KY693941
C. sonorensis	Mexico	RV 13144	—	HQ439179	—
C. strigosipes	China	Dai 15145	KX364795	KX364815	KY693942
C. strigosipes	China	Dai 15586	KU360692	KU360658	KY693943
C. strigosipes	China	Dai15587	KU360693	KU360659	KY693944
C. subcinnamomea	China	Dai 17016	KY693740	KY693755	—
C. subcinnamomea	China	Dai 17022	—	KY693756	—
C. subperennis	China	Dai 11625	KY693735	KY693753	KY693948
C. subperennis	China	Dai 13095	KY693736	KY693754	—
C. subverrucata	China	Dai 12919	MT174242	MT174235	MT133895
C. subverrucata	China	Dai 15600	MT174243	MT174236	MT133896
C. tenuihypha	China	Dai 22684	OL691610	OL691620	OL689397
C. tenuihypha	China	Dai 22690	OL691611	OL691621	—
C. tibetica	China	Cui 12208	MZ484551	MZ437407	—
C. velutina	China	Dai 16980	—	KY693752	—
C. verrucata	China	Dai 15120	KU360694	KU360660	KY693945
C. verrucata	China	Dai 15125	KU360695	KU360661	KY693946

(*Continued*)

Table 1. (Continued).

Species name	Origin	Voucher or strain	GenBank accession numbers		
			ITS	28S	*EF1a*
C. verrucata	China	Dai 16289	—	—	KY693947
C. weii	China	Cui 12624	KX364796	KX364816	KY693950
C. weii	China	Dai 13422	KX364797	KX364817	KY693951
C. weii	China	Cui 11011	KU360698	KU360664	KY693949
C. wenshanensis	China	Dai 15585	KX364798	KX364818	KY693952
C. wenshanensis	China	Dai 18367	MT174244	MT174237	—
C. wuyiensis	China	*Dai 25601*	OR964390	OR964384	—
C. wuyiensis	China	Dai 26431	OR964391	OR964385	—
C. zixishanensis	China	CLZhao7706	OR668922	NG_243414	—
C. baoshanensis	China	Cui 8147	KX364799	KX364819	—
C. baoshanensis	China	Dai 13075	KX364800	KX364820	KY693953
C. dependens	China	Dai 10944	KY693737	KY693757	—
C. dependens	China	Cui 9210	KY693738	KY693758	—
C. globosa	China	Cui 7545	KJ540930	KJ000226	KY693954
C. globosa	Vietnam	Dai 18420	MT174245	MT174238	—
C. minuscula	Indonesia	BO228063	KX086684	—	—
C. navispora	Guyana	MCA 3921	KC155387	KC155386	—
C. navispora	Guyana	TH 9529	KT339262	—	—
C. oblectabilis	Colombia	AMV 2255	KT354690	—	—
C. oblectabilis	Guyana	TH 9187	KC155387	KC155387	—
C. pseudodependens	China	Cui 8138	KJ540931	KJ000227	—
C. pseudodependens	China	Cui 12582	KX364801	KX364821	KY693955
C. pusilla	China	Dai 15168	KU360701	KU360667	KY693956
C. pusilla	China	Dai15581	KY693739	KU360668	KY693957
C. subglobosa	China	Dai 15158	KU360702	KU360669	—
C. subglobosa	China	CLZhao 4122	MK268869	—	—
C. yunnanensis	*China*	CLZhao 4204	OR668921	NG_243413	—
Fomitiporella chinensis	China	Cui 11230	KX181309	KY693759	KY693958
Inonotus griseus	China	Dai 13436	KX364802	KX364823	KY693959

Note. Sequences generated in this study in bold.

ac.uk/software/tracer/), and the first 25% (5000) trees were discarded as burn-in. The remaining trees were used to build the consensus tree using the phylogenetic tree summarization (SumTrees) program within DendroPy 4.3.0. (Sukumaran and Holder 2010, https://github.com/jeetsukumaran/DendroPy). The topologies of the species trees resulting from ML and BI analyses were congruent, which enabled us to combine them. To combine both trees, SumTrees program within DendroPy 4.3.0. (Sukumaran and Holder 2010, https://github.com/jeetsukumaran/DendroPy) was used to add the posterior probabilities (PPs) of the BI on the ML tree. Then, the UFBoot values were added to the best tree obtained by ML that already had values of the posterior probabilities using IQ-TREE (Trifinopoulos et al. 2016). The resulting tree with (UFBoot/PP) is presented in FIG. 1, and the support values of UFBoot and PP are indicated on each node.

