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A phylogenetic and taxonomic study on *Ceriporiopsis* s. str. (Polyporales) in China

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With 4 figures and 1 table

Abstract: Two new resupinate species in Polyporales, *Ceriporiopsis fimbriata* and *C. rosea*, are described from southern China on the basis of morphological and molecular examination. *Ceriporiopsis fimbriata* is characterized by an annual growth habit, resupinate basidiocarps with white to clay-pink pore surface when fresh, become cinnamon to yellow-brown when dry, sterile margin fimbriate, generative hyphae encrusted with pale yellow crystals, oblong-ellipsoid to subcylindrical basidiospores (4.4–5 × 1.7–2.1 µm), and plenty of pale-yellow to pale-orange oily substances present in subiculum and trama. *Ceriporiopsis rosea* is distinguished by annual, resupinate basidiocarps with rose to vinaceous pores when fresh, become orange brown to reddish brown upon drying, generative hyphae bearing crystalline incrustations, broadly ellipsoid basidiospores (4–5.2 × 3.2–3.8 µm). Phylogenetic analysis inferred from the internal transcribed spacer (ITS) regions and nuclear large subunit (nLSU) ribosomal RNA gene regions demonstrated that the two new species were grouped into the phlebia clade. A key to worldwide species of *Ceriporiopsis* sensu stricto in phlebia clade is provided.

Key words: Phanerochaetaceae, phylogeny, Polypore, taxonomy, wood-rotting fungi.

Introduction

Ceriporiopsis Domański (Phanerochaetaceae, Polyporales) is a large, cosmopolitan genus characterized by a combination of annual, resupinate or effused-reflexed basidiocarps, a monomitic hyphal structure with clamp connections, and hyaline, thin-walled, subcylindrical to ellipsoid basidiospores. In addition, its hyphae and spores are acyanophilous and negative in Melzer's reagent. The genus was typified by *Ceriporiopsis gilvescens* (Bres.) Domański and causing a white rot (Gilbertson & Ryvarden 1986, Ryvarden & Gilbertson 1993, Núñez & Ryvarden 2001). So far about 30 species have

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been accepted in the genus worldwide (Hattori 2002, Bernicchia & Ryvarden 2003, Kinnunen & Niemelä 2005, Dai et al. 2007, Fortey & Ryvarden 2007, Læssøe & Ryvarden 2010, Tomšovský et al. 2010, Vlasák et al. 2012, Cui 2013, Zhao & Cui 2014).

Recently, molecular study employing multi-gene datasets by Binder et al. (2013) demonstrated that the type species of *Ceriporiopsis* (*C. gilvescens*) belongs to the phlebioid clade and appeared to be grouped with *Ceraceomyces* Jülich, *Ceriporia* Donk and *Phlebia* Fr. Phylogenetic study of European *Ceriporiopsis* taxa suggested that the genus is polyphyletic, and the type *Ceriporiopsis gilvescens* was grouped with *Phlebia* spp. on the base of the combined data of the nLSU and mitochondrial small subunit rRNA (mtSSU) gene sequences (Tomšovský et al. 2010). Vlasák et al. (2012) described a new species *Ceriporiopsis pseudoplacenta* Vlasák & Ryvarden based on ITS and nLSU sequences, which was clustered into the phlebioid clade, too.

Some *Ceriporiopsis* species including the generic type (*C. gilvescens*) were nested with the genera *Ceraceomyces*, *Mycoacia* Donk, *Phlebia* and *Phanerochaete* P. Karst. based on phylogenetic analysis. However, macroscopically the later genera have smooth, tuberculate, hydnaceous, phlebioid, or merulioid hymenophore (Parmasto & Hallenberg 2000, Nakasone 2002, Moreno et al. 2011, Binder et al. 2013). It seems that the hymenophore configuration for the species in the phlebioid clade is not important. Zhao & Cui 2014 described two new poroid species in *Ceriporiopsis* based on their morphological characters and rDNA sequences, and these two species belong to the phlebioid clade, too.

Polypore diversity in southern China has been extensively studied, and many new species have been described (Dai et al. 2002, 2010, 2011, 2014, Cui et al. 2009, 2011, Dai & Li 2010, Chen & Cui 2012, 2014, Zhou & Dai 2012, 2013, Cui & Dai 2013, Cui & Decock 2013, Li & Cui 2013, Li et al. 2013, Zhao & Cui 2013, Han et al. 2014, Jia et al. 2014, Song et al. 2014), including four new species of *Ceriporiopsis* (Dai et al. 2007, Cui 2013, Zhao & Cui 2014). During investigations on the diversity of polypores in southern China, two additional undescribed species corresponding to *Ceriporiopsis* were found. To confirm the affinity of the two new taxa of *Ceriporiopsis*, phylogenetic analysis was carried out based on ITS and nLSU sequences. In addition, a key to worldwide species of *Ceriporiopsis* sensu stricto in phlebia clade is provided.

Materials and methods

Morphological study: The studied specimens were deposited in the herbaria of the Institute of Microbiology, Beijing Forestry University (BJFC) and the Institute of Applied Ecology, Chinese Academy of Sciences (IFP). Macro-morphological descriptions were based on field notes. Color terms followed Petersen (1996). Microscopic measurements and drawings were made from slide preparations of dried specimens stained with Cotton Blue and Melzer's reagent, the light microscopic study followed Zhao et al. (2013). Sections were studied at ultimate magnification ×1000 using Nikon Eclipse 80i microscopy and phase contrast illumination. Drawings were made with the aid of drawing tube. Spores were measured in tube sections. In presenting spore size variation, 5% of measurements were excluded from each end of the range and given in parentheses. The following abbreviations were used: KOH = 5% potassium hydroxide, CB = Cotton Blue, CB- = acyanophilous, IKI = Melzer's reagent, IKI- = both inamyloid and indextrinoid, L = mean spore length (arithmetic average), W = mean spore width (arithmetic average), Q = L/W ratio for a specimens studied, n (a/b) = number of spores (a) measured from given number of specimens (b).

