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Crepatura ellipsospora gen. et sp. nov. in Phanerochaetaceae (Polyporales, Basidiomycota) bearing a tuberculate hymenial surface

Xiang Ma^{1,2} · Chang-Lin Zhao^{1,2}

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Abstract

A new wood-inhabiting fungal genus, *Crepatura*, typified by *C. ellipsospora* sp. nov., is proposed based on a combination of morphological features and molecular evidence. The genus is characterized by an annual growth habit, resupinate basidiocarps with smooth to irregularly tuberculate hymenial surface, a monomitic hyphal system with thick-walled generative hyphae bearing both clamp connections and simple septa and ellipsoid, hyaline, thick-walled, smooth, negative in Melzer's, acyanophilous basidiospores measuring 6.5–7.5 × 4–5 µm. Sequences of ITS and LSU nrRNA gene regions of the studied samples were generated, and phylogenetic analyses were performed with maximum likelihood, maximum parsimony, and Bayesian inference methods. The phylogenetic analyses based on molecular data of ITS+nLSU sequences showed that *Crepatura* belonged to the Phanerochaetaceae family and nested into the Donkia clade. The result demonstrated that the genus *Crepatura* formed a monophyletic lineage with a strong support and phylogenetically was closely related to *Pirex concentricus*.

Keywords China · Molecular phylogeny · Phanerochaetaceae · Taxonomy · Wood-rotting fungi

Introduction

Polyporales is one of the most intensively studied clades of fungi and the taxa of Polyporales are of interest to both fungal ecologists and applied scientists (Justo et al. 2017). At present, there are 46 genomes of Polyporales hosted by the Joint Genome Institute MycoCosm portal (Grigoriev et al. 2013). However, with roughly 1800 described species, Polyporales account for only about 1.5% of all known species of Fungi (Kirk et al. 2008). Species in this order are the key players among the wood-rotting fungi because of their importance in the pathogenic and potential application in biomedical engineering and biodegradation (Dai et al. 2009; Levin et al. 2016).

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✉ Chang-Lin Zhao
fungichanglinz@163.com

Molecular systematics has played a powerful role in inferring phylogenies within fungal groups since the early 1990s (White et al. 1990; Larsson 2007; Miettinen et al. 2012; Binder et al. 2013; Dai et al. 2015; Choi and Kim 2017). Recently, molecular studies involving Phanerochaetaceae (Polyporales, Basidiomycota) have been carried out (Binder et al. 2005, 2013; Larsson 2007; Wu et al. 2010; Miettinen and Larsson 2011; Miettinen and Rajchenberg 2012; Miettinen et al. 2012, 2016; Floudas and Hibbett 2015; Justo et al. 2017).

Larsson (2007) introduced a new division taxonomic system for part of the Polyporales, effectively renaming the phlebioid and residual polyporoid clades as the Meruliaceae P. Karst., Phanerochaetaceae, and *Byssomerulius* Parmasto families and suggested the adoption of Phanerochaetaceae for a clade of corticioid fungi around the genus *Phanerochaete* P. Karst. The corticioid members of the Phanerochaetaceae have been popular subjects of phylogenetic research, which has resulted in revision of genus concepts within the family and an extended phylogeny of the Phanerochaetaceae was produced, extending the genera *Hjortstamia* Boidin & Gilles and *Phlebiopsis* Jülich (Wu et al. 2010). Furthermore, further study employing a six-gene (5.8S, nrLSU, nrSSU, rpb1, rpb2, tef1) dataset has constructed phylogenetic and phylogenomic overview of the Polyporales, which showed that Phanerochaetaceae was indeed a well-supported subclade of

¹ College of Biodiversity Conservation and Utilization, Southwest Forestry University, Kunming 650224, People's Republic of China

² Key Laboratory for Forest Resources Conservation and Utilization in the Southwest Mountains of China, Ministry of Education, Southwest Forestry University, Kunming 650224, People's Republic of China

the large phlebioid clade, with the polypore genus *Bjerkandera* as the sister clade to the rest of the family (Binder et al. 2013). Floudas and Hibbett (2015) proposed that *Phaeophlebiopsis* Floudas & Hibbett for *Phlebia*-like taxa were phylogenetically separated from the morphologically similar *Phlebiopsis* species and moved a species of *Hjortstamia* Boidin & Gilles to *Phlebiopsis*. Polypores and genus concepts in Phanerochaetaceae have been explored and showed that *Donkia pulcherrima* (Berk. & M.A. Curtis) Pilát, *Hyphoderella rosae* (Bres.) Nakasone, and *Pirex concentricus* (Cooke & Ellis) Hjortstam & Ryvarden nested in the *Donkia* clade belonged to the family Phanerochaetaceae (Miettinen et al. 2016). Justo et al. (2017) proposed a revised family-level classification of the Polyporales (Basidiomycota) and confirmed that Phanerochaetaceae belonged to the order Polyporales and three species *D. pulcherrima*, *H. rosae*, and *P. concentricus* grouped together.

