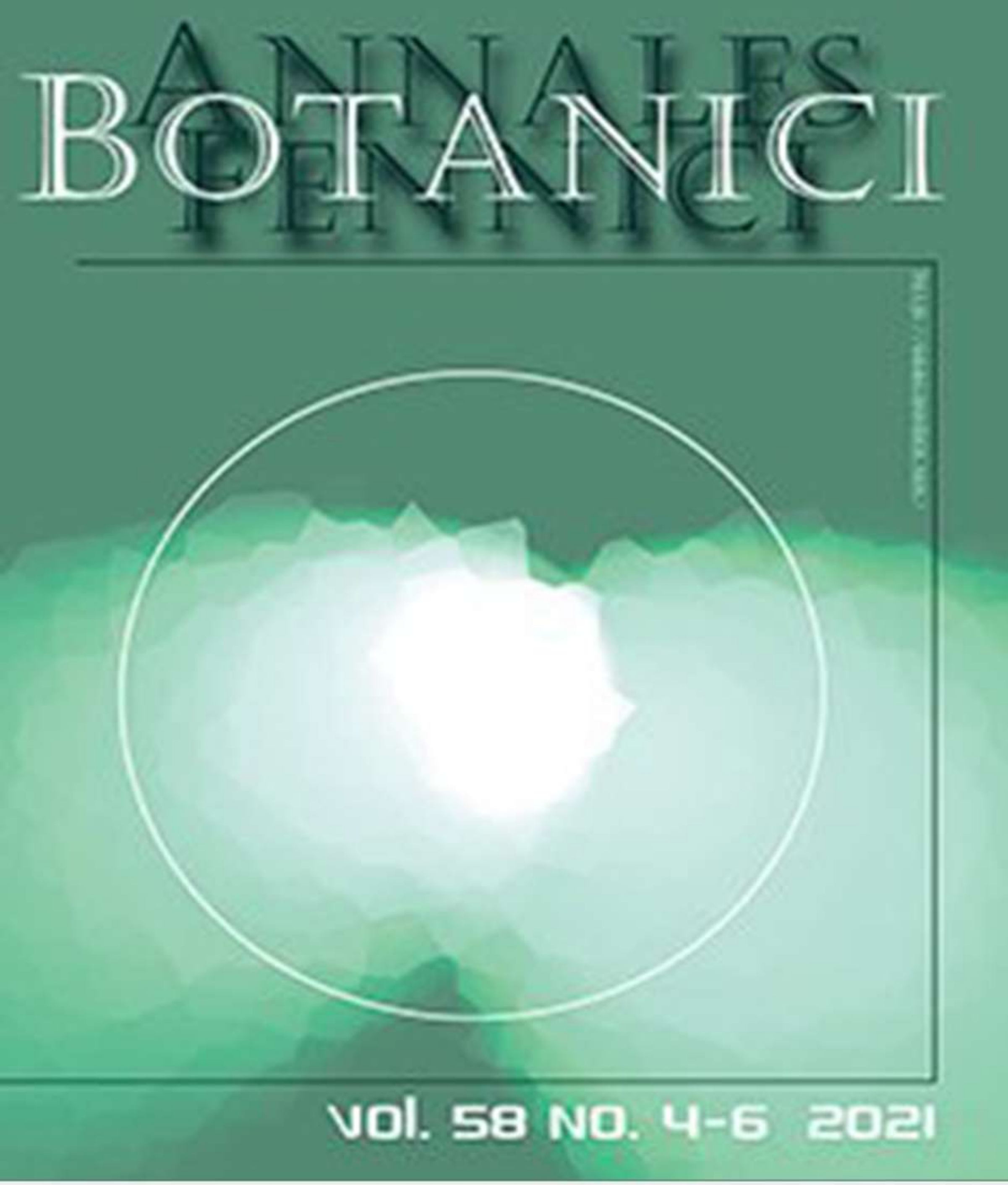

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Fasciodontia yunnanensis (Schizoporaceae, Hymenochaetales), a new species from southern China

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Luo K.Y. & Zhao C.L. 2021: *Fasciodontia yunnanensis* (Schizoporaceae, Hymenochaetales), a new species from southern China. — *Ann. Bot. Fennici* 58: 259–266.

