



## Two new species of aphyllorphoid fungi (Basidiomycota) from southern China

Fu-Chang Huang<sup>1, 2</sup>, Bin Liu<sup>2\*</sup>, Hao Wu<sup>2</sup>, Yuan-Yuan Shao<sup>2</sup>, Pei-Sheng Qin<sup>2</sup>, Jin-Feng Li<sup>2</sup>

<sup>1</sup>College of Life Science and Technology, Guangxi University, Nanning, 530005, China

<sup>2</sup>Institute of Applied Microbiology, College of Agriculture, Guangxi University, Nanning, 530005, China

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### Abstract

Two new species of aphyllorphoid fungi (Basidiomycota) from Nonggang, Guangxi Autonomous Region, tropical, China are described. *Perenniporia nonggangensis* mainly characterized by resupinate to effused-reflexed basidiocarps with cream to greyish cream pore surface, up to 1.4 cm thick, broad-ellipsoid to subglobose, non-truncate and non-dextrinoid basidiospores. *Aporpium obtusisporum* characterized by pileate basidiocarps with poroid to lamellate hymenophore when mature, abundant hyphal pegs on both pileal surface and tubes, oval-elliptic, obtuse apically, cyanophilous basidiospores. Morphology and sequence analysis of the combined ITS and nLSU dataset support their taxonomic position as new species.

**Key words** –Morphological structure – Phylogeny – Polyporaceae – Aporpiaceae – Taxonomy

### Introduction

Nonggang Natural Reserve is located in the Sino-Vietnam border region of southern China. The data of the biodiversity of aphyllorphoid fungi in the reserve are limited, only very few species were reported from the reserve (Yuan & Dai 2012). During an inventory on macrofungal diversity in the reserve, several interesting polypore collections were encountered. *Perenniporia* and *Aporpium* are the possible genera for these collections.

The genus *Perenniporia* Murrill was typified by *Polyporus medulla-panis* Jacq. (Donk 1960), and it is characterized by the ellipsoid to distinctly truncate basidiospores, which are usually thick-walled and have a variable dextrinoid reaction; hyphal system is dimitic to trimitic with clamp connections on generative hyphae, vegetative hyphae are cyanophilous and variably dextrinoid (Decock & Stalpers 2006, Zhao et al. 2013a). Species in *Perenniporia* are lignicolous and cause a white rot, growing on living or dead hardwoods and conifers. Until now, about one hundred species have been described or transferred to the genus (Cui & Zhao 2012, <http://www.indexfungorum.org/names/Names.asp>), out of those 49 species were recorded from China (Zhao et al. 2014), and recent two new species were reported in 2015 (Decock & Ryvarden 2015, Jang et al. 2015).

The genus *Aporpium* Bondartsev & Singer was typified by *Aporpium canescens* (P. Karst.) Bondartsev & Singer [= *A. caryae* (Schwein.) Teixeira & D.P. Rogers], and redefined by Sotome et al. (2014) recently, it is characterized by resupinate to sessile basidiocarps, fleshy to leathery

context, poroid hymenophore, a dimitic hyphal systems with unbranched skeletal hyphae, clavate or ovate to pyriform probasidia, and ellipsoid to cylindrical or allantoid basidiospores (Singer 1944, Sotome et al. 2014). The other relate genera viz. *Elmerina*, *Protodaedalea* and *Protomerulius* have also been described to accommodate polypores with septate basidia, and they have been variably used in the literature by different authors (Ryvarden 1991, Núñez & Ryvarden 2001). Reid (1992) considered *Aporpium* to be a synonym of *Elmerina*. Ryvarden (1991) also treated *Aporpium* as a synonym of *Protomerulius*, which typified by *Protomerulius brasiliensis* and was characterized by resupinate basidiocarps with poroid hymenophore, a dimitic hyphal system, and ovate to pyriform and cruciate epibasidia. Miettinen et al. (2012) treated *Aporpium* as an independent genus distinct from *Elmerina* and *Protomerulius*. Sotome et al. (2014) redefined the concept of *Aporpium* based on the phylogenetic analyses, and they retained *Elmerina* separate from *Aporpium* and *Protodaedalea* since the phylogenetic position of *E. cladophora* was not yet clear. Wu et al. (2017) accepted the concept of the genus *Aporpium* given by Sotome et al. (2014), and added a new species to the genus recently.

During our recent study on macrofungal diversity in southern China, two additional undescribed species of *Perenniporia* and *Aporpium* were found, they were confirmed as new by their special morphological characteristics and the phylogenetic analyses of the combined sequences dataset from internal transcribed spacer (ITS) region and nuclear large subunit ribosomal DNA (nLSU) region.

## Materials & Methods

### Sample collection and morphological studies

Fresh specimens were collected from Nonggang Nature Reserve of Guangxi Autonomous Region in China, on dead angiosperm trunks or twigs. The specimens are deposited at the Herbarium of Guangxi University (GXU). The description of macroscopic characters was based on both fresh and dried specimens. The microscopic procedure followed Dai (2010). In elaborating the variation in the size of the spores, 5% of measurements were excluded from each end of the range, and were given in parentheses. Following were the abbreviations used in text: IKI = Melzer's reagent, IKI- = negative in Melzer's reagent, KOH = 5% potassium hydroxide, CB = Cotton Blue, CB+ = cyanophilous, CB- = acyanophilous, 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. Sections were studied at magnification up to  $\times 1500$  using a Nikon Eclipse 80i microscope and phase contrast illumination microscopy.

### DNA extraction, PCR amplification and sequencing

DNA was extracted from dry material according to conventional CTAB procedure. Nuclear ITS and nLSU regions were amplified with the primer ITS5 and ITS4 (White et al. 1990), and LR0R and LR5 (Vilgalys & Hester 1990) respectively. The PCR procedure was followed as: initial denaturation at 94 °C for 5 min, followed by 30 cycles at 94 °C for 40 s, 56 °C for 40 s and 72 °C for 1 min, and a final extension of 72 °C for 10 min. The PCR products were directly purified and sequenced by Beijing Genomics Institute (BGI) with the same primers. Newly generated sequences from this study were submitted to GenBank. Except sequences obtained from this study, reference taxa were used for phylogenetic analysis through searching in GenBank (Table 1, 2).

### Phylogenetic analyses

Sequence datasets of the ITS and nLSU were aligned with MEGA 5.2 (Tamura et al. 2011) and Clustalx1.83 (Thompson et al. 1997), then performed by SequenceMatrix-Windows-1.7.8 (Vaidya et al. 2011) to obtain their combined dataset sequences. Sequence alignment was deposited at <http://purl.org/phylo/treebase/phyloids/study/TB2:S18433>; *Perenniporia nonggangensis*: *Aporpium obtusisporum*:

<http://purl.org/phylo/treebase/phylovs/study/TB2:S20644>) and was executed by PAUP\* version 4.0b10 (Swofford 2002), MrMtgui 1.01 (<http://www.genedrift.org/mtgui.php>) and MrModeltest 2.3 (Nylander 2004, Posada & Crandall 1998) to find the best-fit model.

