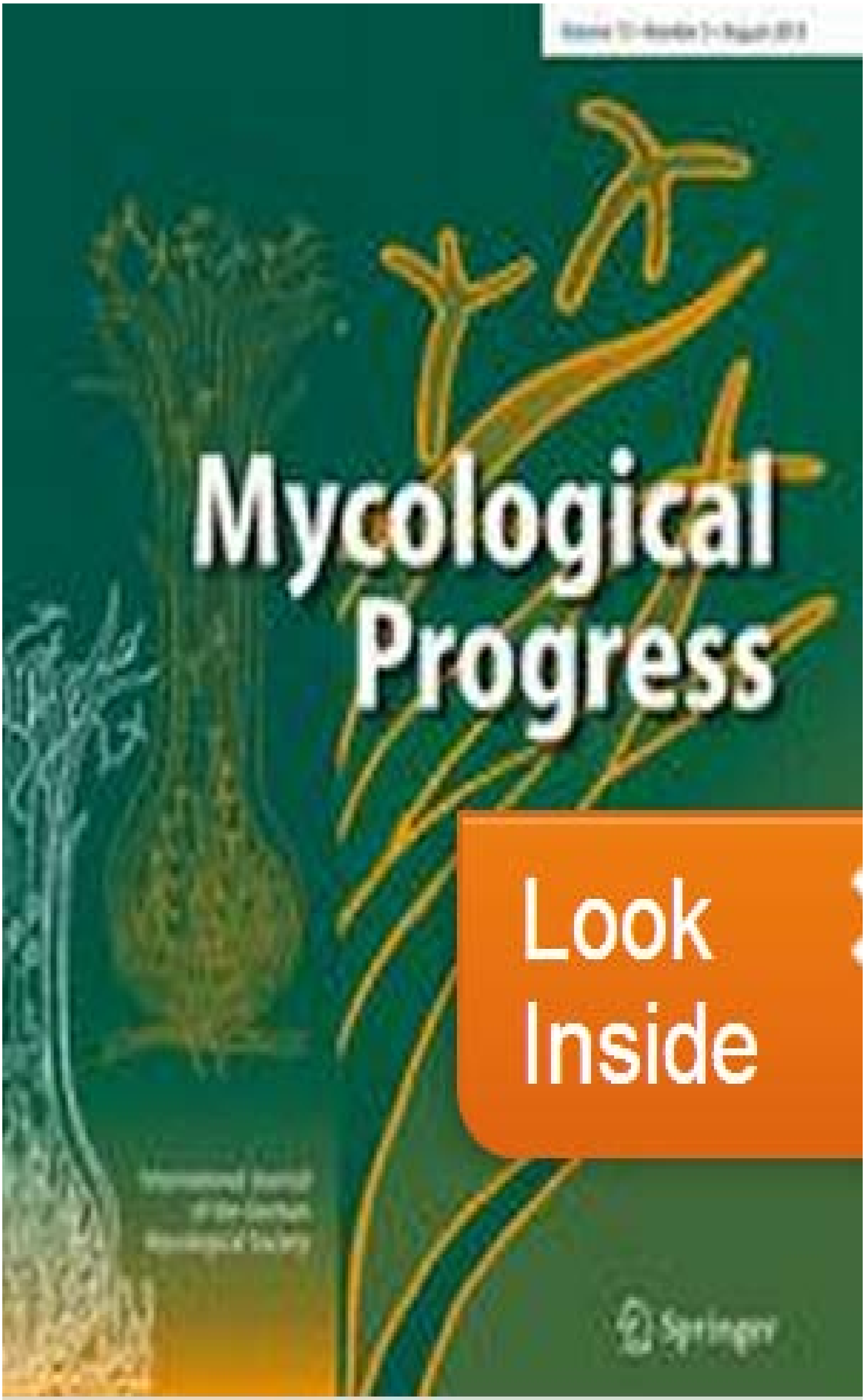
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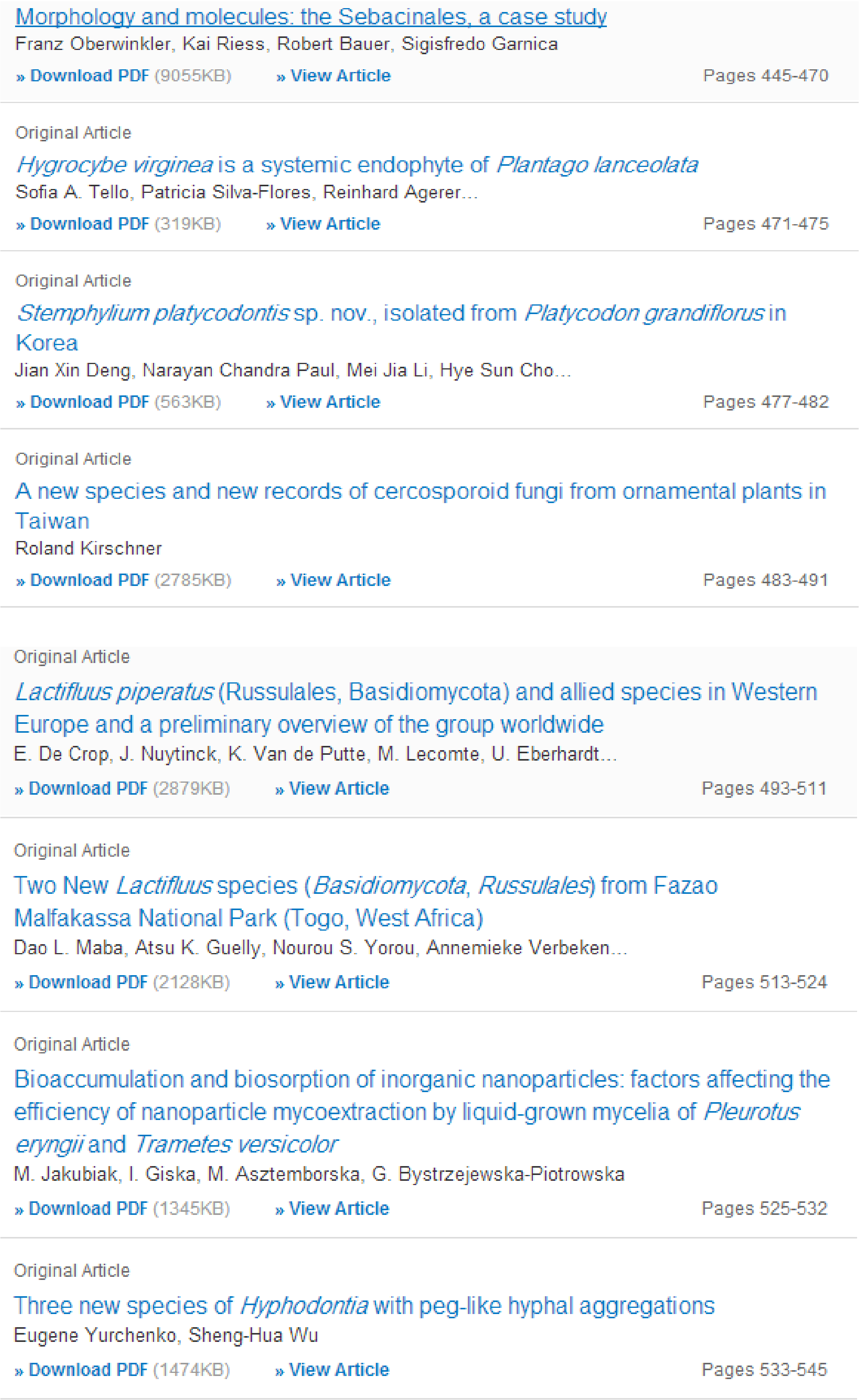

