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ORIGINAL ARTICLE

Revision of the taxonomic status of the genus *Gloeoporus* (Polyporales, Basidiomycota) reveals two new species

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Abstract

Gloeoporus Mont. is characterized by an easily separated gelatinous hymenophore and a continuous hymenium over the pore mouth. Recent molecular taxonomic and phylogenetic research showed that morphological grouping of *Gloeoporus* is polyphyletic. The lack of comprehensive phylogenetic studies of *Gloeoporus* exacerbates confusion in determining the taxonomic position of the genus. To delimit the genus *Gloeoporus*, we performed multi-locus phylogenetic analysis using the internal transcribed spacer (ITS) region, the nuclear large subunit ribosomal DNA (LSU), and the second-largest subunit of RNA polymerase II (*rpb2*). The phylogenetic analyses revealed that current delimitation of *Gloeoporus* is not monophyletic. *Gloeoporus* s.s. includes mostly clamped species lacking cystidia. Some species of *Gloeoporus* featuring simple septa and cystidia are proposed to be renamed to *Meruliopsis*. Two new species of *Gloeoporus* were also observed and they are named *Gloeoporus africanus* and *Gloeoporus orientalis.*

Keywords *Gloeoporus* · Multi-locus analysis · Phylogeny · *rpb2*

Introduction

Gloeoporus Mont. is a morphologically defined group of polypores with easily separated gelatinous hymenophore and a continuous hymenium over the pore mouth (Ryvarden and Johansen 1980). The genus was first established in 1842 by Montagne to describe the subtropical species *Gloeoporus conchoides* Mont. [syn. *Gloeoporus thelephoroides* (Hook.) G. Cunn.]. Species of *Gloeoporus* have pore surfaces with pinkish white, cream, or orange to deep reddish color and have small pores (Gilbertson and Ryvarden 1986). Fresh fruiting bodies have a gelatinous hymenophore, a distinguishing feature of *Gloeoporus*, which becomes resinous and cartilaginous when dry (Ryvarden and Gilbertson 1993). In a recent study on family-level classification of the Polyporales, *Gloeoporus* is located within the family Irpicaceae Spirin & Zmitr. (Justo et al. 2017).

Currently, *Gloeoporus* includes about 13 species mainly based on morphological characters, including a recent addition of *Gloeoporus citrinoalbus* Yuan Yuan & Jia J. Chen and *Gloeoporus hainanensis* Yuan Yuan & Jia J. Chen from tropical China (Coelho et al. 2006; Yuan et al. 2016). Among the species of *Gloeoporus*, two different hyphal systems are observed, either with simple-septate or clamped hyphae (Ryvarden 1991). For example, *Gloeoporus dichrous* (Fr.) Bres. and *Gloeoporus pannocinctus* (Romell) J. Erikss. have generative hyphae with clamp connections while *Gloeoporus taxicola* (Pers.) Gilb. & Ryvarden, *G. thelephoroides*, and *Gloeoporus guerreroanus* G. Coelho, R.M. Silveira &

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Rajchenb. have simple-septate generative hyphae (Coelho et al. 2006; Gilbertson and Ryvarden 1986; Niemelä 1985). Such intrageneric variability has long been perceived as a possible phenomenon in the Corticiaceae s.l. (Ryvarden 1991).

Recent molecular taxonomic and phylogenetic research, however, suggests that previous delimitation of *Gloeoporus* needs considerable revision. Numerous studies on the Polyporales show that a grouping *G. dichrous* and *G. pannocinctus* is well supported while *G. taxicola* has affinity with different genera (Binder et al. 2013; Jia et al. 2014). The lack of comprehensive phylogenetic studies of *Gloeoporus* exacerbates confusion in determining the taxonomic position of the genus. As a result, species in *Gloeoporus* still undergo constant reposition. As of February 2017, for example, Index Fungorum (http://www.indexfungorum.org) lists *G. dichrous* as *Gelatoporia dichroa* (Fr.) Ginns (2014), unlike MycoBank (http://www.mycobank.org) where the species is registered under *Gloeoporus*. Such disagreement calls for a need to define the taxonomic position of *Gloeoporus*.

