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Ripartitella degreefii (Tricholomataceae), a new species from tropical Africa

JEAN-CLAUDE RIZINDE HAKIZIMANA[1,2], MARIO AMALFI[3,4], JÉRÔME DEGREEF[3,4], DENNIS DESJARDIN[5] & CONY DECOCK[1]*

[1] *Mycothèque de l'Université catholique de Louvain (BCCM/MUCL), Earth and Life Institute, Université catholique de Louvain, Croix du Sud 2 bte L7.05.06, 1348 Louvain-la-Neuve, Belgium.*
[2] *Université de Goma, Faculté des Sciences Agronomiques, Goma, BP 204 Goma, Democratic Republic of the Congo.*
[3] *Meise Botanic Garden, Nieuwelaan 38, 1860 Meise, Belgium.*
[4] *Service Général de l'Enseignement Supérieur et de la Recherche Scientifique, Fédération Wallonie-Bruxelles, 1080 Brussels, Belgium.*
[5] *Department of Biology, San Francisco State University, 1600 Holloway Ave., San Francisco, California 94132, USA.*
rizindej@gmail.com; *https://orcid.org/0009-0007-2254-3937*
mario.amalfi@plantentuinmeise.be; *https://orcid.org/0000-0002-1792-7828*
jerome.degreef@botanicgardenmeise.be; *https://orcid.org/0000-0002-2420-2999*
ded@sfsu.edu; *https://orcid.org/0000-0001-8079-5429*
**Corresponding author:* *cony.decock@uclouvain.be;* *https://orcid.org/0000-0002-1908-385X*

Abstract

A new species of *Ripartitella*, *R. degreefii*, is proposed based on phylogenetic, morphological, and ecological evidence from specimens collected in medium elevation (1000 to 2100 masl) forests of the Albertine Rift, in the Democratic Republic of Congo and São Tomé (Africa). The species is described and compared to phylogenetically related or morphologically similar species.

Keywords: Agaricales, Basidiomycota, wood-inhabiting fungus

Introduction

Ripartitella Singer (1947: 85) (Tricholomataceae, Basidiomycota) is a small, pantropical genus, originally typified by *R. squamosidisca* (Murrill) Singer (1947: 85), nowadays a synonym of *R. brasiliensis* (Speg.) Singer (1951: 452) (Ovrebo 1988). *Ripartitella brasiliensis* was originally described from Brazil (Apiaí, São Paulo State) as *Pleurotus brasiliensis* Speg. (1889: 398), whereas *R. squamosidisca* was described as *Marasmiums squamosidisca* Murrill (1940: 151) from Southeastern Florida, USA. Subsequently, several species were added, *viz*., *R. alba* Halling & Franco-Mol. (1996: 669), *R. brunnea* Ming Zhang, T.H. Li & T.Z. Wei (2019: 256), *R. ponderosa* (A.H. Sm. & Singer) Franco-Mol. (1993: 675), *R. rickenii* (Bohus) Singer (1986: 510), and *R. sipariana* (Dennis) Dennis (1970: 58).

However, DNA-based phylogenetic studies showed that *R. ponderosa* belonged to *Cercopemyces* T.J. Baroni, Kropp & V.S. Evenson (2014: 786), whereas *R. sipariana* has been transferred into *Cystodermella* Harmaja (2002: 43) (Capelari & Asai 2009, Zhang *et al.* 2019). *Ripartitella rickenii* was also transferred to *Cercopemyces* (Dima & Nagy 2015), without much comment, however. Therefore, currently, only three species are accepted in *Ripartitella*, *viz., R. brasiliensis*, *R. alba*, and *R. brunnea.*

Ripartitella is a wood-inhabiting genus characterized by the combination of small to medium-sized basidiomata with a collybioid habit; a central to slightly eccentric stipe, variably attached lamellae; hyaline, inamyloid, and rugulose basidiospores, and lageniform pleurocystidia the apex of which is often covered with crystals (Singer 1947, Wartchow *at al.* 2007; Battistin *at al.* 2016, Zhang *et al.* 2019). *Ripartitella* was originally placed in the Agaricaceae Chevall. (1826: 121), Tribe Cystodermatae Fayod, together with *Cystoderma* Fayod (1889: 350) (Singer 1947, 1986). However, DNA-based phylogenetic analyses revealed that *Ripartitella* is phylogenetically closely related to *Cercopemyces* and *Cystodermella* (Harmaja 2002, Saar *et al.* 2009, Baroni *et al.* 2014).

