Taxonomy and Phylogeny of Meruliaceae with Descriptions of Two New Species from China

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Abstract: Two new wood-inhabiting fungi Hermanssonia fimbriata sp. nov. and Phlebia austroasiana sp. nov. in the Meruliaceae family are described and illustrated from southwestern China based on molecular and morphological evidence. The characteristics of H. fimbriata include annual, resupinate basidiomata, the absence of cystidia and cystidioles, oblong ellipsoid basidiospores of 5–6 × 2.4–3 µm, and growth on rotten gymnosperm wood in the east Himalayas. Its basidiomata change drastically upon drying, from being a light-coloured, juicy, papillose-to-wrinkled hymenophore, to a dark-coloured, corky-to-gelatinous, and more or less smooth hymenophore. The characteristics of Ph. austroasiana include annual, resupinate basidiomata, a hydnoid hymenophore, 2–3 spines per mm, the presence of tubular cystidia of 20–25 × 3–3.5 µm, oblong ellipsoid basidiospores of 4.4–5.2 × 2.1–3 µm, and growth on angiosperm wood in tropical forests in the southern Yunnan Province. The phylogenetic analyses based on the combined 2-locus dataset (ITS1-5.8S-ITS2 (ITS) + nuclear large subunit RNA (nLSU)) confirm the placement of two new species, respectively, in Hermanssonia and Phlebia s. lato. Phylogenetically, the closely-related species to these two new species are discussed.

Keywords: diversity; macrofungi; phylogenetic analyses; new taxa; wood-rotting fungi

1. Introduction

The phlebioid clade within Polyporales includes three lineages at a family level, namely Phanerochaetaceae, Irpicaceae, and Meruliaceae [1,2]. The taxonomy of many of the genera belonging to these families is not currently settled, and a case in point example is the genus Phlebia. In a recent study, Chen et al. [3] concluded that Phlebia s.l. is still polyphyletic, with members addressed in all families of the phlebioid clade. Based on their multigene phylogenetic analysis, the core Phlebia clade belongs to the Meruliaceae with three additional clades: the Hydnophlebia clade, the Mycoacia clade, and the Sarcodontia clade. The core Phlebia clade included the genera Aurantiopileus Ginns et al., Aurantiporus Murrill, Pappia Zmitr., and Phlebia s.s., as well as some species of Ceriporiopsis Domaniński s.l. and Mycoacia s.l. [3].

Phlebia Fr. was erected by Fries [4] and typified by Phlebia radiata Fr. As the delimitation of the genus Phlebia s. str. is not yet clarified, in the present paper, we treat Phlebia sensu in the same way as Chen et al. [3]. The genus is characterized by white-rot, resupinate or rarely pileate basidiocarps with a tuberculate, meruloid, folded, odontioid or hydnoid hymenophore, a monomitic hyphal system, generative hyphae with clamp connections, neither amyloid nor dextrinoid, and allantoid to ellipsoid, hyaline, thin-walled, smooth, neither amyloid nor dextrinoid, acyanophilous basidiospores [3,5]. Formerly, several genera have been proposed to accommodate different lineages of Phlebia s. lato, but still many of the species has no modern interpretation, e.g., [3,6]. The monotypic genus Hermanssonia Zmitr. (Meruliaceae, Polyporales) was erected by Zmitrovich [7], based on H. centrifuga...
(P. Karst.) Zmitr. (=Phlebia centrifuga P. Karst.). The genus is characterized by white-rot, resupinate to effuse-reflexed, ceraceous to cartilaginous basidiomata, a phlebioid (radially-costa) or tuberculate hymenophore, a monomitic hyphal system, generative hyphae with clamp connections, and cylindrical, hyaline, thin-walled, smooth, neither amyloid nor dextrinoid basidiospores [7].

Four resupinate phlebioid specimens were collected from southwestern China (Tibet and Yunnan Province) during studies on wood-inhabiting fungi, and their morphology corresponded to concepts of Hermanssonia and Phlebia. Phylogenetic analyses based on the ITS1-5.8S-ITS2 (ITS) and nuclear large subunit RNA (nLSU) rDNA sequences were conducted to confirm their affinity. Both morphological and molecular evidence demonstrated that these four specimens represent two undescribed species of Meruliaceae. Thus, they are described in this paper.

