



A new and unusual species of *Hericium* (Basidiomycota: Russulales, Hericiaceae) from the Dja Biosphere Reserve, Cameroon

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Abstract

Tropical rainforests form the most species-rich biome on the earth. The Dja Biosphere Reserve (DBR) in Cameroon is a biodiverse tropical forest characterized in part by upland monodominant stands of the ectomycorrhizal (ECM) *Gilbertiodendron dewevrei* and ECM *Uapaca* spp. scattered along river banks. This mostly primary Guineo-Congolian evergreen forest harbors natural populations of large megafauna and numerous plant and fungal species. Studies have indicated that some ECM fungal groups of the large order Russulales are abundant in certain localities in the tropics, including the DBR. However, currently, other predominantly wood-decaying families of Russulales are poorly represented in Africa. For example, only three records of the saprotrophic genus *Hericium* (Russulales, Hericiaceae) are known from the African continent. Here, we describe a new species of *Hericium* recently collected from the DBR. Morphological characteristics and molecular phylogenetic analyses support placement of the Cameroonian collection in *Hericium* and its recognition as a new species within a larger *H. coralloides* species complex. The new species, *H. bembedjaense*, differs from *H. coralloides* in its smaller basidiospores ($2.6\text{--}3.0 \times 1.7\text{--}2.2 \mu\text{m}$ compared to $3.5\text{--}5.0 \times 2.8\text{--}4.2 \mu\text{m}$) and longer basidia (up to $27.0 \mu\text{m}$ compared to $15.0 \mu\text{m}$). It differs from all other described *Hericium* species in the production of pleurocystidia. This is the first species of Hericiaceae known from sub-Saharan lowland tropical evergreen forests. This study highlights the need to increase fungal sampling in species-rich tropical forests such as those of the Congo Basin.

Keywords Africa · rDNA systematics · Russulales · Taxonomy · Wood rot fungi

Introduction

Tropical rainforests form the most species-rich biome on earth, harboring over 50% of species on just 7% of the land area (Hill and Hill 2001; Wilson 1988). The Dja Biosphere Reserve (DBR) in the Central African region covers an area of more than 500,000 km² (Carson et al. 2018) and is an integral part of the dense Guineo-Congolian forest encompassing the

Congo Basin. The DBR is exceptionally biodiverse (Hill and Hill 2001) with more than 90% of the forest area still in a natural state (Betti 2004). It consists mostly of primary evergreen forest that supports natural populations of large megafauna as well as various plant and fungal species (Sonké and Couvreur 2014; Verbeken et al. 2008). The reserve is surrounded by 36 villages spread around the buffer zones. More than 6000 people live in these villages including the indigenous Baka (Carson et al. 2018). Within the reserve are patches of forests dominated by a few ectomycorrhizal (ECM) tree species—*Gilbertiodendron dewevrei* (Fabaceae subfam. Detarioideae) and some *Uapaca* spp. (Phyllanthaceae)—scattered along the river banks (Castellano et al. 2016).

Various studies have been conducted to document fungal diversity within tropical forests around the world (e.g., Berndt 2012; Cornejo et al. 1994; Henkel et al. 2012; Piepenbring et al. 2012). Some of these studies have indicated that, locally, the Russulaceae (Russulales) can be the most abundant group of ECM macrofungi (Smith et al. 2017; Verbeken and Walley 2010; Zhou and Dai 2013). Verbeken et al. (2008)

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revealed that *Lactifluus* (Pers.) Roussel and *Russula* Pers. (Russulaceae) were the dominant ECM macrofungal genera in a *G. dewevrei* monodominant Guineo-Congolian rainforest of Central Africa. In the Guiana Shield, the Russulaceae were also abundant in a long-term study in monodominant forests of ECM *Dicymbe* (Henkel et al. 2012; Miller et al. 2012; Smith et al. 2017). In contrast, few tropical studies have revealed representatives of saprotrophic Russulales. In temperate regions, saprotrophic species such as members of Hericiaceae can be important both during wood decay and as causal agents of white rot of hardwood and coniferous trees (Boddy et al. 2011; Das et al. 2011; Hallenberg et al. 2013).