The family Phanerochaetaceae is cosmopolitan and has a rich diversity on the basis of growing on boreal, temperate, subtropical, and tropical vegetation (Núñez and Ryvarden 2001; Dai 2012; Ryvarden and Melo 2014; Dai et al. 2015; Zhou et al. 2016a). During the investigations on wood-inhabiting fungi in southern China, an additional taxon was found, which could not be assigned to any described genus. In this study, we expand samplings from previous studies to examine taxonomy and phylogeny of this new genus within the Phanerochaetaceae based on the internal transcribed spacer (ITS) regions and the large subunit nuclear ribosomal RNA gene (nLSU) sequences.

Materials and methods

Morphology

The specimens studied are deposited at the herbarium of Southwest Forestry University (SWFC). Macromorphological descriptions are based on field notes. Special color terms follow Petersen (1996). Micromorphological data were obtained from the dried specimens, and observed under a light microscope following Dai (2010). The following abbreviations were used: KOH = 5% potassium hydroxide, CB = Cotton Blue, CB- = acyanophilous, IKI = Melzer's reagent, IKI- = both non-amyloid and non-dextrinoid, 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 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. ITS region was amplified with primer pairs ITS5 and ITS4 (White et al. 1990). Nuclear LSU region was amplified with primer pairs LR0R and LR7 (https://sites.duke.edu/vilgalyslab/rDNA_primers_for_fungi/). The 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. 2016). The PCR products were purified and directly sequenced at Kunming Tsingke Biological Technology Limited Company. All newly generated sequences were deposited at GenBank (Table 1).

Sequencher 4.6 (GeneCodes, 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). *Cryptococcus bacillisporus* Kwon-Chung & J.E. Benn. and *C. neoformans* (San Felice) Vuill. were used as outgroups to root trees following Garcia-Sandoval et al. (2011) in the ITS+nLSU analyses (Fig. 1).

Maximum parsimony analysis was applied to the ITS+nLSU dataset sequences. Approaches to phylogenetic analysis followed Li and Cui (2013), 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 TBR branch swapping and 1000 random sequence additions. Max-trees were 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 generated. Sequences were also analyzed using maximum likelihood (ML) with RAxML-HPC2 through the Cipres Science Gateway (www.phylo.org; Miller et al. 2009). Branch support (BS) 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). Bayesian inference was calculated with MrBayes3.1.2 with a general time reversible (GTR+G) model of DNA substitution and a gamma distribution rate variation across sites (Ronquist and Huelsenbeck 2003). Four Markov chains run for 2 runs from random starting trees for 5 million generations and trees were sampled every 100 generations. The first one-fourth

