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Arachnophora dinghuensis sp. nov. and *Websteromyces inaequale* sp. nov., and two new records of anamorphic fungi from dead branches of broad-leaved trees in China Original Research Article

Pages 329-335

Jian Ma, Ji-Wen Xia, Xiu-Guo Zhang, Rafael F. Castañeda-Ruíz

Abstract | Close research highlights | PDF (1488 K)

Highlights

- *Arachnophora dinghuensis* and *Websteromyces inaequale* are described as new species.
- A key to *Arachnophora* species is provided.
- *Websteromyces inaequale* is added as the second species in the genus.
- *Rhexoacrodictys queenslandica* and *Solicorynespora sylvatica* are new records for Chinese mycota.

Fibrodontia alba sp. nov. (Basidiomycota) from Taiwan Original Research Article

Pages 336-343

Eugene Yurchenko, Sheng-Hua Wu

Abstract | Close research highlights | PDF (2569 K)

Highlights

- New species *Fibrodontia alba* was found at the foothills in central Taiwan.
- Phylogenetical study based on ITS and 28S rRNA gene placed *F. alba* in *F. gossypina* complex.
- Main differences of *F. alba* from *F. gossypina* are in morphology of skeletal-like and subicular hyphae.

Three species of *Fulvifomes* (Basidiomycota, Hymenochaetales) associated with rots on mangrove tree *Xylocarpus granatum* in Thailand Original Research Article
Pages 344-354
Tsutomu Hattori, Jariya Sakayaroj, Evan Benjamin Gareth Jones, Satinee Suetrong, Sita Preedanon, Anupong Klaysuban
Abstract | Close research highlights | PDF (2073 K)

Highlights

- We described *Fulvifomes xylocarpicola*, *F. siamensis*, and *F. halophilus*.
- *Fulvifomes mangrovicus* comb. nov. is proposed.
- We examined type specimens of *Fulvifomes mangrovicus*, *F. merrillii*, *F. rimosus*, and *F. swieteniae*.
- A key to the world species of *Fulvifomes* is provided.

Coprinopsis asiaticiphlyctidospora sp. nov., an agaric ammonia fungus from Amami and Okinawa, southern Japan
Pages 355-360
Toshimitsu Fukiharu, Kiminori Shimizu, Hideyuki Utsunomiya, Jay Kant Raut, Ryutaro Goto, Tomoko Okamoto, Makoto Kato, Reiko Horigome, Tatsuo Furuki, Noriko Kinjo
Abstract | Close research highlights | PDF (1551 K)

Highlights

- A new ammonia fungus, *Coprinopsis asiaticiphlyctidospora* is described.
- This new taxon belongs to the *C. phlyctidospora* species complex.
- This new species is distinguished from the related one in basidiospore morphology.

Three new species of *Tilletia* on *Eriachne* from north-western Australia Original Research Article
Pages 361-366
Ying-Ming Li, Roger Graham Shivas, Lei Cai
Abstract | Close research highlights | PDF (1926 K)

Morphological, molecular and biological characterization of *Esteya vermicola*, a nematophagous fungus isolated from intercepted wood packing materials exported from Brazil Original Research Article

Pages 367-377

Xuan Wang, Tingting Wang, Jincheng Wang, Tinglong Guan, Hongmei Li

Abstract | Close research highlights | PDF (2503 K)

Highlights

- South American NKF 13222 was isolated from *Bursaphelenchus rainulfi* intercepted from wood packing materials exported from Brazil.
- NKF 13222 is different from other *E. vermicola* strains in germination mode of conidia.
- NKF 13222 presented higher infectivity to aphelenchids than to tylenchid nematodes.

The genus *Pleurotus* in Brazil: a molecular and taxonomic overview Original Research Article

Pages 378-389

Nelson Menolli Jr., Bruna Suellen Breternitz, Marina Capelari

Abstract | Close research highlights | PDF (1505 K)

Highlights

- Recognition of at least five species of *Pleurotus* certainly known from Brazil.
- *Pleurotus albidus*, *P. djamor*, *P. fuscosquamulosus*, *P. pulmonarius* and *P. rickii*.
- Molecular analysis with ITS sequences confirms the occurrence of these species.
- A list including 71 records of *Pleurotus* names updates the knowledge of the genus in Brazil.