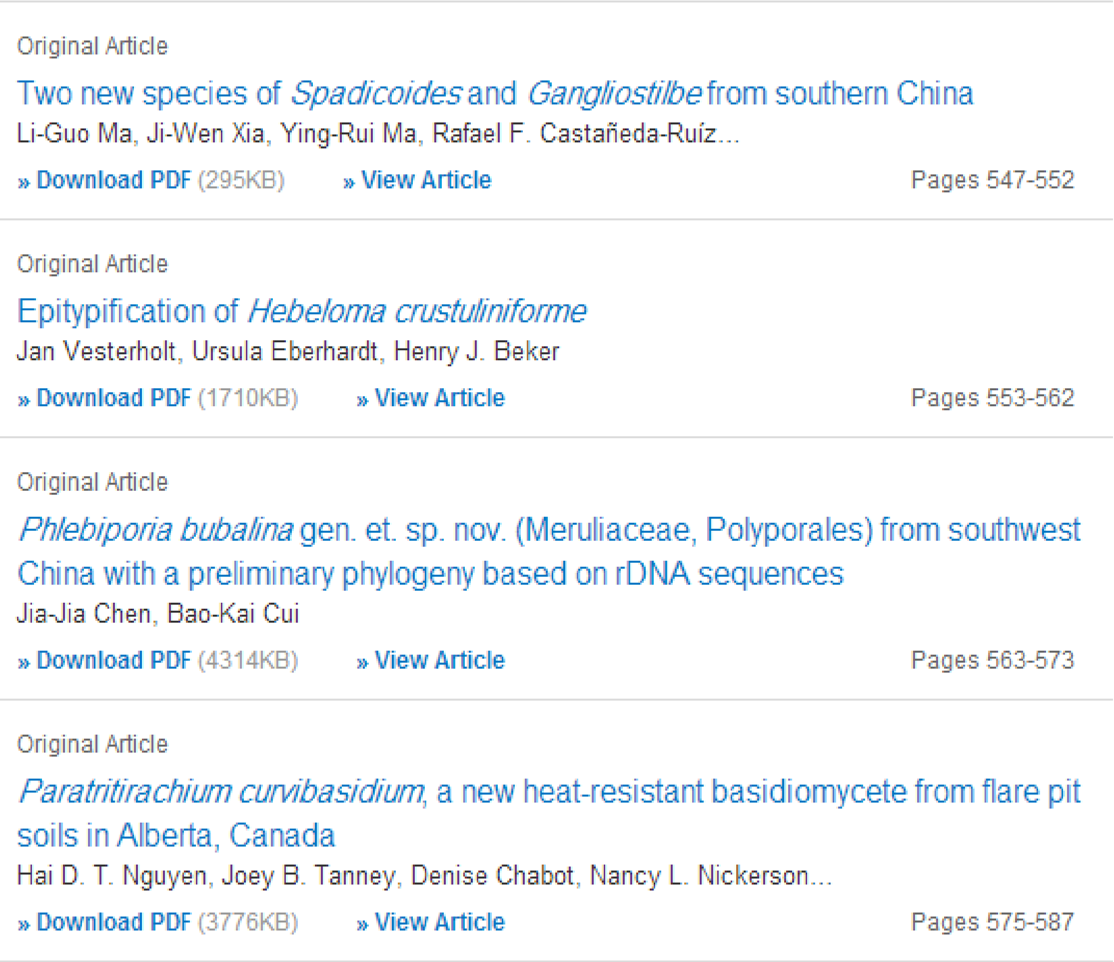

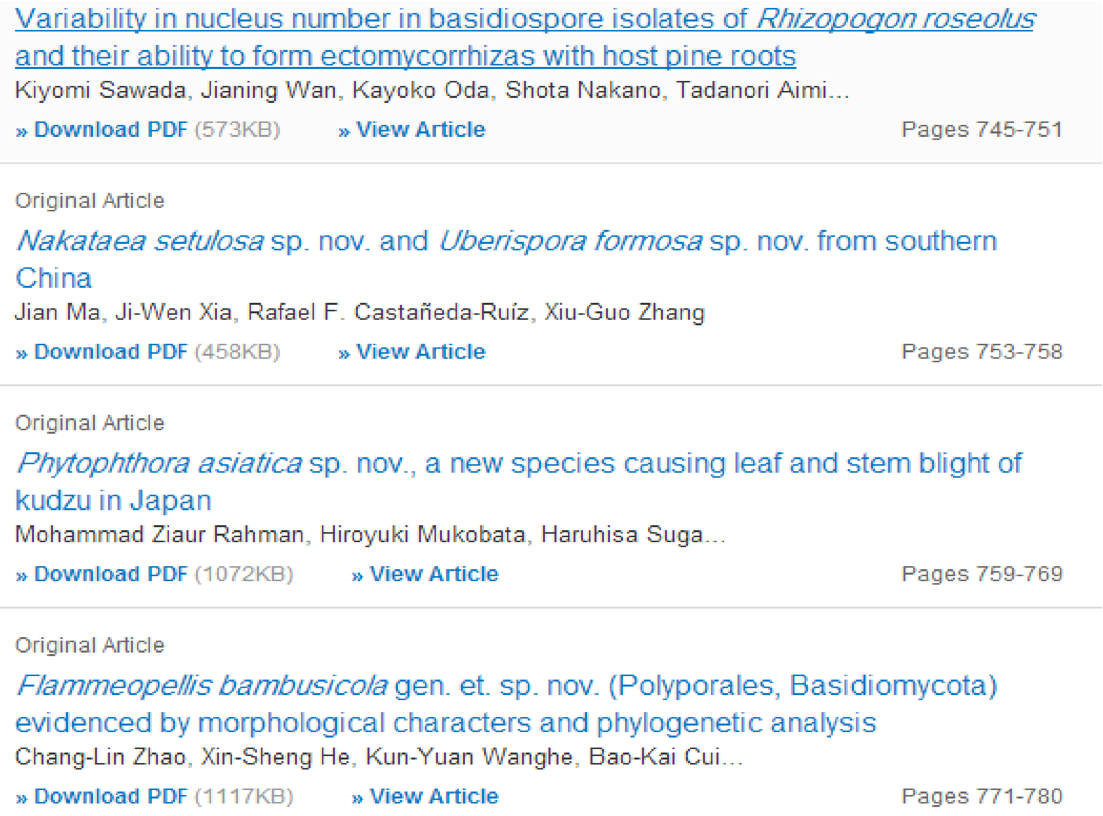

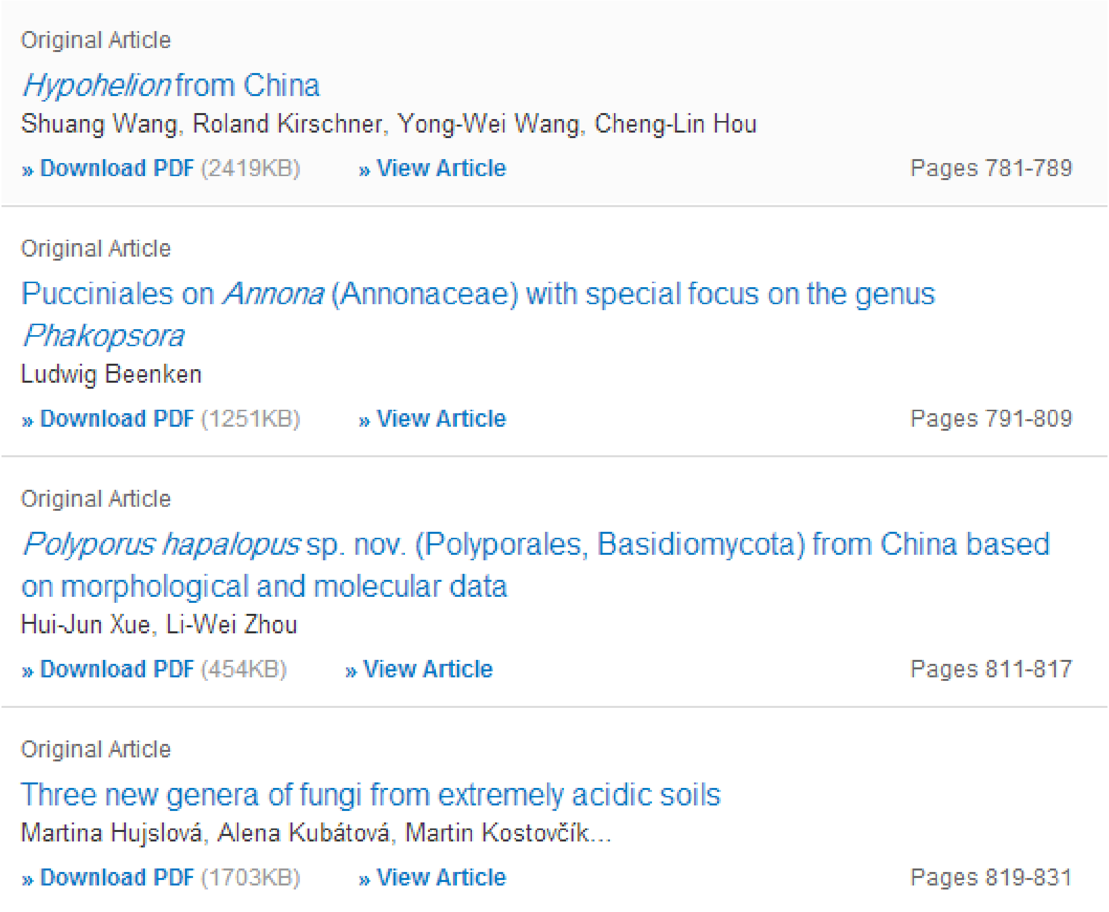

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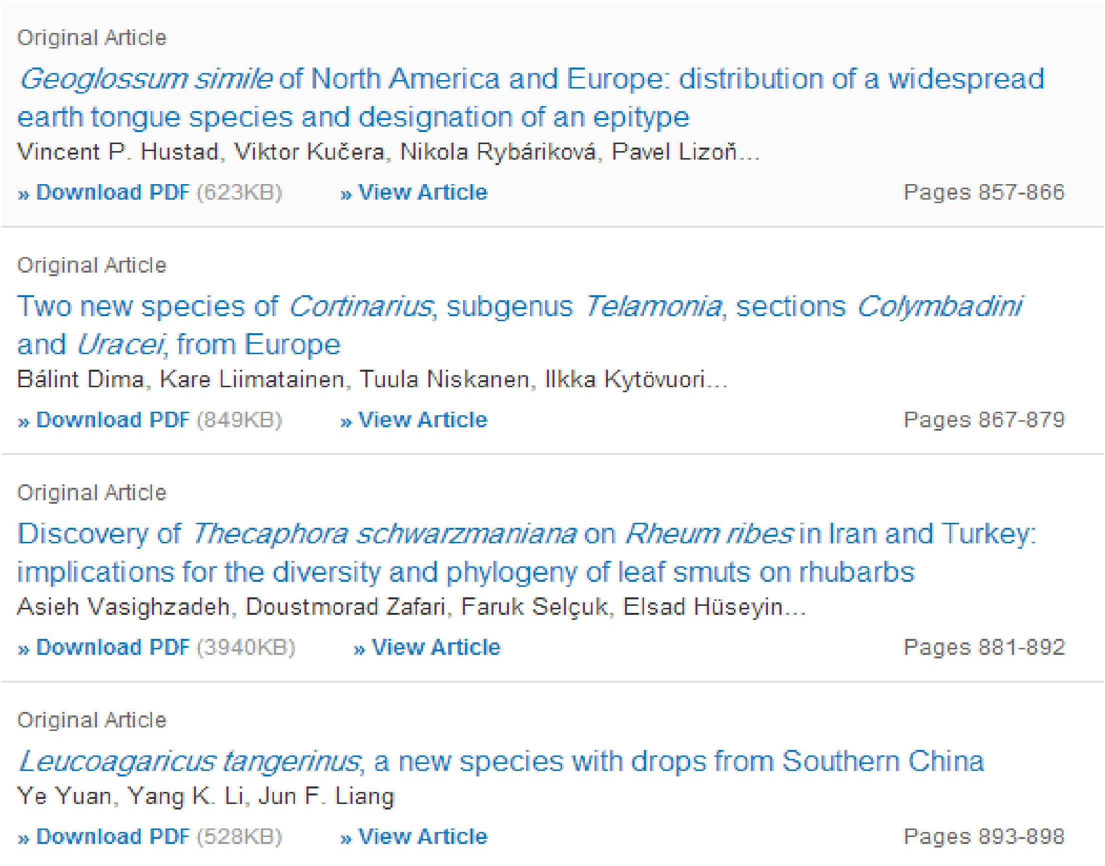

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ORIGINAL ARTICLE

Flammeopellis bambusicola gen. et. sp. nov. (Polyporales, Basidiomycota) evidenced by morphological characters and phylogenetic analysis

Chang-Lin Zhao · Xin-Sheng He · Kun-Yuan Wanghe · Bao-Kai Cui · Yu-Cheng Dai

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Abstract A new poroid wood-inhabiting fungal genus, *Flammeopellis*, is proposed based on morphological characters and molecular evidence. The genus is typified by *Flammeopellis bambusicola* sp. nov., which macroscopically is characterized by an annual growth habit and stipitate basidiocarps with a reddish-brown pileal cuticle. Microscopically, it has a dimitic hyphal system with generative hyphae frequently with simple septa, occasionally with clamp connections, strongly dextrinoid and cyanophilous skeletal hyphae, and ellipsoid to drop-shaped, pale yellowish, thick-walled, smooth, weakly dextrinoid and cyanophilous basidiospores. Phylogenetic analysis based on molecular data of ITS+LSU nrRNA gene regions indicates that *Flammeopellis* belongs to the core polyporoid clade and is closely related to *Perenniporiella*. Combined ITS+nLSU+mtSSU+TEF1 sequence data of representative taxa in *Perenniporia* sensu lato demonstrated that *Flammeopellis bambusicola* grouped with the *Perenniporiella* clade, but formed a monophyletic lineage with a strong support (100 % BP, 1.00 BPP). The morphological and molecular evidence confirmed the placement of the new genus in the core polyporoid clade and established its relationships with similar genera.

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Keywords Multi-marker analysis · *Perenniporia* · Polypores · Taxonomy · Wood-rotting fungi

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 the white-rot fungi of polypores are among the most efficient wood decayers of the biosphere (Zhou et al. 2011; Floudas et al. 2012). Some of these fungi are also forest pathogens and have potential applications in biomedical engineering and biodegradation (Younes et al. 2007; Dai et al. 2007, 2009; Wang et al. 2012, 2013; Cao et al. 2013; Si and Cui 2013; Si et al. 2013).