Hericum Pers. (Hericiaceae) is a dentate and coralloid basidiomycete genus. Ecologically, members are white rotters. But, importantly, many species within the genus are important as sources of food (Hallenberg et al. 2013) and medicinals (e.g., Mori et al. 2008; Pegler 2003; Thongbai et al. 2015) that have a long history of traditional use (e.g., Khan et al. 2013; Ramberg et al. 2010). For example, several species such as *H. erinaceus* (Bull.) Pers., *H. flagellum* (Scop.) Pers., and *H. coralloides* (Scop.: Fr) Pers. are cultivated for food and production of beneficial secondary metabolites. Active compounds (hericenones, hericine, hericerine, erinacines, enzymes, etc.) isolated from members of the genus are useful in therapeutic treatments because they have negligible side effects in patients, unlike chemotherapeutic medication (Thongbai et al. 2015). These extracts also contain antibacterial and anti-aging properties (Kim et al. 2000, 2012; Wittstein et al. 2016; Xu et al. 2010) as well as the ability to prevent the Crohn's disease (Abdulla et al. 2008; Wong et al. 2013). *Hericum* compounds are being used in the prevention and treatment of diabetes and various types of cancers (Kim et al. 2011, 2013; Ma et al. 2012; Yang et al. 2003). In cancer patients, *Hericum* secondary compounds enhance immune responses by increasing their CD4 T cells, which are cytotoxic to tumor cells (Liu et al. 2000) and seem to increase the life span (Ying et al. 1987). Many supplements for cognitive brain function and memory improvement contain compounds from *Hericum* (Obara and Nakahata 2002; Rupcic et al. 2018) and could be used in the treatment of Alzheimer's disease (Allen and Dawbarn 2006; Prine et al. 2014). Finally, *Hericum* is a model for bio-transforming active plant material (Thongbai et al. 2015).

Among species of *Hericum*, variations of micromorphological characters can be very subtle, even when considering specimens from different geographic regions (Hallenberg et al. 2013). Consequently, most species have been differentiated based on a combination of additional features including substratum preference, geographic origin, and molecular data (Ginns 1985; Hallenberg et al. 2013). In terms of phylogenetic analyses, thus far, only the internal transcriber spacer (ITS) region of the ribosomal DNA has been used for species delimitation in

the genus (Das et al. 2011, 2013; Hallenberg et al. 2013). Most of the known species of *Hericum* have been described from higher latitude ecosystems of the Americas and Eurasia. Presently, there are 26 accepted species of *Hericum* (Index Fungorum 2019), all documented from temperate North and South America, Asia, Europe, Australia, and Africa (Tunisia alone) (Boddy et al. 2011; Fraiture and Otto 2015; Ginns 1985; Hallenberg et al. 2013; Kalucka and Olariaga Iburguren n.d.; Ouali et al. 2018). Thus far, no reports are known from the sub-Saharan lowland tropical evergreen forests.

Here, we describe a new species of *Hericum* from the Dja Biosphere Reserve in Cameroon. We provide morphological, molecular phylogenetic, ecological, and geographic data to support recognition of the new species.

Materials and methods

Field collections

Basidiomata were collected in Cameroon during the April–May early rainy season of 2018 from the Dja Biosphere Reserve, Northwest Sector, near the village of Somalomo. Specifically, the study site is in the Upper Dja River Basin, within a 2-km radius of a base camp located at 3° 21' 29.8" N 12° 43' 46.9" E, 650 m a.s.l., in forests dominated by *Gilbertiodendron dewevrei* (Peh et al. 2014). Descriptions of macromorphological features were made from freshly collected basidiomata in the field. Colors were compared with plates in the Online Auction Color Chart (Online Auction Color Chart Co 2004). Fresh specimens were photographed in situ and in the field camp. Basidiomata were dried in the field using silica gel. The holotype collection is deposited at PUL (Kriebel Herbarium, Purdue University); an isotype is deposited at YA (National Herbarium of Cameroon, Yaoundé). Photomicrographs were taken with an Olympus SC30 camera mounted on an Olympus BH2 bright field compound microscope (Olympus Co., Tokyo, Japan) using cellSens 1.18 imaging software.

Micromorphological features were observed from rehydrated sections of specimens. For basidia, cystidia, basidiospores, sterigmata, and hyphal features, rehydrated tissue was mounted in water, 3% KOH or Melzer's reagent, and at least 20 individuals were measured. Line drawings of basidiospores were made using tracing paper from images taken with the cellSens camera mounted to an Olympus BH2 microscope mainly at × 1000 magnification. Drawings of other micromorphological structures (basidia, cystidia, gloeocystidia, etc.) were made from images taken at × 400 magnification. Drawings were edited with Adobe Photoshop Elements 6 ver. 6.0 (Adobe, San Jose, CA, USA). Basidium length excludes sterigmata and

basidiospore dimensions exclude the dimensions of the ornamentations and the hilar appendix. Basidiospores were randomly selected for measurement in side view and their sizes are given as $L_x-L_z-L_y \times W_x-W_z-W_y$ where L_x = minimum value for length of the measured basidiospores, L_y = maximum value for length of the measured pores, L_z = mean value for the length of measured basidiospores, W_x = minimum value for the width of measured basidiospores, W_y = maximum value for the width of measured basidiospores, and W_z = mean value for the width of measured basidiospores. The quotient indicates the length by width ratio ($Q = L/W$) and is given as $Q_x-Q_z-Q_y$ where Q_x = minimum quotient value of the measured basidiospores, Q_y = maximum quotient value of the measured basidiospores, and Q_z = mean quotient value of the measured basidiospores.

