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Phylogenetic analysis demonstrating four new species in *Megasporoporia* sensu lato (Polyporales, Basidiomycota)

Wang YR[1,2], Wu YD[1,3], Vlasák J[4], Yuan Y[1*] and Dai YC[1*]

[1]*Institute of Microbiology, School of Ecology and Nature Conservation, Beijing Forestry University, Beijing 100083, China*
[2]*The college of Forestry, Beijing Forestry University, Beijing 100083, China*
[3]*China Fire and Rescue Institute, Beijing 102202, China*
[4]*Biology Centre, Czech Academy of Sciences, Institute of Plant Molecular Biology, Branišovská 31, CZ-370 05 České Budějovice, Czech Republic*

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Abstract

Megasporoporia sensu lato is a common polypore genus in tropics, the members of which are readily recognized in the field because of their resupinate, light-coloured basidiocarps with big pores. The species of the genus usually grow on fresh fallen trunks and branches. The genus was recognized as polyphyletic by molecular analyses and divided into three genera: *Megasporia*, *Megasporoporia* sensu stricto and *Megasporoporiella*. In the present study, phylogenies based on the combined 2-gene (ITS + nLSU) and 4-gene (ITS + nLSU + mtSSU + TEF) sequences datasets of *Megasporoporia* sensu lato are analysed, and 21 lineages nested in three clades (the *Megasporia* clade, the *Megasporoporia* sensu stricto clade and the *Megasporoporiella* clade) are formed. Based on morphological examination, four new species, *Megasporia bambusae*, *Megasporia fusiformis*, *Megasporoporia inflata* and *Megasporoporiella australiae*, are described based on materials from Australia, China and Malaysia, and a new combination, *Megasporoporiella hubeiensis* comb. nov., is proposed. *Megasporoporiella pseudocavernulosa* is selected as the type species of *Megasporoporiella* because the previous type species *Megasporoporiella cavernulosa* was misidentified. *Polyporus megasporoporus* is the revised name for *Megasporoporiella lacerata*. In addition, a comparison of main characteristics and an identification key of *Megasporoporia* sensu lato are provided.

Keywords – morphology – phylogeny – polymerase – Polyporaceae – taxonomy

Introduction

Ryvarden et al. (1982) established *Megasporoporia* Ryvarden & J.E. Wright in 1982, and four species were addressed in the genus. Species of the genus are easily recognized in the field because of their light coloured, resupinate basidiocarps with big pores. Microscopically, the genus is characterized by a dimitic hyphal structure with generative hyphae bearing clamp connections, skeletal hyphae usually branched and dextrinoid, presence of cystidioles and dendrohyphidia in most species, and hyaline, thin-walled, big basidiospores (Ryvarden et al. 1982, Dai et al. 2004, Li & Cui 2013a, Yuan et al. 2017, Cui et al. 2019). Ecologically, the major members of the genus have a distribution in tropics, and usually grow on fallen trunks, branches and twigs which are not

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Corresponding Author: Yuan Yuan – e-mail – yuanyuan1018@bjfu.edu.cn,
Yu-Cheng Dai – e-mail – yuchengd@yahoo.com

much decayed. The species diversity was for long underestimated, and 14 species were described recently (Dai & Li 2002, Dai & Wu 2004, Cui & Dai 2007, Zhou & Dai 2008, Du & Cui 2009, Li & Cui 2013a, Yuan et al. 2017). In addition, the molecular phylogeny demonstrated that the genus is polyphyletic, and two genera – *Megasporia* B.K. Cui et al. and *Megasporoporiella* B.K. Cui et al. were derived from *Megasporoporia* (Li & Cui 2013a). So, the definition of *Megasporoporia* by Ryvarden et al. (1982) is in sensu lato, including three genera: *Megasporia*, *Megasporoporia* sensu stricto and *Megasporoporiella* (Li & Cui 2013a). These three genera are distinctly different in phylogeny, but it is very difficult to distinguish them morphologically because their major characteristics are overlapped.

Based on more samples of *Megasporoporia* sensu lato from Australia, China and Malaysia, and using combined 2-gene (ITS + nLSU) and 4-gene (ITS + nLSU + mtSSU + TEF) sequences datasets, further phylogenetic analyses on the genus are carried out. Four new species belonging to *Megasporia*, *Megasporoporia* sensu stricto and *Megasporoporiella* are detected, and their illustrated descriptions are provided. *Dichomitus hubeiensis* Hai J. Li & B.K. Cui is nested in the *Megasporoporiella* clade, and its morphology fits well *Megasporoporiella*, so the combination of *Megasporoporiella hubeiensis* is proposed.

Materials & Methods

Morphological studies

The studied specimens are deposited in the herbaria of the Institute of Microbiology, Beijing Forestry University (BJFC), the Institute of Applied Ecology, Chinese Academy of Sciences (IFP), Universidade Federal de Pernambuco (URM), and the private herbarium of Josef Vlasák (JV). Morphological descriptions are based on field notes and herbarium specimens. Microscopic analyses follow Li & Cui (2013a). In the description: CB = Cotton Blue, CB+ = cyanophilous in Cotton Blue, CB– = acyanophilous in Cotton Blue, IKI = Melzer's reagent, IKI– = neither amyloid nor dextrinoid, KOH = 2% potassium hydroxide, L = arithmetic average of all spore length, W = arithmetic average of all spore width, Q = L/W ratios, and n = number of spores/measured from given number of specimens (Yuan et al. 2017). Color terms are cited from Anonymous (1969) and Petersen (1996).

DNA extraction, PCR amplification and sequencing

The total genomic DNA was extracted from the dried specimens using CTAB rapid plant genome extraction kit (Aidlab Biotechnologies Co., Ltd, Beijing), according to the manufacturer's instructions with some modifications (Chen et al. 2016, Shen et al. 2019). The PCR primers for all genes are listed in Table 1. The PCR protocol for ITS, nLSU, mtSSU, and TEF were followed by Rehner & Buckley (2005) and Li & Cui (2013a), and some adjustments were made to suit different species of *Megasporoporia* sensu lato. The PCR products were purified and sequenced in Beijing Genomics Institute (China) with the same primers. All newly generated sequences were deposited at GenBank (http://www.ncbi.nlm.nih.gov/) and listed in Table 2.

Table 1 PCR primers used in this study

Gene	Primer	Primer sequences (5′-3′) [a]	Reference
ITS	ITS5	GGA AGT AAA AGT CGT AAC AAG G	White et al. 1990
	ITS4	TCC TCC GCT TAT TGA TAT GC	White et al. 1990
nLSU	LR0R	ACC CGC TGA ACT TAA GC	Vilgalys & Hester 1990
	LR7	TAC TAC CAC CAA GAT CT	Vilgalys & Hester 1990
mtSSU	MS1	CAG CAG TCA AGA ATA TTA GTC AAT G	White et al. 1990
	MS2	GCG GAT TAT CGA ATT AAA TAA C	White et al. 1990
TEF	983F	GCY CCY GGH CAY CGT GAY TTY AT	Rehner & Buckley 2005
	1567R	ACH GTR CCR ATA CCA CCR ATC TT	Rehner & Buckley 2005

[a] Degeneracr codes: S = G or C, W = A or T, R = A or G, Y = C or T, N = A or T or C or G, D = G or A or T, M = A or C.

Table 2 Information on samples of *Megasporoporia sensu lato* used in this study

Species	Sample no.	Geographic origin	GenBank accessions				References
			ITS	nLSU	mtSSU	TEF	
Cerioporus squamosus	Cui10394	China	KX851635	KX851688	KX851714	KX851789	Cui et al. 2019
C. squamosus	Cui10595	China	KU189778	KU189809	KU189960	KU189925	Zhou et al. 2016
Crassisporus macroporus	Cui14468	China	MK116486	MK116495	MK116505	MK122984	Cui et al. 2019
C. macroporus	Cui14465	China	MK116485	MK116494	MK116504	MK122983	Cui et al. 2019
C. imbricatus	Dai 10788	China	KC867350	KC867425	KX838374	–	Cui et al. 2019
C. imbricatus	Cui6556	China	KC867351	KC867426	–	–	Cui et al. 2019
Daedaleopsis confragosa	Cui6892	China	KU892428	KU892448	KX838381	KX838418	Cui et al. 2019
D. confragosa	Cui9756	China	KU892438	KU892451	–	–	Cui et al. 2019
D. hainanensis	Dai9268	China	KU892434	KU892458	KX838414	–	Li et al. 2016
D. hainanensis	Cui5178	China	KU892435	KU892462	KX838413	KX838441	Li et al. 2016
D. purpurea	Dai8060	Japan	KU892442	KU892475	KX838409	KX838438	Li et al. 2016
D. purpurea	Dai13583a	China	KX832054	KX832063	KX838412	KX838440	Cui et al. 2019
Datronia mollis	Dai11456	China	JX559253	JX559292	KX838388	KX838424	Li et al. 2014
D. mollis	Dai11253	China	JX559258	JX559289	KX838387	–	Li et al. 2014
D. subtropicus	Dai12883	China	KC415184	KC415191	KX838390	KX838427	Li et al. 2014
D. subtropica	Dai12885	China	KC415185	KC415192	KX838391	KX838428	Li et al. 2014
Dichomitus amazonicus	URM87859	Brazil	**MW989394**	**MW965595**	–	–	Present study
D. cylindrosporus	Ryvarden45186	Belize	–	JQ780439	–	–	
D. squalens	Cui9639	China	JQ780407	JQ780426	KX838404	KX838436	Li & Cui 2013a
D. squalens	Cui9725	China	JQ780408	JQ780427	KX838403	KX838435	Li & Cui 2013a
Echinochaete russiceps	Dai13868	China	KX832051	KX832060	KX838406	KX838437	Cui et al. 2019
E. russiceps	Dai13866	China	KX832050	KX832059	KX838405	–	Cui et al. 2019
Favolus acervatus	Cui11053	China	KU189774	KU189805	KU189956	KU189920	Zhou & Cui 2017
F. acervatus	Dai10749b	China	KX548953	KX548979	KX549018	KX549043	Zhou & Cui 2017
F. niveus	Cui11129	China	KX548955	KX548981	KX549019	KX549045	Zhou & Cui 2017
F. niveus	Dai13276	China	KX548956	KX548982	KX549020	KX549046	Zhou & Cui 2017

Table 2 Continued.