**Table 1** A list of species, specimens and GenBank accession number of sequences used in the study on *Perenniporia nonggangensis*.

Fungal taxon	Specimen numbers	GenBank numbers	
		ITS	LSU
<i>Abundisporus sclerosetosus</i>	MUCL 41438	NR111366	NG042479
<i>Abundisporus violaceus</i>	MUCL 38617	FJ411100	FJ393867
<i>Donkioporia expansa</i>	MUCL 35116	FJ411104	FJ393872
<i>Perenniporia aridula</i>	Dai 12398	JQ001855	JQ001847
<i>Perenniporia bannaensis</i>	Cui 8560	JQ291727	JQ291729
<i>Perenniporia bannaensis</i>	Cui 8562	JQ291728	JQ291730
<i>Perenniporia contraria</i>	Knudsen 04-111	JQ861737	JQ861755
<i>Perenniporia detrita</i>	MUCL 42649	FJ411099	FJ393866
<i>Perenniporia fergusii</i>	Gilbertson 16116	HQ876607	JF706337
<i>Perenniporia formosana</i>	Dai 5245	HQ876612	JX941590
<i>Perenniporia fraxinea</i>	Cui 7154	HQ654095	HQ654110
<i>Perenniporia hainaniana</i>	Cui 6364	JQ861743	JQ861759
<i>Perenniporia japonica</i>	Cui 7047	HQ654097	HQ654111
<i>Perenniporia japonica</i>	Cui 9181	JQ001856	JX141468
<i>Perenniporia koreana</i>	KUC20080517-15	KJ156309	KJ156301
<i>Perenniporia lacerata</i>	Cui 7220	JX141448	JX141458
<i>Perenniporia luteola</i>	Harkonen 1308b	JX141457	JX141467
<i>Perenniporia maackiae</i>	Cui 5605	JN048760	JN048780
<i>Perenniporia macropora</i>	Zhou 280	JQ861748	JQ861764
<i>Perenniporia medulla-panis</i>	MUCL 43250	FJ411087	FJ393875
<i>Perenniporia minor</i>	Cui 5782	HQ883475	HQ654115
<i>Perenniporia nanlingensis</i>	Cui 7589	HQ848478	HQ848487
<i>Perenniporia nanlingensis</i>	Cui 7620	HQ848477	HQ848486
<i>Perenniporia narymica</i>	Dai 10510	HQ654101	JF706346
<b><i>Perenniporia nonggangensis</i></b>	<b>GXU 2098</b>	<b>KT894732</b>	<b>KT894733</b>
<i>Perenniporia ochroleuca</i>	MUCL 39563	FJ411097	FJ393864
<i>Perenniporia ohioensis</i>	MUCL 41036	FJ411096	FJ393863
<i>Perenniporia piceicola</i>	Cui 10460	JQ861742	JQ861758
<i>Perenniporia piceicola</i>	Dai 4184	JF706328	JF706336
<i>Perenniporia pyricola</i>	Dai 10265	JN048761	JN048781
<i>Perenniporia rhizomorpha</i>	Cui 7507	HQ654107	HQ654117
<i>Perenniporia robiniophila</i>	Cui 7144	HQ876608	JF706341
<i>Perenniporia russeimarginata</i>	Yuan 1225	JQ861749	JQ861765
<i>Perenniporia straminea</i>	Cui 8858	HQ654104	JF706334
<i>Perenniporia subacida</i>	Dai 8224	HQ876605	JF713024
<i>Perenniporia subacida</i>	MUCL 31402	FJ411103	FJ393880
<i>Perenniporia substraminea</i>	Cui 10177	JQ001852	JQ001844
<i>Perenniporia subtephropora</i>	Dai 10962	JQ861752	JQ861768
<i>Perenniporia tenuis</i>	Wei 2783	JQ001858	JQ001848
<i>Perenniporia tephropora</i>	Cui 6331	HQ848473	HQ848484
<i>Perenniporia tianmuensis</i>	Cui 2648	JX141453	JX141463
<i>Perenniporia tibetica</i>	Cui 9457	JF706326	JF706332
<i>Perenniporia truncatospora</i>	Cui 6987	JN048778	HQ654112
<i>Perenniporia vicina</i>	MUCL 44779	FJ411095	FJ393862

**Table 1** Continued.

Fungal taxon	Specimen numbers	GenBank numbers	
		ITS	LSU
<i>Perenniporiella chaquenia</i>	MUCL 47647	FJ411083	FJ393855
<i>Perenniporiella micropora</i>	MUCL 43581	FJ411086	FJ393858
<i>Pyrofomes demidoffii</i>	MUCL 41034	FJ411105	FJ393873

MrBayesian analysis of *Perenniporia nonggangensis* was performed by MrBayes 3.2.3 (Ronquist et al. 2012) with 200000 generations, and its estimate maximum likelihood phylogenies was performed by PhyML 3.1 (Guindon & Gascuel 2003), which parameters of the model were as follows: tree topology search = SPRs, initial tree = BioNJ, model of nucleotides substitution = Custom, other parameters came from the best-fit model.

MrBayesian analyses of *Aporpium obtusisporum* were performed by MrBayes 3.2.3 (Ronquist et al. 2012) with 300000 generations, and maximum parsimony analyses were performed in PAUP\* version 4.0a151 (Swofford 2002) using tree-bisection reconnection (TBR) branch-swapping algorithm, clade robustness was assessed using a bootstrap (BT) analysis with 1000 replicates. All phylogenetic trees were edited by TreeGraph 2.3.0-425 beta (Stöver & Müller 2010).