Molecular studies involving Polyporaceae have mainly been carried out based on ITS and/or nLSU sequences (Robledo et al. 2009; Justo and Hibbett 2011; Miettinen and Larsson 2011; Miettinen and Rajchenberg 2012). In addition, a six-gene dataset have helped to clarify the generic relationships of 373 polyporoid taxa and provide a phylogenetic and phylogenomic overview of the Polyporales (Binder et al. 2013).

China has a huge land area, including boreal, temperate, subtropical, and tropical vegetation, and the diversity of polypore is very rich (Dai 2012). Most parts of southern China have subtropical to tropical vegetation, but some temperate vegetation occurs in high mountains. Thus, the diversity of trees in southern China is very high, and the climate is suitable for the growth of polypores. The diversity of wood-rotting fungi in southern China has recently been extensively studied (Cui et al. 2011a; Dai et al. 2011; Cui 2013; Cui and Decock 2013; Li et al. 2013; Yuan 2013), and several new genera have been proposed (Niemelä et al. 2007; Dai 2010; Cui et al. 2011b; Li and Cui 2013; Zhao et al. 2013a; Zhou and

Dai 2013). During investigations on wood-inhabiting fungi in southwest China, an additional undescribed fungus was found in Sichuan Province. It is characterized by an annual growth habit, stipitate basidiocarps with reddish-brown cuticle at pileal surface, a dimitic hyphal system with generative hyphae frequently with simple septa, occasionally with clamp connections, strongly dextrinoid and cyanophilous skeletal hyphae, and ellipsoid to drop-shaped, pale yellowish, thick-walled, smooth, weakly dextrinoid and cyanophilous basidiospores; additionally, it grows on bamboo. These characters distinguish it from all known wood-inhabiting fungal taxa. In this study, we expand the phylogenetic sampling of wood-inhabiting poroid taxa using internal transcribed spacer (ITS) regions and the large subunit nuclear ribosomal RNA gene (nLSU) sequences to examine taxonomy and phylogeny of this new genus within the Polyporales. In addition, translation elongation factor 1-α (TEF1) and mitochondrial rRNA gene sequences (mtSSU) were obtained for representative taxa in the *Perenniporia* s.l., and a further investigation on the phylogenetic relationships of the newly described genus and related genera was carried out.