As far as tropical Africa is concerned, *R. brasiliensis* is the sole species currently reported for the continent (Pegler 1977, Desjardin & Perry 2017). Pegler (1977) reported the species from Eastern Africa (Kenya, Tanzania,

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and Uganda), whereas Desjardin & Perry (2017) reported it from a medium elevation forest of the western insular São Tomé. It is noteworthy that Pegler (1977) described the African specimens without cystidia. Based on the known distribution, *R. brasiliensis* in tropical Africa (*sensu* Pegler 1977, Desjardin & Perry 2017) is likely an Afromontane species.

As part of an ongoing survey of agarics (Basidiomycota) in tropical Africa (Degreef & De Kesel, 2017–www.efta-online.org), a collection of a *Ripartitella* species was found in the Kahuzi-Biega mountain range in eastern Democratic Republic of the Congo. Its phylogenetic affinities were inferred using the combined nuclear ribosomal ITS (ITS1–5.8S–ITS2) and LSU sequences. It was shown that it clustered with the specimen of *R. brasiliensis sensu* Desjardin & Perry (2017) from São Tomé, forming a well-supported terminal clade, distinct from the neotropical *R. brasiliensis* clade and any other, named or unnamed, species clade known to date.

Subsequent morphological examinations showed that our specimens from the Congo and São Tomé differed from *R. brasiliensis* by the scarcity of pleurocystidia. Consequently, *Ripartitella degreefii sp. nov*. is proposed, illustrated and described. Similarities and differences with the other species of *Ripartitella* are discussed.

Materials and methods

Site description

The specimens examined are from the Kahuzi Biega mountain range, in the eastern Democratic Republic of the Congo (DRC) (2.331733°S, 28.74848°E, elev. 2139 m. a.s.l, average precipitation 1900 mm/y, average temperature 20°C) and São Tomé (0.27595°N, 6.608767°E, elev. 1100 m a.s.l, average precipitation 1382 mm/y, average temperature 24.7°C). The specimens were collected in old growth forest at São Tomé (Desjardin & Perry 2017) and from a secondary forest in the Kahuzi Biega mountain range, where the vegetation is dominated by the tree species *Maesa lanceolata* Forssk. (Myrsinaceae), *Alangium chinense* (Lour.) Harms (Cornaceae) *Tabernaemontana johnstonii* (Stapf) Pichon (Apocynaceae), and *Polyscias fulva* (Hiern) Harms (Araliaceae).

Morphological examination

Colour codes are according to Kornerup & Wanscher (1981) and were estimated in both fresh and dry specimens. Handmade sections of dry specimens were examined in lactic acid, Cotton blue, Congo Red, and in Melzer's reagent to show any amyloid or dextrinoid staining reaction. All the microscopic measurements were done in Melzer's reagent. In presenting the size range of the microscopic structures, 5 % of the measurements at each end of the range are given in parentheses when relevant. In the text, the following abbreviations are used: Mean = arithmetic mean, Q = ratio of length/width of basidiospores. The dried specimens are deposited at the BR (Meise Botanic Garden, Belgium) and at the H.D. Thiers Herbarium (San Francisco State University (herbarium acronyms according to Thiers, continuously updated (http://sciweb.nybg.org/science2/IndexHerbariorum.asp).

Scanning Electron Microscopy

A few gills were placed in a fold of a filter paper (medium filtration rate; particle retention >5 µm) which was placed in a sample holder (stainless steel tube with meshed top and bottom) for critical point drying. The holder was submerged respectively for 30 min in 12 % ammonia, 2 × 20 min in 70 % ethanol, 4 × 15 min in dimethoxymethane and then 15 min in acetone, after which the sample was dried in a critical point dryer (Leica EP CDP 300). The dried sample was mounted on a 12.7 mm Ø aluminium specimen (Agar Scientific Ltd) stub with a double-sided carbon sticker (Agar Scientific Carbon Tabs). The stub was placed in a High Resolution Fine Sputter Coater for FE-SEM (JFC-2300HR Coating Unit, JEOL) and coated with a layer of approximately 10 nm Pl/Pd (using Argon gas, under 0.05 mbar pressure). The scanning electron microscopy was carried out in Meise Botanic Garden with a JEOL JSM-7100FLV Field Emission SEM with a tension of 2 kV and working distance of 6 mm.

