Morphological and molecular identification of *Phlebia wuliangshanensis* sp. nov. in China

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Abstract — A new white-rot fungus, *Phlebia wuliangshanensis*, is proposed based on a combination of morphological features and molecular evidence. The species is characterized by an annual growth habit, resupinate basidiocarps with a smooth to tuberculate hymenial surface, a monomitic hyphal system with thin- to thick-walled generative hyphae bearing simple septa, presence of cystidia, and narrow ellipsoid to ellipsoid basidiospores (5–6 × 3–3.7 µm). Our phylogenetic analyses of ITS and LSU nrRNA sequences performed with maximum likelihood, maximum parsimony, and Bayesian inference methods support *P. wuliangshanensis* within a phlebioid clade in *Meruliaceae* (*Polyporales*). ITS+nLSU sequence analyses of additional *Phlebia* taxa strongly support *P. wuliangshanensis* within a monophyletic lineage grouped with *P. chrysocreas* and *P. uda*.

Key words — Basidiomycota, Ceriporiopsis, taxonomy, wood-inhabiting fungi, Yunnan Province

Introduction

*Phlebia* Fr. (*Meruliaceae, Polyporales*) is typified by *P. radiata* Fr. (Fries 1821). Basidiocarps are resupinate or rarely pileate with a subceraceous to subgelatinous consistency when fresh and membranaceous to coriaceous when dry. The hymenophore may be smooth, tuberculate, phlebioid,
odontoid, merulioid, or poroid. Microscopic characters include a monomitic (rarely dimitic) hyphal structure with clamp connections or simple-septa, narrowly clavate basidia, and hyaline basidiospores that are thin-walled, smooth, allantoid to ellipsoid, acyanophilous, and negative in Melzer’s reagent (Bernicchia & Gorjón 2010). So far about 100 species have been accepted in the genus worldwide (Fries 1821; Ginns 1969; Nakasone & Burdsall 1984, 1995; Dhingra 1989; Nakasone 1997, 2002, 2003, 2009; Roberts 2000; Gilbertson & Hemmes 2004; Duhem & Michel 2007; Duhem 2009, 2013; Bernicchia & Gorjón 2010; Singh & al. 2010; Westphalen & al. 2018; Gorjón & Greslebin 2012; Kaur & al. 2017; Shen & al. 2018).

Recent, molecular studies have elucidated the classification of *Phlebia* among corticioid homobasidiomycetes (Larsson & al. 2004; Larsson 2007; Tomšovský & al. 2010; Binder & al. 2013, Justo & al. 2017; Shen & al. 2018). Larsson & al. (2004) showed that *Phlebia* clustered into a phlebioid clade and grouped with *Ceriporia* Donk and *Gloeoporus* Mont. Larsson (2007) emended part of *Polyporales* and demonstrated that *Phlebia* was polyphyletic and nested within *Meruliaceae*. A phylogenetic study of European taxa of *Ceriporiopsis* Domański showed that *Phlebia radiata* and the generic type of *Ceriporiopsis*, *C. gilvescens* (Bres.) Domański, grouped closely on the basis of combined nuclear ribosomal large subunit RNA (nLSU) and mitochondrial ribosomal small subunit rRNA (mtSSU) gene sequences (Tomšovský & al. 2010). Binder & al. (2013) multi-gene sequence analyses placed *P. radiata* within a phlebioid clade and apparently grouped with *Ceriporiopsis* and *Climacodon* P. Karst. Also using multi-gene datasets, Justo & al. (2017) revised the family-level classification of *Polyporales*, including eighteen families. They showed that *P. radiata* belonged to *Meruliaceae* and grouped with *Aurantiporus* Murrill and *Ceriporiopsis gilvescens*. Shen & al. (2018) described a new *Phlebia* species based on morphological characters and rDNA sequences. This species belonged within the phlebioid clade and was related to *P. radiata*.

During our investigations of wood-inhabiting fungi in southern China, we found an additional taxon that could not be assigned to any described species. In examining the taxonomy and phylogeny of this new species, we employed a two-gene molecular phylogenetic approach using internal transcribed spacer (ITS) and long subunit (nLSU) plus an expanded sampling of *Phlebia* isolates.