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

Species name	Sample no.	GenBank accession no.		References
		ITS	nLSU	
<i>Aurantiporus croceus</i> (Pers.) Murrill	BRNM 737561	JQ821320	JQ821317	Binder et al. (2013)
<i>Berkandera adusta</i> (Willd.) P. Karst.	HHB 12826	KP134983	KP135198	Floudas and Hibbett (2015)
<i>Boletinellus merulioides</i> (Schwein.) Murrill	AFTOL-ID 575	DQ200922	AY684153	Binder et al. (2005)
<i>Candelabrochaete septicystidia</i> (Burt) Burds.	AS 95	EU118609	EU118609	Binder et al. (2005)
<i>Ceratomyces serpens</i> (Tode) Gimms	HHB 15692	KP135031	KP135200	Floudas and Hibbett (2015)
<i>Ceriporia aurantiocarnescens</i> (Henn.) B. Rivoire	Dai 6055	JX623904	JX644043	Jia et al. (2014)
<i>C. pierii</i> Spirin & Miettinen	Rivoire 1161	KX752604	—	Miettinen et al. (2016)
<i>C. viridiannus</i> (Berk. & Broome) Donk	Miettinen 11701	KX752600	KX752600	Miettinen et al. (2016)
<i>Crepatura ellipsospora</i> C.L. Zhao	CL.Zhao 1265	MR3243692	MR3243696	Present study
<i>C. ellipsospora</i>	CL.Zhao 1260	MR3243693	MR3243697	Present study
<i>C. ellipsospora</i>	CL.Zhao 868	MR3243694	MR3243698	Present study
<i>C. ellipsospora</i>	CL.Zhao 697	MR3243695	MR3243699	Present study
<i>Cryptococcus bacillisporus</i> Kwon-Chung & J.E. Benn.	CBS 10510	FJ534878	FJ534908	Garcia-Sandoval et al. (2011)
<i>C. neoflavicans</i> (San Felice) Vuill.	ATCC 4565	FJ914892	FJ914892	Garcia-Sandoval et al. (2011)
<i>Dacrymyces chrysospermus</i> Berk. & M.A. Curtis	TUFC 13115	AB712452	AF287855	Binder et al. (2005)
<i>Dacryopinax spathularia</i> (Schwein.) G.W. Martin	AFTOL-ID 454	AY854070	AY701525	Binder et al. (2005)
<i>Donkia pulcherrima</i> (Berk. & M.A. Curtis) Pilát	Hausknecht 1998	KX752591	KX752591	Miettinen et al. (2016)
<i>Ennia latemarginata</i> Spirin & Malysheva	Piatek 1997	KX752592	KX752592	Miettinen et al. (2016)
<i>Flavodon flavus</i> (Klotzsch) Ryvarden	10219	JN710543	JN710543	Miettinen et al. (2012)
<i>Globulicium hiemale</i> (Laurila) Hjortstam	5444b	DQ873595	DQ873595	Binder et al. (2005)
<i>Gloeophyllum sepiarium</i> (Wulfen) P. Karst.	Dai 5608	KC782726	KC782737	Garcia-Sandoval et al. (2011)
<i>G. striatum</i> (Fr.) Murrill	NBRC 6429	AB733308	AB733308	Garcia-Sandoval et al. (2011)
<i>Gloeoporus dichrous</i> (Fr.) Bres.	FP 134973	DQ679919	—	Binder et al. (2005)
<i>Grupeinopsis buccina</i> (Pers.) L.L. Kenn.	AFTOL-ID 888	DQ206986	AY475711	Garcia-Sandoval et al. (2011)
<i>Halopeltis eupatori</i> (P. Karst.) Spirin & Miettinen	Dammrich 10744	KX752620	KX752620	Miettinen et al. (2016)
<i>H. percoctus</i> Miettinen	Miettinen 2008	KX752597	KX752597	Miettinen et al. (2016)
<i>H. rutilans</i> (Pers.) Murrill	FD 512	KP135419	—	Floudas and Hibbett (2015)
<i>H. rutilans</i>	Vlasak JV/0206/2	KX752623	KX752623	Miettinen et al. (2016)
<i>Hypodermella capitatum</i> J. Erikss. & Å. Strid	KHL 8464	DQ677491	DQ677491	Garcia-Sandoval et al. (2011)
<i>H. orphanethum</i> (Bourdot & Galzin) Donk	NH 12208	DQ677500	DQ677500	Binder et al. (2005)
<i>Hypodermella corrugata</i> (Fr.) J. Erikss. & Ryvarden	MA-Fungi 24238	FN600378	JN939586	Floudas and Hibbett (2015)
<i>H. rosae</i> (Bres.) Nakasone	PP 150552	KP134978	KP135223	Telleria et al. (2010)
<i>H. rosa</i>	FN600389	FN600389	JN939588	Telleria et al. (2010)
<i>Hypographopeltis aurantiaca</i> (Wulfen) Mai	AI419201	AF352816	AF352816	Garcia-Sandoval et al. (2011)
<i>Ipex lacteus</i> (Fr.) Fr.	Niemela 1932	KX752593	KX752593	Miettinen et al. (2016)
<i>Lepioporus mollis</i> (Pers.) Quél.	RLG 7163	EU402583	EU402583	Binder et al. (2013)
<i>Merulipensis taxicola</i> (Pers.) Bondartsev	EU118648	EU118648	EU118648	Miettinen et al. (2012)
<i>Neolentulus kauffmannii</i> (A.H. Sm.) Redhead & Gimms	HM536097	HM536097	HM536097	Garcia-Sandoval et al. (2011)
<i>Oxycatiae cervinogilva</i> (Jung.) Miettinen	KX752596	KX752596	KX752596	Miettinen et al. (2016)
<i>Phaeophlebiopsis caribbeana</i> Floudas & Hibbett	KP135243	KP135243	KP135243	Floudas and Hibbett (2015)
<i>P. peniophoroides</i> (Glib. & Adask.) Floudas & Hibbett	KP135417	KP135417	KP135417	Floudas and Hibbett (2015)
<i>Phanerina mellea</i> (Berk. & Broome) Miettinen	IX623933	IX623933	IX623933	IX623933