Molecular phylogeny: The fungal taxa used in the phylogenetic analysis were listed in Table 1. A Phire® Plant Direct PCR Kit (Finnzymes, Vantaa, Finland) was used to obtain PCR products from dried specimens, according to the manufacturer's instructions. ITS regions were amplified with primers ITS4 and ITS5 (White et al. 1990), and the nLSU with primers LR0R and LR7 (http://www.biology.duke.edu/fungi/mycolab/primers.htm). PCR conditions was as follows: initial denaturation at 98°C for 5 min, followed by 39 cycles at 98°C for 5 s, 58°C for ITS and 48°C for nLSU for 5 s, 72°C for 5 s, and a final extension of 72°C for 10 min. DNA sequencing was performed at Beijing Genomics Institute, China, with the same primers. All newly generated sequences were submitted to GenBank (Table 1).

Sequences generated in this study were aligned with additional sequences downloaded from GenBank (Table 1) using ClustalX (Thompson et al. 1997) and manually adjusted in BioEdit (Hall 1999). Sequence alignment was deposited at TreeBase (submission ID 15677).

Maximum parsimony phylogenetic analysis followed Li & Cui (2013). It was applied to the combined dataset of ITS and nLSU sequences using PAUP* version 4.0b10 (Swofford 2002). Sequences of *Stereum hirsutum* (Willd.) Pers. and *Heterobasidion annosum* (Fr.) Bref. were used as outgroups to root trees following Binder et al. (2013). All characters were equally weighted and gaps were treated as missing data. Trees were inferred using heuristic search option with TBR branch swapping and 1,000 random sequence additions. Max-trees were set to 5,000, branches of zero length were collapsed and all parsimonious trees were saved. Clade robustness was assessed using bootstrap analysis with 1,000 replicates (Felsenstein 1985). Descriptive tree statistics tree length (TL), consistency index (CI), retention index (RI), rescaled consistency index (RC), and homoplasy index (HI) were calculated for each maximum parsimonious tree generated.

MrModeltest2.3 (Posada & Crandall 1998, Nylander 2004) was used to determine the best-fit evolution model for the combined dataset of ITS and nLSU sequences for estimating Bayesian inference (BI). Bayesian inference was calculated with MrBayes3.1.2 (Ronquist & Huelsenbeck 2003). Four Markov chains were run for 2 runs from random starting trees for 5 million generations, and trees were sampled every 100 generations. The first one-fourth generations were discarded as burn-in. Majority rule consensus tree of all remaining trees was calculated. Branches that received bootstrap support for maximum parsimony (MP) and Bayesian posterior probabilities (BPP) greater than or equal to 75% (MP) and 0.95 (BPP) respectively were considered as significantly supported.

Results

Molecular phylogeny

The ITS+nLSU dataset included sequences from 80 fungal specimens representing 69 species. The dataset had an aligned length of 2, 270 characters, of which 1,172 are constant, 358 are variable but parsimony-uninformative, and 740 are parsimony-informative. Maximum parsimony analysis yielded 100 equally parsimonious trees (TL = 6285, CI = 0.302, RI = 0.530, RC = 0.260, HI = 0.698). Best model of evolution for the combined dataset estimated and applied in the Bayesian analysis was GTR+I+G [lset nst = 6, rates = invgamma; prset statefreqpr = dirichlet (1,1,1,1)]. Bayesian analysis resulted in a similar topology as MP analysis, with an average standard deviation of split frequencies = 0.005355.

The phylogeny (Fig. 1) inferred from ITS+nLSU sequences demonstrates six clades including phlebia clade, residual polyporoid clade, core polyporiod clade, antrodia clade, tyromyces clade and gelatoporia clade. The two new species, *Ceriporiopsis fimbriata* and *C. rosea* grouped into phlebia clade, they are distinct from other species in the phlebioid clade, and form well supported lineages respectively.

Table 1. A list of species, specimens, and GenBank accession number of sequences used in this study.