Materials and methods

Morphological studies

The studied specimens were deposited at the herbarium of Beijing Forestry University (BJFC). The microscopic examinations followed Cui et al. (2007). Sections were studied at magnification up to ×1,000 using a Nikon Eclipse 80i microscope and phase contrast illumination (Nikon, Tokyo, Japan). 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 in the size of the spores, 5 % of measurements were excluded from each end of the range, and were given in parentheses. In the text, the following abbreviations were used: IKI = Melzer's reagent, KOH=5 % potassium hydroxide, CB = Cotton Blue, CB+ = cyanophilous, 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* = number of spores measured from given number of specimens. Special color terms follow Petersen (1996).

Molecular procedures and phylogenetic analyses

The fungal taxa used in this study are listed in Table 1. A Phire® Plant Direct PCR Kit (Thermo, Vilnius, Lithuania) was used to obtain PCR products from dried specimens, according to the manufacturer's instructions. About 0.5 g dried fungal specimen was lysed in 30 μl dilution buffer for DNA extraction. After incubating 3 min at room temperature, 0.75 μl of the supernatant were used as template for a 30-μl PCR reaction. The DNA was amplified with the primers: ITS4 and ITS5 for ITS, MS1 and MS2 for mtSSU (White et al. 1990); LR0R and LR7 for nLSU (http://www.biology.duke.edu/fungi/mycolab/primers.htm), EF1-983 F and EF1-2218R for TEF1 (Rehner and Buckley 2005). The PCR procedure for ITS, mtSSU and TEF1 were as follows: initial denaturation at 98 °C for 5 min, followed by 39 cycles at 98 °C for 5 s, 58 °C for 5 s and 72 °C for 5 s, and a final extension of 72 °C for 10 min. The only difference of the nLSU amplification procedure was its annealing temperature was 48 °C. DNA sequencing was performed at Beijing Genomics Institute, China. All newly generated sequences were submitted to GenBank and are listed in Table 1.

Sequences generated for this study were aligned with additional sequences downloaded from GenBank (Table 1) using BioEdit (Hall 1999) and ClustalX (Thompson et al. 1997). Sequence alignments were deposited in TreeBASE (submission ID 14809).

Maximum parsimony analysis was applied to the combined multiple genes dataset sequences, and this test under heuristic search and 1,000 homogeneity replicates gave a *P* value of 1.000, much greater than 0.01, which means there is no discrepancy among the four loci in reconstructing phylogenetic trees. The tree construction procedure was performed in PAUP* v.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.

MrMODELTEST2.3 (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 2 million generations, and trees were sampled every 100 generations. The first one-fourth of generations were discarded as burn-in. A majority rule consensus tree of all remaining trees was calculated. Branches that received bootstrap support for maximum parsimony (MP) and Bayesian posterior probabilities (BPP) greater than or equal to 75 % (MP) and 0.95 (BPP) were considered as significantly supported, respectively.

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

Species name	Sample no.	GenBank accession nos.				References
		ITS	LSU	mtSSU	TEF1	
Abortiporus biennis	TFRI 274	EU232187	EU232235	—	—	Binder et al. 2005
A. biennis	EL 6503-03	JN649325	JN649325	—	—	Sjökvist et al. 2012
Abundisporus fuscopurpureus	Cui 10950	KC456254[a]	KC456256[a]	KF051025[a]	KF181154[a]	Present study
A. pubertatis	Cui 5776	KC787565[a]	KC787572[a]	KF051029[a]	KF181129[a]	Present study
A. roseoalbus	Dai 12269	KC415908[a]	KC415910[a]	KF051037[a]	KF181131[a]	Present study
A. sclerosetosus	MUCL 41438	FJ411101	FJ393868	—	—	Robledo et al. 2009
A. violaceus	Ryvarden 10775	KF018126[a]	KF018134[a]	KF051058[a]	KF181152[a]	Present study
Amylocystis lapponica	KHL 11755	EU118603	EU118603	—	—	Larsson 2007
Antrodia albida	CBS 308.82	DQ491414	AY515348	—	—	Kim et al. 2007
A. albida	FP 105979	EU232272	EU232272	—	—	Binder et al. 2005
A. heteromorpha	CBS 200.91	DQ491415	—	DQ491442		Kim et al. 2007
A. macra	MUAF 887	EU340898	EU340898	—	—	Cui 2013
Bjerkandera adusta	NBRC 4983	AB733156	AB733333	—	—	Binder et al. 2005
Cinereomyces lindbladii	FBCC 177	HQ659223	—	—	—	Miettinen and Rajchenberg 2012
Climacocystis borealis	KH 13318	JQ031126	JQ031126	—	—	Sjökvist et al. 2012
Coriolopsis caperata	LE(BIN)-0677	AB158316	AB158316	—	EU03059	Justo and Hibbett 2011
Donkioporia expansa	MUCL 35116	FJ411104	FJ393872	—	—	Robledo et al. 2009
Earliella scabrosa	PR1209	JN165009	JN164793	—	JN164894	Justo and Hibbett 2011
Flammeopellis bambusicola	Dai 13443	KF698748[a]	KF698759[a]	KF725877[a]	KF725879[a]	Present study
F. bambusicola	Dai 13506	KF698749[a]	KF698760[a]	KF725878[a]	KF725880[a]	Present study
Ganoderma lingzhi	Wu 1006-38	JQ781858	—	JX029989[a]	JX029976[a]	Present study
G. lingzhi	Dai 12479	JQ781864	—	JX029988[a]	JX029975[a]	Present study
G. australe	Cui 9511	JN048773	JN048792	—	—	Zhao et al. 2013a
G. sinense	Wei 5327	KF494998[a]	KF495008[a]	—	KF494976[a]	Present study
G. applanatum	Dai 12483	KF494999[a]	KF495009[a]	—	KF494977[a]	Present study
Gelatoporia subvermispora	Kotiranta 20823	FN907911	FN907911	—	—	Miettinen and Larsson 2011
Grammothelopsis subtropica	Cui9041	JQ845096[a]	JQ845099[a]	KF051039[a]	KF181133[a]	Present study
Heterobasidion annosum	PFC 5252	KC492906	KC492906	—	KC571646	Binder et al. 2013
Hornodermoporus latissimus	Cui 6625	HQ876604	JF706340	KF051040[a]	KF181134[a]	Zhao and Cui 2012
H. martius	Cui 7992	HQ876603	HQ654114	KF051041[a]	KF181135[a]	Zhao and Cui 2012
H. martius	MUCL 41677	FJ411092	FJ393859	—	—	Robledo et al. 2009
H. martius	MUCL 41678	FJ411093	FJ393860	—	—	Robledo et al. 2009
Hydnopolyporus fimbriatus	LR 40855	JN649347	JN649347	—	—	Sjökvist et al. 2012
Hypochnicium lyndoniae	NL 041031	JX124704	JX124704	—	—	Binder et al. 2005
Lentinus tigrinus	DSH93-181	AY218419	AF518627	U27050	—	Wang et al. 2004
Microporellus violaceocinerascens	MUCL 45229	FJ411106	FJ393874	—	—	Robledo et al. 2009
M. violaceocinerascens	Cui 8459	HQ876606	HQ654113	KF051042[a]	KF181136[a]	Zhao and Cui 2013
Obba rivulosa	KCTC 6892	FJ496693	FJ496710	—	—	Tomšovský et al. 2010
Perenniporia hainaniana	Cui 6364	JQ861743	JQ861759	KF051044[a]	KF181138[a]	Zhao and Cui 2013
P. hainaniana	Cui 6365	JQ861744	JQ861760	KF051045[a]	KF181139[a]	Zhao and Cui 2013
P. hainaniana	Cui 6366	JQ861745	JQ861761	KF494996[a]	KF494981[a]	Zhao and Cui 2013
P. medulla-panis	MUCL 49581	FJ411088	FJ393876	—	—	Robledo et al. 2009
P. medulla-panis	MUCL 43250	FJ411087	FJ393875	—	—	Robledo et al. 2009
P. medulla-panis	Cui 3274	JN112792	JN112793	KF051043[a]	KF181137[a]	Zhao and Cui 2012
P. subacida	Cui 10053	KF495006[a]	KF495017[a]	KF218321[a]	KF286327[a]	Present study
P. substraminea	Dai 10781	KF495007[a]	KF495018[a]	KF494995[a]	KF494983[a]	Present study
P. substraminea	Cui 10177	JQ001852	JQ001844	KF051046[a]	KF181140[a]	Zhao and Cui 2013