In this paper, we present a taxonomic delimitation of the genus *Gloeoporus* based on a global collection of specimens. We aim to taxonomically reorganize the current artificial grouping of the genus through multi-locus phylogenetic analysis and propose *Gloeoporus* s.s. based on molecular and morphological characters of the genus. As DNA sequences of cosmopolitan species of *Gloeoporus* available in GenBank are limited, we collected additional specimens of other *Gloeoporus* species from several countries to perform molecular analyses for this study. In the course of analyses, two undescribed species of *Gloeoporus* were identified and are presented as new species.

Materials and methods

Specimens

For this study, dried specimens of *Gloeoporus* from ten countries, located in Africa, America, Asia, and Europe, were obtained from eight institutes around the world (Table 1). Any misidentified sample (i.e., not *Gloeoporus*) was disregarded from further analysis. Table 1 includes other *Gloeoporus* species collected and DNA sequences of related genera in the *Byssomerulius* clade (Floudas and Hibbett 2015) which also encompasses species of *Gloeoporus*. Microscopic features of the specimens were observed with Eclipse 80i light microscope (Nikon, Japan). Slides were prepared in 5% KOH for measurement. For the description of spore sizes, at least 30 spores were measured.

DNA extraction, amplification, and sequencing

A small piece of fungal tissue from each dried specimen was placed in a 1.5 mL tube containing 2× CTAB buffer. Samples were ground with plastic pestles. Genomic DNA was extracted with the modified CTAB extraction protocol (Rogers and Bendich 1994). Three regions were amplified for the multi-locus analysis: internal transcribed spacer (ITS) region, nuclear large subunit ribosomal DNA (LSU), and the second-largest subunit of RNA polymerase II (*rpb2*). The ITS region was amplified using the primers ITS1F and ITS4-B (Gardes and Bruns 1993) and LSU rDNA region using the primers LR0R and LR5 (Vilgalys and Hester 1990; White et al. 1990). The *rpb2* genes were amplified using primers RPB2-6F1/bRPB2-7.1R (Matheny 2005). The PCR amplification was performed in a C1000™ thermal cycler (Bio-Rad, USA) using the AccuPower® PCR premix (Bioneer Co., Seoul, Korea) in a final volume of 20 μL containing 10 pmol of each primer and 1 μL of genomic DNA. Thermocycler conditions for PCR of ITS and LSU followed Jung et al. (2014). The condition for amplification of *rpb2* is detailed at http://www.clarku.edu/faculty/dhibbett/rpb2%20 primers.htm. DNA sequencing was performed with an ABI3700 automated DNA sequencer (Applied Biosystems, Foster City, CA, USA) at Macrogen (Seoul, Korea).

Molecular phylogeny

For all molecular analyses, alignments were performed with MAFFT online version at http://mafft.cbrc.jp/alignment/server/(Katoh and Standley 2013) and manually adjusted in MEGA5 (Tamura et al. 2011). We used *Bjerkandera adusta* (Willd.) P. Karst. and *Terana caerulea* (Lam.) Kuntze as outgroups based on a previous study (Floudas and Hibbett 2015). Sequences of each gene were separately analyzed by maximum likelihood (ML) method in RAxML 8.2.9 (Stamatakis 2014) from the CIPRES Science Gateway (Miller et al. 2010) with combined rapid bootstrap and search for best-scoring ML tree analysis, the GTRCAT model of sequence evolution, and 1000 bootstrap replicates. Subsequently, we implemented ML analyses with a concatenated dataset of three genes (ITS, LSU, and *rpb2*), partitioned for the inferences. Trees generated from the analyses were checked and modified in FigTree 1.4 (Rambaut and Drummond 2012).

Results

Phylogeny of *Gloeoporus*

The PCR amplification of the ITS, LSU, and *rpb2* regions yielded single bands of about 700, 600, and 500 bp each,

Table 1 Specimens of *Gloeoporus* and related genera used for this study. Accession numbers in italic represent newly generated sequences