A new wood-inhabiting fungal species, *Fasciodontia yunnanensis* C.L. Zhao *sp. nova* (Schizoporaceae, Hymenochaetales) is proposed based on morphological and molecular evidence. *Fasciodontia yunnanensis* is characterised by resupinate basidiomata with minutely odontioid hymenial surface and presence of submoniliform cystidia, and ellipsoid thick-walled basidiospores (3.1–5.7 × 2.1–4.1 µm). Sequences of ITS and 28S rDNA gene regions were generated, and phylogenetic analyses were performed with maximum likelihood, maximum parsimony and Bayesian inference methods. In the phylogenetic reconstruction of *Hyphodontia s. lato* based on a concatenated ITS + 28S data set, the new species nested in *Fasciodontia* where it formed a monophyletic lineage and grouped with *F. brasiliensis* and *F. bugellensis*.

Introduction

Fasciodontia (Schizoporaceae, Hymenochaetales) is a small corticioid genus, typified by *F. bugellensis* (Yurchenko *et al.* 2020) and characterized by resupinate to effused basidiomata with minutely odontioid hymenophore; sterile aculei except bases and consisting of projecting hyphae; a pseudodimitic hyphal system bearing clamp connections, slightly yellowish in KOH, moderately cyanophilous, negative in Melzer's reagent; cylindrical to slightly moniliform and capitate cystidia; utriform to subcylindrical basidia, with two slight constrictions; and ellipsoid, colourless, smooth, slightly thick-walled to thick-walled, slightly to moderately cyanophilous basidiospores (Yurchenko *et al.* 2020). The two currently known species of *Fasciodontia* grow on dead wood and are known from Europe, Canary Islands, Africa (Hjortstam & Ryvarden 2007), East Asia, and South America (Yurchenko *et al.* 2020).

In molecular systematic studies based on the internal transcribed spacer (ITS) and the nuclear large subunit (LSU) ribosomal DNA gene, *Fasciodontia* grouped within a clade comprising *Lyomyces* and *Xylodon* clades. *Fasciodontia brasiliensis* and *F. bugellensis* grouped together in a monophyletic lineage. Yurchenko *et al.* (2020) proposed to separate *Fasciodontia* as a genus distinct from *Xylodon* and *Lyomyces*.

During studies on wood-inhabiting fungi in southern China, we found basidiomata of *Fas-*

ciodontia that could not be assigned to either of the two described species. Hence, we describe it here as new based on morphological and molecular evidence.

Material and methods

Morphological studies

The studied specimens were deposited in the herbarium of Southwest Forestry University (SWFC), Kunming, Yunnan Province, P.R. China. Terms regarding colour follow Petersen (1996). Macromorphological descriptions are based on field notes. Micromorphological features were observed on dried specimens under a Nikon Eclipse E100 light microscope following Cui *et al*. (2019). The following abbreviations are used: KOH = 5% potassium hydroxide; CB = cotton blue; CB+ = cyanophilous; IKI = Melzer's reagent; IKI– = non-amyloid and non-dextrinoid; L = mean spore length (arithmetic average of all spores); W = mean spore width (arithmetic average of all spores); $Q = L/W$ ratio; n (a/b) = number of spores (a) measured from given number (b) of specimens.

