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Phylogeny and taxonomy of *Ceriporiopsis* (Polyporales) with descriptions of two new species from southern China

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Abstract

Phylogenies of *Ceriporiopsis* and related genera were studied using DNA sequences from the ITS+28S nuclear ribosomal RNA gene regions. Two species, *Ceriporiopsis alboaurantia* and *C. semisupina*, are described as new to science. *Ceriporiopsis alboaurantia* is characterized by annual growth habit, resupinate basidiocarps with white pore surface when fresh, turning to apricot-orange to dark orange upon drying, monomitic hyphal system with clamped generative hyphae encrusted with pale yellow crystals, ellipsoid and thin-walled basidiospores ($4-5 \times 3-3.3 \mu m$), and plenty of pale-yellow to pale-orange oily substances in subiculum and trama. *Ceriporiopsis semisupina* is distinguished by annual, effused-reflexed basidiocarps with greyish brown to reddish brown pore surface, monomitic hyphal system with clamped generative hyphae bearing crystalline incrustation, long-clavate basidia, ellipsoid and thin-walled basidiospores ($4-4.5 \times 3-3.3 \mu m$). Like previous study, the phylogenetic analysis presented here also showed that *Ceriporiopsis* is not monophyletic and the sampled species were grouped in four clades, including phlebia clade, residual polyporoid clade, tyromyces clade and gelatoporia clade.

Key words: Phanerochaetaceae, polypore, wood-rotting fungi

Introduction

Ceriporiopsis Domański (Phanerochaetaceae, Polyporales) was typified by *C. gilvescens* (Bres.) Domański. It is characterized by a combination of annual, resupinate basidiocarps, monomitic hyphal structure with clamp connections, and subcylindrical to ellipsoid basidiospores. This combination is not uncommon for many polypores and is likely homoplasious. In addition, its hyphae and spores are acyanophilous and negative in Melzer's reagent. It is a cosmopolitan genus occurring in temperate, boreal, and tropical areas, and causing white rot (Gilbertson & Ryvarden 1986, Ryvarden & Gilbertson 1993, Núñez & Ryvarden 2001).

Lack of robust morphological features for the genus has resulted in a number of names combined under *Ceriporiopsis* generic name. The MycoBank database (http://www.mycobank.org) includes 64 specific and infraspecific names in *Ceriporiopsis* and Index Fungorum (http://www.indexfungorum.org) registers 61 ones, but some species were transferred to other genera according to the Index Fungorum database, and the actual number of species is much lower; until now about 30 species were recognized by polypore specialists in the genus worldwide (Hattori 2002, Bernicchia & Ryvarden 2003, Kinnunen & Niemelä 2005, Fortey & Ryvarden 2007, Læssøe & Ryvarden 2010, Tomšovský *et al.* 2010, Vlasák *et al.* 2012, Cui 2013).

Recently, molecular study employing multi-gene datasets by Binder *et al.* (2013) has helped to clarify the generic relationships of polyporoid fungi and to provide phylogenetic overview of the Polyporales. They demonstrated that the type species of *Ceriporiopsis* (*C. gilvescens*) belongs to the phlebioid clade, but appeared to be grouped with smooth, merulioid and hydnaceous genera, such as *Ceraceomyces* Jülich, *Ceriporia* Donk, *Gloeoporus* Mont., *Merulius* Haller, *Mycoacia* Donk, *Phanerochaete* P. Karst. and *Phlebia* Fr. Phylogenetic study of European *Ceriporiopsis* taxa inferred from the combined data of the large subunit nuclear rRNA gene (nLSU) and mitochondrial small subunit rRNA (mtSSU) gene sequences, suggested that 1) the genus is polyphyletic, 2) the type *Ceriporiopsis gilvescens* was grouped with *Phlebia* spp., 3) the taxa of *Ceriporiopsis* s.l. (Tomšovský *et al.*

2010) were sparsely distributed in the gelatoporia clade, phlebioid clade, residual polyporoid clade and tyromyces clade (Tomšovský *et al.* 2010). Miettinen & Rajchenberg (2012) proposed a new genus *Obba* Miettinen & Rajchenb. to accommodate *Ceriporiopsis rivulosa* (Berk. & M.A. Curtis) Gilb. & Ryvarden based on the ITS and nLSU phylogenies. Vlasák *et al.* (2012) described a new species *Ceriporiopsis pseudoplacenta* Vlasák & Ryvarden, which was clustered into the phlebioid clade based on ITS and nLSU sequences.

