

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 Hymenochaetales, 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 Hymenochaetales, *Fomitiporella* was treated as a synonym of *Phellinus* in most subsequent manuals (Ryvarden & Johansen 1980, Gilbertson & Ryvarden 1987, Larsen & Cobb-Poulsen 1990, Ryvarden 1991, Ryvarden & Gilbertson 1994, Dai 1999, Núñez & Ryvarden 2000).

Based on nuclear large subunit (nLSU) sequences, Wagner and Fischer (2002) con-

firmed *Fomitiporella* as a distinct genus within the Hymenochaetales, 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-

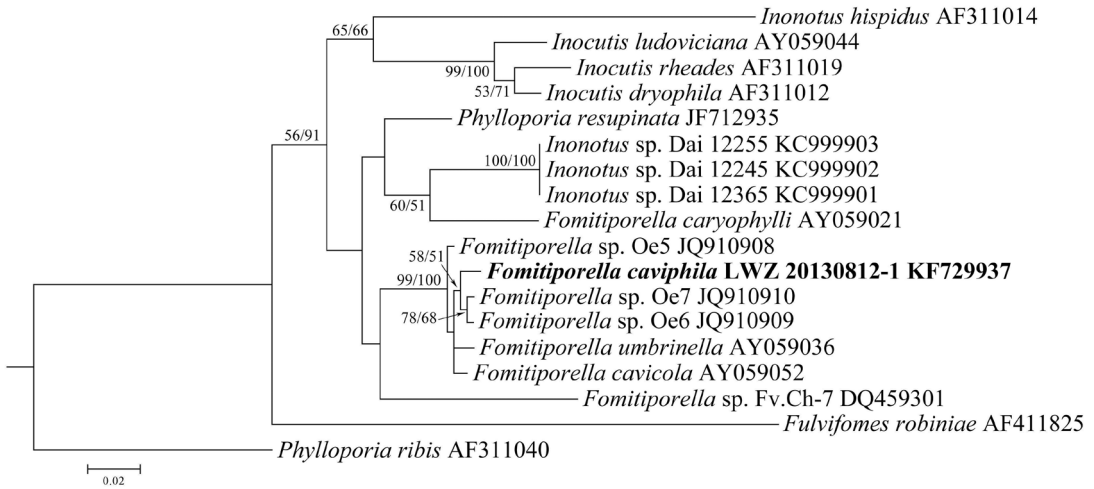


Fig. 1. Phylogenetic position of *Fomitiporella caviphila* inferred from nLSU sequences. The ML tree is presented with BS values from MP analysis after those from the ML analysis. The new species is set in boldface. The voucher numbers of the new species and of the taxa unidentified to species level are provided.

raphies. More than 700 polypore species have been recorded (Dai 2012), including many new members of the Hymenochaetaceae (Dai & Cui 2005, 2011, Cui & Dai 2008, Cui *et al.* 2009, 2010, Dai & Li 2010, Zhou & Jia 2010, Zhou & Dai 2012, Zhou & Qin 2012, 2013, Zhou & Xue 2012, Tian *et al.* 2013, Zhou 2013, Zhou *et al.* 2014). However, no species of *Fomitiporella* has been originally described from China (Dai 2010, 2012). During the field trip in eastern China in 2013, an undescribed species of *Fomitiporella* was collected. Its illustrated description is presented in this paper. The taxonomy of several other species of *Fomitiporella* is also briefly discussed.

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 indextrinoid, 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 (Finnzymes 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. *Phylloporia ribis* was selected as outgroup (Wagner & Fischer 2002). These sequences were aligned using MAFFT 6.935 (Katoh *et al.* 2002, Katoh & Toh

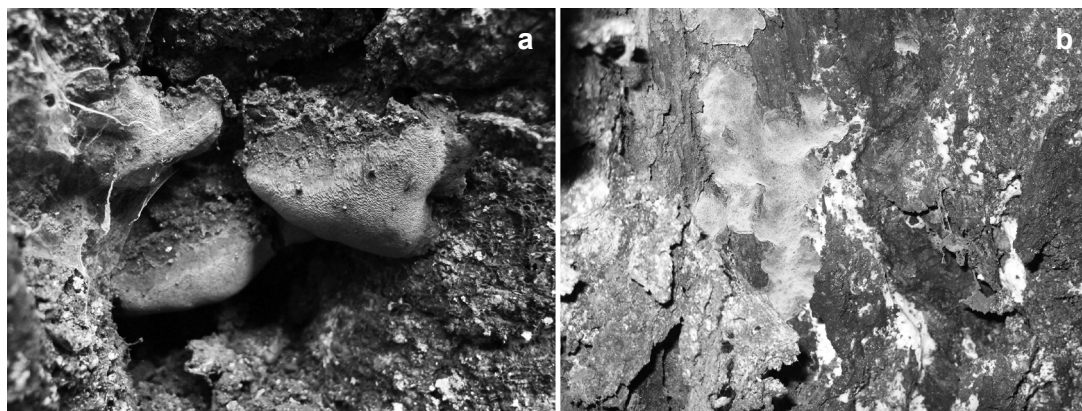


Fig. 2. Basidiocarps of *Fomitiporella caviphila* in situ. — a: Pore surface. — b: Whole basidiocarps.