Species	Collection	Locality	ITS	LSU	*rpb2*
Gloeoporus cystidiatus	776308*	Brazil	*MG572749*	*MG572733*	*MG593278*
G. citrinoalbus	Dai 16,238	China	KU360397	KU360405	–
	Yuan 9654	China	KU360396	KU360404	–
G. dichrous	SFC20111001-71	Korea	*MG572750*	*MG572734*	*MG593279*
	BRNU 631507	Czech Republic	*MG572751*	*MG572735*	*MG593280*
	64251	Norway	*MG572752*	*MG572736*	*MG593281*
	HHB-17181	USA (VA)	*MG572753*	*MG572737*	*MG593282*
G. guerreroanus	ICN 139059**	Brazil	*MG572754*	*MG572738*	*MG593283*
G. hainanensis	Dai 15,268	China	KU360401	KU360411	–
	Yuan 4397	China	KU360400	KU360409	–
G. pannocinctus	FP-135015	USA (NY)	*MG572755*	*MG572739*	*MG593284*
G. taxicola	BU061013-38	Korea	*MG572756*	*MG572740*	*MG593285*
G. thelephoroides	BZ-2896	Belize	*MG572757*	*MG572741*	*MG593286*
G. orientalis	GJ050831-98**	Korea	*MG572758*	*MG572742*	–
	Cui 7261	China	*MG572759*	*MG572743*	*MG593287*
	Cui 8853	China	*MG572760*	*MG572744*	*MG593288*
	F20513	Taiwan	*MG572761*	*MG572745*	*MG593289*
	F-28839	Japan	*MG572762*	*MG572746*	*MG593290*
G. africanus	918063	Uganda	*MG572763*	*MG572747*	*MG593291*
	918572**	Uganda	*MG572764*	*MG572748*	*MG593292*
Bjerkandera adusta	HHB-12826-Sp	USA (AK)	KP134983	KP135198	KP134913
Byssomerulius corium	FP-102382	USA (WI)	KP135007	KP135230	KP134921
Ceraceomyces serpens	HHB-15692-Sp	USA (AK)	KP135031	KP135200	KP134914
Ceriporia lacerata	FP-55521-T	USA (LA)	KP135024	KP135202	KP134915
Ceriporia purpurea	KKN-223-Sp	USA (AZ)	KP135044	KP135203	KP134925
Ceriporia reticulata	RLG-11354-Sp	USA (AZ)	KP135041	KP135204	KP134922
Ceriporia spissa	FD-352	USA (MA)	–	KP135206	KP134924
Ceriporiopsis aneirina	HHB-15629-Sp	USA (AK)	KP135023	KP135207	–
Efibula americana	FP-102165**	USA (KY)	KP135016	KP135256	KP134916
Irpex lacteus	FD-9	USA (MA)	KP135026	KP135224	–
Leptoporus mollis	TJV93-174	USA (WA)	EU402584	EU402510	–
Meruliopsis albostramineus	HHB-10729	USA (VA)	KP135051	KP135229	KP134926
Meruliopsis sp.	FD-278	USA (FL)	KP135057	KP135205	KP134927
Phanerochaete allantospora	KKN-111-Sp	USA (AZ)	KP135038	KP135238	KP134923
Phanerochaete exilis	HHB-6988-Sp	USA (FL)	KP135001	KP135236	KP134918
Phanerochaete sp.	RLG-13408-Sp	USA (LA)	KP135020	KP135257	KP134920
Phanerochaete sp.	HHB-11463	USA (WI)	KP134994	KP135235	KP134892
Phanerochaete sp.	HHB-18104	New Zealand	KP135003	KP135254	KP134917
Phanerochaete xerophila	HHB-8509-Sp	USA (AZ)	KP134996	KP135259	KP134919
Terana caerulea	FP-104073	USA (MD)	KP134980	KP135276	KP134960
Trametopsis cervina	TJV-93-216T	USA (MS)	JN165020	JN164796	JN164877

*Probable isotype; **holotype

respectively. Their sequences were successfully obtained (Table 1). Separate molecular analyses of each gene resulted in phylogenetic trees similar in overall topologies while some discrepancies were observed. All three analyses concurred in clear delimitation of specific *Gloeoporus* species into one clade while the phylogenetic tree of ITS demonstrated lower resolution at basal branches for other specimens (data not shown). The phylogenetic tree of *rpb2* demonstrated overall high bootstrap values at most of the branches. The

phylogenetic analysis based on the concatenated dataset also agrees with the results of single-gene analyses as shown in Fig. 1.

Most of the species previously under *Gloeoporus* combined into a single clade while some *Gloeoporus* taxa lacking clamp connections such as *G. taxicola*, *G. cystidiatus* Ryvarden, and *G. guerreroanus*, intermingled with *Meruliopsis* Bondartsev species. A monophyletic group of *Gloeoporus* encompasses three clades: the first clade includes the two clampless species *G. thelephoroides* and *G. hainanensis*; the second clade has a single species with clamp connections, *G. pannocinctus*; and the third clade includes the clamped species *G. dichrous*, *G. citrinoalbus*, and two new species of *Gloeoporus* (Fig. 1).