DNA isolation, PCR amplification, and sequencing

Total genomic DNA was extracted from basidioma tissue using the Wizard® Genomic DNA Purification kit (Promega Co., Madison, WI, USA), following the manufacturer's protocols. Both the internal transcribed spacer (ITS) DNA barcode region (Dentinger et al. 2011; Schoch et al. 2012) and the large subunit (28S) of the ribosomal DNA (rDNA) were amplified with polymerase chain reaction (PCR) using the primer sets ITS1F/ITS4B for ITS (Gardes and Bruns 1993) and LR0R/LR6 for 28S (Moncalvo et al. 2000; Vilgalys et al. 1994; Vilgalys and Hester 1990). PCR reactions consisted of 12.5 μ L of Promega 2 \times PCR Master Mix, 1.25 μ L of each 10 μ M primer, 9.0 μ L of H₂O, and 1.0 μ L of template DNA. All amplifications were done in an Eppendorf Mastercycler ep Thermal Cycler (Hauppauge, New York, USA) with initial denaturation at 94 °C for 3:00 min; followed by 35 cycles of denaturation at 94 °C for 1:00 min, annealing at 50 °C for 0:45 min and extension at 72 °C for 1:30 min; and final extension at 72 °C for 10:00 min. PCR products were sent to Genewiz (South Plainfield, NJ, USA) for purification and sequencing. Raw sequence reads were assembled and edited using Sequencher v5.2.3 (Gene Codes Co., Ann Arbor, MI, USA) software. Sequences were deposited at the National Center for Biotechnology Information (NCBI) Genbank database, under accession numbers MK683483 and MK683482.

Sequence alignment and phylogenetic analysis

The newly generated sequences were queried against the NCBI GenBank database using the “megablast” algorithm to search for closest relatives (<http://blast.ncbi.nlm.nih.gov/Blast.cgi>). Resulting ITS and 28S sequences of previously described *Hericium* spp. were downloaded. Sequences were aligned using Muscle v3.7 (Edgar 2004). Ambiguously

aligned regions and uninformative regions were removed with TrimAl v1.3 on the command line (Capella-Gutiérrez et al. 2009) with $gt = 0.60$ and $cons = 0.50$. We also constructed a combined ITS+28S dataset using MEGA7 (Kumar et al. 2015). Maximum likelihood (ML) analyses were done using IQ-TREE (Nguyen et al. 2015), of both individual datasets and a smaller concatenated ITS+28S dataset. Appropriate models of nucleotide substitution were selected under the Akaike Information Criterion corrected for small sample size (AICc) using jModelTest2 on XEDE (Darriba et al. 2012) on the CIPRES Science Gateway (Miller et al. 2010). For the ITS dataset, the HKY+G model was selected ($-\ln L = 2657.2323$); for 28S, the TrN+I+G model ($-\ln L = 3332.2045$). The models selected for the concatenated datasets were TrN+G for ITS ($-\ln L = 1998.2828$) and TrN+I+G for 28S ($-\ln L = 1863.5439$). ML was inferred for each individual dataset, as well as for the concatenated ITS+28S dataset under partitioned models (Chernomor et al. 2016). Rapid bootstrapping was inferred under 1000 replicates (Hoang et al. 2017).

Results

Over 4 years of plot-based sampling in DBR, we have vouchered thousands of ECM and saprotrophic taxa. Only a single collection of *Hericium* has ever been observed during this period. BLASTn searches of ITS and 28S sequences of this collection shared the closest identity with other *Hericium* species in GenBank. The final alignment of the *Hericium* ITS rDNA dataset contained 38 sequences and 619 positions of which 116 were parsimony-informative. In the ITS topology resulting from ML inference (Fig. 1), *H. bembedjaense* is part of a clade including 13 specimens of *H. coralloides* sensu lato. *Hericium bembedjaense* is sister to a strain annotated as *H. coralloides* from Argentina (FCUG 3209, Hallenberg et al. 2013), but these share only 90.70% sequence identity. Furthermore, *H. bembedjaense* shares only 89.09% sequence identity with *H. coralloides* FCUG 1229, the specimen that is believed to most closely represent *H. coralloides* sensu stricto (Larsson and Larsson 2003). The 28S rDNA alignment contained 48 sequences and 920 positions, of which 113 were parsimony-informative. The topology resulting from ML inference of the 28S dataset (not shown) revealed that this locus is not informative for *Hericium* at the species level. We also constructed a concatenated ITS+28S dataset, including 26 sequences (Table 1) and 1538 positions, of which 140 were parsimony-informative. The phylogenetic reconstruction of the two-locus dataset (Fig. 2) also places *H. bembedjaense* within the *H. coralloides* species complex. In both analyses (Figs. 1 and 2), taxa in several clades (e.g., *H. alpestre* and *H. erinaceus*) in addition to the *H. coralloides* complex are unresolved.

