

# Pileate *Fomitiporia* species in the USA. New combinations *Fomitiporia calkinsii* and *F. bakeri*

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**Abstract** Sequencing of the ribosomal ITS region was used to resolve the relationship among USA collections of the morphological species *Fomitiporia robusta*. *F. robusta* corresponding to European collections was not found and its occurrence in the USA is regarded as questionable. Birch-growing fungus from mid-western and eastern United States known as *Phellinus bakeri* is a closely related polypore, but because of the absence of typical *F. robusta* here, it should be considered a separate species. Oak-growing pileate fungus from the south-eastern USA, also known as *Fomes calkinsii*, is a distinct species, rather distant from the European *F. robusta*. New combinations *Fomitiporia bakeri* and *F. calkinsii* are proposed. Notes on other similar species are provided.

**Keywords** *Phellinus* · Hymenochaetaceae · Ribosomal DNA · White-rot polypore · Wood-inhabiting fungi

## Introduction

On the basis of DNA sequence data, a number of authors (e.g., Wagner and Fischer 2001, 2002) divided the rich polypore group of *Phellinus* s.l. (Hymenochaetaceae) into several subgroups, currently considered as distinct genera by most authors. One of the best defined is the *Phellinus*

*punctatus-robustus* complex that includes species sharing subglobose, thick-walled, and dextrinoid basidiospores. It was redefined as *Fomitiporia* Murrill, with *Phellinus punctatus* (Fr.) Pilát as type species (Fiasson and Niemelä 1984) and confirmed by Fischer (1996). Murrill originally established this genus for *Fomitiporia langloisii* Murrill (Murrill 1907) which has for a long time been considered a synonym of *Fomitiporia punctata* (Fr.) Murrill, until Decock et al. (2007) demonstrated on the basis of phylogenetic analysis and type studies that it represents a distinct species on its own, and re-established *Fomitiporia langloisii*.

About 30 species of *Fomitiporia* are now recognized ([www.indexfungorum.org](http://www.indexfungorum.org), Decock et al. 2005), and more than 10 of them were described in the past 5 years. Yet, many others will be probably discovered using multigenic phylogenetic tools. Morphology is poorly discriminative within the genus because most species lack setae and have relatively uniform hyphae and spores. Nonetheless, phylogenetic species recognition methods based on DNA sequence often revealed the existence of species complex in *Fomitiporia*. Specific habitat and ecology data provide the first and the simplest implications for the existence of a potentially new species that can be then confirmed by DNA sequencing. This combined approach was successful in the identification of several resupinate, *F. punctata*-like polypores: *F. mediterranea* Fischer (Fischer 2002), *F. tenuis*, *F. aethiopica* (Decock et al. 2005), *F. langloisii* Murr., and *F. maxonii* Murr. (Decock et al. 2007).

In this article, we focused on the *Fomitiporia robusta* species complex in the USA. *Fomitiporia robusta* (P. Karst.) Fiasson & Niemelä is a very characteristic species in Europe, quite common in Central Europe but only scattered in the warmer Mediterranean region (Kotlaba 1984). It grows almost exclusively on living oaks and

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introduced *Robinia* (Kotlaba 1984, p. 39). In the American literature, however, the image of *F. robusta* appears somewhat blurred, as contradictory distribution and substrate records are available. Lowe (1957) and Overholts (1953) reported the species as widespread across the United States, growing on every substrate possible. Gilbertson and Ryvar den (1987), however, reported this only in the southernmost central and western states (Louisiana, Texas, New Mexico, California), in the region of southern oak–pine forest, mostly on oaks.

It is surprising that the oak-growing *F. robusta* is not mentioned in the recent distribution lists of the eastern states, where forests similar to European woods prevail. Nevertheless, we can only confirm this as our numerous mycological excursions in eastern USA—from Maine to Virginia—between 2001 and 2009 did not yield any *F. robusta*-like species on oak (Vlasák 2004). In the Great Smoky Mountains, though, we could quite frequently find an oak-growing *F. robusta*-like, but slightly different in appearance, polypore. We obtained another specimen from northern Florida where it is, according to collectors' comments, also common. Searching the literature, we discovered *Fomes calkinsii* (Murrill) Sacc. & D. Sacc., an oak-growing, hymenochaetoid, pileate polypore with dextrinoid spores (Ryvar den 1985). Overholts (1953) considered *F. calkinsii* a good species that differs from *Fomes robustus* P. Karst. (syn. *Phellinus robustus*) in many, although rather subtle, macro- and microanatomical features. He mentions its occurrence only on oak and beech, in south-central and eastern USA, including North Carolina, Tennessee and Florida where our collections also came from. Lowe (1957), on the other hand, includes *Fomes calkinsii* into *F. robustus*, even though he acknowledges some microscopical differences. Gilbertson and Ryvar den (1987) do not mention this species at all, while Larsen and Cobb-Pouille (1990) regard it as conspecific with *Phellinus robustus*.