Species	Sample no.	Geographic origin	GenBank accessions				References
			ITS	nLSU	mtSSU	TEF	
F. pseudoemerici	Cui11079	China	KX548958	KX548984	KX549022	KX549048	Zhou & Cui 2017
F. pseudoemerici	Cui13757	China	KX548959	KX548985	KX549023	KX549049	Zhou & Cui 2017
H. glabra	Dai12993	China	KX900637	KX900683	KX900733	KX900823	Cui et al. 2019
H. glabra	Cui11367	China	KX900638	KX900684	KX900734	KX900824	Cui et al. 2019
Hornodermoporus latissimus	Cui6625	China	HQ876604	JF706340	KF051040	KF181134	Zhao & Cui 2012
H. latissimus	Dai12054	China	KX900639	KX900686	KF218297	KF286303	Cui et al. 2019
Megasporia bambusae	**Dai22106 (Holotype)**	**China**	**MW694884**	–	**MW694912**	**MZ618631**	Present study
M. bambusae	**Dai20064**	**China**	**MW694885**	**MW694928**	**MW694913**	**MZ618632**	Present study
M. cystidiolophora	Cui2642	China	JQ780390	JQ780432	–	–	Li & Cui 2013a
M. cystidiolophora	Cui2688 (Paratype)	China	JQ780389	JQ780431	–	–	Li & Cui 2013a
M. ellipsoidea	Dai19743	China	**MW694879**	**MW694923**	**MW694899**	**MZ669220**	Present study
M. ellipsoidea	Cui5222 (Holotype)	China	JQ314367	JQ314390	–	–	Li & Cui 2013a
M. fusiformis	**Dai18596 (Holotype)**	**Malaysia**	**MW694892**	**MW694935**	**MW694920**	**MZ618637**	Present study
M. fusiformis	**Dai18578**	**Malaysia**	**MW694893**	**MW694936**	**MW694921**	**MZ618638**	Present study
M. guangdongensis	Cui9130 (Holotype)	China	JQ314373	JQ780428	–	–	Li & Cui 2013a
M. guangdongensis	Cui13986	China	MG847208	MG847217	MG847229	MG867699	Cui et al. 2019
M. hengduanensis	Cui8076 (Holotype)	China	JQ780392	JQ780433	MG847252	KF286337	Li & Cui 2013a
M. hengduanensis	Cui8176	China	JQ314370	KX900697	KX900749	MG867700	Li & Cui 2013a
M. hexagonoides	Cui6592	China	JQ780402	JQ780438	–	–	Li & Cui 2013a
M. hexagonoides	Cui13853	China	**MW694880**	**MW694924**	**MW694900**	**MZ618625**	Present study
M. major	Cui10253	China	JQ314366	JQ780437	MK116502	–	Li & Cui 2013a
M. major	Yuan1183	China	JQ314365	–	–	–	Li & Cui 2013a
M. rimosa	Dai15357 (Holotype)	China	KY449436	KY449447	**MW694908**	–	Yuan et al. 2017
M. rimosa	Dai21997	China	**MW422262**	–	**MW694909**	–	Present study
M. tropica	Cui13740	China	KY449438	KY449449	**MW694910**	**MZ618629**	Yuan et al. 2017
M. tropica	Cui13660 (Holotype)	China	KY449437	KY449448	**MW694911**	**MZ618630**	Yuan et al. 2017
M. violacea	Cui6570 (Holotype)	China	JQ780393	–	–	–	Li & Cui 2013a

Table 2 Continued.

Species	Sample no.	Geographic origin	GenBank accessions				References
			ITS	nLSU	mtSSU	TEF	
M. violacea	Cui13845	China	MG847211	MG847220	MG847232	MG867703	Cui et al. 2019
M. violacea	Cui13838	China	MG847210	MG847219	MG847231	MG867702	Cui et al. 2019
M. yunnanensis	Cui12614A	China	KY449442	KY449453	**MW694922**	**MZ618628**	Yuan et al. 2017
M. yunnanensis	Dai13870 (Holotype)	China	KY449443	KY449454	**MW694907**	–	Yuan et al. 2017
Megasporoporia bannaensis	Dai12306 (Holotype)	China	JQ314362	JQ314379	–	–	Li & Cui 2013a
M. bannaensis	Dai13596	China	KX900653	KX900702	KX900754	KX900838	Cui et al. 2019
M. cavernulosa	JV0904/52J	USA	JF894107	–	–	–	
M. cavernulosa	JV0904/50J	USA	JF894105	–	–	–	
M. cavernulosa	JV0904/81	USA	**MW989395**	–	–	–	Present study
M. inflata	**Dai17882**	**Malaysia**	**MW694886**	**MW694929**	**MW694914**	–	Present study
M. inflata	**Dai17478 (Holotype)**	**Malaysia**	**MW694887**	**MW694930**	**MW694915**	**MZ618633**	Present study
M. mexicana	JV1806/4J	Honduras	**MW989396**	–	–	–	Present study
M. minor	Dai18322	Vietnam	**MW694881**	**MW694925**	**MW694901**	**MZ618624**	Present study
M. minor	Dai12170 (Holotype)	China	JQ314363	JQ314380	**MW694902**	KF494980	Li & Cui 2013a
M. minuta	Zhou120	China	JX163055	JX163056	KF218336	–	
M. minuta	Cui13945	China	**MW989397**	**MW965596**	–	–	Present study
M. setulosa	JV1008_51J	USA	JF894109	–	–	–	Li & Cui 2013a
M. setulosa	JV1008_102J	USA	JF894110	–	–	–	Li & Cui 2013a
Megasporoporiella australiae	**Dai18657 (Holotype)**	**Australia**	**MW694888**	**MW694931**	**MW694916**	**MZ618634**	Present study
M. australiae	**Dai18658**	**Australia**	**MW694889**	**MW694932**	**MW694917**	**MZ618635**	Present study
M. hubeiensis	Dai18102	China	**MW694890**	**MW694933**	**MW694918**	**MZ618636**	Present study
M. hubeiensis	Dai18103	China	**MW694891**	**MW694934**	**MW694919**	–	Present study
M. hubeiensis	Wei2045 (Holotype)	China	JQ780387	JQ780421	KX838396	–	Cui et al. 2019
M. pseudocavernulosa	Yuan1270 (Holotype)	China	JQ314360	JQ314394	–	–	Li & Cui 2013a
M. pseudocavernulosa	Dai19379	China	**MW694882**	–	**MW694904**	**MZ618626**	Present study
M. rhododendri	Dai4226 (Holotype)	China	JQ314356	JQ314392	**MW694905**	–	Li & Cui 2013a
M. rhododendri	Cui12432	China	**MW694883**	**MW694927**	**MW694906**	**MZ618627**	Present study

Table 2 Continued.

Species	Sample no.	Geographic origin	GenBank accessions				References
			ITS	nLSU	mtSSU	TEF	
M. subcavernulosa	Cui9252	China	JQ780378	JQ780416	MG847235	MG867706	Li & Cui 2013a
M. subcavernulosa	Cui14247	China	MG847213	MG847222	MG847234	MG867705	Cui et al. 2019
Neodatronia gaoligongensis	Cui8055	China	JX559269	JX559286	MG847236	KX900846	Li et al. 2014
N. gaoligongensis	Cui8186	China	JX559268	JX559285	MG847237	–	Li et al. 2014
Perenniporia martia	Cui4055	China	KX900641	KX900688	KX900737	–	Cui et al. 2019
P. martia	Cui7992	China	HQ876603	HQ654114	KF051041	KF181135	Zhao & Cui 2012
Polyporus arcularius	Cui10998	China	KX548973	KX548995	KX549029	KX549059	Zhou & Cui 2017
P. arcularius	Cui11398	China	KU189766	KU189797	KU189947	KU189911	Zhou et al. 2016
P. megasporoporus (*Megasporoporiella lacerata*)	Yuan3880 (Holotype)	China	JQ314377	JQ314395	–	KF286334	Li & Cui 2013a
P. megasporoporus (*Megasporoporiella lacerata*)	Yuan3874	China	–	**MW694926**	**MW694903**	–	Present study
P. tuberaster	Dai12462	China	KU507580	KU507582	KU507584	KU507590	Zhou et al. 2016
P. tuberaster	Dai11271	China	KU189769	KU189800	KU189950	KU189914	Zhou et al. 2016
P. varius	Cui12249	China	KU507581	KU507583	KU507585	KU507591	Zhou et al. 2016
P. varius	Dai13874	China	KU189777	KU189808	KU189958	KU189923	Zhou et al. 2016
Trametes hirsuta	RLG5133T	USA	JN164941	JN164801	–	JN164891	Li & Cui 2013a
T. ochracea	HHB13445sp	USA	JN164954	JN164812	–	JN164904	Li & Cui 2013a

New species and sequences are shown in **bold**

Phylogenetic analysis

Sequences generated in this study were aligned with additional sequences downloaded from GenBank (Table 2) using Clustal X (Thompson et al. 1997) and BioEdit (Hall 1999). The data matrixes were edited in Mesquite v3.04 software (Maddison & Maddison 2009). Sequence alignment was deposited at TreeBase (submission ID 28606 and 28610). Previous to phylogenetic analysis, ambiguous sequences at the start and the end were deleted and gaps were manually adjusted to optimize the alignment using BioEdit (Hall 1999). Two combined matrixes were reconstructed for phylogenetic analyses as a 2-gene dataset (ITS + nLSU) and a 4-gene dataset (ITS + nLSU + mtSSU + TEF). The phylogenetic analyses used in this study followed the approach of Zhu et al. (2019) and Sun et al. (2020). Maximum parsimony (MP), Maximum likelihood (ML) and Bayesian inference (BI) were employed to perform phylogenetic analysis.

Sequences of *Trametes hirsuta* (Wulfen) Lloyd and *T. ochracea* (Pers.) Gilb. & Ryvarden were used as outgroups to root trees. All characters were equally weighted and gaps were treated as missing data. Trees were inferred using heuristic search option with TBR branch swapping and 1,000 random sequence additions. Max-trees were set to 5,000, branches of zero length were collapsed and all parsimonious trees were saved. Clade robustness was assessed using bootstrap analysis with 1,000 replicates (Felsenstein 1985). Descriptive tree statistics tree length (TL),

consistency index (CI), retention index (RI), rescaled consistency index (RC), and homoplasy index (HI) were calculated for each maximum parsimonious tree generated (Farris 1989, Farris et al. 1994, Swofford 2002, Yuan et al. 2017).

Maximum likelihood (ML) research was conducted with RAxML-HPC v. 8.2.3 (Stamatakis 2014) involved 1000 ML searches under the GTRGAMMA model, and only the maximum likelihood best tree from all searches was kept. In addition, 1000 rapid bootstrap replicates were run with the GTRCAT model to assess ML bootstrap values (ML) of the nodes.

MrMODELTEST 2.3 (Posada & Crandall 1998, Nylander 2004) also was used to determine the best-fit evolution model for the combined dataset of ITS + nLSU and ITS + nLSU + mtSSU + TEF sequences for estimating Bayesian inference (BI). Bayesian inference was calculated with MrBayes 3.1.2 (Ronquist & Huelsenbeck 2003). Four Markov chains were run for 2 runs from random starting trees for 2 million generations until the split deviation frequency value < 0.01, and sampled every 100 generations. The first one-fourth sampled three were discarded as burn-in, while the remaining ones were used to calculate Bayesian posterior probabilities (BPP) of the clades.