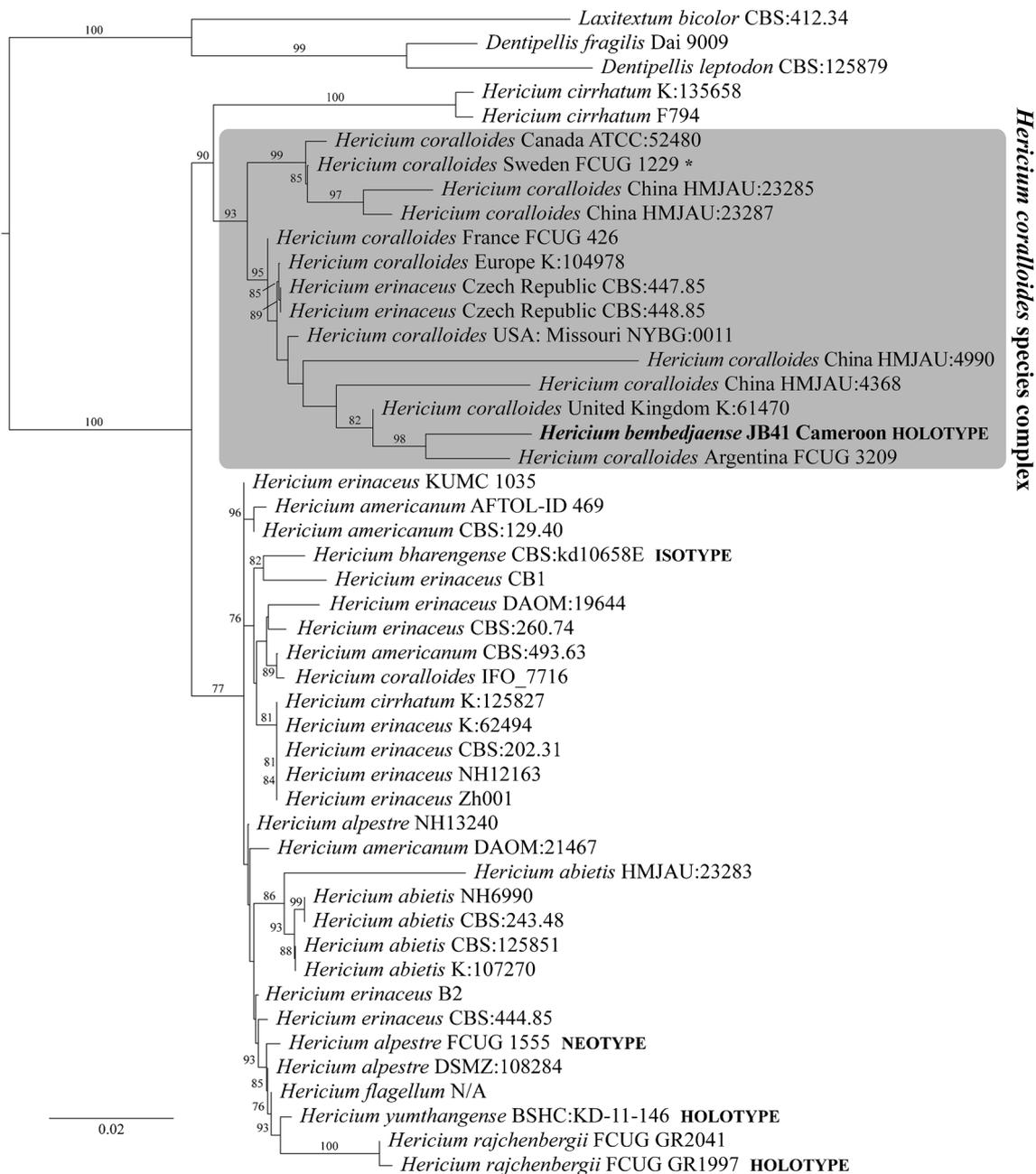


Fig. 1 Phylogeny of *Hericium*, reconstructed from the ITS dataset. The topology is the result of maximum likelihood inference performed with IQ-TREE under partitioned models. Only rapid bootstrapping support values of ≥ 70 are shown. Countries are shown (if known) for isolates

within the *H. coralloides* species complex. The asterisk (*) denotes collection from the same locale as the neotype of *H. coralloides*. The new species from Cameroon is highlighted in bold

Taxonomy

Hericium bembedaense Jumbam and Aime, sp. nov.

Figures 3, 4, and 5

Mycobank number: MB 830806

Type: Cameroon, East region, Dja biosphere reserve, 3° 21' 29.80" N, 12° 43' 46.90" E, alt. 650 m a.s.l., on dead fallen log of *Gilbertiodendron dewevrei* in a monodominant forest, 25 Apr 2018, B. Jumbam JB 41 (HOLOTYPE:

deposited and preserved as dried specimen in the Kriebel Herbarium, PUL F25402; isotype YA) GenBank accession nos. MK683483 (ITS) and MK683482 (28S).

Etymology: Referring to “bembe,” the indigenous Baka vernacular name of the host tree (*Gilbertiodendron dewevrei*) and “dja” for the type locality of the new species.

