Short communication

A new species of Hyphodermella (Polyporales, Basidiomycota) with a poroid hymenophore

Chang-Lin Zhao, Guang-Juan Ren, Fang Wu

Institute of Microbiology, P.O. Box 61, Beijing Forestry University, Beijing 100083, PR China
Yunnan Academy of Biodiversity, Southwest Forestry University, Kunming 650224, PR China

A new poroid wood-inhabiting fungal species, Hyphodermella poroides, is proposed based on morphological and molecular evidences. The species is characterized by resupinate basidiocarps with cream to orange pore surface, a monomitic hyphal system with generative hyphae bearing simple septa, and broadly ellipsoid, hyaline, thin-walled, smooth, IKI-, CB- basidiospores. The phylogenetic analyses based on ITS + nLSU sequences showed that H. poroides formed a single group with a strong support and was closely related to H. corrugata and H. rosae, and then grouped with Pirex concentricus. Both morphological and molecular evidences confirmed the placement of the new species in Hyphodermella.

© 2017 The Mycological Society of Japan. Published by Elsevier B.V. All rights reserved.
studies the polyposes and genus concepts in Phanerochaetaeae based on the morphological and phylogenetic investigations. Their phylogenetic tree based on the internal transcribed spacer (ITS) regions and the large subunit nuclear ribosomal RNA gene (nLSU) sequences showed that H. corrugata and H. rosae placed in the clade labeled as donkia clade together with Donkia pulcherrima (Berk. & M.A. Curtis) Pilat, Phanerochaete deflectens (P. Karst.) Hjortstam, Firex concentricus (Cooke & Ellis) Hjortstam & Ryvarden and two species of Phlebia Fr.

During a study of Chinese wood-inhabiting fungi, two specimens collected from Hainan Province in southern China were characterized by resupinate, cream to orange basidiocarps with poroid hymenophore, a monomitic hyphal structure with simple septa, generative hyphae in subiculum distinctly wider than in trama, and hyaline, thin-walled, ellipsoid basidiospores which are negative in Melzer's reagent and Cotton Blue. These characters made them distinct from all the known wood-rotting fungal taxa, and here we propose a new species for the two specimens. To support this proposal, phylogenetic analyses on the position of the new species and related taxa were done based on ITS and nLSU sequences.

The specimens of Hyphodermella poroides sp. nov. were deposited at the herbarium of Beijing Forestry University (BJFC). Macro-morphological descriptions are based on field notes and indoor observation follows Dai (2010). Special color terms follow Petersen (1996). Micro-morphological data were obtained from the dried specimens, and observed under a light microscope following Dai (2010). The following abbreviations were used: KOH = 5% potassium hydroxide, CB = Cotton Blue, CB− = acyanophilous, IKI = Melzer’s reagent, IKI− = both inamyloid and indextrinoid, L = mean basidiospore length (arithmetic average of all basidiospores), W = mean spore width (arithmetic average of all spores), Q = variation in the L/W ratios between the specimens studied, n(a/b) = number of basidiospores (a) measured from given number (b) of specimens.

CTAB rapid plant genome extraction kit-DN14 (Aidlab Biotechnologies Co., Ltd, Beijing) was used to obtain PCR products from dried specimens, according to the manufacturer’s instructions with some modifications. 2 × EasyTaq PCR SuperMix (TransGen biotech, China) was used to amplify nLSU sequences with primers LR0R and LR7 (http://wwwbiology.duke.edu/fungi/mycolab/primer.htm) and ITS sequences with primers ITS5 and ITS4 (White et al. 1990). The PCR procedure for nLSU was as follows: 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 procedure for ITS was as follows: 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 PCR products were sequenced at Beijing Genomics Institute, China, with primers LR0R and LR7 for nLSU region and primers ITS5 and ITS4 for ITS region. The newly generated sequences were submitted to GenBank (http://www.ncbi.nlm.nih.gov/genbank; Table 1).

