Global Diversity and Taxonomy of Sidera (Hymenochaetales, Basidiomycota): Four New Species and Keys to Species of the Genus

Zhan-Bo Liu 📧, Meng Zhou 📧, Yuan Yuan ⤴ and Yu-Cheng Dai ⤴

Institute of Microbiology, School of Ecology and Nature Conservation, PO Box 61, Beijing Forestry University, Beijing 100083, China; zhanboliu@bjfu.edu.cn (Z.-B.L.); zhoumeng9612@bjfu.edu.cn (M.Z.)
* Correspondence: yuanyuan1018@bjfu.edu.cn (Y.Y.); yuchengdai@bjfu.edu.cn (Y.-C.D.)
Tel.: +86-10-6233-6709 (Y.-C.D.)

Abstract: The genus Sidera is a polypore genus with resupinate, white to cream or buff fresh basidiom, poroid or hydnoid hymenophore, a monomitic or dimitic hyphal system with generative hyphae bearing clamp connections, the presence of rosette-like crystals and allantoid to lunate basidiospores. We study the phylogeny and diversity of Sidera herein by using both morphological and molecular methods. Phylogenetic analyses are based on the ITS dataset, the combined 2-locus dataset (5.8S + nLSU) and 7-locus dataset (ITS + nLSU + RPB1 + RPB2 + TEF1 + mtSSU + nSSU) of 15 taxa of Sidera all over the world. Among them, four species are new to science and described and illustrated in this paper, viz. S. inflata, S. malaysiana, S. punctata and S. roseo-bubalina. In addition, three taxa were treated as Sidera vulgaris sensu lato. An identification key of the 14 accepted species of Sidera worldwide is provided.

Keywords: phylogenetic analysis; Rickenellaceae; wood-rotting fungi

1. Introduction

The genus Sidera Miettinen & K.H. Larss. (Rickenellaceae and Hymenochaetales) was established by Miettinen and Larsson [1] based on molecular and morphological analyses to accommodate Sidera lunata (Romell ex Bourdot & Galzin) K.H. Larss., S. lowei (Rajchenb.) Miettinen, S. lenis (P. Karst.) Miettinen and S. vulgaris (Fr.) Miettinen, with S. lenis selected as its type [1]. Sidera has a worldwide distribution and is characterized by white-rot, resupinate, white to cream or buff, mostly waxy fresh basidiom, poroid or hydnoid hymenophore, a monomitic or dimitic hyphal system with generative hyphae bearing clamp connections, the presence of rosette-like crystals and allantoid to lunate basidiospores [1,2].

To date, ten species are accepted in the genus, i.e., Sidera lenis (= Physisporus lenis P. Karst., Rabenhorst 1886), S. vulgaris (= Polyporus vulgaris Fr., [3]), S. lowei (Rajchenb.) Miettinen (= Ceriporiopsis lowei Rajchenb., [4]), S. lunata (= Grandinia lunata Romell ex Bourdot & Galzin, [5]), S. minutipora (Rodway & Cleland) Y.C. Dai et al. (= Poria minutipora Rodway & Cleland [6]), S. vesiculosa Rui Du & M. Zhou [7], S. minutissima Y.C. Dai et al. [2], S. parallela Y.C. Dai et al. [2], S. srilankensis Y.C. Dai et al. [2] and S. tenuis Y.C. Dai et al. [2].

During investigations on the diversity of polypores in tropical Asia, four resupinate polypore specimens were collected from China and Malaysia. They were characterized by a monomitic or dimitic hyphal system with generative hyphae bearing clamp connections, the presence of rosette-like crystals and allantoid to lunate basidiospores. These morphological characteristics demonstrated that these specimens may represent species of Sidera. To confirm their affinities, phylogenetic analyses were carried out based on the internal transcribed spacer (ITS) regions, the large subunit nuclear ribosomal RNA gene (nLSU), the largest subunit of RNA polymerase II (RPB1), the second largest subunit of...
RNA polymerase II (RPB2), the translation elongation factor 1-α gene (TEF1), the small subunit mitochondrial rRNA gene sequences (mtSSU) and the small subunit (nSSU) of nuclear ribosomal RNA gene. As a result, these specimens were found to represent four new terminal lineages in the Sidera clade. In addition, the specimens or literature and sequences of all 14 currently accepted taxa of Sidera were studied, with their morphological characteristics summarized in Table 1. Furthermore, an identification key of accepted species is provided.

Table 1. The main characteristics of Sidera species. Pore and basidiospore sizes partly from Du et al. (2020) [2], Rajchenberg (1987) [4], Du et al. (2019) [7], Niemelä and Dai (1997) [8] and Niemelä (2005) [9].