Species name	**Sample no.**	**GenBank accession no.**	
		ITS	**nLSU**
Abortiporus biennis (Bull.) Singer	TFRI 274	EU232187	EU232235
Antrodia albida (Fr.) Donk	CBS 308.82	DQ491414	AY515348
A. heteromorpha (Fr.) Donk	CBS 200.91	DQ491415	AY515350
A. xantha (Fr.) Ryvarden	CBS 155.79	DQ491424	DQ491424
Antrodiella americana Ryvarden & Gilb.	Gothenburg 3161	JN710509	JN710509
A. semisupina (Berk. & M.A.Curtis) Ryvarden	FCUG 960	EU232182	EU232266
Bjerkandera adusta (Willd.) P.Karst.	NBRC 4983	AB733156	AF287848
Ceraceomyces serpens (Tode) Ginns	KHL 8478	AF090882	AF090882
Ceriporia aurantiocarnescens (Henn.) Pieri & Rivoire	Yuan 2066	JX623902	JX644042
C. lacerata N.Maek., Suhara & R.Kondo	Dai 10734	JX623916	JX644068
C. purpurea (Fr.) Komarova	Dai 6205	JX623951	JX644046
C. viridans (Berk. & Broome) Donk	Dai 7759	KC182777	–
Ceriporiopsis alboaurantia C.L.Zhao, B.K.Cui & Y.C.Dai	Cui 2877	KF845947	KF845954
C. alboaurantia	Cui 4136	KF845948	KF845955
C. aneirina (Sommerf.) Domański	TAA 181186	FJ496683	FJ496704
C. aneirina	Dai 12657	KF845945[a]	KF845952[a]
C. balaenae Niemelä	H7002389	FJ496669	FJ496717
C. consobrina (Bres.) Ryvarden	Rivoire 977	FJ496667	FJ496716
C. fimbriata C.L.Zhao & Y.C.Dai	Dai 11672	KJ698633[a]	KJ698637[a]
C. fimbriata	Cui 1671	KJ698634[a]	KJ698638[a]
C. gilvescens (Bres.) Domański	BRNM 667882	FJ496685	FJ496719
C. gilvescens	BRNM 710166	FJ496684	FJ496720
C. gilvescens	Yuan 2752	KF845946[a]	KF845953[a]
C. guidella Bernicchia & Ryvarden	HUBO 7659	FJ496687	FJ496722
C. pseudogilvescens (Pilát) Niemelä & Kinnunen	TAA 168233	FJ496673	FJ496702
C. pseudogilvescens	BRNM 686416	FJ496679	FJ496703
C. pseudoplacenta Vlasák & Ryvarden	JV 050952	JN592499	JN592506
C. pseudoplacenta	PRM 899297	JN592497	JN592504
C. pseudoplacenta	PRM 899300	JN592498	JN592505
C. resinascens	Dai 13351	KJ720685[a]	KJ720686[a]
C. rosea C.L.Zhao & Y.C.Dai	Dai 13573	KJ698635[a]	KJ698639[a]
C. rosea	Dai 13584	KJ698636[a]	KJ698640[a]
C. semisupina C.L.Zhao, B.K.Cui & Y.C.Dai	Cui 10222	KF845949	KF845956
C. semisupina	Cui 7971	KF845950	KF845957
C. semisupina	Cui 10189	KF84595	KF845958
Cinereomyces lindbladii (Berk.) Jülich	FBCC 177	HQ659223	HQ659223
Climacocystis borealis (Fr.) Kotl. & Pouzar	KH 13318	JQ031126	JQ031126
Coriolopsis caperata (Berk.) Murrill	LE(BIN)-0677	AB158316	AB158316
Dacryobolus karstenii (Bres.) Oberw. ex Parmasto	KHL 11162	EU118624	EU118624
Daedalea quercina (L.) Pers.	DSM 4953	DQ491425	DQ491425
Earliella scabrosa (Pers.) Gilb. & Ryvarden	PR1209	JN165009	JN164793
Fomitopsis rosea (Alb. & Schwein.) P.Karst.	ATCC 76767	DQ491410	DQ491410
F. pinicola (Sw.) P.Karst.	CBS 221.39	DQ491405	DQ491405

Ganoderma lingzhi Sheng H.Wu, Y.Cao & Y.C.Dai	Wu 1006-38	JQ781858	–
Gelatoporia subvermispora (Pilát) Niemelä	BRNU 592909	FJ496694	FJ496706
Gloeoporus pannocinctus (Romell) J.Erikss.	BRNM 709972	EU546099	FJ496708
G. dichrous (Fr.) Bres.	KHL 11173	EU118627	EU118627
Grammothelopsis subtropica B.K.Cui & C.L.Zhao	Cui 9041	JQ845096	JQ845099
Heterobasidion annosum (Fr.) Bref.	PFC 5252	KC492906	KC492906
Hornodermoporus martius (Berk.) Teixeira	MUCL 41677	FJ411092	FJ393859
Hypochnicium lyndoniae (D.A.Reid) Hjortstam	NL 041031	JX124704	JX124704
Junghuhnia nitida (Pers.) Ryvarden	KHL 11903	EU118638	EU118638
Mycoacia fuscoatra (Fr.) Donk	KHL 13275	JN649352	JN649352
M. nothofagi (G. Cunn.) Ryvarden	KHL 13750	GU480000	GU480000
Obba rivulosa (Berk. & M.A.Curtis) Miettinen & Rajchenb.	KCTC 6892	FJ496693	FJ496710
O. valdiviana (Rajchenb.) Miettinen & Rajchenb.	FF 503	HQ659235	HQ659235
Perenniporia medulla-panis (Jacq.) Donk	MUCL 49581	FJ411088	FJ393876
Perenniporiella neofulva (Lloyd) Decock & Ryvarden	MUCL 45091	FJ411080	FJ393852
Phanerochaete chrysosporium Burds.	BKM-F-1767	HQ188436	GQ470643
Phlebia livida (Pers.) Bres.	FCUG 2189	AF141624	AF141624
P. radiata Fr.	UBCF 19726	HQ604797	HQ604797
P. subserialis (Bourdot & Galzin) Donk	FCUG 1434	AF141631	AF141631
P. unica (H.S.Jacks. & Dearden) Ginns	KHL 11786	EU118657	EU118657
Piloporia sajanensis (Parmasto) Niemelä	Mannine 2733a	HQ659239	HQ659239
Podoscypha venustula (Speg.) D.A.Reid	CBS 65684	JN649367	JN649367
Polyporus tuberaster (Jacq. ex Pers.) Fr.	CulTENN 8976	AF516598	AJ488116
Postia guttulata (Peck ex Sacc.) Jülich	KHL 11739	EU11865	EU11865
Pouzaroporia subrufa (Ellis & Dearn.) Vampola	BRNM 710164	FJ496661	FJ496723
P. subrufa	BRNM 710172	FJ496662	FJ496724
Sebipora aquosa Miett.	Miettinen 8680	HQ659240	HQ659240
Skeletocutis amorpha (Fr.) Kotl. & Pouzar	Miettinen 11038	FN907913	FN907913
S. portcrosensis A.David	LY 3493	FJ496689	FJ496689
S. jelicii Tortič & A.David	H 6002113	FJ496690	FJ496727
S. subsphaerospora A.David	Rivoire 1048	FJ496688	FJ496688
Steccherinum fimbriatum (Pers.) J.Erikss.	KHL 11905	EU118668	EU118668
S. ochraceum (Pers.) Gray	KHL 11902	JQ031130	JQ031130
Stereum hirsutum (Willd.) Pers.	NBRC 6520	AB733150	AB733325
Truncospora ochroleuca (Berk.) Pilát	MUCL 39726	FJ411098	FJ393865
Tyromyces chioneus (Fr.) P. Karst.	Cui 10225	KF698745[a]	KF698756[a]
Xanthoporus syringae (Parmasto) Audet	Gothenburg 1488	JN710607	JN710607