Diagnosis: Different from other species of *Hericium* in the production of pleurocystidia; different from *H. coralloides* in

Table 1 List of ITS and 28S sequences used for molecular phylogenetic analysis, with voucher/isolate, country of collection (when available), accession numbers, and references

Species	Isolate/voucher	Country	ITS	28S	Reference(s)
<i>Dentipellis fragilis</i>	Dai 9009	N/A	JQ349108	JQ349094	Zhou and Dai 2013
<i>Dentipellis leptodon</i>	CBS:125879	New Zealand	MH864083	MH875541	Vu et al. 2019
<i>Hericium abietis</i>	CBS:125851	N/A	MH863807	MH875271	Vu et al. 2019
<i>Hericium abietis</i>	CBS:243.48	Canada	AY534579	MH867882	Park et al. 2004; Vu et al. 2019
<i>Hericium abietis</i>	HMJAU:23283	China	JF430070		Wang et al. 2011
<i>Hericium abietis</i>	K:107270	UK	EU784259		Brock et al. 2009
<i>Hericium abietis</i>	NH6990	N/A	AF506456	AF506456	Larsson and Larsson 2003
<i>Hericium alpestre</i>	DSMZ:108284	Germany	MK491173	MK491173	E. Büttner and H. Kellner unpubl.
<i>Hericium alpestre</i>	FCUG 1555	Romania	JQ716936		Hallenberg et al. 2013
<i>Hericium alpestre</i>	NH13240	N/A	AF506457	AF506457	Larsson and Larsson 2003
<i>Hericium americanum</i>	AFTOL-ID 469	USA: Massachusetts	DQ206987	DQ411538	Matheny et al. 2007
<i>Hericium americanum</i>	CBS:129.40	N/A	MH856062		Vu et al. 2019
<i>Hericium americanum</i>	CBS:493.63	USA: New York	AY534581		Park et al. 2004
<i>Hericium americanum</i>	DAOM:21467	N/A	AF506458	AF506458	Larsson and Larsson 2003
<i>Hericium bharengense</i>	CBS:kd10658E	India	JN185603		Das et al. 2013
<i>Hericium cirrhatus</i>	F794		AF506385	AF506385	Larsson and Larsson 2003
<i>Hericium cirrhatus</i>	K:125827	Europe	EU784260		Brock et al. 2009
<i>Hericium cirrhatus</i>	K:135658	Europe	EU784261		Brock et al. 2009
<i>Hericium coralloides</i>	ATCC:52480	Canada	AY534584		Park et al. 2004
<i>Hericium coralloides</i>	FCUG 3209	Argentina	JQ716934		Hallenberg et al. 2013
<i>Hericium coralloides</i>	FCUG 426	France	JQ716935		Hallenberg et al. 2013
<i>Hericium coralloides</i>	HMJAU:23285	China	JF430072		Wang et al. 2011
<i>Hericium coralloides</i>	HMJAU:23287	China	JF430074		Wang et al. 2011
<i>Hericium coralloides</i>	HMJAU:4368	China	JF430062		Wang et al. 2011
<i>Hericium coralloides</i>	HMJAU:4990	China	JF430064		Wang et al. 2011
<i>Hericium coralloides</i>	IFO_7716	USA	AY534582		Park et al. 2004
<i>Hericium coralloides</i>	K:104978	Europe	EU784262		Brock et al. 2009
<i>Hericium coralloides</i>	K:61470	UK	EU784263		Brock et al. 2009
<i>Hericium coralloides</i>	RD282, FCUG 1229	Sweden	AF506459	AF506459	Larsson and Larsson 2003
<i>Hericium coralloides</i>	NYBG:0011	USA: Missouri	KY432832		B. Bomanz unpubl.
<i>Hericium erinaceus</i>	B2	Slovenia	AM981220		D. Jurc et al. unpubl.
<i>Hericium erinaceus</i>	CB1	China	GU584100		Yin and Chi 2015
<i>Hericium erinaceus</i>	CBS:202.31	The Netherlands	MH855186	MH866638	Vu et al. 2019
<i>Hericium erinaceus</i>	CBS:260.74	The Netherlands	DQ185922	MH872587	Park et al. 2004; Vu et al. 2019
<i>Hericium erinaceus</i>	CBS:444.85	Czech Republic	DQ185927		Park et al. 2004
<i>Hericium erinaceus</i>	CBS:447.85	Czech Republic	DQ185925		Park et al. 2004
<i>Hericium erinaceus</i>	CBS:448.85	Czech Republic	DQ185926		Park et al. 2004
<i>Hericium erinaceus</i>	DAOM:19644	Canada	JN649345	JN649345	Sjökvist et al. 2012
<i>Hericium erinaceus</i>	K:62494	Europe	EU784265		Brock et al. 2009
<i>Hericium erinaceus</i>	KUMC 1035	Korea	DQ185919		Park et al. 2004
<i>Hericium erinaceus</i>	NH12163	N/A	AF506460	AF506460	Larsson and Larsson 2003
<i>Hericium erinaceus</i>	Zh001	Tunisia	KY655903	KY655904	Ouali et al. 2018
<i>Hericium flagellum</i>	N/A	Poland	MG649451		M. Kujawska et al. unpubl.
<i>Hericium bembedjaense</i>	JB41	Cameroon	MK683483	MK683482	This study
<i>Hericium rajchenbergii</i>	FCUG GR1997	Argentina	JX403945		Hallenberg et al. 2013
<i>Hericium rajchenbergii</i>	FCUG GR2041	Argentina	JQ716939		Hallenberg et al. 2013
<i>Hericium yumthangense</i>	BSHC:KD-11-146	India	JX855033	JX855034	Das et al. 2013
<i>Laxitextum bicolor</i>	CBS:412:34	N/A	MH855587	MH867097	Vu et al. 2019

