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Fragiliporiaceae, a new family of Polyporales (Basidiomycota)

Chang-Lin Zhao · Bao-Kai Cui · Jie Song ·
Yu-Cheng Dai

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Abstract *Fragiliporiaceae* fam. nov., a new poroid wood-inhabiting family, is introduced based on the combination of molecular and morphological data, and is typified by *Fragiliporia* gen. nov. The phylogenetic analysis shows that *Fragiliporia fragilis* sp. nov. forms a monophyletic group within Polyporales and warrants the introduction of a new fragiliporia clade based on molecular data of ITS+nLSU rRNA gene regions. Combined ITS, nLSU, mtSSU, TEF1 and RPB2 sequence data also demonstrated that the new family *Fragiliporiaceae* also formed a monophyletic lineage (70 % BS, 57 % BP, 0.99 BPP), and grouped with the phlebioid clade, residual polyporoid clade and core polyporoid clade. *Fragiliporiaceae* has unique macromorphological characters in having resupinate basidiocarps with very soft tubes when fresh, which become brittle when dry (becoming almost powdery when bruised); a monomitic hyphal system with thick-walled generative hyphae, clamp connections, and frequently H-, W- or Y-shaped hyphae branching from the clamp connections.

Keywords *Fragiliporia* clade · Multi-marker analysis · Polypores · Taxonomy

Introduction

The *Polyporales* is a diverse group of Agaricomycetes including more than 1,800 described species in 216 genera and 13

families (Kirk et al. 2008). Polypores are a very important group of wood-inhabiting fungi because of their key role in the carbon cycle and being the most efficient wood decayers in the biosphere (Zhou et al. 2011; Floudas et al. 2012). They may also be pathogenic and have potential application in biomedical engineering and biodegradation (Younes et al. 2007; Dai et al. 2007, 2009; Wang et al. 2012; Si et al. 2013).

Molecular systematics is a powerful tool to infer phylogenies within fungal groups including polypores (White et al. 1990; Hibbett et al. 2007; Justo and Hibbett 2011; Zhang et al. 2011; Binder et al. 2013; Hyde et al. 2013, 2014; Nilsson et al. 2014). Genes coding for ribosomal RNA and proteins have been used to reconstruct the evolutionary history in the Fungi (James et al. 2006), and a higher-level phylogeny including *Polyporales* have been principally resolved (Hibbett et al. 2007). Resolving the taxonomic structure of *Polyporales* has proven difficult based on the nearly exclusive use of ribosomal DNA sequences (Binder et al. 2005). More recent studies have used protein-coding genes (*rpb1*, *rpb2*, *tef1*) for phylogenetic reconstruction (Justo and Hibbett 2011; Miettinen et al. 2012; Sjökvist et al. 2012). Recently, molecular studies employing multi-gene (5.8S, nrLSU, nrSSU, *rpb1*, *rpb2*, *tef1*) datasets has helped to investigate phylogenetic overview of the *Polyporales*. Thirty-four valid families are now placed in *Polyporales* (Binder et al. 2013).

China has a huge land area, including boreal, temperate, subtropical, and tropical vegetations. Most parts of southern China have subtropical to tropical vegetations, in which the diversity of polypores and other fungi is very rich (Dai 2012; Wu et al. 2014). Seven-hundred and four polypore species belonging to 132 genera in ten orders were identified and the majority of them belong in the order *Polyporales* (Dai 2012). Polypore diversity in southern China has been extensively studied during the past 20 years, and a mass of novel genera and new species have been found (Cui et al. 2011; Cao et al. 2012; Dai et al. 2014).

Chang-Lin Zhao and Bao-Kai Cui contributed equally to this work and shared the first author

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In the present study, we examined taxonomy and phylogeny of new samples within the *Polyporales*. A distinct family level clade was found based on combined ITS, nLSU, mtSSU, TEF1 and RPB2 sequence data. Species in the clade have different morphology from the presently known families of *Polyporales*. Thus, a new family is proposed to accommodate this taxon.

Materials and methods

Morphology

The studied specimens are deposited at the herbaria of Beijing Forestry University (BJFC) and the Institute of Applied Ecology, Chinese Academy of Sciences (IFP). Macro-morphological descriptions are based on field notes. Special colour terms follow Petersen (1996). Micro-morphological data were obtained from the dried specimens, and observed under a light microscope following Dai (2010). Sections were studied at a magnification of up to $\times 1,000$ using a Nikon Eclipse 80i microscope and phase contrast illumination. Drawings were made with the aid of a drawing tube. Microscopic features, measurements and drawings were made from slide preparations stained with Cotton Blue and Melzer's reagent. Spores were measured from sections cut from the tubes. In presenting the variation of spore size, 5 % of measurements were excluded from each end of the range, and were 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 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

CTAB rapid plant genome extraction kit-DN14 (Aidlab Biotechnologies Co., Ltd, Beijing) was used to obtain PCR products 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 (<http://www.biology.duke.edu/fungi/mycolab/primers.htm>). Mitochondrial SSU region was amplified with primer pairs MS1 and MS2 (White et al. 1990). TEF1 was amplified with primer pairs EF1-983 F and EF1-2218R (Rehner and Buckley 2005). RPB2 was amplified with primer pairs fRPB2-f5F and bRPB2-7.1R (Liu et al. 1999; Matheny 2005). The PCR procedure for ITS and mtSSU were as follows: initial denaturation at 95 °C for 3 min, followed by

35 cycles at 94 °C for 40 s, 58 °C for ITS and 55 °C for mtSSU for 45 s and 72 °C for 1 min, and a final extension of 72 °C for 10 min. The PCR procedure for nLSU and TEF1 were as follows: initial denaturation at 94 °C for 1 min, followed by 35 cycles at 94 °C for 30 s, 48 °C for nLSU and 59 °C for TEF1 for 1 min and 72 °C for 1.5 min, and a final extension of 72 °C for 10 min. The PCR procedure for RPB2 follows Justo and Hibbett (2011) with slightly modifications: initial denaturation at 94 °C for 2 min, followed by 10 cycles at 94 °C for 40 s, 60 °C for 40 s and 72 °C for 2 min, then followed by 37 cycles at 94 °C for 45 s, 55 °C for 1.5 min and 72 °C for 2 min, and a final extension of 72 °C for 10 min. The PCR products were purified and directly sequenced at Beijing Genomics Institute. All newly generated sequences are deposited at GenBank (Table 1).

Sequences generated in this study were aligned with additional sequences downloaded from GenBank using ClustalX (Thompson et al. 1997) and manually adjusted in BioEdit (Hall 1999). Sequence alignment was deposited at TreeBase (submission ID 15671).

Maximum parsimony analysis followed present studies (He and Dai 2012; Tian et al. 2013). This was applied to the combined multiple genes dataset, under heuristic search and 1,000 homogeneity replicates giving a P value of 1.000, much greater than 0.01, which means there is no discrepancy among the five loci in reconstructing phylogenetic trees. 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 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 a bootstrap (BT) 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 (MPT) generated. RAxML v.7.2.8 was used to construct a maximum likelihood (ML) tree with GTR+G+I model of site substitution including estimation of Gamma-distributed rate heterogeneity and a proportion of invariant sites (Stamatakis 2006). The branch support was evaluated with bootstrapping method of 1,000 replicates (Hillis and Bull 1993).