| Species         | Growing Habit | Hymenophore | Hyphal System | Cystidia     | Skeletal Hyphae in KOH | Spores Shape | Spore Size (µm) |
|-----------------|---------------|-------------|---------------|--------------|-----------------------|--------------|-----------------|
| S. sieraffa     | Annual        | Poreid, 9–10/mm | Dimitic       | Present      | Swollen              | Allantoid    | 3.5–3.7 x 0.3–1.1 |
| S. irinii       | Perennial     | Poreid, 4–6/mm | Dimitic       | Present      | Swollen              | Allantoid    | 0.9–1.5          |
| S. leioi        | Annual        | Poreid, 6–8/mm | Monomitic     | Present, some-branching | -            | Allantoid    | 2.5–2.8         |
| S. leioi        | Annual        | Hydroid, 6–8/mm | Monomitic     | Present      | Swollen              | Allantoid    | 2.5–2.7         |
| S. malaysiana   | Annual        | Poreid, 7–9/mm | Dimitic       | Present      | Swollen              | Allantoid    | 3.5–4.5         |
| S. minutissima  | Annual        | Poreid, 6–8/mm | Dimitic       | Present      | Allantoid to lunate  | Allantoid    | 3.8–4.4 |
| S. minutipora   | Annual        | Poreid, 7–9/mm | Dimitic       | Present      | Swollen              | Allantoid    | 3.5–4.5         |
| S. vesiculosa   | Annual        | Poreid, 8–10/mm | Dimitic       | Present      | Swollen              | Allantoid    | 3.5–4.5         |
| S. punctata     | Annual        | Poreid, 6–8/mm | Monomitic     | Present      | Swollen              | Allantoid    | 3.5–4.5         |
| S. parallela    | Annual        | Poreid, 6–8/mm | Dimitic       | Present      | Almopt-branching     | Allantoid    | 3.8–4.8         |
| S. vulgaris     | Annual        | Poreid, 8–10/mm | Dimitic       | Present      | Almopt-branching     | Allantoid    | 3.8–5.8         |
| S. inflata      | Annual        | Poreid, 9–10/mm | Monomitic     | Present      | Swollen              | Allantoid    | 3.5–4.5         |
| S. lenis        | Perennial     | Poreid, 4–6/mm | Dimitic       | Present      | Almopt-branching     | Allantoid    | 3.5–4.5         |
| S. lowei        | Annual        | Poreid, 6–8/mm | Monomitic     | Present      | Swollen              | Allantoid    | 3.5–4.5         |
| S. inflata      | Annual        | Poreid, 9–10/mm | Monomitic     | Present      | Swollen              | Allantoid    | 3.5–4.5         |
| S. vesiculosa   | Annual        | Poreid, 8–10/mm | Dimitic       | Present      | Swollen              | Allantoid    | 3.5–4.5         |
| S. punctata     | Annual        | Poreid, 6–8/mm | Monomitic     | Present      | Swollen              | Allantoid    | 3.5–4.5         |
| S. parallela    | Annual        | Poreid, 6–8/mm | Dimitic       | Present      | Swollen              | Allantoid    | 3.5–4.5         |
| S. vulgaris     | Annual        | Poreid, 8–10/mm | Dimitic       | Present      | Swollen              | Allantoid    | 3.5–4.5         |
| S. inflata      | Annual        | Poreid, 9–10/mm | Monomitic     | Present      | Swollen              | Allantoid    | 3.5–4.5         |
| S. lenis        | Perennial     | Poreid, 4–6/mm | Dimitic       | Present      | Almopt-branching     | Allantoid    | 3.5–4.5         |
| S. lowei        | Annual        | Poreid, 6–8/mm | Monomitic     | Present      | Swollen              | Allantoid    | 3.5–4.5         |
| S. inflata      | Annual        | Poreid, 9–10/mm | Monomitic     | Present      | Swollen              | Allantoid    | 3.5–4.5         |
| S. lenis        | Perennial     | Poreid, 4–6/mm | Dimitic       | Present      | Almopt-branching     | Allantoid    | 3.5–4.5         |
| S. lowei        | Annual        | Poreid, 6–8/mm | Monomitic     | Present      | Swollen              | Allantoid    | 3.5–4.5         |
| S. inflata      | Annual        | Poreid, 9–10/mm | Monomitic     | Present      | Swollen              | Allantoid    | 3.5–4.5         |
| S. lenis        | Perennial     | Poreid, 4–6/mm | Dimitic       | Present      | Almopt-branching     | Allantoid    | 3.5–4.5         |
| S. lowei        | Annual        | Poreid, 6–8/mm | Monomitic     | Present      | Swollen              | Allantoid    | 3.5–4.5         |
| S. inflata      | Annual        | Poreid, 9–10/mm | Monomitic     | Present      | Swollen              | Allantoid    | 3.5–4.5         |
| S. lenis        | Perennial     | Poreid, 4–6/mm | Dimitic       | Present      | Almopt-branching     | Allantoid    | 3.5–4.5         |
| S. lowei        | Annual        | Poreid, 6–8/mm | Monomitic     | Present      | Swollen              | Allantoid    | 3.5–4.5         |

New species are shown in bold.

2. Materials and Methods
2.1. Morphological Studies

Morphological descriptions were based on field notes and dry herbarium specimens. Microscopic measurements and drawings were made from slide preparations of dry tissues stained with Cotton Blue and Melzer’s reagent following Dai (2010) [10]. Pores were measured by subjectively choosing the straightest line of pores possible and measuring how many fit per mm. The following abbreviations were used: KOH = 5% potassium hydroxide; CB = Cotton Blue; CB– = acyanophilous in Cotton Blue; IKI = Melzer’s reagent; IKI– = neither amyloid nor dextrinoid in Melzer’s reagent; L = mean spore length (arithmetic average of all spores); W = mean spore width (arithmetic average of all spores); Q = variation in the L/W ratios between specimens studied; n = (a/b) number of spores (a) measured from given number of specimens (b). In presenting spore size variation, 5% of measurements were excluded from each end of the range, and this value is given in parentheses. Special color terms follow Anonymous (1969) and Petersen (1996) [11,12]. Herbarium abbreviations follow Thiers (2018) [13]. The studied specimens were deposited at the herbarium of the Institute of Microbiology, Beijing Forestry University (BJFC).

2.2. DNA Extraction, PCR and Sequencing

Total genomic DNA was extracted from dried specimens by a CTAB rapid plant genome extraction kit (Aidlab Biotechnologies Company, Limited, Beijing, China) according to the manufacturer’s instructions with some modifications [14,15]. The ITS regions were amplified with primer pairs ITS5 and ITS4 [16]. The nLSU regions were amplified with primer pairs LR0R and LR7 (https://sites.duke.edu/vilgalyslab/rdna_primers_for_fungi/ (accessed on 24 March 2021)). The mtSSU regions were amplified with primer pairs MS1 and MS2 [16]. The nSSU regions were amplified with primer pairs NS1 and NS4 [16]. The TEF1 regions were amplified with primer pairs EF1-983F and EF1-1567R [17]. The RPB1 regions were amplified with primer pairs RPB1-Af and RPB1-Cf [18]. The RPB2 regions were amplified with primer pairs RPB2-45F and bRPB2-7.1R [19].

The PCR procedure for ITS and mtSSU was as follows: initial denaturation at 95 °C for 3 min, followed by 34 cycles at 94 °C for 40 s, 54 °C for ITS and 55 °C for mtSSU for 45 s and 72 °C for 1 min, and a final extension of 72 °C for 10 min. The PCR procedure for nLSU, nSSU and TEF1 was as follows: initial denaturation at 94 °C for 1 min, followed by 34 cycles at 94 °C for 30 s, 50 °C for nLSU and 59 °C for TEF1 for 1 min and 72 °C
for 1.5 min, and a final extension of 72 °C for 10 min. The PCR procedure for RPB1 and RPB2 was as follows: initial denaturation at 94 °C for 2 min, followed by 10 cycles at 94 °C for 40 s, 60 °C for 40 s and 72 °C for 2 min, then followed by 37 cycles at 94 °C for 45 s, 55 °C for 1.5 min and 72 °C for 2 min, and a final extension of 72 °C for 10 min. The PCR products were purified and sequenced in the Beijing Genomics Institute, China, with the same primers used in the PCR reactions.

2.3. Phylogenetic Analyses

Three combined matrices were reconstructed for phylogenetic analyses as an ITS dataset, a two-gene dataset (5.8S + nLSU) and a 7-gene dataset (ITS + nLSU + RPB1 + RPB2 + TEF1 + mtSSU + nSSU). Phylogenetic analyses were performed with maximum likelihood (ML) and Bayesian Inference (BI) methods. Sequences generated in this study were aligned with additional sequences downloaded from GenBank (Table 2) in MAFFT 6 ([20]; http://mafft.cbrc.jp/alignment/server/ (accessed on 24 March 2021)) using the “G–INS–i” strategy and manually adjusted in BioEdit [21]. Prior to phylogenetic analysis, ambiguous sequences at the start and the end were deleted, and gaps were manually adjusted to optimize the alignment. The data matrix was edited in Mesquite v3.04 software [22]. Sequence alignment was deposited at TreeBase (submission ID 27909, 27910 and 27911). Sequences of Exidia candia Lloyd and Exidiopsis calcea (Pers.) K. Wells outside Hymenochaetales were used as the outgroup [1,12,23] in the combined 2-gene dataset (5.8S + nLSU) and 7-gene dataset (ITS + nLSU + RPB1 + RPB2 + TEF1 + mtSSU + nSSU). The sequence of Sidera lunata (Romell ex Bourdot & Galzin) K.H. Larss. was used as the outgroup in the ITS dataset.