The analysis reveals the existence of new species which are closely related to *G. dichrous* but molecularly and morphologically distinct. These two species exhibit a clamped hyphal system, as with the other two species

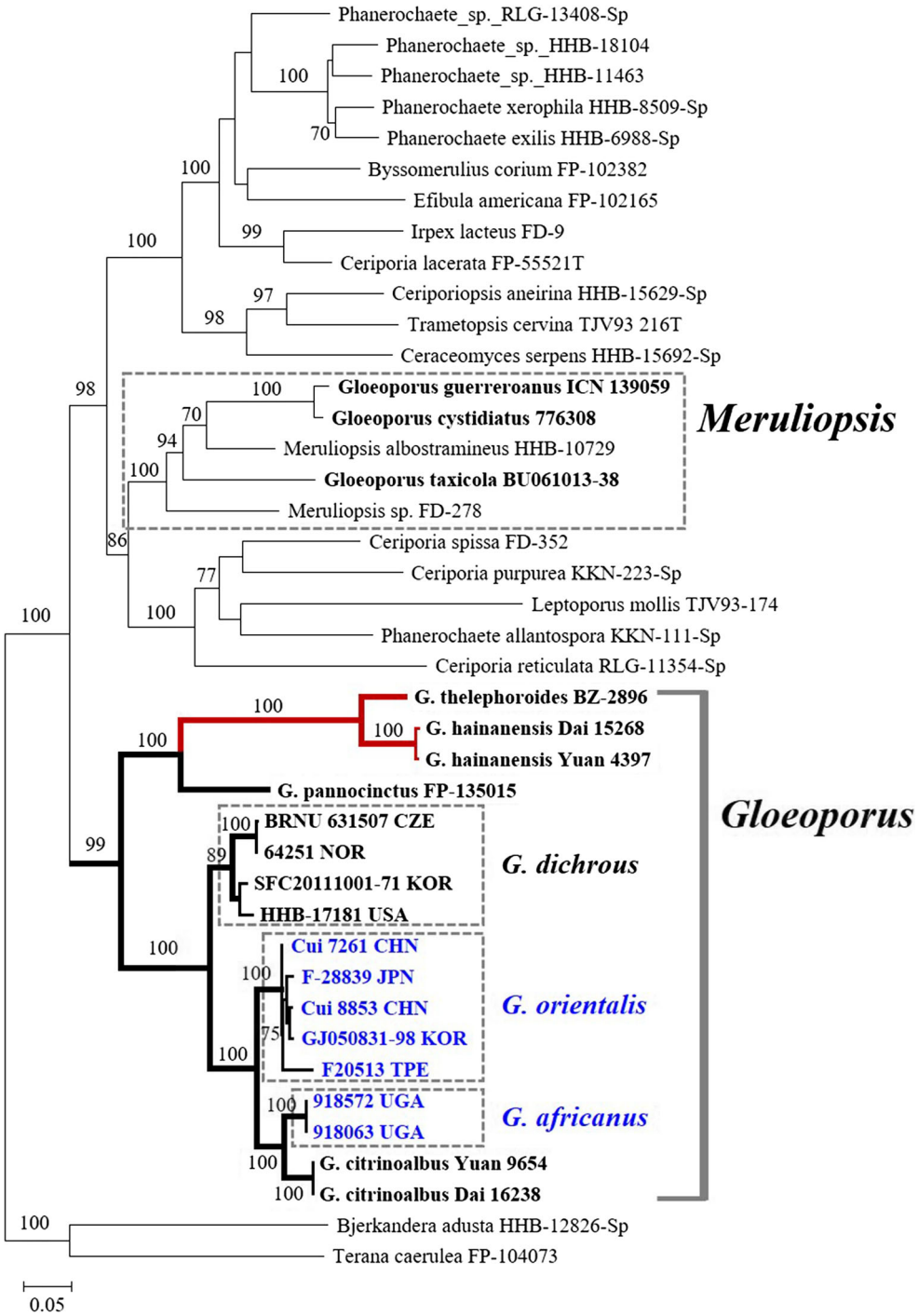

Fig. 1 Maximum likelihood tree of *Gloeoporus* and its related genera based on a combined dataset of three genes, ITS, LSU, and *rpb2*. Red branch represents clampless lineage