[a] Newly generated sequences for this study

Ceriporiopsis fimbriata is closely related to *C. guidella* Bernicchia & Ryvarden with strong supports (96% BP, 1.00 BPP; Fig. 1), and *C. rosea* groups with *C. alboaurantia* C.L.Zhao, B.K.Cui & Y.C.Dai and *C. pseudoplacenta* Vlasák & Ryvarden with a 97% bootstrap value and 1.00 Bayesian posterior probability.

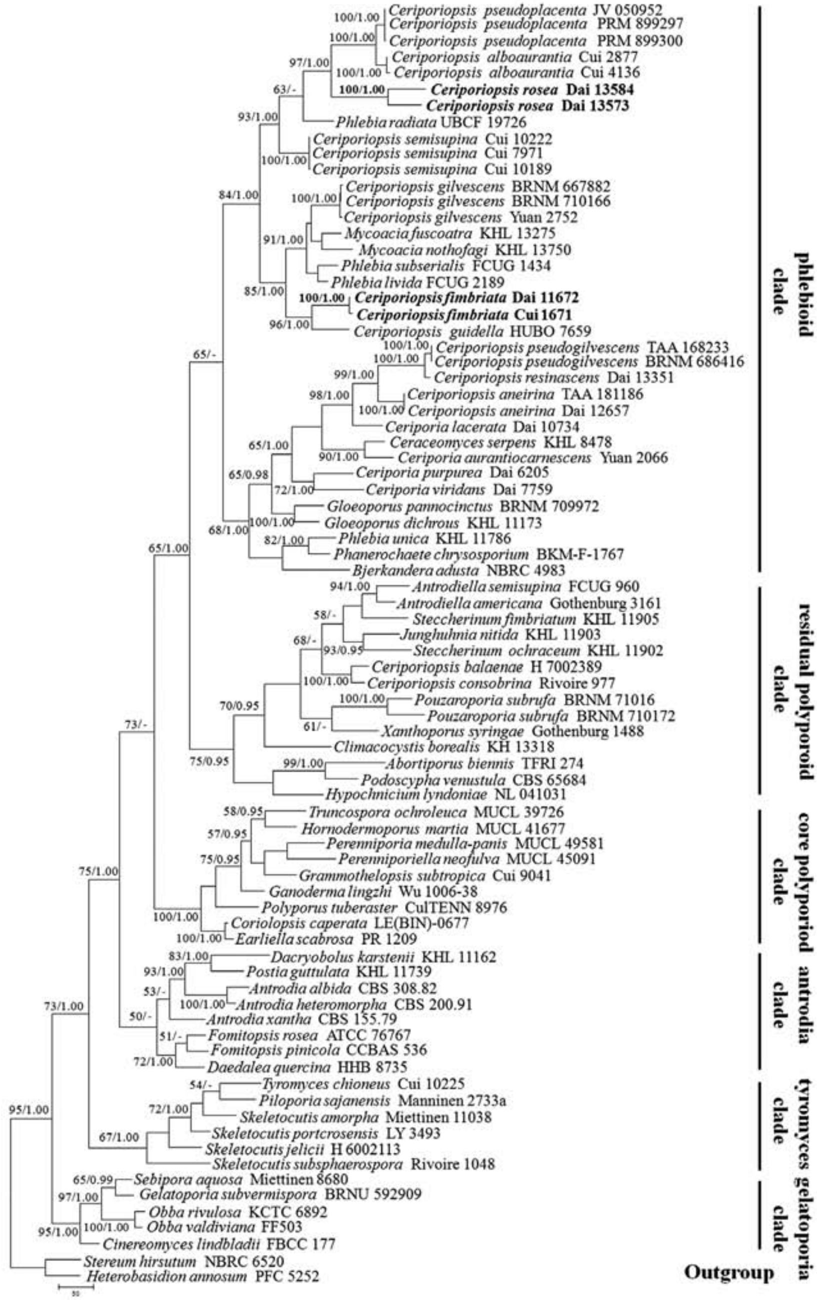

Fig. 1. Maximum Parsimony strict consensus tree illustrating the phylogeny of two new *Ceriporiopsis* species and related taxa based on ITS+nLSU sequences. Branches are labeled with parsimony bootstrap proportions (before slanting line) higher than 50% and Bayesian posterior probabilities (after slanting line) more than 0.95. Bold names = New species. Clade names follow Binder et al. (2013).