Sequences were also analyzed using maximum likelihood (ML) through the CIPRES Science Gateway ([24]; http://www.phylo.org (accessed on 24 March 2021)). Statistical support values (BS) were obtained using nonparametric bootstrapping with 1000 replicates. The optimal substitution models for the combined dataset were determined using the Akaike Information Criterion (AIC) implemented in MrModeltest 2.2 [25] after scoring 24 models of evolution by PAUP* version 4.0 beta 10 [26]. The selected model applied in the Bayesian phylogenetic inference (BI) analyses and maximum likelihood (ML) analyses was the model GTR + I + G.

The BI analysis was performed with MrBayes 3.2.5 [27]. Four Markov chains were run for two runs from random starting trees for 3 million generations (ITS, 5.8S + nLSU and ITS + nLSU + RPB1 + RPB2 + TEF1 + mtSSU + nSSU) until the split deviation frequency value reached <0.01, and trees were sampled 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 Bayesian posterior probabilities (BPP) of the clades.

Branches that received bootstrap support for maximum likelihood (BS), and Bayesian posterior probabilities (BPP) greater than 70% (BS) and 0.95 (BPP) were considered as significantly supported, respectively. FigTree v1.4.2 [28] was used to visualize the resulting tree.
### Table 2. Information for the sequences used in this study.

| Species                          | Specimen No. | Locality          | GenBank Accession No. | ITS                | 5.8S SU | RPB1 | RPB2 | TEF1 | mtSSU | nSSU |
|----------------------------------|--------------|-------------------|-----------------------|--------------------|---------|------|------|------|-------|------|
| Ceriporiopsis anceps             | MUAF 888     | Czech Republic    | EU340895              | U66452             | KX101920 |
| Ceriostereum cordelliforme       | Redhead 7001 | Russia            | KX801973              | AF91226            |
| Eulophyllum setosum              | MW 331       | Canada            | AF91226              |                     |
| Gloeporus rickeri                | KHL 11173    | China             | EU118627              | EU118627           |
| G. lactescens                   | Dai 15223    | Estonia           | EU118627             |                     |
| Gloeophyllum anomalum            | Hpn 19007    | Finland           | DKG78795             | DKG78795           |
| Hyphoderma violascens            | Dai 12045    | Finnd    | DKG78795             |                     |
| Hydnocarpon rossellum           | KHL 13257    | Estonia           | DKG78795             |                     |
| Hydnocarpon pseudocypripedum     | KHL 12258    | USA               | DKG78795             |                     |
| Hypocrea luteola                 | KHL 11779    | Finland           | DKG78795             |                     |
| Hypholoma velutina               | Lascot 74    | USA               | U66452               |                     |
| Hypholoma velutina               | KHL 12224    | USA               | DKG78795             |                     |
| Skvarutia inflecta              | C3 13630     | China             | MF908405             |                     |
| S. lineum                       | Mettietum 12109 | Finland         | FN907914             |                     |
| S. lineatum                     | Mettietum 5426 | New Zealand     | FN907915             |                     |
| S. lineare                      | JH 10860     | Norway            | DKG78795              |                     |
| S. malayanus                     | Dai 14870    | Malaysia          | MF908405             |                     |
| S. naudiniae                     | Cui 16720    | Australia         | MF908405             |                     |
| S. novogardii                   | Dai 19529    | Sri Lanka         | MF908405             |                     |
| S. novogardii                   | Dai 14871A   | China             | MF908405             |                     |
| S. novogardii                   | Cui 10346    | China             | MF908405             |                     |
| S. novogardii                   | Cui 10361    | China             | MF908405             |                     |
| S. novogardii                   | Dai 22119    | China             | MF908405             |                     |
| S. novogardii                   | Dai 15870    | Japan             | MF908405             |                     |
| S. novogardii                   | Dai 19561    | Sri Lanka         | MF908405             |                     |
| S. novogardii                   | Dai 19564    | Sri Lanka         | MF908405             |                     |
| S. novogardii                   | Dai 16097    | Australia         | MF908405             |                     |
| S. novogardii                   | Dai 16098    | Australia         | MF908405             |                     |
| S. novogardii                   | RJCP 025267  | Singapore         | MF908405             |                     |
| S. novogardii                   | RJCP 025277  | Singapore         | MF908405             |                     |
| S. xerogordii seriatus lato     | Ryvarden 73199 | New Zealand   | MF908405             |                     |
| S. xerogordii seriatus lato     | Dai 12370    | USA               | MF908405             |                     |
| S. xerogordii seriatus lato     | Dai 23105    | Belarus           | MF908405             |                     |
| S. xerogordii seriatus lato     | Dai 23457    | Russia            | MF908405             |                     |
| S. xerogordii seriatus lato     | Dai 11258    | China             | MF908405             |                     |
| Sphinctobroma amygdali           | Mettietum 11038 | Finland         | MF908405             |                     |
| S. chrysocoma                   | Mettietum 5426 | Finland         | MF908405             |                     |
| S. dickei                       | HHR 1052Zp   | USA               | MF908405             |                     |
| S. pachycaulis                  | HLC 1132     | China             | MF908405             |                     |
| S. pseudosppense                | Dai 15709    | China             | MF908405             |                     |
| S. scabris                      | L.1053hp     | Canada            | MF908405             |                     |

* Newly generated sequences for this study. New species are shown in bold.*
3. Results

3.1. Phylogenetic Analyses

ITS is the most important locus for barcoding fungi, especially at the generic and species levels. However, the genetic variation inside *Sidera* is significant and, for example, the alignment of the whole ITS region is difficult among *Sidera* polypores [1]. Therefore, we used the most stable and conservative portion of ITS (5.8S) and LSU to analyse the phylogenetic relationship of *Sidera* species (Figure 1). The concatenated 5.8S + nLSU dataset contained sequences from 46 fungal specimens representing 15 *Sidera* taxa (three are treated as *S. vulgaris* sensu lato; (Table 2). Sequences of *Exidia candia* and *Exidiopsis calcea* were used as the outgroup [1,12,23]. The best model for the 5.8S + nLSU dataset estimated and applied in the Bayesian analysis was GTR + I+G. The ML analysis resulted in the best tree (Figure 1). BI analyses resulted in almost identical tree topologies compared to the ML analysis, with an average standard deviation of split frequencies of 0.009930 (BI). Additionally, only the ML tree is presented along with the support values from the BI analyses. Our new species and their related species are nested in Group A and Group B. Thus, we used the whole ITS region to analyse the phylogenetic relationship of new *Sidera* species with their closely related species (Figure 2).

![Figure 1](image-url). Phylogeny of *Sidera* and related species generated by ML analyses based on combined 5.8S + nLSU sequences. Branches are labeled with maximum likelihood bootstrap >50% and Bayesian posterior probabilities >0.90, respectively. New species are indicated in bold.
Figure 2. Phylogeny of *Sidera* new species and related species generated by ML analyses based on ITS sequences. Branches are labeled with maximum likelihood bootstrap >50% and Bayesian posterior probabilities >0.90, respectively. New species are indicated in bold.

