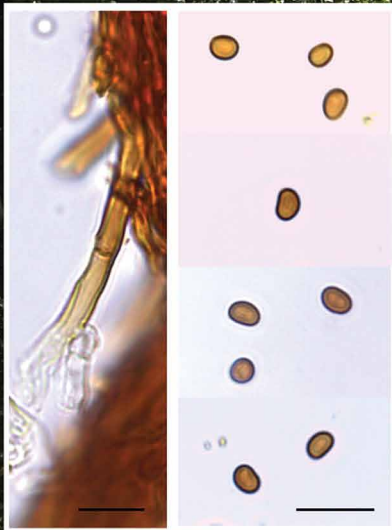
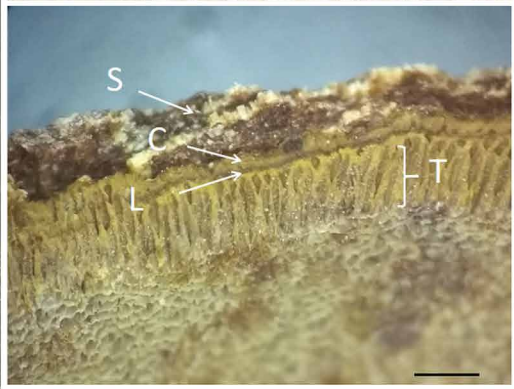


Fomitiporella pertenuis



Fungal Planet 730 – 13 July 2018

Fomitiporella pertenuis V. Xavier de Lima & J.R. Oliveira-Filho, *sp. nov.*

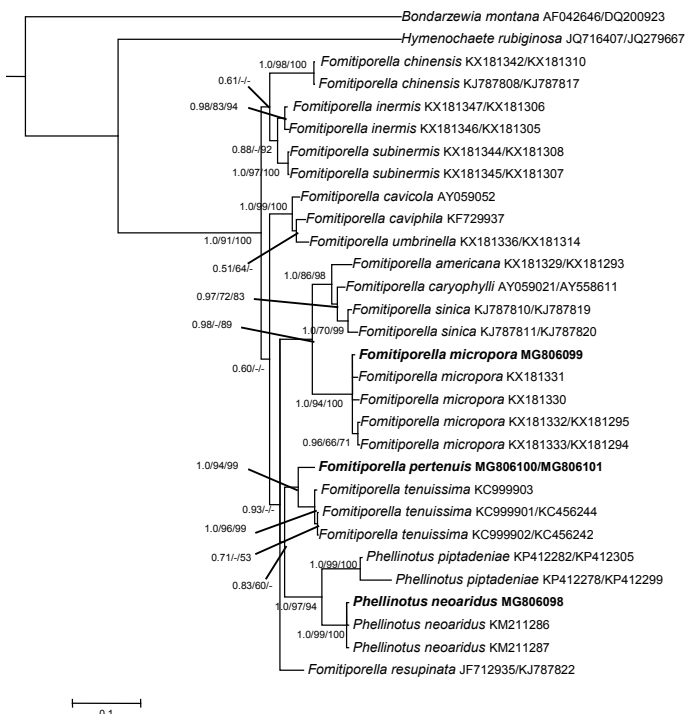
Etymology. Pertenuis (Gr.), referring to the very thin basidioma.

Classification — *Hymenochaetaceae*, *Hymenochaetales*, *Agaricomycetes*.

Basidioma annual, resupinate, up to 1.8 mm thick, margin thin; pore surface hazel (27; Watling 1969) when dry, pores angular, 6–8 per mm; dissepiments thin and entire; context reduced to a thin layer above the substrate, less than 0.5 mm thick, homogeneous hazel (27) to snuff brown (17) with the pore surface, sometimes with a darker line just above the tubes; tubes concolorous with the pore surface. Hyphal system monomitic; generative hyphae hyaline to rust (13), thick-walled with a wide lumen, simple septate, 2.5–4 µm diam, IKI-. Cystidia or other sterile elements absent; basidia not seen; basidiospores ellipsoid to ovoid, thick-walled, smooth, rust (13) to rusty tawny (14), IKI-, 4–5.5 × 3–4 µm.