within the clade. The distinctive microscopic features of the new species are illustrated in Fig. 2. These specimens were originally identified as *G. dichrous* morphologically as their macro-morphology is nearly identical to *G. dichrous*. Further taxonomic descriptions of the two new species are included in the taxonomy section. The monophyletic *Gloeoporus* clade overall includes five species with clamped hyphae (*G. dichrous*, *G. pannocinctus*, *G. citrinoalbus*, and two new *Gloeoporus*) and two species with simple septa (*G. hainanensis* and *G. thelephoroides*). *Gloeoporus thelephoroides*, the type species of the genus, is closely related to *G. hainanensis*, which was recently discovered in Hainan, a tropical island in China (Yuan et al. 2016). *Gloeoporus citrinoalbus* has been reported from the same area in China, but forms a sister group to the African species *G. africanus*. These new species with *G. orientalis* form a sister group to *G. dichrous*. Among *G. dichrous* specimens, European specimens are grouped together against a set of Asian and American counterparts.

Taxonomy

Gloeoporus africanus P.E. Jung & Y.W. Lim, sp. nov.
MycoBank no.: MB 823871

Holotype *Uganda*. Bwindi Forest National Park, Ruhijah, Kabale, on a fallen rotting branch, 2 June 2003, 918572 (holotype in Herb. Oslo).