Branches that received bootstrap support for Maximum parsimony (MP), Maximum Likelihood (ML), and Bayesian posterior probabilities (BPP) more than or equal to 50% (MP and ML) and 0.90 (BPP) were considered as significantly supported. (Figs 1-2). Phylogenetic trees were visualized with the program FigTree v. 1.4.3 (http://tree.bio.ed.ac.uk/software/figtree/).

Results

Phylogenetic analyses

The consequence of phylogeny includes the combined dataset of ITS and nLSU sequences from 96 fungal collections representing 49 species. The dataset has an aligned length of 2074 characters, of which 1148 characters are constant, and 591 are parsimony-informative. MP analysis yields a tree (TL = 2588, CI = 0.388, RI = 0.795, RC = 0.309, HI = 0.612). The best-fit evolutionary model is selected by maximum parsimony (MP) from the combined dataset of ITS + nLSU sequences. The MP and ML values (≥ 50%) and BPP (≥ 0.90) are shown at the nodes. So, the topology from the MP tree is presented along with statistical values from the MP/ML/BPP algorithms (Fig. 1).

The consequence of phylogeny includes the combined dataset of ITS, nLSU, mtSSU, and TEF sequences from 94 fungal collections representing 48 species. The dataset has an aligned length of 3363 characters, of which 2177 characters are constant, and 1093 are parsimony-informative. MP analysis yields a tree (TL = 4864, CI = 0.409, RI = 0.772, RC = 0.316, HI = 0.591). The best-fit evolutionary model is selected by maximum parsimony (MP) from the combined dataset of ITS + nLSU + mtSSU + TEF sequences. The MP and ML values (≥ 50%) and BPP (≥ 0.90) are shown at the nodes. So, the topology from the MP tree is presented along with statistical values from the MP/ML/BPP algorithms (Fig. 2).

Our phylogenies support previous conclusions (Li & Cui 2013a, Yuan et al. 2017), three clades are formed in the topology (Fig. 1): *Megasporia* (79% MP, 99% ML, 1.00 BPP), *Megasporoporia* sensu stricto (91% MP, 99% ML, 1.00 BPP) and *Megasporoporiella* (95% MP, 100% ML, 1.00 BPP).

The *Megasporia* clade includes twelve species: *M. bambusae* sp. nov., *M. cystidiolophora* B.K. Cui & Hai J. Li, *M. ellipsoidea* B.K. Cui & Hai J. Li, *M. fusiformis* sp. nov., *M. guangdongensis* B.K. Cui & Hai J. Li, *M. hengduanensis* B.K. Cui & Hai J. Li, *M. hexagonoides* B.K. Cui et al., *M. major* B.K. Cui & Hai J. Li, *M. rimosa* Y. Yuan et al., *M. tropica* Y. Yuan et al., *M. violacea* B.K. Cui et al. and *M. yunnanensis* Y. Yuan et al.

The *Megasporoporia* sensu stricto clade includes four species: *M. bannaensis* B.K. Cui & Hai J. Li, *M. inflata* sp. nov., *M. minor* B.K, Cui & Hai J. Li, and *M. setulosa* Rajchenb.

The *Megasporoporiella* clade includes five species: *M. australiae* sp. nov., *M. hubeiensis* comb. nov., *M. pseudocavernulosa* B.K. Cui & Hai J. Li, *M. rhododendri* B.K. Cui & Hai J. Li, and *M. subcavernulosa* B.K. Cui & Hai J. Li.

In addition, another clade (the unnamed clade of *Megasporoporia* sensu lato, Figs 1–2) includes three species: *Dichomitus amazonicus* Gomes-Silva et al., *Megasporoporia cavernulosa* (Berk.) Ryvarden and *M. mexicana* Ryvarden.

Four new species, *Megasporia bambusae*, *Megasporia fusiformis*, *Megasporoporia inflata*, *Megasporoporiella australiae*, and a new combination, *Megasporoporiella hubeiensis*, formed well-supported phylogenetic lineages (100% ML, 100% ML, 1.00 BPP) distinct from other known lineages (species) of *Megasporoporia* sensu lato (Fig. 2).

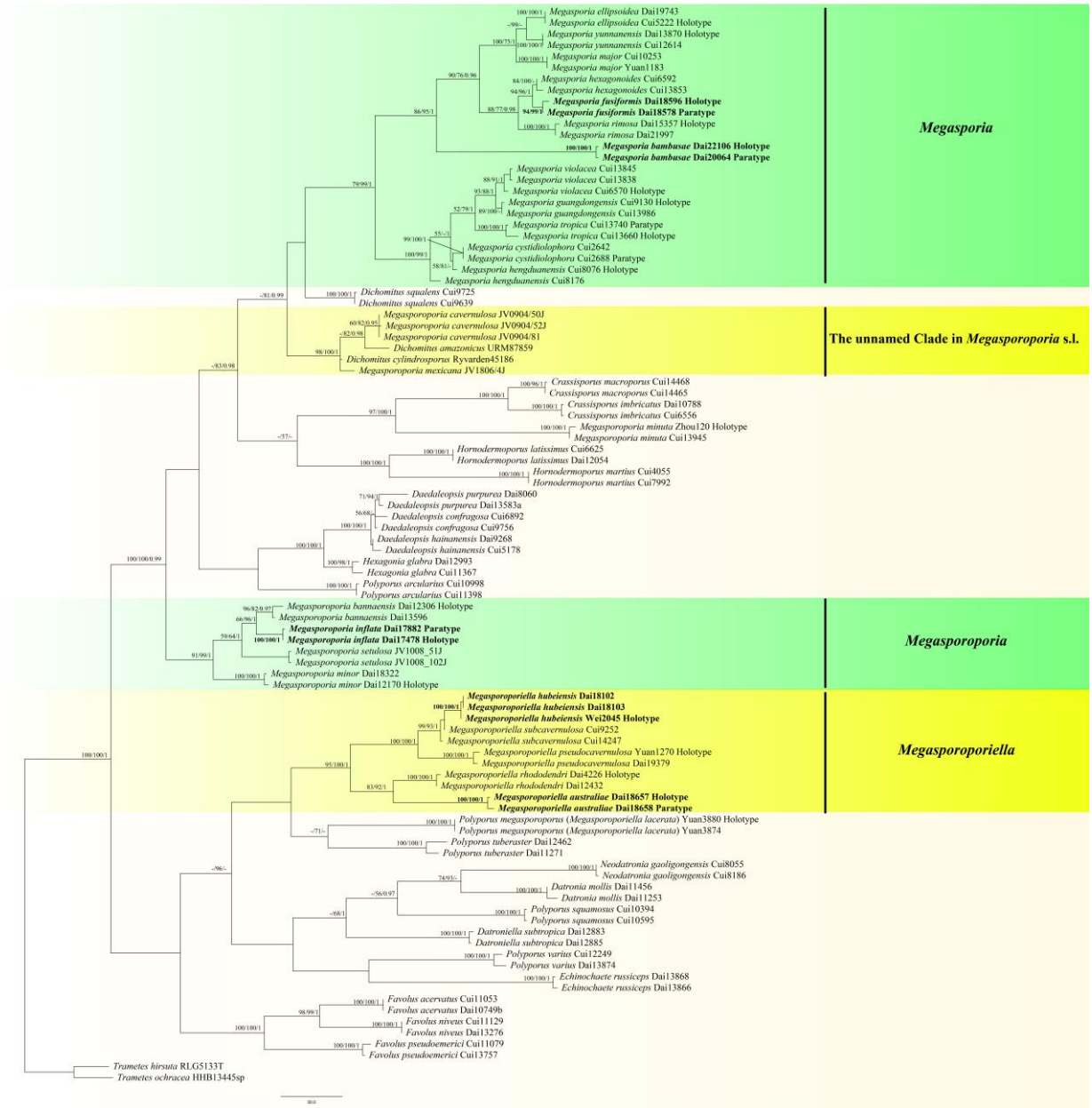

Figure 1 – Phylogeny of *Megasporoporia* sensu lato and related species generated by Maximum Parsimony based on combined ITS + nLSU sequences. Bootstrap supports for Maximum parsimony (MP), Maximum Likelihood (ML) and Bayesian posterior probabilities (BPP) were not lower than: 50% (MP and ML) and 0.90 (BPP) on the branches. The new species and combination were in **bold**.

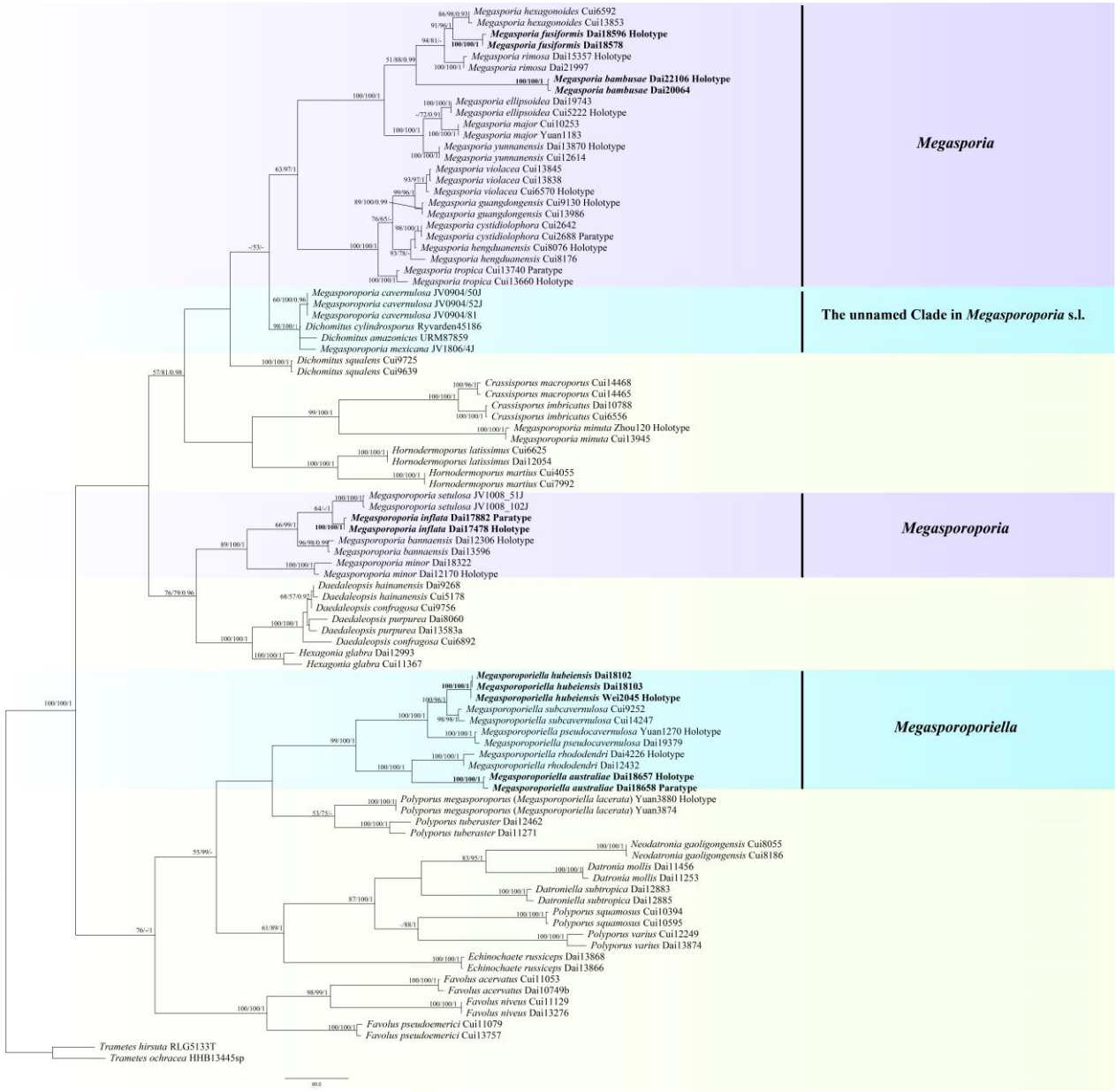

Figure 2 – Phylogeny of *Megasporoporia* sensu lato and related species generated by Maximum Parsimony based on combined ITS + nLSU + mtSSU + TEF sequences. Bootstrap supports for MP, ML and BPP were not lower than: 50 % (MP and ML) and 0.90 (BPP) on the branches. The new species and combination were in bold.