2. Materials and Methods

2.1. Morphological Studies

Macro-morphological descriptions were based on voucher specimens and field notes. Microscopic structures were prepared from slide preparations of dried tissues stained with Cotton Blue and Melzer’s reagent as described by Wu et al. [8]. The following abbreviations are used in the description: CB = Cotton Blue; CB– = acyanophilous in Cotton Blue; IKI = Melzer’s reagent; IKI– = neither amyloid nor dextrinoid in Melzer’s reagent; KOH = 5% potassium hydroxide; L = mean spore length (arithmetic average of basidiospores); W = mean spore width (arithmetic average of basidiospores); and Q = variation in the L/W ratios between the specimens studied, (n = a/b) = number of spores (a) measured from given number of specimens (b). When the variation in spore size is shown, 5% of the measurements were excluded from each end of the range, and these values are shown in parentheses. Special colour terms follow Petersen [9] and herbarium abbreviations follow Thiers [10]. The voucher specimens for the present study are deposited in the herbarium of the Institute of Microbiology, Beijing Forestry University (BJFC), Beijing, China.

2.2. DNA Extraction, PCR, and Sequencing

Total genomic DNA was extracted from dried specimens using a CTAB Rapid Plant Genome Extraction Kit (Aidlab Biotechnologies Company, Ltd., Beijing, China) according to the manufacturer’s instructions with some modifications [11]. The ITS regions were amplified with primers ITS4 and ITS5 [12]. The nLSU regions were amplified with primers LR0R and LR7 [13].

The polymerase chain reaction (PCR) procedure for the ITS was as follows: initial denaturation at 95 °C for 3 min, followed by 35 cycles at 94 °C for 40 s, 54 °C for 45 s, 72 °C for 1 min, and a final extension of 72 °C for 10 min. The PCR procedure for the nLSU was as follows: initial denaturation at 94 °C for 1 min, followed by 35 cycles at 94 °C for 30 s, 48 °C for 1 min, and 72 °C for 1.5 min, and a final extension of 72 °C for 10 min [14]. The purification and sequencing of the PCR products was conducted by the Beijing Genomics Institute, Beijing, China, with the same primers used in the PCR reactions. Species were identified by sequence comparison with accessions in the NCBI databases using the BLAST program.

2.3. Phylogenetic Analyses

Phylogenetic trees were constructed using ITS + nLSU rDNA sequences, and phylogenetic analyses were performed with the Maximum Likelihood (ML), Maximum Parsimony (MP), and Bayesian Inference (BI) methods. Sequences of the species and strains were primarily adopted from ITS-based and 28S-based tree topology, as described by Huang et al. [5] and Chen et al. [3]. New sequences generated in this study, along with reference sequences retrieved from GenBank (Table 1), were aligned by MAFFT 7 (Katoh et al. [15]; http://mafft.cbrc.jp/alignment/server/, accessed on 18 April 2022) using the “G-INS-i” strategy and manually adjusted in BioEdit v. 7.2.5 [16]. Unreliably
aligned sections were removed before the analyses, and efforts were made to manually inspect and improve the alignment. The data matrix was edited in Mesquite v3.70 (https://www.mesquiteproject.org/ (accessed on 18 April 2022). [17]. The sequence alignment was deposited at TreeBase. Sequences of *Hyphoderma mutatum* (Peck) Donk and *H. setigerum* (Fr.) Donk obtained from GenBank (https://www.ncbi.nlm.nih.gov/genbank/ (accessed on 18 April 2022) were used as outgroups to root the trees in the ITS + nLSU analysis.

