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Ceriporiopsis kunmingensis sp. nov. (Polyporales, Basidiomycota) evidenced by morphological characters and phylogenetic analysis

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Abstract A new poroid wood-inhabiting fungal species, *Ceriporiopsis kunmingensis* sp. nov., is proposed based on morphological and molecular characters. The species is characterized by resupinate basidiocarps with pale cinnamon-buff to ochreous color when dry; generative hyphae unbranched and subparallel along the tubes; presence of hyphal ends; allantoid basidiospores, $4.5\text{--}5 \times 1.5\text{--}2 \mu\text{m}$. The internal transcribed spacer (ITS) and large subunit (LSU) regions of nuclear ribosomal RNA gene sequences of the studied samples were generated, and phylogenetic analyses were performed with maximum likelihood, maximum parsimony, and Bayesian inference methods. The phylogenetic analysis based on molecular data of ITS + nLSU sequences showed that *C. kunmingensis* belonged to the phlebioid clade, formed a monophyletic lineage with a strong support (100% BS, 100% BP, 1.00 BPP), and was closely related to *Phlebia aurea*, and then grouped with *P. livida* and *P. subserialis*. Both morphological and molecular characters confirmed the placement of the new species in *Ceriporiopsis*.

Keywords *Phlebia* · Phylogenetic analysis · Polypores · Taxonomy · Wood-rotting fungi

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Introduction

Ceriporiopsis Domański (Phanerochaetaceae, Polyporales) was erected by Domanski (1963). It 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 basidiospores are acyanophilous and negative in Melzer's reagent. The genus was typified by *C. gilvescens* (Bres.) Domański and causing a white rot (Gilbertson and Ryvarden 1986–1987; Núñez and Ryvarden 2001; Ryvarden and Melo 2014). So far, about 30 species have been accepted in the genus worldwide (Hattori 2002; Bernicchia and Ryvarden 2003; Kinnunen and Niemelä 2005; Dai et al. 2007; Fortey and Ryvarden 2007; Læssøe and Ryvarden 2010; Tomšovský et al. 2010; Vlasák et al. 2012; Cui 2013a; Zhao and Cui 2014; Zhao et al. 2015b).

Recently, phylogenetic study of European *Ceriporiopsis* taxa suggested that the genus is polyphyletic, and the type *C. gilvescens* was grouped with *Phlebia* spp. on the base of the combined data of the large subunit nuclear ribosomal RNA gene (nLSU) sequences 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. Binder et al. (2013) employed molecular study based on multigene datasets and 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. by using ribosomal DNA sequences. Zhao and Cui (2014) resolved four major clades for *Ceriporiopsis* sensu lato, including phlebia, residual polyporoid, tyromyces, and gelatoporia clades. Zhao et al.

(2015b) described two new poroid species in *Ceriporiopsis* based on their morphological characters and rDNA sequences, and these two species belonged to the phlebioid clade, and were related to the type species of *Ceriporiopsis* (*C. gilvescens*).

During investigations on the diversity of polypores in southwestern China, an additional undescribed species corresponding to *Ceriporiopsis* was found. To confirm the affinity of the undescribed species of *Ceriporiopsis*, phylogenetic analysis was carried out based on the ITS and nLSU sequences.

Materials and methods

Morphology

The specimens studied are deposited at the herbarium of Southwest Forestry University (SWFC). Macro-morphological descriptions are based on field notes. Special color terms follow Petersen (1996). Micro-morphological data were obtained from the dried specimens, and observed under a light microscope following Zhao et al. (2014). 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 of all spores), W = mean spore width (arithmetic average of all spores), Q = variation in the L/W ratios between the specimens studied, n (a/b) = number of spores (a) measured from a given number (b) of specimens.