**Materials & methods**

The specimens studied are deposited at the herbarium of Southwest Forestry University (SWFC). Macro-morphological descriptions are based on field notes. Colour terms follow Petersen (1996). Micro-morphological data were obtained
Table 1. Species, specimens, and sequence data used in this study.
New sequences in **bold**.

| Species name                  | Sample no. | GenBank accession no. | References                  |
|-------------------------------|------------|-----------------------|-----------------------------|
| **Abortiporus biennis**       | TFRI 274   | EU232187 EU232277     | Unpublished                 |
| **Antrodia albida**           | CBS 308.82 | DQ491414 AY515348     | Kim & al. 2007              |
| **A. heteromorpha**           | CBS 200.91 | DQ491415 AY515350     | Kim & al. 2007              |
| **Antrodiella americana**     | Gothenburg 3161 | JN710509 JN710509      | Binder & al. 2013           |
| **A. semisupina**             | FCUG 960   | EU232182 EU232266     | Binder & al. 2005           |
| **Ceriporiopsis gilvescens**  | BRNM 710166 | FJ496684 FJ496720     | Tomšovský & al. 2010       |
| **Climacocystis borealis**    | KH 13318   | JQ031126 JQ031126     | Binder & al. 2013           |
| **Coriolopsis caperata**      | LE(BIN)-0677 | AB158316 AB158316     | Tomšovský & al. 2010       |
| **Dacryobolus karstenii**     | KHL 11162  | EU118624 EU118624     | Binder & al. 2005           |
| **Daedalea quercina**         | HHH 8735   | FJ403214 FJ403214     | Lindner & al. 2011          |
| **Earliella scabra**          | PR 1209    | JN165009 JN164793     | Binder & al. 2005           |
| **Fomitopsis pinicola**       | ATCC 76767 | DQ491410 DQ491410     | Kim & al. 2007              |
| **F. rosea**                  | ATCC 76767 | DQ491410 DQ491410     | Kim & al. 2007              |
| **Fragiliporia fragilis**     | Dai 13080  | KJ734260 KJ734264     | Zhao & al. 2015a            |
| **Ganoderma lingzhi**         | BRNU 592909 | FJ496694 FJ496706     | Tomšovský & al. 2010       |
| **Gelatoporia subvermispora** | Dai 13559  | KJ734261 KJ734265     | Zhao & al. 2015a            |
| **G. pannocinctus**           | Dai 13561  | KJ734262 KJ734266     | Zhao & al. 2015a            |
| **Grammothelopsis subtropica**| Wu 1006-38 | JQ781858              | —                            |
| **Heterobasidion annosum**    | BRNU 592909 | FJ496694 FJ496706     | Tomšovský & al. 2010       |
| **Hornodermoporus martius**   | MUCL 41677 | FJ411092 FJ393859     | Robledo & al. 2009          |
| **Hydnophlebia chrysorhiza**  | FD-282     | KPI135338 KPI135216   | Floudas & Hibbett 2015     |
| **Hypocnemium lyndae**        | NL 041031  | JX124704 JX124704     | Unpublished                 |
| **Junghuhnia nitida**         | KHL 11903  | EU118638 EU118638     | Binder & al. 2005           |
| **Obba rivulosa**             | KCTC 6892  | FJ496693 FJ496710     | Miettinen & Rajchenberg 2012 |
| **O. valdiviana**             | FF 503     | HQ659235 HQ659235     | Miettinen & Rajchenberg 2012 |
| **Phanerochaete chrysosporium**| BKM-F-1767 | HQ188436 GQ470643     | Wu & al. 2010               |
| **P. velutina**               | HHB-15343  | KP135184 —            | Floudas & Hibbett 2015     |
| **Perenniporia medulla-panis**| MUCL 49581 | FJ411087 FJ393875     | Robledo & al. 2009          |
| **Perenniporia neofulva**     | MUCL 45091 | FJ411080 FJ393852     | Robledo & al. 2009          |
| **Phlebia acanthocystis**     | FP 150571  | KPY948767 KPY948844   | Justo & al. 2017            |
| **P. acerina**                | FD-301     | KP135378 KP135378     | Justo & al. 2017            |
| **Phlebia acanthocystis**     | HHH-11146  | KP135372 —            | Floudas & Hibbett 2015     |
| **P. acerina**                | FP-135252  | KP135371 —            | Floudas & Hibbett 2015     |
| **Phlebia wuliangshanensis**  | DR-60      | KP135375 KF691615     | Floudas & Hibbett 2015     |
| Species name                  | Sample no.     | GenBank accession no. | References         |
|------------------------------|----------------|-----------------------|--------------------|
| *P. ailaoshanensis*          | CLZhao 3996    | MH784926 MH784936     | Shen & al. 2018    |
| *P. ailaoshanensis*          | CLZhao 4036    | MH784927 MH784937     | Shen & al. 2018    |
| *P. aurea*                   | DLL 2011-100   | KJ140614 —            | Unpublished        |
| *P. centrifuga*              | HHB-9239       | KP135380 KP135262     | Floudas & Hibbett 2015 |
| *P. chrysoceras*             | L-15541        | KP135381 —            | Floudas & Hibbett 2015 |
| *P. floridensis*             | HHH 9905       | KP135383 KP135264     | Justo & al. 2017   |
| *P. hydnoidea*               | HHH 1993       | KY948778 KY948853     | Justo & al. 2017   |
| *P. lindtneri*               | GB-501         | KY948772 KY948847     | Justo & al. 2017   |
| *P. livida*                  | FCUG 2189      | AF141624 AF141624     | Tomšovský & al. 2010 |
| *P. ludoviciana*             | FD-427         | KP135342 —            | Floudas & Hibbett 2015 |
| *P. nantahaliensis*          | HHH 2816       | KY948777 KY948852     | Justo & al. 2017   |
| *P. nothofagi*               | HHH 4273       | KP135369 KP135266     | Floudas & Hibbett 2015 |
| = *Mycoacia nothofagi*        | HHH 6906       | KP135368 —            | Floudas & Hibbett 2015 |
| *P. nantahaliensis*          | HHH 12067      | KP135370 —            | Floudas & Hibbett 2015 |
| *P. radiata*                 | KHL 13750      | GU480000 GU480000     | Tomšovský & al. 2010 |
| *P. setulosa*                | HBB-6891       | KP135382 KP135267     | Justo & al. 2017   |
| *P. subochracea*             | KPL 1571       | GU461512 —            | Binder & al. 2005  |
| *P. subserialis*             | FCUG 1434      | AF141631 AF141631     | Tomšovský & al. 2010 |
| *P. subserialis*             | FCUG 2452      | AF141614 —            | Unpublished        |
| *P. udu*                     | USDA Kropp-1   | AB084621 —            | Suhara & al. 2002  |
| *P. wuliangshanensis*        | CLZhao 3475 T  | MK881787 MK881897     | Present study      |
| *P. wuliangshanensis*        | CLZhao 3639    | MK881788 MK881898     | Present study      |
| *P. wuliangshanensis*        | CLZhao 3645    | MK881789 MK881899     | Present study      |
Table 1, concluded