Taxonomy

Megasporia bambusae Y.C. Dai, Yuan Yuan & Ya. R. Wang sp. nov. Figs 3–4

Index Fungorum number: IF558811; Facesoffungi number: FoF10470

Etymology – *bambusae* (Lat.): referring to the species growing on bamboo.

Basidiocarps annual, resupinate, corky, without odor or taste when fresh, becoming hard corky upon drying, up to 2.7 cm long, 2.2 cm wide, and 0.2 mm thick at center; sterile margin distinct, white, up to 1 mm wide. Pore surface white to cream when fresh, cream to buff when dry; pores angular, 4–5 per mm; dissepiments thick, entire; subiculum pale buff, corky, up to 0.05 mm thick; tubes cream, paler than subiculum, corky, up to 0.15 mm long. *Hyphal system* dimitic; generative hyphae bearing clamp connections; skeletal hyphae weakly dextrinoid, CB+; tissues unchanged in KOH (not dissolved). *Subicular* generative hyphae hyaline, thin-walled, occasionally branched, 1.5–1.8 µm in diam; skeletal hyphae dominant, thick-walled with a narrow to wide

lumen, frequently branched, mostly flexuous, interwoven, 2.5–3 µm in diam. *Tramal* generative hyphae hyaline, thin-walled, occasionally branched, 1.5–1.8 µm in diam; skeletal hyphae dominant, thick-walled with a narrow to medium lumen, frequently branched, mostly flexuous, interwoven, 1.5–2 µm in diam. *Dendrohyphidia* present. *Hyphal pegs* absent. *Cystidia* absent; *cystidioles* present, subulate or ventricose, thin-walled, smooth, 14–41 × 4.8–14.8 µm. *Basidia* clavate to pear-shaped, usually constricted in middle, with four sterigmata and a basal clamp connection, 20–35.2 × 10–14.8 µm; *basidioles* in shape similar to basidia, but distinctly smaller. Small tetrahedric or polyhedric crystals frequently present among hymenium. *Basidiospores* ellipsoid, hyaline, fairly thick-walled, smooth, IKI–, CB–, (10.5–)11.8–14(–14.8) × (5.5–)5.8–6.8(–7.5) µm, L = 12.67 µm, W = 6.53 µm, Q = 1.91–1.96 (n = 90/3).

Known distribution – widespread in tropical and subtropical regions.

Materials examined – China, Hainan Prov., Haikou, Jinniuling Park, on dead bamboo, 18 Nov 2020, Y.C. Dai 22106 (BJFC035998, holotype), Y.C. Dai 22113 (BJFC036005); Guangxi Auto. Reg., Yulin, Guishan Forest Park, on dead bamboo, 3 Jul 2019, Y.C. Dai 20064 (BJFC031738).

Notes – *Megasporia bambusae* is found from the tropical zone of China. It is readily distinguished from other species in *Megasporoporia* sensu lato by its fairly thick-walled basidiospores and growing on bamboo, all other members of *Megasporoporia* sensu lato have thin-walled basidiospores and growing on dicotyledon. *Megasporia bambusae* resembles *Megasporia cystidiolophora*, *Megasporia guangdongensis* and *Megasporoporiella rhododendri* by the overlapped distribution and almost the same size of pore (3–5 per mm), but the latter three species have thin-walled basidiospores and lacks dendrohyphidia. Phylogenetically, *Megasporia bambusae* is related to *Megasporia ellipsoidea*, *M. yunnanensis*, *M. major*, *M. hexagonoides*, *M. fusiformis* and *M. rimosa* (Figs 1–2), but the latter six species have thin-walled basidiospores and growing on another angiosperm rather than bamboo (Ryvarden et al. 1982, Yuan et al. 2017).

Figure 3 – Basidiocarps of *Megasporia bambusae* (the holotype, Dai 22106).

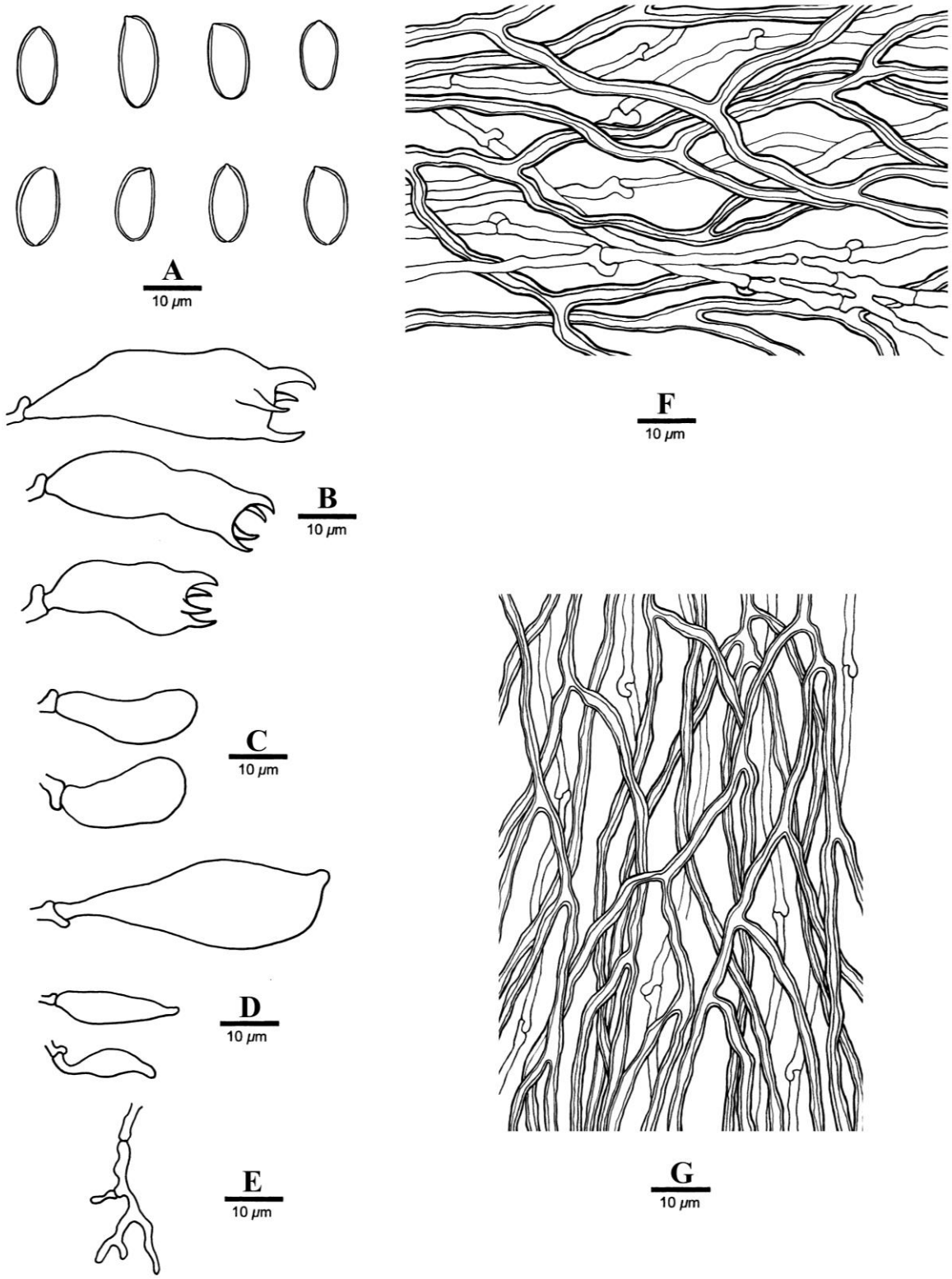

Figure 4 – Microscopic structures of *Megasporia bambusae* (drawn from the holotype, Dai 22106). A Basidiospores. B Basidia. C Basidioles. D Cystidioles. E Dendrohyphidia. E Hyphae from subiculum. G Hyphae from tubes.

Megasporia fusiformis Y.C. Dai, Yuan Yuan & Ya.R. Wang, sp. nov. Figs 5–6

Index Fungorum number: IF558812; Facesoffungi number: FoF10471

Etymology – *fusiformis* (Lat.): referring to the species producing fusiform basidiospores.

Basidiocarps annual, resupinate, corky, without odor or taste when fresh, becoming hard corky when dry, up to 11.6 cm long, 2.2 cm wide, and 0.4 mm thick at center; sterile margin distinct, white, up to 1 mm wide. Pore surface cream when fresh, cream to buff-yellow when dry; pores angular, 3.5–4 per mm; dissepiments thick, entire; subiculum cream, corky, up to 0.2 mm thick; tubes cream, paler than subiculum, corky, up to 0.2 mm long. *Hyphal system* dimitic; generative hyphae bearing clamp connections; skeletal hyphae sometime simple septate, IKI–, CB+; tissues unchanged in KOH (not dissolved). *Subicular* generative hyphae infrequent, hyaline, thin-walled, occasionally branched, 2–2.5 µm in diam; skeletal hyphae dominant, thick-walled with a narrow to wide lumen, frequently branched, occasionally simple septate, mostly flexuous, interwoven, 2.8–3 µm in diam. *Tramal* generative thin-walled, occasionally branched, 2–3 µm in diam; skeletal hyphae dominant, thick-walled with a narrow to medium lumen, frequently branched, mostly flexuous, interwoven, 2–3.5 µm in diam. *Dendrohyphidia* present. *Hyphal pegs* absent. *Cystidia* absent; *cystidioles* present, ventricose, thin-walled, smooth, 23.2–28.5 × 5.2–9.5 µm. *Basidia* clavate, usually constricted in middle, with four sterigmata and a basal clamp connection, 25.2–38.2 × 8.2–11.5 µm; *basidioles* in shape similar to basidia, but distinctly smaller. Small tetrahedric or polyhedric crystals frequently present among hymenium. *Basidiospores* fusiform, hyaline, thin-walled, smooth, sometimes with one or two guttules, IKI–, CB–, (14.1–)15–19.8(–20.2) × (4–)4.2–6.8(–7) µm, L = 17.59 µm, W = 5.12 µm, Q = 3.24–3.68 (n = 60/2).