Morphological examination.—Descriptions of macro- and microstructures were based on dried specimens of *Coltricia* spp. Macromorphological characters were described with the aid of a dissecting microscope. The microstructures were described using a Leica DM2700M compound light microscope. For the microstructures, fine sections through the dried basidiomata were prepared using a razor blade under a dissecting microscope and mounted in 10% aqueous solution of potassium hydroxide (KOH). Melzer's reagent and cotton blue were used to test dextrinoid or amyloid and cyanophilic reactions, respectively. The following abbreviations are used: IKI+ = amyloid or dextrinoid in Melzer's reagent, IKI– = neither amyloid nor dextrinoid, CB+ = blue in cotton blue, CB– = acyanophilous. The basidiospore size is given as length and width of the spores. For measurements, we present the mean value with standard deviation and minimum and maximum values in parentheses. The length (L), arithmetic average of all spore lengths, and the width (W), arithmetic average of all spore widths, were calculated. In addition, the ratio of length/width (Q) was calculated.

RESULTS

Phylogenetic analyses.—Six specimens of *Coltricia* spp. recently collected in Benin, Guinea, and Togo (OAB1033, OAB1085, OAB1152, OAB1153, OAB1218, and OAB1221) were included in a phylogenetic analysis of *Coltricia* spp. To this end, 16 sequences comprising six ITS rDNA, six 28S rDNA, and four *EF1α* gene sequences were generated and supplemented with

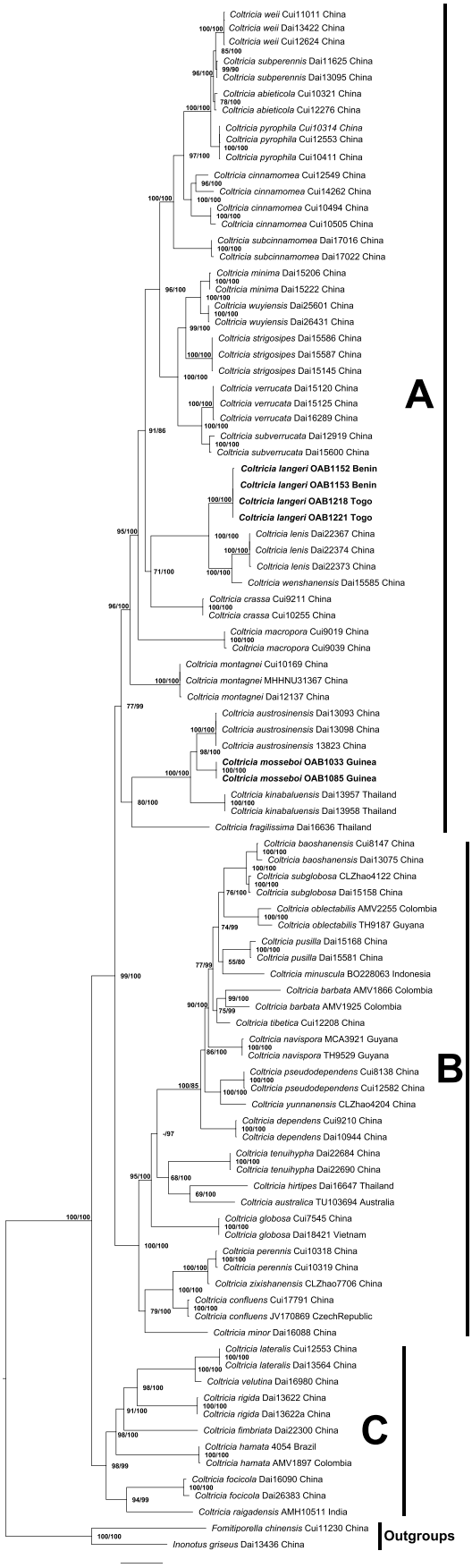


Figure 1. Maximum likelihood (ML) and Bayesian analysis (BI) analyses of the combined ITS-28S-*EF1a* data set of *Coltricia* and *Coltriciella*. Branch support values given as UFBoot/PP. Newly generated sequences are highlighted in bold. The sequence names are followed by voucher or strain number and country of origin.