MrModeltest 2.3 (Posada and Crandall 1998; Nylander 2004) was used to determine the best-fit evolution model for each data set for Bayesian inference (BI). Bayesian inference 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 2 runs from random starting trees for 5 million generations (ITS+nLSU), for 10 million generations (ITS+LSU+mtSSU+TEF1+RPB2) and

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

Species name	Sample no.	GenBank accessions					References
		ITS	nLSU	mtSSU	TEF1	RPB2	
<i>Abortiporus biennis</i>	TFRI 274	EU232187	EU232235	—	—	—	Binder et al. 2005
<i>Antrodia albida</i>	CBS 308.82	DQ491414	AY515348	DQ491441	—	DQ491387	Kim et al. 2007
<i>A. heteromorpha</i>	CBS 200.91	DQ491415	AY515350	DQ491442	—	DQ491388	Kim et al. 2007
<i>A. xantha</i>	CBS 155.79	DQ491424	DQ491424	DQ491451	—	DQ491397	Kim et al. 2007
<i>Antrodiella americana</i>	Gothenburg 3161	JN710509	JN710509	JN710656	JN710711	—	Miettinen et al. 2012
<i>A. semisupina</i>	FCUG 960	EU232182	EU232266	—	—	—	Binder et al. 2005
<i>Bjerkandera adusta</i>	NBRC 4983	AB733156	AF287848	U27025	—	—	Binder et al. 2013
<i>Boletinellus merulioides</i>	AFTOL-ID 575	DQ200922	AY684153	DQ534581	DQ056287	—	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 aneirina</i>	TAA 181186	FJ496683	FJ496704	—	—	—	Tomšovský et al. 2010
<i>C. aneirina</i>	Dai 12657	KF845945	KF845952	—	—	—	Zhao and Cui 2014
<i>C. balaenae</i> Niemelä	H7002389	FJ496669	FJ496717	FJ496746	—	—	Tomšovský et al. 2010
<i>C. consobrina</i>	BRNM 710167	FJ496664	FJ496712	FJ496742	—	—	Tomšovský et al. 2010
<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. guidella</i>	HUBO 7659	FJ496687	FJ496722	FJ496740	—	—	Tomšovský et al. 2010
<i>C. pseudogilvescens</i>	Niemelä 7447	FJ496680	FJ496700	FJ496735	—	—	Tomšovský et al. 2010
<i>Cinereomyces lindbladii</i>	FBCC 177	HQ659223	HQ659223	—	—	—	Binder et al. 2013
<i>Climacocystis borealis</i>	KH 13318	JQ031126	JQ031126	—	—	—	Binder et al. 2013
<i>Climacodon septentrionalis</i>	AFTOL 767	AY854082	AY684165	JN710741	AY885151	AY780941	Binder et al. 2013
<i>Corioloopsis caperata</i>	LE(BIN)-0677	AB158316	AB158316	—	—	—	Tomšovský et al. 2010
<i>Cryptococcus bacillisporus</i>	CBS 10510	FJ534878	FJ534908	—	FJ534862	FJ534939	Garcia-Sandoval et al. 2011
<i>C. neoformans</i>	ATCC 4565	FJ914892	FJ914892	—	—	—	Garcia-Sandoval et al. 2011
<i>Dacrymyces chrysospermus</i>	TUFC 13115	AB712452	AF287855	—	—	AB712536	Binder et al. 2005
<i>Dacryobolus karstenii</i>	KHL 11162	EU118624	EU118624	—	—	—	Binder et al. 2005
<i>Dacryopinax spathularia</i>	AFTOL-ID 454	AY854070	AY701525	—	AY701525	—	Binder et al. 2005
<i>Daedalea quercina</i>	DSM 4953	DQ491425	DQ491425	DQ491452	—	DQ491398	Kim et al. 2007
<i>Earliella scabrosa</i>	PR1209	JN165009	JN164793	—	—	—	Justo and Hibbett 2011
<i>Fomitopsis pinicola</i>	CBS 221.39	DQ491405	DQ491405	DQ491432	—	DQ491378	Kim et al. 2007
<i>F. rosea</i>	ATCC 76767	DQ491410	DQ491410	DQ491437	—	—	Kim et al. 2007
<i>Fragiliporia fragilis</i>	Dai 13080	KJ734260 ^a	KJ734264 ^a	KJ734268 ^a	KJ790245 ^a	KJ790248 ^a	in the present study
<i>F. fragilis</i>	Dai 13559	KJ734261 ^a	KJ734265 ^a	KJ734269 ^a	KJ790246 ^a	KJ790249 ^a	in the present study
<i>F. fragilis</i>	Dai 13561	KJ734262 ^a	KJ734266 ^a	KJ734270 ^a	KJ790247 ^a	KJ790250 ^a	in the present study
<i>F. fragilis</i>	Yuan 5516	KJ734263 ^a	KJ734267 ^a	KJ734271 ^a	—	—	in the present study
<i>Ganoderma lingzhi</i>	Wu 1006-38	JQ781858	—	JX029988	JX029975	—	Zhao et al. 2014
<i>Gelatoporia subvermispora</i>	BRNU 592909	FJ496694	FJ496706	—	—	—	Tomšovský et al. 2010
<i>Globulicium hiemale</i>	5444b	DQ873595	DQ873595	—	—	—	Binder et al. 2005
<i>Gloeophyllum sepiarium</i>	Dai 5608	KC782726	KC782737	—	—	—	Garcia-Sandoval et al. 2011
<i>G. striatum</i>	NBRC 6429	AB733125	AB733308	—	—	—	Garcia-Sandoval et al. 2011
<i>Gloeoporus pannocinctus</i>	BRNM 709972	EU546099	FJ496708	—	—	—	Tomšovský et al. 2010

Table 1 (continued)

Species name	Sample no.	GenBank accessions					References
		ITS	nLSU	mtSSU	TEF1	RPB2	
<i>G. dichrous</i>	KHL 11173	EU118627	EU118627	—	—	—	Tomšovský et al. 2010
<i>Grammothelopsis subtropica</i>	Cui 9041	JQ845096	JQ845099	—	—	—	Zhao et al. 2013
<i>Guepiniospiza buccina</i>	AFTOL-ID 888	DQ206986	AY745711	—	—	—	Garcia-Sandoval et al. 2011
<i>Heterobasidion annosum</i>	PFC 5252	KC492906	KC492906	—	KC571646	—	Binder et al. 2013
<i>Hornodermoporus martius</i>	MUCL 41677	FJ411092	FJ393859	—	—	—	Zhao et al. 2013
<i>Hypophoropsis aurantiaca</i>	MA-Fungi 47694	AJ419201	AF352816	—	—	—	Garcia-Sandoval et al. 2011
<i>Hyphoderma capitatum</i>	KHL 8464	DQ677491	DQ677491	—	—	—	Garcia-Sandoval et al. 2011
<i>H. orphanellum</i>	NH 12208	DQ677500	DQ677500	—	—	—	Binder et al. 2005
<i>H. setigerum</i>	Hallenberg 8544	FN907905	FN907905	—	—	—	Binder et al. 2013
<i>Hypochnicium lyndoniae</i>	NL 041031	JX124704	JX124704	—	—	—	Binder et al. 2005
<i>Junghuhnia nitida</i>	KHL 11903	EU118638	EU118638	AF352892	N710721	JN710736	Binder et al. 2005
<i>Merulius tremellosus</i>	FCUG 1813	AF141632	AF141632	—	—	—	Binder et al. 2013
<i>Microporus xanthopus</i>	Cui 8242	JX290074	JX290071	—	—	JX559313	Li and Cui 2013
<i>Mycoacia fuscoatra</i>	KHL 13275	JN649352	JN649352	—	—	—	Tomšovský et al. 2010
<i>M. nothofagi</i>	KHL 13750	GU480000	GU480000	—	—	—	Tomšovský et al. 2010
<i>Mycorrhaphium adustum</i>	KHL 12255	JN710573	JN710573	JN710692	JN710727	—	Miettinen et al. 2012
<i>Neolentinus kauffmanii</i>	DAOM 214904	HM536097	HM536073	—	—	—	Garcia-Sandoval et al. 2011
<i>Obba rivulosa</i>	KCTC 6892	FJ496693	FJ496710	—	—	—	Miettinen and Rajchenberg 2012
<i>O. valdiviana</i>	FF 503	HQ659235	HQ659235	—	—	—	Miettinen and Rajchenberg 2012
<i>Perenniporia medulla-panis</i>	Dai 3274	JN112792	JN112793	KF051043	KF181137	—	Zhao et al. 2013
<i>Perenniporiella neofulva</i>	MUCL 45091	FJ411080	FJ393852	—	—	—	Robledo et al. 2009
<i>Phanerochaete chrysosporium</i>	BKM-F-1767	HQ188436	GQ470643	—	—	—	Tomšovský et al. 2010
<i>P. velutina</i>	FP 102157	AY219351	DQ679917	—	—	—	Binder et al. 2013
<i>Phlebia livida</i>	FCUG 2189	AF141624	AF141624	—	—	—	Tomšovský et al. 2010
<i>P. radiata</i>	AFTOL 484	AY854087	—	—	AY885156	AY218502	Binder et al. 2013
<i>P. subserialis</i>	FCUG 1434	AF141631	AF141631	—	—	—	Tomšovský et al. 2010
<i>P. unica</i>	KHL 11786	EU118657	EU118657	—	—	—	Tomšovský et al. 2010
<i>Piloporia sajanensis</i>	Mannine 2733a	HQ659239	HQ659239	—	—	—	Tomšovský et al. 2010
<i>Piptoporus betulinus</i>	CBS 378.51	DQ491423	DQ491423	DQ491450	—	DQ491396	Kim et al. 2007
<i>Podosecypha multizonata</i>	Gothenburg 3005	JN710581	JN710581	JN710697	JN710645	—	Binder et al. 2013
<i>P. venustula</i>	CBS 65684	JN649367	JN649367	—	—	—	Tomšovský et al. 2010
<i>Polyporus tuberaster</i>	WD 2382	AB474086	AB368104	—	—	AB368161	Sotome et al. 2008
<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>P. subrufa</i>	BRNM 710172	FJ496662	FJ496724	—	—	—	Tomšovský et al. 2010
<i>Rickenella mellea</i>	Lamoure 74	U66438	U66438	—	—	—	Tomšovský et al. 2010
<i>Sebipora aquosa</i>	Miettinen 8680	HQ659240	HQ659240	—	—	—	Miettinen and Rajchenberg 2012
<i>Serpula himantioides</i>	MA-Fungi 24446	AJ419213	AJ419213	—	—	—	Binder et al. 2005
<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. portrosensis</i>	LY 3493	FJ496689	FJ496689	—	—	—	Tomšovský et al. 2010
<i>Steccherinum fimbriatum</i>	KHL 11905	EU118668	EU118668	JN710667	—	—	Tomšovský et al. 2010