Known distribution – widespread in subtropical regions.

Materials examined – Malaysia. Selangor, Kota Damansara, Community Forest Reserve, on rotten angiosperm wood, 16 April 2018, Y.C. Dai 18596 (BJFC026884, holotype), Y.C. Dai 18578 (BJFC026866).

Figure 5 – Basidiocarps of *Megasporia fusiformis* (the holotype, Dai 18596).

Notes – Morphologically, *Megasporia rimosa* is similar to *M. fusiformis* by white to cream pore surface and extremely thin basidiocarp (less than 0.5 mm thick), but *M. rimosa* is different from *M. fusiformis* by its dextrinoid skeletal hyphae, cylindrical basidiospores and skeletal hyphae

without any septa (Yuan et al. 2017). Phylogenetically *M. fusiformis* is closer to *M. hexagonoides* and *M. rimosa* (Figs 1–2), but *M. hexagonoides* differs from *M. fusiformis* by the bigger pores (0.5–1 per mm vs. 3.5–4 per mm), the absence of dendrohyphidia, and skeletal hyphae without any septa (Dai & Cui 2008).

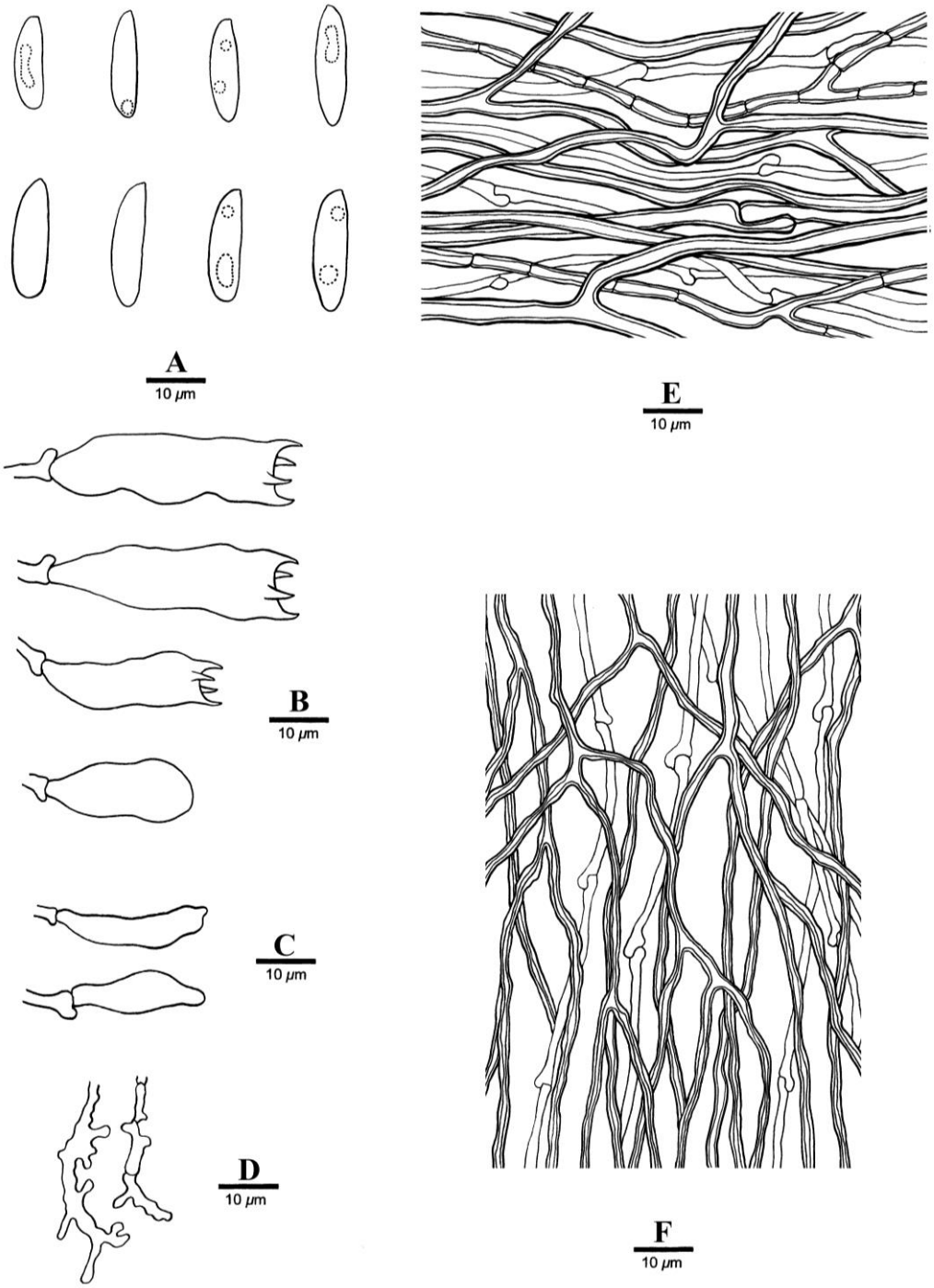

Figure 6 – Microscopic structures of *Megasporia fusiformis* (drawn from the holotype, Dai 18596). A Basidiospores. B Basidia and basidioles. C Cystidioles. D Dendrohyphidia. E Hyphae from subiculum. F Hyphae from tubes.

Megasporoporia inflata Y.C. Dai, Yuan Yuan & Ya.R. Wang, sp. nov. Figs 7–8

Index Fungorum number: IF558813; Facesoffungi number: FoF10472

Etymology – *inflata* (Lat.): referring to the skeletal hyphae of the species become swollen in KOH.

Basidiocarps annual, resupinate, cushion-shaped, corky, without odor or taste when fresh, becoming hard corky upon drying, up to 9.5 cm long, 2 cm wide, and 3.5 mm thick at center; sterile margin thinning out, cream to clay buff, up to 1 mm wide. Pore surface cream to buff when fresh, buff when dry; pores round to angular, 2.5–3 per mm; dissepiments thick, entire; subiculum buff, corky, up to 1 mm thick; tubes pale buff, corky, up to 2.5 mm long. *Hyphal system* dimitic; generative hyphae bearing clamp connections; skeletal hyphae strongly dextrinoid, CB+; tissues more or less dissolved and skeletal hyphae become strongly swollen in KOH. *Subicular* generative hyphae infrequent, hyaline, thin-walled, moderately branched, mostly flexuous, 2–2.5 µm in diam; skeletal hyphae dominant, thick-walled with a narrow to medium lumen, moderately branched, mostly flexuous, interwoven, 2–3.5 µm in diam. *Tramal* generative hyaline, thin-walled, moderately branched, 2–2.5 µm in diam; skeletal hyphae dominant, thick-walled with a narrow lumen to subsolid, moderately branched, mostly flexuous, interwoven, 2.5–3 µm in diam. *Dendrohyphidia* absent. *Hyphal pegs* absent. *Cystidia* and *cystidioles* absent. *Basidia* broadly barrel-shaped to pyriform, with four sterigmata and a basal clamp connection, 14.2–22.5 × 7–8.9 µm; *basidioles* dominant in hymenium, in shape similar to basidia, but smaller. Big rhomboid or polyhedric crystals frequently present among hymenium. *Basidiospores* cylindrical, hyaline, thin-walled, smooth, with one big guttule, IKI–, CB–, (9.8–)10–11.8(–12) × 3.5–4.2 µm, L = 10.38 µm, W = 3.86 µm, Q = 2.69–2.98 (n = 60/2).

Known distribution – widespread in tropical and subtropical regions.

Materials examined – Malaysia. Selangor, Kota Damansara Community Forest Reserve, on fallen angiosperm twig, 19 June 2017, Y.C. Dai 17478 (BJFC025011, holotype). Singapore. Bukit, Timah Natural Reserve, on fallen angiosperm branch, 20 July 2017, Y.C. Dai 17882 (BJFC025414).

Figure 7 – Basidiocarps of *Megasporoporia inflata* (the holotype, Dai 17478).