Taxonomy

Ceriporiopsis fimbriata C.L.Zhao & Y.C.Dai, **sp. nov.** Figs 2a, 3

MycoBank no.: MB 809166

Differs from other *Ceriporiopsis* species by resupinate basidiocarps with white to clay-pink pores when fresh, become cinnamon to yellowish-brown when dry; sterile margin fimbriate; generative hyphae encrusted with pale-yellow crystals, and plenty of pale-yellow oily substance present in subiculum and trama, oblong-ellipsoid to subcylindrical basidiospores, distinctly tapering at apiculus, usually bearing one or two guttules, 4.4–5 × 1.7–2.1 µm.

Type: China, Hunan Province, Zhangjiajie, Zhangjiajie Forest Park, on fallen angiosperm trunk, 17 August 2010, Dai 11672 (Holotype in BJFC).

rDNA sequence ex holotype: KJ698633 (ITS), KJ698637 (nLSU).

Etymology: *fimbriata* (Lat.) referring to characteristic on sterile margin of the basidiocarps.

Fruiting body: Basidiocarps annual, resupinate, soft corky, without odor or taste when fresh, becoming corky upon drying, up to 13 cm long, 5 cm wide, 2 mm thick at centre. Pore surface white to cream to clay-pink when fresh, turning to cinnamon to yellowish-brown upon drying; pores angular, 2–3 per mm; dissepiments thin, entire. Sterile margin distinct, white, fimbriate, up to 2 mm wide. Subiculum cream, up to 0.5 mm thick. Tubes concolorous with pore surface, corky, up to 1.5 mm long.

Hyphal structure: Hyphal system monomitic; generative hyphae with clamp connections, IKI–, CB–; tissues unchanged in KOH.

Subiculum: Generative hyphae hyaline, thin- to thick-walled, rarely branched, interwoven, 4–6 µm in diameter, encrusted with pale-yellow crystals. Plenty of pale-yellow oily substance present among hyphae.

Tubes: Generative hyphae hyaline, thin- to thick-walled, unbranched, subparallel along the tubes, 3–5 µm in diameter, occasionally encrusted with pale-yellow crystals. Plenty of pale-yellow oily substance present among hyphae. Cystidia and cystidioles absent; basidia long-clavate to pyriform, with four sterigmata and a basal clamp connection, 16–18 × 4.5–5.5 µm; basidioles dominant, in shape similar to basidia, but slightly smaller.

Spores: Basidiospores oblong-ellipsoid to subcylindrical, hyaline, thin-walled, smooth, distinctly tapering at apiculus, usually bearing one or two guttules, IKI-, CB-, (4.2–)4.4–5(–5.2) × 1.7–2.1 µm, L = 4.76 µm, W = 1.91 µm, Q = 2.47–2.5 (n = 60/2).

Additional specimen examined: China, Jiangsu Province, Nanjing, Zijinshan Forest Park, on rotten wood of *Liquidambar*, 3 June 2005, Cui 1671 (Paratype in BJFC).

Ceriporiopsis rosea C.L.Zhao & Y.C.Dai, **sp. nov.** Figs 2b, 4

MycoBank no.: MB 809167

Differs from other *Ceriporiopsis* species by resupinate basidiocarps with rose to rosaceous pore surface when fresh, become orange brown to reddish brown up upon

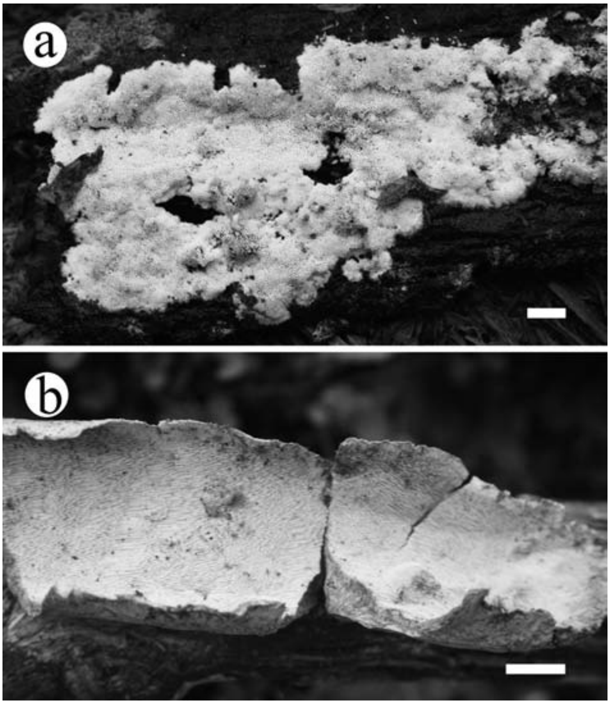

Fig. 2. Basidiomata of two new *Ceriporiopsis* species. a *C. fimbriata*, b *C. rosea*. Scale bars: a, b = 1 cm.

drying, tissues becoming black in KOH, generative hyphae encrusted with crystals, broadly ellipsoid basidiospores, 4–5.2 × 3.3–3.8 µm.

TYPE: China, Yunnan Province, Jingdong County, Ailaoshan Nature Reserve, on fallen angiosperm trunk, 15 October 2013, Dai 13573 (Holotype in BJFC).

rDNA SEQUENCE EX HOLOTYPE: KJ698635 (ITS), KJ698639 (nLSU).

ETYMOLOGY: *rosea* (Lat.) referring to rose to vinaceous pore surface.

FRUITING BODY: Basidiocarps annual, resupinate, without odor or taste when fresh, becoming corky upon drying, up to 12 cm long, 5 cm wide, 8.5 mm thick at centre. Pore surface rose to vinaceous when fresh, become orange brown to reddish brown upon drying; pores angular, 2–3 per mm; dissepiments thin, lacerate. Sterile margin brown, up to 1 mm wide. Subiculum cinnamon to orange-brown, up to 3.5 mm thick. Tubes reddish brown, corky, up to 5 mm long.