Table 1 (continued)

Species name	Sample no.	GenBank accessions					References
		ITS	nLSU	mtSSU	TEF1	RPB2	
<i>S. ochraceum</i>	KHL 11902	JN710590	JN710590	JN710700	JN710730	JN710738	Miettinen et al. 2012
<i>Stereum hirsutum</i>	NBRC 6520	AB733150	AB733325	—	—	—	Binder et al. 2013
<i>Suillus pictus</i>	AFTOL-ID 717	AY854069	AY684154	—	AY883429	—	Binder et al. 2005
<i>Truncospora ochroleuca</i>	MUCL 39726	FJ411098	FJ393865	—	—	—	Robledo et al. 2009
<i>Tyromyces chioneus</i>	Cui 10225	KF698745 ^a	KF698756 ^a	—	—	—	in the present study
<i>Xanthoporus syringae</i>	Gothenburg 1488	JN710607	JN710607	—	—	—	Miettinen et al. 2012

^a Newly generated sequences for this study

trees were sampled every 100 generations. The first one-fourth 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 (MP) and Bayesian posterior probabilities (BPP) greater than or equal to 75 % (MP) and 0.95 (BPP) were considered as significantly supported, respectively.

Results

The ITS-nLSU dataset included sequences from 81 fungal specimens representing 73 taxa. The dataset had an aligned length of 2,380 characters, of which 1,076 characters are constant, 357 are variable and parsimony-uninformative, and 947 are parsimony-informative. Maximum parsimony analysis yielded four equally parsimonious trees (TL=7792, CI=0.312, RI=0.532, RC=0.170, HI=0.681). Best model for the combined ITS+nLSU dataset estimated and applied in the Bayesian analysis: GTR+I+G, lset nst=6, rates=invgamma; prset statefreqpr=dirichlet (1,1,1,1). Bayesian analysis and ML analysis resulted in a similar topology as MP analysis, with an average standard deviation of split frequencies=0.007523 (BI). Sequences of *Cryptococcus bacillisporus* Kwon-Chung & J.E. Benn. and *C. neoformans* (San Felice) Vuill. obtained from GenBank were used as outgroups to root trees following Garcia-Sandoval et al. (2011).

The phylogeny (Fig. 1) inferred from ITS+nLSU sequences demonstrates seven major clades for 73 species of the *Polyporales*. The new family *Fragiliporiaceae* formed a monophyletic lineage and the new fragiliporia clade is proposed.

The five gene (ITS, LSU, mtSSU, TEF1, RPB2) sequence dataset did not show any conflicts in tree topology for the reciprocal bootstrap trees, which allowed us to combine them (P=0.07). The dataset had an aligned length of 4,517

characters, of which 2,431 characters are constant, 812 are variable and parsimony-uninformative, and 1,274 are parsimony-informative. Maximum parsimony analysis yielded 3 equally parsimonious trees (TL=4322, CI=0.598, RI=0.507, RC=0.253, HI=0.503). Best model for the combined ITS+nLSU+mtSSU+TEF1+RPB2 dataset estimated and applied in the Bayesian analysis: GTR+I+G. Bayesian analysis and ML analysis resulted in a similar topology as MP analysis, with an average standard deviation of split frequencies=0.003863 (BI). Sequences of *Stereum hirsutum* (Willd.) Pers. and *Heterobasidion annosum* (Fr.) Bref. obtained from GenBank were used as outgroups to root trees following Binder et al. (2013).

A further phylogeny (Fig. 2) inferred from multiple genes of the combined ITS+nLSU+mtSSU+TEF1+RPB2 sequences was obtained for 44 fungal specimens representing 40 taxa in the *Polyporales* and demonstrated that the new family formed a monophyletic entity, but with a low 70 % BS, 57 % BP and 0.99 B.P. and then grouped with phlebia clade, residual polyporoid clade and core polyporoid clade.

In addition, the results of BLAST queries in NCBI based on ITS and nLSU separately showed the sequences producing significant alignments descriptions: in ITS blast results, the top ten taxa are *Ceriporia lacerata* N. Maek. only (Maximum record descriptions: Max score 303; Total score 303; Query cover 37 %; E value 1e-78; Ident 88 %). In nLSU blast results, the top ten taxa are *Griseoporia carbonaria* (Berk. & M.A. Curtis) Ginns, *Neolentinus kauffmanii* (A.H. Sm.) Redhead & Ginns and *Veluticeps fimbriata* (Ellis & Everh.) Nakasone (Maximum record descriptions: Max score 1,626; Total score 1,626; Query cover 99 %; E value 0.0; Ident 93 %).

Taxonomy

Fragiliporiaceae Y.C. Dai, B.K. Cui & C.L. Zhao, fam. nov.
Mycobank no.: MB 809338