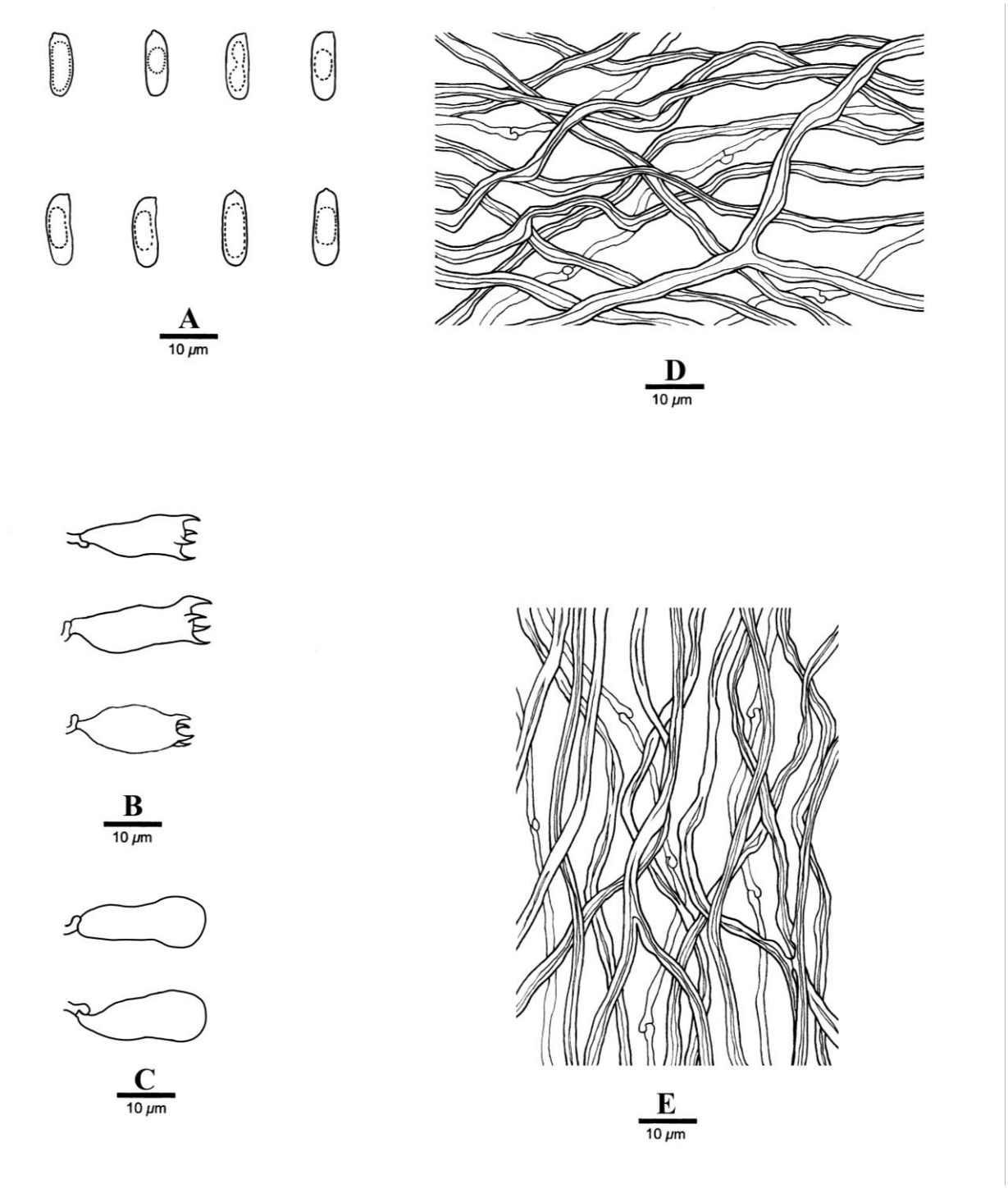

Figure 8 – Microscopic structures of *Megasporoporia inflata* (drawn from the holotype, Dai 17478). A Basidiospores. B Basidia. C Basidioles. D Hyphae from subiculum. E Hyphae from tubes.

Notes – The skeletal hyphae of *Megasporoporia inflata* strongly swell in KOH, and this feature is unique in *Megasporoporia* sensu lato. In addition, *Megasporoporia inflata* lacks hyphal pegs, cystidioles and dendrohyphidia. So, the above characteristics stand out the new species from other members of *Megasporoporia* sensu lato. *Megasporia tropica* is similar to *Megasporoporia inflata* by occurring in tropical China, almost the same size of pores, strongly dextrinoid skeletal hyphae, the absence of hyphal pegs and dendrohyphidia, but the former has cystidioles and bigger basidiospores (14.7–18.8 × 5–6.5 µm vs. 10–11.8 × 3.5–4.2 µm), and its skeletal hyphae are unchanged in KOH (Yuan et al. 2017). Phylogenetically, *M. inflata* is closely related to

M. bannaensis (Figs 1–2), but the latter species has bigger pores (1–2 per mm) and their skeletal hyphae unchanged in KOH (Li & Cui 2013a).

Megasporoporiella australiae Y.C. Dai, Yuan Yuan & Ya.R. Wang, sp. nov. Figs 9–10

Index Fungorum number: IF558814; Facesoffungi number: FoF10473

Etymology – *australiae* (Lat.): referring to the species found from Australia.

Basidiocarps annual, resupinate, corky, without odor or taste when fresh, becoming hard corky and cracked upon drying, up to 5.4 cm long, 2 cm wide, and 0.4 mm thick at center; sterile margin distinct, white to cream, cottony, up to 3 mm wide. Pore surface white to cream when fresh, vinaceous buff to fulvous when dry; pores round to angular, 3–4 per mm; dissepiments thick, entire; subiculum pale buff, corky, up to 0.2 mm thick; tubes cream, paler than subiculum, corky, up to 0.2 mm long. *Hyphal system* dimitic; generative hyphae bearing clamp connections; skeletal hyphae IKI–, CB+; tissues unchanged in KOH (not dissolved). *Subicular* generative hyphae infrequent, hyaline, thin-walled, occasionally branched, 2–3 µm in diam; skeletal hyphae dominant, thick-walled with a narrow to medium lumen, frequently branched, strongly flexuous, strongly interwoven, 2–3.5 µm in diam. *Tramal* generative hyphae hyaline, thin-walled, occasionally branched, 2–2.5 µm in diam; skeletal hyphae dominant, thick-walled with a narrow lumen, moderately branched, strongly flexuous, strongly interwoven, 2–3 µm in diam. *Dendrohyphidia* absent. *Hyphal pegs* absent. *Cystidia* absent; *cystidioles* present, tubular to fusoid, thin-walled, smooth, 29–41 × 2.5–11.5 µm. *Basidia* pear-shaped, with four sterigmata and a basal clamp connection, 35–38 × 9.5–12 µm; *Basidioles* in shape similar to basidia, but smaller, some with a few guttules. All the hymenial cells (cystidioles, basidia and basidioles) with abundant oily substance. Small tetrahedric or polyhedric crystals frequently present among hymenium. *Basidiospores* cylindrical, hyaline, thin-walled, smooth, sometimes with one big guttule, IKI–, CB–, (11.5–)11.8–15(–16.5) × (3.5–)4–6(–6.5) µm, L = 13.4 µm, W = 4.98 µm, Q = 2.52–2.64 (n = 60/2).

Known distribution – widespread in temperate region.

Figure 9 – Basidiocarp of *Megasporoporiella australiae* (the paratype, Dai 18658).

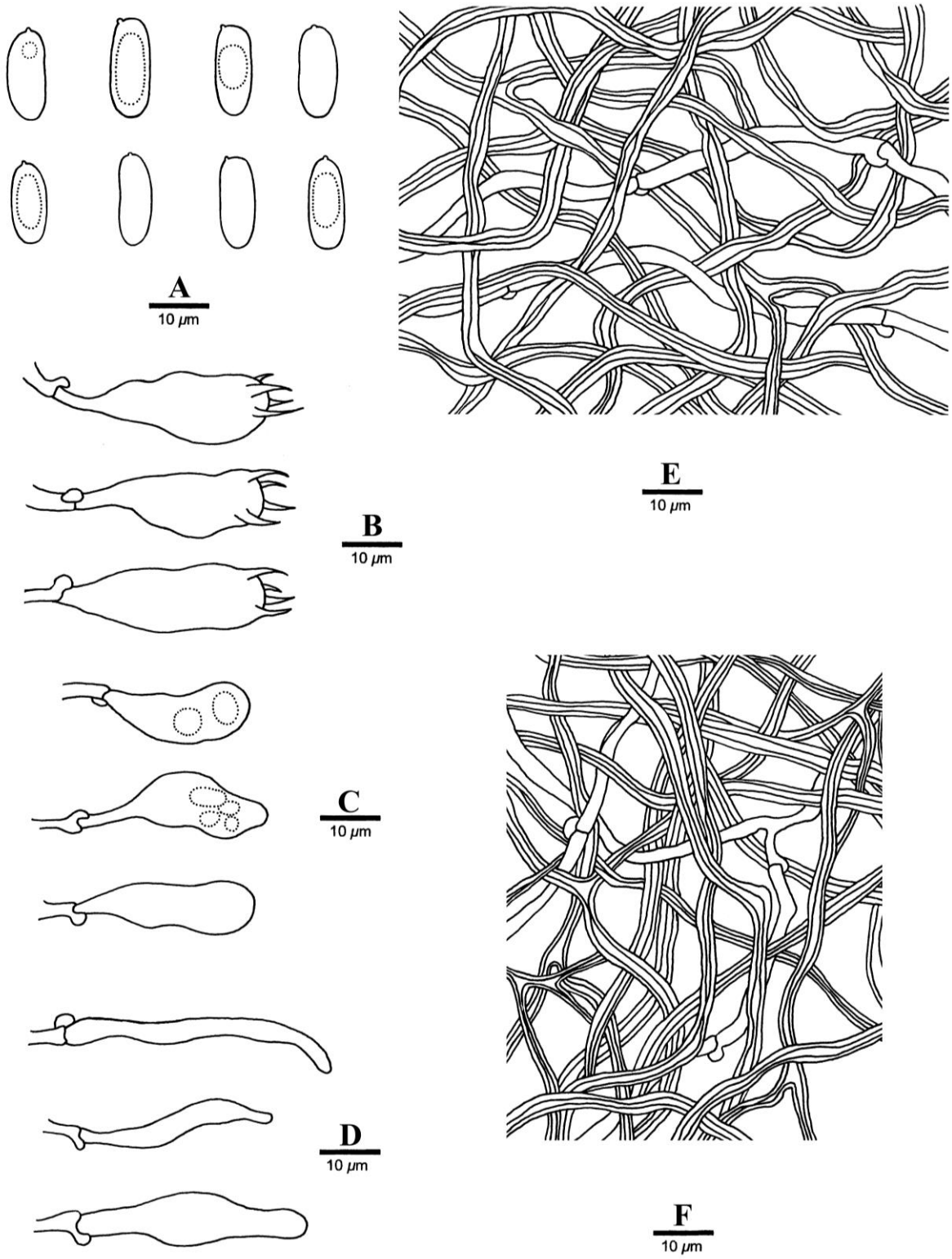

Figure 10 – Microscopic structures of *Megasporoporiella australiae* (drawn from the holotype, Dai 18658). A Basidiospores. B Basidia. C Basidioles. D Cystidioles. E Hyphae from subiculum. F Hyphae from tubes.

Materials examined – Australia. Melbourne. Dandenong Ranges Botanic Garden, on dead tree of *Rhododendron*, 12 May 2018, Y.C. Dai 18657 (BJFC27125, holotype), Y.C. Dai 18658 (BJFC27126).

Notes – Morphologically, *Megasporoporiella australiae* resembles *Megasporia cystidiolophora*, *Megasporia hengduanensis* and *Megasporoporia cavernulosa* by sharing almost the same size of pores and basidiospores, but the latter three species can be readily distinguished from *Megasporoporiella australiae* by their dextrinoid skeletal hyphae (Ryvarden et al. 1982, Cui & Dai 2007, Li & Cui 2013a). Phylogenetically, *M. australiae* is closely related to *M. rhododendri* (Figs 1, 2), but *M. rhododendri* can be distinguished from *M. australiae* by dextrinoid skeletal hyphae and ellipsoid basidiospores measuring as 11–14 × 6.5–8 µm (Dai et al. 2004).