additional sequences retrieved from GenBank. The combined ITS, 28S, and *EF1α* alignment contained 95 sequences, resulting in 3209 alignment columns, 1839 distinct patterns, 1385 parsimony-informative sites, 198 singleton sites, and 1626 constant sites. The resulting phylogenetic tree revealed three distinct groups or lineages, each with strong support values. Three groups recovered from the phylogenetic tree are named here A, B, and C (FIG. 1). Group A is made up of 22 clades, including two new clades of the two new species we present below. These 22 clades represent the sequences of 21 species, all belonging to *Coltricia*. Group B is made up of 18 clades representing the sequences of 18 species, some of which originally belonged to *Coltriciella* and others to *Coltricia*. The last group, Group C, is the basal group of the phylogenetic tree and is made up of seven clades that represent the sequences of seven different species, all belonging to *Coltricia* (FIG. 1). Sequences generated from specimens from Benin and Togo grouped together and formed a distinct clade, separate from those of Guinea. The Benin and Togo clade is closely related to *Coltricia lenis* L.S. Bian, M. Zhou & Jian Yu and *Coltricia wenshanensis* L.S. Bian & Y.C. Dai, whereas the Guinea clade is sister clade to *Coltricia austrosinensis* L.S. Bian & Y.C. Dai and *Coltricia kinabaluensis* Corner ex Y.C. Dai & Hai J. Li. The phylogenetic analyses provide strong support for the distinctiveness of the newly generated sequences, thereby justifying their recognition as novel species.

TAXONOMY

Coltricia langeri Olou, sp. nov. FIGS. 2, 3
MycoBank MB858500

Typification: BENIN. BORGOU PROVINCE: Woodlands of Okpara/Parakou, 9°15′36.62″N, 2°43′28.40″E, altitude 331 m above sea level (a.s.l.), on the soil in a woodland forest dominated by *Isoberlinia doka* Craib & Stapf., leg. *Boris A. Olou*, 14 Sep 2022, OAB1153 (**holotype** UNIPAR, isotype BR). Holotype sequences: ITS = PV448892; 28S = PV383200; *EF1α* = PV468594.

Diagnosis: *Coltricia langeri* differs from known species of *Coltricia* by the combination of the following characteristics: Basidiomata centrally stipitate, solitary or in groups of two to three basidiomata, pilei surface rust brown, velutinate. Pilei circular as seen from above, up to 2.5 cm diam and 1 mm thick at the center. Setae, cystidia, and cystidioles absent. Basidia 25–31.5 × 7.5–10.5 µm. Basidiospores ellipsoid, 8.5–12.0 × 5.5–7.5 µm.

Etymology: *langeri* (Latin), in honor to Prof. Ewald Langer, a mycologist who significantly contributed to the documentation of Aphyllophorales fungi globally, with a particular focus on Benin and Cameroon.

Description: Basidiomata seasonal, centrally stipitate, solitary or in groups of two to three basidiomata, without odor or taste when fresh, brittle and light weight when dry. Pilei circular as seen from above, flat to slightly infundibuliform, up to 2.5 cm diam and 1 mm thick at the center, pilei surface rust brown, velutinate, with indistinct concentric zones and radially aligned lines, margin thin and sharp, rolled inside when dry. Pore surface light brown, pores slightly decurrent, angular to irregular, up to 2 mm wide, dissepiments thin, entire. Context rust brown, soft, spongy, up to 1 mm thick. Tubes dark brown, up to 4 mm thick. Stipe long, reddish brown, corky, up to 2–5 cm long, 7 mm diam, very fragile, easily breaking during collection. Hyphal system: monomitic, generative hyphae with simple septae; tissue becoming blackish brown in KOH. Contextual hyphae yellowish, slightly thick-walled, branched, interwoven, 8–15 µm diam. Tramal hyphae thick-walled with a wide lumen, branched, frequently simple septate, straight, subparallel along the tubes, 4–8 µm diam. Setae, cystidia, and cystidioles absent. Basidia clavate, with four sterigmata each, with a simple septum at the base, 25–31.5 × 7.5–10.5 µm; basidioles similar in shape but slightly smaller. Basidiospores: ellipsoid, yellowish, thick-walled, smooth, IKI–, CB–, (8.4–)10.2–11.8(–12.2) × (5.5–)6.5–7.4(–7.5) µm, L = 10.22 µm, W = 6.5 µm, Q = 1.57 (n = 89/1).

Ecology and distribution: Basidiomata grow on the soil under angiosperm trees in a woodland forest. This species is currently only known from Benin and Togo.

Other material morphologically examined: BENIN. BORGOU PROVINCE: woodlands of Okpara/Parakou, 9°15′36.62″N, 2°43′28.40″E, altitude 331 m a.s.l., on the soil in a woodland forest dominated by *I. doka*, leg. *Boris A. Olou*, 14 Sep 2022, OAB1152 (UNIPAR). TOGO. ASSOLI PROVINCE: Alédjo Wildlife Reserve, 9°16′12.0″N, 1°13′12.0″E, on the soil in a gallery forest with *Berlinia grandiflora* (Vahl) Hutch. & Dalziel and *Uapaca guineensis* Müll.Arg., leg. *Boris A. Olou, C. Tétéli, N.S. Yorou & M. Demakou*, 24 Jun 2024, OAB1218 (UNIPAR), OAB1221 (UNIPAR).