Table 1 (continued)

Species name	Sample no.	GenBank accession nos.				References
		ITS	LSU	mtSSU	TEF1	
P. substraminea	Cui 10191	JQ001853	JQ001845	KF051047[a]	KF181141[a]	Zhao and Cui 2013
Perenniporiella chaquenia	MUCL 47647	FJ411083	FJ393855	—	HM467609	Robledo et al. 2009
P. chaquenia	MUCL 47648	FJ411084	FJ393856	—	HM467610	Robledo et al. 2009
P. micropora	MUCL43581	FJ411086	FJ393858	—	HM467608	Robledo et al. 2009
P. neofulva	MUCL 45091	FJ411080	FJ393852	—	HM467599	Robledo et al. 2009
P. pendula	MUCL 46034	FJ411082	FJ393853	—	HM467601	Robledo et al. 2009
Phanerochaete chrysosporium	BKM-F-1767	HQ188436	GQ470643	—	—	Binder et al. 2005
Phlebia unica	KHL 11786	EU118657	EU118657	—	—	Larsson 2007
Physisporinus sanguinolentus	BRNM 699576	FJ496671	FJ496725	FJ496750	—	Tomšovský et al. 2010
Piloporia sajanensis	Mannine 2733a	HQ659239	HQ659239	—	—	Miettinen and Rajchenberg 2012
Polyporus brumalis	KHL 8558	AF347108	AF347108	—	—	Larsson 2007
P. tuberaster	CulTENN 8976	AF516598	AJ488116	—	—	Binder et al. 2005
Postia alni	X 1400	KC595932	KC595932	—	—	Beatriz et al. 2013
P. caesia	CIEFAP 174	JX090109	JX090130	—	—	Binder et al. 2013
P. guttulata	KHL 11739	EU11865	EU11865	—	—	Beatriz et al. 2013
P. lactea	X 1391	KC595939	KC595939	—	—	Beatriz et al. 2013
P. venata	CIEFAP 346	JX090113	JX090133	—	—	Beatriz et al. 2013
Pycnoporus cinnabarinus	AFTOL-ID 772	DQ411525	AY586703	U27059	—	Binder et al. 2005
Pyrofomes demidoffii	MUCL 41034	FJ411105	FJ393873	—	—	Robledo et al. 2009
Sebipora aquosa	Miettinen 8680	HQ659240	HQ659240	—	—	Miettinen and Rajchenberg 2012
Skeletocutis amorpha	Miettinen 11038	FN907913	FN907913	—	—	Miettinen and Larsson 2011
Stereum hirsutum	NBRC 6520	AB733150	AB733325	—	—	Binder et al. 2013
Trametes elegans	FP105679	JN048766	JN048785	—	—	Zhao et al. 2013a
T. hirsuta	Cui 7784	JN048768	JN048787	—	—	Zhao et al. 2013a
T. hirsuta	RLG5133T	JN164854	JN164801	AF042154	JN164891	Justo and Hibbett 2011
T. pubescens	PRM 900586	AY684173	AY855906	—	—	Tomšovský et al. 2006
Truncospora ochroleuca	Dai 11486	HQ654105	JF706349	KF051048[a]	KF181142[a]	Zhao and Cui 2012
T. ochroleuca	MUCL 39726	FJ411098	FJ393865	—	—	Robledo et al. 2009
T. ochroleuca	Cui 5671	JX941584	JX941602	KF218309[a]	KF286315[a]	Zhao and Cui 2013
T. ochroleuca	Cui 5673	JX941585	JX941603	KF218308[a]	KF286314[a]	Zhao and Cui 2013
T. ohiensis	Cui 5714	HQ654103	HQ654116	KF051056[a]	KF181150[a]	Zhao and Cui 2012
T. ohiensis	MUCL 41036	FJ411096	FJ393863	—	—	Robledo et al. 2009
Tyromyces chioneus	Miettinen 7487	HQ659224	HQ659224	—	—	Miettinen and Rajchenberg 2012
T. kmetii	Penttilä 13474	KF705040[a]	KF705041[a]	—	—	Present study
Vanderbylia delavayi	Dai 6891	JQ861738[a]	KF495019[a]	KF218287[a]	KF286293[a]	Present study
V. fraxinea	DP 83	AM269789	AM269853	—	—	Robledo et al. 2009
V. fraxinea	Cui 7154	HQ654095	HQ654110	KF218288[a]	KF286294[a]	Zhao and Cui 2012
V. fraxinea	Cui 8871	JF706329	JF706345	KF051050[a]	KF181144[a]	Zhao and Cui 2012
V. fraxinea	Cui 8871	JF706329	JF706345	KF051050[a]	KF181144[a]	Zhao and Cui 2012
V. robiniophila	Cui 7144	HQ876608	JF706341	KF051052[a]	KF181146[a]	Zhao and Cui 2012
V. vicina	MUCL 44779	FJ411095	AF518666	—	—	Robledo et al. 2009
Yuchengia narymica	Dai 6998	JN048775	JN048794	KF051055[a]	KF181149[a]	Zhao et al. 2013a

[a] Newly generated sequences for this study

Results

Molecular phylogeny

Eighty-eight new gene sequences were generated in this study (Table 1). The ITS+nLSU dataset included sequences from 61 fungal specimens representing 55 taxa. The dataset had an aligned length of 2,148 characters, of which 1,207 characters are constant, 256 are variable and parsimony-uninformative, and 685 are parsimony-informative. Maximum parsimony analysis yielded 5 equally parsimonious trees (TL=4,520, CI=0.344, RI=0.517, RC=0.277, HI=0.656). Best model for ITS+nLSU estimated and applied in the Bayesian analysis: GTR+I+G. Bayesian analysis resulted in the same topology compared to maximum parsimony analysis with an average standard deviation of split frequencies=0.007869. 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).

The phylogeny (Fig. 1) inferred from ITS+nLSU sequences demonstrated six major clades for 55 sampled species of the Polyporales. The new genus *Flammeopellis* clustered into the core polyporoid clade and was closely related to *Perenniporiella* Decock & Ryvarden based on phylogenetic analysis with a low support (77 % BP, 0.97 BPP), and then grouped with the clades of *Abundisporus* Ryvarden, *Ganoderma* P. Karst, *Grammothelopsis* Jülich and *Truncospora* Pilát.

The four-gene (ITS+LSU+mtSSU+TEF1) sequence dataset did not show any conflicts in tree topology for the reciprocal bootstrap trees, which allowed us to combine them ($P>0.01$). The combined dataset included sequences from 50 fungal specimens representing 31 taxa. The dataset had an aligned length of 4,035 characters, of which 2,545 characters