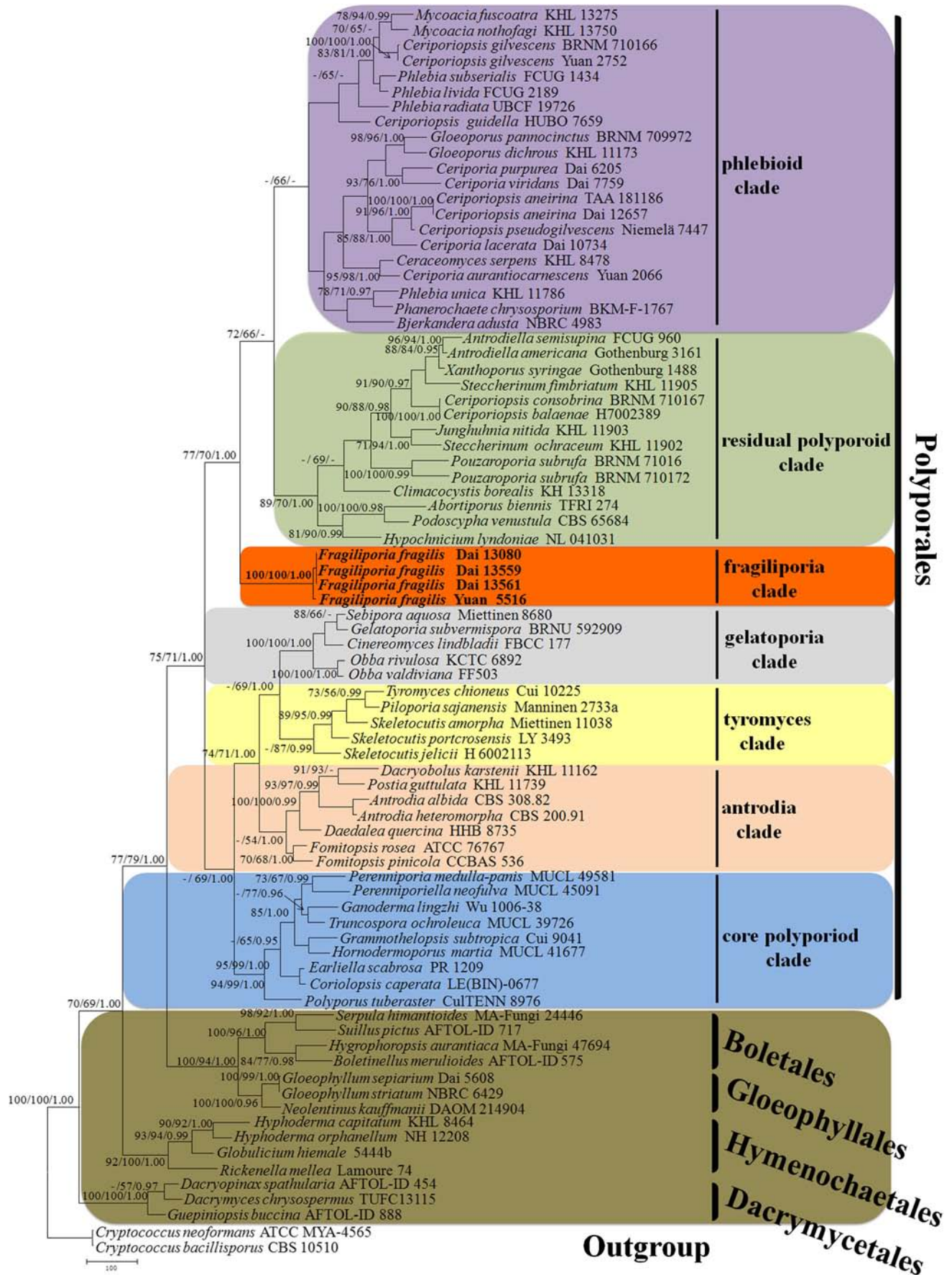


Fig. 1 Maximum Parsimony strict consensus tree illustrating the phylogeny of *Fragiliporia fragilis*, and related species in Agaricomycetes based on ITS+nLSU sequences. Branches are labeled with maximum likelihood bootstrap higher than 70 %, parsimony bootstrap proportions higher than 50 % and Bayesian posterior probabilities more than 0.95 respectively. Clade names follow Binder et al. (2013)

Type genus. Fragiliporia.

Basidiocarps resupinate, tubes very soft when fresh, becoming brittle when dry (become almost powdery when bruised). Hyphal system monomitic, generative hyphae thick-walled with clamp connections, hyphae frequently branched from clamp connections, the branches mostly as H-, W- or Y-shaped. Basidiospores hyaline, thin-walled.

Fragiliporia Y.C. Dai, B.K. Cui & C.L. Zhao, gen. nov.

Mycobank no.: MB 809339

Type species. Fragiliporia fragilis.

Etymology. fragiliporia (Lat.): referring to brittle basidiocarps.

Basidiocarps resupinate, very soft when fresh, becoming brittle when dry. Hyphal system monomitic, generative hyphae thick-walled with clamp connections, hyphae frequently branched from clamp connections, usually encrusted by crystals, IKI-, CB-, branched hyphae mostly H-, W- or Y-shaped; hyphae swollen in KOH. Basidiospores hyaline, thin-walled, allantoid, IKI-, CB-.

Fragiliporia fragilis Y.C. Dai, B.K. Cui & C.L. Zhao, sp. nov. (Figs. 3 and 4).

Mycobank no.: MB 809343

Holotype. CHINA. Yunnan Prov., Baoshan, Gaoligongshan Nature Reserve, on rotten stump of *Alnus*, 28 October 2012, *Dai 13080* (BJFC013304, BJFC).

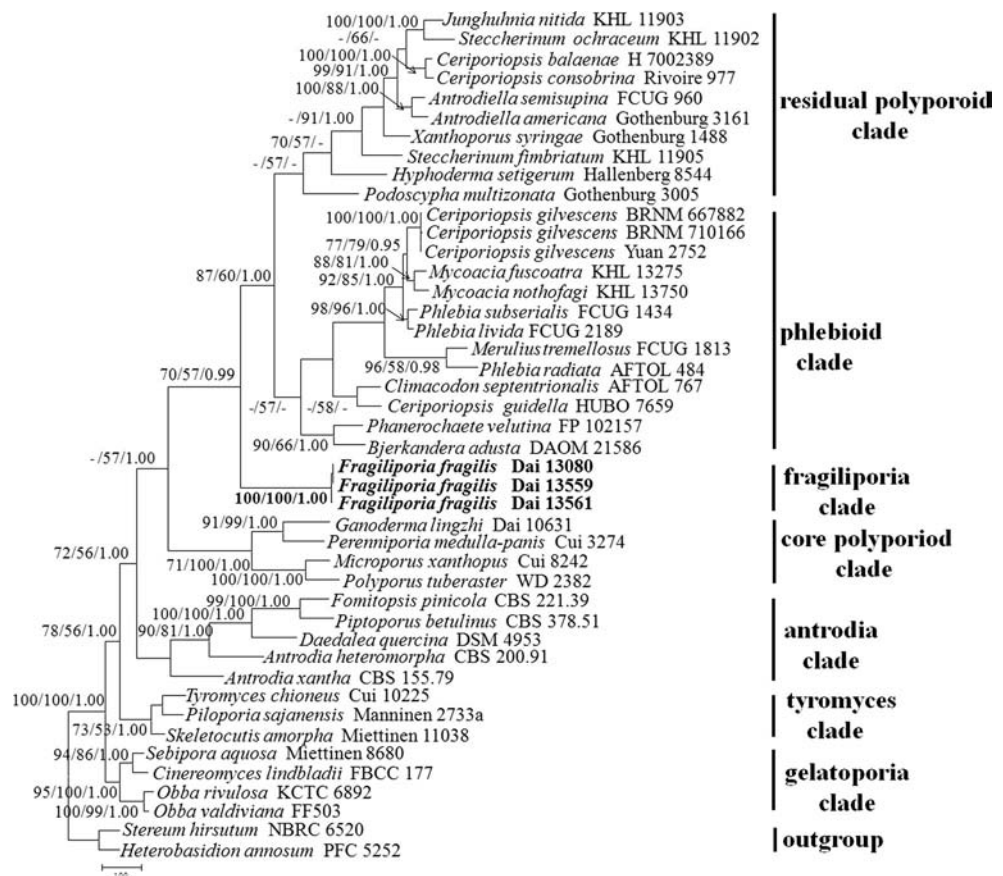
Etymology. fragilis (Lat.) referring to the brittle basidiocarps.

Fruitbody. Basidiocarps annual, resupinate, very soft, without odor or taste when fresh, when dry becoming brittle and powdery when bruised, up to 15 cm long, 5 cm wide, 6 mm thick at center. Pore surface grayish-buff to lavender when fresh, turning to vinaceous gray to grayish brown upon drying; pores angular, 0.5–1 per mm; dissepiments thin, entire. Sterile margin distinct, white, more or less fimbriate, up to 6 mm wide. Subiculum orange-yellow, up to 0.5 mm thick. Tubes concolorous with pore surface, fragile when dry, up to 5.5 mm long.

Hyphal structure. Hyphal system monomitic; generative hyphae thick-walled, bearing clamp connections, hyphae frequently branched from clamp connections, branched hyphae mostly H-, W- or Y-shaped; all hyphae usually encrusted with crystals, IKI-, CB-; hyphae swollen in KOH.

Subiculum. Generative hyphae hyaline, thick-walled, frequently branched, interwoven, 4–6 µm in diameter.