Coltricia mosseboi Olou, sp. nov. FIGS. 4, 5
MycoBank MB858501

Typification: GUINEA. FARANAH REGION: Dabola Province, Moussaya, National Park of Upper Niger, 10°32′50.7″N, 10°34′45.8″W, altitude 422.9 m, on the soil in the vicinity of *Anthonotha crassifolia* (Baill.) J. Léonard plants, leg. *Boris A. Olou,*



Figure 2. Fresh basidiomata of *Coltricia langeri* from different collections. A. OAB1221, Togo. B. OAB1218, Togo. C. OAB1153, Benin. Bars = 1 cm.

G. Konomou, A. Verbeken & N.S. Yorou, 12 Aug 2022, OAB1085 (holotype UNIPAR, isotype Meise Botanic Garden). Holotype sequences: ITS = PV448896; 28S = PV383204; *EF1α* = PV468596.

Diagnosis: *Coltricia mosseboi* differs from known species of *Coltricia* by the combination of the following characteristics: Basidiomata centrally stipitate, solitary, pilei surface brown, tomentose. Pilei large, circular, flat, up to 9 cm diam and 2 cm thick at the center. Setae, cystidia, and cystidioles absent. Basidia 16.5–26.4 × 5.2–8.1 µm. Basidiospores ellipsoid 5.8–8.3 × 3.7–6.1 µm.

Etymology: *mosseboi* (Latin), named in honor of the late Prof. Dominique Claude Mossebo, a distinguished African mycologist and world-renowned expert on polypores, who coauthored several seminal works on African polypores.

Description: Basidiomata seasonal, centrally stipitate, solitary, without odor or taste when fresh, brittle and light weight when dry. Pilei circular, flat, up to 9 cm diam and 2 cm thick at center, pilei surface brown, tomentose, margin thin and sharp. Pore surface light brown, pores angular, 0.5–2 per mm, dissepiments thin, entire. Context rust brown, soft, spongy, up to 1.5 cm thick. Tubes dark brown, up to 3 mm thick. Stipe long, reddish brown, corky, up to 4 cm long, 1.2 cm diam. Hyphal structure: monomitic, generative hyphae with simple septae; tissue becoming blackish brown in KOH. Contextual hyphae yellowish, slightly thick-walled, branched, interwoven, 5–10 µm diam. Tramal hyphae, thick-walled with a wide lumen, branched, frequently simple septate, straight, subparallel along the tubes, 3–7 µm diam. Setae, cystidia, and cystidioles absent.

