Two new species of *Perenniporia* (Polyporales, Basidiomycota)

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Abstract

Two new species of *Perenniporia*, *P. pseudotephropora* sp. nov. and *P. subcorticola* sp. nov., are introduced respectively from Brazil and China based on morphological characteristics and molecular data. *Perenniporia pseudotephropora* is characterised by perennial, pileate basidiocarps with distinctly stratified tubes, grey pores, tissues becoming dark in KOH, a dimitic hyphal system with slightly dextrinoid arboriform skeletal hyphae and broadly ellipsoid to subglobose, truncate, weakly dextrinoid, cyanophilous basidiospores, measuring 4.9–5.2 × 4–4.8 μm. *Perenniporia subcorticola* is characterised by resupinate basidiocarps, yellow pores with thick dissepiments, tissues becoming dark in KOH, flexuous skeletal hyphae, ellipsoid, truncate and slightly dextrinoid basidiospores, measuring 4.2–5 × 3.5–4.2 μm. The morphologically-similar species and phylogenetically closely-related species to the two new species are discussed.

Keywords

phylogeny, polypore, taxonomy, wood-decaying fungi

Introduction

*Perenniporia* Murrill (Polyporales, Basidiomycetes) is typified by *Polyporus unitus* Pers. (Decock and Stalpers 2006). Species in the genus are important, not only for the wood-decaying, but also for their potential application in both biomedical engineering and biodegradation (Younes et al. 2007; Dai et al. 2009; Zhao et al. 2013; Si et al. 2016). *Perenniporia* is characterised by mostly perennial, resupinate to pileate ba-
sidiocarps, a dimitic to trimitic hyphal system with generative hyphae bearing clamp connections, cyanophilous and variably dextrinoid skeletal hyphae or skeletal-binding hyphae in most species and ellipsoid, to subglobose, truncate or not, thick-walled, variably dextrinoid and cyanophilous basidiospores. All *Perenniporia* species cause a white rot (Ryvarden and Gilbertson 1994; Decock and Ryvarden 1999; Cui et al. 2019).

Extensive studies on the genus have been carried out during the last 20 years showing a high species diversity and nowadays, 120 taxa have been found (e.g. Hattori and Lee 1999; Decock 2001a, b; Decock et al. 2001; Dai et al. 2002; Decock and Stalpers 2006; Cui et al. 2007; Xiong et al. 2008; Cui and Zhao 2012; Zhao and Cui 2012; Zhao et al. 2013; Decock and Ryvarden 2015; Jang et al. 2015; Decock 2016; Viacheslav and Ryvarden 2016; Huang et al. 2017; Ji et al. 2017; Liu et al. 2017; Shen et al. 2018; Cui et al. 2019; Zhao and Ma 2019).

According to the phylogenetic analysis, based on ITS and nuclear ribosomal partial LSU DNA sequences, Robledo et al. (2009) demonstrated the fundamental phylogeny of *Perenniporia* s.l., combined with such characteristics as a diversity of the vegetative hyphae and basidiospores morphology. In their study, *Perenniporia* s.s. and *Perenniporia* s.l. were scattered into distinct clades, which is also supported by different morphological traits. Zhao et al. (2013) divided *Perenniporia* s.l. into seven clades, based on ITS and nLSU DNA phylogenetic inferences, each of these seven clades being distinguished by a specific combination of morphological characteristics that supported recognition at the genus level. Some genera, having similar morphological characteristics to *Perenniporia*, such as *Amylosporia* B.K. Cui et al., *Murinicarpus* B.K. Cui & Y.C. Dai, *Vanderbylia* D.A. Reid, *Truncospora* Pilát and *Hornodermoporus* Teixeira, were also proved to form distinct lineages in DNA-based phylogenetic analyses (Cui et al. 2019). Besides, several new species were proved to belong to *Perenniporia*, based on morphological characteristics and phylogenetic evidence, which improved the understanding of the phylogenetic structure of *Perenniporia* (Jang et al. 2015; Huang et al. 2017; Ji et al. 2017; Liu et al. 2017; Zhao and Ma 2019).