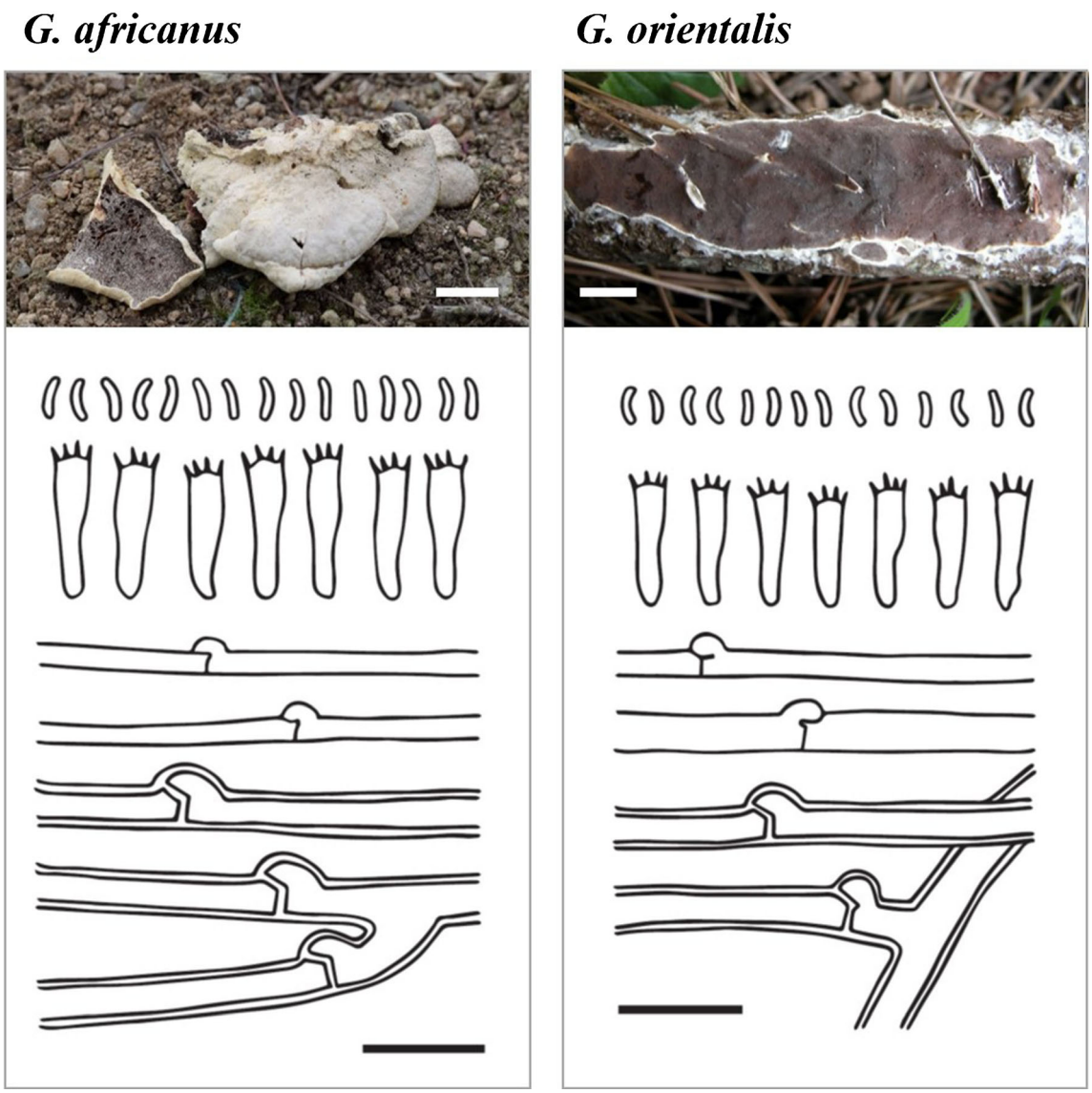

Fig. 2 Fruiting bodies and microscopic features of *Gloeoporus africanus* and *G. orientalis*. Fruiting body, basidiospores, basidia, and generative hyphae with clamp connections are shown from top to bottom. Scale bar = 1 cm in fruiting bodies and = 10 μm in microscopic features

Etymology Africanus (Lat.): referring to the African continent where this species was collected.

Basidiomata Annual, pileate, soft when fresh, somewhat brittle when dry. Pilei imbricate and some fused, up to 5 cm wide, typically less than 1 cm wide at base. Upper surface smooth, first white to cream, becoming beige with age. As pilei mature, a white edge forms near the margin, up to 5 mm wide. A brown line present between newly formed whiter edge and inner pileus in beige. Edge deflexed when dry. Pileus in section showing context of white edge distinguished from inward beige context by a thin brown line. Pore surface cartilaginous and gray to black when dry, edge distinguished from inward surface by a thin black line. Base cream to beige, byssoid, clearly contrasting with tube layer which easily separating from the context, pores circular and shallow, less than 0.5 mm deep, 6–8 per mm. Context white, up to 1 mm thick close to edge and up to 8 mm thick at base, clearly thicker than the tube layer.

Hyphal structure Hyphal system monomitic; generative hyphae with clamp connections.

Subiculum Generative hyphae, thick walled with large clamp connections, 4–5 μm wide.

Tubes Generative hyphae, 1.7–2.5 μm. Cystidia absent. Basidia clavate, 13.7–14.8 × 2.8–3.5 μm.

Spores Basidiospores allantoid, 3.8–4.2 × 0.6–0.7 μm.

Other material examined (paratype) *Uganda*. Bwindi Forest National Park, Rukingiri, on a rotting log, 8 November 2002, 918063

Distribution *Gloeoporus africanus* is only known in Uganda, Africa.

Remarks *Gloeoporus africanus* somewhat resembles *Bjerkandera adusta* in terms of the pore surface color. The latter, however, has angular pores and distinctive white edges on the pore surface when actively growing. *G. citrinoalbus* is easily distinguished from this species by a distinct lemon yellow pore surface. Microscopically, *G. africanus* can be differentiated from *G. dichrous* by the shorter basidia (Table 2).

Gloeoporus orientalis P.E. Jung & Y.W. Lim, sp. nov. MycoBank no.: MB 823872

Holotype *Korea*. Geoje Island, Gyeongsangnam-do, on a fallen angiosperm trunk, 31 August 2005 GJ050831-98 (holotype in SFC).

Etymology Orientalis (Lat.): referring to the Asian continent where this species was collected.

Basidiomata Annual, resupinate to effused-reflexed, soft when fresh, somewhat brittle when dry. Pore surface at first chestnut to light redwood color changing to reddish brown and brownish black with age. Margin cream to beige, byssoid and mostly wide (often 3–4 mm when actively growing), clearly contrasting with tube layer which easily separating from subiculum. Pores circular and shallow, less than 0.5 mm deep, 7–9 per mm. Subiculum white, up to 2 mm thick at margin, less than 1 mm in the middle, clearly thicker than the tube layer at margin.

Hyphal structure Hyphal system monomitic; generative hyphae with clamp connections.

Subiculum Generative hyphae, thick walled with large clamp connections, 4–6.3 μm wide.

Tubes Generative hyphae, 2.2–3.5 μm. Cystidia absent. Basidia clavate, 11.4–12.5 × 2.5–2.8 μm.

Spores Basidiospores allantoid, 3.0–3.6 × 0.6–0.8 μm.