Four original specimens of *F. calkinsii* collected in 1886 and 1887 by W.W. Calkins in northern Florida (including the type) are preserved in NYBG herbarium with photos available on the Internet, and their similarity with our collections is striking. Also, we have inspected and sequenced a collection of M.A. Donk from 1970: an oak-growing, *Phellinus robustus*-like polypore, kindly provided by the University of Tennessee Herbarium. This collection was from the Great Smoky Mountains, similar to our oak collections.

On the basis of ecological and morphological characteristics of *F. calkinsii*, and comments on its microanatomy made by L.O. Overholts (1953) and J.L. Lowe (1957), we have concluded that it is identical with our collections from the Great Smoky Mountains and northern Florida, even though we have not studied NYBG herbarium collections directly.

We have also compared our *F. robusta/calkinsii* collections to other similar species from the *F. robusta* group, namely the recently described *F. dryophila* Murrill (Decock et al. 2007) and conifer-growing and birch-growing types. Semipileate *F. dryophila* is a well-defined species that grows abundantly on live oak (*Q. virginiana* Miller) in the very south of Florida. Its morphology is rather similar to *F. robusta* in early development but sequences show only a distant relationship (Decock et al. 2007). Conifer-growing *Fomitiporia robusta*-like fungi, usually named *F. hartigii* (Allesch. & Schnabl) Fiasson & Niemelä or *F. tsugina* Murrill are common in the eastern as well as western USA. They are distinctly different from the true *F. robusta*, as was shown, for example, by Fischer and Binder (2004), and are treated only marginally in this paper. Some comments on the identity of American collections are included in the “Discussion”. *Betula*-specific, *F. robusta*-like polypore *Phellinus bakeri* (Murrill) A. Ames was described by W. A. Murrill (Murrill 1908) from Wisconsin, and its range was reported as “Wisconsin, Missouri and westward” (Murrill 1914). Because of the substrate, *P. bakeri* was sometimes mistaken for *Phellinus igniarius* (L.) Quél. Overholts (1920) stressed some morphological and type-of-rot differences between *P. bakeri* and *P. igniarius* (both as *Fomes*) and described three collections from eastern USA. According to our field experience, this fungus is common in eastern states where *Betula lenta* L. and/or *B. nigra* L. grow (Vlasák 2004), but in the Great Smoky Mountains it also colonizes *B. allegheniensis*. *P. bakeri* was often identified as a birch-specific variety of *P. robustus* (Lowe 1957). Gilbertson and Ryvar den (1987) do not mention it at all, but Larsen and Cobb-Pouille (1990) regard it as a good species.

In this article, we present the results of our collections of *P. calkinsii*, including ribosomal RNA sequence data that demonstrate unequivocally that it is a distinct species, rather distant from *F. robusta*. We also show that the birch-growing *P. bakeri* is much more similar to European *F. robusta* judging by ribosomal RNA sequence, but still different, in our opinion. Comments on some other pileate *Fomitiporia* species occurring in the USA are added.

## Materials and methods

### Specimens studied

Fresh material was collected by the first author and his son (collections signed -J) in 2001–2009 across eastern USA (Table 1); the European material studied for the comparison was retrieved from the private herbarium of the first author (<http://mykoweb.prf.jcu.cz/polypores>) where are also preserved all specimens collected in the USA. Duplicates of

most of the specimens are also preserved in Prague Museum Herbarium (PRM). The collection of M.A. Donk 35560 is preserved at the University of Tennessee Herbarium (TENN). Herbarium acronyms follow Holmgren and Holmgren (1998).

The microscopic inspections were performed in Melzer's reagent. A total of 30 basidiospores from each specimen were measured.

### Sequencing

About 20 mg of basidiocarp context material was disintegrated for 30 s in a ball mill (MM301 RETSCH), and DNA was isolated using CTAB/NaCl extraction buffer as described by Murray and Thompson (1980), followed by repeated extractions with chloroform, and isopropanol precipitation. Crude DNA was dissolved in 100 µl of water with 5 µg of RNaseA, incubated for 30 min at 37°C and purified with GENOMED JetSorb silica kit. The resulting DNA solution was ten times diluted and 1 µl was used as a template for amplification with ITS1 and ITS4 primers (White et al. 1990) in 25 µl of reaction mixture, using 55°C annealing temperature. Then, 0.5 µl of the amplified DNA reaction mixture was sequenced using ITS1 and ITS4 primers. The sequencing was performed in the Genomics

laboratory of Biology Centre, Academy of Sciences of the Czech Republic, České Budějovice, on an ABI 3730xl DNA analyzer, using BigDye Terminator 3.1 kit. The sequences obtained in this study were deposited at GenBank (Table 1).

