Fomitiporella caviphila sp. nova (Hymenochaetales, Basidiomycota) from eastern China, with a preliminary discussion on the taxonomy of Fomitiporella

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Fomitiporella caviphila L.W. Zhou (Hymenochaetales, Basidiomycota) sp. nova is described and illustrated from eastern China. Its perennial, resupinate and inseparable basidiocarps, thin subiculum, stratified tubes, a dimitic hyphal system, lack of setae, and brown basidiospores fit well to the current concept of Fomitiporella. The new species resembles F. cavicola by inhabiting cavities of living logs and having thick basidiocarps, but it differs by the lighter pore surface, smaller pores and smaller basidiospores. In DNA analysis, F. caviphila is nested within the clade including the generic type, F. umbrinella. The current phylogeny does not support F. caryophylli and Phylloporia resupinata as members of Fomitiporella.

Introduction

Fomitiporella, belonging to the Hymenochaetaeae, was erected by Murrill (1907), including nine species with F. umbrinella as the generic type. The genus is characterized by perennial, resupinate and inseparable basidiocarps, a thin subiculum, stratified tubes, and subglobose and brown basidiospores (Murrill 1907). As several other genera within the Hymenochaetaeae, Fomitiporella was treated as a synonym of Phellinus in most subsequent manuals (Ryvarden & Johansen 1980, Gilbertson & Ryvarden 1987, Larsen & Cobb-Pouille 1990, Ryvarden 1991, Ryvarden & Gilbertson 1994, Dai 1999, Núñez & Ryvarden 2000).

Based on nuclear large subunit (nLSU) sequences, Wagner and Fischer (2002) confirmed Fomitiporella as a distinct genus within the Hymenochaetaeae, and combined Phellinus caryophylli and P. cavicola into this genus.

Dai (2010) did not accept Fomitiporella as an independent genus because no clear morphological differences between Fomitiporella and Fulvifomes were detected, and he combined Fomitiporella umbrinella into Fulvifomes. However, the lack of differences mentioned by Dai (2010) between the two genera results from inappropriately broadening the concept of Fulvifomes to accommodate resupinate species. This broadened delimitation without any phylogenetic support is against the original concept proposed by Murrill (1914) and it was rejected by Zhou (2014). Therefore, I accept Fomitiporella as a good genus here.

In China, there are large areas of natural forests across multiple climatic zones and topog-
Fig. 1. Phylogenetic position of *Fomitiporella cavipila* inferred from nLSU sequences. The ML tree is presented with BS values from MP analysis after those from the ML analysis. The new species is set in boldface. The voucher numbers of the new species and of the taxa unidentified to species level are provided.

Material and methods

The studied specimens are deposited in the herbaria of the Institute of Applied Ecology, Chinese Academy of Sciences (IFP) and Botanical Museum, Finnish Museum of Natural History (H). The special color terms follow Petersen (1996) and the microscopic procedure follows He and Dai (2012). The sections were prepared in 5% potassium hydroxide (KOH), Melzer’s reagent (IKI) and Cotton Blue (CB). The following abbreviations are used: \( L \) = mean spore length (arithmetical average of all spores), \( W \) = mean spore width (arithmetical average of all spores), \( Q \) = the ratio of \( L/W \), \( n \) = the number of spores measured from given number of specimens, IKI− = inamyloid and indetrinoid, CB+ = cyanophilous, and CB− = acyanophilous. In presenting the size range of spores, 5% of the measurements were excluded from each end of the range, and are given in parentheses. Drawings were made with the aid of a drawing tube.

The nLSU sequence of the specimen LWZ 20130812-1 was directly amplified using Phire® Plant Direct PCR Kit (Finzymes Oy, Finland) according to the manufacturer’s instruction with primers LR0R and LR7 (Vilgalys & Hester 1990). The PCR procedure was as follows: initial denaturation at 98 °C for 5 min, followed by 39 cycles at 98 °C for 5 s, 48 °C for 5 s and 72 °C for 5 s, and a final extension of 72 °C for 10 min. The PCR product was sequenced in the Beijing Genomics Institute, China, with primers LR0R, LR7, LR3R and LR3 (Vilgalys & Hester 1990). The newly generated sequence was deposited at GenBank (http://www.ncbi.nlm.nih.gov/genbank; Fig. 1).

To infer the phylogenetic position, some nLSU sequences (Fig. 1) from related genera were downloaded from GenBank. *Phyllopora ribis* was selected as outgroup (Wagner & Fischer 2002). These sequences were aligned using MAFFT 6.935 (Katoh et al. 2002, Katoh & Toh...
2008) with auto option. The resulting alignment was used for phylogenetic analyses. Maximum likelihood (ML) analysis was performed by raxmlGUI 1.2 (Stamatakis 2006, Silvestro & Michalak 2012) under GTR + I + G model and auto FC option (Pattengale et al. 2010) for bootstrap (BS) replicates. PAUP* 4.0b10 (Swofford 2002) was used to construct a maximum parsimony (MP) tree. Heuristic searches with one thousand BS searches were conducted. All characters were equally weighted and gaps were set as missing data. Other parameters were as follows: starting tree obtained via stepwise addition, tree-bisection-reconnection branch swapping, steepest descent option not in effect, and 'multtrees' option in effect.

Fig. 2. Basidiocarps of *Fomitiporella caviphila* in situ. — a: Pore surface. — b: Whole basidiocarps.

Fig. 3. Microscopic structures of *Fomitiporella caviphila* (from the holotype). — a: Basidiospores. — b: Hyphae from trama. — c: Hyphae from subiculum.