DNA extraction, amplification and sequencing

Genomic DNA was extracted from fresh tissues of specimens using a CTAB 3 % solution isolation procedure adapted from Doyle & Doyle (1990). PCR amplification of the ITS region (nuclear ribosomal internal transcribed spacer) and LSU (large subunit ribosomal DNA) was performed using the primer pairs ITS1/ITS4, and LR0R/LR5, respectively (White *et al*. 1990). PCR products were purified by adding 1 U of Exonuclease I and 0.5 U FastAP Alkaline Phosphatase (Thermo Scientific, St. Leon-Rot, Germany) and incubating at 37 °C for 1 h, followed by inactivation at 80 °C for 15 min.

Sequencing was performed by Macrogen Inc. (Korea and The Netherlands) using the same primer combinations as for PCR. The sequences were assembled in Geneious Pro v. 6.0.6 (Biomatters).

Phylogenetic analysis

Materials and sequences used in this study are listed in Table 1. Initial BLAST searches (http://blast.ncbi.nlm.nih.gov) of both LSU and ITS-5.8S sequences were performed to estimate similarity with *Ripartitella* /other Agaricales sequences already present in the GenBank database (Table 1). Following the results of the BLAST search, sixteen sequences of *Ripartitella*, three of *Cercopemyces*, twelve of *Cystodermella*, 21 of *Cystoderma* and six *Ripartites* sequences were included in the dataset, including the newly generated sequences from our own specimens of *Ripartitella* from DRC and São Tomé (Table 1).

A combined dataset (including nuclear ribosomal partial LSU and ITS-5.8S) comprising sequences from 59 collections including the outgroup was constructed and used for further phylogenetic analyses. *Lepiota cristata* (Bolton) P. Kumm. (1871: 137), strain HKAS 61649, was used as the outgroup for the combined ITS-LSU dataset, following Capelari & Asai (2009).

Nucleotide sequences were automatically aligned using the MUSCLE algorithm (Edgar 2004) with default settings. The alignment was further optimized and manually adjusted as necessary by direct examination with the software Se-Al v. 2.0a11 (University of Oxford).

Potential ambiguously aligned segments, especially in ITS-5.8S alignment, were detected by Gblocks v0.91b (Castresana 2000; http://molevol.cmima.csic.es/castresana/Gblocks.html) with the following parameter settings: minimum number of sequences for a conserved position = 30 (minimum possible); minimum number of sequences for a flank position = 30 (minimum possible); maximum number of contiguous non-conserved positions = 4 bp, minimum block size = 4 bp, and gaps allowed within selected blocks in half of the sequences.

To detect the possible bias from substitution saturation and evaluate the phylogenetic signal, we tested each partition by using Xia's test (Xia *et al.* 2003, Xia & Lemey 2009), as implemented in DAMBE (Xia & Xie 2001). Because the Iss.c is based on simulation results, there is a problem with more than 32 species. To circumvent this problem, DAMBE was used to randomly sample subsets of 4, 8, 16 and 32 OTUs multiple times and to perform the test for each subset to see if substitution saturation exists for these subsets of sequences. In order to confirm the results of the Xia's method we also plotted the raw number of transversions and transitions against Tamura-Nei genetic distances with the aid of the DAMBE package, with an asymptotic relationship indicating the presence of saturation.

Models of evolution for BI were estimated using the Akaike information criterion (AIC) as implemented in Modeltest 3.7 (Posada & Crandall 1998).

Phylogenetic analyses were performed separately for each individual and concatenated loci using Bayesian Inference (BI) as implemented in MrBayes v3. 2 (Ronquist *et al.* 2011) and Maximum Likelihood (ML) as implemented in RAxML 7.2.7 (Stamatakis *et al.* 2008).

The best-fit models for each partition were implemented as partition specific models within partitioned mixed-model analyses of the combined dataset. All parameters were unlinked across partitions. Bayesian analyses were implemented with two independent runs, each with four simultaneous independent chains for six million generations, starting from random trees, and keeping one tree every 1000th generation. All trees sampled after convergence (average standard deviation of split frequencies < 0.01 and confirmed using Tracer v1.4 [Rambaut & Drummond 2007]) were used to reconstruct a 50 % majority-rule consensus tree (BC) and to calculate Bayesian Posterior Probabilities (BPP). BPP of each node was estimated based on the frequency at which the node was resolved among the sampled trees with the consensus option of 50 % majority-rule (Simmons *et al.* 2004). A probability of 0.95 was considered significant. Maximum Likelihood (ML) searches conducted with RAxML involved 1000 replicates under the GTRGAMMAI model, with all model parameters estimated by the program. In addition, 1000 bootstrap (ML BS) replicates were run with the same GTRGAMMAI model. We provided an additional alignment partition file to force RAxML software to search for a separate evolution model for each dataset. Clades with Maximum Likelihood bootstrap values of 75 % or greater were considered supported by the data.