Sequences were aligned in MAFFT 6 (Katoh and Toh 2008; http://mafft.cbrc.jp/alignment/server/) using “E-INS-I” strategy for ITS + nLSU, and manually adjusted in BioEdit (Hall 1999). Alignment datasets were deposited in TreeBase (submission ID 19081). Phanerina mella (Berk. & Broome) Miettinen was selected as outgroup for phylogenetic analyses combined dataset of ITS and nLSU regions (Miettinen et al. 2016).

Maximum parsimony (MP) analysis was applied to the ITS + nLSU datasets. The tree construction procedure was performed in PAUP* version 4.0b10 (Swoford 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 5,000, branches of zero length were collapsed and all parsimonious trees were saved. A bootstrap analysis with 1000 replicates was assessed (Felsenstein 1985). Descriptive tree statistics tree length (TL), consistency index (CI), retention index (RI), rescaled consistency index (RC), and homoplasy index (HI) were calculated for each Maximum Parsimonious Tree generated. Maximum Likelihood (ML) analysis with RAXML-HPC2 was conducted ITS + nLSU data-sets on Abe through the Cipres Science Gateway (www.phylo.org; Miller et al. 2009). Branch support for MP and ML analysis was determined by 1000 bootstrap replicates.

MrModeltest 2.3 (Posada and Crandall 1998; Nylander 2004) was used to determine the best-fit evolution model for each dataset for Bayesian inference (BI). Bayesian inference was calculated with MrBayes 3.1.2 with a general time reversible (GTR) model of DNA substitution and a gamma distribution.

Table 1 – A list of species, specimens, and GenBank accession number of sequences used in this study.

<table>
<thead>
<tr>
<th>Species name</th>
<th>Sample no.</th>
<th>GenBank accession no.</th>
<th>References</th>
</tr>
</thead>
<tbody>
<tr>
<td>Donkia pulcherrima</td>
<td>Gothenburg 2022</td>
<td>KX752591</td>
<td>Miettinen et al. 2016</td>
</tr>
<tr>
<td>Hyphodermella corrugata</td>
<td>MA-Fungi 26186</td>
<td>CNN00379</td>
<td>Foudas and Hibbett 2015</td>
</tr>
<tr>
<td>H. corrugata</td>
<td>MA-Fungi 24238</td>
<td>CNN00378</td>
<td>Foudas and Hibbett 2015</td>
</tr>
<tr>
<td>H. poroides</td>
<td>Dai 12045</td>
<td>KX008367</td>
<td>Present study</td>
</tr>
<tr>
<td>H. poroides</td>
<td>Dai 10848</td>
<td>KX008368</td>
<td>Present study</td>
</tr>
<tr>
<td>H. roae</td>
<td>FP 150552</td>
<td>KP134978</td>
<td>Foudas and Hibbett 2015</td>
</tr>
<tr>
<td>Phanerina mella</td>
<td>MA-Fungi 38071</td>
<td>FN003089</td>
<td>Telleria et al. 2010</td>
</tr>
<tr>
<td>Phlebia deflectens</td>
<td>Ryvarden 10132</td>
<td>KX752611</td>
<td>Miettinen et al. 2016</td>
</tr>
<tr>
<td>P. firma</td>
<td>Edman K268</td>
<td>EU118654</td>
<td>Larsson 2007</td>
</tr>
<tr>
<td>P. lilascens</td>
<td>FCUG 1568</td>
<td>AF141619</td>
<td>Larsson 2007</td>
</tr>
<tr>
<td>Pirex concentricus</td>
<td>OSC-41587</td>
<td>KP134984</td>
<td>Foudas and Hibbett 2015</td>
</tr>
</tbody>
</table>
rate variation across sites (Ronquist and Huelsenbeck 2003). Four Markov chains were run for 2 runs from random starting trees for 5 million generations, and trees were sampled every 100 generations. The first one-fourth generations were discarded as burn-in. A majority rule consensus tree of all remaining trees was calculated. Branches that received bootstrap support were considered as significantly supported for maximum likelihood (BL), maximum parsimony (BP) and Bayesian posterior probabilities (BPP) greater than or equal to 80% (BL), 75% (BP) and 0.95 (BPP) were considered as significantly supported, respectively.