The ITS dataset contained sequences from ten fungal specimens representing eight *Sidera* taxa (four new species and another four *Sidera* taxa). The sequence of *Sidera lunata* was used as the outgroup. The best model for the ITS dataset estimated and applied in the Bayesian analysis was GTR + I + G. The ML analysis resulted in the best tree (Figure 2). BI analyses resulted in almost identical tree topologies compared to the ML analysis, with an average standard deviation of split frequencies of 0.001361 (BI). Thus, only the ML tree is presented along with the support values from the BI analyses.

The concatenated ITS + nLSU + RPB1 + RPB2 + TEF1 + mtSSU + nSSU dataset contained sequences from 46 fungal specimens representing 15 *Sidera* taxa (three were treated as *S. vulgaris* sensu lato; Table 2). Sequences of *Exidia candidia* and *Exidiopsis calcea* were used as the outgroup [1,12,23]. The best model for the ITS + nLSU + RPB1 + RPB2 + TEF1 + mtSSU + nSSU dataset estimated and applied in the Bayesian analysis was GTR + I+G. The ML analysis resulted in the best tree (Figure 3). BI analyses resulted in almost identical tree topologies compared to the ML analysis, with an average standard deviation of split frequencies of 0.009821 (BI). Additionally, only the ML tree is presented along with the support values from the BI analyses.

The phylogenetic trees (Figures 2 and 3) revealed four new and independent lineages represented by our specimens, indicating that they are phylogenetically distinct from the species currently known in the genus. In addition, another three taxa were treated as *S. vulgaris* sensu lato, although they formed four independent lineages too.
**Figure 3.** Phylogeny of *Sidera* and related species generated by ML analyses based on combined ITS + nLSU + RPB1 + RPB2 + TEF1 + mtSSU + nSSU sequences. Branches are labeled with maximum likelihood bootstrap >50% and Bayesian posterior probabilities >0.90, respectively. New species are indicated in bold.

### 3.2. Taxonomy

1. **Sidera inflata** Z.B. Liu & Y.C. Dai, sp. nov. Figures 4 and 5.
   
   MycoBank number: MB 838380.
   
   Etymology—*Inflata* (Lat.): referring to the species having inflated skeletal hyphae in KOH.
Type—China, Hainan Province, Baisha County, Yinggeling Nature Reserve, on rotten angiosperm wood, 17 November 2015, B.K. Cui 13610 (holotype BJFC 028475).

Basidioma—Annual, resupinate, soft corky when fresh and dry, up to 4 cm long, 1.5 cm wide and less than 1 mm thick at center; pore surface white to buff and shiny when fresh, becoming cream to buff yellow and shiny when dry; sterile margin distinct, white, cottony, thinning out; pores angular, 9–10 per mm; dissepiments thin, lacerate; subiculum very thin to almost absent; tubes concolorous with the poroid surface, less than 1 mm long.

Hyphal structure—Hyphal system dimitic; generative hyphae bearing clamp connections; skeletal hyphae dominant; all hyphae IKI–, CB–, skeletal hyphae obviously becoming swollen in KOH.

Subiculum—Generative hyphae hyaline, thin-walled, occasionally branched, 1–2 µm in diameter; skeletal hyphae thick-walled with a wide lumen, rarely branched, interwoven, 2–4 µm diameter; rosette-like crystals rarely present.

Tubes—Generative hyphae hyaline, thin-walled, occasionally branched, 1–2 µm in diameter; skeletal hyphae thick-walled with a wide lumen, rarely branched, interwoven, usually covered by abundant fine thorn-like crystals at dissepiment edge, 2–4 µm diameter; rosette-like crystals abundant, 2–8 µm in diameter; cystidia absent; cystidioles present, fusoid, hyaline, thin-walled, basally swollen, with a sharp or often hyphoid neck, 13–15 × 2.5–3 µm; basidia clavate, hyaline, bearing four sterigmata and a basal clamp connection, 7–8 × 3.5–4.5 µm; basidioles similar in shape to basidia, but slightly shorter.

Basidiospores—Allantoid, hyaline, thin-walled, smooth, occasionally with one or two guttules, IKI–, CB–, (2.9–)3.3(–3.5) × (0.8–)0.9–1.1 µm, L = 3.03 µm, W = 1 µm, Q = 3.03 (n = 60/1).

Notes—*Sidera inflata* was found in China, and the species is characterized by annual, resupinate basidioma with a white to buff fresh pore surface, which becomes cream to buff-yellow upon drying; angular pores (9–10 per mm); a dimitic hyphal system; skeletal hyphae at dissepiment edge bearing abundant fine thorn-like crystals; skeletal hyphae in all structures obviously swelling in KOH; and allantoid basidiospores measuring 3–3.3 × 0.9–1.1 µm. Morphologically, *S. inflata* can be distinguished from other species in *Sidera* by its skeletal hyphae at the dissepiment edge, which are usually covered by abundant fine thorn-like crystals. Although *S. inflata* clustered together with the *S. vulgaris* sensu lato (Dai 21057 and Dai 22151) with a moderate support (87% BS, 0.94 BPP; Figure 3), the latter taxon had perennial basidioma, and its skeletal hyphae were unchanged in KOH.

Figure 4. A basidioma of *Sidera inflata* (from the holotype Cui 13610). Scale bar = 10 mm.
2. *Sidera malaysiana* Z.B. Liu & Y.C. Dai, sp. Nov. Figures 6 and 7

MycoBank number: MB 838381.

Etymology—*Malaysiana* (Lat.): referring to the species occurring in Malaysia.

Type—Malaysia, Selangor, Forest Research Institute of Malaysia, on rotten angiosperm wood, 15 April 2018, Y.C. Dai 18570 (holotype BJFC 026859).

Basidioma—Annual, resupinate, very difficult to separate from substrate, soft corky when fresh and dry, up to 4 cm long, 2 cm wide and less than 1 mm thick at center; pore surface white to cream when fresh and dry; sterile margin indistinct; pores round to angular, 9–11 per mm; dissepiments thin, entire; subiculum very thin to almost absent; tubes white, less than 1 mm long.

Hyphal structure—Hyphal system dimitic; generative hyphae bearing clamp connections; skeletal hyphae dominant; all hyphae IKI–, CB–, skeletal hyphae slightly swollen in KOH.
Subiculum—Generative hyphae hyaline, thin-walled, rarely branched, 1–2 µm in diameter; skeletal hyphae dominant, occasionally branched, interwoven, usually covered by abundant irregular crystals and fine thorn-like crystals, 1.5–3.5 µm diameter; rosette-like crystals occasionally present, 3–5 µm in diameter.