China has a huge land area covering boreal, temperate, subtropical, and tropical vegetation, and the diversity of polypores in the country is very rich (Dai 2012). Polypore diversity in southern China has been extensively studied, and many new species have been described (Dai *et al.* 2002, 2010, 2011, Cui *et al.* 2009, 2011, Du & Cui 2009, Dai 2010, 2012, Cui & Dai 2013, Cui & Decock 2013, Li & Cui 2013, Zhao & Cui 2013), including two new species of *Ceriporiopsis* (Dai *et al.* 2007, Cui 2013). Additional two undescribed species morphologically corresponding to *Ceriporiopsis* were found recently. To confirm the affinity of the two new species, phylogenetic analysis was carried out based on the ITS and 28S sequences.

Materials and methods

Morphological studies.—The studied specimens were deposited in the herbarium of the Institute of Microbiology, Beijing Forestry University (BJFC). 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, by light microscopy following 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), Q = L/W ratio for a specimens studied, n (a/b) = number of spores (a) measured from given number of specimens (b).

DNA extraction, amplification, sequencing and phylogenetic analyses.—The fungal taxa examined in this study are 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 28S 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 28S 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 14954).

Maximum parsimony phylogenetic analysis followed Li & Cui (2013). It was applied to the combined dataset of ITS and 28S sequences using PAUP* version 4.0b10 (Swofford 2002). Sequences of *Stereum hirsutum* (Willd.) Pers. and *Heterobasidion annosum* (Fr.) Bref. were used as an outgroup 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 28S 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 3 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.

TABLE 1. A list of species, specimens and GenBank accession number of sequences used in this st	udy
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	G I	GenBank acc	ession no.
Species name	Sample no.	ITS	28 S
Abortiporus biennis (Bull.) Singer	TFRI 274	EU232187	EU232235
Antrodia albida (Fr.) Donk	CBS 308.82	DQ491414	AY515348
Antrodiella americana Ryvarden & Gilb.	Gothenburg 3161	JN710509	JN710509
A. semisupina (Berk. & M.A. Curtis) Ryvarden	FCUG 960	EU232182	EU232266
Ceraceomyces serpens (Tode) Ginns	KHL 8478	AF090882	AF090882
Ceriporia viridans (Berk. & Broome) Donk	Dai 7759	KC182777	-
Ceriporiopsis alboaurantia C.L. Zhao, B.K. Cui & Y.C. Dai	Cui 2877	KF845947 ª	KF845954 ^a
C. alboaurantia	Cui 4136	KF845948 ^a	KF845955 ^a
C. aneirina (Sommerf.) Domański	TAA 181186	FJ496683	FJ496704
C. aneirina	Dai 12657	KF845945 ª	KF845952 ^a
C. aneirina	BRNM 706970	EU340895	EU368503
C. balaenae Niemelä	H 7002389	FJ496669	FJ496717
C. balaenae	H 7002390	FJ496668	FJ496718
C. consobrina (Bres.) Ryvarden	Rivoire 977	FJ496667	FJ496716
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. pseudogilvescens	Niemelä 7447	FJ496680	FJ496700
C. pseudoplacenta Vlasák & Ryvarden	JV 050952	JN592499	JN592506
C. pseudoplacenta	PRM 899297	JN592497	JN592504
C. pseudoplacenta	PRM 899300	JN592498	JN592505
C. semisupina C.L. Zhao, B.K. Cui & Y.C. Dai	Cui 10222	KF845949 ^a	KF845956 ^a
C. semisupina	Cui 7971	KF845950 ^a	KF845957 ^a
C. semisupina	Cui 10189	KF845951ª	KF845958 ^a
Cinereomyces lindbladii (Berk.) Jülich	KHL 12078	FN907906	FN907906
C. lindbladii	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
Earliella scabrosa (Pers.) Gilb. & Ryvarden	PR1209	JN165009	JN164793
Ganoderma lingzhi Sheng H. Wu, Y. Cao & Y.C. Dai	Wu 1006-38	JQ781858	-
Gelatoporia subvermispora (Pilát) Niemelä	BRNU 592909	FJ496694	FJ496706
G. subvermispora	HK 20823	FN907911	FN907911
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	JQ845096ª	JQ845099 ª
Heterobasidion annosum (Fr.) Bref.	PFC 5252	KC492906	KC492906
Hornodermoporus martius (Berk.) Teixeira	MUCL 41677	FJ411092	FJ393859