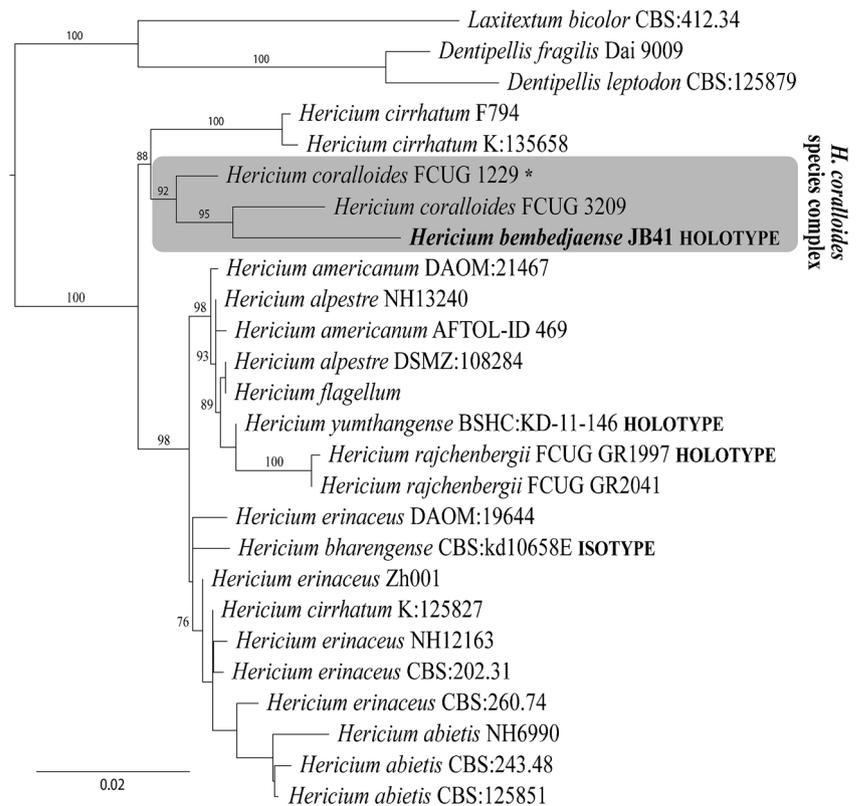
N/A not available

smaller basidiospores, longer and narrower basidia, and presence of pleurocystidia.

Description: *Basidioma* solitary, thick, fleshy, pendant, 120 × 70 mm, pale yellow (oac816) throughout, unchanging, branching up to six times from the main stipe attached to the underside of the host log, thicker primary branches diverging downward into progressively thinner secondary, tertiary, and

quaternary branches giving rise to numerous spines; *spines* ~ 3 mm long, irregularly distributed laterally, clustered terminally, tapering apically, concolorous with the branches, drying to become orange brown (oac740–oac741). *Exposed context* wet, unchanging. *Odor* fragrant, reminiscent of hibiscus. *Taste* indistinct to slightly sweet. *Hyphal system* monomitic; *contextual hyphae* generative, 3.0–8.3 μm wide, branching

Fig. 2 Phylogeny of *Hericium*, reconstructed from the concatenated ITS+28S rDNA dataset. The topology is the result of maximum likelihood inference performed with IQ-TREE under partitioned models. Only rapid bootstrapping support values of ≥ 70 are shown. The asterisk (*) denotes collection from the same locale as the neotype of *H. coralloides*. The new species from Cameroon is highlighted in bold



frequently, walls up to 0.4 μm wide; *hymenial tramal hyphae* 3.5–4.0 μm wide, hyaline in KOH, branching, walls < 0.4 μm wide; *gloeopleurous hyphae* 4.5–6.7 μm wide, abundant with dense yellowish-green content, aseptate, apex rounded to somewhat clavate. *Basidiospores* (2.6–)2.8(–3.0) \times (1.7–)2.0(–2.2) μm ; $Q = (1.0\text{--})1.35\text{--}1.70$), subglobose to broadly ovate, hyaline, amyloid, smooth to slightly roughened; *hilar appendix* 0.44 μm long. *Basidia* 13.5–27.0 \times 3.5–4.5 μm , subclavate to clavate, 2- to 4-sterigmate; *sterigmata* 3.4–4.5 \times 1.0–1.5 μm . *Gloeocystidia* 3.4–6.7 μm wide, cylindrical to aciculate, extending beyond

the hymenial palisade, with dense content. *Pleurocystidia* 13.5–24.7 \times 3.4–4.5 μm including the acuminate tip, ventricose–rostrate to mucronate–acuminate. *Hymenium* inamyloid; *subhymenial hyphae* thin-walled, up to 4.35 μm wide. *Clamp connections* abundant on hyphae of all tissues.