Tubes—Generative hyphae hyaline, thin-walled, rarely branched, 1–2.5 µm in diameter, dominating at dissepiment edges; skeletal hyphae thick-walled, occasionally branched, interwoven, 1.5–3.5 µm diameter; rosette-like and irregular rhomboidal crystals abundant at dissepiment edges; cystidia absent; cystidioles present, fusoid, hyaline, thin-walled, basally swollen, with a sharp or often hyphoid neck, 9–13 × 2.2–3.5 µm; basidia clavate, hyaline, with a basal clamp connection and four sterigmata, 7.8–15 × 3–4.3 µm; basidioles similar in shape to basidia, but slightly shorter.

Basidiospores—Lunate, hyaline, thin-walled, smooth, usually with two or three guttules, IKI–, CB–, (2.8–)2.9–3.2(–3.3) × 1–1.2(–1.4) µm, L = 3.16 µm, W = 1.12 µm, Q = 2.82 (n = 60/1).

Notes—*Sidera malaysiana* was found in Malaysia, and the species is characterized by annual, resupinate basidioma with a white to cream pore surface, round to angular pores (9–11 per mm), a dimitic hyphal system, skeletal hyphae in all structures become slightly swollen in KOH, subicular skeletal hyphae bearing rosette-like crystals, irregular crystals and fine thorn-like crystals and lunate basidiospores measuring 2.9–3.2 × 1–1.2 µm. Morphologically, *S. malaysiana* can be distinguished from other species in *Sidera* by its subicular skeletal hyphae, which are usually covered by abundant irregular crystals and fine thorn-like crystals. *S. malaysiana* is closely related to *S. srilankensis* in our phylogeny (100% BS, 1.00 BPP; Figure 2), but *S. malaysiana* is different from *S. srilankensis* due to its smaller pores (9–11 per mm vs. 6–8 per mm, [2]) and skeletal hyphae in all structures becoming slightly swollen in KOH, while skeletal hyphae are unchanged in KOH in *S. srilankensis*. *S. malaysiana* resembles *S. parallela* due to its white fresh pore surface. However, *S. malaysiana* differs from *S. parallela* due to its smaller pores (9–11 per mm vs. 6–8 per mm, [2]). In addition, tramal hyphae are parallel in *S. parallela*, while they are interwoven in *S. malaysiana*. Additionally, they are phylogenetically distant (Figure 2).

![Figure 6. A basidioma of *Sidera malaysiana* (from the holotype Dai 18570). Scale bar = 10 mm.](image-url)
Figure 7. Microscopic structures of *Sidera malaysiana* (holotype, Dai 18570). (a) Basidiospores. (b) Basidia and basidioles. (c) Cystidioles. (d) Hyphae from subiculum. (e) Hyphae from trama. (f) Hyphae at dissepiment edge. Drawing by Meng Zhou.

3. **Sidera punctata** Z.B. Liu & Y.C. Dai, sp. nov. Figures 8 and 9.

   MycoBank number: MB 838384.

   Etymology—*Punctata* (Lat.): referring to the species having cushion-shaped basidioma.

   Type—China, Hainan Province, Haikou, Guanlanhu, on rotten angiosperm wood, 18 November 2020, Y.C. Dai 22119 (holotype BJFC 036011).

   Basidioma—Annual, resupinate, soft coryck when fresh and dry; up to 13 cm long, 4 cm wide and less than 1 mm thick at center; pore surface white to cream when fresh, becoming cinnamon buff to white when dry; sterile margin distinct, white, cottony, thinning out; pores round, 8–9 per mm; dissepiments thin, entire; subiculum very thin to almost absent; tubes darker than the poroid surface, less than 1 mm long.

   Hyphal structure—Hyphal system monomitic; generative hyphae bearing clamp connections; all hyphae IKI−, CB−, unchanged in KOH.

   Subiculum—Generative hyphae hyaline, thin-walled, often branched, interwoven, 1.5–2.5 μm in diameter; rosette-like crystals frequently present, 2–7 μm in diameter.

   Tubes—Generative hyphae hyaline, thin-walled, sometimes branched, loosely interwoven, 1.5–3 μm in diameter, some hyphae, especially hyphae at dissepiment edge with swollen tips which are globose, bottle-shaped or irregularly elongated; rosette-like crystals occasionally present; cystidia absent; cystidioles absent; basidia clavate, hyaline, bearing four sterigmata and a basal clamp connection, 12.5–13.5 × 3.5–4.5 μm; basidioles similar in shape to basidia, but slightly shorter.
Figure 8. A basidioma of *Sidera punctata* (from the holotype Dai 22119). Scale bar = 10 mm.

Figure 9. Microscopic structures of *Sidera punctata* (holotype, Dai 22119). (a) Basidiospores. (b) Basidia and basidioles. (c) Hyphae from subiculum. (d) Hyphae from trama. (e) Hyphae at dissepiment edge. Drawing by Meng Zhou.
Basidiospores—Allantoid to lunate, hyaline, thin-walled, smooth, occasionally with one to three guttules, IKI–, CB–, (3.5–)3.8–4.8(–5) × 1–1.3(–1.4) μm, L = 4.27 μm, W = 1.21 μm, Q = 3.53 (n = 60/1).

Notes—*Sidera punctata* was discovered in China, and the species is characterized by annual, resupinate basidioma with a white to cream fresh pore surface which becomes cinnamon-buff to white upon drying, round pores (8–9 per mm), a monomitic hyphal system, and allantoid to lunate basidiospores measuring 3.8–4.8 × 1–1.3 μm. Phylogenetically, *S. punctata* is close to *S. vesiculosa* (100% BS, 1.00 BPP; Figure 2) and it is similar to *S. vesiculosa* by annual, resupinate basidioma and some generative hyphae with swollen tips, but *S. punctata* has a cinnamon-buff to white dry pore surface, while the pore surface is cream upon drying in *S. vesiculosa*. Above all, *S. punctata* can be distinguished from other species in *Sidera* by its rosette-like crystals are more abundant in subiculum than in tubes, while rosette-like crystals are more abundant in tubes than in subiculum in other members of the genus.

4. *Sidera roseo-bubalina* Z.B. Liu & Y.C. Dai, sp. nov. Figures 10 and 11.

Mycobank number: MB 838382.

Etymology—*Roseo-bubalina* (Lat.): referring to the species having pinkish buff hymenophore.

Type—China, Henan Province, Neixiang County, Baotianman Nature Reserve, on rotten wood of *Quercus*, 22 September 2009, Y.C. Dai 11277 (holotype BJFC 007251).

Basidioma—Annual, resupinate, soft corky when dry, up to 7 cm long, 3 cm wide, and less than 1 mm thick at center; pore surface pinkish buff to yellowish brown when dry; sterile margin distinct, white, cottony, thinning out; pores round, 6–7 per mm; dissepiments thin, entire to lacerate; subiculum very thin to almost absent; tubes concolorous with the poroid surface, less than 1 mm long.

Hyphal structure—Hyphal system monomitic; generative hyphae bearing clamp connections; all hyphae IKI–, CB–, unchanged in KOH.

Subiculum—Generative hyphae hyaline, thin-walled, often branched, interwoven, 2–3 μm in diameter; rosette-like crystals occasionally present.