**Table 2** A list of species, specimens and GenBank accession number of sequences used in the study on *Aporpium obtusisporum*

Fungal taxon	Specimen no.	GenBank numbers	
		ITS	nLSU
<i>Aporpium caryae</i>	WD2207	AB871751	AB871730
<i>Aporpium hexagonoides</i>	ML297	AB871754	AB871735
<i>Aporpium hexagonoides</i>	TFM F-27498	AB871755	AB871736
<i>Aporpium hexagonoides</i>	Wei 5584	JQ764667	JQ764645
<i>Aporpium hexagonoides</i>	Wei 5680	JQ764668	JQ764646
<b><i>Aporpium obtusisporum</i></b>	<b>GXU 2084</b>	<b>KY655346</b>	<b>KY655347</b>
<b><i>Aporpium obtusisporum</i></b>	<b>GXU 2237</b>	<b>KY655348</b>	<b>KY655349</b>
<i>Aporpium strigosum</i>	TFM F-27651	AB871757	AB871738
<i>Aporpium strigosum</i>	TUFC14542	AB871760	AB871741
<i>Aporpium strigosum</i>	TUFC10589	AB871756	AB871737
<i>Aporpium strigosum</i>	WD1710	AB871759	AB871740
<i>Aporpium strigosum</i>	WD680	AB871758	AB871739
<i>Aporpium strigosum</i>	Wei 5621	JQ764659	JQ764634
<i>Aporpium strigosum</i>	Wei 5990	JQ764660	JQ764635
<i>Auricularia villosula</i>	Cui 8688	KM396810	KM396858
<i>Auricularia villosula</i>	HMAS 130446	KM396817	KM396864
<i>Elmerina caryae</i>	Dai 3952	JQ764651	JQ764630
<i>Elmerina caryae</i>	Dai 4549	JQ764652	JQ764631
<i>Elmerina dimidiata</i>	O 18238	JQ764663	JQ764640
<i>Elmerina dimidiata</i>	O 18261	JQ764664	JQ764641
<i>Elmerina efibulata</i>	Dai 9322	JQ764669	JQ764647
(= <i>Protomerulius efibulatu</i> )			
<i>Elmerina foliacea</i>	Yuan 5691	JQ764666	JQ764644
(= <i>Protodaedalea foliacea</i> )			
<i>Exidia recisa</i>	MW 315	AF291276	AF291322
<i>Exidia saccharina</i>	RoKi 88	AF291277	AF291323
<i>Protodaedalea hispida</i>	E701	AB871767	AB871748
<i>Protodaedalea hispida</i>	WD548	AB871768	AB871749

## Results

### Phylogeny of *Perenniporia nonggangensis*

The combined ITS + nLSU dataset included sequences from 47 fungal specimens representing 42 taxa. The dataset had an aligned length of 1643 characters including gaps in the dataset (706 characters for ITS, 927 characters for nLSU), *Pyrofomes demidoffii* (Lév.) Kotl. & Pouzar (MUCL 41034) and *Donkioporia expansa* (Desm.) Kotl. & Pouzar (MUCL 35116) were used as outgroups. Best model for the ITS + nLSU dataset estimated and applied in the Bayesian analysis: GTR + I + G, lset nst = 6, rates = invgamma; prset statefreqpr = dirichlet (1, 1, 1, 1). The average standard deviation of split frequencies of Bayesian analysis was 0.005698. The parameters of the maximum likelihood phylogenetic model: Gamma shape parameter = 0.536, Proportion of invariant = 0.370, Nucleotides frequencies of f (A) = 0.2433, f (C) = 0.2123, f (G) = 0.2696, f (T) = 0.2748. The phylogenetic tree topology of the estimated maximum likelihood tree was the same as the tree from Bayesian analysis (Fig. 1).

### Phylogeny of *Aporpium obtusisporum*

The combined ITS + nLSU dataset included sequences from 26 fungal specimens representing 10 taxa. There were 1095 total characters (530 characters for ITS, 565 characters for nLSU) in the alignment, of which, 798 characters were constant, 65 were variable and parsimony-uninformative, and 232 were parsimony informative. The consensus tree was shown in Fig. 2 (TL = 522, CI = 0.736, RI = 0.863, RC = 0.635, HI = 0.264). Best model for the ITS + nLSU dataset estimated and applied in the Bayesian analysis: SYM+I+G, Lset nst = 6 rates = invgamma; Prset statefreqpr = fixed (equal). The average standard deviation of split frequencies of Bayesian analysis was 0.006729. Tree topology of the maximum parsimony analysis showed similar to the tree from Bayesian analysis (Fig. 2).

## Taxonomy

*Perenniporia nonggangensis* F.C. Huang & Bin Liu, sp. nov.