Melampsora salicis-sinicae (Melampsoraceae, Pucciniales), a new rust fungus found on willows in China Original Research Article

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Melampsora salicis-sinicae (Melampsoraceae, Pucciniales), a new rust fungus found on willows in China Original Research Article

Pages 390-399

Peng Zhao, Cheng-Ming Tian, Yi-Jian Yao, Qi Wang, Makoto Kakishima, Yuichi Yamaoka

Abstract | Close research highlights | PDF (1132 K) | Supplementary content

Highlights

- A new rust fungus, *Melampsora salicis-sinicae*, is described on five willow species in China.
- This species is characterized by amphigenous telia and subcuticular teliospores with apparently thickened apices.
- This new species is morphologically similar to *M. capraearum* and *M. epiphylla*.

A new species of *Entoloma* from India

Pages 400-404

K.N. Anil Raj, K.P. Deepna Latha, T.K. Arun Kumar, Patinjareveettil Manimohan

Abstract | Close research highlights | PDF (1407 K)

Synthesis of Japanese *Boletus edulis* ectomycorrhizae with Japanese red pine Original Research Article

Pages 405-416

Naoki Endo, Fuminori Kawamura, Ryoko Kitahara, Daisuke Sakuma, Masaki Fukuda, Akiyoshi Yamada

Abstract | Close research highlights | PDF (4221 K) | Supplementary content

Highlights

- *Boletus edulis* basidiomata collected from Japanese boreal forests were identified microscopically and phylogenetically.
- *Boletus edulis* was isolated efficiently on malt extract agar medium.
- In vitro synthesis of *B. edulis* ectomycorrhizae with *Pinus densiflora* host was successful.
- Synthesized *B. edulis* ectomycorrhizae were acclimatized under laboratory conditions.

Perenniporia cinereofusca sp. nov. (Polyporales, Basidiomycota) evidenced by morphological characters and phylogenetic analysis

Pages 417-422

Chang-Lin Zhao, Lu-Lu Shen, Bao-Kai Cui

Abstract | Close research highlights | PDF (1981 K) | Supplementary content

Highlights

- A new species, *Perenniporia cinereofusca*, matching the concept of *Perenniporia* was described.
- Phylogenetic analysis was carried out based on ITS + nLSU sequences of *Perenniporia* sensu lato.
- Phylogenetic analysis revealed nine clades for 47 species of *Perenniporia* sensu lato used in this study.

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Short communication

Perenniporia cinereofusca sp. nov. (Polyporales, Basidiomycota) evidenced by morphological characters and phylogenetic analysis

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ABSTRACT

A new *Perenniporia* species, *P. cinereofusca*, is described based on morphological and molecular characters. It is characterized by an annual growth habit, resupinate basidiocarps with gray to pale brown pore surface, tissues becoming black in 5% potassium hydroxide (KOH), a dimitic hyphal system with weakly dextrinoid skeletal hyphae and hyaline to pale yellowish, distinctly thick-walled and indextrinoid basidiospores (6.5–7.7 × 5.3–6.3 μm), and presence of dendrohyphidia and large rhomboid crystals. Both morphological and molecular evidence confirmed the placement of the new species in *Perenniporia* sensu stricto and showed its relationships with similar species in the genus.

Perenniporia Murrill is a large, cosmopolitan genus characterized by poroid basidiomata, thick-walled, ellipsoid to distinctly truncate basidiospores, and cyanophilous and variable dextrinoid and amyloid reactions. The hyphal system of *Perenniporia* species is di- or trimitic with clamp connections on generative hyphae, while the vegetative hyphae are cyanophilous and variably dextrinoid or amyloid (Decock and Stalpers 2006). Until now about one hundred species have been described or transferred to the genus (http://www.indexfungorum.org/names/Names.asp).