Other materials examined (paratypes) CHINA. GUANGDONG: Chebaling, on a fallen angiosperm trunk, 26 June 2010, *Cui 8853* (BJFC); HENAN: Yuntai Mountain, on angiosperm stump, 4 September 2009, *Cui 7261* (BJFC). TAIWAN. NANTOU: Lienhuachih, on rotten angiosperm trunk, 14 December 2006, *F20513* (TNM). JAPAN. TOKYO: Bonin Island, 13 November 2013, *F-28839* (TFM).

Table 2 Comparison of microscopic features of *Gloeoporus dichrous* and new *Gloeoporus* species

	Specimen	No. of pores (mm)	Basidia size (μm)	Spore size (μm)
G. africanus	918063 UGA	6–8	13.7–14.8 × 2.8–3.5	3.8–4.2 × 0.6–0.7
G. dichrous	HHB-17181 USA	4–6	13.1–16.9 × 3.7–4.1	3.6–5.2 × 0.6–1.2
	916456 NZL	4–5	15.6–17.6 × 3.3–4.3	4.0–5.6 × 1.2–1.8
	F20963 TPE	4–6	15.6–16.9 × 3.2–4.0	(3.6–4.8 × 1.0–1.4)
	286284 NOR	4–6	(14.0–18.0 × 3.0–4.0)	(3.5–5.5 × 0.7–1.5)
G. orientalis	GJ050831-98 KOR	7–9	11.4–12.5 × 2.5–2.8	3.0–3.6 × 0.6–0.8

Distribution *Gloeoporus orientalis* is found in East Asian countries, China, Taiwan, Japan, and Korea. The geographic habitat of *G. orientalis* overlaps with *G. dichrous*; yet, specimens of *G. orientalis* are reported from somewhat remote areas, such as a nature reserve of China and a remote island of Japan, suggesting that the species may not be as common as *G. dichrous*.

Remarks The fruiting body of *G. orientalis* is resupinate to effused-reflexed. While the macro-morphology of *G. orientalis* resembles *G. dichrous*, the latter has larger pores, larger basidia, and more cylindrical basidiospores (Table 2). *Gloeoporus africanus* can be distinguished from *G. orientalis* by its imbricate pilei and slightly larger basidia and spores (Table 2).

Meruliopsis cystidiata (Ryvarden) P.E. Jung & Y.W. Lim, comb. nov.

MycoBank no.: MB 823876

Basionym: *Gloeoporus cystidiatus* Ryvarden, Mycotaxon 28 (2): 528 (1987)

= *Gloeoporus guerreroanus* G. Coelho, R.M. Silveira & Rajchenb., Mycologia 98 (5): 821 (2006)

Materials examined BRAZIL. AMAZONAS, on wood, 12 13 Mar 1984, 776,308 (NYBG), holotype of *G. cystidiatus*; BRAZIL, Rio Grande do Sul: Santa Maria, Boca do Monte, FEPAGRO, on bamboo, 3 Oct 2005, ICN 139059 (ICN), holotype of *G. guerreroanus*.

Notes Ryvarden (1987) described this species as a "characteristic species in *Gloeoporus*" due to the presence of cystidia in the hymenium. The molecular phylogeny of this study, however, demonstrates that *Gloeoporus* sensu stricto lacks cystidia in the hymenium. Coelho et al. (2006) stated that *G. guerreroanus* differs from *G. cystidiatus* based on the microscopic features such as cystidia size and basidiospore shape and its bamboo host. The size ranges of cystidia of two proposed species, however, largely overlap and different basidiospore shapes may be considered as an intraspecies variation. These two species have noticeably similar morphological characteristics (e.g., purpuraceous hymenophore and microscopic features), and phylogenetic analysis supports that the two species are conspecific (Fig. 1).

Meruliopsis taxicola (Pers.) Bondartsev

MycoBank no.: MB 300911

Basionym: *Xylomyzon taxicola* Pers., Mycologia Europaea 2: 32 (1825)

≡ *Merulioporia taxicola* (Pers.) Bondartsev & Singer, Annales Mycologici 39 (1): 48 (1941)

≡ *Merulioporia taxicola* (Pers.) Bondartsev & Singer, Trut. Grib Evrop. Chasti SSSR Kavkaza: 593 (1953)

≡ *Gloeoporus taxicola* (Pers.) Gilb. & Ryvarden, Mycotaxon 22 (2): 364 (1985)

Notes *Meruliopsis taxicola* has been often misguidedly referred to as *Gloeoporus taxicola* due to morphological similarities with *G. dichrous*. Numerous phylogenies inferred from multi-locus genes (Binder et al. 2013; Wu et al. 2010), including this study, demonstrate that this species is clearly separated from *Gloeoporus* s.s. and should be denoted as *Meruliopsis*.