Molecular phylogeny

The CTAB rapid plant genome extraction kit-DN14 (Aidlab Biotechnologies Co., Ltd., Beijing) was used to obtain genomic DNA from dried specimens, according to the manufacturer's instructions, with some modifications in that a small piece of dried fungal specimen (about 30 mg) was ground to powder with liquid nitrogen. The powder was transferred to a 1.5-mL centrifuge tube, suspended in 0.4 mL of lysis buffer, and incubated in a 65 °C water bath for 60 min. After that, 0.4 mL phenol-chloroform (24:1) was added to each tube and the suspension was shaken vigorously. After centrifugation at 13,000 rpm for 5 min, 0.3 mL of supernatant was transferred to a new tube and mixed with 0.45 mL of binding buffer. The mixture was then transferred to an adsorbing column (AC) for centrifugation at 13,000 rpm for 0.5 min. Then, 0.5 mL of inhibitor removal fluid was added in the AC for a centrifugation at 12,000 rpm for 0.5 min. After washing twice with 0.5 mL of washing buffer, the AC was transferred to a clean centrifuge tube, and 100 mL of elution buffer was added to the middle of the adsorbed film to elute the genome DNA. The ITS region was amplified with primer pairs ITS5 and ITS4

(White et al. 1990). The nuclear LSU region was amplified with primer pairs LR0R and LR7 (<http://www.biology.duke.edu/fungi/mycolab/primers.htm>). The polymerase chain reaction (PCR) procedure for ITS was as follows: initial denaturation at 95 °C for 3 min, followed by 35 cycles at 94 °C for 40 s, 58 °C for 45 s, and 72 °C for 1 min, and a final extension of 72 °C for 10 min. The PCR procedure for nLSU was as follows: initial denaturation at 94 °C for 1 min, followed by 35 cycles at 94 °C for 30 s, 48 °C for 1 min, and 72 °C for 1.5 min, and a final extension of 72 °C for 10 min (Chen et al. 2015). The PCR products were purified and directly sequenced at Beijing Genomics Institute. All newly generated sequences were deposited at GenBank (Table 1).

Sequencher 4.6 (Gene Codes, Ann Arbor, MI, USA) was used to edit the DNA sequence. Sequences were aligned in MAFFT 6 (Katoh and Toh 2008; <http://mafft.cbrc.jp/alignment/server/>) using the "G-INS-i" strategy and manually adjusted in BioEdit (Hall 1999). The sequence alignment was deposited in TreeBase (submission ID 19868). Sequences of *Heterobasidion annosum* (Fr.) Bref. and *Stereum hirsutum* (Willd.) Pers. obtained from GenBank were used as outgroups to root trees following Binder et al. (2013) in the ITS + nLSU analysis.

Maximum parsimony analysis was applied to the ITS + nLSU dataset sequences. Approaches to phylogenetic analysis followed Song et al. (2016), and the tree construction procedure was performed in PAUP* version 4.0b10 (Swofford 2002). All characters were equally weighted and gaps were treated as missing data. Trees were inferred using the heuristic search option with tree bisection and reconnection (TBR) branch swapping and 1000 random sequence additions. maxtrees was set to 5000, branches of zero length were collapsed, and all parsimonious trees were saved. Clade robustness was assessed using a bootstrap (BT) analysis with 1000 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 (MPT) generated. Sequences were also analyzed using maximum likelihood (ML) with RAxML-HPC2 through the CIPRES Science Gateway (<http://www.phylo.org>; Miller et al. 2009). Branch support for ML analysis was determined by 1000 bootstrap replicates.

MrModeltest 2.3 (Posada and Crandall 1998; Nylander 2004) was used to determine the best-fit evolution model for each dataset for Bayesian inference (BI). BI was calculated with MrBayes3.1.2 with a general time reversible (GTR) model of DNA substitution and a gamma distribution rate variation across sites (Ronquist and Huelsenbeck 2003). Four Markov chains were run for two runs from random starting trees for 5 million generations (ITS + nLSU), and trees were sampled every 100 generations. The first one-fourth of

Table 1 List of species, specimens, and GenBank accession numbers of sequences used in this study