During a study of wood-inhabiting polypore from Brazil and China, two unknown species of *Perenniporia* were distinguished by both morphology and molecular data. In this study, the two species are described and illustrated.

**Materials and methods**

**Morphological studies**

The studied specimens are deposited in the herbaria of the Institute of Microbiology, Beijing Forestry University (BJFC) and Universidade Federal de Pernambuco (URM). Morphological descriptions are based on field notes and herbarium specimens. Microscopic analyses follow Zhao and Cui (2013). In the description: KOH = 5% potassium hydroxide, IKI = Melzer’s reagent, IKI– = neither amyloid nor dextrinoid, CB = Cotton Blue, CB+ = cyanophilous in Cotton Blue, CB– = acyanophilous, L = arithmetic
average of all spore length, $W = \text{arithmetic average of all spore width}$, $Q = \frac{L}{W}$ ratios, $n = \text{number of spores/number of specimens}$. Colour terms are cited from Anonymous (1969) and Petersen (1996).

**Molecular studies and phylogenetic analysis**

A CTAB rapid plant genome extraction kit-DN14 (Aidlab Biotechnologies Co., Ltd, Beijing) was used to obtain PCR products from dried specimens, according to the manufacturer’s instructions with some modifications (Shen et al. 2019; Sun et al. 2020). Two DNA gene fragments, ITS and nrLSU were amplified using the primer pairs ITS5/ITS4 (White et al. 1990) and LR0R/LR7 (http://www.biology.duke.edu/fungi/mycolab/primers.htm). The PCR procedures for ITS and nLSU followed Zhao et al. (2013) in the phylogenetic analyses. DNA sequencing was performed at Beijing Genomics Institute and the newly-generated sequences were deposited in the GenBank database. Sequences generated for this study were aligned with additional sequences downloaded from GenBank, 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 (submission ID 26254). Sequences of *Donkioporia expansa* (Desm.) Kotl. and Pouzar and *Pyrofomes demidoffii* (Lév.) Kotl. and Pouzar, obtained from GenBank, were used as outgroups (Zhao et al. 2013).

Phylogenetic analyses, used in this study, followed the approach of Han et al. (2016) and Zhu et al. (2019). Maximum parsimony (MP) and Maximum Likelihood (ML) analyses were conducted for the datasets of ITS and nLSU sequences. The best-fit evolutionary model was selected by hierarchical likelihood ratio tests (hLRT) and Akaike Information Criterion (AIC) in MrModeltest 2.2 (Nylander 2004) after scoring 24 models of evolution by PAUP* version 4.0b10 (Swofford 2002).

The MP topology and bootstrap values (MP-BS) obtained from 1000 replicates were performed using PAUP* version 4.0b10 (Swofford 2002). All characters were equally weighted and gaps were treated as missing. Trees were inferred using the heuristic search option with TBR branch swapping and 1000 random sequence additions. Max-trees were set to 5,000, branches of zero length were collapsed and all parsimonious trees were saved. 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. Sequences were also analysed using Maximum Likelihood (ML) with RAxML-HPC2 through the CIPRES Science Gateway (www.phylo.org; Miller et al. 2009). Branch support (BT) for ML analysis was determined by 1000 bootstrap replicates.

Bayesian phylogenetic inference and Bayesian posterior probabilities (BPP) were performed with MrBayes 3.1.2 (Ronquist and Huelsenbeck 2003). Four Markov chains were run for 4,650,000 generations until the split deviation frequency value was less than 0.01 and trees were sampled every 100 generations. The first 25% of the
sampled trees were discarded as burn-in and the remaining ones were used to reconstruct a majority rule consensus and calculate Bayesian posterior probabilities (BPP) of the clades.

Branches that received bootstrap support for maximum likelihood (ML), maximum parsimony (MP) and Bayesian posterior probabilities (BPP) ≥ 75% (ML-BS), 75% (MP-BT) and 0.95 (BPP) were considered as significantly supported, respectively.