To detect topological conflicts among data partitions, the nodes between the majority-rule consensus trees obtained in the ML analysis from the individual data sets were compared with the software compat.py (available at www.lutzonilab.net/downloads). Paired trees were examined for conflicts only involving nodes with ML BS > 75 % (Mason-Gamer & Kellogg 1996, Lutzoni *et al.* 2004, Reeb *et al.* 2004). A conflict was assumed to be significant if two different relationships for the same set of taxa (one being monophyletic and the other not) were observed in rival trees.

TABLE 1. List of collections used for DNA analyses, with origin, GenBank accession numbers and references.

Name of the speices	Specimen Voucher	Country	GenBank accession no.		**Reference**
			ITS	LSU	
Cercopemyces crocodilinus holotype	UTC 258260	USA	JX409899	NG071239	Kropp B and Baroni T 2012, unpublished
Cercopemyces ponderosus holotype	NR_119888	USA, Tennesseee	NR_119888	-	Matheny PB and Wolfenbarger AD 2014, unpublished
Cercopemyces rickenii	G0771	Hungary	-	MK277686	Varga *et al.* 2019
Cystoderma amianthinum	AFTOL-ID 1553	Sweden	DQ192177	DQ154108	Matheny PB and Hibbett DS 2005, unpublished
Cystoderma andinum isotype	C57998	Ecuador	NR_119475	AM946425	Saar *et al.* 2009
Cystoderma arcticum	KA16-1045	Kyrgyzstan	MK351684	-	Cho S 2018, unpublished
Cystoderma carcharias var. fallax	I. Kytovuori 92-1309	Finland	AM946485	AM946430	Saar *et al.* 2009
Cystoderma carcharias var. fallax	H (as holotype C. intermedium)	Finland	AM946488	-	Saar *et al.* 2009
Cystoderma castellanum holotype	LOU-F19663	Spain	LN878148	-	Saar 2016
Cystoderma chocoanum	NY-EFM629	Colombia	-	U85302	Johnson 1999
Cystoderma clastotrichum	PDD 83705	New Zealand	AM946490	AM946434	Saar *et al.* 2009
Cystoderma granosum	ZRL 20181937	-	MW242931	MW242943	Li J 2020, unpublished
Cystoderma japonicum holotype	Hongo 6221/ BR5020079022647	Japan	NR_119476	AM946435	Saar *et al.* 2009
Cystoderma jasonis	RAS200	USA	MG773835	-	Matheny PB, Hobbs AM and Swenie RA 2017, unpublished
Cystoderma jasonis	GLM 45917	Germany	-	AY207196	Walther *et al.* 2005
Cystoderma jasonis var. jasonis	TAA 182013	Estonia	AM946492	AM946436	Saar *et al.* 2009
Cystoderma jasonis var. lilacipes	TAA 147362	Finland	AM946495	AM946437	Saar *et al.* 2009
Cystoderma jasonis var. niveum	R. Saarenoksa 52585 (H)	Finland	AM946497	AM946438	Saar *et al.* 2009
Cystoderma jasonis var. saarenoksae	TAA 147361	Finland	AM946499	AM946440	Saar *et al.* 2009
Cystoderma liliaceum holotype	ZRL 20161878	China	MW242922	MW242948	Li J 2020, unpublished