Species name	Sample no.	GenBank accession no.		References
		ITS	nLSU	
<i>Abortiporus biennis</i>	TFRI 274	EU232187	EU232235	Binder et al. (2005)
<i>Antella americana</i>	Gothenburg 3161	JN710509	JN710509	Binder et al. (2013)
<i>Antrodia albida</i>	CBS 308.82	DQ491414	AY515348	Kim et al. (2007)
<i>A. heteromorpha</i>	CBS 200.91	DQ491415	AY515350	Kim et al. (2007)
<i>A. semisupina</i>	FCUG 960	EU232182	EU232266	Binder et al. (2005)
<i>Ceraceomyces serpens</i>	KHL 8478	AF090882	AF090882	Binder et al. (2005)
<i>Ceriporia aurantiocarnescens</i>	Yuan 2066	JX623902	JX644042	Jia et al. (2014)
<i>C. lacerata</i>	Dai 10734	JX623916	JX644068	Jia et al. (2014)
<i>C. purpurea</i>	Dai 6205	JX623951	JX644046	Jia et al. (2014)
<i>C. viridans</i>	Dai 7759	KC182777	–	Jia et al. (2014)
<i>Ceriporiopsis alboaurantia</i>	Cui 2877	KF845947	KF845954	Zhao and Cui (2014)
<i>C. alboaurantia</i>	Cui 4136	KF845948	KF845955	Zhao and Cui (2014)
<i>C. aneirina</i>	TAA 181186	FJ496683	FJ496704	Tomšovský et al. (2010)
<i>C. aneirina</i>	Dai 12657	KF845945	KF845952	Zhao and Cui (2014)
<i>C. fimbriata</i>	Dai 11672	KJ698633	KJ698637	Zhao et al. (2015b)
<i>C. fimbriata</i>	Cui 1671	KJ698634	KJ698638	Zhao et al. (2015b)
<i>C. gilvescens</i>	BRNM 710166	FJ496684	FJ496720	Tomšovský et al. (2010)
<i>C. gilvescens</i>	Yuan 2752	KF845946	KF845953	Zhao and Cui (2014)
<i>C. gilvescens</i>	BRNM 667882	FJ496685	FJ496719	Tomšovský et al. (2010)
<i>C. guidella</i>	HUBO 7659	FJ496687	FJ496722	Tomšovský et al. (2010)
<i>C. herbicola</i>	K 132752	KX008364	KX081076	Present study
<i>C. lagerheimii</i>	58240	KX008365	KX081077	Present study
<i>C. kunmingensis</i>	C.L. Zhao 152	KX081072	KX081074	Present study
<i>C. kunmingensis</i>	C.L. Zhao 153	KX081073	KX081075	Present study
<i>C. pseudogilvescens</i>	TAA 168233	FJ496673	FJ496702	Tomšovský et al. (2010)
<i>C. pseudogilvescens</i>	BRNM 686416	FJ496679	FJ496703	Tomšovský et al. (2010)
<i>C. pseudogilvescens</i>	Niemelä 7447	FJ496680	FJ496700	Tomšovský et al. (2010)
<i>C. pseudoplacenta</i>	PRM 899300	JN592498	JN592505	Vlasák et al. (2012)
<i>C. pseudoplacenta</i>	JV 050952	JN592499	JN592506	Vlasák et al. (2012)
<i>C. pseudoplacenta</i>	PRM 899297	JN592497	JN592504	Vlasák et al. (2012)
<i>C. rosea</i>	Dai 13573	KJ698635	KJ698639	Zhao et al. (2015b)
<i>C. rosea</i>	Dai 13584	KJ698636	KJ698640	Zhao et al. (2015b)
<i>C. semisupina</i>	Cui 10222	KF845949	KF845956	Zhao and Cui (2014)
<i>C. semisupina</i>	Cui 7971	KF845950	KF845957	Zhao and Cui (2014)
<i>C. semisupina</i>	Cui 10189	KF84595	KF845958	Zhao and Cui (2014)
<i>Climacocystis borealis</i>	KH 13318	QJ031126	JQ031126	Binder et al. (2013)
<i>Coriopolis caperata</i>	LE(BIN)-0677	AB158316	AB158316	Tomšovský et al. (2010)
<i>Dacryobolus karstenii</i>	KHL 11162	EU118624	EU118624	Binder et al. (2005)
<i>Daedalea quercina</i>	DSM 4953	DQ491425	DQ491425	Kim et al. (2007)
<i>Earliella scabrosa</i>	PR 1209	JN165009	JN164793	Binder et al. (2005)
<i>Fomitopsis pinicola</i>	CBS 221.39	DQ491405	DQ491405	Kim et al. (2007)
<i>F. rosea</i>	ATCC 76767	DQ491410	DQ491410	Kim et al. (2007)
<i>Fragiliporia fragilis</i>	Dai 13080	KJ734260	KJ734264	Zhao et al. (2015a)
<i>F. fragilis</i>	Dai 13559	KJ734261	KJ734265	Zhao et al. (2015a)
<i>F. fragilis</i>	Dai 13561	KJ734262	KJ734266	Zhao et al. (2015a)
<i>Ganoderma lingzhi</i>	Wu 1006-38	JQ781858	–	Zhao et al. (2013)
<i>Gelatoporia subvermispota</i>	BRNU 592909	FJ496694	FJ496706	Tomšovský et al. (2010)
<i>Gloeoporus pannocinctus</i>	BRNM 709972	EU546099	FJ496708	Tomšovský et al. (2010)
<i>G. dichrous</i>	KHL 11173	EU118627	EU118627	Binder et al. (2005)
<i>Grammothelopsis subtropica</i>	Cui 9035	JQ845094	JQ845097	Zhao et al. (2013)
<i>Heterobasidium annosum</i>	PFC 5252	KC492906	KC492906	Binder et al. (2013)
<i>Hornodermoporus martius</i>	MUCL 41677	FJ411092	FJ393859	Robledo et al. (2009)
<i>Hypochnicium lyndoniae</i>	NL 041031	JX124704	JX124704	Binder et al. (2005)
<i>Junghuhnia nitida</i>	KHL 11903	EU118638	EU118638	Binder et al. (2005)
<i>Mycocacia fuscoatra</i>	KHL 13275	JN649352	JN649352	Tomšovský et al. (2010)
<i>M. nothofagi</i>	KHL 13750	GU480000	GU480000	Tomšovský et al. (2010)
<i>Niemelaea balaenae</i>	H7002389	FJ496669	FJ496717	Tomšovský et al. (2010)
<i>N. consobrina</i>	Rivoire 977	FJ496667	FJ496716	Tomšovský et al. (2010)
<i>Obba rivulosa</i>	KCTC 6892	FJ496693	FJ496710	Miettinen and Rajchenberg (2012)
<i>O. valdiviana</i>	FF 503	HQ659235	HQ659235	Miettinen and Rajchenberg (2012)