Table 1 (continued)

Species name	Sample no.	GenBank accession no.		References
		ITS	nLSU	
<i>P. mellaea</i>	Miettinen 9134	KX752599	KX752602	Jia et al. (2014)
<i>P. mellaea</i>	Dai 9453	JX623932	JX644059	Jia et al. (2014)
<i>Phanerochaete arizonica</i> Burds. & Gilb.	RLG 10248	KP135170	KP135239	Floudas and Hibbett (2015)
<i>P. buriti</i> (Romell ex Burt) Parmasto	HHB 4618	KP135117	KP135241	Floudas and Hibbett (2015)
<i>P. chrysosporium</i> Burds.	HHB 6251	KP135094	KP135246	Floudas and Hibbett (2015)
<i>P. citrinosanguinea</i> Floudas & Hibbett	PP 105385	KP135100	KP135234	Floudas and Hibbett (2015)
<i>P. ericina</i> (Boudot) J. Erikss. & Ryvarden	HHB 2288	KP135167	KP135247	Floudas and Hibbett (2015)
<i>P. laevis</i> (Fr.) J. Erikss. & Ryvarden	HHB 15519	KP135149	KP135249	Floudas and Hibbett (2015)
<i>P. sanguineocarnosa</i> Floudas & Hibbett	FD 359	KP135122	KP135245	Floudas and Hibbett (2015)
<i>P. sordid</i> (P. Karst.) J. Erikss. & Ryvarden	FD 241	KP135136	KP135252	Floudas and Hibbett (2015)
<i>P. subceracea</i> (Burt) Burds.	PP 105974-R	KP135162	KP135255	Floudas and Hibbett (2015)
<i>Phlebia ignota</i> Fr.	AFTOL-ID 484	AY854087	AF287885	Binder et al. (2005)
<i>Phlebiopsis crassa</i> (Lév.) Floudas & Hibbett	KRN 86	KP135394	KP135215	Floudas and Hibbett (2015)
<i>P. flavidula</i> (Cooke) Hjortstam	FD 263	KP135402	KP135271	Floudas and Hibbett (2015)
<i>P. gigantean</i> (Fr.) Jülich	PP 70857	KP135390	KP135272	Floudas and Hibbett (2015)
<i>P. pilatii</i> (Parmasto) Spirin & Miettinen	Spirin 5048	KX752590	KX752590	Miettinen et al. (2016)
<i>Pixex concentricus</i> (Cooke & Ellis) Hjortstam & Ryvarden	OSC-41587	KP134984	KP135275	Floudas and Hibbett (2015)
<i>Porostereum spadiceum</i> (Pers.) Hjortstam & Ryvarden	Wu 9708-104	DQ679918	Wu et al. (2010)	Miettinen et al. (2016)
<i>Riopa metamorphosa</i> (Fuckel) Miettinen & Spirin	Pouzar 1988	KX752612	—	Miettinen et al. (2016)
<i>R. metamorphosa</i>	Vhasak JV0511/5	KX752613	KX752613	Bindet et al. (2005)
<i>Rhizopeltis brunnea</i> Gresl., Nakasone & Rajchenb.	M/R 229	AY219389	AY219389	Bindet et al. (2005)
<i>Rhizopeltis fowleriæ</i> Nakasone & Rajchenb.	KKN 121	AY219390	AY219390	Tomšovský et al. (2010)
<i>Rickenella mellea</i> (Singer & Cléménçon) Lamoure	Lamoure 74	U66438	U66438	Miettinen et al. (2016)
<i>Riopa pudens</i> Miettinen	Miettinen 8772	KX752598	—	Bindet et al. (2005)
<i>Suillus pictus</i> (Peck) Kunze	AFTOL-ID 717	AY854069	AY844154	Miettinen et al. (2012)
<i>Trametopsis cervina</i> (Schwein.) Tomšovský	TJV 93216T	JN165020	—	Miettinen et al. (2012)

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 (BT), and Bayesian posterior probabilities (BPP) greater than or equal to 75% (BT) and 0.95 (BPP) were considered as significantly supported, respectively.