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TABLE 1 (Continued**)**

Name of the speices	Specimen Voucher	Country	GenBank accession no.		**Reference**
			ITS	LSU	
Cystoderma muscicola	MEL 2362094	Australia	KP311425	KP311368	Bonito G and May TW 2014, unpublished
Cystoderma subvinaceum	WU19742	Austria	AM946501	AM946441	Saar *et al.* 2009
Cystoderma superbum	BR22288-75	Belgium	AM946504	AM946442	Saar *et al.* 2009
Cystoderma tuomikoskii holotype	H	Finland	AM946505	AM946444	Saar *et al.* 2009
Cystodermella adnatifolia	TAA 175640	Estonia	AM946510	AM946421	Saar *et al.* 2009
Cystodermella cinnabarina	TAA 147423	Estonia	AM946512	AM946429	Saar *et al.* 2009
Cystodermella cinnabarina f. nogalesi	BR5020002523012	Spain	LN878147	-	Saar 2016
Cystodermella cristallifera holotype	BR5020031802836	Africa, RDC	LN878146	-	Saar 2016
Cystodermella granulosa	TAA 147491	Estonia	AM946518	AM946431	Saar *et al.* 2009
Cystodermella granulosa var. ambrosii	T. Ulvinen 23 Aug 1974 (H)	Finland	AM946516	AM946422	Saar *et al.* 2009
Cystodermella lactea holotype	LUG9395	Switzerland	LN878144	-	Saar 2016
Cystodermella myriadocystis holotype	BR5020018682581	Belgium	LN878145	-	Saar 2016
Cystodermella papallactae isotype	C58002	Ecuador	NR_119478	AM94643	Saar *et al.* 2009
Cystodermella sp	PDD 94849	New Zealand	KF727402	KF727340	Johnston PR, and Park D 2013, unpublished
Cystodermella sp	Smith-2018 iNaturalist # 17339256	USA, Wisconsin	MK573917	-	Russell SD 2019, unpublished
Cystodermella terryi	2016-295	China	KY820054	-	Zhang et al 2019
Lepiota cristata	HKAS 61649	China	JN944090	JN940284	Ge ZW 2011, unpublished
Ripartitella alba isotype	NY 80066	Costa Rica	NR_119479	NG_060064	Saar *et al.* 2009
Ripartitella alba	R.E. Halling 7182 (NY)	Costa Rica	AM946525	AM946464	Saar *et al.* 2009
Ripartitella brasiliensis	A.E. Franco-Molano 499 (NY)	Colombia	AM946524	AM946465	Saar *et al.* 2009
Ripartitella brasiliensis	NY-EFM744	Colombia	-	U85300	Johnson and Vilgalys 1998

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TABLE 1 (Continued**)**

Name of the speices	Specimen Voucher	Country	GenBank accession no.		**Reference**
			ITS	LSU	
Ripartitella brasiliensis	FLAS-F-61262	USA, Florida	MH211841	-	Kaminsky et al 2018, unpublished
Ripartitella brunnea	GDGM 70592	China	MH660405	MH660408	Zhang et al 2019
Ripartitella brunnea	GDGM 70834	China	MH660406	MH660409	Zhang et al 2019
Ripartitella brunnea	HMAS 279808	China	MH660407	MH660410	Zhang et al 2019
Ripartitella degreefii sp. nov.	**SFSU DED 8323**	**Africa, São Tomé**	**MF100952**	-	**Desjardin & Perry 2017**
Ripartitella degreefii sp. nov.	**RHJ305 / BR5020189043549**	**Africa, RDC**	**OQ813454**	**OQ813455**	**this study**
Ripartitella sp	4-841	Japan, Yakushima Island	AB509988	-	Sato et al 2009, unpublished
Ripartitella sp	4-201	Japan, Yakushima Island	AB509611	-	Sato et al 2009, unpublished
Ripartitella sp	BZ-1689	Belize	JX462554	JX462553	Kropp and Baroni., unpublished
Ripartitella sp	FLAS-F-61822	USA, Florida	MH281887	-	Kaminsky et al 2018, unpublished
Ripartitella sp	PDD 71285	New Zealand	KF727403	KF727348	Johnston PR, and Park D 2013, unpublished
Ripartitella sp	FUNNZ 2017/1339	New Zealand	MF461603	-	Matheny PB, Swenie RA and Cooper J, unpublished
Ripartites albidoincarnatus	16177	Italy	JF908756	-	Garbelotto MM et al 2013, unpublished
Ripartites metrodii	5981	Italy	JF908748	-	Garbelotto MM et al 2013, unpublished
Ripartites odorus	ma010	Italy	MN595290	-	Rita *et al.* 2020
Ripartites sp	JAC 13105	Australia	KP191949	KP191768	Lebel T and Cooper J 2014, unpublished
Ripartites sp	Mushroom Observer 248705	USA	MK559718	MF765759	Clements TA 2019, unpublished
Ripartites tricholoma	CBS 484.50	France	MH856715	MH868234	Vu *et al.* 2019

Results

Phylogenetic analysis

The test of substitution saturation showed that the observed index of substitution saturation (*Iss*) for the ITS and LSU partitions (considered individually) was significantly lower than the corresponding critical index substitution saturation (*Iss.c*), indicating that there was little saturation in our sequences (P<0.001) (Table 2).

By comparing the tree topologies obtained for the individual datasets, no significant conflict involving significantly supported nodes was found using the 75 % ML BP criterion; the datasets were therefore combined.

Once excluding the 16 ambiguously aligned characters, the combined data set comprised 59 sequences including the outgroup and 1940 positions (840 position the ITS-5.8S partition and 1100 the nucLSU partition).