Table 1 (continued)

Species name	Sample no.	GenBank accession no.		References
		ITS	nLSU	
<i>Perenniporia medulla-panis</i>	MUCL 49581	FJ411087	FJ393875	Robledo et al. (2009)
<i>Perenniporiella neofulva</i>	MUCL 45091	FJ411080	FJ393852	Robledo et al. (2009)
<i>P. chryso sporium</i>	BKM-F-1767	HQ188436	GQ470643	Binder et al. (2005)
<i>Phlebia aurea</i>	DLL2011-263	KJ140747	KJ140747	Binder et al. (2013)
<i>P. aurea</i>	DLL2011-100	KJ140614	AY586691	Binder et al. (2013)
<i>P. aurea</i>	FCUG2767	HQ153409	HQ153409	Binder et al. (2013)
<i>P. livida</i>	FCUG 2189	AF141624	AF141624	Tomšovský et al. (2010)
<i>P. radiata</i>	UBCF 19726	HQ604797	HQ604797	Binder et al. (2013)
<i>P. subserialis</i>	FCUG 1434	AF141631	AF141631	Tomšovský et al. (2010)
<i>P. unica</i>	KHL 11786	EU118657	EU118657	Binder et al. (2013)
<i>Piloporia sajanensis</i>	Manninen 2733a	HQ659239	HQ659239	Tomšovský et al. (2010)
<i>Podoscypa multizonata</i>	Gothenburg 3005	JN710581	JN710581	Binder et al. (2013)
<i>Polyporus tuberaster</i>	CuTENN 10197	AF516596	AJ488116	Binder et al. (2013)
<i>Postia guttulata</i>	KHL 11739	EU11865	EU11865	Kim et al. (2007)
<i>Pouzaroporia subrufa</i>	BRNM 710164	FJ496661	FJ496723	Tomšovský et al. (2010)
<i>Sehipora aquosa</i>	Miettinen 8680	HQ659240	HQ659240	Miettinen and Rajchenberg (2012)
<i>Skeletocutis amorpha</i>	Miettinen 11038	FN907913	FN907913	Tomšovský et al. (2010)
<i>S. jelicii</i>	H 6002113	FJ496690	FJ496727	Tomšovský et al. (2010)
<i>S. portcrossensis</i>	LY 3493	FJ496689	FJ496689	Tomšovský et al. (2010)
<i>Steccherinum fimbriatum</i>	KHL 11905	EU118668	EU118668	Tomšovský et al. (2010)
<i>S. ochraceum</i>	KHL 11902	JQ031130	JQ031130	Tomšovský et al. (2010)
<i>Stereum hirsutum</i>	NBRC 6520	AB733150	AB733325	Tomšovský et al. (2010)
<i>Truncospora ochroleuca</i>	MUCL 39726	FJ411098	FJ393865	Robledo et al. (2009)
<i>Tyromyces chioneus</i>	Cui 10225	KF698745	KF698756	Zhao et al. (2013)
<i>Xanthoporus syringae</i>	Gothenburg 1488	JN710607	JN710607	Tomšovský et al. (2010)