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 ‘multrees’ option in effect.

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-parsimonious 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*,

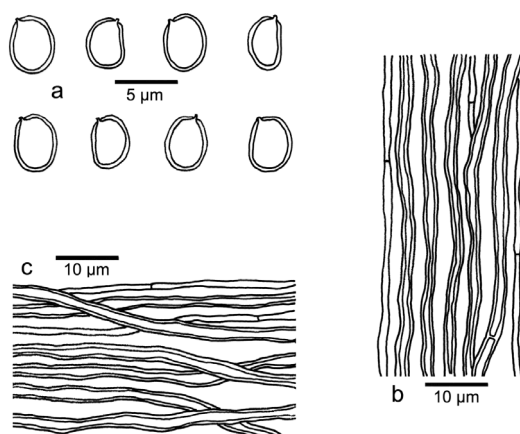


Fig. 3. Microscopic structures of *Fomitiporella caviphila* (from the holotype). — a: Basidiospores. — b: Hyphae from trama. — c: Hyphae from subiculum.

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, Kaihua County, Gutianshan National Nature Reserve, in a cavity within the

base of living *Quercus phillyraeoides*, 12 Aug. 2013, LWZ 20130812-1 (holotype IFP).

ETYMOLOGY: *caviphila* (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, distinctly glancing; sterile margin distinct, buff-yellow to curry-yellow, 1.5 mm wide; pores circular, 6–8 per mm; dissepiments 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 absent. Cystidia and cystidioles absent. Basidia and basidioles not seen.

BASIDIOSPORES. Broadly ellipsoid, sometimes one side collapsed, brown, thick-walled, smooth, IKI–, CB+, (4.1–)4.2–5(–5.2) \times (3.3–)3.4–4(–4.2) μm , $L = 4.72 \mu\text{m}$, $W = 3.75 \mu\text{m}$, $Q = 1.26$ ($n = 30/1$).

OTHER SPECIMENS STUDIED. — *Fomitiporella caryophylli*. **Indonesia.** Sumatera, *M. Núñez* 824 (duplicate H 7015133). **India.** Nilambur, on dead wood (duplicate H 7015132). — *Fomitiporella cavicola*. **Czech Republic.** Central Bohemia, Průhonice, *F. Kotlaba* (IFP 015059). — *Fomitiporella umbrinella*. **USA.** Florida, Chiefland, *J.L. Lowe* 4146 (duplicate H). — *Fulvifomes inermis*. **USA.** New York, Ulster, Ashokan, *J. Gimms* 2294 (duplicate H); New York, Saratoga, Mount McGregor, *S.J. Smith* 45130 (duplicate H). — *Phylloporia resupinata*. **Cameroon.** Centre Province, Nyong-et-So, *DMC* 476 (isotype IFP 015195).

Discussion

Fomitiporella caviphila has perennial, resupinate and inseparable basidiocarps, a thin subiculum, stratified tubes with thick and entire pore dissepiments, a dimitic hyphal system, no setae, and brown basidiospores. This combination of characters fits *Fomitiporella* as defined by Murrill (1907). In the current phylogeny (Fig. 1), *F. caviphila* is close to the generic type, *F. umbrinella*. Morphologically, *F. caviphila* 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 \times 4–4.5 μm ; Kotlaba & Pouzar 1995). In addition, *F. cavicola* is known from Europe only. *Fomitiporella umbrinella* resembles *F. caviphila* in the similar pore (6–8 per mm) and basidiospore sizes (4–5 \times 3.5–4 μm), but its basidiocarps are much thinner than in the latter (Gilbertson & Ryvarden 1987). Another species morphologically related to *F. caviphila* 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 \times 4–4.5 μm ; Gilbertson & Ryvarden 1987).

Based on the phylogeny from nLSU sequences, Wagner and Fischer (2002) accepted *Fomitiporella* as a genus within the Hymenochaetaceae, and accommodated the effused-reflexed species *F. caryophylli* in it. However, in the current phylogeny (Fig. 1), *F. caryophylli* 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 considered as a principal character of *Fomitiporella*.

Phylloporia resupinata was recently described from Cameroon (Douanla-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 phylogeny (Fig. 1) does not support a placement of *Phylloporia resupinata* in *Fomitiporella*.

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