Table 1. Taxa information and GenBank accession numbers of the sequences used in this study.

| Species                        | Sample         | GenBank Accession No. | References |
|--------------------------------|----------------|------------------------|------------|
|                                |                | ITS                   | nLSU       |            |
| *Aurantiopileus mayaensi*      | JV 1504/128    | KT156706               | —          | —          |
| *A. mayaensi*                  | TJB1022        | HM772140               | HM772139   | —          |
| *Aurantiporus croceus*         | Miettinen-16483| KY948745               | KY948901   | —          |
| *A. roseus*                    | Dai 13573      | KJ698635               | KJ698639   | —          |
| Ceriporopsis alboaurantia      | Cui 4136       | KF845955               | KF845948   | —          |
| *C. alboaurantia*              | Cui 2877       | KF845954               | KF845947   | —          |
| *C. fimbriata*                 | Cui 1671       | KJ698634               | KJ698638   | —          |
| *C. fimbriata*                 | Dai 11672      | KJ698633               | KJ698637   | —          |
| *C. gilvescens*                | BRNM 710166    | FJ496684               | FJ496684   | —          |
| *C. guidella*                  | HUBO 7659      | FJ496687               | FJ496722   | —          |
| *C. kunmingensis*              | CLZhao 152     | KX081072               | KX081074   | —          |
| *C. kunmingensis*              | CLZhao 153     | KX081073               | KX081075   | —          |
| *C. lagerheimii*               | 58240          | KX008365               | KX081077   | —          |
| *C. pseudoplacenta*            | PRM 899297     | JN592497               | JN592504   | —          |
| *C. pseudoplacenta*            | PRM 899300     | JN592498               | JN592505   | —          |
| *C. semisupina*                | Cui 10222      | KF845956               | KF845949   | —          |
| *C. semisupina*                | Cui 7971       | KF845957               | KF845950   | —          |
| *Climacodon septentrionalis*   | AFTOL-767      | AY854082               | AY864165   | —          |
| *C. septentrionalis*           | RLG-6890-Sp    | KP135344               | —          | [26]       |
| Crustodontia chrysocreas       | HHB-3946       | KP135357               | —          | [26]       |
| *C. chrysocreas*               | HHB-6333-Sp    | KP135358               | KP135263   | —          |
| *C. nigrodonca*                | CLZhao 2758    | MT896824               | —          | [5]        |
| *C. nigrodonca*                | CLZhao 2445    | MT896821               | MT896818   | —          |
| *C. sp.*                       | KUC20121123-24 | KJ668482               | —          | [28]       |
| *C. longxiniana*               | CLZhao 2255    | MT020773               | MT020751   | —          |
| *C. longxiniana*               | CLZhao 2316    | MT020774               | MT020752   | —          |
| Geesterania carneola           | MCW 388/12     | KY174999               | KY174999   | —          |
| *G. davidii*                   | MCW 396/12     | KY174998               | KY174998   | —          |
| Hermanssonia centrifuga        | CBS 125890     | MH864088               | MH875547   | —          |
| *H. centrifuga*                | HHB-9239-Sp    | KP135380               | KP135262   | —          |
| *H. fimбриata*                | Dai 23266      | ON135436               | ON135440   | Present study|
| *H. fimбриata*                | Dai 23305      | ON135437               | ON135441   | Present study|
| *H. fimбриata*                | Dai 23306      | ON135438               | ON135442   | Present study|
| Hydnophanerochaete odontoeida  | CLZhao 3882    | MH784919               | MH784929   | —          |
| *H. odontoeida*                | CLZhao 4036    | MH784927               | MH784937   | —          |
| *Hydnophlebia chrysorhiza*     | FD-282         | KP135338               | KP135217   | —          |
| *H. chrysorhiza*               | HHB-18767      | KP135337               | —          | —          |
| Hyphoderma mutatum             | HHB-15479-Sp   | KP135296               | KP135221   | —          |
| *H. setigerum*                 | FD-312         | KP135297               | KP135222   | —          |
| Lilaceophlebia livida          | FCUG 2189      | AF141624               | AF141624   | —          |
| *L. livida*                    | FCUG 1290      | HQ153414               | —          | —          |
| *L. subserialis*               | FCUG 1434      | AF141631               | AF141631   | —          |
| Luteochaete subglobosa         | CLZhao 3639    | MK881898               | MK881788   | —          |