Molecular methods

CTAB rapid plant genome extraction kit-DN14 (Aidlab Biotechnologies Co., Ltd., Beijing, P.R. China) was used to obtain genomic DNA from dried specimens according to the manufacturer's instructions. The ITS region was amplified with the primer pair ITS5 and ITS4 (White *et al*. 1990). The nuclear 28S region was amplified with the primer pair LR0R and LR7. The PCR cycling procedure for ITS (after Shen *et al*. 2019) was as follows: initial denaturation at 95 °C for 3 min, followed by 35 cycles at 94 °C for 40 s, 58 °C for 45 s and 72 °C for 1 min, and final extension at 72 °C for 10 min. The PCR procedure for 28S was as follows: initial denaturation at 94 °C for 1 min, followed by 35 cycles at 94 °C for 30 s, at 48 °C for 1 min and 72 °C for 1.5 min, and final extension of 72 °C for 10 min. The PCR products were purified and directly sequenced at the Kunming Tsingke Biological Technology Limited Company (P.R. China). All newly generated sequences (Table 1) were deposited in GenBank (https://www.ncbi.nlm.nih.gov/nuccore/?term=Fasciodontia).

Phylogenetic analyses

Sequencher 4.6 (GeneCodes, Ann Arbor, Michigan, USA) was used to assemble and edit the generated sequence reads. Sequences were aligned in MAFFT 7 (https://mafft.cbrc.jp/alignment/server/) using the "G-INS-I" strategy and manually adjusted in BioEdit (Hall 1999). The sequence alignment was deposited in TreeBase (ID 28006) (https://treebase.org/treebase-web/search/studySearch.html). *Oxyporus populinus* was selected as an outgroup for phylogenetic analyses using ITS + 28S (Yurchenko *et al.* 2020). *Skeletocutis odora* was selected as an outgroup for analyses of ITS phylogenetic trees (Yurchenko *et al.* 2020).

Maximum parsimony (MP), Maximum Likelihood (ML) and Bayesian Inference (BI) analyses were applied to the ITS + 28S and ITS dataset sequences. Phylogenetic analyses followed Zhao and Wu (2017). MP analysis was performed in PAUP* ver. 4.0b10 (Swofford 2002). All characters were equally weighted and gaps were treated as missing data. Trees were inferred using the heuristic search option with TBR branch swapping and 1000 random sequence additions. Max-trees were set to 5000, branches of zero length were collapsed and all most-parsimonious trees were saved. Clade robustness was assessed using bootstrap (BT) analysis with 1000 replicates (Felsenstein 1985). Tree tree length (TL), consistency index (CI), retention index (RI), rescaled consistency index (RC) and homoplasy index (HI) were calculated for each most-parsimonious tree generated. ML was inferred using RAxML-HPC2 through the Cipres Science Gateway (http://www.phylo.org/sub_sections/portal). Branch support (BS) for ML analysis was determined by 1000 bootstrap replicates and evaluated under the gamma model.

MrModeltest 2.3 (Nylander 2004) was used to determine the best-fit evolution model for the data set for Bayesian Inference (BI). Bayesian

Inference was performed with MrBayes 3.1.2 with a general time reversible (GTR + I + G) model of DNA substitution and a gamma distribution rate variation across sites (Ronquist & Huelsenbeck 2003). Four Markov chains were used in each of the two runs from random starting trees for 720 000 generations (Fig. 1), with trees and parameters sampled every 100 generations. The first quarter of generations were discarded as burn-in. The majority rule consensus tree for all remaining trees was calculated. Branches were considered significantly supported if they received maximum likelihood bootstrap value (BS) > 70%, maximum parsimony bootstrap value (BT) > 70%, or Bayesian posterior probabilities (BPP) > 0.95.

Results

The ITS + 28S data set (Fig. 1) included sequences from 27 fungal specimens representing 23 species. The data set had an aligned length of 2388 characters, of which 1087 characters were constant and 532 parsimony-informative. The MP analysis yielded two equally parsimonious trees (TL = 3080, CI = 0.5951, HI = 0.4049, RI = 0.5646, RC = 0.3360). The best model for the ITS + 28S data set estimated and applied in the Bayesian analysis was GTR + I + G, lset nst = 6, rates = invgamma; prset statefreqpr = dirichlet (1, 1, 1, 1). Bayesian and ML analyses resulted in a similar topology as MP analysis, with an average standard deviation of split frequencies

Table 1. List of species, specimens and GenBank accession numbers of sequences used in this study.