The general time reversible model (GTR+I+G), using the proportion of invariant sites and distribution of rates at variable sites modelled on a discrete gamma distribution with four rate classes, was estimated as the best-fit likelihood model of evolution for the [28S + ITS] full dataset, for BI and ML, using the Akaike information criterion (AIC) as implemented in Modeltest 3.7 (Posada and Crandall 1998). The two Bayesian runs (6,000,000 generations) converged to stable likelihood values after 1,000,000 generations; the first 25 % of the tree were discarded as burnin. The remaining stationary trees from each analysis were used to compute a 50 % majority rule consensus tree (BC) and to calculate posterior probabilities. In the ML searches, the alignment had 772 distinct patterns with a proportion of gaps and undetermined characters of 37.10 %.

TABLE 2. Summary of data sets used for phylogenetic inferences.

	Datasets	
Properties	ITS	LSU
Alignment size	840	1100
Excluded characters	16	-
Model selected	GTR+I+G	GTR+I+G
-Likelihood score	5875.1128	3211.9116
Base frequencies		
Freq. A =	0.2715	0.2753
Freq. C =	0.1830	0.1940
Freq. G =	0.1929	0.2760
Freq. T =	0.3526	0.2547
Proportion of invariable sites	0.2877	0.6059
Gamma shape	1.0176	0.5928
Test of substitution saturation		
Iss	0.453	0.445
Iss.cSym	0.692	0.754
P (Sym)	< 0.0001	< 0.0001
Iss.cAsym	0.364	0.454
P (Asym)	< 0.0001	< 0.0001

Note: Iss: index of substitution saturation. Iss.cSym: critical value for symmetrical tree topology. Iss.cAsym: critical value for extremely assymetrical tree topology. P: probability that Iss is significantly different from the critical value (Iss.cSym or Iss.cAsym).

The topologies of the consensus tree obtained from the Bayesian Inference (BI) and the most likelihood tree were nearly identical. The 50 % majority-rule consensus tree from BI of the combined dataset is presented in Figure 1. The phylogenetic analyses recovered the specimens from the eastern African and São Tomé Mountain range as a single, independent lineage that is sister to the *R. brunnea* clade, and distant from all other species clades shown to date (Fig. 1).

From these results, we concluded that our collections of *Ripartitella* from DRC and São Tomé correspond to a distinct phylogenetic species.

FIGURE 1. The 50 % majority-rule consensus tree from Bayesian Inference of the combined dataset. Thickened branches in bold represent ML BS support greater than 75 % and BPP greater than 0.95; thickened branches in black denote branches supported by either ML BS or BPP; for selected nodes ML BS support value and BPP are respectively indicated to the left and right of slashes; the new taxa are highlighted in the shaded box.

Taxonomy

Ripartitella degreefii Rizinde, Desjardin, Amalfi, & Decock, *sp. nov.* Figs. 2, 3

[Mycobank: MB842786]

Diagnosis:—The species is similar to *R. brasiliensis* in the basidioma habit, but differs in the paucity of pleurocystidia, a pileipellis as a cutis, and its habitat in mountain areas of tropical Africa.

Description:—*Basidiomata* cespitose, small to medium-sized (Fig. 2A, B). *Pileus* 25–70 mm diam., convex to plano-convex, becoming applanate and depressed, with (or without) a small obtuse umbo; surface dull, dry, pure white to off-white, disc with (or without) tiny, brownish orange (ferruginous 7C6–7]) scales when young, wearing off with age. *Margin* decurved to sometimes uplifted in age, centrally pure white to cream (4A3) with white appendiculate veil remnants. *Context* 1–2 mm thick, soft, white. *Lamellae* shallowly adnexed to adnate, crowded to very crowded, unequal, (24 (L+l) / cm), with 2–4 series of lamellulae, narrow (2–3 mm deep), with smooth edge, pale yellowish white (4A2). *Stipe* central to slightly eccentric, terete, subclavate to bulbous, 15–70 (–100) mm long, 3–10 mm broad, solid,

annulate, concolorous with pileus, squarrose, with superficial, scattered white velar remnants toward base, glabrous above the annulus. *Annulus* evanescent, single, membranous, felted, often incomplete, attached to the upper quarter of the stipe. *Odor* fungoid*, taste* not tested. *Spore print* white *Hyphal system* monomitic, composed of generative hyphae with clamp connections in all tissues. *Pileipellis* a cutis, made up of repent, subparallel, radially oriented, cylindric hyphae, 3.5–7 µm diam, smooth, thin-walled. *Pileus squamules* composed of subcatenulate, rarely encrusted hyphae, 5–10 µm diam. *Pileitrama* made up of interwoven hyaline, smooth, thin- to slightly thick-walled, hyphae, 2.5–7 µm diam. *Lamellar trama* similar to pileitrama. *Stipitipellis* a layer of ±parallel, longitudinally oriented hyphae, with scattered clusters of subcatenulate elements similar to those of pileipellis (Fig. 3C), individual cells 3.5–7 µm diam, smooth, thin-walled.