**Results**

The analysed 18 nLSU sequences generated an alignment with 900 characters. Among these characters, 85 were parsimony-informative. The ML search was stopped after 400 BS replicates, while seven equally most-parsimmonous trees of 289 steps (CI = 0.734, RI = 0.717) were saved. Because the topologies from ML and MP analyses were similar, only that from the ML analysis is presented, while the BS values from ML and MP analyses are given when they are above 50% (Fig. 1).

The current phylogeny (Fig. 1) shows that specimen LWZ 20130812-1 formed a strongly supported clade with *Fomitiporella cavicola*, *F. umbrinella* and three unidentified *Fomitiporella* collections (Oe 5, Oe 6 and Oe 7), and occupied a distinct lineage within this clade. *Fomitiporella caryophylli*, an unidentified *Fomitiporella* collection (Fv. Ch-7) and *Phylloporia resupinata* were placed out of this clade.

**Taxonomy**

*Fomitiporella caviphila* L.W. Zhou, sp. nova (Figs. 2 and 3)

Mycobank No.: MB 805918.

Type: China. Zhejiang Province, Kailua County, Gutianshan National Nature Reserve, in a cavity within the
base of living Quercus phyllyraceoides, 12 Aug. 2013, LWZ 20130812-1 (holotype IFP).

**ETYMOLOGY:** cavifila (Lat.) refers to the fungus growing in a cavity of the host.

**FRUITBODY.** Basidiocarps perennial, resupinate, inseparable, without odor or taste when
fresh, woody hard, about 20 cm long, 8 cm wide and 2 cm thick. Pore surface dark brown, dis-
tinctly glancing; sterile margin distinct, buff-yellow to curry-yellow, 1.5 mm wide; pores cir-
cular, 6–8 per mm; disseminets thick, entire. Subiculum yellowish brown, woody hard, up to
0.5 mm thick. Tubes yellowish brown, woody hard, single layer up to 2 mm long, stratified,
separated by a thin layer of context; white mycelial strands present in old tubes.

**HYPHAL STRUCTURE.** Hyphal system dimitic; generative hyphae simple septate, CB–; skeletal
hyphae CB–; tissue darkening but otherwise unchanged in KOH.

**SUBICULUM.** Generative hyphae rare, hyaline, thin-walled, frequently septate, rarely branched,
1–1.5 µm in diam; skeletal hyphae dominant, yellow to brown, thick-walled with a wide to
narrow lumen, rarely septate, unbranched, relatively regularly arranged, 2–3 µm in diam.

**TUBES.** Generative hyphae frequent, hyaline, thin-walled, frequently septate, unbranched,
1–1.8 µm in diam; skeletal hyphae dominant, yellow to brown, thick-walled with a wide to
narrow lumen, rarely septate, unbranched, parallel along the tubes, 1.4–2.6 µm in diam. Setae

**BASIDIOPORES.** Broadly ellipsoid, sometimes one side collapsed, brown, thick-walled, smooth,
IKI–, CB+, (4.1–)4.2–5(–5.2) × (3.3–)3.4–4(–4.2) µm, L = 4.72 µm, W = 3.75 µm, Q = 1.26 (n = 30/1).

India. Nilambur, on dead wood (duplicate H 7015132).
So, DMC 476 (isotype IFP 015195).

**Discussion.**

Fomitiporella cavifila has perennial, resupinate and inseparable basidiocarps, a thin subiculum,
stratified tubes with thick and entire pore disseminets, a dimitic hyphal system, no setae,
and brown basidiospores. This combination of characters fits Fomitiporella as defined by
Murill (1907). In the current phylogeny (Fig. 1), F. cavifila is close to the generic type, F. umbrin-
ella. Morphologically, F. cavifila is most similar to F. cavicola which also inhabits cavities in
angiosperms and has thick basidiocarps (Kotlaba & Pouzar 1995). However, F. cavicola has a
darker pore surface, larger pores (5–6 per mm) and larger basidiospores (4.7–5.5 × 4.4–5.5 µm;
Kotlaba & Pouzar 1995). In addition, F. cavicola is known from Europe only. Fomitiporella
umbrinella resembles F. cavifila in the similar pore (6–8 per mm) and basidiospore sizes (4.5–5 ×
3.5–4 µm), but its basidiocarp is much thinner than in the latter (Gilbertson & Ryvarden 1987).
Another species morphologically related to F. cavifila is Fulvifomes inermis, not included in
the current phylogeny. Fulvifomes inermis however differs in having thinner basidiocarps, and
more importantly, larger pores (4–6 per mm) and bigger basidiospores (5–6 × 4.4–5 µm; Gilber-
tson & Ryvarden 1987).

Based on the phylogeny from nLSU sequences, Wagner and Fischer (2002) accepted
Fomitiporella as a genus within the Hymeno-
chaetaceae, and accommodated the effused-
reflexed species F. caryophylli in it. However,
in the current phylogeny (Fig. 1), F. caryo-
phylli does not form a strongly supported clade
with the generic type. Therefore, it is doubtful
whether that species belongs to Fomitiporella,
and non-resupinate basidiocarps may not be con-
considered as a principal character of Fomitiporella.

Phylloporia resupinata was recently described from Cameroon (Douania-Meli et al. 2007). That resupinate species did not well cluster together with other species of Phylloporia (Zhou & Dai 2012). Decock et al. (2013) further showed that P. resupinata has a closer relationship with Fomitiporella caryophylli and F. cavicola in nLSU-based phylogeny. However, the current phylog-
eny (Fig. 1) does not support a placement of
Phylloporia resupinata in Fomitiporella.
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