| Species name               | Sample no. | GenBank accession no. | References             |
|----------------------------|------------|-----------------------|------------------------|
| *Phlebia wuliangshanensis* sp. nov. (China) |            |                       |                        |
| *Piloporia sajanensis*     | MANNINE 2733a | HQ659239              | Tomšovský & al. 2010  |
| *Podoscypha venustula*     | CBS 65684  | JN649367              | Sjoekvist & al. 2012  |
| *Polyporus tuberaster*     | CuTTENN 10197 | AF516596              | Binder & al. 2013     |
| *Postia guttulata*         | KHL 11739  | EU11865               | Kim & al. 2007        |
| *Pouzaroporia subrufa*     | BRNM 710164 | FJ496661              | Tomšovský & al. 2010  |
| *Sebipora aquosa*          | Miettinen 8680 | HQ659240              | Miettinen & Rajchenberg 2012 |
| *Skeletocutis amorpha*     | Miettinen 11038 | FN907913              | Tomšovský & al. 2010  |
| *S. jelicii*               | H 6002113  | FJ496690              | Tomšovský & al. 2010  |
| *S. portcrosensis*         | LY 3493    | FJ496689              | Tomšovský & al. 2010  |
| *S. subphaeospora*         | Rivoire 1048 | FJ496688              | Tomšovský & al. 2010  |
| *Steccherinum fimbriatum*  | KHL 11905  | EU118668              | Tomšovský & al. 2010  |
| *S. ochraceum*             | KHL 11902  | JQ031130              | Tomšovský & al. 2010  |
| *Stereum hirsutum*         | NBRC 6520  | AB733150              | Tomšovský & al. 2010  |
| *Truncospora ochroleuca*   | MUCI 39726 | FJ411098              | Robledo & al. 2009    |
| *Tyromyces chionaeus*      | Cui 10225  | KF698745              | Zhao & al. 2013       |
| *Xanthoporus syringae*     | Gothenburg 1488 | JN710607              | Tomšovský & al. 2010  |

from the dried specimens and observed under light microscopy following Dai (2012). Abbreviations are: KOH = 5% potassium hydroxide, CB = Cotton Blue, 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 among the specimens studied, n (a/b) = number of spores (a) measured from given number (b) of specimens.

We extracted genomic DNA from dried specimens using HiPure Fungal DNA Mini Kit II (Magen Biotech Co.) according to the manufacturer’s instructions with some modifications. A small piece (c. 30 mg) of dried fungal material was ground to powder with liquid nitrogen. The powder was transferred to a 1.5 ml centrifuge tube, suspended in 0.4 ml of lysis buffer, and incubated in a 65 °C water bath for 60 min, after which 0.4 ml phenol-chloroform (24:1) was added to each tube and the suspension was shaken vigorously. After centrifugation at 13,000 rpm for 5 min, 0.3 ml supernatant was transferred to a new tube and mixed with 0.45 ml binding buffer. The mixture was then transferred to an adsorbing column (AC) for centrifugation at 13,000 rpm for 0.5 min. Then, 0.5 ml inhibitor removal fluid was added in AC for centrifugation at 12,000 rpm for 0.5 min. After washing twice with 0.5 ml washing buffer, the AC was transferred to a clean centrifuge tube, and 100 ml elution buffer was added to the middle of adsorbed film to elute the genomic DNA. The ITS region was amplified with primer pairs ITS5 and ITS4 (White & al. 1990). Nuclear LSU region was amplified with primer pairs LR0R and LR7 (Vilgalys 2018). The ITS was amplified by 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 a final extension of 72 °C for 10 min. The nLSU was amplified by initial denaturation at 94 °C for 1 min, followed by 35 cycles at 94 °C for
30 s, 48 °C 1 min, and 72 °C for 1.5 min, and a final extension of 72 °C for 10 min. The PCR products were purified and directly sequenced at Kunming Tsingke Biological Technology Limited Company. All newly generated sequences were deposited in GenBank (Table 1).