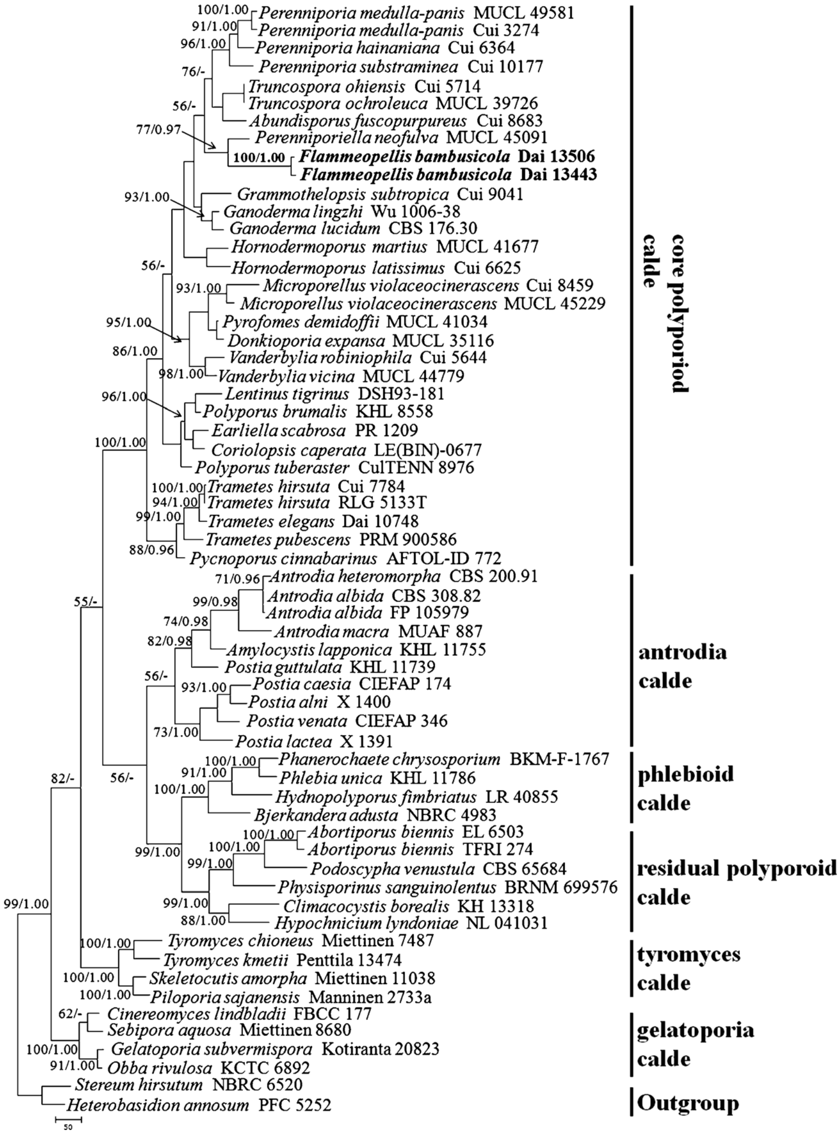

Fig. 1 One of the most parsimonious trees illustrating the phylogeny of *Flammeopellis bambusicola* and related species in Polyporales, based on ITS+ nLSU sequences. Parsimony bootstrap proportions (*before the slash markers*) higher than 50 % and Bayesian posterior probabilities (*after the slash markers*) more than 0.95 are indicated along branches

are constant, 230 are variable and parsimony-uninformative, and 1,260 are parsimony-informative. Maximum parsimony analysis yielded 8 equally parsimonious trees (TL=4,484, CI=0.492, RI=0.659, RC=0.323, HI=0.509). Best model for the combined ITS+nLSU+mtSSU+TEF1 estimated and applied in the Bayesian analysis: GTR+I+G. Bayesian analysis resulted in the same topology with an average standard deviation of split frequencies=0.008430. Sequences of *Donkioporia expansa* (Desm.) Kotl. & Pouzar and *Pyrofomes demidoffii* (Lév.) Kotl. & Pouzar obtained from GenBank were used as outgroups to root trees following Zhao et al. (2013b).

A further phylogeny (Fig. 2) inferred from multiple genes of the combined ITS+nLSU+mtSSU+TEF1 sequences was obtained for representative taxa in the *Perenniporia* s.l. and demonstrated that *Flammeopellis bambusicola* grouped with *Perenniporiella* clade, but two sampled specimens of the new species *F. bambusicola*, formed a monophyletic lineage with a strong support (100 % BP, 1.00 BPP), and then grouped with *Grammothelopsis subtropica* B.K. Cui & C.L. Zhao with a 94 % bootstrap value and 0.99 Bayesian posterior probability.

Taxonomy

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

MycoBank no.: MB 807157

Differs from other genera by a stipitate basidiocarp with reddish cuticle on pileus and stipe surface, a dimitic hyphal system with generative hyphae frequently with simple septa, occasionally with clamp connections, strongly dextrinoid and cyanophilous skeletal hyphae, and thick-walled, pale yellowish, smooth, weakly dextrinoid and cyanophilous basidiospores.

Type species: *Flammeopellis bambusicola.*

Etymology: *flammeopellis* (Lat.): referring to reddish upper cuticle surface.

Basidiocarps annual, stipitate, soft corky when fresh, corky when dried. Pileus convex, pileal surface bearing a reddish cuticle on pileus and stipe surface. Pore surface white to cream. Context white to cream, soft corky when fresh, corky when dried. Tubes concolorous with pore surface, soft corky when fresh, corky when dried. Stipe distinctly reddish, corky. Hyphal system dimitic; generative hyphae frequently with simple septa, occasionally with clamp connections; skeletal hyphae strongly dextrinoid, CB+. Basidiospores pale yellowish, thick-walled, smooth, weakly dextrinoid, CB+.

Flammeopellis bambusicola Y.C. Dai, B.K. Cui & C.L. Zhao, sp. nov. Figs. 3 and 4

MycoBank no.: MB 807158

Basidiocarps annual, stipitate, solitary or gregarious, soft corky when fresh, corky when dried. Pilei more or less semicircular to spathulate. Pileus convex, pileal surface bearing a reddish brown cuticle. Pore surface white when fresh, cream upon drying; pores round; dissepiments thick, entire. Context

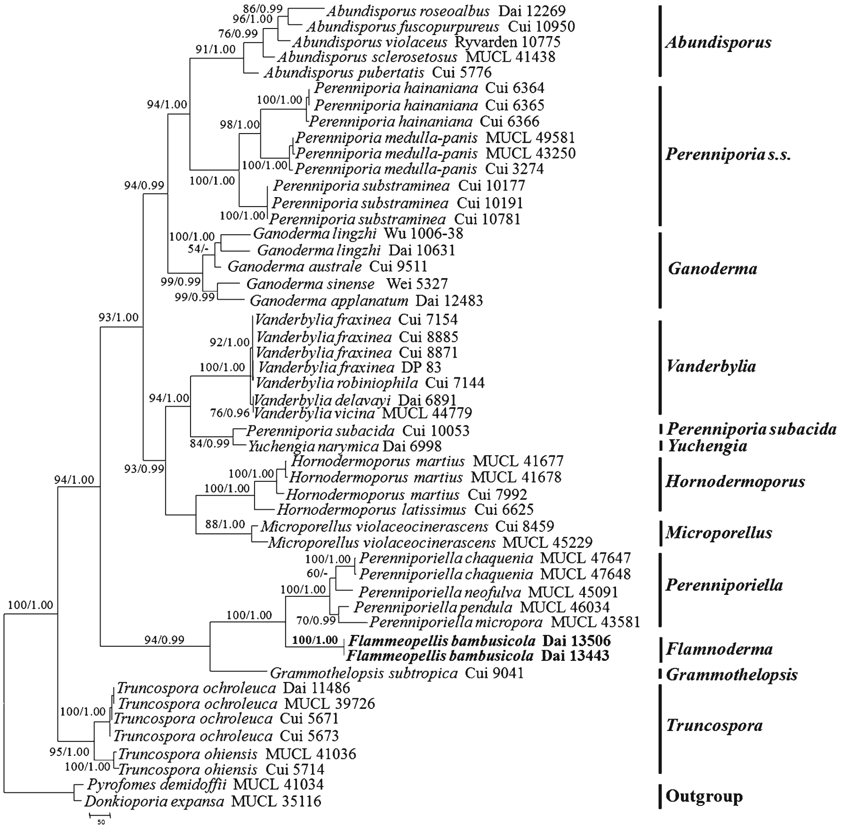

Fig. 2 One of the most parsimonious trees illustrating the phylogeny of *Flammeopellis bambusicola* species and related species obtained for more representative taxa in the *Perenniporia* s.l., based on the combined ITS+LSU+mtSSU+TEF1 sequence datasets. Parsimony bootstrap proportions (*before the slash markers*) higher than 50 % and Bayesian posterior probabilities (*after the slash markers*) more than 0.95 are indicated along branches

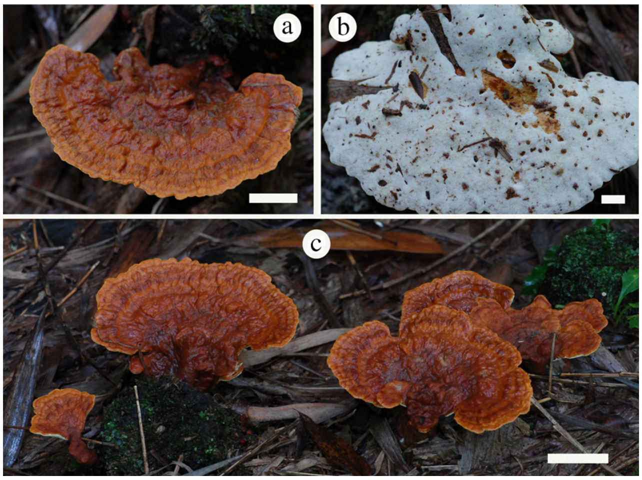

Fig. 3 Basidiocarps of *Flammeopellis bambusicola* (holotype). *Bars* (**a**) 1.5 cm, (**b**) 0.5 cm, (**c**) 2 cm

white to cream, soft corky when fresh, corky when dried. Tubes concolorous with pore surface, soft corky when fresh, corky when dried. Stipe surface distinctly reddish, corky. Tissues unchanged in KOH. Hyphal system dimitic; generative hyphae frequently with simple septa, occasionally with clamp connections; skeletal hyphae strongly dextrinoid, CB+, unbranched. Basidiospores ellipsoid to drop-shaped, pale yellowish, thick-walled, smooth, weakly dextrinoid, cyanophilous, 4.5–5.1 × 3.5–4 μm.