The ITS + nLSU dataset included sequences from 12 fungal specimens or isolates representing 9 species (Table 1), in which the taxon sampling of this phylogenetic analyses except for outgroup are member of donkia clade. The dataset had an aligned length of 2093 characters, of which 1734 characters are constant, 199 are variable and parsimony-uninformative, and 160 are parsimony-informative. Maximum parsimony analysis yielded five equally parsimonious trees (TL = 585, CI = 0.763, HI = 0.238, RI = 0.556, RC = 0.424). Best model for the ITS + nLSU dataset estimated and applied in the Bayesian analysis as GTR + I + G. Bayesian analysis and ML analysis resulted in a similar topology as MP analysis, with an average standard deviation of split frequencies = 0.009426 (BI). The phylogeny (Fig. 1) inferred from ITS + nLSU sequences showed that the new species grouped with the related species Hyphodermella corrupgata and H. rosae with a strong support (100% BS, 100% BP, 1.00 BPP).

**Hyphodermella poroides** Y.C. Dai & C.L. Zhao, sp. nov. Figs. 2, 3. MycoBank no.: MB 820991.

The species has unique morphological characters by having an annual growth habit, a poroid hymenophore with cream to orange surface, a monomitic hyphal system with simple septa, generative hyphae in subiculum distinctly wider than in trama, and broadly ellipsoid, hyaline, thin-walled, smooth, IKI–, CB– basidiospores.


Etymology: Poroides, referring to the species having a poroid hymenophore.

Fruiting body: Basidiocarps annual, resupinate, adnate, soft, without odor or taste when fresh, ceraceous-crustaceous to hard corky when dry, up to 7 cm long, 5 cm wide, 2 mm thick at center. Pore surface white when fresh, cream to orange when dry; pores angular, 2–3 per mm; dissepiments thin, slightly lacerate. Sterile margin distinctly fimbriate, determinate, white, up to 2 cm wide. Subiculum white, ceraceous-crustaceous, up to 0.5 mm thick. Tubes concolorous with pore surface, ceraceous-crustaceous, up to 1.5 mm long.

Hyphal structure: Hyphal system monomitic; generative hyphae hyaline, thin- to slightly thick-walled, bearing simple septa, IKI–, slightly cyanophilous; tissues unchanged in KOH.

Subiculum: Generative hyphae hyaline, thin- to slightly thick-walled, frequently branched, interwoven, 4.5–7 μm diam.

Tubes: Generative hyphae hyaline, thin-walled, frequently branched, loosely interwoven to subparallel along the tubes, 2.5–4.5 μm in diam; hyphal ends occasionally capitated. Cystidia absent, but fusoid cystidioles occasionally present, hyaline, thin-walled, 20–23 × 3–4 μm; basidia long and clavate, with four sterigmata and a simple septum, 22–27 × 4–5 μm; basidioles dominant, in shape similar to basidia, but slightly smaller.

Spores: Basidiospores broadly ellipsoid, hyaline, thin-walled, smooth, IKI–, CB–, (2.5–)3–3.5–(4) × 2.5–3 μm, L = 3.26 μm, W = 2.77 μm, Q = 1.07–1.21 (n = 60/2).

Associated wood-rot: White.


In the present study, a new species *Hyphodermella poroides* was described based on phylogenetic analyses and morphological characters. The species has unique morphological
characters by having a poroid hymenophore in *Hyphodermella* and the new species grouped with the related species *H. corrugata* and *H. rosae* with a strong support (100% BS, 100% BP, 1.00 BPP).