DNA sequences were edited using Sequencher 4.6. Sequences were aligned in MAFFT 7 (Katoh & Toh, 2008) using the “G-INS-I” strategy and manually adjusted in BioEdit (Hall 1999). The sequence alignment (ID 24249) was deposited in TreeBase. In Fig. 1, *Heterobasidion annosum* (Fr.) Bref. and *Stereum hirsutum* (Willd.) Pers. were used as outgroup to root the tree following Binder & al. (2013). In Fig. 2, *Hydnophlebia chrysorhiza* (Eaton) Parmasto and *Phanerochaete velutina* (DC.) P. Karst. were used as outgroup to root the tree following Floudas & Hibbett (2015).

Phylogenetic analyses of the ITS+nLSU sequences were performed using maximum parsimony, maximum likelihood, and Bayesian inference methods. Maximum parsimony (MP) analyses followed Zhao & Wu (2017), and tree construction 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 bootstrap (BP) analysis with 1,000 replicates (Felsenstein 1985). Tree statistics tree length (TL), consistency index (CI), retention index (RI), rescaled consistency index (RC), and homoplasy index (HI) were calculated for each Maximum Parsimonious Tree generated. Sequences were analyzed using Maximum Likelihood (ML) with RAxML-HPC2 through the Cipres Science Gateway (Miller & al. 2009). Branch support (BS) for ML analysis was determined by 1000 bootstrap replicates.

MrModeltest 2.3 (Posada & Crandall 1998; Nylander 2004) was used to determine the best-fit evolution model for each data set for Bayesian inference (BI). Bayesian inference was calculated with MrBayes_3.1.2 using a general time reversible (GTR+G) model of DNA substitution and a gamma distribution rate variation across sites (Ronquist & Huelsenbeck 2003). Four Markov chains were run for 2 runs from random starting trees for 8 million generations (ITS+nLSU) in Fig. 1, for 5 million generations (ITS+LSU) in Fig. 2 and trees were sampled every 100 generations. The first 25% of the generations were discarded as burn-in. A majority rule consensus tree of all remaining trees was calculated. Branches that received bootstrap support for maximum likelihood (BS), maximum parsimony (BP) and Bayesian posterior probabilities (BPP) greater than or equal to 75% (BP) and 0.95 (BPP) were considered significantly supported, respectively.

**Molecular phylogeny**

The first ITS+nLSU dataset (Fig. 1) included sequences from 57 fungal specimens representing 49 species of *Polyporales* plus the outgroup had an aligned length of 2104 characters, of which 1236 characters were constant, 248 variable and parsimony-uninformative, and 620 parsimony-informative.
Fig. 1. Maximum Parsimony strict consensus tree illustrating the phylogeny of *Phlebia wuliangshanensis* and related species in *Polyporales* based on ITS+nLSU sequences. Branches are labeled with maximum likelihood bootstrap >70%, parsimony bootstrap proportions >50% and Bayesian posterior probabilities >0.95. Clade names follow Binder & al. (2013).

Maximum parsimony analysis yielded 3 equally parsimonious trees (TL = 4783, CI = 0.307, HI = 0.693, RI = 0.526, RC = 0.162). Best model for this dataset estimated and applied in the Bayesian analysis: GTR+I+G, lset nst = 6, rates = invgamma; prset statefreqpr = dirichlet (1,1,1,1). Bayesian analysis and ML analysis produced a similar topology as MP analysis (average standard deviation of split frequencies = 0.003241 (BI). The tree clustered the 57 polypore species into seven major clades, placing our new species, *Phlebia wuliangshanensis*, in the phlebioid clade (Fig. 1).