Taxonomic studies of *Perenniporia* in China have been carried out recently, and 49 species were recorded from the country (Dai et al. 2002; Cui et al. 2007; Xiong et al. 2008), including several new species described from the country in recent three years (Dai 2010; Dai et al. 2011; Cui and Zhao 2012; Zhao and Cui 2012, 2013a b; Zhao et al. 2013). As a continuation of these surveys, an undescribed species matching the concepts of *Perenniporia* was found. To confirm the affinity of the new species of *Perenniporia*, phylogenetic analysis was carried out based on the internal transcribed spacer (ITS) regions and the large subunit nuclear ribosomal RNA gene (nLSU) sequences of *Perenniporia* sensu lato.

The specimens of *Perenniporia cinereofusca* were deposited at the herbaria of the Institute of Microbiology, Beijing Forestry University (BJFC) and the Institute of Applied Ecology, Chinese Academy of Sciences (IFP). The microscopic routine

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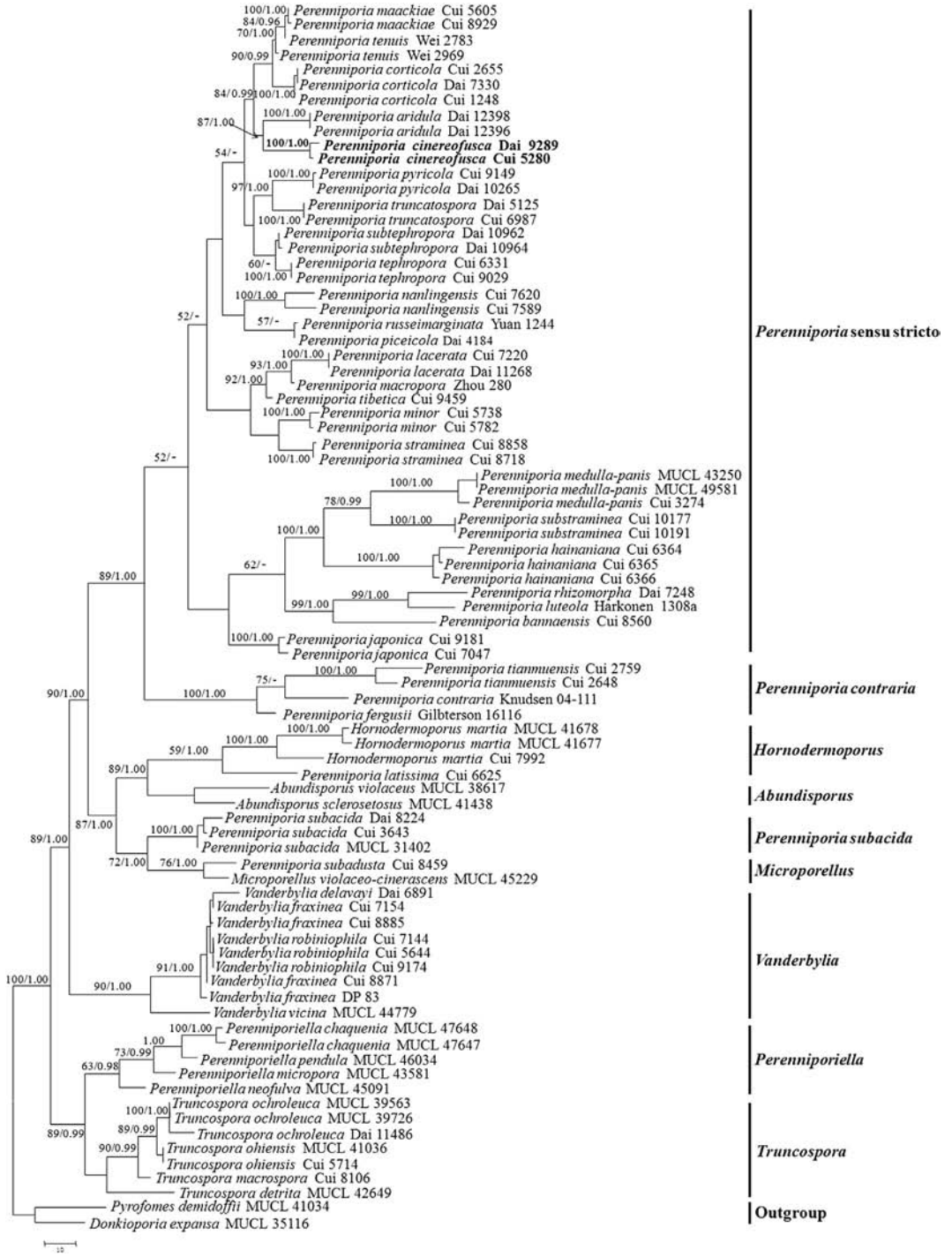