Fig. 2 Maximum Parsimony strict consensus tree illustrating the phylogeny of the new family Fragiliporiaceae, and more representative available families in Polyporales, based on the combined ITS+nLSU+mtSSU+TEF1+RPB2 sequence datasets. Branches are labeled with maximum likelihood bootstrap higher than 70 %, parsimony bootstrap proportions higher than 50 % and Bayesian posterior probabilities more than 0.95. Clade names follow Binder et al. (2013)



Tubes. Generative hyphae hyaline, thick-walled, occasionally branched, subparallel along the tubes, 3–5 µm in diameter. Cystidia and cystidioles absent; basidia long clavate to pyriform, with four sterigmata and a basal clamp connection, 15–18×5–6 µm; basidioles abundant (hymenia dominant by basidioles), in shape similar to basidia, but slightly smaller.

Spores. Basidiospores allantoid, hyaline, thin-walled, smooth, IKI–, CB–, (4.6–)4.8–5.4(–5.6)×(1.5–)1.7–2(–2.2) µm, L=5.05 µm, W=1.89 µm, Q=2.57–2.73 (n=180/6).

Rot type. A white rot.

Additional specimens (paratypes) examined: CHINA. Yunnan Prov., Jinghong County, Ailaoshan Nature Reserve, on fallen angiosperm trunk, 15 October 2013, *Dai 13559* & *13561* (BJFC015021 & BJFC015023, BJFC); Zhejiang Prov., Lin'an County, Tianmushan Nature Reserve, on rotten angiosperm wood, 16 October 2004, *Dai 6437* (BJFC000421, BJFC); 10 October 2005, *Cui 2634* (BJFC000415, BJFC); Guizhou Prov., Jiangkou County, Fanjingshan Nature Reserve, on fallen angiosperm trunk, 21 August 2010, *Yuan 5516* (IFP014297, IFP).

Discussion

In the present study, a new family, *Fragiliporiaceae*, is described based on phylogenetic analyses and morphological characters. The family has unique morphological characters and forms a monophyletic lineage within the order *Polyporales*.

Previously, six clades were found in the *Polyporales*: antrodia clade, core polyporoid clade, gelatoporia clade, phlebioid clade, residual polyporoid clade and tyromyces clade (Binder et al. 2013). According to our result the new family did not nest in the six known clades when analysed using combined ITS and nLSU sequence data (Fig. 1). Therefore, a new clade is recognized in *Polyporales* as the fragiliporia clade. The phylogeny inferred from combined ITS, nLSU, mtSSU, TEF1 and RPB2 gene sequences (Fig. 2) shows that *Fragiliporiaceae* also formed a monophyletic lineage (70 % BS, 57 % BP, 0.99 BPP), and then grouped with phlebioid clade, residual polyporoid clade and core polyporoid clade, which showed similar result with the combined ITS and nLSU sequences. The molecular analysis (Figs. 1 and 2) shows that the new taxon is justified at the family level.

Based on the results of BLAST queries in NCBI, *Ceriporia lacerata*, *Griseoporia carbonaria*, *Neolentinus kauffmanii* and *Veluticeps fimbriata* are related to *Fragiliporia fragilis*. However, there are low similarity parameters in the ITS BLAST result. In addition, morphologically, *Ceriporia lacerata* differs from *Fragiliporia fragilis* in having simple-septate generative hyphae (Suhara et al. 2003). Moreover, *C. lacerata* nested into phlebioid clade in previous molecular

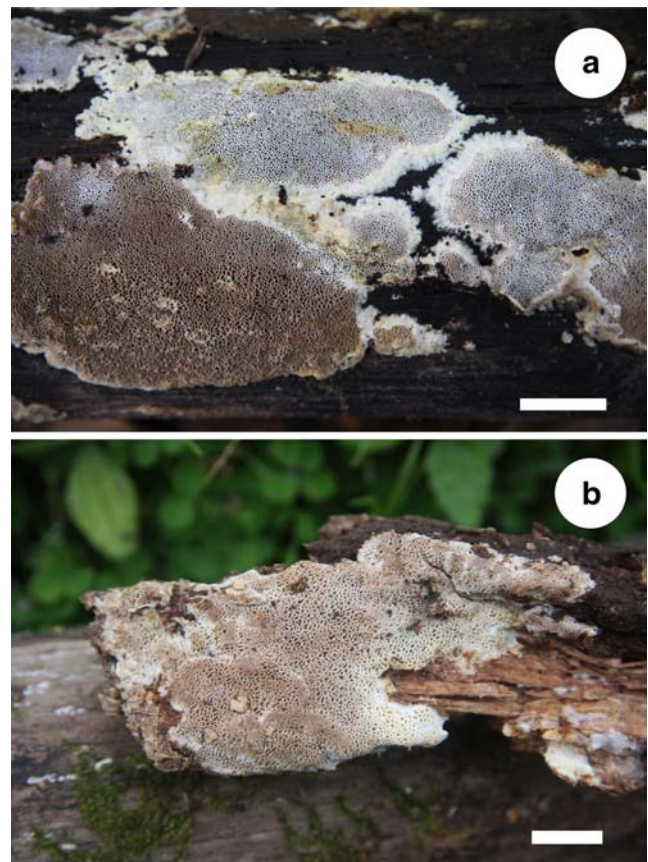
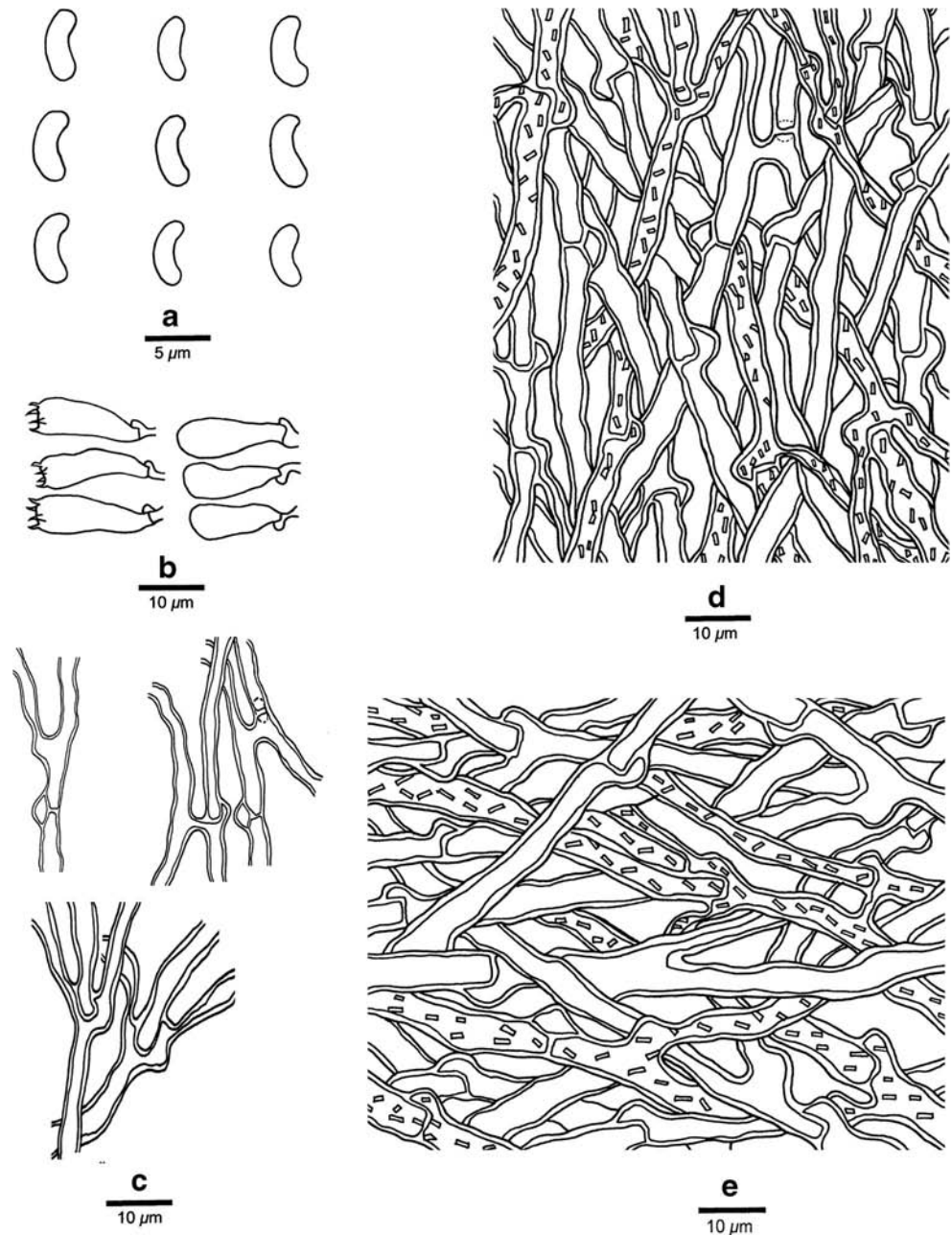