**Results**

**Phylogeny results**

The combined ITS and nLSU dataset contained 101 sequences from 101 specimens referring to 59 taxa in this study. They were downloaded from GenBank and the sequences about *Perenniporia corticola*, *P. pseudotephropora* and *P. subcorticola* are new (Table 1). The dataset had an aligned length of 2089 characters in the dataset, of which, 1400 characters are constant, 181 are variable and parsimony-uninformative and 508 are parsimony informative. Maximum Parsimony analysis yielded one equally-parsimonious tree (TL = 2627, CI = 0.389, RI = 0.711, RC = 0.277, HI = 0.611) and a strict consensus tree of these trees is shown in Fig. 1. Best model applied in the Bayesian analysis: GTR+I+G, lset nst = 6, rates = invgamma; prset statefreqpr = dirichlet (1, 1, 1, 1). Bayesian analysis resulted in a same topology with an average standard deviation of split frequencies = 0.009950.

From the phylogenetic tree (Fig. 1), *P. pseudotephropora* and *P. subcorticola* were absorbed in the genus *Perenniporia*. Moreover, *P. subcorticola* formed a direct lineage with a high approval rating (98/99/1.00) and *P. pseudotephropora* produced an independent lineage.

**Taxonomy**

*Perenniporia pseudotephropora* Chao G. Wang & F. Wu, sp. nov.

MycoBank No: 835122

Figs 2, 3

**Diagnosis.** The very thick dissepiments (thicker than pore diameter), tissues becoming pale olivaceous to dark in KOH, flexuous and arboriform skeletal hyphae, ellipsoid to globose, truncate and slightly dextrinoid basidiospores measuring 4.9–5.2 × 4–4.8 μm highlight the species in *Perenniporia*.

**Holotype.** Brazil. Manaus, Parque Municipal Cachoeira das Orqideas, on rotten angiosperm wood, 12. V. 2017, Y.C. Dai 17383 (BJFC024919).

**Etymology.** *Pseudotephropora* (Lat.): referring to the species similar to *Perenniporia tephropora*. 
Two new species of *Perenniporia* (Polyporales, Basidiomycota)

Figure 1. Phylogeny of *Perenniporia* and related species generated by maximum parsimony analysis, based on combined ITS and nLSU sequences. Bootstrap supports for Maximum Likelihood (ML), Maximum parsimony (MP) and Bayesian posterior probabilities (BPP) are not lower than: 50% (ML-BS), 50% (MP-BT) and 0.90 (BPP) on the branches.
Table 1. Information for the sequences used in this study.