generations were discarded as burn-in. A majority rule consensus tree of all remaining trees was calculated. Branches that received bootstrap support for maximum likelihood (BS), maximum parsimony (BP), and Bayesian posterior probabilities (BPP) greater than or equal to 75% (BP) and 0.95 (BPP) were considered as significantly supported, respectively.

Results

The ITS + nLSU dataset included sequences from 86 fungal specimens, representing 69 species. The dataset had an aligned length of 2431 characters, of which 1348 characters are constant, 281 are variable and parsimony-uninformative, and 802 are parsimony-informative. Maximum parsimony analysis yielded nine equally parsimonious trees (TL = 6641, CI = 0.283, HI = 0.717, RI = 0.580, RC = 0.164). Best model for the ITS + nLSU dataset estimated and applied in the Bayesian analysis was GTR + I + G. Bayesian analysis and ML analysis resulted in a similar topology as MP analysis, with an average standard deviation of split frequencies of 0.004427 (BI).

The phylogeny (Fig. 1) inferred from ITS + nLSU sequences demonstrated seven major clades for 69 species of the Polyporales. The new species *Ceriporiopsis kunmingensis* clustered into the phlebioid clade and was closely related to

Phlebia aurea (Fr.) Nakasone with a high support (100% BS, 95% BP, 0.99 BPP), and then grouped with *P. livida* (Pers.) Bres. and *P. subserialis* (Bourdot & Galzin) Donk.

Taxonomy

Ceriporiopsis kunmingensis C.L. Zhao, sp. nov. Figs. 2 and 3
Mycobank no.: MB 818989

Differs from other *Ceriporiopsis* species by resupinate basidiocarps with pale cinnamon-buff to ochreous color when dry; generative hyphae unbranched, subparallel along the tubes; presence of hyphal ends; allantoid basidiospores, 4.5–5 × 1.5–2 μm.

Holotype. CHINA. Yunnan Prov., Kunming, Yeyahu Forest Park, on fallen angiosperm trunk, 26 August 2016, C.L. Zhao 153 (SWFC).

Etymology. *Kunmingensis* (Lat.): referring to the locality (Kunming) of the type specimen.

Fruiting body. Basidiocarps annual, resupinate, soft corky, without odor or taste when fresh, becoming ceraceous-crustaceous to hard corky upon drying, up to 12 cm long, 3 cm wide, 2 mm thick at center. Pore surface buff to ochreous when fresh, turning to pale cinnamon-buff to ochreous upon drying; pores angular, 4–5 per mm; dissepiments thin, lacerate. Sterile margin distinct, cream, up to 2 mm wide.