HYPHAL STRUCTURE: Hyphal system monomitic; generative hyphae with clamp connections, IKI-, CB-; tissues becoming black in KOH.

SUBICULUM: Generative hyphae hyaline, thick-walled, unbranched, interwoven, 4–5 µm in diameter, occasionally encrusted with pale-yellow crystals.

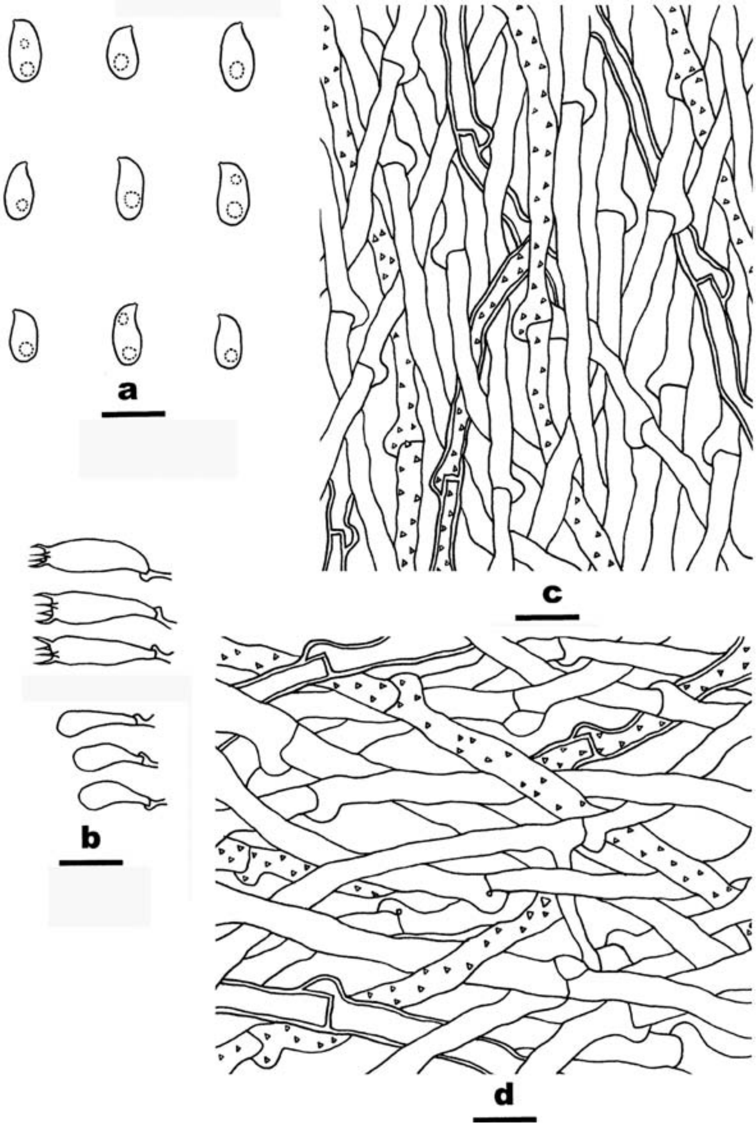

Fig. 3. Microscopic structures of *Ceriporiopsis fimbriata* (Holotype). a: Basidiospores. b: Basidia and basidioles. c: Hyphae from trama. d: Hyphae from subiculum. Bars: a = 5 µm; b–d = 10 µm.

TUBES: Generative hyphae hyaline, thin- to thick-walled, unbranched, interwoven, 2.5–4 µm in diameter, occasionally encrusted with pale-yellow crystals. Cystidia absent, but fusoid to ventricose cystidioles present, hyaline, thin-walled, 15–19 × 4–5 µm; basidia long-clavate, with four sterigmata and a basal clamp connection, 18–22 × 6–7 µm; basidioles dominant, in shape similar to basidia, but distinctly smaller.