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[17] [18] [19] [20] [21] [22] [23] [24] [25] [26] [27] [28] [29] [30] [31] [32] [33]
| Species                     | Sample          | GenBank Accession No. | References |
|-----------------------------|-----------------|-----------------------|------------|
|                            |                 | ITS                   | nLSU       |            |
| L. subglobosa               | CLZhao 3475     | MK881897              | MK881787   | [33]       |
| L. albomarginata            | Dai 15229       | KU598873              | KU598878   | [34]       |
| L. albomarginata            | GC 1702-1       | LC379003              | LC379155   | [35]       |
| L. citriniporia             | Dai 19507       | MT872218              | MT872216   | [36]       |
| L. citriniporia             | Dai 19622       | MT872219              | MT872217   | [36]       |
| L. lutea                    | CHWC 1506-68    | MZ636997              | MZ637157   | [3]        |
| L. lutea                    | GC 1409-1       | MZ636998              | MZ637158   | [3]        |
| Mycocalicia aurea           | DII 2011263     | KY40747               | —          | [1]        |
| M. aurea                    | RLG-5075-Sp     | KY40747               | MZ637161   | [2,3]      |
| Mycoaciella bispora         | EL13 99         | —                     | AY386692   | [38]       |
| Mycoaciella bispora         | WEI 19-057      | MZ637012              | MZ637172   | [3]        |
| Mycoaciella bispora         | WEI 16-172      | MZ637011              | MZ637171   | [3]        |
| Odoria alborubescens        | BP106943        | MG097864              | MG097867   | [39]       |
| O. alborubescens            | BRNU 627479     | JQ821319              | JQ801318   | [40]       |
| Pappia fissilis             | 814             | HQ728291              | HQ728290   | [41]       |
| P. fissilis                 | BRNM 699803     | HQ728292              | HQ728290   | [41]       |
| Phelebia acanthocystis      | KUC20131001-33  | KJ66848               | KJ668337   | [26]       |
| P. acanthocystis            | FP150571        | KY40747               | KY408444   | [2]        |
| P. acerina                  | FD 301          | KP135378              | —          | [2]        |
| P. acerina                  | HHH 11146       | KP135372              | —          | [26]       |
| P. austroasiana             | Dai 17556       | ON135439              | ON135443   | Present study |
| P. brevispora               | HHH 7030        | KP135387              | —          | [26]       |
| P. brevispora               | FBCC1463        | LN611135              | LN611135   | [43]       |
| P. floridens                | HHH 7175        | KP135384              | —          | [26]       |
| P. floridens                | HHH-9905-Sp     | KP135383              | KP135264   | [26]       |
| P. fuscotuberculata         | CLZhao 10227    | MT020739              | MT020737   | [27]       |
| P. fuscotuberculata         | CLZhao 10239    | MT020760              | MT020738   | [27]       |
| P. hydnoidea                | HHH-1993-Sp     | KY40747               | KY40853    | [2]        |
| P. lindtneri                | GB-1027         | AB210076              | —          | [44]       |
| P. lindtneri                | GB-301          | KY408772              | KY408447   | [2]        |
| P. ludoviciiana             | HHH-8715-Sp     | KY408770              | KY408446   | [2]        |
| P. ludoviciiana             | FD-427          | KP135342              | —          | [26]       |
| P. nantahaliensis           | HHH-2816-Sp     | KY408577              | KY408582   | [2]        |
| P. radiata                  | CBS 285.56      | MH857642              | MH869187   | [30]       |
| P. radiata                  | AFTOL-484       | AY854087              | AF287885   | [29]       |
| P. radiata                  | UBC: F19726     | HQ064797              | HQ064797   | [1]        |
| P. rufa                     | FBCC297         | LN611092              | LN611092   | [43]       |
| P. rufa                     | HHH-14924       | KP135374              | —          | [26]       |
| P. serialis                 | FCUG 2868       | HQ153429              | —          | [32]       |
| P. serialis                 | UC2023146       | KP141951              | —          | [33]       |
| P. setulosia                | PH 11749        | GU461312              | —          | [1]        |
| P. setulosia                | HHH-6891-Sp     | KP135382              | KP135267   | [26]       |
| P. setulosia                | AH31879         | GQ259417              | GQ259417   | [45]       |
| P. subochracea I            | KGN 162/95      | EU118656              | EU118656   | [46]       |
| P. subochracea II           | FBCC295         | LN611116              | LN611116   | [43]       |
| P. subochracea II           | HHH-8494-Sp     | KY408577              | KY408445   | [2]        |
| P. tomentopileata           | CLZhao 9563     | MT020765              | MT020743   | [27]       |
| P. tomentopileata           | CLZhao 9515     | MT020764              | MT020742   | [27]       |
Table 1. Cont.