Fig. 1 – One of the most parsimonious trees illustrating the phylogeny of *Perenniporia cinereofusca* and related species based on ITS + nLSU sequences. Parsimony bootstrap proportions (before the slash markers) higher than 50% and Bayesian posterior probabilities (after the slash markers) more than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

followed Li and Cui (2013). Sections were studied at magnification up to ×1000 using a Nikon Eclipse 80i microscope and phase contrast illumination (Nikon, Tokyo). Drawings were made with the aid of a drawing tube. Microscopic features, measurements and drawings were made from slide preparations stained with Cotton Blue and Melzer's reagent. Spores were measured from sections cut from the tubes. In presenting the variation in the size of the spores, 5% of measurements were excluded from each end of the range, and were given in parentheses. In the text the following abbreviations were used: IKI = Melzer's reagent, KOH = 5% potassium hydroxide, IKI– = negative in Melzer's reagent, CB = Cotton Blue, CB+ = cyanophilous, *L* = mean spore length (arithmetic average of all spores), *W* = mean spore width (arithmetic

average of all spores), Q = variation in the *L*/*W* ratios between the specimens studied, *n* = number of spores measured from given number of specimens. Special color terms followed Petersen (1996).

Phire® Plant Direct PCR Kit (Finnzymes, Vantaa, Finland) was used to obtain PCR products from dried specimens, according to the manufacturer's instructions. A small piece of dried fungal specimen was lysed in 30 μl dilution buffer for DNA extraction. After incubating 3 min at room temperature, 0.75 μl of the supernatant were used as template for a 30 μl PCR reaction. The ITS regions were amplified with the primers ITS4 and ITS5 (White et al. 1990), and the nLSU with the primers LR0R and LR7 (http://www.biology.duke.edu/fungi/mycolab/primers.htm). The PCR procedure for ITS was as follows: initial denaturation at 98 °C for 5 min, followed by 39 cycles at 98 °C for 5 s, 58 °C for 5 s and 72 °C for 5 s, and a final extension of 72 °C for 10 min. The only difference of the nLSU amplification procedure was its annealing temperature was 48 °C. DNA sequencing was performed at Beijing Genomics Institute, China, with the same primers. Four newly generated sequences from *Perenniporia cinereofusca* were submitted to GenBank (KF568892–KF568895).

The four new sequences from specimens of *Perenniporia cinereofusca* were aligned with additional sequences of *Perenniporia* sensu lato downloaded from GenBank (Supplementary data) using BioEdit (Hall 1999) and ClustalX (Thompson et al. 1997). In the study, nuclear ribosomal RNA genes were used to determine the phylogenetic position of the new species. Sequence alignment was deposited at TreeBASE (http://purl.org/phylo/treebase/phylows/study/TB2:S14660?x-access-code=eb02240e3f4a920134fb1b49f169ad53&format=html).

Maximum parsimony analysis was applied to the combined dataset of ITS and nLSU sequences. Sequences of *Donkioporia expansa* (Desm.) Kotl. & Pouzar and *Pyrofomes demidoffii* (Lév.) Kotl. & Pouzar obtained from GenBank were used as outgroups (Zhao and Cui 2013a). The tree construction procedure was performed in PAUP* version 4.0b10 (Swofford 2002). All characters were equally weighted and gaps were treated as missing data. Trees were inferred using the heuristic search option with TBR branch swapping and 1000 random sequence additions. Max-trees were set to 5000, branches of zero length were collapsed and all parsimonious trees were saved. Clade robustness was assessed using a bootstrap (BT) analysis with 1000 replicates (Felsenstein 1985). Descriptive tree statistics tree length (TL), consistency index (CI), retention index (RI), rescaled consistency index (RC), and homoplasy index (HI) were calculated for each Maximum Parsimonious Tree (MPT) generated.