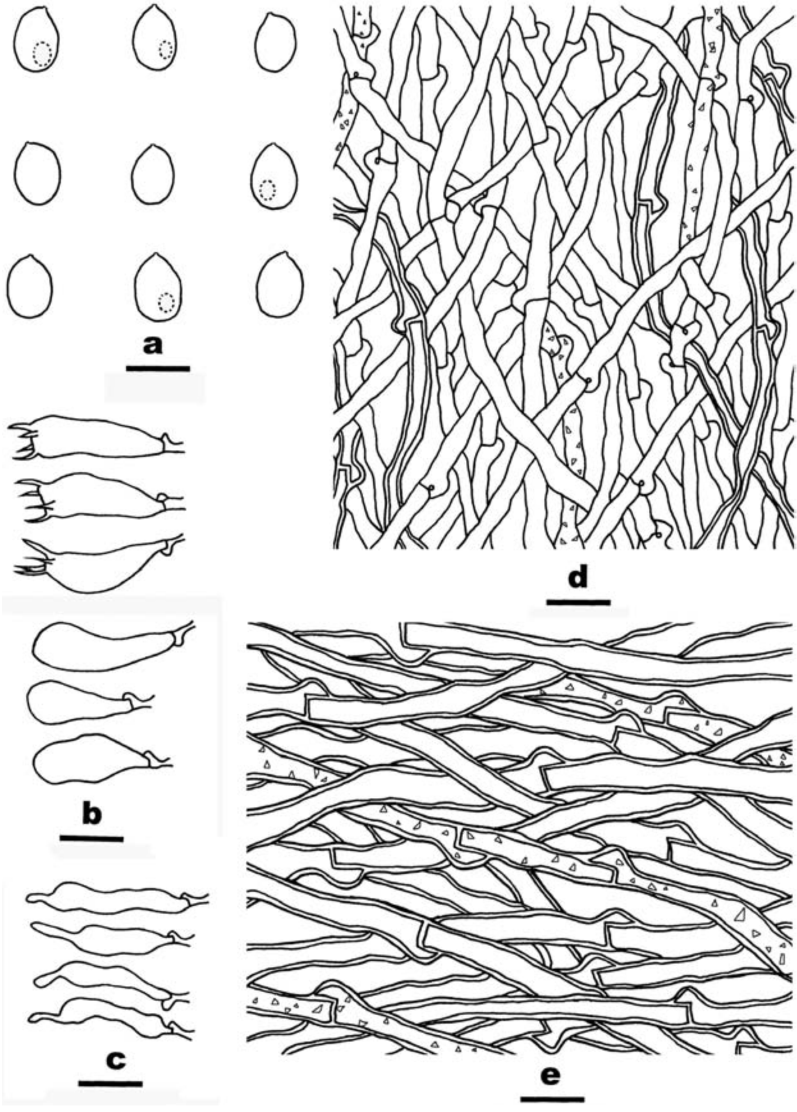

Fig. 4. Microscopic structures of *Ceriporiopsis rosea* (Holotype). a: Basidiospores. b: Basidia and basidioles. c: Cystidioles. d: Hyphae from trama. e: Hyphae from subiculum. Bars: a = 5 µm; b–e = 10 µm.

Spores: Basidiospores broadly ellipsoid, hyaline, thin-walled, smooth, IKI–, CB–, (3.8–)4–5.2(–5.4) × (2.9–)3.2–3.8(–4) µm, L = 4.5 µm, W = 3.51 µm, Q = 1.24–1.34 (n = 60/2).

Additional specimen examined: China, Yunnan Province, Puer, Taiyanghe Nature Reserve, on rotten angiosperm wood, 18 October 2013 Dai 13584 (Paratype in BJFC).

Discussion

In the present study (Fig. 1), ITS+nLSU rRNA gene regions revealed six clades for sampled taxa: phlebia clade, residual polyporoid clade, core polyporiod clade, antrodia clade, tyromyces clade and gelatoporia clade, and this result is consistent with previous studies (Tomšovský et al. 2010, Binder et al. 2013, Zhao and Cui 2014). The two new species, *Ceriporiopsis fimbriata* and *C. rosea*, grouped into phlebia clade.

Ceriporiopsis fimbriata and *C. rosea* seem to be related to *Phlebia* species in the phylogeny (Fig. 1). However, morphological characters of two new species match the concept of *Ceriporiopsis* quite well.

Ceriporiopsis fimbriata is closely related to *C. guidella* Bernicchia & Ryvarden in the rDNA based phylogeny (Fig. 1). But morphologically, *Ceriporiopsis guidella* produces a dull yellow to greenish pore surface with smaller pores (4–5 per mm) and wider basidiospores (4–5 × 2.1–2.4 µm; Bernicchia & Ryvarden 2003). *Ceriporiopsis gilvescens* is another species with oblong-ellipsoid to subcylindrical basidiospores, but it differs from *C. fimbriata* by having both smaller pores (4–5 per mm) and basidiospores (3.5–4.5 × 1.5–2 µm; Gilbertson & Ryvarden 1986). In addition, *C. gilvescens* was not closely related to *C. fimbriata* in phylogeny (Fig. 1). *Ceriporiopsis cremea* (Parmasto) Ryvarden is similar to *C. fimbriata* by having fimbriate sterile margin; however, *C. cremea* differs in its both larger pores (1–2 per mm) and basidiospores (4.5–5.5 × 2.5–3.5 µm; Núñez & Ryvarden 2001).

Ceriporiopsis rosea grouped with *C. alboaurantia* and *C. pseudoplacenta* with a strong support (96% BP, 1.00 BPP). However, morphologically *Ceriporiopsis alboaurantia* differs in white to cream pore surface when fresh, turning to apricot-orange to dark orange upon drying, and frequently branched generative hyphae (Zhao & Cui 2014). *Ceriporiopsis pseudoplacenta* differs from *C. rosea* by having smaller pores (3–4 per mm) with thick dissepiments, and smaller basidiospores (3.5–4.5 × 2.2–3 µm; Vlasák et al. 2012). *Ceriporiopsis balaenae* Niemelä may be confused with *C. rosea* in similar sized pores (2–3 per mm) and basidiospores (4–5 × 2.5–3.5 µm), but *C. balaenae* differs in having yellow to straw-colored pore surface and weakly amyloid generative hyphae (Ryvarden & Gilbertson 1993).

Recently, eight *Ceriporiopsis* sensu stricto species in worldwide have been grouped into phlebia clade based on phylogenetic analysis (Tomšovský et al. 2010, Vlasák et al. 2012, Binder et al. 2013, Zhao & Cui 2014). In the present study, seven species from China, which include two new species, have been nested into phlebia clade and they do belong to *Ceriporiopsis* s.s. evidenced by morphological characters and molecular analysis. A key to ten worldwide species of *Ceriporiopsis* s.s. in phlebia clade is provided in the following.

1. Basidiospores < 2.1 µm in width 2
1. Basidiospores > 2.1 µm in width 3

2. Pores < 3 per mm .... *C. fimbriata*
Basidiocarps resupinate, pore surface white to cream to clay-pink when fresh, turning to cinnamon to yellowish-brown upon drying, pores 2–3 per mm; generative hyphae thin- to thick-walled, rarely

branched, encrusted with crystals; basidiospores oblong-ellipsoid to subcylindrical, (4.2–)4.4–5(–5.2) × 1.7–2.1 µm, L = 4.76 µm, W = 1.91 µm, Q = 2.47–2.5 (n = 60/2).