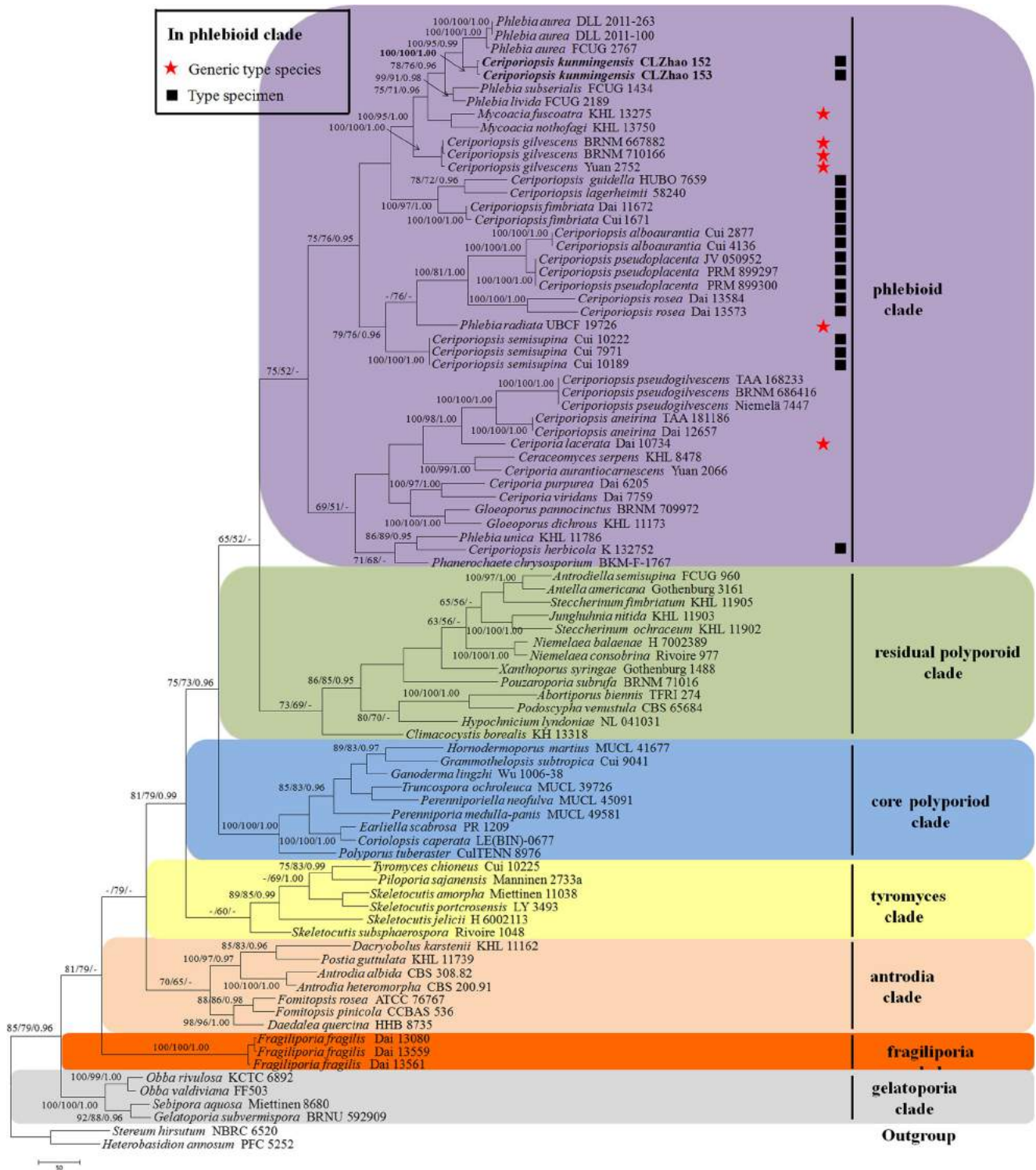


Fig. 1 Maximum parsimony strict consensus tree illustrating the phylogeny of *Ceriporiopsis kunmingensis* and related species in Polyporales based on ITS + nLSU sequences. Branches are labeled with

maximum likelihood bootstrap higher than 70%, parsimony bootstrap proportions higher than 50%, and Bayesian posterior probabilities more than 0.95, respectively. Clade names follow Binder et al. (2013)

Subiculum cream, soft corky, up to 0.5 mm thick. Tubes concolorous with pore surface, ceraceous-crustaceous to hard corky, up to 1.5 mm long.