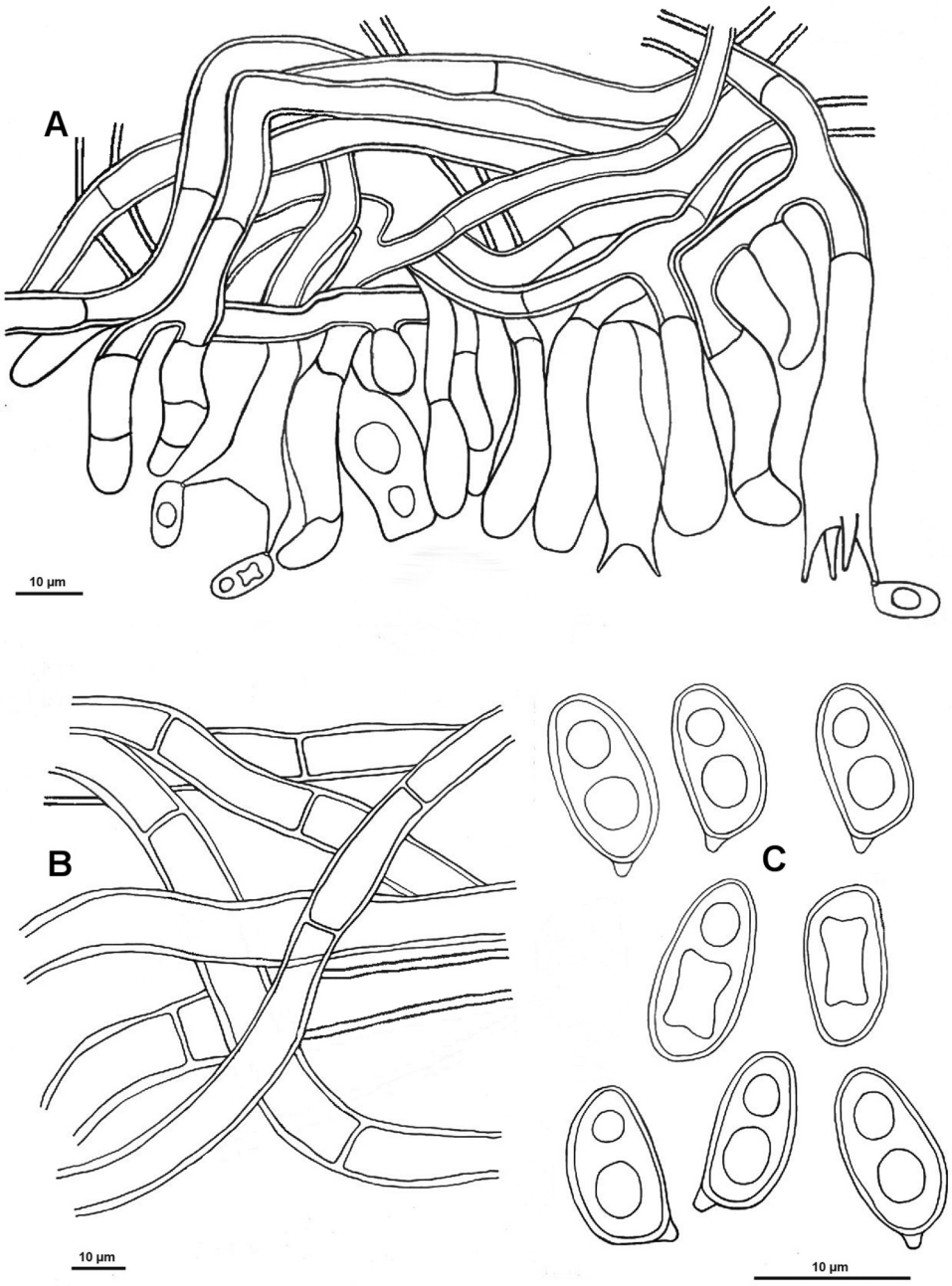


Figure 3. *Coltricia langeri* (OAB1153). A. Hyphae of the trama close to a pore and basidia, basidia with young basidiospores. B. Contextual hyphae. C. Basidiospores. Cellular contents correspond to oil drops. Bars = 10 µm.

Basidia clavate, with four sterigmata and a basal simple septate at the base, 16.5–26.4 × 5.2–8.1 µm; basidioles similar in shape but slightly smaller. Basidiospores: ellipsoid, yellowish, thick-walled, smooth, IKI–, CB–, (6–)5.8–7.7(–8.3) × (3.7–)4.4–5.9(–6.1) µm, L = 6.78 µm, W = 5.18 µm, Q = 1.31 (n = 62/1).

Ecology and distribution: Basidiomata grow on the soil under ectomycorrhizal angiosperm trees in a dense dry forest. This species is currently only known from the type locality in Guinea.

Other material morphologically examined: GUINEA. KANKAN REGION: Kouroussa Province, National Park of Upper Niger, 10°06′50.5″N, 10°26′07.4″W, altitude 421.7 m, on the soil in the vicinity of *Uapaca togoensis* Pax., leg. *Boris A. Olou, G. Konomou, A. Verbeken & N.S. Yorou*, 8 Aug 2022, OAB1033 (Meise Botanic Garden).

DISCUSSION

Our findings, based on specimens collected from Benin, Togo, and Guinea, introduce two novel species to the genus *Coltricia*, broadening the known diversity of this group in tropical West Africa.