The second ITS+nLSU dataset (Fig. 2) comprising sequences from 51 fungal specimens representing 22 *Phlebia* species plus the outgroup had an aligned length of 2102 characters, of which 1588 characters were constant, 142 variable
Fig. 2. Maximum parsimony strict consensus tree illustrating the phylogeny of *Phlebia wuliangshanensis* and related species in *Phlebia* based on ITS+nLSU sequences. Branches are labeled with maximum likelihood bootstrap >70%, parsimony bootstrap proportions >50% and Bayesian posterior probabilities >0.95.

and parsimony-uninformative, and 372 parsimony-informative. Maximum parsimony analysis yielded 10 equally parsimonious trees (TL = 1113, CI = 0.518, HI = 0.482, RI = 0.873, RC = 0.403). Best model for the ITS+nLSU dataset estimated and applied in the Bayesian analysis: GTR+I+G, lset nst = 6,
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rates = invgamma; prset statefreqpr = dirichlet (1,1,1,1). Here also Bayesian analysis and ML analysis generated a similar topology as MP analysis (average standard deviation of split frequencies = 0.002221 (BI). The phylogeny (Fig. 2) inferred from the combined ITS+nLSU sequences from 49 Phlebia isolates grouped the new species with P. chrysocreas (Berk. & M.A. Curtis) Burds. and P. uda (Fr.) Nakasone.

Taxonomy

**Phlebia wuliangshanensis** C.L. Zhao, sp. nov. Figs 3, 4

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Differs from *Phlebia chrysocreas* by its narrower ellipsoid basidiospores and from *P. uda* by its smooth to tuberculate hymenium and generative hyphae with simple septa.

**Type:** China. Yunnan Province: Puer, Jingdong County, Wuliangshan National Nature Reserve, on angiosperm trunk, 2 October 2017, CLZhao 3475 (Holotype, SWFC 003475; GenBank MK881787, MK881897).

**Etymology:** The specific epithet *wuliangshanensis* (Lat.) refers to the locality (Wuliangshan) of the type specimen.

**Basidiomata** annual, resupinate, easily separable from the substratum, ceraceous to gelatinous, without odor or taste when fresh, becoming membranaceous upon drying, ≤12 cm long, 200–700 µm thick. Hymenial
Fig. 4. Microscopic structures of *Phlebia wuliangshanensis* (drawn from the holotype, SWFC 003475). A. Basidiospores; B. Basidia and basidioles; C. Cystidia; D. Basidiocarp section; E. Hymenium section; F. Hyphae from subiculum. Scale bars: A = 5 µm; B–F = 10 µm.
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surface smooth to tuberculate, white to cream to pale brown when fresh, cream to pale brown upon drying. Sterile margin distinct, white.

**Hyphal structure** monomitic; generative hyphae with simple septa, negative in Melzer’s reagent, CB–; tissues unchanged in KOH.

**Subiculum** generative hyphae hyaline, thin- to thick-walled, branched, 3–5.5 µm in diam.

**Hymenium** cystidia of two kinds: 1) hyaline, cylindrical, numerous, thick-walled, strongly encrusted, 20–55 × 6–10.5 µm; 2) hyaline, lanceolate, few, thin-walled, 12–18 × 3–4.5 µm; basidia barrel-shaped, with four sterigmata and a simple basal septum, 10–16 × 4–5 µm; basidioles dominant, in shape similar to basidia, but slightly smaller.

**Basidiospores** narrowly ellipsoid to ellipsoid, more or less curved, hyaline, thin-walled, smooth, negative in Melzer’s reagent, CB–, 5–6(–6.5) × 3–3.7 µm, L = 5.42 µm, W = 3.32 µm, Q = 1.64–1.73 (n = 180/3).

**Type of rot:** white.

**Additional specimens examined:** CHINA. YUNNAN PROVINCE. Puer: Jingdong County, Wuliangshan National Nature Reserve, on angiosperm trunk, 2 October 2017, CLZhao 3639 (SWFC 003639; GenBank MK881788, MK881898), CLZhao 3645 (SWFC 003645; GenBank MK881789, MK881899).

**Discussion**

We describe a new species, *Phlebia wuliangshanensis*, based on phylogenetic analyses and morphological characters.

Previously, seven clades were found in *Polyporales*: /antrodia, /core polyporoid, /fragiliporia, /gelatoporia, /phlebioid, /residual polyporoid, and /tyromyces (Binder & al. 2013, Zhao & al. 2015). Our combined ITS+nLSU sequence analysis (Fig. 1) strongly supports *Phlebia wuliangshanensis* (100% BS, 100% BP, 1.00 BPP) within the phlebioid clade and related to the type species, *P. radiata*.

*Phlebia wuliangshanensis* is closely related to *P. chrysocreas* and *P. uda* in the ITS+nLSU phylogenetic tree (Fig. 2). Morphologically, *P. chrysocreas* differs from *P. wuliangshanensis* by having ochraceous-buff to yellow ochre color hymenophore and narrowly ovoid basidiospores (4–6 × 2–2.5 µm, Lombard & al. 1975), while *P. uda* presents an odontoid hymenophore, generative hyphae bearing clamp connections, and smaller basidiospores (5–5.5 × 2–2.5 µm, Bernicchia & Gorjón 2010).