Tubes—Generative hyphae hyaline, thin-walled, often branched, interwoven, 2–3.5 μm in diameter, some hyphae, especially hyphae at dissepiment edge with swollen tips which are globose, bottle-shaped or irregularly elongated; rosette-like crystals abundant, 4–6 μm in diameter; cystidia absent; cystidioles present, fusoid, hyaline, thin-walled, basally swollen, with a sharp or often hyphoid neck, 15–22 × 4–4.5 μm; basidia clavate, hyaline, bearing four sterigmata and a basal clamp connection, 8.5–11 × 4.5–5 μm; basidioles similar in shape to basidia, but slightly shorter.

Basidiospores—Lunate, hyaline, thin-walled, smooth, occasionally with one to four guttules, IKI–, CB–, (3.5–)3.9–4.5(–4.8) × (0.7–) 0.8–1 μm, L = 4.22 μm, W = 0.93 μm, Q = 4.53 (n = 60/1).

Notes—*Sidera roseo-bubalina* was discovered in China, and the species is characterized by annual, resupinate basidioma with a pinkish buff to yellowish brown dry pore surface, round pores (6–7 per mm), a monomitic hyphal system and lunate basidiospores measuring 3.9–4.5 × 0.8–1 μm. Morphologically, *S. roseo-bubalina* and *S. lowei* share annual, resupinate basidioma and similar pores (6–7 per mm in *S. roseo-bubalina* vs. 6–8 per mm in *S. lowei* [1]), but *S. roseo-bubalina* has lunate basidiospores, which are usually <1 μm wide, while *S. lowei* has allantoid basidiospores, which are usually >1 μm wide. Phylogenetically, *S. roseo-bubalina* is close to *S. punctata* and *S. vesiculosa* (100% BS, 1.00 BPP; Figure 2), and these three species share annual and resupinate basidioma, and some generative hyphae with swollen tips, but *S. roseo-bubalina* has a pinkish buff to yellowish brown dry pore surface, while the pore surface is cream upon dried in *S. vesiculosa* and cinnamon-buff to white when dried in *S. punctata*. In addition, *S. roseo-bubalina* differs from the other two species due to its larger pores (6–7 per mm in *S. roseo-bubalina*, 8–9 per mm in *S. punctata* and 7–9 per mm in *S. vesiculosa*, [7]).
Figure 10. A dry basidioma of *Sidera roseo-bubalina* (from the holotype Dai 11277). Scale bar = 10 mm.

Figure 11. Microscopic structures of *Sidera roseo-bubalina* (holotype, Dai 11277). (a) Basidiospores. (b) Basidia and basidioles. (c) Cystidioles. (d) Hyphae from subiculum. (e) Hyphae from trama. (f) Hyphae at dissepiment edge. Drawing by Meng Zhou.

5. *Sidera vulgaris sensu lato*

Specimens examined—Belarus, Brestskaya Voblasts, Belavezhskaya Pushcha National Park, on rotten wood of *Picea*, 19 October 2019, Y.C. Dai 21057 (BJFC 032716 and MSK). China, Guangxi Province, Guiping County, Xishan Scenic Spot, on rotten wood of *Pinus*, 25 December 2020, Y.C. Dai 22151 (BJFC 036043); Shannxi Province, Zhashui County, Niu-ubeliang Forest Park, on fallen angiosperm trunk, 16 September 2013, B.K. Cui 11216 (BJFC 015331). USA, Connecticut, New Haven, West Rock Park, on rotten stump of *Pinus*, 15 July 2012, Y.C. Dai 12730 (BJFC 013037).
Previously, the ten species of Sidera, viz. *S. lenis*, *S. lowei*, *S. lunata*, *S. minutipora*, *S. minutissima*, *S. parallela*, *S. srilankensis*, *S. tenuis*, *S. vesiculosa* and *S. vulgaris* were described or transferred to the genus. In this paper, *S. inflata*, *S. malaysiana*, *S. punctata* and *S. roseo-bubalina* were described as new to science, and they have resupinate, white to cream or buff fresh basidiocarps; a monomitic or dimitic hyphal system with generative hyphae bearing clamp connections; the presence of rosette-like crystals; and allantoid to lunate basidiospores. These characteristics fit well with the generic concept of Sidera. Thus far, 14 species are accepted in Sidera, and a key of accepted species is provided below.

**A key to species of Sidera worldwide**

1. Hymenium grandinioid to odontioid
   - **S. lunata**
1. Hymenium poroid
2. Hyphal system monomitic
   - **S. vesiculosa**
2. Hyphal system dimitic
3. Basidiospores mostly <1 µm in width
   - **S. roseo-bubalina**
3. Basidiospores mostly >1 µm in width
4. Pores 7–9 per mm; basidiospores 2.9–3.7 µm long
   - **S. lenis**
4. Pores 6–7 per mm; basidiospores 3.9–4.5 µm long
   - **S. inflata**
5. Pores 6–8 per mm; cystidioles present, some branched
   - **S. punctata**
5. Pores 8–9 per mm; cystidioles absent
6. Basidiospores >1.5 µm in width
   - **S. malaysiana**
6. Basidiospores <1.5 µm in width
7. Skeletal hyphae becoming swollen in KOH
   - **S. minutipora**
7. Skeletal hyphae almost unchanged in KOH
8. Pores 5–7 per mm; basidiospores 3.7–4.3 µm long
   - **S. tenuis**
8. Pores 9–11 per mm; basidiospores 2.9–3.3 µm long
   - **S. vulgaris**
9. Basidiospores allantoid, skeletal hyphae distinctly swollen in KOH
   - **S. srilankensis**
9. Basidiospores lunate, skeletal hyphae slightly swollen in KOH
10. Tramal hyphae parallel along the tubes
   - **S. parallela**
10. Tramal hyphae interwoven
11. Generative hyphae at dissepiments even
   - **S. srilankensis**
11. Generative hyphae at dissepiments with swollen tips
12. Basidiospores <3.6 µm long
   - **S. vulgaris**
12. Basidiospores >3.8 µm long
13. Sterile margin distinct, fimbriate; basidiospore Length/width <4
   - **S. minutissima**
13. Sterile margin indistinct to almost absent; basidiospore Length/width >4

4. Discussion

As is well known, the genus *Sidera* is challenging for distinguishing species morphologically, and two species, *S. lenis* and *S. vulgaris*, were recognized before phylogenetical analyses. *Poria krawtzewii* Pilát was treated as a synonym of *P. lenis* (P. Karst.) Sacc. [29], but it is different from the *S. lenis* complex because of ellipsoid spores [30]. We summarize another five synonyms of *Sidera lenis* (Index Fungorum and MycoBank): *Poria lunulispora* Pilát (type from Siberia), *P. chakassensis* Pilát (type from Siberia), *P. earlei* Murrill (type from Jamaica), *P. tenuipora* Murrill (type from Jamaica) and *P. montana* Murrill (type from Jamaica).