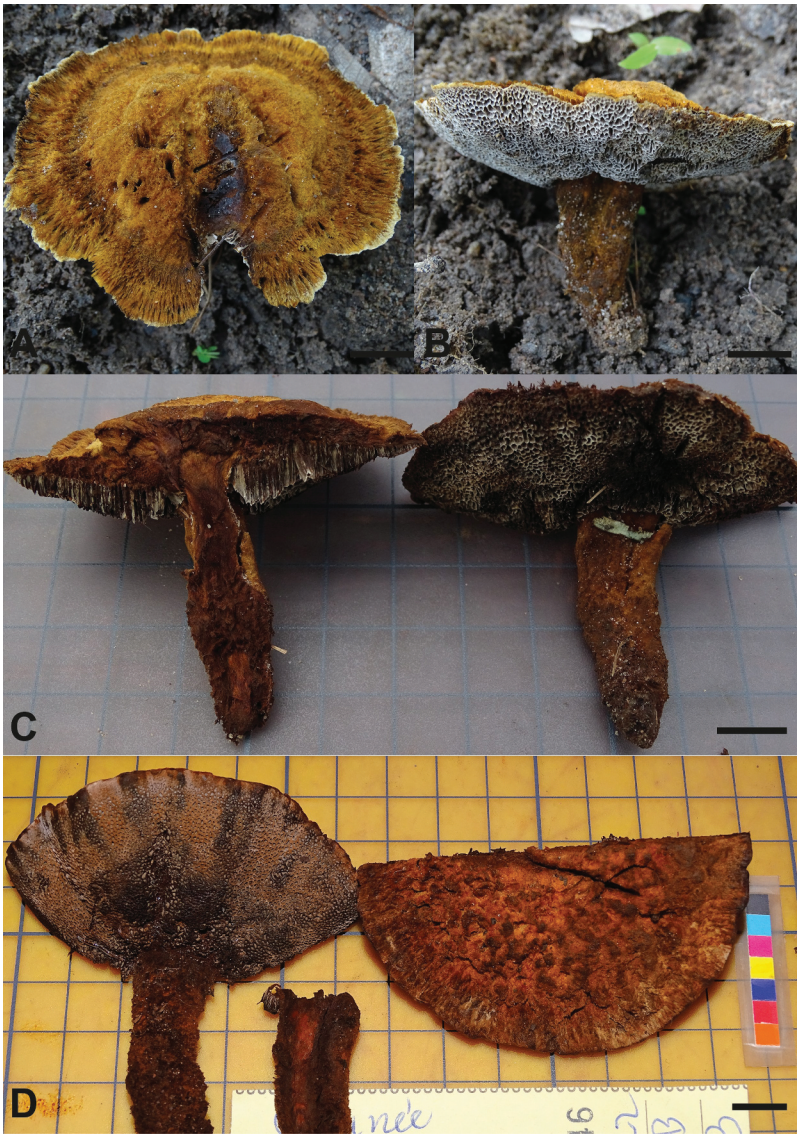


Figure 4. Fresh basidiomata of *Coltricia mosseboi*. A, B. Basidiomes in the natural habitat (OAB1085, Guinea). C. Basidiomata a few hours after collection prepared for drying (OAB1085, Guinea). D. Basidiomata a few hours after collection prepared for drying (OAB1033, Guinea). Bars = 1 cm.

***Morphology, ecology, and phylogenetic position of the two new* Coltricia *species.*—**The phylogenetic analysis based on the combined data set confirms the generic placement of the two newly described species within *Coltricia*. The species selected for comparison were chosen based on their close phylogenetic placement in our tree. Subsequently, their morphological characteristics, based on the literature on holotypes, were used to further compare and discriminate between species (Dai and Li 2012; Bian et al. 2016, 2022; Bian and Dai 2017).

Coltricia langeri shares several morphological characteristics with *C. lenis* and *C. wenshanensis*, particularly its centrally stipitate basidiomata, which occur either solitarily or in groups of two to three, and its ellipsoid basidiospores. However, *C. langeri* can be distinguished from these species by its larger basidiospores, measuring 8.4–12.2 × 5.5–7.5 µm, which are notably wider than those of *C. lenis* (6–9 × 5–6 µm; Bian et al. 2022) and *C. wenshanensis* (7–8 × 6–7 µm; Bian and Dai 2017). These distinctions in spore size are significant, as they represent a key diagnostic feature separating *C. langeri* from closely related species. Moreover, *C. langeri* is currently known only from woodland forests in Benin and Togo, an ecological and geographic range that further sets it apart from other species in the genus.

Coltricia mosseboi forms a distinct clade with *C. austrosinensis* and *C. kinabaluensis*, sharing several morphological traits such as centrally stipitate, solitary