Species	Specimen	GenBank accession no.		Source	Country
		ITS	28S		
Fasciodontia brasiliensis	MSK-F7245a, holotype	MK575201	MK598734	Yurchenko *et al.* 2020	Brazil
F. bugellensis	KAS-FD10705a	MK575203	MK598735	Yurchenko *et al.* 2020	France
F. bugellensis	MSK-F5548	MK575204	MK598736	Yurchenko *et al.* 2020	Belarus
F. yunnanensis	CLZhao6255	MZ146325	–	Present study	China
F. yunnanensis	CLZhao6280	MK811275	MZ146327	Present study	China
F. yunnanensis	CLZhao6385	MK811277	–	Present study	China
F. yunnanensis	CLZhao9414	MZ146326	–	Present study	China
Hastodontia halonata	HHB-17058 (CFMR)	MK575207	MK598738	Yurchenko *et al.* 2020	Mexico
H. hastata	KHL14646 (GB)	MH638232	MH638232	Viner *et al.* 2018	Norway
Hyphodontia arguta	Wu0806-44	JN571548	–	Wang & Chen 2017	Réunion
	KHL11938 (GB)	–	EU118633	Larsson 2007	
H. borbonica	FR-0219441, holotype	KR349240	–	Riebesehl *et al.* 2015	Réunion
		–	MH884915	Riebesehl *et al.* 2019	
H. pallidula	GEL2097	DQ340317	–	Riebesehl & Langer 2017	USA
		–	DQ340372	Yurchenko *et al.* 2020	
Kneiffiella abieticola	GEL2924	DQ340332	–	Unpublished	Sweden
	KHL12498 (GB)	–	DQ873601	Larsson *et al.* 2006	
K. barba-jovis	KHL11730 (GB)	DQ873609	–	Larsson *et al.* 2006	Sweden
		–	DQ873610		
K. palmae	KAS-GEL3456	DQ340333	DQ340369	Yurchenko *et al.* 2020	China
K. subalutacea	KAS-GEL2196	DQ340341	DQ340362	Yurchenko *et al.* 2020	Norway
Lyomyces fimbriatus	Wu911204-4	MK575210	MK598740	Yurchenko *et al.* 2020	China
L. mascarensis	KAS-GEL4833, holotype	KY800399	KY795964	Yurchenko *et al.* 2017	Réunion
L. organensis	MSK-F7247, holotype	KY800403	KY795967	Yurchenko *et al.* 2017	Brazil
L. pruni	GB90287	MK575211	MK598741	Yurchenko *et al.* 2020	Sweden
L. sambuci	KAS-JR7	KY800402	KY795966	Yurchenko *et al.* 2017	Germany
Oxyporus populinus	CBS218.39	MH855986	MH867486	Vu *et al.* 2019	USA
Xylodon detriticus	Zíbarová26.05.17	MH320794	MH638264	Viner *et al.* 2018	Czechia
X. exilis	TUB-FO42565, holotype	MH880198	MH884898	Riebesehl *et al.* 2019	China
X. flaviporus	MA-Fungi79440	MH260071	MH260066	Fernández-López *et al.* 2018	Germany
X. hyphodontinus	LIPGG-MAR12-238	MH880207	MH884905	Riebesehl *et al.* 2019	Martinique
X. quercinus	CBS333.62	MH858169	MH869761	Vu *et al.* 2019	France