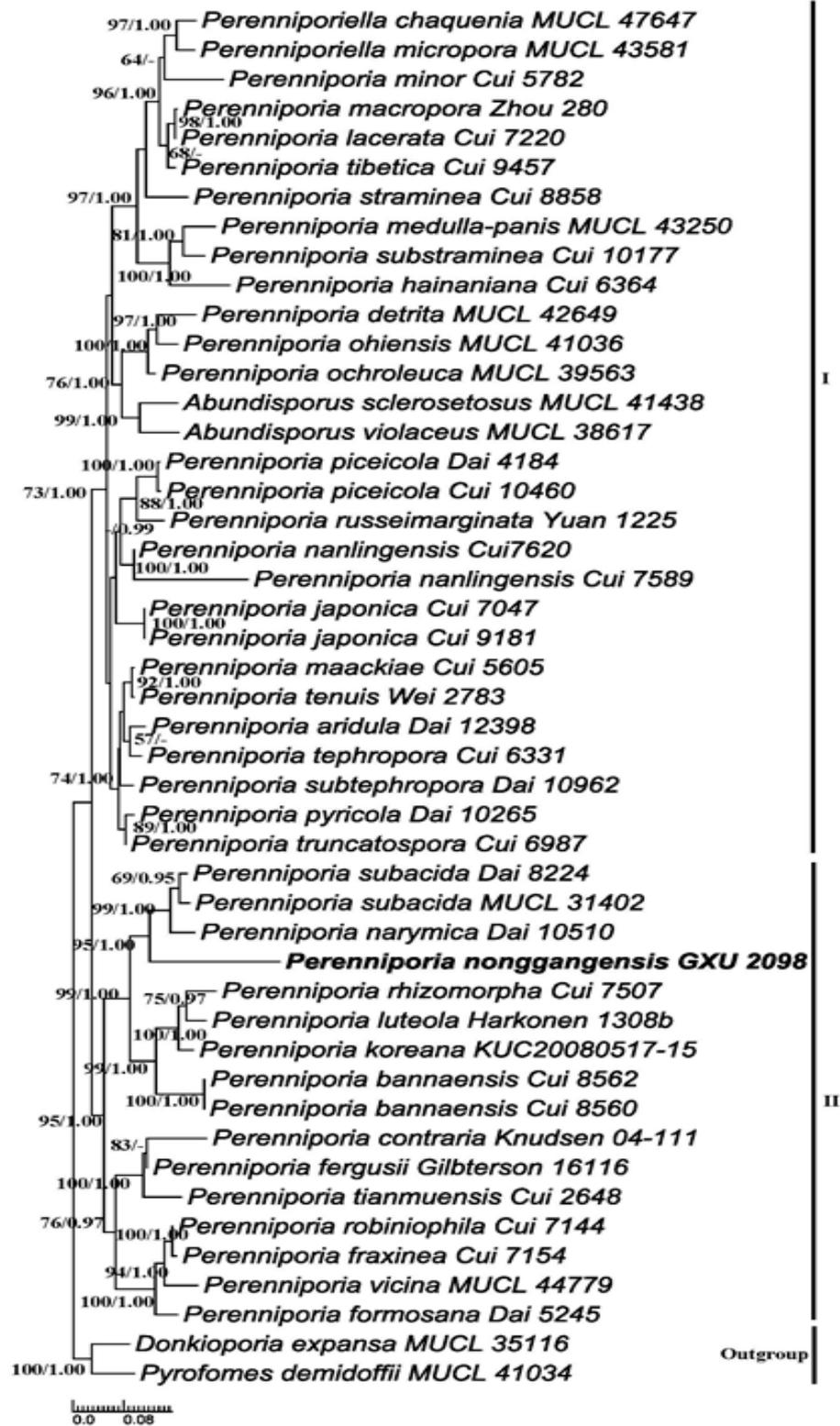
Figs 3–5

Mycobank number: MB816217; Facesoffungi number: FOF03876

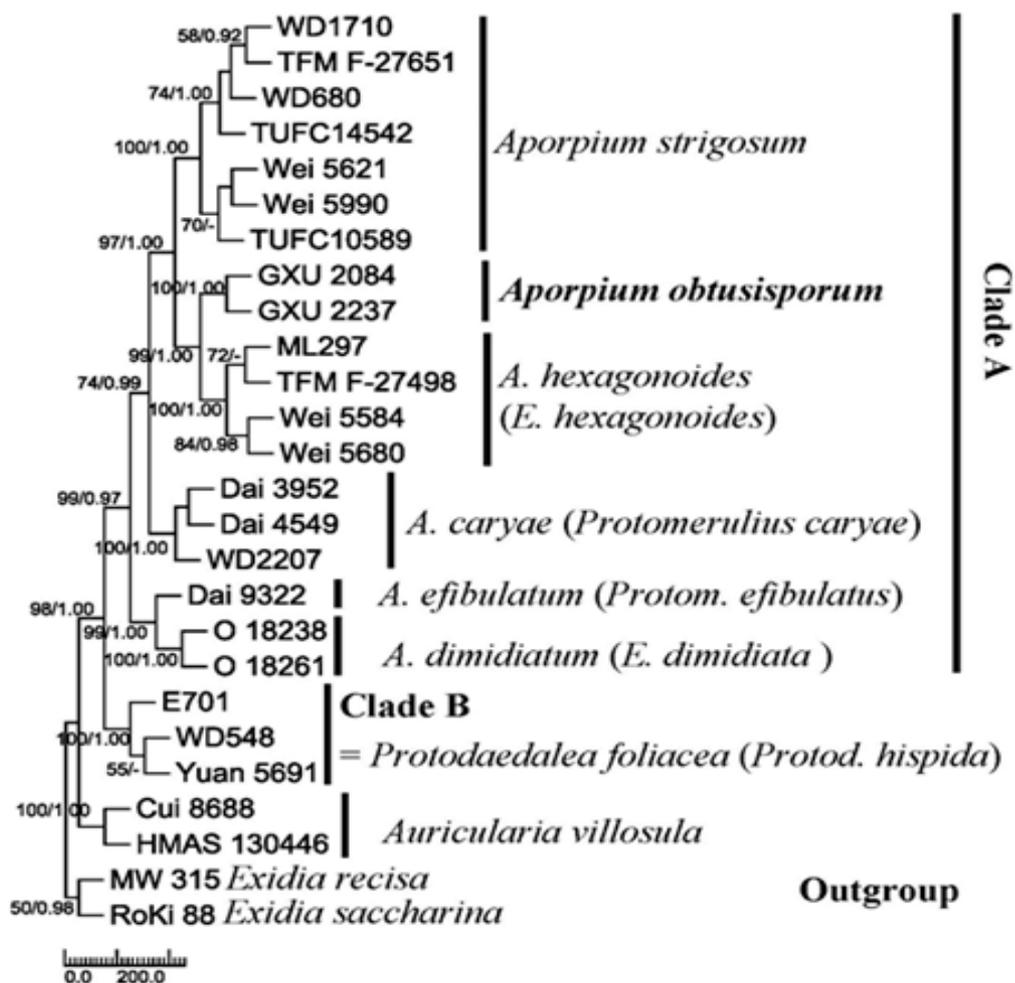
Holotype – CHINA, Guangxi, Chongzuo, Nonggang Nature Reserve, on fallen angiosperm trunk, July 11, 2014, GXU 2098 (Holotype).

Etymology – *Nonggangensis* (Lat.), referring to the locality of the type specimen.

Basidiocarps annual, resupinate to effused-reflexed, separable, soft and leathery when fresh, becoming corky upon drying, up to 35 cm long, 14 cm wide and 2.0 cm thick when resupinate; Pore surface cream to greyish cream when fresh, pale yellow-orange, capucine buff to sudan brown when dry (Ridgway 1912), the bruised part becoming brownish dark upon drying, some small pilei projecting on the edge of mature basidiocarps. Sterile margin white to cream, finely velutinate, sometimes radially fimbriate, up to 2.1 cm wide; pores round, angular, 4–5 per mm; dissepiments thin, entire to lacerate; subiculum white to cream when fresh, white to capucine buff when dry, up to 1.4 cm thick. Tubes concolorous with pore surface, corky, up to 6 mm long. Hyphal system dimitic; generative hyphae with clamp connections; skeleto-binding hyphae dextrinoid and cyanophilous; tissues changed to dark brown in KOH. Contextual generative hyphae frequent, 1.9–7.4  $\mu\text{m}$  diam, thin- to thick-walled, limited branched with clamp connections, generative hyphae common, tightly interwoven. Contextual skeleto-binding hyphae dominant, thick-walled with a wide to narrow lumen, or subsolid, limited branched, interwoven, 2.0–4.5  $\mu\text{m}$  diam. Tramal generative hyphae frequent, 1.7–3.1  $\mu\text{m}$  diam, thin-walled, limited branched with clamp connections, parts of generative hyphae tightly interwoven. Tramal skeleto-binding hyphae frequent, thick-walled, with a wide to narrow lumen, or subsolid, limited branched, interwoven, 1.7–3.6  $\mu\text{m}$  diam. Cystidia absent; cystidioles fusoid, hyaline, thin-walled, 12.9–25.7  $\times$  3.3–6.6  $\mu\text{m}$ ; basidia clavate to barrel-shaped, with four sterigmata and a basal clamp connection, 8.7–18.1  $\times$  3.9–7.1  $\mu\text{m}$ ; basidioles oblong-ellipsoid to barrel-shaped, 7.9–15.9  $\times$  4.4–7.6  $\mu\text{m}$ . Basidiospores



**Figure 1** – The phylogenetic tree was generated by Maximum Likelihood method based on combined ITS + nLSU sequences. Bootstrap values (before the/) higher than 50 % and Bayesian posterior probabilities (after the/) more than 0.95 were indicated along branches.