Fig. 3 Basidiomata of *Fragiliporia fragilis*. Bars: **a**–4 cm (holotype); **b**–2 cm (Dai 13561)

studies (Binder et al. 2013; Jia et al. 2014). In nLSU BLAST, the descriptions produce good similarity parameters. However, morphologically *Griseoporia carbonaria* differs from *Fragiliporia fragilis* by brown basidiocarps, and dimitic hyphal system with yellowish to rusty brown skeletal hyphae (Ginns 1984; Ryvarden and Gilbertson 1993). *Veluticeps fimbriata* is separated from the new taxon by having perennial and hard basidiocarps, smooth hymenophore configuration, solitary or fascicled cystidia, rather large basidia and basidiospores (usually 10–25 µm long) and in causing a brown rot (Hjortstam and Telleria 1990; Nakasone 1990). *Neolentinus kauffmanii* is distinct from *F. fragilis* by pileate and corky basidiocarps with lamellate to daedaleoid hymenophore and a dimitic hyphal system and causing a brown rot (Rune 1994). In phylogeny, the three species *Griseoporia carbonaria*, *Neolentinus kauffmanii* and *Veluticeps fimbriata* are not closely related to *Fragiliporia fragilis* based on molecular studies (Kim and Jung 2000; Hibbett and Binder 2002; Hibbett et al. 2007; Garcia-Sandoval et al. 2011).

Binder et al. (2005) studied the phylogenetic distribution of resupinate forms the mushroom-forming fungi and showed that variations of basidiocarps existed, and there was no morphological synapomorphy in the order *Polyporales*. This order is highly heterogeneous, and a wide variety of

Fig. 4 Microscopic structures of *Fragiliporia fragilis* (drawn from the holotype). **a.** Basidiospores; **b.** Basidia and basidioles; **c.** H-, Y- and W-shaped generative hyphae; **d.** Hyphae from trama; **e.** Hyphae from subiculum. Bars: **a**–5 μm ; **b**–**e**–10 μm



basidiocarps types: bracket-shaped (e.g. *Fomitopsis* P. Karst., *Trametes* Fr.), resupinate to effused-reflexed (*Ceriporiopsis* Domański, *Phlebia* Fr., *Antrodia* (Fr.) Donk), stipitate (*Polyporus* P. Micheli) and hymenophore configuration: poroid (*Perenniporia* Murrill), lamellate (*Lentinus* Fr.), hydnceous (*Steccherinum* Gray) and smooth (*Podoscypha* Pat.) are included (Binder et al. 2013).

The family *Phanerochaetaceae* (typified by *Phanerochaete*) is morphologically similar to *Fragiliporiaceae*, which is mainly characterized by its tyromycetoid, merulioid, corticioid basidiocarps with smooth, lamellate, tuberculate, spinose, odontoid hymenophore configuration and rather soft corky to spongy context and ceraceous tubes (Jülich 1981; Binder et al.

2005; Wu et al. 2010). However, several genera in this family have poroid hymenophores and they share similar characters with the new genus *Fragiliporia*. *Ceriporia* and *Ceriporiopsis* are similar to *Fragiliporia* by an annual growth habit, causing a white rot, and producing resupinate basidiocarps. However, *Ceriporia* differs in its simple-septate generative hyphae (Donk 1933; Gilbertson and Ryvarden 1986; Núñez and Ryvarden 2001). *Ceriporiopsis* is separated from *Fragiliporia* by its soft corky to corky basidiocarps, its dry basidiocarps are never become powdery when bruised and most importantly the branches in this genus are not from clamp connections, and hyphae are never H-, W- or Y-shaped (Gilbertson and Ryvarden 1986; Ryvarden and Gilbertson 1993; Núñez and Ryvarden 2001).