| Species                          | Sample number | ITS        | nLSU       |
|----------------------------------|---------------|------------|------------|
| Abundisporus sclerosetosus       | MUCL 41438    | FJ411101   | FJ393868   |
| A. violaceus                     | MUCL 38617    | FJ411100   | FJ393867   |
| Donkioporia expansa              | MUCL 35116    | FJ411104   | FJ393872   |
| Hornodermoporus latissima        | Cui 6625      | HQ876604   | JF706340   |
| H. martius                       | MUCL 41678    | FJ411093   | FJ393860   |
| Microporellus violaceo-cinerascens| MUCL 45229    | FJ411106   | FJ393874   |
| Perenniporia africana            | Cui 8674      | KF018119   | KF018128   |
| P. africana                      | Cui 8676      | KF018120   | KF018129   |
| P. aridae                        | Dai 12396     | JQ001854   | JQ001846   |
| P. corticola                     | Dai 17778     | MT117219   | MT117224   |
| P. corticola                     | Dai 18526     | MT117216   | MT117221   |
| P. bambusicola                   | Cui 11050     | KX900668   | KX900719   |
| P. bannaensis                    | Cui 8560      | JQ291727   | JQ291729   |
| P. bostonensis                   | CL Zhao 2855  | MG491285   | MG491288   |
| P. chiangraiensis                | Dai 16637     | KY475566   | –          |
| P. cinereofusca                  | Dai 9289      | KF568893   | KF568895   |
| P. subcorticola                  | Cui 2655      | HQ654093   | HQ848483   |
| P. ellipsopora                   | Cui 10276     | KF018124   | KF018132   |
| P. fraxinea                      | Cui 10284     | JQ861739   | KF018133   |
| P. gomezii                       | Dai 9656      | KX900672   | KX900722   |
| P. japonica                      | Cui 7047      | JQ861744   | JQ861760   |
| P. macropora                     | KUC 20090129  | JX141448   | JX141458   |
| P. maackiae                      | Cui 8929      | HQ654102   | JF706338   |
| P. lacerata                      | Dai 11268     | JX141449   | JX141459   |
| P. luteola                       | Harkonen 1308a| JX141456   | JX141466   |
| P. medulla-panii                 | Zhou 280      | JX141457   | JX141467   |
| P. minor                         | Dai 9198      | JQ861748   | JQ861764   |
| P. minutissima                   | Cui 10979     | KF495003   | KF495013   |
| P. mopanshanensis                | CL Zhao 5145  | MH784912   | MH784916   |
| P. nanlingensis                  | Cui 7620      | HQ848477   | HQ848486   |
| Species                        | Sample number | ITS          | nLSU        |
|-------------------------------|---------------|--------------|-------------|
| *P. nonggangensis*             | Dai 17857     | MT232521     | MT232515    |
|                               | GXU 2098      | KT894732     | KT894733    |
| *P. piceicola*                 | Cui 10460     | JQ861742     | JQ861758    |
|                               | Dai 4181      | JF706328     | JF706336    |
| *P. pseudotephropora*          | Dai 17383     | MT117215     | MT117220    |
| *P. pyricola*                  | Dai 10265     | JN048761     | JN048781    |
|                               | Cui 9149      | JN048762     | JN048782    |
| *P. rhizomorpha*               | Dai 7248      | JF706330     | JF706348    |
|                               | Cui 7507      | HQ564107     | HQ564117    |
| *P. robiniphila*               | Cui 7144      | HQ876608     | JF706341    |
|                               | Cui 5644      | HQ876609     | JF706342    |
| *P. ruseimarginata*            | Yuan 1244     | JQ861750     | JQ861766    |
| *P. straminea*                 | Cui 8858      | HQ564104     | JF706334    |
|                               | Cui 8718      | HQ876600     | JF706335    |
| *P. subacida*                  | Cui 10053     | KF495006     | KF495017    |
|                               | Dai 8224      | HQ876605     | JF713024    |
| *P. subadusta*                 | Cui 8459      | HQ876606     | HQ564113    |
| *P. substraminea*              | Cui 10177     | JQ001852     | JQ001844    |
|                               | Cui 10191     | JQ001853     | JQ001845    |
| *P. subtephropora*             | Dai 10964     | JQ861753     | JQ861769    |
|                               | Dai 10962     | JQ861752     | JQ861768    |
| *P. tenuis*                    | Wei 2969      | JQ001859     | JQ001849    |
|                               | Wei 2783      | JQ001858     | JQ001848    |
| *P. tephropora*                | Cui 9029      | HQ876601     | JF706339    |
|                               | Cui 6331      | HQ848473     | HQ848484    |
| *P. tibetica*                  | Cui 9459      | JF706327     | JF706333    |
| *P. tianmuensis*               | Cui 2648      | JX141453     | JX141463    |
|                               | Cui 2715      | JX141454     | JX141464    |
| *P. truncatospora*             | Cui 6987      | JN048778     | HQ564112    |
|                               | Dai 5125      | HQ654098     | HQ848481    |
| *P. yinggelingensis*           | Cui 13856     | MH427957     | MH427965    |
|                               | Cui 13625     | MH427960     | MH427967    |
| *Perenniporiella chaquenia*    | MUCL 47647    | FJ411083     | FJ393855    |
| *P. chaquenia*                 | MUCL 47648    | FJ411084     | FJ393856    |
| *P. micropora*                 | MUCL 43581    | FJ411086     | FJ393858    |
| *P. neofulva*                  | MUCL 45091    | FJ411080     | FJ393852    |
| *Pyrofomes demidoffii*         | MUCL 41034    | FJ411105     | FJ393873    |
| *Truncospora detrita*          | MUCL 42649    | FJ411099     | FJ393866    |
| *T. macropora*                 | Cui 8106      | JX941573     | JX941596    |
| *T. ochroleuca*                | MUCL 39563    | FJ411097     | FJ393864    |
|                               | MUCL 39726    | FJ411098     | FJ393865    |
|                               | Dai 11486     | HQ564105     | JF706349    |
| *T. obtiens*                   | MUCL 41036    | FJ411096     | FJ393863    |
|                               | Cui 5714      | HQ564103     | HQ564116    |
| *Vanderbylia delavavi*         | Dai 6891      | JQ861738     | KF495019    |
| *V. fraxinea*                  | DP 83         | AM269789     | AM269853    |
| *V. vicina*                    | MUCL 44779    | FJ411095     | FJ393862    |