| Species                  | Sample          | GenBank Accession No. | References |
|--------------------------|-----------------|-----------------------|------------|
| *P. tremellosa*          | ES 20082        | JX109859 JX109859     | [1]        |
| *P. tremellosa*          | CBS 217.56      | MH857589 MH869138     | [30]       |
| *Phlebiporia tubalina*   | Dai 13168       | KC782526 KC782528     | [47]       |
| *P. tubalina*            | Dai 15179       | KY131843 KY131902     | [48]       |
| *Sarcodontia uda*        | Dai 15179       | KY135361 KY135232     | [26]       |
| *S. hydnoides*           | USDA Kropp 1    | KY948764 —            | [2]        |
| *Scopuloides hydnoides*  | FP-150473       | KP135355 KP135284     | [26]       |
| *S. hydnoides*           | WEI 17-569      | MZ637085 MZ637283     | [3]        |
| *Stereophlebia tuberculata* | FCUG 3157  | HQ153427 —            | [32]       |
| *S. tuberculata*         | Wu 1708-107     | MZ637089 MZ637286     | [3]        |

New sequences are in bold.

Maximum Parsimony analysis was applied to the ITS + nLSU dataset sequences. The approaches to phylogenetic analysis utilized those conducted by Chen and Cui [47], and the tree was constructed using PAUP* version 4.0 beta 10 [49]. All the characters were equally weighted, and gaps were treated as missing data. Trees were inferred using the heuristic search option with tree bisection and reconnection (TBR) branch swapping, and 1000 random sequence addition maxtrees were set to 5000. Branches of zero length were collapsed, and all the parsimonious trees were saved. Clade robustness was assessed using a bootstrap (BT) analysis with 1000 replicates [50]. Descriptive tree statistics, including the Consistency Index (CI), Homoplasy Index (HI), Rescaled Consistency index (RC), Retention Index (RI), and tree length (TL), were calculated for each Maximum Parsimonious Tree (MPT) generated.

The research using ML was conducted using RAxML-HPC v. 8.2.3 [51] and RAxML-HPC through the CIPRES Science Gateway ([52]; http://www.phylo.org, accessed on 18 April 2022). Statistical support values (BS) were obtained using nonparametric bootstrapping with 1000 replicates. The BI analysis was performed with MrBayes 3.2.7a [53]. Four Markov chains were run for two runs from random starting trees for 3 million generations until the split deviation frequency value < 0.01, and the trees were sampled at every 1000 generation. The first 25% of the sampled trees were discarded as burn-in, and the remaining ones were used to reconstruct a majority rule consensus tree and calculate the Bayesian Posterior Probabilities (BPP) of the clades.

A total of 24 models of evolution were scored using PAUP* version 4.0 beta 10 [49]. Optimal substitution models for the combined dataset were then determined using the Akaike Information Criterion (AIC) implemented in MrModeltest 2.3 [54,55]. The model GTR + I + G was selected for use in the Maximum Likelihood (ML) and Bayesian Inference (BI) analyses.

Branches that received bootstrap support for Maximum Likelihood (BS), Maximum Parsimony (BP), and Bayesian Posterior Probabilities (BPP) > 75% (BS), 50% (BP), and 0.9 (BPP) were considered to be significantly supported. In addition, the ML analysis resulted in the best tree, and only the ML tree is shown along with the support values from the MP and BI analyses. FigTree v1.4.4 [56] was used to visualize the resulting tree.

3. Results
3.1. Phylogenetic Analyses

The combined ITS + nLSU dataset included sequences from 110 specimens representing 61 taxa (Table 1). The dataset had an aligned length of 2349 characters, of which 1503 were constant, 195 were variable but parsimony-uninformative, and 651 were parsimony-informative. MP analysis yielded nine equally parsimonious trees (TL = 3586, CI = 0.377, RI = 0.752, RC = 0.283, HI = 0.623). The best model for the ITS + nLSU dataset estimated and applied in the Bayesian analysis was GTR + I + G. Bayesian analysis and
MP analysis resulted in a similar topology to the ML analysis, with an average standard deviation of split frequencies of 0.006112 (BI).