**Figure 2** – The phylogenetic tree was generated by maximum parsimony analyses based on the combined ITS + nLSU dataset. Bootstrap values (before the/) higher than 50 % and Bayesian posterior probabilities (after the/) more than 0.80 were indicated along branches.

broad-ellipsoid to subglobose, hyaline, thick-walled, smooth, occasionally with a large guttule, IKI–, slightly CB+, (2.9–)3.1–4.4(–5.1) × (2.6–)2.7–3.6(–3.9) μm, L = 3.79 μm, W = 3.12 μm, Q = 1.21 (n = 60).

Notes – *Perenniporia nonggangensis* differs from other *Perenniporia* species by resupinate to effused-reflexed basidiocarps with cream to greyish fresh pore, thick subiculum up to 1.4 cm, a dimitic hyphal system with dextrinoid and cyanophilous skeleto-binding hyphae, the presence of long fusoid cystidioles, IKI–, slightly cyanophilous, and broad-ellipsoid to subglobose basidiospores.

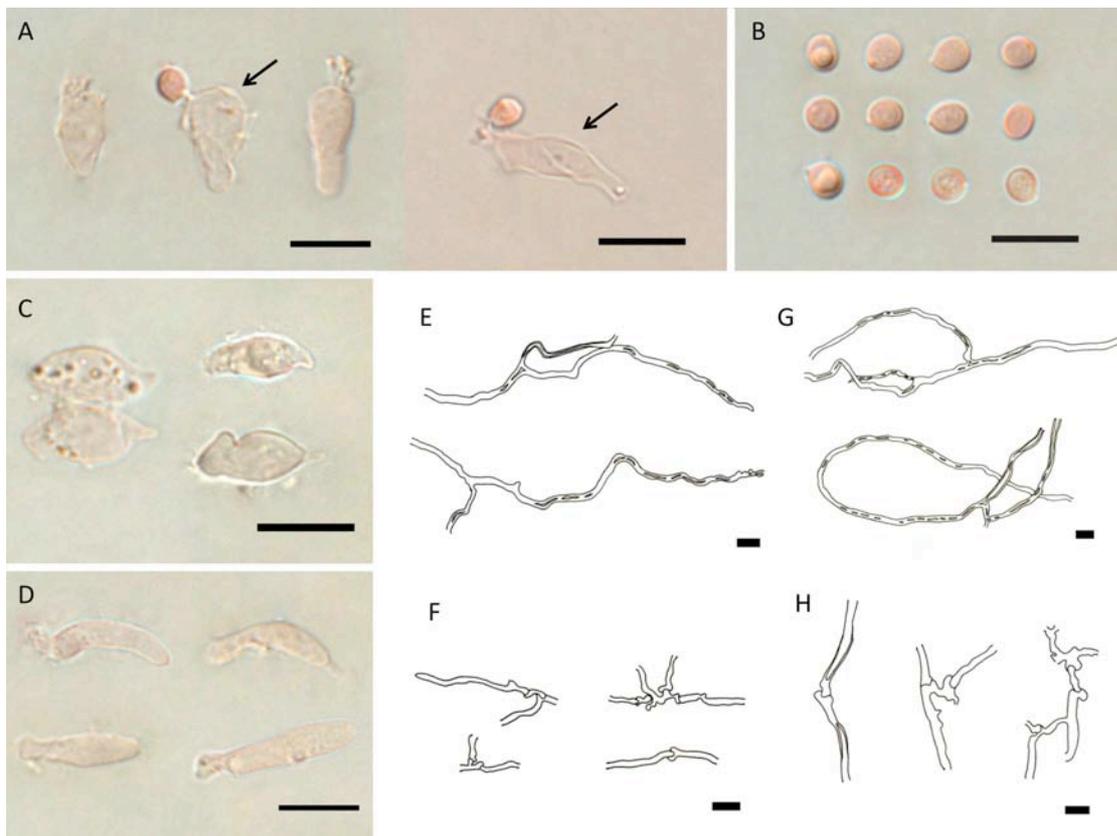
***Aporpium obtusisporum*** F.C. Huang & Bin Liu, sp. nov. Figs 6–7

Mycobank number: MB820107; Facesoffungi number: FOF03877

Etymology – *Obtusisporum* (Lat.), referring to the basidiospores obtuse apically.

Holotype – CHINA, Guangxi, Chongzuo, Nonggang Nature Reserve, on fallen angiosperm trunks or twigs, July 10, 2014, GXU 2084 (Holotype)

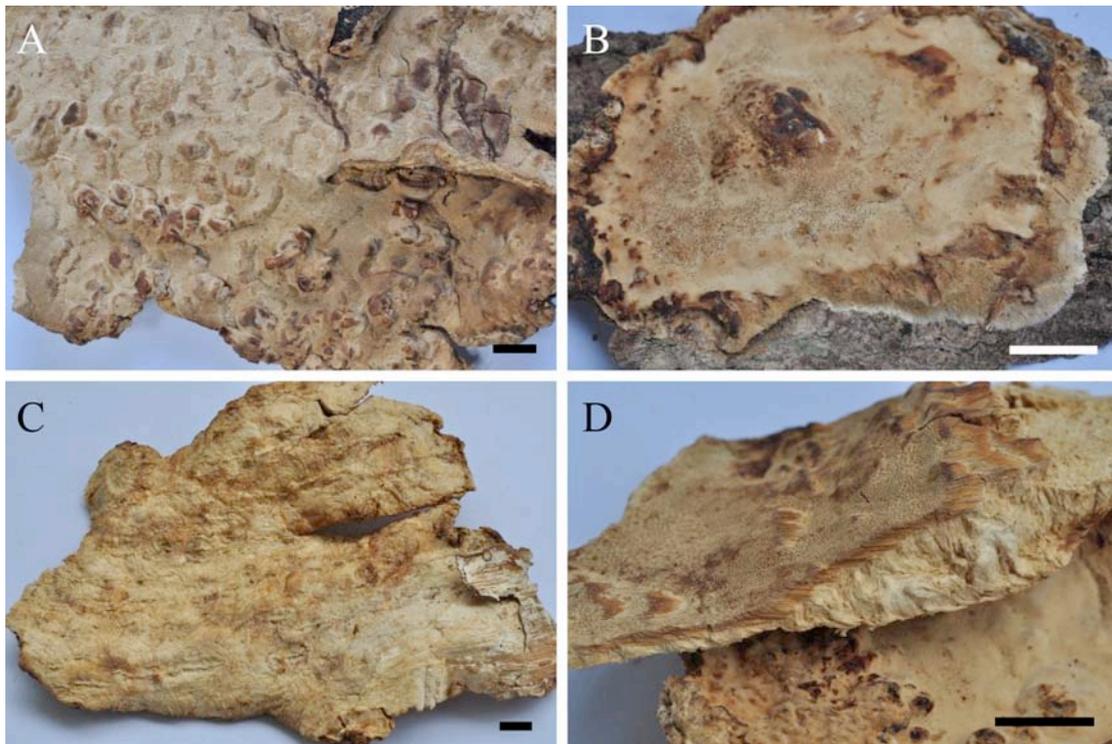
Basidiocarps annual, pileate, leathery, without odor; pilei projecting up to 8.3 cm, 11.3 cm wide and 4.0 mm thick at base, margin acute, entire, frequently incurved when dry, occasionally several pilei fused along the adjacent margins. Pilei spatulate or flabellate, bearing an elongated strap-like attachment base; upper surface from pale ochraceous buff to white toward the margin when fresh, salmon-buff, salmon to liver brown (Ridgway 1912) when dry, indistinctly concentrically zonate when fresh but distinct when dry, longitudinal stripes present, hyphal pegs