MrMODELTEST2.3 (Posada and Crandall 1998; Nylander 2004) was used to determine the best-fit evolution model for each dataset for Bayesian inference (BI). Bayesian inference was calculated with MrBayes3.1.2 with a general time reversible (GTR) model of DNA substitution and a gamma distribution rate variation across sites (Ronquist and Huelsenbeck 2003). Four Markov chains were run for 2 runs from random starting trees for 2 million generations, and trees were sampled every 100 generations. The first one-fourth generations were discarded as burn-in. A majority rule consensus tree of all remaining trees was calculated. Branches that received bootstrap support for maximum parsimony (MP) and Bayesian posterior probabilities (BPP) greater than or equal to 75% (MP) and 0.95 (BPP) respectively were considered as significantly supported.

Perenniporia cinereofusca B.K. Cui & C.L. Zhao, sp. nov.

Figs. 2, 3.

MycoBank no.: MB 805466.

Differs from other *Perenniporia* species by an annual growth habit, resupinate basidiocarps with gray to pale brown pore surface, tissues pale brown to black in KOH, and a dimitic hyphal system with weakly dextrinoid skeletal hyphae and hyaline to pale yellowish, distinctly thick-walled, smooth, indextrinoid basidiospores (6.5–7.7 × 5.3–6.3 μm), and presence of dendrohyphidia and large rhomboid crystals.

Type: China, Hainan Prov., Ledong County, Jianfengling Nature Reserve, on fallen angiosperm trunk, 18 November 2007, Dai 9289 (Holotype in BJFC).

rRNA gene sequence ex holotype: KF568893 (ITS), KF568895 (nLSU).

Etymology: *Cinereofusca* (Lat.), referring to the gray to pale brown pore surface.

Basidiocarps annual, resupinate, adnate, without odor or taste when fresh, becoming corky upon drying, up to 8 cm long, 5 cm wide, 1.5 mm thick at center. Pore surface cream to clay-buff when fresh, gray to pale brown upon drying; pores round to angular, 4–6 per mm; dissepiments thin to thick, entire. Sterile margin wide, brown, up to 3 mm wide. Subiculum clay-buff to brown, thin, up to 0.5 mm thick. Tubes concolorous with pore surface, corky, up to 1 mm long. Hyphal system dimitic; generative hyphae with clamp connections; skeletal hyphae weakly dextrinoid, CB+; tissues pale brown to black in KOH. Generative hyphae in subiculum infrequent, hyaline, thin-walled, usually unbranched, 2.0–3.0 μm in diameter; subicular skeletal hyphae dominant, hyaline to pale yellowish, thick-walled with a wide lumen, frequently branched, interwoven, 2.5–3.5 μm in diameter. Tramal generative hyphae infrequent, hyaline, thin-walled, usually unbranched, 2.0–2.5 μm in diameter; skeletal hyphae in trama dominant, hyaline to pale yellowish, thick-walled with a wide to narrow lumen, frequently branched, interwoven, 2.0–3.0 μm in diameter. Dendrohyphidia common at the dissepiments. Cystidia absent, but fusoid cystidioles present, hyaline, thin-walled, 22.0–33.0 × 6.0–7.0 μm; basidia clavate, with four sterigmata and a basal clamp connection,

Fig. 2 – Basidiocarp of *Perenniporia cinereofusca* (holotype). *Bar*: 1 cm.