The phylogeny (Figure 1) inferred from the ITS and nLSU sequences demonstrated that the new species, *Hermanssonia fimbriata* and *Phlebia austroasiana*, clustered into the genera *Hermanssonia* and *Phlebia*, respectively. *Hermanssonia fimbriata* grouped with *H. centrifuga* with strong support (100% BS, 100% BP, and 1.00 BPP, Figure 1) and *Phlebia austroasiana* grouped with *Ph. brevispora* Nakasone with strong support (92% BP, 97% BS, 1.00 BPP, Figure 1).

**Figure 1.** Phylogeny of Meruliaceae by MP analysis based on combined ITS and nLSU rDNA sequences. Branches are labelled with maximum likelihood bootstrap > 75%, parsimony bootstrap proportions > 50%, and Bayesian posterior probabilities > 0.9, respectively. New species are in bold.
3.2. Taxonomy

1. **Hermanssonia fimbriata** Z.B. Liu & Y.C. Dai, sp. Nov. (Figure 2A,B and Figure 3)

![Figure 2. Basidiomata of Hermanssonia fimbriata and Phlebia austroasiana.](image)

MycoBank number: MB 844038.

**Diagnosis**—*Hermanssonia fimbriata* is characterized by annual, resupinate basidiomata, a monomitic hyphal system with clamp connections, the absence of cystidia and cystidioles, and basidiospores which are oblong ellipsoid, hyaline, thin-walled, smooth, IKI−, CB−, and 5–6 × 2.4–3 μm. Its basidiomata change drastically upon drying, from being a light-coloured, juicy, papillose-to-wrinkled hymenophore, to a dark-coloured, corky-to-gelatinous, and more or less smooth hymenophore.

**Etymology**—*Fimbriata* (Lat.): refer to the species having fimbriate margin.

**Type**—China. Tibet, Linzhi, Milin County, Nanyi Valley, ca. 94°22′E, 29°37′N, elev. 3000 m, on rotten wood of *Picea*, 22 October 2021, Dai 23266 (BJFC 037837).

**Basidiomata**—Annual, resupinate, adnate, when fresh ceraceous and salmon (6A4) when juvenile, gelatinous, darkening to pale mouse grey (7C2) to light vinaceous grey (13B2/3) when mature, becoming corky, salmon (6A4) and reddish brown (8/9E7) upon drying, first as small colonies, later confluent up to 10 cm or more in the longest dimension, 4 cm in the widest dimension, and less than 0.1 mm thick at center when dry; hymenial surface irregularly papillose and partly radially or unevenly wrinkled; margin white and fimbriate; subiculum very thin to almost absent.
Hyphal structure—Hyphal system monomitic; generative hyphae with clamp connections, IKI–, CB–; tissue unchanged in KOH.

Subiculum—Generative hyphae hyaline, thin- to thick-walled, smooth, rarely branched, loosely interwoven, 2–4 µm in diam.

Hymenium—Generative hyphae in subhymenium hyaline, thin-walled, smooth, occasionally branched, loosely interwoven, 1.5–3 µm in diam; cystidia and cystidioles absent; basidia clavate, hyaline, bearing four sterigmata and a basal clamp connection, 25–30 × 5–6 µm; basidioles in shape similar to basidia, but slightly shorter.

Basidiospores—Ellipsoid to oblong ellipsoid, hyaline, thin-walled, smooth, IKI–, CB–, (4.5–) 5–6 × (2.2–) 2.4–3 µm, L = 5.51 µm, W = 2.78 µm, Q = 1.88–2.04 (n = 60/2).

Additional specimens (paratypes) examined—China. Tibet, Linzhi, Milin County, Nanyi Valley, ca. 94°22′E, 29°37′N, elev. 3000 m, on rotten wood of *Picea*, 22 October 2021, Dai 23305 (BJFC 037876), Dai 23306 (BJFC 037877).