.....continued on the next page

TABLE 1. (Continued)

Species nome	Sampla na	GenBank accession no.	
Species name	Sample no.	ITS	28S
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 alni Niemelä & Vampola	X 1400	KC595932	KC595932
P. floriformis (Quél.) Jülich	Gothenburg 4120	KC595937	KC595937
P. guttulata (Peck ex Sacc.) Jülich	KHL 11739	EU11865	EU11865
P. lactea (Fr.) P. Karst.	X 1391	KC595939	KC595939
P. sericeomollis (Romell) Jülich	X 1332	KF112878	KF112878
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
Trametes pubescens (Schumach.) Pilát	PRM 900586	AY684173	AY855906
Truncospora ochroleuca (Berk.) Pilát	MUCL 39726	FJ411098	FJ393865
Tyromyces chioneus (Fr.) P. Karst.	Cui 10225	KF698745 °	KF698756 ^a
Xanthoporus syringae (Parmasto) Audet	Gothenburg 1488	JN710607	JN710607

^a Sequences newly generated in this study

Results

Molecular phylogeny

The ITS+28S dataset included sequences from 76 fungal specimens representing 61 species. The dataset had an aligned length of 2,175 characters, of which 1,164 are constant, 315 are variable but parsimony-uninformative, and

695 are parsimony-informative. Maximum parsimony analysis yielded 9 equally parsimonious trees (TL = 5455, CI = 0.315, RI = 0.583, RC = 0.243, HI = 0.685). 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 the same topology as MP analysis, with an average standard deviation of split frequencies = 0.007323.

The phylogeny (Fig. 1) inferred from ITS+28S sequences demonstrates four major clades for *Ceriporiopsis* sensu lato, including phlebia clade, residual polyporoid clade, tyromyces clade and gelatoporia clade.



FIGURE 1. Maximum Parsimony strict consensus tree illustrating the phylogeny of two new *Ceriporiopsis* species and related taxa based on ITS+28S 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. Numbers after taxon names = Sample numbers. Clade names follow Binder (2013).

Sampled specimens of the two new species, *Ceriporiopsis alboaurantia*, and *C. semisupina*, form well supported lineages respectively. They are distinct from other species in the phlebioid clade. *Ceriporiopsis alboaurantia* is closely related to *C. pseudoplacenta* Vlasák & Ryvarden (100% BP, 1.00 BPP), and *C. semisupina* groups with *Phlebia radiata* Fr. (98% BP, 1.00 BPP).

Taxonomy

Ceriporiopsis alboaurantia C.L. Zhao, B.K. Cui & Y.C. Dai, *sp. nov* MycoBank no.: MB 808039

(Figs. 2a, 3)

Differs from other *Ceriporiopsis* species by white to cream pore surface when fresh, turning to apricot-orange to dark orange upon drying, plenty of pale-yellow to pale-orange oily substance present among hyphae, and ellipsoid, thin-walled basidiospores, $4-5 \times 3-3.3 \mu m$.

Type.—CHINA. Fujian Prov.: Wuyishan County, Longfenggu Forest Park, alt. 500 m, on fallen trunk of *Cunninghamia*, 27 August 2006, *Cui 4136* (holotype, BJFC!).



FIGURE 2. Basidiomata of two new Ceriporiopsis species. a C. alboaurantia, b C. semisupina. Scale bars = 1 cm.

Etymology.—alboaurantia (Lat.) referring to the color of pore surface in fresh and dry state.