**Basidiocarps.** Perennials, resupinate or effused-reflexed to pileate, without odour or taste when fresh, becoming hard corky when dry. Pilei applanate, semicircular to fan-shaped, projecting up to 1 cm, 3.5 cm wide and about 1 cm thick at base. Pile-
al surface pinkish-buff, grey to greyish-brown, smooth. Pore surface greyish to pale brown; pores tiny, round, 8–9 per mm; dissepiments thick, thicker than pore diameter, entire. Context thin, fawn to brown, coryx, up to 0.5 mm thick. Tubes buff to brown, darker than pore surface, distinctly stratified, hard coryx, up to 9.5 mm long.

**Hyphal structure.** Hyphal system dimitic; generative hyphae bearing clamp connections; skeletal hyphae arboriform branched, slightly dextrinoid, CB+; tissues becoming pale olivaceous to dark in KOH.

**Context.** Generative hyphae infrequent, hyaline, thin-walled, bearing clamp connections, 1.6–2.2 μm in diam.; skeletal hyphae dominant, thick-walled with a wide lumen, hyaline to pale brown, frequently arboriform branched, flexuous, interwoven, 1.5–2.8 μm.

**Tubes.** Generative hyphae infrequent, hyaline, thin-walled, bearing clamp connections, 1.5–2 μm in diam.; skeletal hyphae dominant, thick-walled with a wide lumen, hyaline to pale brown, frequently arboriform branched, flexuous, interwoven, 1.5–3 μm in diam. Cystidia absent, cystidioles present, clavate or fusoid, hyaline, thin-walled, 11–12.5 × 3–4 μm; basidia barrel- to pear-shaped, with four sterigmata and a basal clamp connection, 12.3–13.7 × 6.2–7.5 μm; basidioles in shape similar to basidia, but smaller.
Figure 3. Microscopic structures of *Perenniporia pseudotephropora* (Holotype, Dai17383) **a** basidiospores **b** A basidium **c** basidioles **d** cystidioles **e** arboriform skeletal hyphae **f** hyphae from trama **g** hyphae from context.

**Spores.** Basidiospores broadly ellipsoid to subglobose, hyaline to pale brown, truncate, thick-walled, smooth, slightly dextrinoid, CB+, (4.5–)4.9–5.2(–5.3) × 4–4.8(–5) μm, L = 5.02 μm, W = 4.22 μm, Q = 1.19 (n = 30/1).
**Perenniporia subcorticola** Chao G. Wang & F. Wu, sp. nov.

Mycobank No: 835519

Figs 4, 5

**Diagnosis.** *Perenniporia subcorticola* is characterised by resupinate basidiocarps, yellow pores with thick dissepiments, tissues becoming dark in KOH, flexuous skeletal hyphae, ellipsoid, truncate and slightly dextrinoid basidiospores measuring 4.2–5 × 3.5–4.2 μm.