Megasporoporiella hubeiensis (Hai J. Li & B.K. Cui) Y.C. Dai, Yuan Yuan & Ya. R. Wang, comb. nov. Figs 11–12

Index Fungorum number: IF558815; Facesoffungi number: FoF10468

Basidiocarps biennial, resupinate, cushion-shaped, corky, without odor or taste when fresh, becoming hard corky upon drying, up to 2.4 cm long, 12 cm wide, and 2.4 mm thick at center; sterile margin thinning out, very narrow to almost lacking. Pore surface white to cream when fresh, vinaceous buff to fulvous when dry; pores round to angular, 1–2 per mm; dissepiments thick, entire; subiculum pale buff, corky, up to 0.6 mm thick; tubes concolorous with the pore surface, corky, up to 1.8 mm long. *Hyphal system* dimitic; generative hyphae bearing clamp connections; skeletal hyphae IKI–, CB+; tissues unchanged in KOH. (not dissolved). *Subicular* generative hyphae hyaline, thin-walled, occasionally branched, 2.5–2.8 µm in diam; skeletal hyphae dominant, thick-walled with a narrow to medium lumen, frequently branched, mostly flexuous, interwoven, 2.8–3 µm in diam. *Tramal* generative hyphae hyaline, thin-walled, occasionally branched, 1.8–2.5 µm in diam; skeletal hyphae dominant, thick-walled with a narrow lumen, frequently branched, mostly flexuous, interwoven, 2.5–3 µm in diam. *Dendrohyphidia* present. *Hyphal pegs* absent. *Cystidia* absent; *cystidioles* present, subulate or ventricose, thin-walled, smooth, 18.2–37.2 × 6.3–10.5 µm. *Basidia* clavate, with four sterigmata and a basal clamp connection, 26.8–34.2 × 7.8–11.2 µm; *basidioles* in shape similar to basidia, but smaller. Small tetrahedric or polyhedric crystals frequently present among hymenium. *Basidiospores* cylindrical, hyaline, thin-walled, smooth, usually with one big guttule, IKI–, CB–, (11–)12–14.3(–14.8) × (4–)4.5–5.7(–6.5) µm, L = 13.26 µm, W = 5.12 µm, Q = 2.37–2.55 (n = 60/2).

Figure 11 – Basidiocarps of *Megasporoporiella hubeiensis* (Dai 18102).

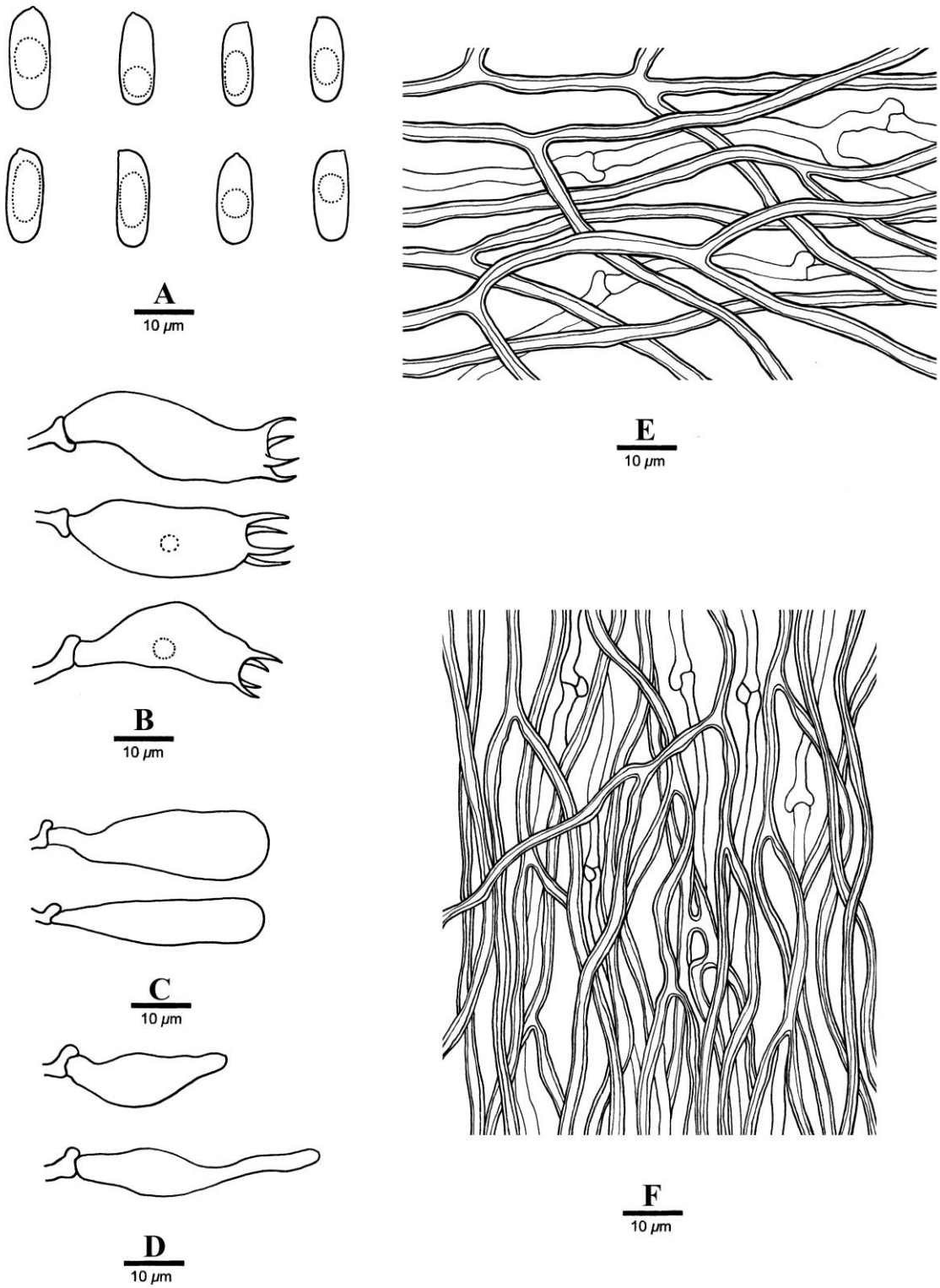

Figure 12 – Microscopic structures of *Megasporoporiella hubeiensis* (drawn from Dai 18103). A Basidiospores. B Basidia. C Basidioles. D Cystidioles. E Hyphae from subiculum. F Hyphae from tube.

≡ *Dichomitus hubeiensis* Hai J. Li & B.K. Cui, Nordic Journal Botany 31: 118 (2013).

Known distribution – widespread in temperate and subtropical regions.

Materials examined – China, Hebei, Zhuolu County, Xiaowutai Natural Reserve, Shanjiankou, on dead branch of *Salix*, 10 September 2017, Y.C. Dai 18102 (BJFC025632), Y.C.

Dai 18103 (BJFC025633); Hubei, Fang County, Shennongjia Natural Reserve, on fallen angiosperm branch, 22 September 2004, Wei 2045 (BJFC012314, holotype).

Notes – *Megasporoporiella hubeiensis* was originally described as *Dichomitus hubeiensis* Hai J. Li & B.K. Cui from subtropical China (Li & Cui 2013b). But our phylogenies (Figs 1–2) show the species nested in *Megasporoporiella* clade with a robust support (100% MP, 100% ML, 1.00 BPP). So, the above combination is proposed.

In addition, Li & Cui (2013a) defined *Megasporoporiella cavernulosa* as type species of the genus (Li & Cui 2013a), and they used the specimen Wu 9508-328 (AY333800) for phylogeny, however, the specimen represents *Megasporoporiella subcavernulosa* rather than *Megasporoporia cavernulosa* (Dai & Wu 2004). *Megasporoporia cavernulosa* was originally described from America, specimens JV0904/50J, JV0904/52J and JV0904/81 collected from America are analyzed, and they are distantly related to *Megasporoporiella* (Fig. 1). In the present study we select *Megasporoporiella pseudocavernulosa* as the type species of *Megasporoporiella*.

For conveniences for the readers, a comparison of main characteristics (Table 3) and an identification key of *Megasporia*, *Megasporoporia* sensu stricto and *Megasporoporiella* are provided as following.

Table 3 The main characteristics of species of *Megasporia*, *Megasporoporia* sensu stricto and *Megasporoporiella*

Species	Pores (per mm)	Dextrinoid of skeletals	KOH reaction of skeletals	Cystidioles	Gloeocystidioles	Basidia (µm)	Shape of basidiospores	Basidiospores (µm)	Dendrohyphidia	Hyphal pegs	References
Megasporia bambusae	4–5	[+]	[–]	+	–	20–35 × 10–15	ellipsoid	11.8–14 × 5.8–6.8	+	–	Present study
M. cystidiolophora	3–5	[++]	[–]	+	–	18–25 × 7–10	cylindrical	11.7–14.9 × 4.1–5.6	–	–	Cui & Dai (2007)
M. ellipsoidea	1–1.5	[+]	[–]	+	+	23–40 × 9–15	ellipsoid	12–15 × 6–8.2	+	+	Du & Cui (2009)
M. fusiformis	3.5–4	[–]	[–]	+	–	25–38 × 8–12	fusiform	15–19.8 × 4.2–6.8	+	–	Present study
M. guangdongensis	4–5	[+++]	[–]	+	–	20–28 × 5–8	cylindrical	11–14.9 × 3.4–4.5	–	–	Li & Cui (2013a)
M. hengduanensis	2–3	[++]	[–]	+	–	30–37 × 9–12	cylindrical	11–15 × 4.2–5.2	–	–	Li & Cui (2013a)
M. hexagonoides	0.5–1	[+]	[–]	+	–	38–40 × 8–12	allantoid	17–21 × 5–6	–	–	Dai & Cui (2008)
M. major	1–1.5	[+++]	[+]	+	–	24–38 × 12–16	cylindrical	15.2–20 × 5.5–7.1	+	+	Dai & Li (2002)
M. rimosa	3–4	[+]	[–]	+	–	20–28 × 5–8	cylindrical	16.8–20.2 × 4.3–5.5	+	–	Yuan et al. (2017)
M. tropica	2–3	[+++]	[–]	+	–	20–25 × 7–10	cylindrical	14.7–18.8 × 5–6.5	–	–	Yuan et al. (2017)

Table 3 Continued.