Basidiocarps.—Annual, resupinate, soft, without odor or taste when fresh, becoming tough upon drying, impregnated with resinous substance, not readily separable, up to 4.5 cm long, 2.5 cm wide, 2 mm thick at centre. Pore surface white to cream when fresh, turning to apricot-orange to dark orange with reddish tinge upon drying; pores round to angular, 2–3 per mm; dissepiments thin, entire. Sterile margin distinct, white to pale orange, up to 3 mm wide. Subiculum buff to cinnamon-buff, up to 0.5 mm thick. Tubes concolorous with pore surface, tough, up to 1.5 mm long.

Hyphal structure.—Hyphal system monomitic; generative hyphae with clamp connections, IKI–, CB–; tissues becoming vinaceous brown to black in KOH.

Subiculum.—Generative hyphae hyaline, thin-walled, occasionally branched, interwoven, 4–6 µm in diameter, occasionally encrusted with pale-yellow crystals. Pale-yellow to pale-orange oily substance is abundant among hyphae.

Tubes.—Generative hyphae hyaline, thin-walled, frequently branched, interwoven, 2.5–4.5 μ m in diameter, occasionally encrusted with pale-yellow crystals. Plenty of pale-yellow to pale-orange oily substance present among hyphae. Cystidia absent, but fusoid cystidioles present, hyaline, thin-walled, 15–17 × 4.5–5 μ m; basidia short-clavate, with four sterigmata and a basal clamp connection, 17–20 × 5–6 μ m; basidioles dominant, in shape similar to basidia, but slightly smaller.

Spores.—Basidiospores ellipsoid, hyaline, thin-walled, smooth, usually tapering at apiculus, IKI–, CB–, $4-5(-5.2) \times 3-3.3(-3.5) \mu m$, L = 4.36 μm , W = 3.17 μm , Q = 1.34–1.41 (n = 60/2).

Additional specimen examined.—CHINA. Fujian Prov.: Wuyishan County, Longchuan Valley, alt. 500 m, on fallen trunk of *Cunninghamia*, 16 October 2005, *Cui* 2877 (paratype, BJFC!).

Ceriporiopsis semisupina C.L. Zhao, B.K. Cui & Y.C. Dai, sp. nov.	(Figs. 2b, 4)
MycoBank no.: MB 808040	

Differs from other *Ceriporiopsis* species by resupinate to effused-reflexed basidiocarps with greyish brown to reddish brown pore surface, generative hyphae encrusted with crystals, long-clavate basidia, ellipsoid basidiospores, $4-4.5 \times 3-3.3 \mu m$.

Type.—CHINA. Zhejiang Prov.: Taishun County, Wuyanling Nature Reserve, alt. 1200 m, on fallen angiosperm trunk, 22 August 2011, *Cui 10222* (holotype, BJFC!).

Etymology.—semisupina (Lat.) referring to partly effused basidiocarps.

Basidiocarps.—Annual, resupinate to effused-reflexed, adnate, without odor or taste when fresh, becoming tough upon drying, when resupinate up to 6 cm long, 4 cm wide, 3 mm thick at centre. Pilei usually semicular to fan-shaped, often imbricate, projecting up to 1.5 cm, 0.6 cm wide, and 2 mm thick at base. Pileal surface buff to buff-yellow, glabrous; margin obtuse. Pore surface olivaceous-buff to greyish brown when fresh, greyish brown to reddish brown upon drying; pores round to angular, 6–7 per mm; dissepiments thin, entire to lacerate. Sterile margin brown, up to 1 mm wide. Subiculum buff, up to 0.5 mm thick. Tubes concolorous with pore surface, tough, up to 2.5 mm long.

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

Subiculum.—Generative hyphae hyaline, thick-walled, unbranched, interwoven, $4.5-7 \mu m$ in diameter, occasionally encrusted with crystals.

Tubes.—Generative hyphae hyaline, thick-walled, unbranched, subparallel along tubes, $3-5 \mu m$ in diameter, frequently encrusted with crystals. Cystidia absent, but fusoid to ventricose cystidioles present, hyaline, thin-walled, $17-19.5 \times 5-6.5 \mu m$; basidia long-clavate, with four sterigmata and a basal clamp connection, $26-32 \times 5.5-8 \mu m$; basidioles dominant, in shape similar to basidia, but distinctly smaller.