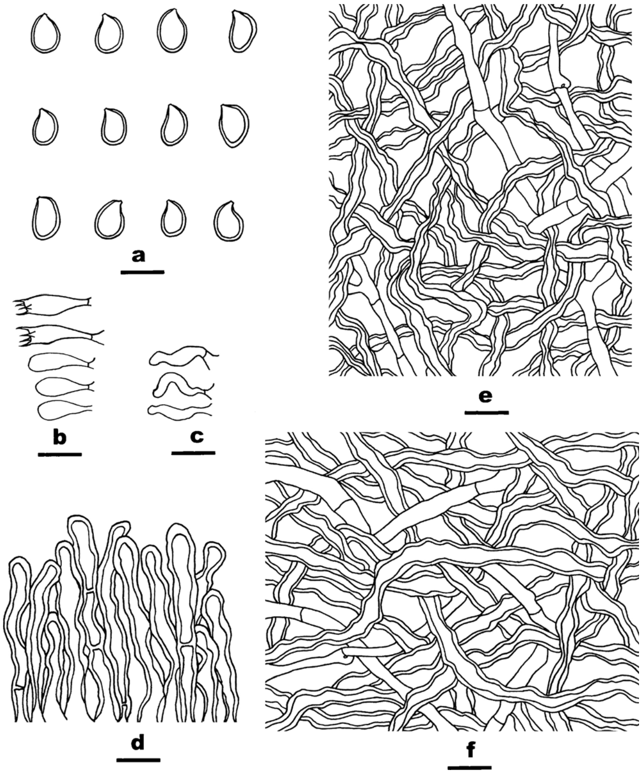

Fig. 4 Microscopic structures of *Flammeopellis bambusicola* (drawn from the holotype). **a** Basidiospores; **b** basidia and basidioles; **c** cystidioles; **d** palisade of cells from the upper surface cuticle; **e** hyphae from trama; **f** hyphae from context. *Bars*: (**a**) 5 μm, (**b**–**f**) 10 μm

Holotype: CHINA. Sichuan Prov., Qionglai County, Pingle, Lugouzhuhai, on stump of *Bambusa*, 12 August 2013 *Dai 13443* (BJFC).

Etymology: *bambusicola* (Lat.): referring to growth on bamboo stump.

Basidiome: Basidiocarps annual, laterally stipitate, solitary or gregarious, soft corky and without odor or taste when fresh, becoming corky upon drying. Pilei more or less semicircular to spathulate, up to 7 cm long, 5 cm wide, 4 mm thick at centre. Pileus convex, pileal surface bearing a reddish brown cuticle which becoming dark reddish brown with age, irregularly rough, distinctly sulcate. Pore surface white when fresh, white to cream upon drying; pores round, 6–7 per mm; dissepiments thick, entire. Sterile margin narrow, cream to pale brown, up to 1 mm wide. Context white to cream, soft corky when fresh, corky when dried, up to 1.5 mm thick. Tubes concolorous with pore surface, soft corky when fresh, corky when dried, up to 2.5 mm long. Stipe surface distinctly reddish, soft corky when fresh, corky when dried, up to 4.5 cm long, 1.5 mm in diam.

Hyphal structure: Hyphal system dimitic; generative hyphae frequently with simple septa, occasionally with clamp connections; skeletal hyphae strongly dextrinoid, CB+; tissues unchanged in KOH.

Context: Generative hyphae infrequent, hyaline, thin-walled, occasionally branched, 3.5–5 μm in diameter; skeletal hyphae dominant, hyaline, thick-walled with a wide lumen, unbranched, interwoven, occasionally collapsed, 4–6 μm in diameter.

Cuticle: Composed of a vertical and closely-packed palisade of cells; cells mostly clavate, yellowish to pale brown, thick-walled, with 1–2 septa, weakly dextrinoid, 31–45 × 5–7 μm.

Tubes: Generative hyphae infrequent, hyaline, thin-walled, occasionally branched, 3–4.5 μm in diameter; skeletal hyphae dominant, hyaline, thick-walled with a wide to narrow lumen, unbranched, interwoven, 3.5–5 μm in diameter. Cystidia absent, but fusoid cystidioles present, hyaline, thin-walled, 10–14 × 3–4 μm; basidia clavate to barrel-shaped, with four sterigmata and a basal clamp connection, 15–16 × 5–6.5 μm; basidioles dominant, in shape similar to basidia, but slightly smaller.

Stipe: Generative hyphae infrequent, hyaline, thin-walled, occasionally branched, 3–5 μm in diameter; skeletal hyphae dominant, hyaline, thick-walled with a wide lumen, unbranched, interwoven, 3.5–6 μm in diameter.

Spores: Basidiospores ellipsoid to drop-shaped, pale yellowish, thick-walled, smooth, weakly dextrinoid, CB+, (4.3–)4.5–5.1(−5.4) × (3.3–)3.5–4(−4.2) μm, $L = 4.83$ μm, $W = 3.8$ μm, $Q = 1.25–1.28$ ($n = 60/2$).

Rot type: White rot.

Additional specimen examined: CHINA. Sichuan Prov., Qionglai County, Pingle, Lugouzhuhai, on stump of *Bambusa*, 10 September 2013 *Dai 13506* (BJFC, paratype).

Discussion

Flammeopellis bambusicola is characterized by an annual growth habit, laterally stipitate basidiocarps with a reddish-brown pileal cuticle, a dimitic hyphal system with generative hyphae frequently with simple septa, occasionally with clamp connections, strongly dextrinoid, cyanophilous, unbranched skeletal hyphae, and ellipsoid to drop-shaped, pale yellowish, thick-walled, smooth, weakly dextrinoid and cyanophilous basidiospores (4.5–5.1×3.5–4 μm).

In the present study, *Flammeopellis bambusicola* is described based on morphological characters and molecular phylogenetic analyses. The molecular data show that *Flammeopellis* belongs to the core polyporoid clade and is closely related to *Perenniporiella* based on ITS+LSU-nrRNA gene regions with a low support (77 % BP, 0.97 B.P. Fig. 1). A further study with representative taxa in the *Perenniporia* s.l. used combined ITS+nLSU+mtSSU+TEF1 sequence data analysis. *Flammeopellis bambusicola* grouped with the *Perenniporiella* clade, but formed a monophyletic lineage with a strong support (100 % BP, 1.00 B.P. Fig. 2). *Flammeopellis* is therefore confirmed as a new genus in the core polyporoid clade.

Phylogenetically, the genus *Perenniporiella* groups with *Flammeopellis* (Figs. 1, 2); however, the former differs from the latter by its dimitic hyphal system, generative hyphae with only clamp connections, and hyaline basidiospores (Decock and Ryvarden 2003). *Grammothelopsis subtropica* is closely related to *Flammeopellis bambusicola* in phylogenetic trees (Figs. 1, 2), but it differs from *F. bambusicola* in producing resupinate basidiocarps, larger pores (1–2 per mm), presence of dendrohyphidia, and hyaline and larger basidiospores (12.7–15.2×4.9–5.9 μm; Zhao and Cui 2012).

Morphologically, stipitate basidiocarps with a reddish pileal cuticle is typical of some wood-rotting fungal species in *Ganoderma* and *Pyrrhoderma* Imazeki. *Ganoderma* differs from *Flammeopellis* in having double-walled basidiospores with an echinulae endospore (Moncalvo and Ryvarden 1997). *Pyrrhoderma* is separated from *Flammeopellis* by a monomitic hyphal structure with simple septate generative hyphae, and hyaline and thin-walled basidiospores (Dai 2010).