*Poria earlei*, *P. montana* and *P. tenuipora* were described from the Caribbean (Jamaica) (Murrill [31,32]). The type of specimens of three species were studied by Niemelä and Dai [8]. They found that *P. earlei* and *P. montana* are conspecific, and the species is perennial, resupinate and has small pores (7–9 per mm). *Sidera punctata* and *S. vesiculosa* have similar pores (8–9 per mm in *S. punctata* vs. 7–9 per mm in *S. vesiculosa* [7]) to *P. tenuipora* as well, but the former two species have a monomitic hyphal system, while *P. tenuipora* has a dimitic hyphal system. *S. vesiculosa* differs from *S. punctata* due to the presence of vesicular cells of swollen hyphae in the subiculum.

*Poria chakassensis* and *P. lunulispora* were described from Siberia [33,34]. Kotlaba and Pouzar [30,35] found that *P. chakassensis* has basidiospores measuring 5.5–8.5 × 2–2.4 µm and represents *Ceriporia purpurea* (Fr.) Donk; *P. lunulispora* was collected on the wood.
of Pinus, and is true Diplomitoporus lenis (= Sidera lenis). Hence, P. chakasskensis and P. lunulispora are different from our newly described species.

Du et al. [2] summarized three synonyms of Sidera vulgaris (Index Fungorum and MycoBank): Boletus papyraceus Schrank, B. proteus Bolton and B. cellulosus O.F. Müll, and all of them were originally described from Europe. In addition, the specimen Ryvarden 37198 from New Zealand was named S. vulgaris by Miettinen and Larsson too [1]. In the present paper, we found three taxa with similar morphologies to S. vulgaris, but we did not study the types of the above-mentioned taxa, and no sequence data are available for them. Although our three taxa formed three distinct lineages in our phylogenies (Figure 3), we refrained from describing these as new, and treated them as S. vulgaris sensu lato in this paper (Table 2). The description of these species is the subject of a forthcoming paper.

Ceriporiopsis lowei (= Sidera lowei) was described from Northern Brazil [4]. The specimen Miettinen X426 (Ryvarden 38817) from New Zealand clustered together with a Venezuelan specimen Miettinen X419, and both specimens were considered as Sidera lowei by Miettinen and Larsson [1]. We did not examine the type of Sidera lowei; thus, we regard Miettinen X419 and Miettinen X426 as “S. lowei”.

The sequence of OTU1581 is from GenBank. We failed to obtain specimens of the taxa, but it formed a distinct lineage within the Sidera clade, so we treated OTU1581 as Sidera sp. temporarily here.

Polypores are an extensively studied group of Basidiomycota, and more than 1500 species have been recorded in the world [36–42]. Molecular phylogenies have demonstrated that more new taxa exist in the world [43–47], and more crypto species will be confirmed after molecular analyses of some traditional species in sensu lato. Thus, in order to understand the diversity, phylogeny and evolution of the fungi, future taxonomic and phylogenetic work should be based on both molecular and morphological characteristics.

**Author Contributions:** Conceptualization, Y.-C.D. and Z.-B.L.; methodology, Z.-B.L.; performing the experiment, Z.-B.L.; formal analysis, Z.-B.L.; validation, Z.-B.L., Y.-C.D., M.Z. and Y.Y.; resources, Y.-C.D.; writing—original draft preparation, Z.-B.L.; writing—review and editing, Y.-C.D.; visualization, Z.-B.L.; supervision, Y.-C.D. and Y.Y.; project administration, Y.Y.; funding acquisition, Y.-C.D. 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 No. 31870007; 31530002).

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

**Informed Consent Statement:** Not applicable.

**Data Availability Statement:** Publicly available datasets were analyzed in this study. This data can be found here: https://www.ncbi.nlm.nih.gov/; https://www.mycobank.org/page/Simple%20names%20search; http://purl.org/phylo/treebase, submission ID 27909, 27910 and 27911.

**Acknowledgments:** Not applicable.

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

**References**

1. Miettinen, O.; Larsson, K.H. Sidera. A new genus in Hymenochoetales with poroid and hydnoid species. *Mycol. Prog.* 2011, 10, 131–141. [CrossRef]

2. Du, R.; Wu, F.; Gate, G.M.; Dai, Y.C.; Tian, X.M. Taxonomy and phylogeny of Sidera (Hymenochoetales, Basidiomycota): Four new species and keys to species of the genus. *MycokEys* 2020, 68, 115–135. [CrossRef]

3. Fries, E.M. Systema Mycologicum. *Berlingius Lindae*. 1821, 1, 1–520.

4. Rajchenberg, M. Type studies of Polyporaceae (Aphyllophorales) described by J. Rick. *Nord. J. Bot.* 1987, 7, 553–568. [CrossRef]

5. Bourdot, H.; Galzin, A. Hyménomycètes de France. I. Hétérobasidiées. *Bull. Soc. Mycol. Fr.* 1909, 25, 15–36.

6. Rodway, L.; Cleland, J.B. Notes on the genus Poria No. 3. *Pap. Proc. R. S. Tasman.* 1929, 17, 7–24.

7. Du, R.; Wang, L.; Zhou, M.; Chen, J.J. A new species of Sidera (Hymenochoetales, Basidiomycota) from tropical Asia. *Phytotaxa.* 2019, 387, 165–171. [CrossRef]

8. Niemelä, T.; Dai, Y.C. Polypore *Skeletocutis lenis* and its sib *S. vulgaris*. *Ann. Bot. Fenn.* 1997, 34, 133–140.

9. Niemelä, T. Polypores, lignicolous fungi. *Norrlinia* 2005, 13, 1–320, (In Finnish, with English summary).
27. Ronquist, F.; Teslenko, M.; Mark, P.; Avres, D.L.; Darling, A.; Höhna, S.; Larget, B.; Liu, L.; Suchard, M.A.; Huelsenbeck, J.P.

44. Miettinen, O.; Ryvarden, L. Polypore genera

43. Decock, C.; Yombiyeni, P.; Memiaghe, H. Hymenochaetaceae from the Guineo-Congolian rainforest: Mycoscience

40. Dai, Y.C. Polypore diversity in China with an annotated checklist of Chinese polypores. Synop. Fungorum.

39. Ryvarden, L. Neotropical polypores 1.

38. Núñez, M.; Ryvarden, L. East Asian polypores 2. Synop. Fungorum. 2001, 14, 165–252.

37. Buchanan, P.K.; Ryvarden, L. An annotated checklist of polypore and polypore-like fungi recorded from New Zealand. N. Z. J. Bot. 2000, 38, 265–323. [CrossRef]

36. White, T.J.; Bruns, T.; Lee, S.; Taylor, J. Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. PCR Protocols: A Guide to Methods and Applications

35. Kotlaba, F.; Pouzar, Z. Type studies of polypores described by A. Pilát-III. Ceska Mykol. 1989, 43, 36–44. [PubMed]

34. Pilát, A. Polyporaceae. In Atlas des Champignons de l’s Europe; Kavina, C., Pilát, A., Eds.; Privately Published: Prague, Czech Republic, 1936–1942; pp. 1–624,374.

33. Pilát, A. Polyporaceae. In Atlas des Champignons de l’s Europe; Kavina, C., Pilát, A., Eds.; Privately Published: Prague, Czech Republic, 1936–1942; pp. 1–624,374.