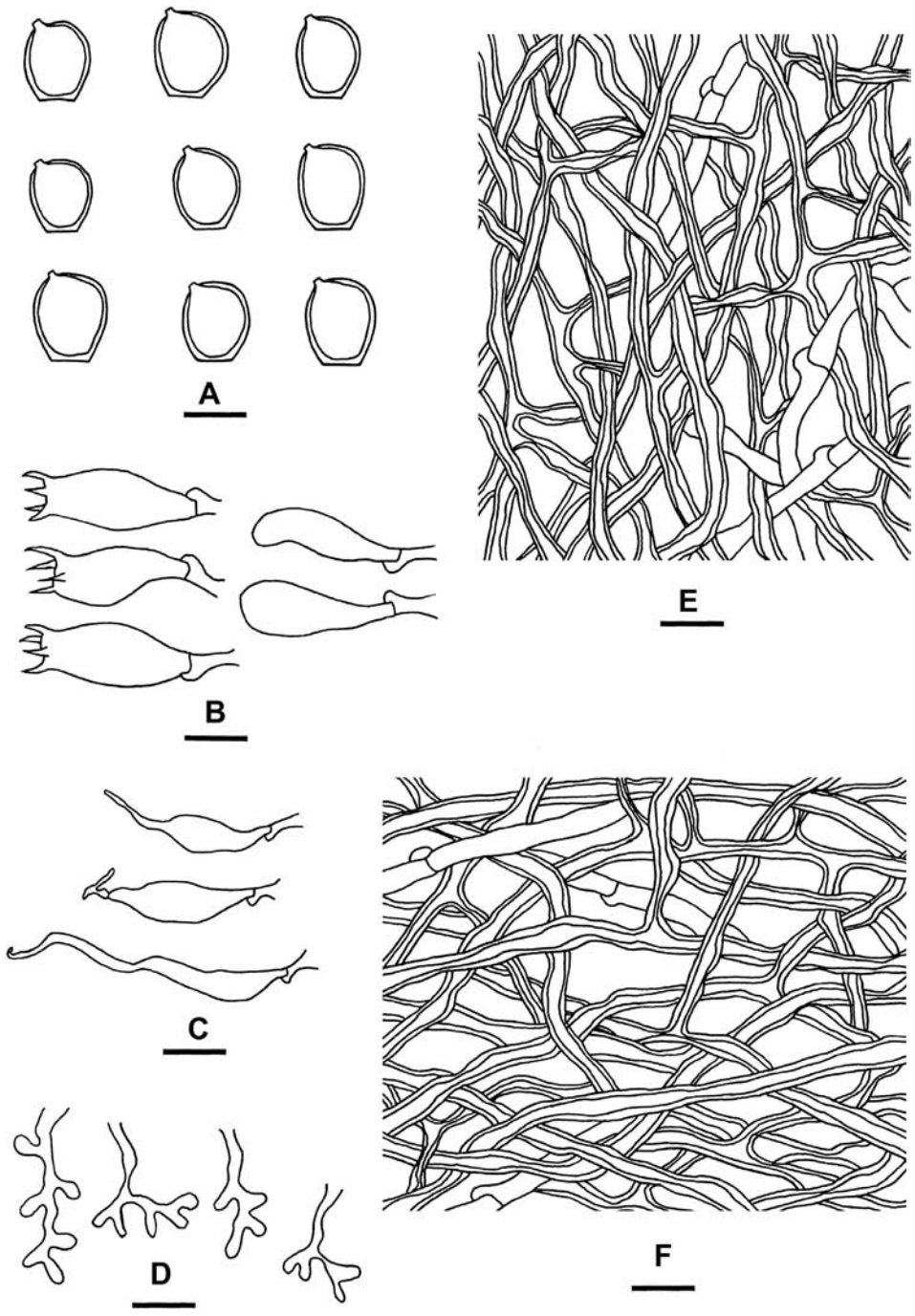

Fig. 3 – Microscopic structures of *Perenniporia cinereofusca* (drawn from the holotype). A: Basidiospores. B: Basidia and basidioles. C: Cystidioles. D: Dendrohyphidia. E: Hyphae from trama. F: Hyphae from subiculum. *Bars*: A 5 μm; B–F 10 μm.

20.0–25.0 × 9.5–11.5 μm; basidioles dominant, in shape similar to basidia, but slightly smaller. Large rhomboid crystals abundant. Basidiospores ellipsoid, truncate, hyaline to pale yellowish, distinctly thick-walled, smooth, IKI–, CB+, (6.2–)6.5–7.7(–8.0) × (5.1–)5.3–6.3(–6.5) μm, L = 7.02 μm, W = 5.75 μm, Q = 1.15–1.22 (n = 60/2).

Type of rot: White rot.

Additional specimen examined: China, Hainan Prov., Lingshui County, Diaoluoshan Forest Park, on fallen angiosperm trunk, 20 November 2007, Cui 5280 (BJFC & IFP).