Results

The ITS+nLSU dataset (Fig. 1) included sequences from 68 fungal specimens representing 60 taxa. The dataset had an aligned length of 2352 characters, of which 1292 characters were constant, 300 parsimony-uninformative, and 760

parsimony-informative. MP analysis yielded 10 equally parsimonious trees (TL = 4757, CI = 0.377, HI = 0.623, RI = 0.577, RC = 0.218). The best-fit model for ITS+nLSU alignment estimated and applied in the BI was GTR+I+G, lset nst = 6, rates = invgamma; prset statefreqpr = dirichlet (1,1,1,1). BI resulted in a similar topology with an average standard deviation of split frequencies = 0.007374.

The phylogenetic tree (Fig. 1) inferred from ITS+nLSU sequences demonstrated four major clades in Phanerochaetaceae for 55 sampled species of the Polyporales. The new genus *Crepatura* fell into the Donkia clade. The new genus formed a monophyletic entity with a high 100% BS, 100% BP, and 1.00 BPP, and was closely related to *Pirex concentricus* (Cooke & Ellis) Hjortstam & Ryvarden with a strong support (100% BS, 98% BP, 1.00 BPP) and then grouped with

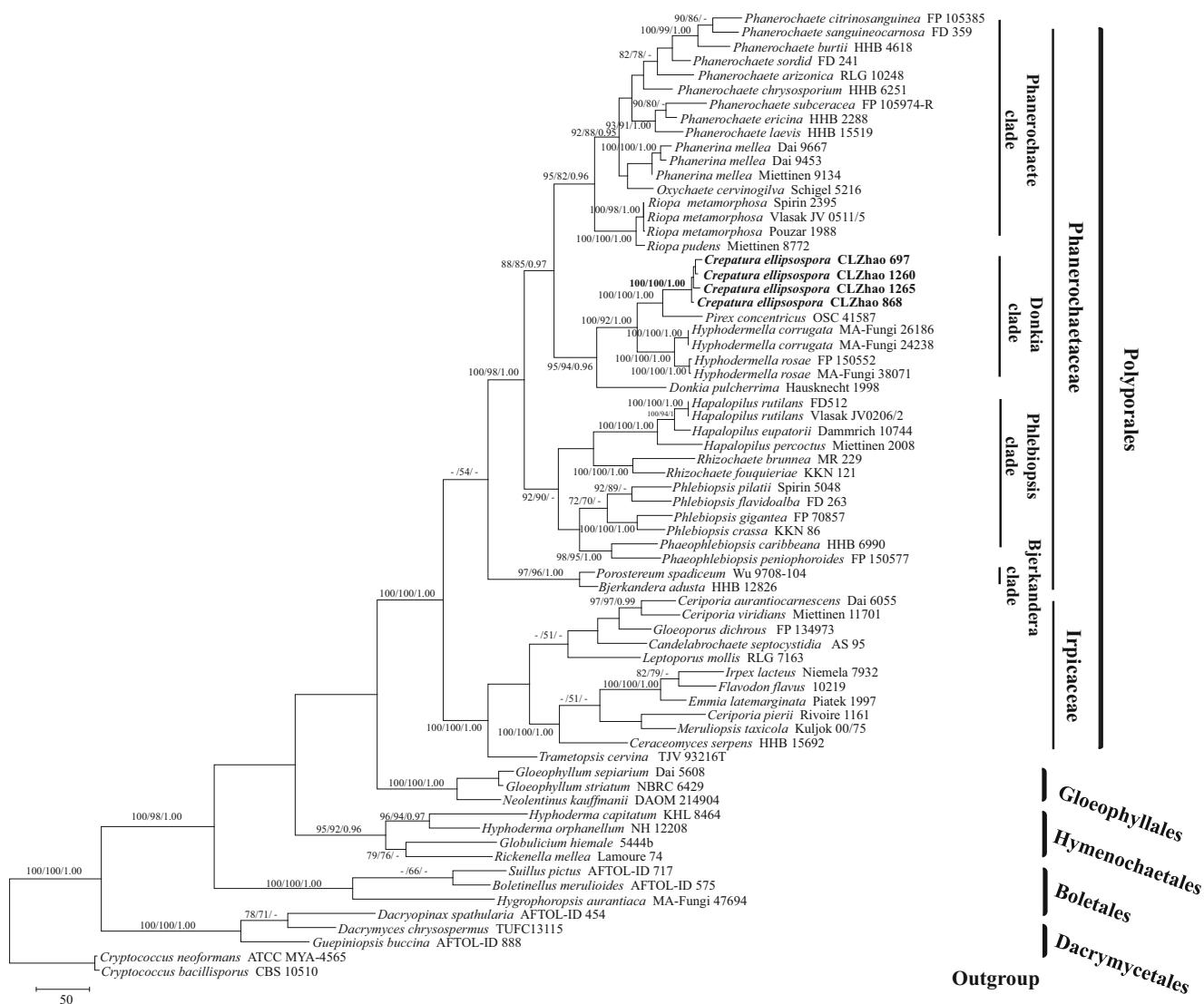


Fig. 1 Maximum parsimony strict consensus tree illustrating the phylogeny of *Crepatura ellipsospora* and related species in Polyporales based on ITS+nLSU sequences. Branches are labeled with parsimony