32. Murrill, W.A. Light-colored resupinate polypores 2. Mycologia 1920, 12, 299–308. [CrossRef]

31. Murrill, W.A. Light-colored resupinate polypores 1. Mycologia 1920, 12, 77–92. [CrossRef]

30. Kotlaba, F.; Pouzar, Z. Type studies of polypores described by A. Pilát. Ceska Mykol. 1991, 45, 91–97. [CrossRef]

29. Pilát, A. Additamenta ad floram Sibiriae Asiaeque orientalis mycologicum. Bull. Soc. Mycol. Fr. 1933, 49, 256–339.

28. Rambaut, A. Molecular Evolution, Phylogenetics and Epidemiology. FigTree ver. 1.4 Software. Available online: http://tree.bio.ed.ac.uk/software/figtree/ (accessed on 24 March 2021).

27. Ronquist, F.; Teslenko, M.; Mark, P.; Avres, D.L.; Darling, A.; Höhna, S.; Larget, B.; Liu, L.; Suchard, M.A.; Huelsenbeck, J.P.

26. White, T.J.; Bruns, T.; Lee, S.; Taylor, J. Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. PCR Protocols: A Guide to Methods and Applications

25. Nylander, J.A.A. MrModeltest v2. Program Distributed by the Author

24. Miller, M.A.; Holder, M.T.; Vos, R.; Midford, P.E.; Liebowitz, T.; Chan, L.; Hoover, P.; Warnow, T. The CIPRES Portals. CIPRES. Available online: http://www.phylo.org/sub_sections/portal (accessed on 4 August 2009).

23. Yuan, Y.; Ji, X.H.; Wu, F.; He, S.H.; Chen, J.J. Two new Gloeoporus (Polyporales, Basidiomycota) from tropical China. Nova Hedwig. 2016, 103, 169–183. [CrossRef]

22. Maddison, W.P.; Maddison, D.R. Mesquite: A Modular System for Evolutionary Analysis. Available online: https://www.mesquiteproject.org/ (accessed on 24 March 2021).

21. Hall, T.A. Bioedit: A user–friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. Nucleic Acids Symp. Ser. 1999, 41, 95–98. [CrossRef]

20. Hall, T.A. Bioedit: A user–friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. Nucleic Acids Symp. Ser. 1999, 41, 95–98. [CrossRef]

19. Nylander, J.A.A. MrModeltest v2. Program Distributed by the Author; Evolutionary Biology Centre: Uppsala, Sweden, 2004.

18. Maddison, W.P.; Maddison, D.R. Mesquite: A Modular System for Evolutionary Analysis. Available online: https://www.mesquiteproject.org/ (accessed on 24 March 2021).

17. Hall, T.A. Bioedit: A user–friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. Nucleic Acids Symp. Ser. 1999, 41, 95–98. [CrossRef]

16. White, T.J.; Bruns, T.; Lee, S.; Taylor, J. Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In PCR Protocols: A Guide to Methods and Applications; Innis, M.A., Gefland, D.H., Sninsky, J.J., White, J.T., Eds.; Academic Press: San Diego, CA, USA, 1990; pp. 315–322. [CrossRef]

15. Matheny, P.B.; Liu, Y.J.; Ammirati, J.F.; Hall, B.D. Using RPBI sequences to improve phylogenetic inference among mushrooms (Inocybe, Agaricales). Am. J. Bot. 2002, 89, 688–698. [CrossRef] [PubMed]

14. Matheny, P.B. Improving phylogenetic inference of mushrooms with RPBI1 and RPBI2 nucleotide sequences (Inocybe, Agaricales). Mol. Phylogenet. Evolut. 2005, 35, 1–20. [CrossRef] [PubMed]

13. Thiers, B. Fungal Divers. 1996; pp. 1–6.

12. Petersen, J.H. A Preliminary Polypore Flora of East Africa

11. Anonymous. Flora of British Fungi. Colour Identification Chart; Her Majesty's Stationery Office: London, UK, 1969.

10. Dai, Y.C. Hymenochaetaceae (Basidiomycota) in China. Fungal Divers. 2010, 45, 131–343. [CrossRef]

9. Matheny, P.B.; Liu, Y.J.; Ammirati, J.F.; Hall, B.D. Using RPBI sequences to improve phylogenetic inference among mushrooms (Inocybe, Agaricales). Am. J. Bot. 2002, 89, 688–698. [CrossRef] [PubMed]

8. Matheny, P.B. Improving phylogenetic inference of mushrooms with RPBI1 and RPBI2 nucleotide sequences (Inocybe, Agaricales). Mol. Phylogenet. Evolut. 2005, 35, 1–20. [CrossRef] [PubMed]

7. Kotah, K.; Toh, H. Recent developments in the MAFFT multiple sequence alignment program. Brief. Bioinform. 2008, 9, 286–298. [CrossRef]

6. Miller, M.A.; Holder, M.T.; Vos, R.; Midford, P.E.; Liebowitz, T.; Chan, L.; Hoover, P.; Warnow, T. The CIPRES Portals. CIPRES. Available online: http://www.phylo.org/sub_sections/portal (accessed on 4 August 2009).

5. Nylander, J.A.A. MrModeltest v2. Program Distributed by the Author; Evolutionary Biology Centre: Uppsala, Sweden, 2004.

4. Swofford, D.L. PAUP: Phylogenetic Analysis using Parsimony Version 4.0b10; Sinauer Associates: Sunderland, MA, USA, 2002.

3. Ronquist, F.; Teslenko, M.; Mark, P.; Avres, D.L.; Darling, A.; Höhna, S.; Larget, B.; Liu, L.; Suchard, M.A.; Huelsenbeck, J.P. MrBayes3.2: Efficient Bayesian phylogenetic inference and model choice, across a large model space. Syst. Biol. 2012, 61, 539–542. [CrossRef]

2. Rambaut, A. Molecular Evolution, Phylogenetics and Epidemiology. FigTree ver. 1.4 Software. Available online: http://tree.bio.ed.ac.uk/software/figtree/ (accessed on 24 March 2021).

1. Pilát, A. Polyporaceae. In Atlas des Champignons de l’s Europe; Kavina, C., Pilát, A., Eds.; Privately Published: Prague, Czech Republic, 1936–1942; pp. 1–624,374.
45. Ji, X.H.; He, S.H.; Chen, J.J.; Si, J.; Wu, F.; Zhou, L.W.; Vlasák, J.; Tian, X.M.; Dai, Y.C. Global diversity and phylogeny of *Onnia* (Hymenochaetaceae) species on gymnosperms. *Mycologia* 2017, 109, 27–34. [CrossRef] [PubMed]

46. Spirin, V.; Vlasák, J.; Miettinen, O. Studies in the *Antrodia serialis* group (Polyporales, Basidiomycota). *Mycologia* 2017, 109, 217–230. [CrossRef] [PubMed]

47. Wu, F.; Dai, S.J.; Vlasák, J.; Spirin, V.; Dai, Y.C. Phylogeny and global diversity of *Porodaedalea*, a genus of gymnosperm pathogens in the Hymenochaetales. *Mycologia* 2019, 111, 40–53. [CrossRef]