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References

- Binder M, Hibbett DS, Larsson KH, Larsson E, Langer E, Langer G (2005) The phylogenetic distribution of resupinate forms across the major clades of mushroom-forming fungi (Homobasidiomycetes). *Syst Biodivers* 3:113–157. doi:10.1017/S1477200005001623
- Binder M, Justo A, Riley R, Salamov A, López-Giráldez F, Sjökvist E, Copeland A, Foster B, Sun H, Larsson E, Larsson KH, Townsend J, Grigoriev IV, Hibbett DS (2013) Phylogenetic and phylogenomic overview of the Polyporales. *Mycologia* 105:1350–1373. doi:10.3852/13-003
- Cao Y, Wu SH, Dai YC (2012) Species clarification of the prize medicinal *Ganoderma* mushroom “Lingzhi”. *Fungal Divers* 56:49–62. doi:10.1007/s13225-012-0178-5
- Cui BK, Zhao CL, Dai YC (2011) *Melanoderma microcarpum* gen. et sp. nov. (Basidiomycota) from China. *Mycotaxon* 116:295–302. doi:10.5248/116.295
- Dai YC (2010) Hymenochaetaceae (Basidiomycota) in China. *Fungal Divers* 45:131–343. doi:10.1007/s13225-010-0066-9
- Dai YC (2012) Polypore diversity in China with an annotated checklist of Chinese polypores. *Mycoscience* 53:49–80. doi:10.1007/s10267-011-0134-3
- Dai YC, Cui BK, Yuan HS, Li BD (2007) Pathogenic wood-decaying fungi in China. *Forest Pathol* 37:105–120. doi:10.1111/j.1439-0329.2007.00485.x
- Dai YC, Yang ZL, Cui BK, Yu CJ, Zhou LW (2009) Species diversity and utilization of medicinal mushrooms and fungi in China (Review). *Int J Med Mushrooms* 11:287–302. doi:10.1615/IntJMedMushr.v11.i3.80
- Dai YC, Xue HJ, Vlasák J, Rajchenberg M, Wang B, Zhou LW (2014) Phylogeny and global diversity of *Polyporus* group *Melanopus* (Polyporales, Basidiomycota). *Fungal Divers* 64:133–144. doi:10.1007/s13225-013-0248-3
- Donk MA (1933) Revision de niederlandischen homobasidiomycetes. *Aphyllophoraceae* 2. *Medd Bot Mus Herb Rijhs Universit Utrecht* 9: 1–278
- Felsenstein J (1985) Confidence intervals on phylogenetics: an approach using bootstrap. *Evolution* 39:783–791
- Floudas D, Binder M, Riley R, Bary K, Blanchette RA, Henrissat B, Martínez AT, Otilar R, Spatafora JW, Yadav JS, Aerts A, Benoit I, Boyd A, Carlson A, Copeland A, Coutinho PM, de Vries RP, Ferreira P, Findley K, Foster B, Gaske J, Glotzer D, Górecki P, Heitman J, Hesse C, Hori C, Igarashi K, Jurgens JA, Kallen N, Kersten P, Kohler A, Kües U, Kumar TK, Kuo A, LaButti K, Larrondo LF, Lindquist E, Ling A, Lombard V, Lucas S, Lundell T, Martin R, McLaughlin DJ, Morgenstern I, Morin E, Murat C, Nagy LG, Nolan M, Ohm RA, Patyshakuliyeva A, Rokas A, Ruiz-Dueñas FJ, Sabat G, Salamov A, Samejima M, Schmutz J, Slot JC, St John F, Stenlid J, Sun H, Sun S, Syed K, Tsang A, Wiebenga A, Young D, Pisabarro A, Eastwood DC, Martin F, Cullen D, Grigoriev IV, Hibbett DS (2012) The Paleozoic origin of enzymatic lignin decomposition reconstructed from 31 fungal genomes. *Science* 336: 1715–1719. doi:10.1126/science.1221748
- García-Sandoval R, Wang Z, Binder M, Hibbett DS (2011) Molecular phylogenetics of the Gloeophyllales and relative ages of clades of Agaricomycotina producing a brown rot. *Mycologia* 103:510–524. doi:10.3852/10-209
- Gilbertson RL, Ryvarden L (1986) North American polypores 1. *Fungiflora*, Oslo
- Ginns J (1984) *Griseoporia* a new genus for *Hexagonia carbonaria* (Polyporaceae). *Mycotaxon* 20:559–565
- Hall TA (1999) Bioedit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. *Nucleic Acids Symp Ser* 41:95–98
- He SH, Dai YC (2012) Taxonomy and phylogeny of *Hymenochaete* and allied genera of Hymenochaetaceae (Basidiomycota) in China. *Fungal Divers* 56:77–93. doi:10.1007/s13225-012-0174-9
- Hibbett DS, Binder M (2002) Evolution of complex fruiting body morphologies in homobasidiomycetes. *Proc Biol Sci* 269:1963–1969. doi:10.1098/rspb.2002.2123
- Hibbett DS, Binder M, Bischoff JF, Blackwell M, Cannon PF, Eriksson OE, Huhndorf S, James T, Kirk PM, Lücking R, Thorsten Lumbsch H, Lutzoni F, Matheny PB, McLaughlin DJ, Powell MJ, Redhead S, Schoch CL, Spatafora JW, Stalpers JA, Vilgalys R, Aime MC, Aptroot A, Bauer R, Begerow D, Benny GL, Castlebury LA, Crous PW, Dai YC, Gams W, Geiser DM, Griffith GW, Gueidan C, Hawksworth DL, Hestmark G, Hosaka K, Humber RA, Hyde KD, Ironside JE, Køljalg U, Kurtzman CP, Larsson KH, Lichtwardt R, Longcore J, Miadlikowska J, Miller A, Moncalvo JM, Mozley-Standridge S, Oberwinkler F, Parmasto E, Reeb V, Rogers JD, Roux C, Ryvarden L, Sampaio JP, Schüssler A, Sugiyama J, Thorn RG, Tibell L, Untereiner WA, Walker C, Wang Z, Weir A, Weiss M, White MM, Winka K, Yao YJ, Zhang N (2007) A higher-level phylogenetic classification of the Fungi. *Mycol Res* 111:509–547. doi:10.1016/j.mycres.2007.03.004
- Hillis DM, Bull JJ (1993) An empirical test of bootstrapping as a method for assessing confidence in phylogenetic analysis. *Syst Biol* 42:182–192. doi:10.1093/sysbio/42.2.182
- Hjortstam K, Telleria MT (1990) *Columnocystis*, a synonym of *Veluticeps*. *Mycotaxon* 37:53–56
- Hyde KD, Nilsson RH, Alias SA, Ariyawansa HA, Blair JE, Cai L, de Cock AWAM, Dissanayake AJ, Glockling SL, Goonasekara ID, Gorczak M, Hahn M, Jayawardena RS, van Kan IAL, Laurence MH, Lévesque CA, Li XH, Liu JK, Maharachchikumbura SSN, Manamgoda DS, Martin FN, McKenzie EHC, McTaggart AR, Mortimer PE, Nair PVR, Pawłowska J, Rintoul TL, Shivas TG, Spies ARCFJ, Summerell BA, Taylor PWJ, Terhem RB, Udayanga D, Vaghefi N, Walther G, Wilk M, Wrzosek M, Xu JC, Yan JY, Zhou N (2014) One stop shop: backbones trees for important phytopathogenic genera. *Fungal Diversity* 68 (in press)
- Hyde KD, Jones EBG, Liu JK, Ariyawansa H, Boehm E, Boonmee S, Braun U, Chomnunti P, Crous P, Dai DQ, Diederich P, Dissanayake A, Doilom M, Doveri F, Hongsanan S, Jayawardena R, Lawrey JD, Li YM, Liu YX, Lücking R, Monkal J, Nelsen MP, Phookamsak R, Muggia L, Pang KL, Senanayake I, Shearer CA, Wijayawardene N, Wu HX, Thambugala M, Suetrong S, Tanaka K, Wikee S, Zhang Y, Hudson BA, Alias SA, Aptroot A, Bahkali AH, Bezerra LJ, Bhat JD, Camporesi E, Chukeatirote E, Hoog SD, Gueidan C, Hawksworth DL, Hirayama K, Kang JC, Knudsen K, Li WJ, Liu ZY, McKenzie EHC, Miller AN, Nadeeshan D, Phillip AJL, Mapook A, Raja HA, Tian Q, Zhang M, Scheuer C, Schumm F, Taylor J, Yacharoen S, Tibpromma S, Wang Y, Yan J, Li X (2013) Families of Dothideomycetes. *Fungal Divers* 63:1–313. doi:10.1007/s13225-013-0263-4
- James TY, Kauff F, Schoch CL, Matheny PB, Hofstetter V, Cox CJ, Celio G, Gueidan C, Fraker E, Miadlikowska J, Lumbsch HT, Rauhut A, Reeb V, Arnold AE, Amtoft A, Stajich JE, Hosaka K, Sung GH, Johnson D, O'Rourke B, Crockett M, Binder M, Curtis JM, Slot JC, Wang Z, Wilson AW, Schüssler A, Longcore JE, O'Donnell K, Mozley-Standridge S, Porter D, Letcher PM, Powell MJ, Taylor JW, White MM, Griffith GW, Davies DR, Humber RA, Morton JB, Sugiyama J, Rossman AY, Rogers JD, Pfister DH, Hewitt D, Hansen K, Hambleton S, Shoemaker RA, Kohlmeyer J, Volkmann-Kohlmeyer B, Spotts RA, Serdani M, Crous PW, Hughes KW, Matsuura K, Langer E, Langer G, Untereiner WA, Lücking R, Bidel B, Geiser DM, Aptroot A, Diederich P, Schmitt I, Schultz