Typus. BRAZIL, Alagoas, Biological Reserve of Pedra Talhada, on dead wood, July 2017, V. Xavier de Lima, PPT 111 (holotype URM 91181, ITS and LSU sequences GenBank MG806101 and MG806100, MycoBank MB824040).

Additional material examined. ***Fomitiporella micropora***. BRAZIL, Maranhão, São José de Ribamar, Panaquatira beach, on dead branch of living angiosperm, Jan. 2017, J.R.C. Oliveira-Filho, JRF135, URM 91186, LSU sequence GenBank MG806099. ***Phellinotus neoaridus***. BRAZIL, Sergipe, Poço Redondo, Apr. 2016, T.B. Gibertoni, PH5, URM 91187, LSU sequence GenBank MG806098.



Colour illustrations. Environment where the type specimen was collected in Biological Reserve of Pedra Talhada, AL, Brazil; close-up showing the thin dissepiments and rather angular pores (scale bar = 1 mm); transversal view of the basidioma: substrate (S), context (C), darker line (L) and tube layer (T) are visible (scale bar = 1 mm); photomicrographs of a septate generative hyphae and basidiospores (scale bar = 10 µm).

Notes — According to our phylogenetic analyses (ITS+LSU), *F. pertenuis* clustered in a clade with high support with specimens of *F. tenuissima* from China (GenBank KC999901, KC999902, KC999903), but diverged significantly from the Chinese specimens and it is distantly related from other species of *Fomitiporella*. Both *F. pertenuis* and *F. tenuissima* have thin basidiomata and lack sterile elements, but *F. pertenuis* has smaller pores (6–8 per mm vs 3–4 per mm in *F. tenuissima*) and monomital hyphal system (both monomitic and dimitic hyphal system in *F. tenuissima*; Yu et al. 2013). The clade of *F. tenuissima* and *F. pertenuis* shows relation to *Phellinotus* (Dreschler-Santos et al. 2016), which is placed in *Fomitiporella* in our analyses. Thus, synonymising *Phellinotus* under *Fomitiporella* is suggested; however, both species of *Phellinotus* (*P. neoaridus* and *P. piptadeniae*) are pileate and are host-specific on living *Ceasalpinia* and *Piptadeniae*, and *Fomitiporella*, a resupinate genus whose species occur mostly on dead trees, would have to be emended. Another specimen collected in Brazil was identified as *F. micropora*; the specimen is morphologically very similar to the type description, but it has larger pores (4–5 per mm in the Brazilian specimen, 8–10 per mm in the type). *Fomitiporella micropora* is only superficially similar to the new species, from which it differs by the perennial, thicker basidioma (up to 10 mm), smaller pores (8–10 per mm), dimitical hyphal system, and slightly smaller basidiospores, (3–)3.5–4(–4.5) × (2–)2.5–3(–3.5) µm. Besides, *F. micropora* clustered in a clade with specimens collected in the type locality (Virgin Islands) and Costa Rica, distantly related from the new species.

The 50 % majority rule Bayesian tree inferred from ITS+LSU sequences with the model K80 + G using MrBayes v. 3.2.6 (Ronquist et al. 2012). Maximum parsimony (PAUP v. 4.0b10, Swofford 2003) and maximum likelihood (MEGA5, Tamura et al. 2011) analyses were done and similar topologies were obtained (not shown). Bayesian posterior probabilities (PP) from 10 M generations; Maximum parsimony bootstrap (MPbs) and Maximum likelihood bootstrap (MLbs) support values from 1 000 replications. Values next to nodes represent PP/MLbs/MPbs. Sequences generated in this study are shown in **bold**. *Bondarzewia montana* represents the outgroup. The alignment is deposited in TreeBASE (Submission ID 22272).