**Figure 3** – Anatomical details of *Perenniporia nonggangensis* A: Basidia; B: Basidiospores; C: Basidioles; D: Cystidioles; E: Skeleto-binding hyphae from tube trama; F: Generative hyphae from tube trama; G: Skeleto-binding hyphae from subiculum; H: Generative hyphae from subiculum. Scale bars: A–H = 10  $\mu$ m.



**Figure 4** – A fresh basidiocarp of *Perenniporia nonggangensis*. Scale bars: 1cm.



**Figure 5** – Dry basidiocarps of *Perenniporia nonggangensis* A: part of the fruiting body; B: a juvenile basidiocarp with radially fimbriate margin; C: back surface of fruiting body; D: Context. Scale bars: A–D = 1 cm.

abundant on pileal surface. Pore surface from pale ochraceous buff to white toward the margin when fresh, and salmon color to buckthorn brown or liver brown when dried, sterile margin lacking; pores angular, hexagonal, 0.5–2.5 mm in diam, or radially elongate when juvenile, and hymenophore poroid to lamellate when mature; thin dissepiments often bearing densely hyphal pegs. Subiculum white to pale ochraceous buff when fresh, and light ochraceous salmon to liver brown, rigid and leathery when dried, up to 2 mm thick. Tubes concolorous with pore surface, leathery, up to 2 mm long. Hyphal system dimitic; generative hyphae with clamp connections; skeletal hyphae IKI–, CB+; tissues unchanged in KOH. Contextual generative hyphae frequent, thin-walled, hyaline, with clamp-connections, moderately branched, 1.5–3.6  $\mu\text{m}$  wide; contextual skeletal hyphae dominant, rarely branched, almost straight with a wide to narrow lumen or subsolid, 1.9–5.7  $\mu\text{m}$  wide. Tramal generative hyphae frequent, thin-walled, hyaline, with clamp-connections, moderately branched, 1.5–3  $\mu\text{m}$  wide; tramal skeletal hyphae rarely branched, almost straight, dominant, thick-walled with a wide to narrow lumen or subsolid, 2.3–4.6  $\mu\text{m}$  wide. Hyphal pegs abundant in the hymenium, cylindrical, usually encrusted crystal, 46.4–131.8  $\times$  13.2–41.9  $\mu\text{m}$ . Cystidioles present, thin-walled, hyaline, more often fusoid, sometimes clavate, 7.4–24.3  $\times$  2–5.2  $\mu\text{m}$ . Basidia short clavate with a basal constriction, or barrel-shaped, cruciately septate in the apical portion, 11.6–29.9  $\times$  5–8.8  $\mu\text{m}$ , four sterigmata up to 23.8  $\mu\text{m}$  long, basidioles aseptate, short clavate often with a basal constriction, or barrel-shaped, 9.6–22.6  $\times$  4.2–8.6  $\mu\text{m}$ . Basidiospores oval-elliptic, obtuse apically, smooth, hyaline, thin-walled, IKI–, CB+, (4.9–) 5.9–9.6 (–9.7)  $\times$  (3.2–) 3.5–5.5 (–6.2)  $\mu\text{m}$ , L = 7.8  $\mu\text{m}$ , W = 4.7  $\mu\text{m}$ , Q = 1.66 (n = 62).

Other materials examined (paratypes) – CHINA, Guangxi, Chongzuo, Nonggang Nature Reserve, on fallen angiosperm trunks or twigs, June 20, 2012, GXU 0489; July 19, 2012, GXU 0584; July 10, 2016, GXU 2237.

Notes – *Aporpium obtusisporum* was confirmed as a novel species based on morphological and phylogenetic supports. It differs from *Aporpium hexagonoides* by pileal surface covered by abundant hyphal pegs, hymenophore poroid to lamellate when mature. Basidiospores are shorter in average, cystidioles present and without dendrohyphidia.