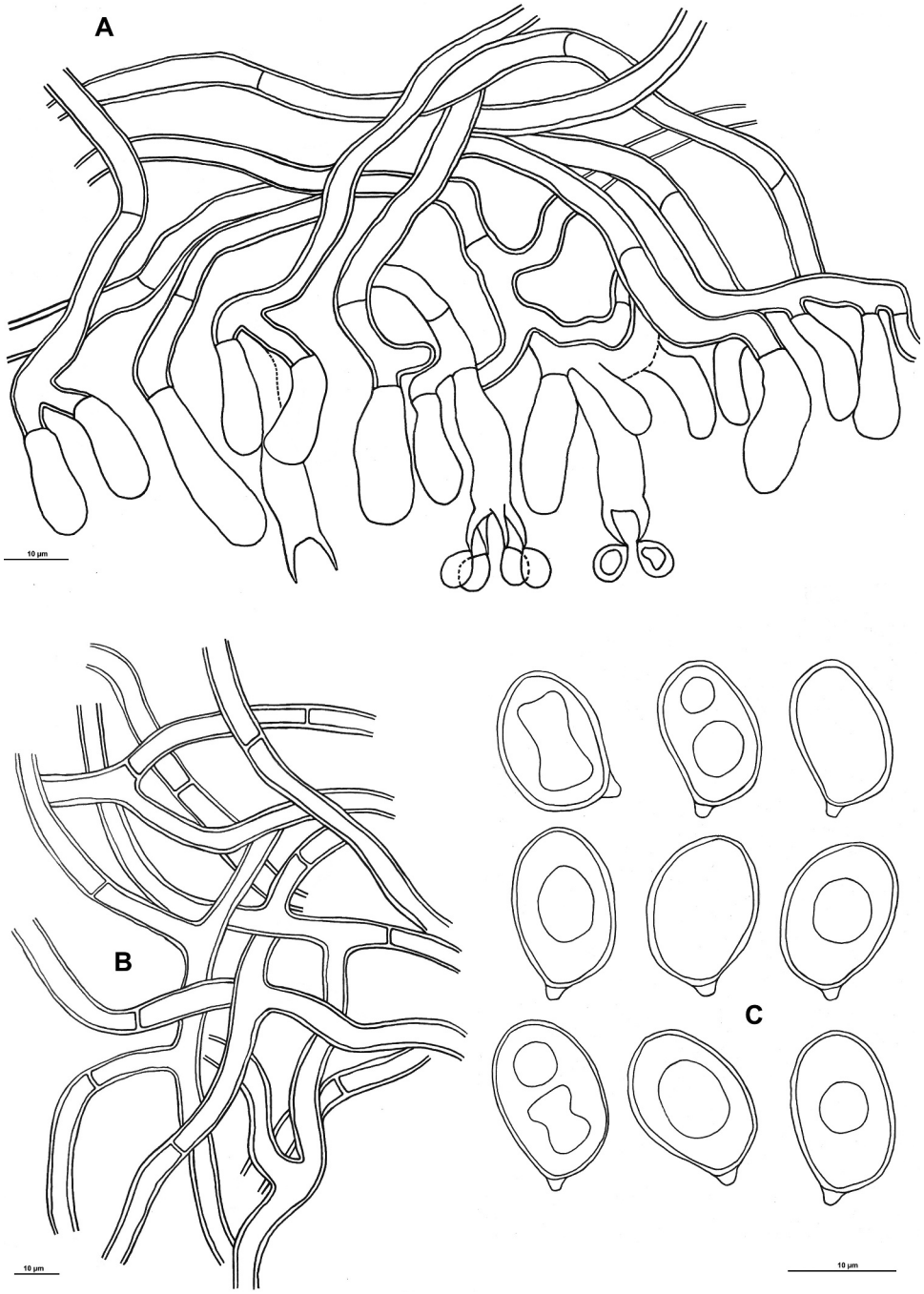


Figure 5. *Coltricia mosseboi* (OAB1085). A. Hyphae of the trama close to a pore and basidia, basidia with young basidiospores. B. Contextual hyphae. C. Basidiospores. Bars = 10 µm.

basidiomata, and ellipsoid basidiospores. Despite these similarities, *C. mosseboi* is distinguishable from *C. austrosinensis* by its shorter basidiospores, measuring 5.8–8.3 × 3.7–6.1 µm, whereas *C. austrosinensis* has longer basidiospores, ranging from 8 to 10 µm (Bian et al. 2016). *Coltricia kinabaluensis*, on the other hand, has basidiospores that are almost identical in size to those of *C. mosseboi* (6–8 × 4–5 µm in *C. kinabaluensis* versus 5.8–8.3 × 3.7–6.1 µm in *C. mosseboi*). However, ecological and substrate differences clearly distinguish these species: *C. kinabaluensis* is wood-inhabiting (Dai and Li 2012), whereas *C. mosseboi* is soil-dwelling, found under ectomycorrhizal trees such as *A. crassifolia* and *U. togoensis*. Additionally, *C. kinabaluensis* is geographically restricted so far to Malaysia and Thailand (Dai and Li 2012; Bian and Dai 2017), whereas *C. mosseboi* has been reported only from its type locality in Guinea. These

ecological, geographic, and phylogenetic distinctions collectively highlight the unique characteristics of *C. mosseboi* and support its recognition as a new species.