The ITS + nLSU dataset included sequences from 82 fungal specimens representing 47 taxa of *Perenniporia* sensu lato. The dataset had an aligned length of 2044 characters including gaps in the dataset (659 characters for ITS, 1385 characters for nLSU), of which 1532 characters are constant, 128 are variable and parsimony-uninformative, and 384 are parsimony-informative. Maximum parsimony analysis yielded 100 equally parsimonious trees (TL = 1754, CI = 0.410, RI = 0.729, RC = 0.299, HI = 0.589). Best model for ITS + nLSU estimated and applied in the Bayesian analysis: GTR + I + G, lset nst = 6,

rates = invgamma; prset statefreqpr = dirichlet (1,1,1,1). Bayesian analysis resulted in the same topology with an average standard deviation of split frequencies = 0.007869.

The phylogeny (Fig. 1) inferred from ITS + nLSU sequences demonstrates nine major clades for 47 sampled species of *Perenniporia* sensu lato. Two sampled specimens of the new species, *P. cinereofusca*, formed a well-supported lineage distinct from other species, which recovered in the *Perenniporia* sensu stricto clade.

In the present study, *Perenniporia cinereofusca* is described as new based on morphological differences and molecular phylogenetic analyses. Molecular study based on sequence data from the ribosomal ITS + nLSU regions (Fig. 1) confirmed the generic placement of the new species, and it formed monophyletic lineage with strong support (100% MP, 1.00BPP).

Morphologically, the truncate and large basidiospores ($L > 6$ μm) of the new species remind several similar *Perenniporia* species in China. *Perenniporia pyricola* Y.C. Dai & B.K. Cui may be confused with *P. cinereofusca* in producing resupinate basidiocarps, a dimitic hyphal system and similar basidiospores (6.3–7.6 × 4.8–6.5 μm); however, *P. pyricola* differs in its perennial basidiocarps and dextrinoid basidiospores (Dai 2010). *Perenniporia lacerata* B.K. Cui & C.L. Zhao is similar to *P. cinereofusca* by annual, resupinate basidiocarps, a dimitic hyphal system and ellipsoid, truncate basidiospores (6.1–7.0 × 5.0–5.7 μm); however, it differs by having lacerate pores and dextrinoid basidiospores (Zhao and Cui 2013b).

The following four *Perenniporia* species produce basidiocarps with tissues turning pale brown to black in KOH: *P. centrali-africana* Decock & Mossebo (Decock and Mossebo 2001), *P. inflexibilis* (Berk.) Ryvarden (Decock et al. 2002), *P. subtephropora* B.K. Cui & C.L. Zhao (Zhao and Cui 2013a) and *P. tephropora* (Mont.) Ryvarden (Gilbertson and Ryvarden 1987). *Perenniporia centrali-africana* differs from *P. cinereofusca* in having small sized pores (7–8 per mm) and basidiospores (4.8–6.0 × 3.8–5.3 μm; Decock and Mossebo 2001). *Perenniporia inflexibilis* is distinguished from *P. cinereofusca* by having pileate basidiocarps and smaller basidiospores (4.1–5.0 × 3.5–4.3 μm; Decock et al. 2002). *Perenniporia subtephropora* is separated from *P. cinereofusca* by its small sized pores (7–8 per mm) and dextrinoid basidiospores (Zhao and Cui 2013a). *Perenniporia tephropora* is unique in having perennial basidiocarps and unbranched skeletal hyphae (Núñez and Ryvarden 2001).

Phylogenetically, *Perenniporia aridula* B.K. Cui & C.L. Zhao sisters to *P. cinereofusca* inferred from the ITS + nLSU rRNA gene regions with strong supports (87% BP, 1.00BPP; Fig. 1). However, morphologically, *P. aridula* differs from *P. cinereofusca* by its distinctly perennial basidiocarps with cream to buff-yellow pore surface, smaller pores (6–7 per mm) and indextrinoid skeletal hyphae and dextrinoid basidiospores (Zhao et al. 2013).

Disclosure

The authors declare no conflict of interest. All the experiments undertaken in this study comply with the current laws of the People's Republic of China.

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Appendix A. Supplementary data

Supplementary data related to this article can be found at http://dx.doi.org/10.1016/j.myc.2013.11.006.

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