Species	Pores (per mm)	Dextrinoid of skeletals	KOH reaction of skeletals	Cystidioles	Gloeocystidioles	Basidia (µm)	Shape of basidiospores	Basidiospores (µm)	Dendrohyphidia	Hyphal pegs	References
M. violacea	5–7	[+++]	[–]	+	–	13–19 × 5–10	cylindrical	11–14.9 × 3.2–5	+	–	Du & Cui (2009)
M. yunnanensis	2–3	[+]	[–]	+	–	30–35 × 9–11	cylindrical	15–20.8 × 5.5–7.1	+	–	Yuan et al. (2017)
Megasporoporia bannaensis	1–2	[+++]	[–]	+	–	20–32 × 8–10	cylindrical	10–14 × 3.9–4.6	–	+	Li & Cui (2013a)
M. inflata	2.5–3	[+++]	[+++]	–	–	14–23 × 7–9	cylindrical	10–11.8 × 3.5–4.2	–	–	Present study
M. minor	6–7	[+++]	[–]	+	–	18–26 × 6–8	ellipsoid	6–7.8 × 2.6–4	–	+	Li & Cui (2013a)
M. setulosa	1–2	[+++]	[–]	–	–	18–29 × 7–10	cylindrical	10–14 × 4.2–5.7	–	+	Ryvarden et al. (1982)
Megasporoporiella australiae	3–4	[–]	[–]	+	+	35–38 × 10–12	cylindrical	11.8–15 × 4–6	–	–	Present study
M. hubeiensis	1–2	[–]	[–]	+	–	27–34 × 8–11	cylindrical	12–14.3 × 4.5–5.7	+	–	Li & Cui (2013a), Present study
M. pseudocavernulosa	1.5–2.5	[++]	[–]	+	–	34–52 × 10–12	allantoid	10.8–14 × 5.3–6.5	–	+	Li & Cui (2013a)
M. rhododendri	4–5	[++]	[–]	+	–	23–40 × 9–14	ellipsoid	11–14 × 6.5–8	–	–	Dai et al. (2004)
M. subcavernulosa	2–4	[+]	[–]	–	–	18–24 × 8–11	cylindrical	9–12.1 × 4.2–5.2	+	+	Dai & Wu (2004)

Abbreviations: [+] = weakly dextrinoid / slightly swollen; [++] = moderately dextrinoid; [+++] = strongly dextrinoid / distinctly swollen; [–] = indextrinoid/not swollen; + = present; – = absent.

Key to known species of *Megasporia, Megasporoporia* sensu stricto and *Megasporoporiella*

1. Pores < 1 per mm ……..*Megasporia hexagonoides*
1. Pores > 1 per mm ……..2
2. Pores 5–7 per mm ……..3
2. Pores 1–5 per mm ……..4
3. Pore surface violet to greyish violet ……..*Megasporia violacea*
3. Pore surface cream to buff ……*Megasporoporia minor*
4. Basidiospores ellipsoid ……..5

4. Basidiospores cylindrical, allantoid or fusiform ……7
5. Pores 1–2 per mm ……...*Megasporia ellipsoidea*
5. Pores 4–5 per mm ……...6
6. Dendrohyphidia present; on bamboo ……...*Megasporia bambusae*
6. Dendrohyphidia absent; on *Rhododendron* ……...*Megasporoporiella rhododendri*
7. Basidiospores fusiform ……*Megasporia fusiformis*
7. Basidiospores cylindrical or allantoid ……8
8. Hyphal pegs present ……9
8. Hyphal pegs absent ……...13
9. Skeletal hyphae strongly dextrinoid ……..10
9. Skeletal hyphae weakly to moderately dextrinoid ……12
10. Basidiospores > 15 µm long ……*Megasporia major*
10. Basidiospores < 15 µm long ……...11
11. Cystidioles present; Asian species ……*Megasporoporia bannaensis*
11. Cystidioles absent; African and American species ……*Megasporoporia setulosa*
12. Dendrohyphidia present, cystidioles absent ……...*Megasporoporiella subcavernulosa*
12. Dendrohyphidia absent, cystidioles present ……*Megasporoporiella pseudocavernulosa*
13. Skeletal hyphae strongly dextrinoid ……14
13. Skeletal hyphae indextrinoid, weakly to moderately dextrinoid ……16
14. Pores 4–5 per mm ……*Megasporia guangdongensis*
14. Pores 2–3 per mm ……...15
15. Skeletal hyphae distinctly swollen in KOH ……..*Megasporoporia inflata*
15. Skeletal hyphae unchanged in KOH ……...*Megasporia tropica*
16. Dendrohyphidia present ……..17
16. Dendrohyphidia absent ……...19
17. Basidiospores < 15 µm long ……...*Megasporoporiella hubeiensis*
17. Basidiospores > 15 µm long ……...18
18. Basidiocarps cracked when dry ……...*Megasporia rimosa*
18. Basidiocarps uncracked when dry ……..*Megasporia yunnanensis*
19. Gloeocystidioles present, skeletal hyphae indextrinoid ……..*Megasporoporiella australiae*
19. Gloeocystidioles absent, skeletal hyphae moderately dextrinoid ……...20
20. Pore surface cream to buff, pores 2–3 per mm ……...*Megasporia hengduanensis*
20. Pore surface pale pinkish brown to salmon, pores 3–5 per mm ……*Megasporia cystidiolophora*

Discussion

Dichomitus D.A. Reid resembles *Megasporoporia* sensu lato by light colored and resupinate basidiocarps, a dimitic hyphal system with generative hyphae bearing clamp connections, cyanophilous skeletal hyphae, and hyaline, thin-walled basidiospores; that is why Masuka & Ryvarden (1999), Robledo & Rajchenberg (2007) merged them, but without molecular analysis. Type species of *Dichomitus*, *D. squalens*, is included in our phylogeny and it is distantly related to *Megasporia*, *Megasporoporia* sensu stricto, *Megasporoporiella*, and the unnamed clade of *Megasporoporia* sensu lato. (Figs 1–2). Morphologically, *Dichomitus* lacks hyphal pegs and dendrohyphidia, its skeletal hyphae are indextrinoid and dendritically branched in which they are very similar to *Polyporus* sensu stricto; while the most species of *Megasporia*, *Megasporoporia* sensu stricto and *Megasporoporiella* have hyphal pegs and dendrohyphidia, and their skeletal hyphae are dextrinoid in most species. So, we treat *Dichomitus*, *Megasporia*, *Megasporoporia* sensu stricto and *Megasporoporiella* as independent genera.

As mentioned in the introduction, *Megasporia*, *Megasporoporia* sensu stricto and *Megasporoporiella* are distinct in phylogeny, but it is impossible to separate each other by morphology. So, we treat our new species and the combination in *Megasporia*, *Megasporoporia* sensu stricto and *Megasporoporiella*, but for the discussion of their similar species, all the members of *Megasporoporia* sensu lato are included. In our phylogeny (Figs 1, 2), *Dichomitus amazonicus*,

Megasporoporia cavernulosa and *M. mexicana* are nested in three lineages and formed a clade. *Dichomitus amazonicus* was described from neotropics (Gomes-Silva et al. 2012), corresponding specimen URM 87859 is examined, and the specimen has strongly dextrinoid skeletal hyphae and hyphal pegs (not mentioned in the original description). *Megasporoporia cavernulosa* was originally described from Brazil (Ryvarden 1984), and it has dendrohyphidia and dextrinoid skeletal hyphae. *Megasporoporia mexicana* was originally described from Mexico (Ryvarden et al. 1982), and it was combined in *Dichomitus* without DNA data (Ryvarden 2007). A specimen of *Megasporoporia mexicana* from Honduras (JV1806/4J, sequenced) is studied, and it has hyphal pegs and dextrinoid skeletal hyphae. So, all these three species have dextrinoid skeletal hyphae which are different from *D. squalens* (the type species of *Dichomitus*). Phylogenetically, these three species are distantly related to *Dichomitus*, *Megasporia*, *Megasporoporia* sensu stricto and *Megasporoporiella*. A new genus might be set up to accommodate them, for the time being, we treat them as present names because more materials need to be examined and phylogenetically analyzed.

Megasporoporia minuta Y.C. Dai & X.S. Zhou was described from China without phylogenetic analysis (Zhou & Dai 2008), but our phylogenies show its type is distantly related to *Megasporoporia* sensu lato (Figs 1–2). Its type (Zhou 120) and another specimen Cui 13945 are studied, they have perennial basidiocarps, small pores (6–8 per mm), indextrinoid skeletal hyphae, narrowly ovoid basidiospores, lack hyphal pegs, dendrohyphidia and tetrahedric or polyhedric crystals. These characteristics do not fit the definition of *Megasporoporia* sensu lato. So, the species is excluded from *Megasporia*, *Megasporoporia* sensu stricto and *Megasporoporiella*. Moreover, *Megasporoporiella lacerata* B.K. Cui & Hai J. Li was described from China based on morphology and a single gene phylogeny (Li & Cui 2013a). Although its morphological characteristics are similar to that of *Megasporoporia* sensu lato. However, our phylogenies based on 2-gene and 4-gene sequences datasets show that *M. lacerata* is closer to *Polyporus tuberaster* (type species of *Polyporus* sensu stricto, Figs 1, 2). So, the species should be combined into *Polyporus*. However, *Polyporus laceratus* Berk. (Ann. nat. Hist., Mag. Zool. Bot. Geol. 3: 392, 1839) is existed, and the species is re-named as following.

Polyporus megasporoporus Y.C. Dai, Yuan Yuan & Ya.R. Wang, nomen. nov.

Index Fungorum number: IF558816; Facesoffungi number: FoF10469

Etymology – *megasporoporus* (Lat.): referring to the species similar with *Megasporopoia*.

As given by Li and Cui 2013: 377.

= *Megasporoporiella lacerata* B.K. Cui & Hai J. Li, Mycologia 105(2): 377 (2013).

Material examined – China. Yunnan Province. Baoshan County, Gaoligong Mountains, Baihualing Nature Reserve, on fallen angiosperm branch, 09 Sep 2007, Yuan 3880 (holotype in IFP, isotype in BJFC).

Besides the species in our phylogeny and the above discussion, the taxa *Dichomitus affixus* (Corner) T. Hatt. (Hattori 2002), *D. africanus* Ryvarden (Ryvarden 2019), *D. amygdalinus* (Berk & Ravenel) Ryvarden (Ryvarden 1977), *D. anoectoporus* (Berk & M.A. Curtis) Ryvarden (Ryvarden 1984), *D. cameroonensis* Ryvarden (Ryvarden 2018), *D. citricremeus* Masuka & Ryvarden (Masuka & Ryvarden 1999), *D. costaricensis* Ryvarden (Ryvarden 2012), *D. cylindrosporus* Ryvarden (Ryvarden 2007), *D. delicatulus* (Henn.) Masuka & Ryvarden (Masuka & Ryvarden 1999), *D. densiporus* Ryvarden (Ryvarden 2019), *D. deviatus* Ipulet & Ryvarden (Ipulet & Ryvarden 2005), *D. ecuadorensis* Ryvarden (Læssøe & Ryvarden 2010), *D. efibulatus* A.M. Ainsw. & Ryvarden (Ainsworth & Ryvarden 2008), *D. epitephrus* (Berk.) Ryvarden (Cunningham 1965), *D. grandisporus* Aime & Ryvarden (Aime et al. 2007), *D. leucoplacus* (Berk.) Ryvarden (Ryvarden 1977), *D. newhookii* P.K. Buchanan & Ryvarden (Buchanan & Ryvarden 2000), *D. papuanus* Quanten (Quanten 1996), *D. perennis* Ryvarden (Ryvarden 2007) & *D. sinuolatus* H.S. Yuan (Yuan 2013) are recorded in *Dichomitus*, but most of these taxa lack DNA data, and we did not yet exam their vouchers, and for the time being they are not included in *Megasporoporia*

sensu lato. By comparing the original descriptions of these species, the new species we have recently described are different from them.

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