**Holotype.** China. Fujian Province, Wuyishan Nature Reserve, on rotten wood of *Pinus*, 21.X.2005, Y.C. Dai 7330 (BJFC001421).

**Etymology.** Subcorticola (Lat.): referring to the species similar to *Perenniporia corticola*.

**Basidiocarps.** Perennial, resupinate, soft corky and without odour or taste when fresh, becoming corky when dry, up to 10 cm long, 5 cm wide, 3.5 mm thick at centre. Pore surface yellow when fresh, becoming buff-yellow to curry-yellow when dry; margin narrow, thinning out; pores tiny, round, 7–8 per mm; dissepiments thick, entire. Subiculum thin, cream, up to 2 mm thick. Tubes concolorous with pore surface, up to 1.5 mm long.

**Hyphal structure.** Hyphal system dimitic; generative hyphae with clamp connections; skeletal hyphae weakly dextrinoid, CB+; tissues darkening in KOH.

**Subiculum.** Generative hyphae infrequent, hyaline, thin-walled, occasionally branched, 2–3 μm in diam.; skeletal hyphae dominant, thick-walled with a wide lumen, frequently branched, interwoven, 2–3.5 μm in diam.

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**Figure 4.** A basidiocarp of *Perenniporia subcorticola* (from Dai 3257). Scale bar: 1 cm. Photo by Yu-Cheng Dai.
Figure 5. Microscopic structures of *Perenniporia subcorticola* (Holotype, Dai 7330) a basidiospores b basidia and basidioles c cystidioles d hyphae from trama e hyphae from subiculum.
Tubes. Generative hyphae infrequent, hyaline, thin-walled, occasionally branched, 2–3 μm in diam.; skeletal hyphae dominant, thick-walled with a wide lumen, frequently branched, interwoven, 1.8–3 μm in diam. Cystidia absent, fusoid cystidioles present, hyaline, thin-walled, 14–18 × 4.5–7.5 μm; basidia barrel-shaped, with four sterigmata and a basal clamp connection, 13–16 × 6.5–9 μm; basidioles dominant, mostly pear-shaped to capitulate, slightly smaller than basidia.

Spores. Basidiospores ellipsoid, truncate, hyaline, thick-walled, smooth, dextrinoid, CB+, (4–)4.2–5(–5.5) × (3–)3.5–4.2(–4.7) μm, L = 4.66 μm, W = 3.91 μm, Q = 1.16–1.23 (n = 60/2).

Additional specimens (paratypes) examined. China. Hunan Province, Liuyang, Daweishan Forest Park, fallen angiosperm trunk, 21.XII.2000, Dai 3257 (BJFC009205); Zhejiang Province, Tianmushan Nature Reserve, on fallen angiosperm branch, 10.X.2005, Cui 2655 (BJFC001422).

Perenniporia corticola (Corner) Decock, Mycologia 93: 776 (2001)

Fig. 6

Note. Perenniporia corticola and P. dipterocarpicola Hattori & S.S. Lee were described from Malaysia (Corner 1989; Hattori and Lee 1999). Decock (2001a) restudied the types of the two taxa and treated P. dipterocarpicola as a synonym of P. corticola. Perenniporia corticola grows on Dipterocarpus in lowland forests of Southeast Asia (Decock 2001a; Hattori and Lee 1999) and was not phylogenetically analysed. In this study, P. corticola is closely related to P. citrinoalba and P. pseudotephropora. However, P. citrinoalba has larger basidiospores, 5.5–6 × 4.7–5.2 μm (Cui et al. 2019); while basidiospores are 4.6–5(–5.1) × 3.5–4(–4.1) μm in P. corticola (4.4–5 × 3.4–4 μm from the type, Decock 2001a). Perenniporia pseudotephropora differs from P. corticola by resupinate or effused-reflexed to pileate basidiocarps with greyish to pale brown pores, absence of dendrohyphidia and larger basidiospores (4.9–5.2 × 4–4.8 μm vs. 4.6–5 × 3.5–4 μm).