FIGURE 2. Basidiomes of *Ripartitella degreefii* (A=RHJ 305, holotype; B=DED 8323). Scale bar = 10 mm. Photos by J.C. Rizinde (RHJ 305) and D. Desjardin (DED 8323).

Basidiospores hyaline (Fig. 3G, H), broadly ellipsoid to subglobose, thin-walled, verrucose, inamyloid, acyanophilous, (3.5–) 4–5 × 3–3.8 µm (n = 30, mean = 4.3 × 3.4 µm, Q = 1.13–1.5). *Basidia* with a basal clamp, clavate, with 4 sterigmata (Fig. 3F), not siderophilous, 14–24 × 6–8 µm. *Pleurocystidia* absent or present (Fig. 3D), then scarce, difficult to observe, with a basal clamp, lageniform, thin- to thick-walled, apically smooth or slightly, finely or coarsely incrusted (Fig. 3E), 32–40 × 5.0–7.5 µm, the apical digitate part 2–2.5 µm diam (mean =36 × 6.5 µm, 2.3 µm in the apical section). *Cheilocystidia* not observed.

Distribution:—AFRICA. Known from the Eastern Democratic Republic of the Congo and São Tomé.

Ecology (substrate, host, habitat):—On fallen trunks of angiosperms, including, in DRC, *Xymalos monospora* (Harv.) Baill. (Monimiaceae, locally named "Cinyalubombo"), mountain forests, at 1100 and 2139 m a.s.l.

Etymology:—The species name is a tribute to Jérôme Degreef, scientific director at Meise Botanic Garden for his devotion to African mycology and his efforts for promoting the training of students from tropical Africa.

Material examined:—AFRICA. Democratic Republic of the Congo, South Kivu: Kahuzi Biega mountain range, Kahuzi Biega National Park, 2.331733°S, 28.74848°W, 2139 m a.s.l., on fallen trunk of *Xymalos monospora* (Harv.) Baill. (Monimiaceae), November 2018, *J.C. Rizinde* leg., *RHJ 305* (BR #5020189043549**, Holotype)**, culture ex-holotype MUCL 57374; SÃO TOMÉ: Macambrara radio antenna area; 0.27595°N, 6.608767°E, 1100 m elev., 25 April 2008, *D. E. Desjardin* leg. *DED 8323*; SÃO TOMÉ; Macambrara radio antenna area; 0.27595°N, 6.608767°E; 1100 m elev., April 2006, D. E. Desjardin leg., *DED 7937* (but material lost in transit to the USA).

Notes:—*Ripartitella degreefii* is phylogenetically distant from all other *Ripartitella* known to date (Fig. 1). Morphologically, *R. degreefii* is similar in many respects to *R. brasiliensis* (Capelari & Asai 2009, Desjardin & Perry 2017), but differs in having a pileipellis as a cutis (Fig. 3C) as opposed to a trichoderm (Capelari & Asai 2009), scarce (Fig. 3D–E) in contrast to abundant pleurocystidia (Capelari & Asai 2009), and a distribution in Afromontane forests in contrast to lowland neotropics. *Ripartitella brasiliensis* also has dense, brown to reddish brown squamules, covering the whole cap when young (Capelari & Asai 2009, Battistin *et al*. 2016). Squamules are variably present in young specimens of *R. degreefii* (Fig. 2), but soon wear off with age.