Discussion

The current morphological circumscription of *Gloeoporus* sensu lato is polyphyletic based on the molecular phylogenetic analyses of this study. According to these results, the clade with the type species *G. thelephoroides* includes species with either clamped or simple-septate generative hyphae and lacking cystidia. While mixed hyphal systems in *Gloeoporus* may appear somewhat counterintuitive, other genera in the phlebioid clade also exhibit the same phenomenon. *Phanerochaete* P.Karst. and *Rhizochaete* Gresl., Nakasone & Rajchenb. (Greslebin et al. 2004) are such examples. Floudas and Hibbett (2015) also stated that existence of clamped species in *Phanerochaete* (which mostly encompasses species lacking clamp connections) should be accepted in defining *Phanerochaete* sensu stricto. The clade of *Gloeoporus* s.s. is robustly supported by each phylogenetic analysis (ITS, LSU, *rpb2*) and the combined analysis.

Two species with simple-septate hyphae, *G. cystidiatus* and *G. guerreroanus*, have closer affinities with species of *Meruliopsis*, typified by *Meruliopsis* (*Gloeoporus*) *taxicola*. The taxonomic relationship of the two well-known species *G. dichrous* and *G. taxicola* has been uncertain and questioned by numerous taxonomists. Based on their morphology, *G. dichrous* and *G. taxicola* were often considered congeneric. Recent taxonomic studies suggest that they are both positioned in the phlebioid clade of the Polyporales, but not as closely related as previous taxonomists had believed (Binder et al. 2013; Skaven Seierstad et al. 2013; Wu et al. 2010). *Gloeoporus guerreroanus* was published as a new species in 2006 based on morphology only (Coelho et al. 2006). Phylogenetic analyses of this study, however, reveal that the species is not part of *Gloeoporus* s.s. Furthermore, *G. guerreroanus* has noticeably similar morphological characteristics with *G. cystidiatus* (e.g., purpuraceous hymenophore and microscopic features), and the two species should be considered as conspecific. In brief, we propose that cystidium-forming species of *Gloeoporus* be renamed to *Meruliopsis*.

The genus *Gloeoporus* includes several species which are found in tropical/subtropical regions and have not been sequenced for molecular analyses. For example, *G. longisporus*, the recent new species published in 2010 is reported from Costa Rica. Mata and Ryvarden (2010) describe the species as lacking both cystidia and clamp connections;

thus, phylogenetic assessment is required to verify the taxonomic position of this species. Extensive studies of the tropical mycobiota, based on molecular taxonomic methods, will be needed to realize the diversity of this genus.

Gloeoporus dichrous and the new species of *Gloeoporus* have nearly identical macro-morphology. *Gloeoporus dichrous* and *G. orientalis* display white cottony (byssoid) margins which sharply contrast with the dark pore surfaces. The pore surface of *G. dichrous* has a varying color from light reddish to dark purplish and brown depending on the degree of senescence. While the *G. dichrous* has a reddish brown pore surface typical at its earlier stage (Lim et al. 2010), *G. orientalis* has dark purplish color which may easily be considered as *G. dichrous* at its mature stage.

Due to remarkably similar morphology to *G. dichrous*, both new species of *Gloeoporus* may have been repeatedly identified as *G. dichrous* based on their physical traits. Moreover, sympatric distribution of the new species with *G. dichrous* may have hindered discovery of these species. *Gloeoporus orientalis* occurs throughout Korea, China, Taiwan, and Japan and *G. africanus* in Uganda. *Gloeoporus orientalis* is observed from areas where anthropogenic effect is rather small, such as a remote island of Japan and nature reserves of China. *G. africanus* was recorded from Bwindi Impenetrable Forest, a primeval forest in Uganda. While more research is required to understand their ecology and distribution pattern, these species may possibly be rare and easily affected by environmental disturbance. Thorough and extensive sampling, coupled with molecular analysis, may further uncover the diversity hidden under the macroscopic familiarity.

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