***Comparison with previously known African species of* Coltricia.—**Among the four *Coltricia* species previously reported from Africa, namely, *C. africana, C. cinnamomea, C. grandispora*, and *C. pyrophila*, our phylogenetic analysis reveals that available sequences of *C. cinnamomea* and *C. pyrophila* are not closely related to the two new species described in this study. In addition, *C. pyrophila* differs from other species by growing in post-fire environments (Ryvarden 1972; Ryvarden and Johansen 1980; Ryvarden et al. 2022). In contrast, the newly introduced species were discovered in undisturbed forest areas, showing no signs of post-fire habitat adaptation. For *C. africana* and *C. grandispora*, sequences are not available on GenBank, but morphological and ecological differences allow us to distinguish the two new species from these African taxa. The two new species exhibit smaller basidiomata but possess larger pores and basidiospores when compared with *C. africana*, which is characterized by large, robust basidiomata with relatively smaller pores and basidiospores (Masuka and Ryvarden 1993; Ryvarden et al. 2006). In contrast, *C. grandispora* is readily distinguished from both new species by its notably larger basidiospores, measuring 11.5–14 × 7–9 µm (Ryvarden et al. 2006). In terms of distribution, *C. africana* is known only from its type locality in Malawi, where it grows on the ground beneath *Widdringtonia nodiflora* (L.) Powrie, a tree species native to southern Africa. *Coltricia grandispora*, on the other hand, has a more insular distribution, being recorded exclusively on the ground in the Seychelles, specifically on Mahé and Praslin islands (Ryvarden et al. 2022). Although genetic comparisons were not possible for *C. africana* and *C. grandispora*, the combination of morphological differences and habitat distinctions supports the recognition of the two new species as taxonomically and ecologically distinct.

These findings contribute to the growing understanding of *Coltricia* diversity in Africa and highlight the importance of continued research on African fungal species to uncover their evolutionary and ecological significance.

Taxonomic implications of phylogenetic results.—Our phylogenetic analyses using the ITS, 28S, and *EF1α* regions revealed three distinct groups within *Coltricia*, referred to here as Groups A, B, and C. As part of our phylogenetic analysis, the grouping of *C. perennis* and *Co. dependens* (the type species of their respective genera) within a single group suggests that basidiospore morphology alone may not provide sufficient justification for maintaining *Coltricia* and *Coltriciella* as separate genera. Our findings support the merging of *Coltricia* and *Coltriciella* (Wu et al. 2022; Zeng et al. 2025).

Importantly, we note that the available sequences used to represent generic type species (e.g., *Coltricia perennis* from China and *Coltriciella dependens*) were not derived from type material or collections near the type localities. This limitation, common in fungal systematics, reflects the scarcity of verified type-based sequences in public databases. Although these sequences are widely used for comparative purposes, we acknowledge that their interpretation for generic delimitation should be approached with caution.

DICHOTOMOUS KEY TO TROPICAL AFRICAN *COLTRICIA* SPECIES

1. Spores (11–)12–14 × 7–9 µm..... *Coltricia grandispora*
1′. Spores smaller 2
2. Spores 6.5–8 × 5–6 µm ..... *Coltricia cinnamomea*
2′. Spores smaller or narrower than above..... 3
3. Pores 6–7 per mm; under *Widdringtonia* in Malawi. ..... *Coltricia africana*
3′. Pores 2–4 per mm; not under *Widdringtonia*..... 4
4. Basidiomata found on burnt areas *Coltricia pyrophila*
4′. Basidiomata not associated with burnt areas..... 5
5. Pileus brown to rusty brown, velvety to tomentose; margin incurved at maturity; basidia long (35–45 µm); spores 10–11.5 × 4.5–6 µm .... *Coltricia langeri*
5′. Pileus dark brown to blackish, strongly velvety; context darkening with age; spores ovoid to subglobose, 9–10.5 × 6–7 µm ..... *Coltricia mosseboi*

DISCLOSURE STATEMENT

No potential conflict of interest was reported by the author(s).

DATA AVAILABILITY STATEMENT

The alignment used in this study is provided as SUPPLEMENTARY FILE 1. The newly generated sequences have been submitted to GenBank, with the accession numbers listed in TABLE 1. All alignments, phylogenetic trees, and GenBank accession numbers for the newly generated sequences will be made publicly available upon publication of this paper. The collected specimens are deposited in the Mycological Herbarium of the University of Parakou (UNIPAR). The newly described species are registered in

MycoBank, with their registration numbers provided in the Taxonomy section of this paper.

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