Spores.—Basidiospores ellipsoid, hyaline, thin-walled, smooth, distinctly tapering to the apiculus, IKI–, CB–, $4-4.5(-4.8) \times 3-3.3(-3.5) \mu m$, L = $4.25 \mu m$, W = $3.14 \mu m$, Q = 1.32-1.38 (n = 90/3).

Additional specimens examined.—CHINA. Zhejiang Prov.: Taishun County, Wuyanling Nature Reserve, alt. 1200 m, on dead angiosperm tree, 22 August 2011, *Cui 10189* (paratype, BJFC!); Yunnan Prov.: Kunming, Qiongzhusi, alt. 1800 m, on angiosperm stump, 21 October 2009, *Cui 7971* (paratype, BJFC!).



FIGURE 3. Microscopic structures of *Ceriporiopsis alboaurantia* (drawn from the holotype). a Basidiospores. b Basidia and basidioles. c Cystidioles. d Hyphae from trama. e Hyphae from subiculum. Bars: $a = 5 \mu m$; $b-f = 10 \mu m$.



FIGURE 4. Microscopic structures of *Ceriporiopsis semisupina* (drawn from the holotype). a Basidiospores. b Basidia and basidioles. c Cystidioles. d Hyphae from trama. e Hyphae from subiculum. Bars: $a = 5 \mu m$; $b-f = 10 \mu m$.

Discussion

In present study (Fig. 1), *Ceriporiopsis* s.l. species are sparsely distributed in four clades: phlebia clade, residual polyporoid clade, tyromyces clade and gelatoporia clade, and this result is the same as previous studies (Tomšovský *et al.* 2010, Binder *et al.* 2013). The two new species, *Ceriporiopsis alboaurantia* and *C. semisupina* grouped into phlebia clade.

In phlebia clade (Fig. 1), the sampled *Ceriporiopsis* species including the generic type are nested with the genera *Ceraceomyces*, *Ceriporia*, *Gloeoporus*, *Mycoacia*, *Phlebia* and *Phanerochaete*. Macroscopically the genera *Ceraceomyces*, *Mycoacia*, *Phanerochaete* and *Phlebia* have smooth, tuberculate, phlebioid, or merulioid hymenophore (Parmasto & Hallenberg 2000, Nakasone 2002, Moreno *et al.* 2011, Binder *et al.* 2013). Even though the basidiocarp configuration may not be a good character to differentiate taxa at a generic level, for the time being we decided to describe the two new species here in the genus *Ceriporiopsis*, mainly because their morphological characters match the concept of *Ceriporiopsis* quite well. Although the two new species (Fig. 1) seem closely related to *Phlebia radiata* (generic type of *Phlebia*), rather than *Ceriporiopsis gilvescens* in the phylogenetic analysis (Fig. 1), but *Phlebia* (established in 1821) is an earlier name than *Ceriporiopsis* (set up in 1963), and many new combinations should be proposed if the two genera are merged. *Ceriporia viridans* (Berk. & Broome) Donk (generic type) differs from *Ceriporiopsis* by having simple-septate generative hyphae (Núñez & Ryvarden 2001). *Gloeoporus dichrous* (Fr.) Bres. (generic type) differs in its partly fluffy subiculum contrasting to dense trama (Eriksson 1958).

Ceriporiopsis alboaurantia is closely related to *C. pseudoplacenta* in the rDNA-based phylogeny (Fig. 1). However, *Ceriporiopsis pseudoplacenta* has a dark reddish brown pore surface with smaller, thick-walled pores (3–4 per mm), black subiculum, and smaller basidiospores (3.5–4.5 $^{\prime}$ 2.2–3 µm, Vlasák *et al.* 2012). There are no sequence data for *Ceriporiopsis cremeicarnea* (Corner) T. Hatt. and *C. herbicola* Fortey & Ryvarden, so the comparisons are made morphologically only. *Ceriporiopsis cremeicarnea* is another species that has white pore surface when fresh, turning to dull pinkish and brownish-orange upon drying. It differs from *C. alboaurantia* by both larger pores (1–2 per mm) and basidiospores (5.5–7.5 × 3–4 µm, Hattori 2002). *Ceriporiopsis herbicola* Fortey & Ryvarden and *C. alboaurantia* share pale cinnamon pore surface with reddish tinge and generative hyphae covered with small crystals. However, *Ceriporiopsis herbicola* differs by larger pores (1–2 per mm) and narrower basidiospores (4–4.5 $^{\prime}$ 2–2.5 µm, Fortey & Ryvarden 2007).