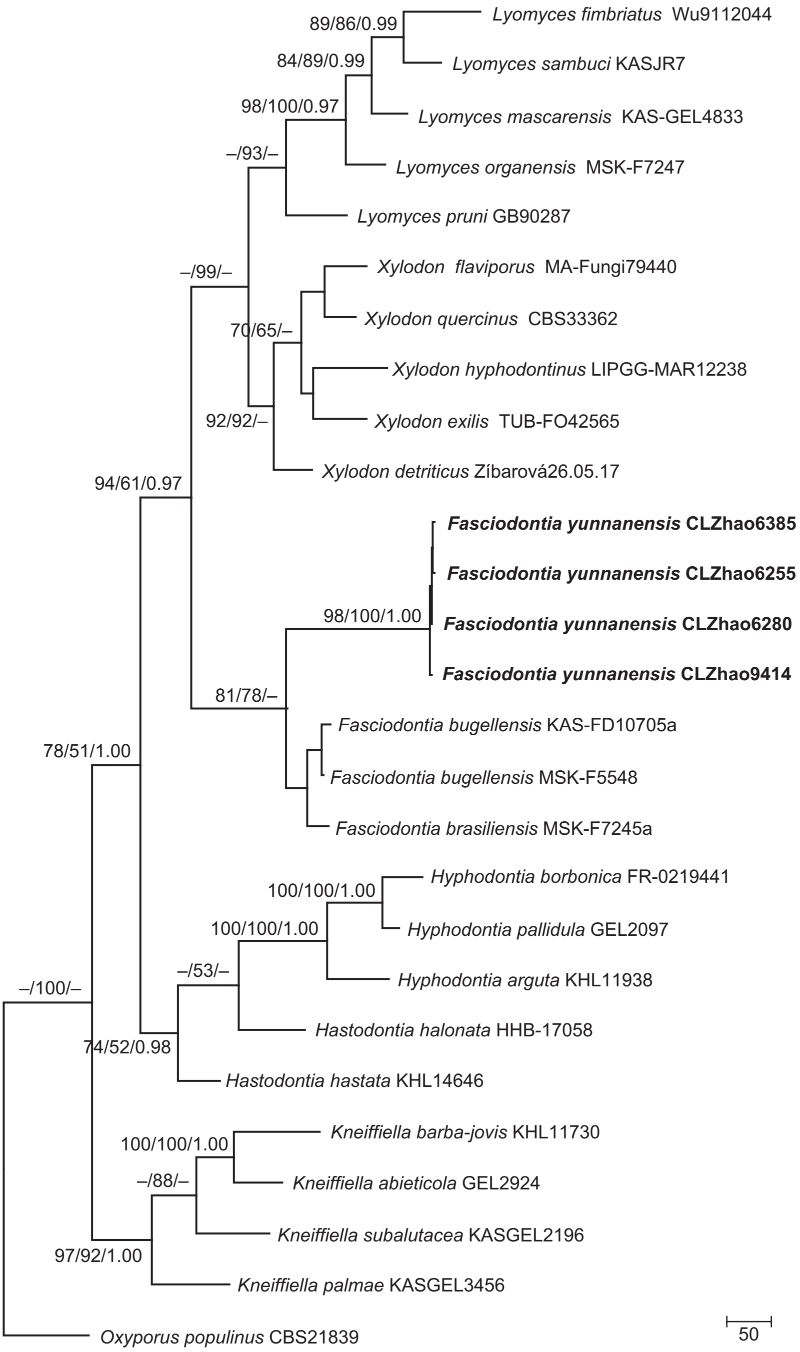

Fig. 1. Maximum parsimony strict consensus tree illustrating the phylogeny of *Fasciodontia yunnanensis* and related species in *Hyphodontia s. lato* based on ITS + 28S sequences. Branches are labelled with maximum likelihood bootstrap values > 70%, parsimony bootstrap values > 50%, and Bayesian posterior probabilities > 0.95.

equalling 0.008396 (BI), and the effective sample size (ESS) across the two runs is the double of the average ESS (avg ESS) equalling 948.5. In the phylogenetic reconstruction (Fig. 1) of *Hyphodontia s. lato*, the new species was nested in *Fasciodontia* and formed a well-supported lineage.