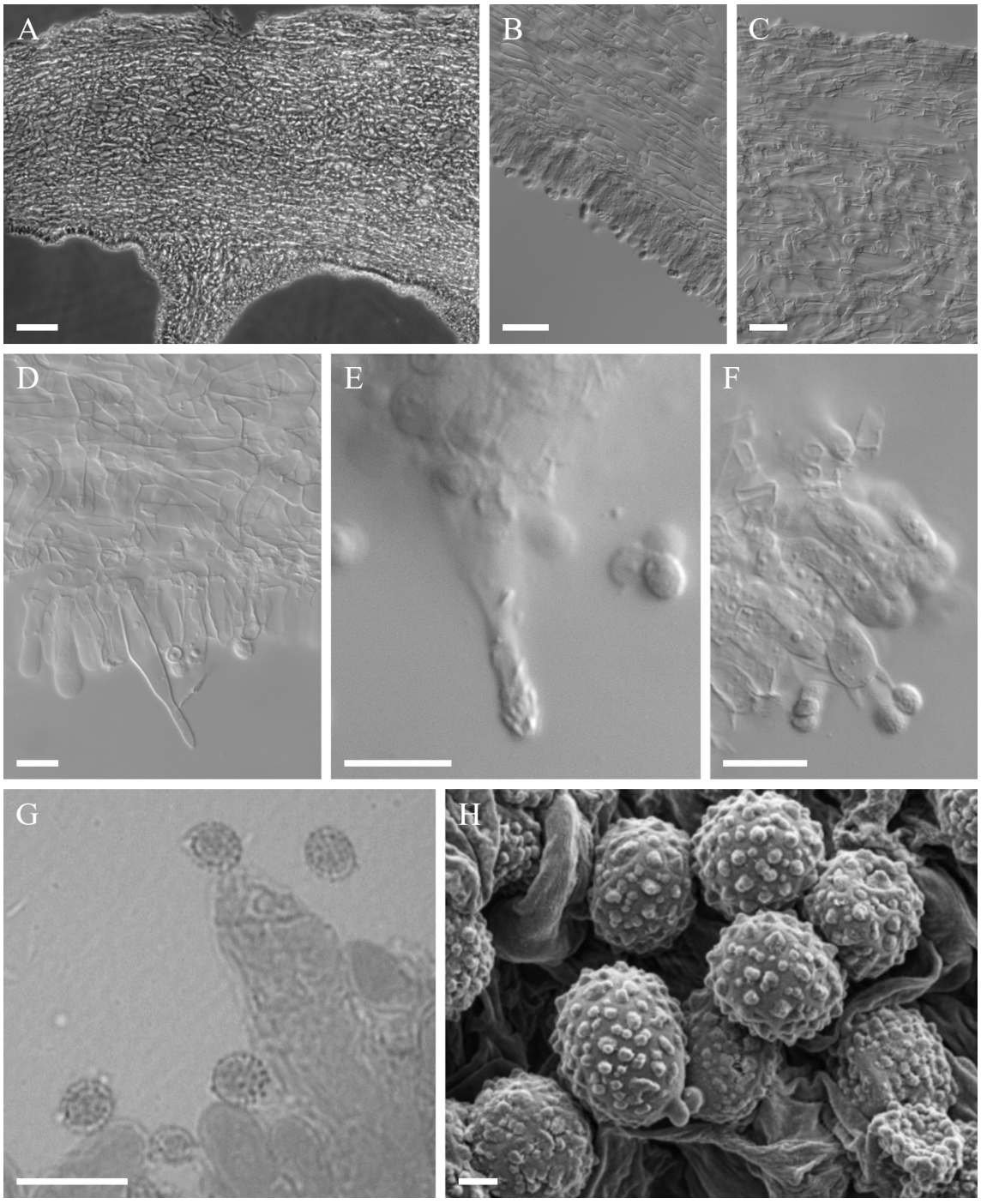

FIGURE 3. A. section of pileus; B. transversal section of lamellae; C. Pileipellis; D, E. Cystidia; F. Basidia; G = basidiospores from RHJ 305, optical microscopy; H = verrucose basidiospores from RHJ 305, SEM. Photos by C. Decock (A–F) and Mario Amalfi (G–H). Scale bars A= 100 µm; B, C = 20 µm; D–G= 10 µm.

Ripartitella degreefii is known so far from two collections originating from two spots of medium elevation forests, in the continental and insular Afromontane range, in the Albertine rift (DRC) and São Tomé. It is the first *Ripartitella* described from Tropical Africa. Pegler (1977) reported *R. brasiliensis* from Eastern Africa, in Kenya, Tanzania, and

Uganda. He described the eastern African collections as lacking cystidia (Pegler 1977). Pleurocystidia were observed in *R. degreefii*, in both specimens available. However, they are scarce and difficult to see. Desjardin and Perry (2017) reported *R. degreefii* under *R. brasiliensis* from São Tomé, stating that it matched "nicely the description of African material provided by Pegler (1977)". A closer examination of the São Tomé specimen revealed the presence of scarce pleurocystidia. The identity of the specimens cited by Pegler (1977) remains to be ascertained but they could represent *R. degreefii*.

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