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

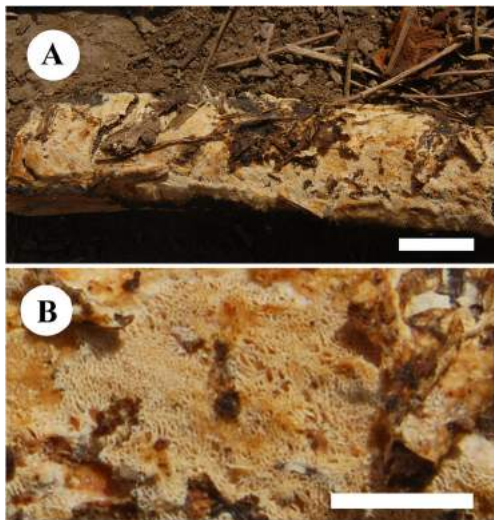


Fig. 2 Basidiomata of *Ceriporiopsis kunmingensis*. Scale bars: **a** 2 cm; **b** 4 mm (holotype)

Subiculum. Generative hyphae hyaline, thin, unbranched, subparallel along the tubes, 3.5–6 μm in diameter.

Tubes. Generative hyphae hyaline, thin-walled, unbranched, subparallel along the tubes, 2–4 μm in diameter;

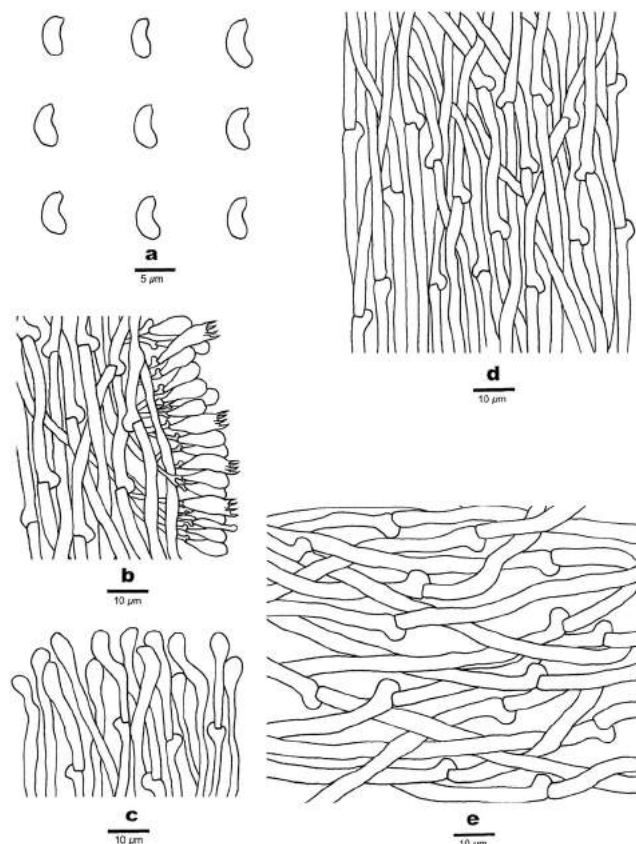


Fig. 3 Microscopic structures of *Ceriporiopsis kunmingensis* (drawn from the holotype). **a** Basidiospores. **b** A section of hymenium. **c** Hyphal ends. **d** Hyphae from trama. **e** Hyphae from subiculum. Scale bars: **a** 5 μm ; **b–e** 10 μm

presence of hyphal ends. Cystidia absent, but fusoid cystidioles occasionally present, hyaline, thin-walled, 9–11 \times 2–2.5 μm ; basidia clavate to pyriform, with four sterigmata and a basal clamp connection, 11–16 \times 4–5 μm ; basidioles dominant, in shape similar to basidia, but slightly smaller.

Spores. Basidiospores allantoid, hyaline, thin-walled, smooth, IKI–, CB–, (4–)4.5–5(–5.5) \times 1.5–2 μm , L = 4.88 μm , W = 1.87 μm , Q = 2.56–2.67 (n = 60/2).

Ecology and habitat. Known only from the Yeyahu Forest Park of Kunming in Yunan province and collected on rotten wood of *Castanea*, causing a white rot.

Additional specimen (paratype) examined: CHINA. Yunnan Prov., Kunming, Yeyahu Forest Park, on rotten wood of *Castanea*, 26 August 2016, C.L. Zhao 152 (SWFC).