2. Pores > 3 per mm..*C. gilvescens*
Basidiocarps resupinate to effused-reflexed, pore surface white to pale pinkish yellow when fresh, turning to ochraceous upon drying, pores 4–5 per mm; generative hyphae thin-walled, branched, occasionally encrusted with crystals; basidiospores oblong-ellipsoid to cylindrical, (3.4–)3.6–4.4(–4.6) × 1.6–2 µm, L = 4 µm, W = 1.8 µm, Q = 2.05–2.24 (n = 180/6; specimens: BJFC003588 in BJFC; BJFC000400, BJFC012278 & BJFC012279 in BJFC; BJFC000397/IFP 001037 & BJFC000398/IFP 001030 in BJFC and IFP).

3. Tissues becoming black in KOH 4
3. Tissues unchanged in KOH 5

4. Generative hyphae unbranched...*C. rosea*
Basidiocarps resupinate, pore surface rose to vinaceous when fresh, become orange brown to reddish brown upon drying, pores 2–3 per mm; generative hyphae thin- to thick-walled, unbranched, occasionally encrusted with crystals, tissues becoming black in KOH; basidiospores broadly ellipsoid, (3.8–)4–5.2(–5.4) × (2.9–)3.2–3.8(–4) µm, L = 4.5 µm, W = 3.51 µm, Q = 1.24–1.34 (n = 60/2).

4. Generative hyphae branched... *C. alboaurantia*
Basidiocarps resupinate, pore surface white to cream when fresh, turning to apricot-orange to dark orange with reddish tinge upon drying, pores 2–3 per mm; generative hyphae thin-walled, branched, encrusted with crystals, tissues becoming black in KOH; basidiospores ellipsoid, 4–5(–5.2) × 3–3.3(–3.5) µm, L = 4.36 µm, W = 3.17 µm, Q = 1.34–1.41 (n = 60/2; specimens: BJFC000412 holotype in BJFC; BJFC000416 paratype in BJFC).

5. Pores < 3 per mm..6
5. Pores > 3 per mm..7

6. Basidiospores > 3.5 µm in width ....*C. aneirina*
Basidiocarps resupinate, pore surface whitish straw or young amber when fresh, turning to cream to honey upon drying, pores 1–3 per mm; generative hyphae thin-walled, branched, encrusted with crystals; basidiospores ellipsoid, 5.5–6.7(–7) × 3.5–4.5 µm, L = 6.2 µm, W = 3.95 µm, Q = 1.5–1.61 (n = 180/6; specimens: BJFC005381 & BJFC005421 in BJFC; BJFC000391 & BJFC012238 in BJFC; BJFC000389/IFP 001009 & BJFC000390/IFP 001012 in BJFC and IFP). (5.6–7 × 3.7–4.4 µm, BPI 242279 type in H; Kinnunen & Niemelä 2005).

6. Basidiospores < 3.5 µm in width .... *C. pseudogilvescens*
Basidiocarps resupinate, pore surface white to cream when fresh, turning to pale brown upon drying, pores 2–3 per mm; generative hyphae thin- to thick-walled, rarely branched, encrusted with crystals; basidiospores ellipsoid to subcylindrical, 3.8–6 × 2.6–3.1 µm, PRM 498233 type in PRM; Kinnunen & Niemelä 2005).

7. Basidiospores > 5 µm in length ....*C. resinascens*
Basidiocarps resupinate, pore surface cream when fresh, turning to straw to pale brown upon drying, pores 3–5 per mm; generative hyphae thin- to thick-walled, branched, encrusted with crystals; basidiospores oblong-ellipsoid to subcylindrical, 5.1–6.1(–6.4) × 2.2–2.5(2.7) µm, L = 5.5 µm, W = 2.35 µm, Q = 2.1–2.4 (n = 120/4; specimens: BJFC005311 in BJFC; BJFC000410, BJFC000413 & BJFC014813 in BJFC). (4.9–6.2 × 2.2–2.6 µm, LE 23049 type in LE; Kinnunen & Niemelä 2005).

7. Basidiospores < 5 µm in length 8

8. Pores > 5 per mm... *C. semisupina*
Basidiocarps resupinate to effused-reflexed, pore surface olivaceous-buff to greyish brown when fresh, turning to greyish brown to reddish brown upon drying, pores 6–7 per mm; generative hyphae thick-walled, unbranched, encrusted with crystals; basidiospores ellipsoid, 4–4.5(–4.8) × 3–3.3(–3.5) µm, L = 4.25 µm, W = 3.14 µm, Q = 1.32–1.38 (n = 90/3; specimens: BJFC011116 holotype in BJFC; BJFC006460 & BJFC011084 paratypes in BJFC).

8. Pores < 5 per mm..9

9. Pore surface greenish-yellow.. *C. guidella*
Basidiocarps resupinate, pore surface dull yellow to greenish when fresh, getting darker upon drying, pores 4–5 per mm; generative hyphae thin-walled, unbranched, encrusted with crystals; basidiospores oblong-ellipsoid to subcylindrical, 4–5 × 2.1–2.4 µm, Pancaldi 7600 holotype in HUBO; Bernicchia & Ryvarden 2003).

9. Pore surface salmon-pink to reddish brown .... *C. pseudoplacenta*
Basidiocarps resupinate, pore surface pale apricot to salmon-pink when fresh, turning to dark reddish brown upon drying, pores 3–4 per mm; generative hyphae thin-walled, branched; basidiospores ellipsoid, 3.5–4.5(–5) × 2.2–3 µm, PRM 899297 holotype in PRM; Vlasák et al. 2012).

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