*Phlebia wuliangshanensis* morphologically resembles other *Phlebia* species: *P. bispora* (Stalpers) Nakasone, *P. capitata* Bernicchia & Gorjón, *P. coccineofulva* Schwein., *P. femsjoeensis* (Litsch. & S. Lundell) J. Erikss.
& Hjortstam, *P. livida* (Pers.) Bres., *P. nothofagi* (G. Cunn.) Nakasone, *P. radiata*, *P. rufa* (Pers.) M.P. Christ., *P. segregata* (Bourdot & Galzin) Parmasto, and *P. subserialis* (Bourdot & Galzin) Donk. These species differ from *P. wuliangshanensis* as follows: *P. bispora* by a hydnoid hymenophore, dimitic hyphal system, and smaller basidiospores (4–5 × 2.5–3 µm, Nakasone 2002); *P. capitata* by an odontoid hymenophore, generative hyphae with clamps, and the presence of capitate cystidia (Bernicchia & Gorjón 2010); *P. coccineofulva* by a granular hymenophore with vivid yellow radiating margin and metuloid cystidia (Schweinitz 1832); *P. femsjoeensis* by orange to violaceous basidiocarps (Eriksson & al. 1981); *P. livida* by its reddish hymenophore and a monomitic hyphal system with generative hyphae with clamps (Bernicchia & Gorjón 2010); *P. nothofagi* by effused basidiocarps with a hydnoid hymenophore, a monomitic hyphal system with generative hyphae with clamps, and narrower basidiospores (4–6 × 2–3 µm, Nakasone 1997); *P. rufa* by its effused basidiocarps with the reticulate or subporoid hymenophore (Christiansen 1960); *P. segregata* by its smooth hymenophore and cylindrical basidiospores (6–7 × 2–2.5 µm, Parmasto 1967); and *P. subserialis* by a white hymenium, clamped generative hyphae, and allantoid basidiospores (6–7 × 1.5–2 µm, Bernicchia & Gorjón 2010).

Although wood-rotting fungi are an extensively studied group in *Basidiomycota* (Gilbertson & Ryvarden 1987, Núñez & Ryvarden 2001, Bernicchia & Gorjón 2010, Dai 2012, Ryvarden & Melo 2014, Dai & al. 2015), Chinese wood-rotting fungi diversity is still not well known, especially in the subtropics and tropics. The new species *Phlebia wuliangshanensis* is from the Chinese subtropics, where many new taxa in the *Polyporales* have been described (Cui & al. 2007, 2009, 2010, 2011; Cui & Dai 2008; Du & Cui 2009; Li & Cui 2010; He & Li 2011; Jia & Cui 2011; Yu & al. 2013; Yang & He 2014; Chen & al. 2015; Zhao & Wu 2017; Zhao & Ma 2019). We anticipate that more new polypore taxa will be found in China after further investigations and molecular analyses.