Fasciodontia yunnanensis C.L. Zhao, *sp. nova* (Figs. 2 and 3)

MycoBank MB 839639. — Holotype: China. Yunnan Province: Yuxi, Xinping County, Mopanshan National Forestry Park, 23.98°N, 102.04°E, on fallen branch of angiosperm, 18 January 2018 *CLZhao6385 (SWFC006385)*. — Para-

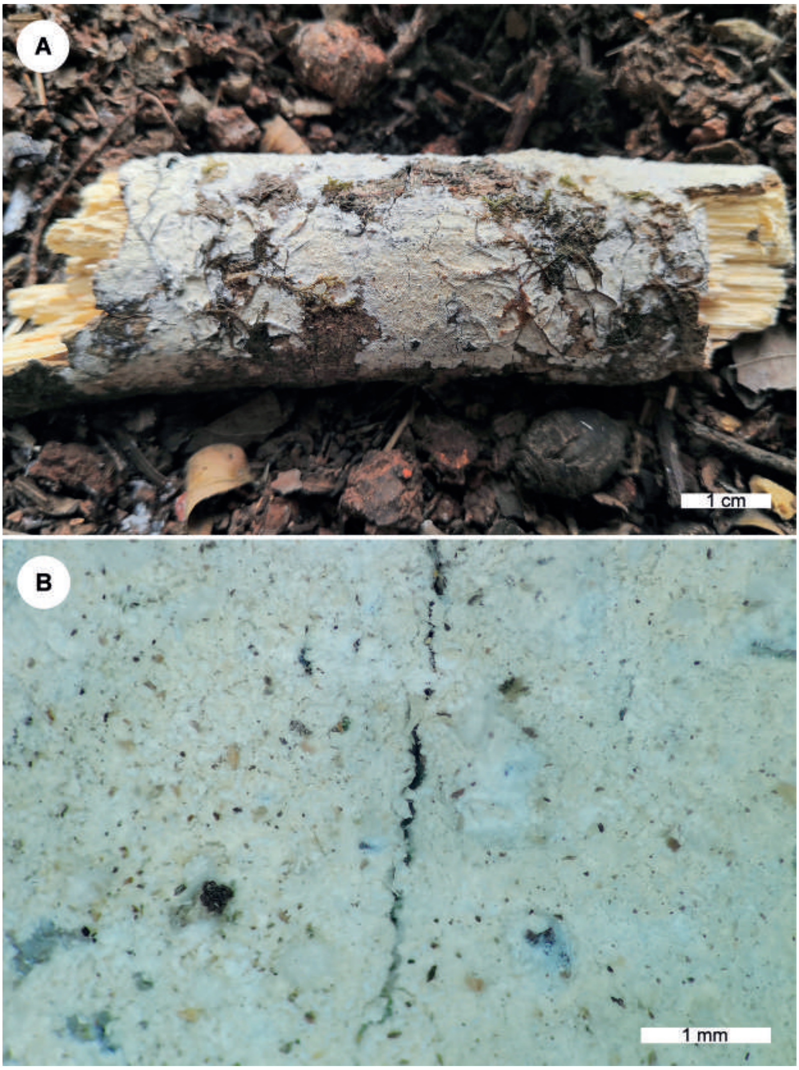

Fig. 2. Basidiomata of *Fasciodontia yunnanensis* (holotype).

TYPES: China. Yunnan Province: Yuxi, Xinping County, Mopanshan National Forestry Park, 23.98°N, 102.04°E, on fallen branch of angiosperm, 18 January 2018 *CLZhao6255* (*SWFC006255*), *CLZhao 6280* (*SWFC006280*); China. Yunnan Province: Puer, Jingdong County, The Forestry of Pineapple, 24.39°N, 100.78°E, on fallen branch of angiosperm, 4 January 2019 *CLZhao9414* (*SWFC009414*).

ETYMOLOGY: *yunnanensis* (Lat.), referring to the provenance (Yunnan Province) of the type specimens.