bootstrap values (before slash) higher than 50% and Bayesian posterior probabilities (after slash) equal to and more than 0.95. Clade names follow Miettinen et al. (2016)

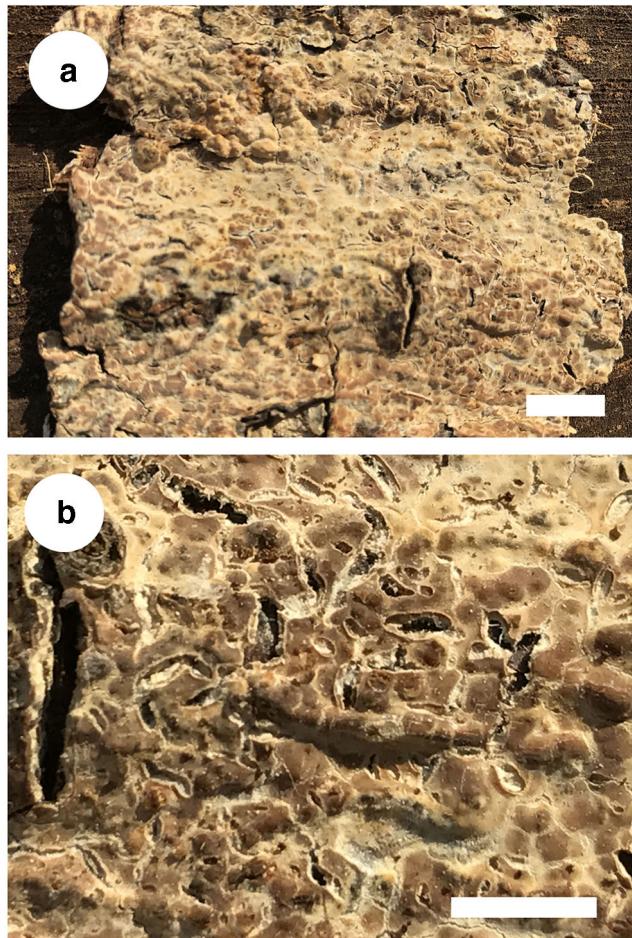


Fig. 2 Basidiomata of *Crepatura ellipsospora* (holotype). Bars: **a** 1 cm, **b** 5 mm s

two genera *Hyphodermella* J. Erikss. & Ryvarden and *Donkia* Pilát.

Taxonomy

Crepatura C.L. Zhao, gen. nov.

Mycobank no.: MB 830230

Differs from other genera in Polyporales by resupinate basidiocarps, a monomitic hyphal system, thick-walled generative hyphae bearing both clamp connections and simple septa, and hyaline, thick-walled, smooth, IKI–, CB– basidiospores.

Type species. *Crepatura ellipsospora* C.L. Zhao.

Etymology. *Crepatura* (Lat.): referring to the cracking hymenial surface.

Basidiocarps annual, resupinate. Hymenial surface smooth to irregularly tuberculate, concentrically and radially cracking. Hyphal system monomitic; generative hyphae thick-walled bearing both clamp connections and simple septa, IKI–, CB–; tissues unchanged in KOH. Cystidia and cystidioles

absent; numerous crystals present among the hyphae, basidia clavate, with two sterigmata. Basidiospores ellipsoid, hyaline, thick-walled, smooth, IKI–, CB–.