**Acknowledgments**

Special thanks are due to Jason Karakehian (Harvard University, USA) and Dr. Mei-Ling Han (Langfang Normal University, P.R. China) who reviewed the manuscript. The research was supported by the National Natural Science Foundation of China (Project No. 31700023) and the Key Laboratory of State Forestry Administration for Highly Efficient Utilization of Forestry Biomass Resources in Southwest China (Southwest Forestry University) (Project No. 2019-KF10).
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Literature cited
Bernicchia A, Gorjón SP. 2010. Fungi Europaei 12: Corticiaceae 1. Edizioni Candusso, Lomazzo. 1007 p.
Binder M, Justo A, Riley R, Salamov A, López-Giráldez F, Sjökvist E, Copeland A, Foster B, Sun H, Larsson E, Larsson KH, Townsend J, Grigoriev IV, Hibbett DS. 2013. Phylogenetic and phylogenomic overview of the Polyporales. Mycologia 105: 1350–1373. https://doi.org/10.3852/13-003
Christiansen MP. 1960. Danish resupinate fungi. Part II. Homobasidiomycetes. Dansk botanisk Arkiv 19: 57–388.
Chen JJ, Shen LL, Dai YC. 2015. Dentipellicula austroafricana sp. nov. supported by morphological and phylogenetic analyses. Mycotaxon 130: 17–25. https://doi.org/10.5248/130.17
Cui BK, Dai YC. 2008. Skeletocutis luteolus sp. nov. from southern and eastern China. Mycotaxon 104: 97–101.
Cui BK, Dai YC, Decock C. 2007. A new species of Perenniporia (Basidiomycota, Aphyllophorales) from eastern China. Mycotaxon 99: 175–180.
Cui BK, Dai YC, Bao HY. 2009. Wood-inhabiting fungi in southern China 3. A new species of Phellinus (Hymenochaetae) from tropical China. Mycotaxon 110:125–130. https://doi.org/10.5248/110.125
Cui BK, Dai YC, Yuan HS. 2010. Two new species of Phyllopora (Basidiomycota, Hymenochaetae) from China. Mycotaxon 113:171–178. https://doi.org/10.5248/113.171
Cui BK, Zhao CL, Dai YC. 2011. Melanoderma microcarpum gen. et sp. nov. (Basidiomycota) from China. Mycotaxon 116:295–302. https://doi.org/10.5248/116.295
Dai YC. 2012. Polypore diversity in China with an annotated checklist of Chinese polypores. Mycoscience 53: 49–80. https://doi.org/10.1007/s10267-011-0134-3
Dai YC, Cui BK, Si J, He SH, Hyde KD, Yuan HS, Lui XY, Zhou LW. 2015. Dynamics of the worldwide number of fungi with emphasis on fungal diversity in China. Mycological Progress 14: 62. https://doi.org/10.1007/s11557-015-1084-5
Dhingra GS. 1989. Genus Phlebia Fr. in the eastern Himalaya. Journal of the Indian Botanical Society 84: 111–117.
Duhem B. 2009. Phlebia pyrenaica sp. nov., une nouvelle espèce méditerranéenne. Cryptogamie Mycologie 30: 319–328.
Duhem B. 2013. Phlebia rhodana sp. nov. et Phlebia jurassica sp. nov. (Agaricomycotina). Cryptogamie Mycologie 34: 291–301. https://doi.org/10.7872/crym.v34.iss4.2013.291
Duhem B, Michel H. 2007. Une espèce nouvelle de Phlebia possédant des fibres arboriformes. Cryptogamie Mycologie 28: 29–38.
Du P, Cui BK. 2009. Two new species of Meganasperoporaria (Polyporales, Basidiomycota) from tropical China. Mycotaxon 110: 131–138. https://doi.org/10.5248/110.131
Eriksson J, Hjortstam K, Ryvarden L. 1981. The Corticiaceae of North Europe. Synopsis Fungorum 6: 1048–1276.
Felsenstein J. 1985. Confidence intervals on phylogenetics: an approach using bootstrap. Evolution 39: 783–791. https://doi.org/10.1111/j.1558-5566.1985.tb00420.x
Floudas D, Hibbett DS. 2015. Revisiting the taxonomy of Phanerochaete (Polyporales, Basidiomycota) using a four gene dataset and extensive ITS sampling. Fungal Biology 119: 679–719. https://doi.org/10.1016/j.funbio.2015.04.003
Fries EM. 1821. Systema mycologicum. Greifswald 1: 1–520.
Ginns JH. 1969. The genus Merulius 2. Species of Merulius and Phlebia proposed by Lloyd. Mycologia 61: 357–372. https://doi.org/10.1080/00275514.1969.12018737
Gilbertson RL, Hemmes DE. 2004. New species of lignicolous basidiomycetes from Hawaii. Memoirs of the New York Botanical Garden 89: 81–92.
Gilbertson RL, Ryvarden L. 1987. North American polypores 2. Fungiflora, Oslo. 448 p.
Gorjón SP, Greslebin AG. 2012. Type studies of the species of Odontia described by G.H. Cunningham. New Zealand Journal of Botany 50: 289–301.
https://doi.org/10.1080/0028825X.2012.681385
Hall TA. 1999. Bioedit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. Nucleic Acids Symposium Series 41: 95–98
He SH, Li HJ. 2011. Hymenochaete in China. 2. A new species and three new records from Yunnan Province. Mycotaxon 118: 411–422. https://doi.org/10.5248/118.411
Jia BS, Cui BK. 2011. Notes on Ceriporia (Basidiomycota, Polyporales) in China. Mycotaxon 116: 457–468. https://doi.org/10.5248/116.457
Justo A, Miettinen O, Floudas D, Ortiz-Santana B, Sjökvist E, Lindner D, Nakasone K, Niemelä T, Larsson KH, Ryvarden L, Hibbett DS. 2017. A revised family-level classification of the Polyporales (Basidiomycota). Fungal Biology 121: 798–824. https://doi.org/10.1016/j.funbio.2017.05.010
Katoh K, Toh H. 2008. Recent developments in the MAFFT multiple sequence alignment program. Briefings in Bioinformatics 9: 286–298. https://doi.org/10.1093/bib/bbn013
Kaur G, Singh AP, Dhingra GS. 2017. Phlebia brevibasidia sp. nov. from India. Mycotaxon 132: 95–97. https://doi.org/10.5248/132.95
Larsson KH. 2007. Re-thinking the classification of corticioid fungi. Mycological Research 111: 1040–1063. https://doi.org/10.1016/j.mycres.2007.08.001
Larsson KH, Larsson E, Kõljalg U. 2004. High phylogenetic diversity among corticioid homobasidiomycetes. Mycological Research 108: 983–1002. https://doi.org/10.1017/S0953756204000851
Li HJ, Cui BK. 2010. A new Trametes species from Southwest China. Mycotaxon 113: 263–267. https://doi.org/10.5248/113.263
Lombard FF, Burdsall HH, Gilbertson RL. 1975. Taxonomy of Corticium chrysocreas and Phlebia livida. Mycologia 67: 495–510. https://doi.org/10.1080/00275514.1975.12019775
Miller MA, Holder MT, Vos R, Midford PE, Liebowitz T, Chan L, Hoover P, Warnow T. 2009. The CIPRES Portals. CIPRES. http://www.phylo.org/sub_sections/portal. 2009-08-04. ( Archived by WebCite(r) at http://www.webcitation.org/5imQlJeQa).
Nakasone KK. 1997. Studies in Phlebia. Six species with teeth. Sydowia 49: 49–79.
Nakasone KK. 2002. Mycoaciella, a synonym of Phlebia. Mycotaxon 81: 477–490.
Nakasone KK. 2003. Type studies of resupinate hydnaceous hymenomycetes described by Patouillard. Cryptogamie Mycologie 24: 131–145.
Nakasone KK. 2009. Type studies of corticioid hymenomycetes (Basidiomycota) with aculei. Sydowia 61: 273–285.
Nakasone KK, Burdsall Jr HH. 1984. Merulius, a synonym of Phlebia. Mycotaxon 21: 241–246.
Nakasone KK, Burdsall Jr HH. 1995. Phlebia species from eastern and southeastern United States. Mycotaxon 54: 335–359.
Núñez M, Ryvarden L. 2001. East Asian polypores 2. Polyporaceae s. lato. Synopsis Fungorum 14: 165–522.
Nylander JAA. 2004. MrModeltest v2. Program distributed by the author. Evolutionary Biology Centre, Uppsala University.
Parmasto E. 1967. Corticiaceae U.R.S.S. IV. Descriptiones taxorum novarum. Combinationes novae. Eesti NSV Teaduse Akadeemia Toimetised 16: 377–394.
Phlebia wuliangshanensis sp. nov. (China)...