Figure 3. Microscopic structures of *Hermanssonia fimbriata* (Holotype, Dai 23266). (a) Basidiospores. (b) Basidia and basidioles. (c) Hyphae from subiculum. (d) Hyphae from subhymenium. Drawings by: Zhan-Bo Liu.
2. *Phlebia austroasiana* Z.B. Liu & Y.C. Dai, sp. Nov. Figures 2C and 4

**Figure 4.** Microscopic structures of *Phlebia austroasiana* (Holotype, Dai 17556). (a) Basidiospores. (b) Basidia and basidioles. (c) Cystidia. (d) Hyphae from spine trama. Drawings by: Zhan-Bo Liu.

MycoBank number: MB 844039.

Diagnosis—*Phlebia austroasiana* is characterized by annual, resupinate basidiomata, a hymenophore with spines, 2–3 spines per mm, a monomitic hyphal system with clamp connections, the presence of tubular cystidia of 20–25 × 3–3.5 µm, and basidiospores which are oblong ellipsoid, hyaline, thin-walled, smooth, IKI–, CB–, 4.4–5.2 × 2.1–3 µm.

Etymology—*Austroasiana* (Lat.): refer to the species which is distributed in southeast Asia.

Type—China. Yunnan Province, Jinghong, Primeval Forest Park, ca. 100°52′E, 22°01′N, elev. 763 m, on angiosperm stump, 17 June 2017, Dai 17556 (BJFC 025088).
Basidiomata—Annual, resupinate, tightly adnate, gelatinous when dry, up to 5 cm long, 4 cm wide; hymenophore hydnoid, clay buff (6D4) when dry, not cracked; margin indistinct; spines crowded, clay buff (6D4), subulate, mostly separated, rarely fused, up to 2 mm long, 2–3 per mm at the base. Subiculum white, very thin to almost absent.

Hyphal structure—Hyphal system monomitic; generative hyphae with clamp connections, IKI–, CB–; tissue unchanged in KOH. Spines—Generative hyphae in spine trama hyaline, thin-walled, smooth, frequently branched, loosely interwoven, 2–3.5 μm in diam; cystidia tubular, thin-walled, with a basal clamp connection, 20–25 × 3–3.5 μm; cystidioles absent; basidia clavate, hyaline, bearing four sterigmata and a basal clamp connection, 18–26 × 4–5 μm; basidiomes in shape similar to basidia, but slightly shorter.

Basidiospores—Ellipsoid to oblong ellipsoid, hyaline, thin-walled, smooth, IKI–, CB–, (4.1–)4.4–5.2 × (2–)2.1–3 μm, L = 4.86 μm, W = 2.53 μm, Q = 1.92 (n = 60/1).

4. Discussion

Chen et al. [3] divided the taxa of Meruliaceae into four clades: the core Phlebia clade, the Hydnophlebia clade, the Mycoacia clade, and the Sarcodeontia clade. Two new species, Hermanssonia fimbriata and Phlebia austroasiana, are described in this study, based on morphological characters and phylogenetic analyses. Phylogenetically, they are nested in the core Phlebia clade, based on the ITS + nLSU sequence data (Figure 1).