Ceriporiopsis semisupina sisters to *Phlebia radiata* and then groups with *C. alboaurantia* and *C. pseudoplacenta*. Nevertheless, *Ceriporiopsis alboaurantia* differs from *C. semisupina* by having larger pores (2–3 per mm) in morphology. *Ceriporiopsis pseudoplacenta* differs in its smaller basidiospores (3.5–4.5 \cdot 2.2–3 µm, Vlasák *et al.* 2012). *Ceriporiopsis aneirina* (Sommerf.) Domański is similar to *C. semisupina* by having tan to reddish-brown pore surface and long-clavate basidia (mostly 30 µm), but this species has larger pores (1–3 per mm) and basidiospores (5–8 \cdot 3.5–5.5 µm, Núñez & Ryvarden 2001), and *C. aneirina* is distant from *C. semisupina* in the phylogenetic analysis (Fig. 1). There is no sequence data for *Ceriporiopsis jensii* Læssøe & Ryvarden, so the comparison is made morphologically only. *Ceriporiopsis jensii* and *C. semisupina* share pale brown to reddish-brown pore surface with similarly sized pores (6–8 per mm) and generative hyphae encrusted with crystals; however, the former species has narrower basidiospores (3.5–4.5 \cdot 2–2.5 µm, Læssøe & Ryvarden 2010).

In the residual polyporoid clade, *Ceriporiopsis balaenae* Niemelä, *C. consobrina* (Bres.) Ryvarden and *C. subrufa* (Berk. & M.A. Curtis) Gilb. & Ryvarden were grouped together. *Ceriporiopsis balaenae* may be confused with *C. alboaurantia* in resupinate basidiocarps with similar sized pores (2–3 per mm) and basidiospores (4–5 $^{2.5-3.5} \mu$ m). However, *Ceriporiopsis balaenae* differs in having yellow to straw-colored pore surface and weakly amyloid generative hyphae (Ryvarden & Gilbertson 1993).

In tyromyces clade, *Skeletocutis jelicii* Tortič & A. David, and *S. portcrosensis* A. David, and *S. subsphaerospora* A. David were transferred to *Ceriporiopsis* by Gilbertson & Ryvarden (1993). Tomšovský *et al.* (2010) indicated that these three *Ceriporiopsis* species belong to the tyromyces clade, and proposed that the original genus *Skeletocutis* is more suitable for these three species (Tomšovský *et al.* 2010). Morphologically they are similar to the two new species by having encrusted with crystals. However, they are not related to *Ceriporiopsis alboaurantia* and *C. semisupina* in phylogenetic trees (Fig. 1).

In gelatoporia clade, *Poria subvermispora* Pilát was combined in *Gloeoporus* by Eriksson (1958) based on its resupinate basidiocarps and monomitic hyphal system. Later Niemelä (1985) transferred it to the genus

Gelatoporia for its acyanophilous hyphae and allantoid basidiospores. Gilbertson & Ryvarden (1985) put it into *Ceriporiopsis* by its resupinate basidiocarps with white to pale cream pore surface. Tomšovský *et al.* (2010) revealed that the taxon belongs to the phlebia clade, and put it into *Gelatoporia*. However, recent phylogenetic studies showed that it clustered into the gelatoporia clade (Miettinen & Rajchenberg 2012, Binder 2013). Our research also showed that it is clustered in a separate gelatoporia clade (Fig. 1). Morphologically, *Gelatoporia subvermispora* (Pilát) Niemelä differs from *Ceriporiopsis alboaurantia* and *C. semisupina* by having allantoid basidiospores (Niemelä 1985).

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