The genus *Microporellus* Murrill is similar to *Flammeopellis* in having stipitate basidiocarps and unbranched skeletal hyphae; however, *Flammeopellis* is not close to *Microporellus* species based on DNA sequence data (Figs. 1, 2), and morphologically it differs from *Flammeopellis* in having a dimitic hyphal system with generative hyphae only bearing clamp connections, and skeletal hyphae often absent in the context, presence of cystidia and subglobose, slightly thick-walled basidiospores (David and Rajchenberg 1985; Decock 2007).

Two other species in *Perenniporia* s.l. have been reported to grow on bamboo as follows: *P. bambusicola* Choeyklin, T. Hatt. & E.B.G. Jones (Choeyklin et al. 2009) and *P. aridula* B.K. Cui & C.L. Zhao (Zhao et al. 2013b). *Perenniporia bambusicola* differs in its resupinate basidiocarps with orange to orange brown pore surface, presence of rhizomorphs, and truncate, hyaline, narrower basidiospores (1.8–2.5 μm wide; Choeyklin et al. 2009). *Perenniporia aridula* is distinguished by perennial, resupinate basidiocarps, frequently branched skeletal hyphae, and truncate and larger basidiospores (6–7×5.1–6 μm; Zhao et al. 2013b).

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References

Beatriz OS, Lindner DL, Miettinen O, Justo A, Hibbett DS (2013) A phylogenetic overview of the antrodia clade (Basidiomycota, Polyporales). Mycologia 105:1391–1411. doi:10.3852/13-051

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 CL, Peng F, Cui BK (2013) Chemical characterization and structure of exopolysaccharides from submerged culture of new medicinal mushroom from China, *Phellinus mori* (Higher Basidiomycetes). Int J Med Mushrooms 15:57–69. doi:10.1615/IntJMedMushr.v15.i1.70

Choeyklin R, Hattori T, Jaritkhuan S, Jones EBG (2009) Bambusicolous polypores collected in central Thailand. Fungal Divers 36:121–128

Cui BK (2013) *Antrodia tropica* sp. nov. from southern China inferred from morphological characters and molecular data. Mycol Prog 12:223–230. doi:10.1007/s11557-012-0829-7

Cui BK, Decock C (2013) *Phellinus castanopsidis* sp. nov. (Hymenochaetaceae) from southern China, with preliminary phylogeny based on rDNA sequences. Mycol Prog 12:341–351. doi:10.1007/s11557-012-0839-5

Cui BK, Dai YC, Decock C (2007) A new species of *Perenniporia* (Basidiomycota, Aphyllophorales) from eastern China. Mycotaxon 99:175–180

Cui BK, Du P, Dai YC (2011a) Three new species of *Inonotus* (Basidiomycota, Hymenochaetaceae) from China. Mycol Prog 10:107–114. doi:10.1007/s11557-010-0681-6

Cui BK, Zhao CL, Dai YC (2011b) *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. For 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, Cui BK, Yuan HS, He SH, Wei YL, Qin WM, Zhou LW, Li HJ (2011) Wood-inhabiting fungi in southern China 4. Polypores from Hainan Province. Ann Bot Fenn 48:219–231. doi:10.5735/085.048.0302

David A, Rajchenberg M (1985) Pore fungi from French Antilles and Guiana. Mycotaxon 22:285–325

Decock C (2007) On the genus *Microporellus*, with two new species and one recombination (*M. papuensis* spec. nov., *M. adextrinoideus* spec. nov., and *M. terrestris* comb. nov.). Czech Mycol 59:153–170

Decock C, Ryvarden L (2003) *Perenniporiella* gen. nov. segregated from *Perenniporia*, including a key to neotropical *Perenniporia* species with pileate basidiomes. Mycol Res 107:93–103. doi:10.1017/S0953756202006986

Felsenstein J (1985) Confidence intervals on phylogenetics: an approach using bootstrap. Evolution 39:783–791

Floudas D, Binder M, Riley R, Barry K, Blanchette RA, Henrissat B, Martínez AT, Otillar 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

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

Justo A, Hibbett DS (2011) Phylogenetic classification of *Trametes* (Basidiomycota, Polyporales) based on a five-marker dataset. Taxon 60:1567–1583

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, Wallingford

Larsson KH (2007) Re-thinking the classification of corticioid fungi. Mycol Res 111:1040–1063. doi:10.1016/j.mycres.2007.08.001

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

Li HJ, Han ML, Cui BK (2013) Two new *Fomitopsis* species from southern China based on morphological and molecular characters. Mycol Prog 12:709–718. doi:10. 1007/s11557-012-0882-2

Miettinen O, Larsson KH (2011) *Sidera*, a new genus in Hymenochaetales with poroid and hydnoid species. Mycol Prog 10:131–141. doi:10.1007/s11557-010-0682-5

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

Moncalvo JM, Ryvarden L (1997) A nomenclatural study of the Ganodermataceae Donk. Syn Fung 11:1–114

Niemelä T, Larsson KH, Dai YC, Larsson E (2007) *Anomoloma*, a new genus separated from *Anomoporia* on the basis of decay type and nuclear rDNA sequence data. Mycotaxon 100:305–317

Nylander 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 teleomorphs*. 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

Si J, Cui BK (2013) A new fungal peroxidase with alkaline-tolerant, chloride-enhancing activity and dye decolorization capacity. J Mol Catal B 89:6–14. doi:10.1016/j.molcatb.2012.12.002

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

Swofford DL (2002) PAUP*: phylogenetic analysis using parsimony (*and other methods). Version 4.0b10. Sinauer, Massachusetts

Thompson JD, Gibson TJ, Plewniak F, Jeanmougin F, Higgins DG (1997) The Clustal_X windows interface: flexible strategies formultiple sequence alignment aided by quality analysis tools. Nucleic Acids Res 25:4876–4882. doi:10.1093/nar/25.24.4876

Tomšovský M, Kolarík M, Pažoutová S, Homolka L (2006) Molecular phylogeny of European *Trametes* (Basidiomycetes, Polyporales) species based on LSU and ITS (nrDNA) sequences. Nova Hedwigia 82:269–280

Tomšovský 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 Z, Binder M, Dai YC, Hibbett DS (2004) Phylogenetic relationships of *Sparassis* inferred from nuclear and mitochondrial ribosomal DNA and RNA polymerase sequences. Mycologia 96:1015–1029. doi:10.2307/3762086

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

Wang W, Yuan TQ, Cui BK (2013) Fungal treatment followed by FeCl3 treatment to enhance enzymatic hydrolysis of poplar wood for high sugar yields. Biotechnol Lett 35:2061–2067. doi:10.1007/s10529-013-1306-3

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 Press, San Diego, pp 315–322

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 decolourization of synthetic dyes. J Appl Microbiol 102:1033–1042

Yuan HS (2013) *Antrodiella chinensis* sp. nov., a Chinese representative of the *Antrodiella americana* complex. Mycol Prog 12:437–443. doi:10.1007/s11557-012-0852-8

Zhao CL, Cui BK (2012) A new species of *Grammothelopsis* (Polyporales, Basidiomycota) described from southern China. Mycotaxon 121:291–296. doi:10.5248/121.291

Zhao CL, Cui BK (2013) Morphological and molecular identification of four new resupinate species of *Perenniporia* (Polyporales) from southern China. Mycologia 105:945–958. doi:10.3852/12-201

Zhao CL, Cui BK, Steffen KT (2013a) *Yuchengia*, a new polypore genus segregated from *Perenniporia* (Polyporales, Basidiomycota) based on morphological and molecular characters. Nord J Bot 31:331–338. doi:10.1111/j.1756-1051.2012.00003.x

Zhao CL, Cui BK, Dai YC (2013b) New species and phylogeny of *Perenniporia* based on morphological and molecular characters. Fungal Divers 58:47–60. doi:10.1007/s13225-012-0177-6

Zhou LW, Dai YC (2013) Taxonomy and phylogeny of wood-inhabiting hydnoid species in Russulaes: two new genera, three new species and two new combinations. Mycologia 105:636–649. doi:10.3852/12-011

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