Discussion

In the present study, a new species, *Ceriporiopsis kunmingensis*, is described based on phylogenetic analyses and morphological characters. The species has unique morphological characters in *Ceriporiopsis* and forms a monophyletic lineage within the phlebioid clade.

Previously, seven clades were found in the Polyporales: antrodia clade, core polyporoid clade, fragiliporia clade, gelatoporia clade, phlebioid clade, residual polyporoid clade, and tyromyces clade (Binder et al. 2013; Zhao et al. 2015a). According to our result based on the combined ITS + nLSU sequence data (Fig. 1), *C. kunmingensis* is nested into the phlebioid clade with strong support (100% BS, 100% BP, 1.00 BPP).

In the phlebioid clade (Fig. 1), the sampled *Ceriporiopsis* species, including the generic type, are nested with the genus *Phlebia*. Macroscopically, *Phlebia* has a smooth, tuberculate, or phlebioid hymenophore (Parmasto and 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 new species here in the genus *Ceriporiopsis*, mainly because their morphological characters match the concept of *Ceriporiopsis* quite well. Although the new species (Fig. 1) seems closely related to *Phlebia* species, rather than to *Ceriporiopsis gilvescens* in the phylogenetic analysis (Fig. 1), *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.

In present molecular analyses (Fig. 1), *C. kunmingensis* groups with *P. aurea* inferred from the ITS + nLSU analyses. However, morphologically, *P. aurea* differs from *C. kunmingensis* by its odontoid hymenophore with cylindrical aculei, and fimbriate at margin (Nakasone 1997;

Bernicchia and Gorjón 2010). In addition, *C. lagerheimii* Læssøe & Ryvarden and *C. herbicola* Fortey & Ryvarden are sequenced based on type specimens in the present study, and *C. lagerheimii* is as a sister species with *C. guidella* Bernicchia & Ryvarden and *C. herbicola* groups with *P. unica* (H.S. Jacks. & Dearden) Ginns (Fig. 1).

Ceriporiopsis kunmingensis seems to be related to *Phlebia* species in the phylogeny (Fig. 1). However, morphological characters of the new species match the concept of *Ceriporiopsis* quite well. *Ceriporiopsis kunmingensis* is closely related to *C. fimbriata* C.L. Zhao & Y.C. Dai, *C. gilvescens* (Bres.) Domański, *C. guidella*, and *C. lagerheimii* in the rDNA-based phylogeny (Fig. 1). But morphologically, *C. fimbriata* produces larger pores (2–3 per mm) and oblong-ellipsoid to subcylindrical basidiospores (Zhao et al. 2015b). *Ceriporiopsis gilvescens* is another species with subcylindrical to allantoid basidiospores, but it differs from *C. kunmingensis* by having straw to orange brown pore surface upon drying and presence of fimbriate margin, and generative hyphae bearing crystalline incrustations (Gilbertson and Ryvarden 1986–1987; Núñez and Ryvarden 2001; Ryvarden and Melo 2014). *Ceriporiopsis guidella* differs in having a dull yellow to greenish pore surface and wider basidiospores (4–5 × 2.1–2.4 µm; Bernicchia and Ryvarden 2003). *Ceriporiopsis lagerheimii* is separated from the new species by white to cream pore surface, smaller pores (5–8 per mm), and cylindrical basidiospores (Læssøe and Ryvarden 2010).

Polypores are an extensively studied group of Basidiomycota (Gilbertson and Ryvarden 1986–1987; Núñez and Ryvarden 2001; Ryvarden and Melo 2014), but the Chinese polypore diversity is still not well known, especially in the subtropics and tropics; many recently described taxa of polypores were from these areas (Cui 2013b; Li and Cui 2013; Li et al. 2013; Chen and Cui 2014; Song et al. 2014; Dai et al. 2015; Chen et al. 2016a, b; Shen et al. 2016; Zhou et al. 2016). The new species in the present study, *C. kunmingensis*, is from the subtropics, too. Recently, 11 *Ceriporiopsis sensu stricto* species from around the world have been grouped into the phlebioid clade based on phylogenetic analysis (Tomšovský et al. 2010; Vlasák et al. 2012; Binder et al. 2013; Zhao and Cui 2014; Zhao et al. 2015b). It is possible that new polypore taxa will be found after further investigations and molecular analyses.

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