Petersen JH. 1996. Farvekort. The Danish Mycological Society’s colour-chart. Foreningen til Svampekundskabens Fremme, Greve.

Posada D, Crandall KA. 1998. Modeltest: testing the model of DNA substitution. Bioinformatics 14: 817–818. https://doi.org/10.1093/bioinformatics/14.9.817

Roberts P. 2000. Corticioid fungi from Korup National Park, Cameroon. Kew Bulletin 55: 803–842. https://doi.org/10.2307/4113628

Ryvarden L, Melo I. 2014. Poroid fungi of Europe. Synopsis Fungorum 31:1–455.

Schweinitz LD. 1832. Synopsis fungorum in America boreali media degentium. Transactions of the American Philosophical Society 4: 141–316. https://doi.org/10.2307/1004834

Shen S, Ma X, Xu TM, Zhao CL. 2018. Phlebia ailyshanensis sp. nov. (Polyporales, Basidiomycota) evidenced by morphological characters and phylogenetic analyses. Phytotaxa 373: 184–196. https://doi.org/10.11646/phytotaxa/373.3.2

Singh AP, Dhingra GS, Singla N. 2010. A new species of Phlebia (Basidiomycetes) from India. Mycotaxon 112: 21–24. https://doi.org/10.5248/112.21

Swofford DL. 2002. PAUP*: phylogenetic analysis using parsimony (*and other methods). Version 4.0b10. Sinauer Associates, Massachusetts.

Tomšovský M, Menkis A, Vasaitis R. 2010. Phylogenetic relationships in European Ceriporiopsis species inferred from nuclear and mitochondrial ribosomal DNA sequences. Fungal Biology 114: 350–358. https://doi.org/10.1016/j.funbio.2010.02.004

Vilgalys R. 2018. Conserved primer sequences for PCR amplification of fungal rDNA. Retrieved from: https://sites.duke.edu/vilgalyslab/rdna_primers_for_fungi/ (Duke University, Vilgalys Lab).

Yang J, He SH. 2014. Hymenochaete in China. 8. H. biformisetosa sp. nov. with a key to species with denticulate setae. Mycotaxon 128: 137–144. https://doi.org/10.5248/128.137

Yu HY, Zhao CL, Dai YC. 2013. Inonotus niveomarginatus and I. tenuissimus spp. nov. (Hymenochaetales), resupinate species from tropical China. Mycotaxon 124: 61–68. https://doi.org/10.5248/124.61

Zhao CL, Cui BK, Song J, Dai YC. 2015. Fragiliporiaceae, a new family of Polyporales (Basidiomycota). Fungal Diversity 70: 115–126. https://doi.org/10.1007/s13225-014-0299-0

Zhao CL, Wu ZQ. 2017. Ceriporiopsis kunmingensis sp. nov. (Polyporales, Basidiomycota) evidenced by morphological characters and phylogenetic analysis. Mycological Progress 16: 93–100. https://doi.org/10.1007/s11557-016-1259-8

Zhao CL, Ma X. 2019. Perenniporia mopanshanensis sp. nov. from China. Mycotaxon 134: 125–137. https://doi.org/10.5248/134.125