Crepatura ellipsospora C.L. Zhao, sp. nov. (Figs. 2 and 3)
Mycobank no.: MB 830231

Holotype. CHINA. Yunnan Province, Kunming, Xishan District, Haikou Forestry Park, 22 April 2017, on fallen branch of *Quercus*, CLZhao 1265 (SWFC).

Etymology. *ellipsospora* (Lat.): referring to the ellipsoid basidiospores.

Fruiting body. Basidiocarps annual, resupinate, not separable, coriaceous, without odor or taste when fresh, becoming rigid up on drying, up to 18 cm long, 100–300 µm thick. Hymenial surface smooth to irregularly tuberculate, cream to pale yellow when fresh, turn to yellow to yellowish brown upon drying, concentrically and radially cracking. Sterile determined, concolorous with hymenial surface.

Hyphal structure. Monomitic; generative hyphae thick-walled bearing both clamp connections and simple septa, simple septa more frequent than clamps, IKI–, CB–; tissues unchanged in KOH. Subiculum absent or indistinct, hymenium thickening, hyphae colorless, more or less interwoven, thick-walled, rarely branched, 3.5–5 µm in diam.

Hymenium. Cystidia and cystidioles absent; numerous crystals present among the hyphae, basidia clavate, with two sterigmata and a basal clamp connection, 18.5–35.5 × 5.5–6.5 µm; basidioles dominant, similar in shape to basidia, but slightly smaller. Basidiospores ellipsoid, hyaline, thick-walled, smooth, IKI–, CB–, (6–)6.5–7.5(–8.5) × (3.5–)4–5(–5.5) µm, L = 7.15 µm, W = 4.57 µm, Q = 1.51–1.63 (n = 120/4).

Type of rot. White rot.

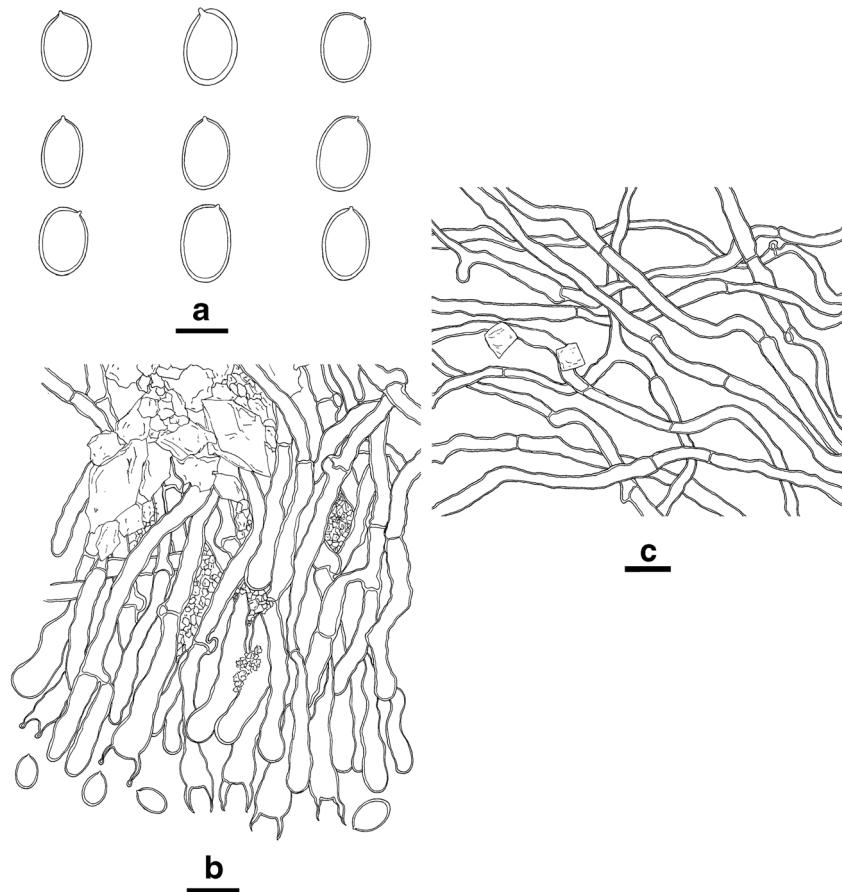
Additional specimens (paratypes) examined: CHINA. Yunnan Province, Kunming, Xishan District, Haikou Forestry Park, 22 April 2017, on fallen branch of *Quercus*, CLZhao 1260 (SWFC); 11 January 2017, on trunk of Alder, CLZhao 697 (SWFC); 16 January 2017, on fallen branch of *Quercus*, CLZhao 868 (SWFC).