Specimens examined. Malaysia. Selangor, Kota Damansara, Community Forest Reserve, on angiosperm stump, 17. IV. 2018, Y.C. Dai 18641 (BJFC026929), Y.C. Dai 18633 (BJFC026921); Taman Botani Negara Shah Alam, on rotten angiosperm wood, 12. IV. 2018, Y.C. Dai 18526 (BJFC026815), Singapore. Singapore Botanical Garden, on rotten angiosperm wood, 17. VII. 2017, Y.C. Dai 17778 (BJFC025310).

Discussion

Perenniporia pseudotephropora is somehow related to P. corticola and P. citrinoalba B.K. Cui, C.L. Zhao & Y.C. Dai in our phylogeny (Fig. 1). However, the latter two species have completely resupinate basidiocarps with white to yellow pores. Perenniporia corticola has smaller basidiospores, 4.6–5 × 3.5–4 μm, while P. citrinoalba has larger basidiospores, 5.5–6 × 4.7–5.2 (Cui et al. 2019) vs. 4.9–5.2 × 4–4.8 μm in P. pseudotephropora.
Two new species of *Perenniporia* (Polyporales, Basidiomycota)

*Perenniporia tephropora* (Mont.) Ryvarden is similar to *P. pseudotehropora* in having perennial, resupinate to pileate basidiocarps with grey or greyish to pale brown pore surface, tissues becoming pale olivaceous to dark in KOH and broadly ellipsoid, truncate, dextrinoid basidiospores (Ryvarden and Johansen 1980; Corner 1989). However, *P. tephropora* has larger pores (4–6 per mm, Ryvarden and Johansen 1980). In addition, the two species are phylogenetically distantly related.

Phylogenetically, *Perenniporia subcorticola* is related to *P. maackiae* (Bondartsev & Ljub.) Parmasto and *P. tenuis* (Schwein.) Ryvarden (Fig. 1) and all these three species have yellow pores. However, *P. maackiae* has effused-reflexed basidiocarps, strongly dextrinoid skeletal hyphae, ellipsoid basidiospores measuring 5–6.5 × 3.5–4.5 μm and grows exclusively on *Maackia* (Dai et al. 2002); while *P. subcorticola*

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**Figure 6.** Basidiocarps of *Perenniporia corticola* **a** Dai 18641 **b** Dai 18633 **c** Dai 17778. Scale bars: 1 cm. Photos by Yu-Cheng Dai.
has completely resupinate basidiocarps, weakly dextrinoid skeketal hyphae, basidiospores measuring 4.2–5 × 3.5–4.2 μm and grows on a different tree. *Perenniporia tenuis* is different from *P. subcorticola* by larger pores (3–5 per mm), distinct dextrinoid skeketal hyphae and slightly larger basidiospores measuring 5.5–6.5 × 4.5–5.5 μm (Dai et al. 2002).

Macromorphologically, *Perenniporia subcorticola* is similar to *P. corticola* by its yellow pores and almost the same size of basidiospores and that is the reason why the specimens of *P. subcorticola* were previously treated as *P. cf. subcorticola* (Dai et al. 2002). However, *P. corticola* has arboriform branched skeletal hyphae and dendrohyphidia at dissepiments and it is a tropical species usually growing on the wood of Dipterocarpaceae (Decock 2001a); while *P. subcorticola* lacks arboriform branched skeletal hyphae and dendrohyphidia and it seems to be a warm temperate species growing on both gymnosperm and angiosperm wood.

*Perenniporia xantha* Decock & Ryvarden and *P. subcorticola* have yellow hynemnophore and almost the same size of pores and basidiospores, but *P. xantha* has arbo-riform skeletal hyphae, lacks cystidioles and its basidiospores are weakly dextrinoid (Decock and Ryvarden 1999); while *P. subcorticola* lacks arboriform skeletal hyphae, has cystidioles and its basidiospores are distinctly dextrinoid.

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