- M, Yahr R, Hibbett DS, Lutzoni F, McLaughlin DJ, Spatafora JW, Vilgalys R (2006) Reconstructing the early evolution of fungi using a six-gene phylogeny. *Nature* 443:818–822. doi:10.1038/nature05110
- Jia BS, Zhou LW, Cui BK, Rivoire B, Dai YC (2014) Taxonomy and phylogeny of *Ceriporia* (Polyporales, Basidiomycota) with an emphasis of Chinese collections. *Mycol Prog* 13:81–93. doi:10.1007/s11557-013-0895-5
- Jülich W (1981) Higher taxa of Basidiomycetes. *Bibliotheca Mycol* 85:1–485
- Justo A, Hibbett DS (2011) Phylogenetic classification of *Trametes* (Basidiomycota, Polyporales) based on a five-marker dataset. *Taxon* 60:1567–1583
- Kim SY, Jung HS (2000) Phylogenetic relationships of the Aphyllophorales inferred from sequence analysis of nuclear small subunit ribosomal DNA. *J Microbiol* 38:122–131
- Kim KM, Lee JS, Jung HS (2007) *Fomitopsis incarnatus* sp. nov. based on generic evaluation of *Fomitopsis* and *Rhodofomes*. *Mycologia* 99:833–841. doi:10.3852/mycologia.99.6.833
- Kirk PM, Cannon PF, David JC, Minter DW, Stalpers JA (2008) *Ainsworth and bisby's dictionary of the fungi*, 10th edn. CAB International Press, Wallingford
- Li HJ, Cui BK (2013) Taxonomy and phylogeny of the genus *Megasporoporia* and its related genera. *Mycologia* 105:368–383. doi:10.3852/12-114
- Liu YL, Whelen S, Hall BD (1999) Phylogenetic relationships among ascomycetes: evidence from an RNA polymerase II subunit. *Mol Biol Evol* 16:1799–1808
- Matheny PB (2005) Improving phylogenetic inference of mushrooms with RPB1 and RPB2 nucleotide sequences (*Inocybe*; Agaricales). *Mol Phylogenet Evol* 35:1–20. doi:10.1016/j.ympev.2004.11.014
- Miettinen O, Rajchenberg M (2012) *Obba* and *Sebipora*, new polypore genera related to *Cinereomyces* and *Gelatoporia* (Polyporales, Basidiomycota). *Mycol Prog* 11:131–147. doi:10.1007/s11557-010-0736-8
- Miettinen O, Larsson E, Sjökvist E, Larsson KL (2012) Comprehensive taxon sampling reveals unaccounted diversity and morphological plasticity in a group of dimittic polypores (Polyporales, Basidiomycota). *Cladistics* 28:251–270. doi:10.1111/j.1096-0031.2011.00380.x
- Nakasone KK (1990) Taxonomic study of *Veluticeps* (Aphyllophorales). *Mycologia* 82:622–641
- Nilsson RH, Hyde KD, Pawłowska J, Ryberg M, Tedersoo L, Aas AB, Alias SA, Alves A, Anderson CL, Antonelli A, Arnold AE, Bahnmann B, Bahram M, Bengtsson-Palme J, Berlin A, Branco S, Chomnunti P, Dissanayake A, Drenkhan R, Friberg H, Frøslev TG, Halwachs B, Hartmann M, Henricot B, Jayawardena R, Jumpponen A, Kausserud H, Koskela S, Kulik T, Liimatainen K, Lindahl BD, Lindner D, Liu J-K, Maharachchikumbura S, Manamgoda D, Martinsson S, Neves MA, Niskanen T, Nyländer S, Pereira OL, Pinho DB, Porter TM, Queloz V, Riit T, Sánchez-García M, Sousa F, Stefańczyk E, Tadych M, Takamatsu S, Tian Q, Udayanga D, Unterseher M, Wang Z, Wikee S, Yan J, Larsson E, Larsson K-H, Kõljalg U, Abarenkov K (2014) Improving ITS sequence data for identification of plant pathogenic fungi. *Fungal Divers*. doi:10.1007/s13225-014-0291-8, in press
- Núñez M, Ryvarden L (2001) East Asian polypores 2. *Synopsis Fungorum* 14:165–522
- Nyländer JAA (2004) MrModeltest v2. Program distributed by the author. Evolutionary Biology Centre, Uppsala University
- Petersen JH (1996) Farvekort. The Danish Mycological Society's colour-chart. Foreningen til Svampekundskabens Fremme, Greve
- Posada D, Crandall KA (1998) Modeltest: testing the model of DNA substitution. *Bioinformatics* 14:817–818
- Rehner SA, Buckley E (2005) A *Beauveria* phylogeny inferred from nuclear ITS and EF1-alpha sequences: evidence for cryptic diversification and links to *Cordyceps teleomorpha*. *Mycologia* 97:84–98. doi:10.3852/mycologia.97.1.84
- Robledo GL, Amalfi M, Castillo G, Rajchenberg M, Decock C (2009) *Perenniporiella chaquenia* sp. nov. and further notes on *Perenniporiella* and its relationships with *Perenniporia* (Poriales, Basidiomycota). *Mycologia* 101:657–673. doi:10.3852/08-040
- Ronquist F, Huelsenbeck JP (2003) MrBayes 3: bayesian phylogenetic inference under mixed models. *Bioinformatics* 19:1572–1574. doi:10.1093/bioinformatics/btg180
- Rune F (1994) *Neolentinus*: a well founded genus in Pleurotaceae that includes *Heliocybe*. *Mycol Res* 98:542–544. doi:10.1016/S0953-7562(09)80476-0
- Ryvarden L, Gilbertson RL (1993) European polypores 1. *Synopsis Fungorum* 6:1–387
- Si J, Peng F, Cui BK (2013) Purification, biochemical characterization and dye decolorization capacity of an alkali-resistant and metal-tolerant laccase from *Trametes pubescens*. *Bioresour Technol* 128:49–57. doi:10.1016/j.biortech.2012.10.085
- Sjökvist E, Larsson E, Eberhardt U, Ryvarden L, Larsson KH (2012) Stipitate stereoid basidiocarps have evolved multiple. *Mycologia* 104:1046–1055. doi:10.3852/11-174
- Sotome K, Hattori T, Ota Y, To-anun C, Salleh B, Kakishima M (2008) Phylogenetic relationships of *Polyporus* and morphologically allied genera. *Mycologia* 100:603–615. doi:10.3852/07-191R
- Stamatakis A (2006) RAxML-VI-HPC: maximum likelihood-based phylogenetic analyses with thousands of taxa and mixed models. *Bioinformatics* 22:2688–2690. doi:10.1093/bioinformatics/btl446
- Suhara H, Maekawa N, Kaneko S, Hattori T, Sakai K, Kondo R (2003) A new species, *Ceriporia lacerata*, isolated from white-rotted wood. *Mycotaxon* 86:335–347
- Swofford DL (2002) PAUP*: phylogenetic analysis using parsimony (*and other methods). Version 4.0b10. Sinauer Associates, Massachusetts
- Thompson JD, Gibson TJ, Plewniak F, Jeanmougin F, Higgins DG (1997) The CLUSTAL X windows interface: flexible strategies for multiple sequence alignment aided by quality analysis tools. *Nucleic Acids Res* 25:4876–4882. doi:10.1093/nar/25.24.4876
- Tian XM, Yu HY, Zhou LW, Decock C, Vlasák J, Dai YC (2013) Phylogeny and taxonomy of the *Inonotus linteus* complex. *Fungal Divers* 58:159–169. doi:10.1007/s13225-012-0202-9
- Tomšůvský M, Menkis A, Vasaitis R (2010) Phylogenetic relationships in European *Ceriporiopsis* species inferred from nuclear and mitochondrial ribosomal DNA sequences. *Fungal Biol* 114:350–358. doi:10.1016/j.funbio.2010.02.004
- Wang W, Yuan TQ, Wang K, Cui BK, Dai YC (2012) Combination of biological pretreatment with liquid hot water pretreatment to enhance enzymatic hydrolysis of *Populus tomentosa*. *Bioresour Technol* 107:282–286. doi:10.1016/j.biortech.2011.12.116
- White TJ, Bruns T, Lee S, Taylor J (1990) Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In: Innis MA, Gelfand DH, Sninsky JJ, White TJ (eds) *PCR protocols: a guide to methods and applications*. Academic, San Diego, pp 315–322
- Wu SH, Nilsson HR, Chen CT, Yu SY, Hallenberg N (2010) The white-rotting genus *Phanerochaete* is polyphyletic and distributed throughout the phleboid clade of the Polyporales (Basidiomycota). *Fungal Divers* 42:107–188. doi:10.1007/s13225-010-0031-7
- Wu G, Feng B, Xu JP, Zhu XT, Li YC, Zeng NK, Hosen Md I, Yang ZL (2014) Molecular phylogenetic analyses redefine seven major clades and reveal 22 new generic clades in the fungal family *Boletaceae*. *Fungal Divers*. doi:10.1007/s13225-014-0283-8, in press
- Younes SB, Mechichi T, Sayadi S (2007) Purification and characterization of the laccase secreted by the white rot fungus *Perenniporia tephropora* and its role in the decolorization of synthetic dyes. *J Appl Microbiol* 102:1033–1042
- Zhang Y, Crous PW, Schoch CL, Bahkali AH, Guo LD, Hyde KD (2011) A molecular, morphological and ecological re-appraisal of Venturiales—a new order of *Dothideomycetes*. *Fungal Divers* 51:249–277. doi:10.1007/s13225-011-0141-x
- Zhao CL, Cui BK (2014) Phylogeny and taxonomy of *Ceriporiopsis* (Polyporales) with descriptions of two new species from southern China. *Phytotaxa* 164:17–28. doi:10.11646/phytotaxa.164.1.2

- Zhao CL, Cui BK, Dai YC (2013) New species and phylogeny of *Perenniporia* based on morphological and molecular characters. *Fungal Divers* 58:47–60. doi:[10.1007/s13225-012-0177-6](https://doi.org/10.1007/s13225-012-0177-6)
- Zhao CL, He XS, WangHe KY, Cui BK, Dai YC (2014) *Flammeopellis bambusicola* gen. et. sp. nov. (Polyporales, Basidiomycota) evidenced by morphological characters and phylogenetic analysis. *Mycol Prog* 13:771–780. doi:[10.1007/s11557-014-0960-8](https://doi.org/10.1007/s11557-014-0960-8)
- Zhou LW, Hao ZQ, Wang Z, Wang B, Dai YC (2011) Comparison of ecological patterns of polypores in three forest zones in China. *Mycology* 2:260–275