Phylogenetically, three specimens of Hermanssonia fimbriata formed a lineage with strong support (100% BS, 100% BP, and 1.00 BPP, Figure 1) and grouped with H. centrifuga with strong support (100% BS, 100% BP, and 1.00 BPP). Both species share annual, resupinate basidiomata, a monomitic hyphal system, generative hyphae with clamp connections, thin-walled, IKI–, CB– basidiospores, and growth on rotten gymnosperm wood [57]. Hermanssonia fimbriata can be distinguished from H. centrifuga by its shorter basidiospores (5–6 × 2.4–3 μm vs. 6.5–9 × 2.5–3 μm, [57]). Hermanssonia centrifuga was described as Phlebia centrifuga P. Karst. from Finland [58], and an Asian taxon, Phlebia macra Litsch., was described from Siberia [59]. The latter was treated as a synonym of Ph. centrifuga [60]. Phlebia macra differs from Hermanssonia fimbriata by larger basidiospores (6–7.5 × 3–3.2 μm vs. 5–6 × 2.4–3 μm, [59]). Morphologically, H. fimbriata is similar to Phlebia coccineofulva Schwein., Ph. femsjoeensis (Litsch. & S. Lundell) J. Erikss. & Hjortstam, and Ph. radiata. These four species share the phlebioid hymenophore, but the last three species have cystidia, while cystidia are absent in Hermanssonia fimbriata. Above all, basidiospores of H. fimbriata are larger than that of Phlebia femsjoeensis (4–5 × 2–2.5 μm, [61]) and Ph. radiata (4–5 × 1.8–2 μm, [61]), but thinner than that of Ph. coccineofulva (2.8–3.5 μm in width, [61]). Hermanssonia fimbriata also resembles Phlebia subserialis (Bourdôt & Galzin) Donk and Luteochaete subglobosa (Sheng H. Wu) C.C. Chen & Sheng H. Wu (=Phlebia wulingshanensis C.L. Zhao) by the resupinate and ceraceous basidiomata when fresh, a monomitic hyphal system, and generative hyphae with clamp connections; however, cystidia are abundant in L. subglobosa and Phlebia subserialis, while cystidia are absent in Hermanssonia fimbriata. In addition, basidiospores of H. fimbriata are wider than that of Phlebia subserialis (2.4–3 μm vs. 2–2.5 μm, [61]), but thinner than that of Luteochaete subglobosa (2.4–3 μm vs. 3–3.7 μm, [5]). Hermanssonia remained a monotypic genus until the present paper which contributes the second species in the genus.

An ITS sequence KJ654590 of sample E8898A, named Phlebia sp. from GenBank, is almost identical to Dai 17556 in the ITS regions and the similarity between them is up to 99.65%. Hence, we believe the sample E8898A collected from Indonesia [42] represents the same species as our specimen (Dai 17556) collected from the Yunnan Province, China. Both samples were collected in tropical Asia, and formed a lineage with strong support (100% BS, 100% BP, and 1.00 BPP, Figure 1) in our phylogeny. Hence, Phlebia austroasiana is described based on these two samples. Ph. austroasiana is closely related to Ph. brevispora (92% BP, 97% BS, 1.00 BPP, Figure 1), however, morphologically, Ph. brevispora differs from Ph. austroasiana by its tuberculate hymenophore [62], while Ph. austroasiana has a hydnoid hymenophore. In addition, Ph. austroasiana is distinguished from Ph. brevispora by its
larger basidiospores (4.4–5.2 × 2.1–3 µm vs. 4–4.5 × 2–2.5 µm, [62]). Morphologically, *Ph. austroasiana* is similar to *Ph. capitata* Bernichia & Gorjón, in macromorphology, but the cystidia in *Ph. capitata* are capitate [61], while the cystidia in *Ph. austroasiana* are tubular. In addition, *Ph. austroasiana* is distinguished from *Ph. capitata* by its smaller basidiospores (4.4–5.2 × 2.1–3 µm vs. 5–5.5 × 2.5–3 µm, [61]).

**Author Contributions:** Conceptualization, Y.-C.D. and Z.-B.L.; methodology, Z.-B.L.; software, Z.-B.L.; validation, Z.-B.L., J.-L.Z. and V.P.; formal analysis, Z.-B.L.; investigation, Z.-B.L., Y.-C.D. and J.-L.Z.; resources, Y.-C.D.; data curation, Z.-B.L. and V.P.; writing—original draft preparation, Z.-B.L.; writing—review and editing, Y.-C.D.; visualization, Z.-B.L. and V.P.; supervision, Y.-C.D.; project administration, Y.-C.D.; funding acquisition, Y.-C.D. and V.P. All authors have read and agreed to the published version of the manuscript.

**Funding:** The research is supported by the National Natural Science Foundation of China (Project Nos. 32161143013, U1802231), and the Second Tibetan Plateau Scientific Expedition and Research Program (STEP, Grant No. 2019QZKK0503).

**Institutional Review Board Statement:** Not applicable.

**Informed Consent Statement:** Not applicable.

**Data Availability Statement:** Not applicable.

**Acknowledgments:** The support of the János Bolyai Research Scholarship of the Hungarian Academy of Sciences to Viktor Papp is highly appreciated.

**Conflicts of Interest:** The authors declare that there are no conflict of interest.

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