Discussion

An integrative taxonomic approach using multiple properties including morphology, ecology, host specificity, molecular phylogenetic data, and/or mating behavior is increasingly being employed for accurate delimitation of fungal species (e.g., Aime 2004; Araújo et al. 2015; Haelewaters et al. 2018; Sochorová et al. 2019), and has been applied to some species in *Hericium*, although accurate delimitations are far from resolved in this genus (Hallenberg et al. 2013). A contributing factor to this situation is the relative paucity of *Hericium* collections. Some species have been collected so infrequently that they are considered locally rare and added to regional Red Lists. This is the case for two taxa in some European countries: *H. coralloides* and *H. erinaceus* (Boddy et al. 2011; Kalucka and Olariaga Ibaruren n.d.). Other factors such as seasonal fruiting phenology may contribute to the low rate of *Hericium* encounters. In Cameroon, we found a single *Hericium* basidioma during a field survey from 21



Fig. 3 Field photograph of *Hericium bembedaense* at the Dja Biosphere Reserve, showing the irregularly branched basidiomata freshly collected from a fallen *Gilbertiodendron dewevrei* tree trunk. Photo: Bryn T.M. Dentinger

Fig. 4 Microscopic features of *Hericium bembedjaense* (Jumbam 41, holotype). **a** Pleurocystidia. **b** Basidia. **c** Gloeocystidia. **d** Basidiospores. Scale bars = **a–b** = 10 μ m, **c** = 20 μ m, **d** = 2.5 μ m

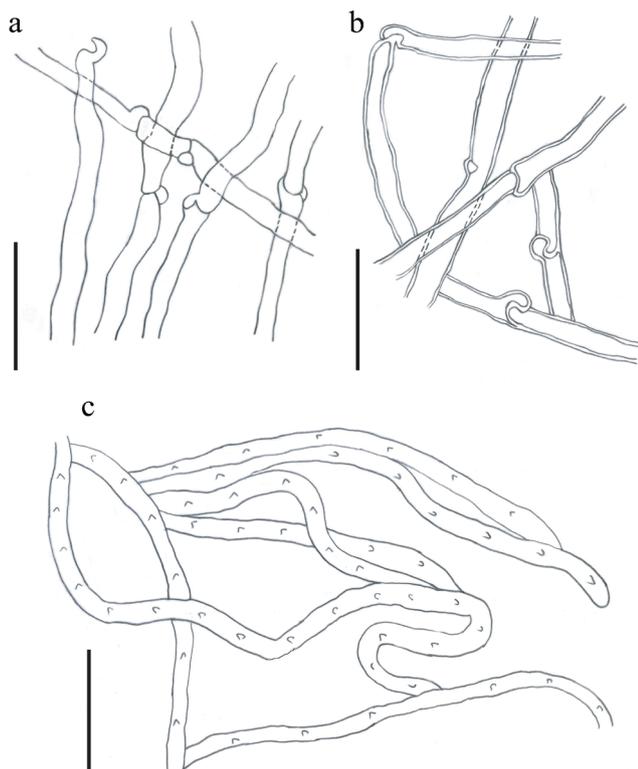
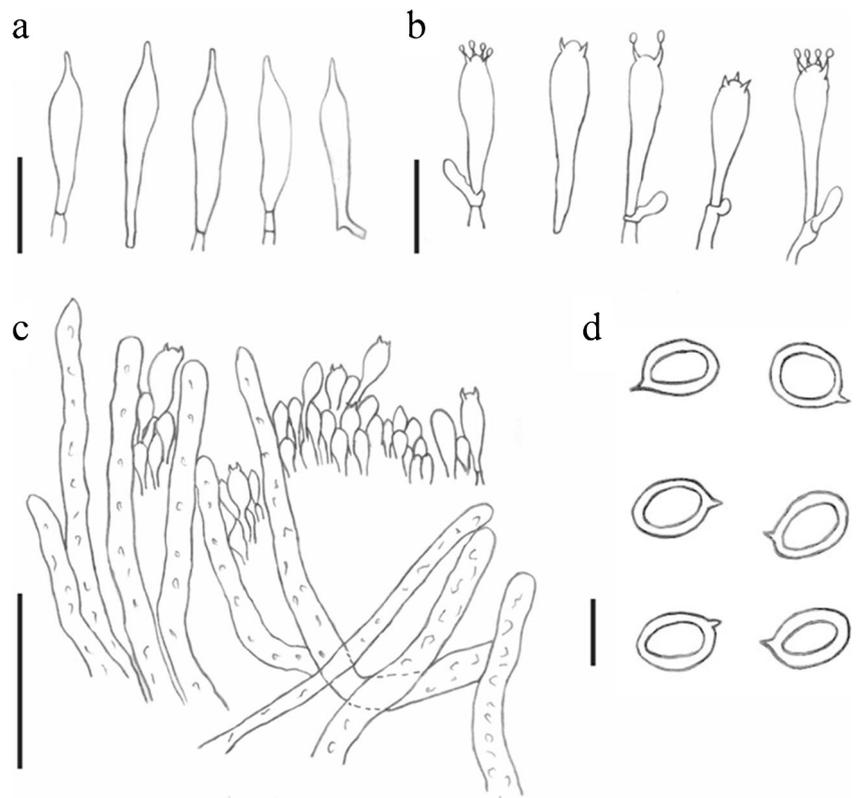