Basidiomata annual, resupinate, membranaceous when fresh, becoming hard membranaceous, up to 11 cm long and 3 cm wide, 100–300 μm thick. Hymenial surface minutely odontioid, aculei 50–100 μm long, 10–13 aculei/mm, consisting of projecting hyphae with numerous encrusted crystals, cream when fresh, turning cream to pale pink upon drying, cracking with age. Margin narrow, slightly cream. Hyphal system pseudodimitic; generative hyphae with clamp connections, colourless, thin- to slight thick-walled, rarely branched, 1.5–2.5 μm in diameter; moderately CB+ , IKI–, tissues slightly yellowish in KOH. Cystidia of two types: (1) submoniliform cystidia, numerous, colourless, thin-walled, smooth, 18–39.5 × 3–5 μm, and (2) tramacystidia skeletal-like in aculei loosely encrusted, thin-walled, 70–120 × 4–7 μm; cystidioles absent. Basidia clavate to utriform with one constriction, thin-walled, with four sterigmata and a basal clamp connection,

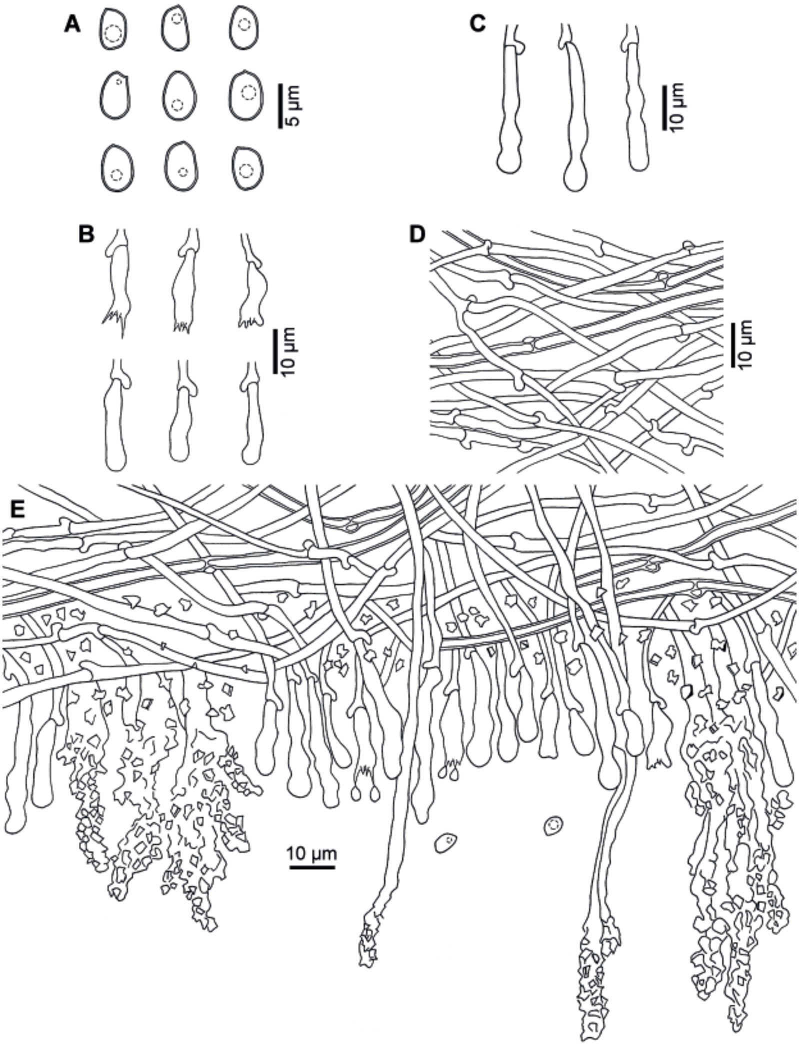

Fig. 3. Microscopic structures of *Fasciodontia yunnanensis*. — **A**: Basidiospores. — **B**: Basidia and basidioles. — **C**: Cystidia. — **D**: Hyphae from subiculum. — **E**: A section of hymenium.