Discussions

In the present study, a new genus, *Crepatura*, is described based on phylogenetic analyses and morphological characters. The genus has unique morphological characters in Phanerochaetaceae.

Previously, three families were studied in the Polyporales—Phanerochaetaceae, Irpicaceae Spirin & Zmitr., and Meruliaceae P. Karst.—and four clades were found in the Phanerochaetaceae: Phanerochaete clade, Donkia clade, Phlebiopsis clade, and Bjerkandera clade (Miettinen et al. 2016). According to our result based on the combined ITS+ nLSU sequence data (Fig. 1), the new genus is nested into the

Fig. 3 Microscopic structures of *Crepatura ellipsospora* (drawn from the holotype). **a** Basidiospores; **b** a section of hymenium; **c** Subiculum. Bars: **a** 5 μm ; **b, c** 10 μm



Donkia clade with strong support (100% BS, 100% BP, 1.00 BPP) and belongs to the family Phanerochaetaceae.

Miettinen et al. (2016) analyzed a higher-level phylogenetic classification of polypores and the genus concepts in Phanerochaetaceae (Polyporales, Basidiomycota) and showed that the macromorphology of fruiting bodies and hymenophore construction did not reflect monophyletic groups. The current phylogeny shows that the new genus is closely related to *Pirex concentricus* and then grouped with *Hyphodermella* and *Donkia* based on ITS+LSU nrRNA gene regions with a strong support (Fig. 1). However, morphologically, the genus *Pirex* is characterized by resupinate basidiocarps with hydnoid hymenophore and brown subiculum, and a monomitic hyphal system bearing clamp connections and ellipsoid, hyaline, thin-walled, smooth basidiospores (Hallenbergs et al. 1985). In addition, the tissues changed to a reddish color in KOH. *Pirex* Hjortstam & Ryvarden differs from *Crepatura* by a hydnoid hymenophore and chrome yellow basidiocarps, a dark brown context, and thin-walled basidiospores (Hallenbergs et al. 1985). *Hyphodermella* is separated from *Crepatura* by the grandiniod to odontiod hymenophore and the presence of encrusted hyphal ends (Bernicchia and Gorjón 2010). *Donkia* differs in its pileate basidiocarps with hydnoid or

dentate hymenophore and the thick-walled cystidia and thin-walled basidiospores (Bernicchia and Gorjón 2010).

Morphologically, *Crepatura* resembles *Hypochnicium* J. Erikss. and *Phlebiiporia* Jia J. Chen, B.K. Cui & Y.C. Dai. *Hypochnicium* is similar to *Crepatura* in the resupinate basidiome with smooth, tuberculate hymenophore, and a monomitic hyphal structure and thick-walled basidiospores. However, *Hypochnicium* differs from *Crepatura* by having the generative hyphae bearing only clamps, and basidia with four sterigmata and cyanophilous basidiospores (Bernicchia and Gorjón 2010). In addition, *Hypochnicium* grouped with *Abortiporus biennis* (Bull.) Singer and *Podoscypha multizonata* (Berk. & Broome) Pat. belonging to the family Meruliaceae (Miettinen et al. 2012).

Phlebiiporia is similar to *Crepatura* by having generative hyphae bearing both simple septa and clamp connections, but it is separated from *Crepatura* by having a poroid hymenophore, dextrinoid generative hyphae, tissues becoming brownish in KOH, and the presence of thin-walled quasi-binding hyphae in the subiculum (Chen and Cui 2014).

Wood-rotting fungi are an extensively studied group of Basidiomycota (Núñez and Ryvarden 2001; Bernicchia and Gorjón 2010; Dai 2012; Ryvarden and Melo 2014; Dai et al. 2015; Zhou et al. 2016a), but the Chinese wood-rotting fungus

diversity is still not well known, especially in subtropics and tropics, where many recently described taxa of wood-rotting fungi were from these areas (Cui 2013; Li et al. 2013, 2014; Chen and Cui 2014; Chen et al. 2016; Zhou et al. 2016b; Kan et al. 2017). The new genus in the present study, *Crepatura*, is from the subtropics, too. It is possible that new taxa will be found after further investigations and molecular analyses.

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