## Discussion

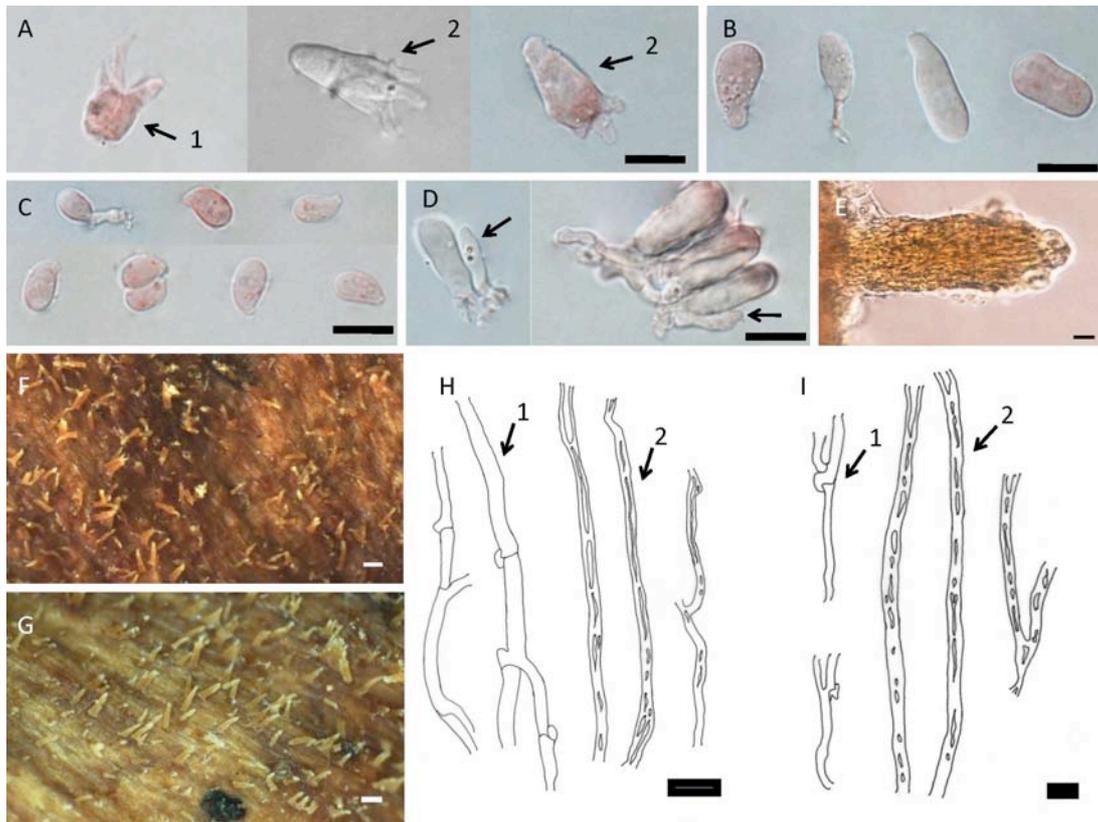
The phylogeny of *Perenniporia nonggangensis* (Fig. 1) based on the combined ITS + nLSU formed a well supported lineage; species in the phylogeny included two groups (I and II). The relationships among species in our analysis are similar to those of Jang et al. (2015), but slightly different from those of Zhao & Cui (2013) and Zhao et al. (2013a). Group I included species with typically truncate basidiospores, and group II included the non-truncate basidiospore species, such as *Perenniporia luteola* B.K. Cui & C.L. Zhao, *P. rhizomorpha* B.K. Cui et al., and *P. bannaensis* B.K. Cui & C.L. Zhao (except for *P. fergusii* Gilb. & Ryvarden). *Perenniporia nonggangensis* clustered with *P. subacida* (Peck) Donk and *P. narymica* (Pilát) Pouzar with a high support (bootstrap values, BP = 95; Bayesian posterior probabilities, BPP = 1.00), and then these three taxa clustered with *P. rhizomorpha*, *P. luteola*, *P. koreana* Y. Jang & J.J. Kim, and *P. bannaensis* in a clade also with high support (BP = 99; BPP = 1.00).



**Figure 6** – Fresh basidiocarps of *Aporrium obtusisporum*. Scale bars: 1cm.

*Perenniporia subacida* is similar to *P. nonggangensis* by resupinate basidiocarp, dextrinoid and cyanophilous skeletal hyphae, fusoid cystidioles, and non-truncate, non-dextrinoid basidiospores (Ryvarden & Gilbertson 1994, Zhao & Cui 2013, Zhao et al. 2013b), while *P. subacida* differs in its cream to pale yellowish pore surface, tissues unchanged in KOH, rarely branched skeletal hyphae, and longer basidiospores ( $4.3\text{--}5.4 \times 3.2\text{--}4.1 \mu\text{m}$ , Dai et al. 2002). *Perenniporia narymica* (Zhao et al. 2013b) is similar to *P. nonggangensis* by annual and resupinate basidiocarps, a dimitic hyphal system with clamped generative hyphae, fusoid cystidioles, and non-truncate, non-dextrinoid basidiospores. But it distinguishes from the latter by amyloid and acyanophilous skeletal hyphae which dissolved in KOH, and cyanophilous basidiospores, and it was treated as an independent genus *Yuchengia* by Zhao et al. (2013b).

Morphologically, *Perenniporia luteola*, *P. koreana* and *P. bannaensis* are very similar to *P. nonggangensis* by sharing the similar characteristics of resupinate basidiocarps, dextrinoid and cyanophilous skeletal hyphae, fusoid cystidioles, and non-truncate basidiospores. But *P. luteola* differs from *P. nonggangensis* by buff to buff-yellow fresh pores, thin subiculum up to 0.5 mm thick, hyphae unchanged in KOH, and bigger basidiospores ( $6.1\text{--}6.9 \times 5.1\text{--}5.4 \mu\text{m}$ , Zhao & Cui 2013).



**Figure 7** – Anatomical details of *Aporpium obtusisporum* A1: Epibasidium, A2: Basidia; B: Basidioles; C: Basidiospores; D: Cystidioles; E: Hyphal pegs from tubes; F, G: Hyphal pegs from pileal surface; H1: Generative hyphae from tube trama; H2: Skeletal hyphae from tube trama; I1: Generative hyphae from context; I2: Skeletal hyphae from context. Scale bars: A–I = 10  $\mu$ m; F, G = 100  $\mu$ m.

*Perenniporia koreana* distinguishes from *P. nonggangensis* by yellowish pores, rarely branched skeletal hyphae, dextrinoid, cyanophilous and bigger basidiospores (6–7  $\times$  3.9–5.2  $\mu$ m, Jang et al. 2015). *Perenniporia bannaensis* differs from *P. nonggangensis* by cream to buff fresh pores, thinner fruiting body up to 2 mm thick, smaller pores (6–8 per mm), unbranched skeletal hyphae, longer and strongly dextrinoid basidiospores (5.2–6  $\times$  4–4.6  $\mu$ m, Zhao et al. 2013a).

*Perenniporia rhizomorpha* is also similar to *P. nonggangensis* by resupinate basidiocarps, dextrinoid and cyanophilous skeletal hyphae, and non-truncate basidiospores, but it is easy to distinguish from the latter by rhizomorphic basidiocarps, cream-buff to yellow-buff fresh pores, tissue unchanged in KOH, skeletal hyphae usually encrusted with fine crystals, the absence of cystidioles, and bigger, dextrinoid, cyanophilous basidiospores (5.3–6.5  $\times$  4.1–5.2  $\mu$ m, Cui et al. 2007).

The phylogenetic tree of *Aporpium obtusisporum* (Fig. 2) based on the combined ITS + nLSU sequence also formed a well-supported lineage. The relationships among species in the phylogeny are similar to those of Sotome et al. (2014). Clade A included type species *Aporpium caryae* and other species also from the same genus, *A. strigosum* Sotome & T. Hatt., *A. obtusisporum*, *A. hexagonoides* A. David & Jaq., *A. efibulatum* (Y.C. Dai & Y.L. Wei) Sotome & T. Hatt. and *A. dimidiatum* A. David; however, the species of clade B came from *Protodaedalea*, *P. hispida* Imazeki (Fig. 2). Moreover, the new species *A. obtusisporum* is genetically closely related to *A. hexagonoides* with strongly supported (bootstrap values, BP = 99; Bayesian posterior probabilities, BPP = 1.00).