Morphologically, *Hyphodermella bruneonecta* is separated from *H. poroides* by an odontioid hymenophore, a brown subiculum and larger basidiospores (4.5–5 × 3.5–4 μm; Duhem and Buyck 2013). The type species of *Hyphodermella*, *H. corrugata* differs from *H. poroides* by its grandinioid hymenophore and larger basidia (35–50 × 6–7 μm; Eriksson and Ryvarden 1976; Bernicchia and Gorjón 2010). *Hyphodermella maunakeaensis* differs by a hydnoid hymenophore and larger basidiospores (4.5–5 × 3.5–4 μm; Gilbertson et al. 2001). *Hyphodermella ochracea* differs from *H. poroides* by its odontioid hymenophore, ochraceous subiculum and larger basidiospores (8–12 × 4–5.5 μm; Duhem 2010). *Hyphodermella rosea* differs from *H. poroides* by its odontioid hymenophore and cream to brown subiculum when drying (Bernicchia and Gorjón 2010).

Having resupinate basidiocarps with a poroid hymenophore and a monomitic hyphal system bearing simple septa reminds of the genus Ceriporia Donk. *Ceriporia* differs from *Hyphodermella* by having white to tan or brightly colored purple, orange, pink or greenish basidiocarps and cylindrical or allantoid basidiospores (Ryvarden and Melo 2014).

*Hyphodermella poroides* is put into the genus *Hyphodermella* mainly based on the phylogenetic analyses, in which three species of *H. corrugata*, *H. poroides* and *H. rosae* group together (Fig. 1). In addition, the morphological characters of *H. poroides* by having a poroid hymenophore is unique in this genus, and it shares the common characteristics with the genus *Hyphodermella* by having a monomitic hyphal system bearing simple septa with generative hyphae, the presence of hyphal ends, clavate to suburniform basidia and hyaline, thin-walled, smooth, IKI-, CB– basidiospores (Bernicchia and Gorjón 2010; Duhem and Buyck 2011). Hence, the generic concept of *Hyphodermella* is enlarged after *H. poroides* added in the genus, in which the hymenophore may be grandinioid to odontioid, hydnoid or poroid.

The poroid wood-rotting fungi is an extensively studied group of Basidiomycota (Gilbertson and Ryvarden 1986, 1987; Núñez and Ryvarden 2001; Ryvarden and Melo 2014), but the Chinese diversity is still not well known, especially in the subtropics and tropics, from where many taxa have recently been described (Dai 2012a,b; Li and Cui 2013; Chen et al. 2014; Zhao et al. 2014; Bian and Dai 2015; Han and Cui 2015). *Hyphodermella poroides* is from the subtropics, and it is likely that more new wood-rotting fungi will be found after further investigations.

**Key to species of *Hyphodermella***

1a Basidiospores ≥8 μm in length.................................................2
1b Basidiospores <8 μm in length.................................................3
   2a Hymenophore surface orange to yellow orange; basidia ≥35 μm in length.................................................*H. corrugata*
   2b Hymenophore surface ochraceous; basidia <35 μm in length.................................................*H. ochracea*
   3a Hymenophore poroid; basidiospores <4.5 μm in length.................................................*H. poroides*
   3b Hymenophore odontioid to hydnoid; basidiospores ≥4.5 μm in length.................................................4
   4a Hymenophore surface cream to pale orange yellow, margin fimbriate.................................................*H. rosae*
   4b Hymenophore brownish, margin entire..............................5
   5a Hymenophore hydnoid; basidiospores narrowly ellipsoid........................................................................*H. maunakeaensis*
   5b Hymenophore odontioid; basidiospores broadly ellipsoid to subglobose.................................................*H. bruneonecta*

**Disclosure**

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

**Acknowledgments**

The research was supported by the National Natural Science Foundation of China (Project No. 31372115).

**References**