Fig. 5 Microscopic features of *Hericium bembedjaense* (Jumbam 41, holotype). **a** Tramal hyphae. **b** Thick-walled contextual hyphae. **c** Gloeopleurous hyphae. Scale bars = 20 μ m

Apr to 3 May 2018. Three previous expeditions conducted at the same site between Aug and Oct in 2015–2017 yielded no *Hericium* collections. This absence of fruiting body observations may be due, at least in part, to interspecific variations in fruiting seasons, leading to the possibility of missing individual fungal species during short periods of fieldwork (De Crop et al. 2019).

Hericium coralloides is believed to be a complex containing cryptic species (Hallenberg et al. 2013). Our Cameroonian species, *H. bembedjaense*, falls within this complex (Figs. 1 and 2). *Hericium coralloides* (Scop.) Pers. was designated as the type species for the genus (Persoon 1794) and the species was neotypified by Hallenberg (1983) using a specimen collected in 1948 from Femsjö (Småland Province) in Sweden that was growing on *Fagus silvatica*. No sequences are available for the neotype, though we included in our analyses a sequence from a more recent Swedish specimen (indicated by * in Figs. 1 and 2), collected in Östergötland Province, Åby, growing on a dead coniferous tree, culture FCUG 1229, GenBank accession no. AF506459 (Larsson and Larsson 2003). The neotype and FCUG 1229, collected in neighboring provinces in the southern part of Sweden (Göteborg), are presumed to be conspecific and so FCUG 1229 can be considered representative of *H. coralloides* sensu stricto. In both of our analyses, *H. bembedjaense* appears in a separate lineage from all northern temperate collections,

including FCUG 1229 (Figs. 1 and 2). *Hericium bembedjaense* and FCUG 1229 share only 89.09% sequence identity at the ITS locus, well below the threshold recommended for delimiting fungal species (e.g., Blaaid et al. 2013; Garnica et al. 2016; Niu et al. 2015).

Hericium bembedjaense differs from all other described species of *Hericium* in the presence of pleurocystidia (Fig. 4a). Additionally, *H. bembedjaense* differs from *H. coralloides* in several macro- and micromorphological features (*vide* Koski-Kotiranta and Niemela 1988), including shorter spines (~5 mm); smaller basidiospores ($3.5\text{--}5.0 \times 2.8\text{--}4.2 \mu\text{m}$ vs. $2.6\text{--}3.0 \times 1.7\text{--}2.2 \mu\text{m}$ in *H. bembedjaense*); and longer, more narrow basidia up to $15.0 \times 5 \mu\text{m}$. Apart from these morphological features, *H. bembedjaense* can be differentiated from other members of the *H. coralloides* complex by different substratum preferences (*G. dewevrei* for *H. bembedjaense* vs. Fagaceae spp. for *H. coralloides*) and geographic ranges (tropical Central Africa for *H. bembedjaense* vs. temperate North America and Eurasia for *H. coralloides*). *Hericium bembedjaense* is the first taxon after *H. coralloides sensu stricto* to receive a formal description in the *H. coralloides* species complex.

Hericium bembedjaense likely causes white rot of *G. dewevrei* and potentially other Congo Basin hardwoods, similar to rots caused by other members of *Hericium* on temperate hardwoods and conifers. From the African continent, only a few records of *Hericium* are known; *H. erinaceus* was recently reported from Tunisia (Ouali et al. 2018) and one (unvouchered) observation from Algeria has been submitted to the citizen-science platform iNaturalist (<https://www.inaturalist.org/observations/22251773>). Both of these countries are floristically part of the Mediterranean province of the Boreal floristic kingdom (Good 1974), where the fungi are more likely to share biogeographic connections with Europe. A single unvouchered observation in Madagascar is also present on iNaturalist (<https://www.inaturalist.org/observations/10099211>), but its affinities cannot be determined due to the absence of DNA data and micromorphology.

Conclusion

In this study, we present the first *Hericium* species from the sub-Saharan African tropical evergreen forest using data from morphology, DNA sequences, and ecology. Thus far, basidiomata of *Hericium* have been very rarely collected on the African continent. Most countries, especially in the Central African sub-region, are mycologically poorly explored because of a scarcity of trained African mycologists (Gryzenhout et al. 2012), political instability, and challenging field work conditions (De Crop et al. 2019). In addition, the timing of sampling around rainy seasons can be critical but

logistically difficult. Many *Hericium* species are important as sources of food and secondary metabolites; the documentation of a new species—the first from sub-Saharan Africa—highlights the importance of efforts to document tropical fungal diversity for potential future application.

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