Morphologically, *Aporpium obtusisporum* is very similar to *A. hexagonoides*. Both species shared many similar features including the pileate basidiocarps, tubes densely covered with hyphal pegs, a dimittic hyphal system, epibasidia septate when mature. However, the latter was distinct

from *A. obtusisporum* by hirsute pileal surface without hyphal pegs, white to cream fresh pore surface, angular to partly sinuous or elongated pores, longer basidiospores in average ( $8\text{--}10 \times 4\text{--}5 \mu\text{m}$ ,  $L = 9.0 \mu\text{m}$ ), the presence of dendrohyphidia (Sotome et al. 2014).

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### References

- Cui BK, Dai YC, Decock CA 2007 – A new species of *Perenniporia* (Basidiomycota, Aphyllophorales) from eastern China. *Mycotaxon* 99, 175–180.
- Cui BK, Zhao CL 2012 – Morphological and molecular evidence for a new species of *Perenniporia* (Basidiomycota) from Tibet, southwestern. *Mycoscience* 53, 365–372.
- Decock C, Ryvarden L 2015 – Studies in *Perenniporia* s.l. African taxa IX: *Perenniporia vanhullii* sp. nov. from open woodlands. *Synopsis Fungorum* 33, 44.
- Decock C, Stalpers J 2006 – Studies in *Perenniporia*: *Polyporus unitus*, *Boletus medulla-panis*, the nomenclature of *Perenniporia*, *Poria* and *Physisporus*, and a note on European *Perenniporia* with a resupinate basidiome. *Taxon* 53, 759–778.
- Dai YC 2010 – *Hymenochaetaceae* (Basidiomycota) in China. *Fungal Diversity* 45, 131–343.
- Dai YC, Niemelä T, Kinnunen J 2002 – The polypore genera *Abundisporus* and *Perenniporia* (Basidiomycota) in China, with notes on *Haploporus*. *Annales Botanici Fennici* 39, 169–182.
- Donk MA. 1960 – The generic names proposed for Polyporaceae. *Persoonia* 1, 173–302.
- Guindon S, Gascuel O 2003 – A simple, fast and accurate algorithm to estimate large phylogenies by maximum likelihood. *Systematic Biology* 52, 696–704.
- Jang Y, Jang S, Lim YW, Kim C, Kim JJ 2015 – *Perenniporia koreana*, a new wood-rotting basidiomycete from South Korea. *Mycotaxon* 130, 173–179.
- Miettinen O, Spirin V, Niemelä T 2012 – Notes on the genus *Aporpium* (Auriculariales, Basidiomycota), with a new species from temperate Europe. *Annales Botanici Fennici* 49, 359–368.
- Núñez M, Ryvarden L 2001 – East Asian polypores 2. *Synopsis Fungorum* 14, 170–522.
- Nylander JAA 2004 – MrModeltest v2. Evolutionary Biology Center, Uppsala University, Uppsala, Sweden.
- Posada D, Crandall KA 1998 – Modeltest: testing the model of DNA substitution. *Bioinformatics* 14, 817–818.
- Reid DA 1992 – The genus *Elmerina* (Tremellales) with accounts of two species from Queensland, Australia. *Persoonia* 14, 465–474.
- Ridgway R 1912 – Color Standards and Color Nomenclature. United States National Museum, Washington, D.C.
- Ronquist F, Teslenko M, Mark P van der, Ayres D, Darling A, Höhna S, Larget B, Liu L, Suchard MA, Huelsenbeck JP 2012 – MrBayes 3.2: Efficient Bayesian phylogenetic inference and model choice across a large model space. *Systematic Biology* 61, 539–542.
- Ryvarden L 1991 – Genera of polypores, nomenclature and taxonomy. *Synopsis Fungorum* 5, 1–363.
- Ryvarden L, Gilbertson RL 1994 – European polypores. Part 2. *Synopsis Fungorum* 7, 394–743
- Singer R 1944 – Notes on taxonomy and nomenclature of the polypores. *Mycologia* 36, 65–69.

- Sotome K, Maekawa N, Nakagiri A, Lee SS, Hattori T 2014 – Taxonomic study of Asian species of poroid Auriculariales. *Mycological Progress* 13, 987–997.
- Stöver BC, Müller KF 2010 – TreeGraph 2: Combining and visualizing evidence from different phylogenetic analyses. –*BMC Bioinformatics* 11, 7.
- Swofford DL 2002 – PAUP \*, phylogenetic analysis using parsimony (\*and other methods), ver. 4.0b10. –Sinauer Associates.
- Tamura K, Peterson D, Peterson N, Stecher G, Nei M, Kumar S 2011 – MEGA5: Molecular evolutionary genetics analysis using maximum likelihood, evolutionary distance, and maximum parsimony methods. *Molecular Biology and Evolution* 28, 2731–2739.
- Thompson JD, Gibson TJ, Plewniak F, Jeanmougin F, Higgins DG 1997 – The Clustal X windows interfaces: flexible strategies for multiple sequence alignment aided by quality analysis tools. *Nucleic Acids Research* 24, 4876–4882.
- Vaidya G, Lohman DJ, Meier R 2011 – SequenceMatrix: concatenation software for the fast assembly of multi-gene datasets with character set and codon information. *Cladistics* 27, 171–180.
- Vilgalys R, Hester M 1990 – Rapid genetic identification and mapping of enzymatically amplified ribosomal DNA from several *Cryptococcus* species. *Journal of Bacteriology* 172, 4238–4246.
- White TJ, Bruns T, Lee S, Taylor J 1990 – Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenies. In: Innis MA, Gelfand DH, Sninsky JJ, White TJ (eds) *PCR protocols, a guide to methods and applications*. Academic, San Diego
- Wu F, Zhou LW, Yuan Y, Dai YC 2017 – *Aporpium miniporum*, a new polypore species with vertically septate basidia from southern China. *Phytotxa* (in press)
- Yuan HS, Dai YC 2012 – A Wood-inhabiting fungi in southern China. 6. Polypores from Guangxi Autonomous Region. *Annales Botanici Fennici* 49:341–351.
- Zhao CL, Cui BK 2013 – Three new *Perenniporia* (Polyporales, Basidiomycota) species from China based on morphological and molecular data. *Mycoscience* 54, 231–240.
- Zhao CL, Cui BK, Dai YC 2013a – New species and phylogeny of *Perenniporia* based on morphological and molecular characters. *Fungal Diversity* 58, 47–60.
- Zhao CL, Cui BK, Steffen KT 2013b – *Yuchengia*, a new polypore genus segregated from *Perenniporia* (Polyporales, Basidiomycota) based on morphological and molecular characters. *Nordic Journal of Botany* 31, 331–338.
- Zhao CL, Shen LL, Cui BK 2014 – *Perenniporia cinereofusca* sp. nov. (Polyporales, Basidiomycota) evidenced by morphological characters and phylogenetic analyses. *Mycoscience* 55, 417–422.