9.5–21.5 × 3.5–4.5 µm; basidioles abundant, in shape similar to basidia, but slightly smaller. Basidiospores ellipsoid, colourless, thick-walled, smooth, IKI–, slightly to moderately cyanophilous, with 1 globule, 3.1–5.7 × 2.1–4.1 µm, L = 4.67 µm, W = 3.31 µm, Q = 1.3–1.5 (n = 90/3).

SUBSTRATE AND DISTRIBUTION: Lignicolous, causing white rot. Thus far known only from the type locality (Yunnan Province, China).

Discussion

The phylogenetic analysis of ITS + nLSU data set by Yurchenko *et al*. (2020) revealed that seven main clades were nested in *Hyphodontia s. lato*: *Fasciodontia*, *Hastodontia*, *Hyphodontia*, *Kneiffiella*, *Lyomyces*, *Tubulicrinis* and *Xylodon*. The two species of *Fasciodontia* grouped with *Lyomyces* and *Xylodon*. In our study, *F. yunnanensis* nested in *Fasciodontia*, formed a monophyletic lineage, and grouped with *F. brasiliensis* and *F. bugellensis* (Fig. 1). However, *F. brasiliensis* differs from *F. yunnanensis* by having larger aculei (7–10 mm), narrower cystidia (15–25 × 3–5 µm) and separating projecting generative hyphae (Yurchenko *et al*. 2020). *Fasciodontia bugellensis* differs in having white to chalky or cream hymenial surface, and larger basidiospores (5.5–6.5 × 3.5–4.5 µm; Bernicchia & Gorjón 2010).

Morphologically, *Lyomyces bambusinus*, *L. cremeus*, *L. macrosporus*, *L. wuliangshanensis* and *Xylodon exilis* resemble *F. yunnanensis* by having thick-walled basidiospores. *Lyomyces bambusinus* differs from *F. yunnanensis* by its colliculose to tuberculate hymenial surface and presence of capitate and tapering cystidia, *L. cremeus* by its smooth hymenial surface, *L. macrosporus* by its reticulate hymenial surface and larger basidiospores (6.7–8.9 × 4.4–5.4 µm), *L. wuliangshanensis* by its smooth to more or less tuberculate hymenial surface and capitate cystidia (Chen & Zhao 2020), and *X. exilis* by its narrowly utriform basidia (Riebesehl *et al.* 2019).

Hyphodontia arguta, *Xylodon borealis*, *X. filicinus*, *X. pseudolanatus* and *X. vesiculosus* resmble *F. yunnanensis* by having minutely odontioid hymenophore. *Hyphodontia arguta* differs from *F. yunnanensis* by having a hyphoid hymenophore and tubular cystidia; *X. borealis F. yunnanensis* by having capitate cystidia and thin-walled basidiospores (Bernicchia & Gorjón 2010); *X. filicinus* by having subcylindrical cystidia and globose to subglobose, thin-walled basidiospores; *X. pseudolanatus* by having capitate cystidia and cylindrical, constricted basidia; and *X. vesiculosus* by having utriform to subcylindrical basidia and ellipsoid to narrowly ellipsoid basidiospores (Riebesehl *et al.* 2019).

Hastodontia halonata, *H. hastata* and *Xylodon brevisetus* resmble *F. yunnanensis* by having moniliform cystidia. *Hastodontia halonata* differs from *F. yunnanensis* by having narrower basidiospores (4.5–5.5 × 1.5–2 µm), *H. hastata* by having subulate cystidia, and *X. brevisetus* by having thin-walled basidiospores (Bernicchia & Gorjón 2010).

The family Schizoporaceae belongs to the order Hymenochaetales, which is an extensively studied group (Dai 2012, Qin & Zhou 2013, Spirin *et al*. 2014, Zhou 2014, Zhou *et al*. 2014, Viner *et al*. 2018, Cui *et al*. 2019, Riebesehl *et al*. 2019, Shi *et al*. 2019, He *et al*. 2020, Xu *et al*. 2020, Wang & Zhao 2021), but the species diversity, especially in the subtropical and tropical areas of China, is still not well known.

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