Most of the sequences contained some heterozygous sites due to genetically different nuclei (alleles) present in polykaryotic tissues. In about 30% of specimens (but none of *Fomitiporia calkinsii*), insertions/deletions were detected in one genome compared to the other, which led to overlapping peaks in parts of the sequence scanner output. These sectors had to be re-sequenced with additional primers ITS2 and ITS3 (White et al. 1990) that anneal behind the heterozygous region. Ribosomal RNA sequence of such collections had to be published under two different accession numbers referring to individual alleles.

### Phylogenetic analysis

The sequences were aligned by Clustal X and manually curated. The evolutionary history was inferred using the Neighbor-Joining method (Saitou and Nei 1987) and the evolutionary distances were computed using the Maximum Composite Likelihood method (Tamura et al. 2004). All

**Table 1** List of collections studied and their GenBank accession numbers

Specimens of <i>Fomitiporia</i>	Substrate	Herbarium	GenBank number
<i>F. calkinsii</i> JV0212/12-J	Bulow Creek St. Pk, Ormond Beach, FL, USA, <i>Carya sp.</i>		GU136226
<i>F. calkinsii</i> JV0404/11-J,	Boogerman Trail, Great Smoky Mt., NC, USA, <i>Quercus sp.</i>	PRM915978	GU136225
<i>F. calkinsii</i> JV0509/36	Maddron Trail, Great Smoky Mt., TN, USA, <i>Quercus rubra</i>	PRM915979	GU136223
<i>F. calkinsii</i> JV0509/113	Porters Creek Trail, Great Smoky Mt., TN, USA, <i>Quercus rubra</i>	PRM915980	GU136224
<i>F. calkinsii</i>	Cades Cove, Great Smoky Mt., TN, USA, <i>Quercus falcata</i> , Coll. M.A. Donk	TN 35560	<sup>a</sup>
<i>F. robusta</i> (P. Karst.) Fiasson & Niemelä JV0908/27	Hluboká, Czech republic, Europe, <i>Quercus robur</i>	PRM915946	GU136218
<i>F. robusta</i> JV0911/1	Hluboká, Czech republic, Europe, <i>Robinia pseudoacacia</i>		HQ162313
<i>F. robusta</i> JV0911/4	Hluboká, Czech republic, Europe, <i>Robinia pseudoacacia</i>	PRM915947	<sup>b</sup>
<i>F. bakeri</i> , JV0309/144	Valley Forge, PA, USA, <i>Betula lenta</i>	PRM915948	GU136219 and 220
<i>F. bakeri</i> , JV0404/18-J	Great Smoky Mt., TN, USA, <i>Betula allegheniensis</i>	-	GU136221 and 222
<i>F. dryophila</i> Murr., JV0904/30	Everglades NP, Royal Palm, FL, USA, <i>Quercus virginiana</i>	PRM915950	GU136213 and 214
<i>F. dryophila</i> , JV0904/31	Everglades NP, Royal Palm, FL, USA, <i>Quercus virginiana</i>	PRM915951	GU136212
<i>F. sp.</i> JV0407/16-J	Henry Cowell Redwoods St. Pk, Santa Cruz, CA, USA, <i>Quercus sp.</i>		GU136227 and 228
<i>F. tsugina</i> JV0108/123	Hickory Run, Allentown, PA, USA, <i>Tsuga sp.</i>		GU594156
<i>F. tsugina</i> JV0709/128	Crater Lake, OR, USA, <i>Tsuga mertensiana</i>		GU594157
<i>F. tsugina</i> JV0809/100	Sawyer Pond, White Mt., NH, USA, <i>Abies sp.</i>		HQ162314 and 315
<i>F. tsugina</i> JV0309/29-J	Mt. Rainier, WA, USA, <i>Pseudotsuga menziesii</i>		HQ162316
<i>F. hartigii</i> JV0911/5	Hluboká, Czech republic, Europe, Castle park, <i>Tsuga sp.</i>		HQ162317

<sup>a</sup> Sequence identical with GU136224

<sup>b</sup> Identical with GU136218

positions containing gaps and missing data were eliminated from the dataset (Complete deletion option). There were a total of 628 positions in the final dataset.

## Results

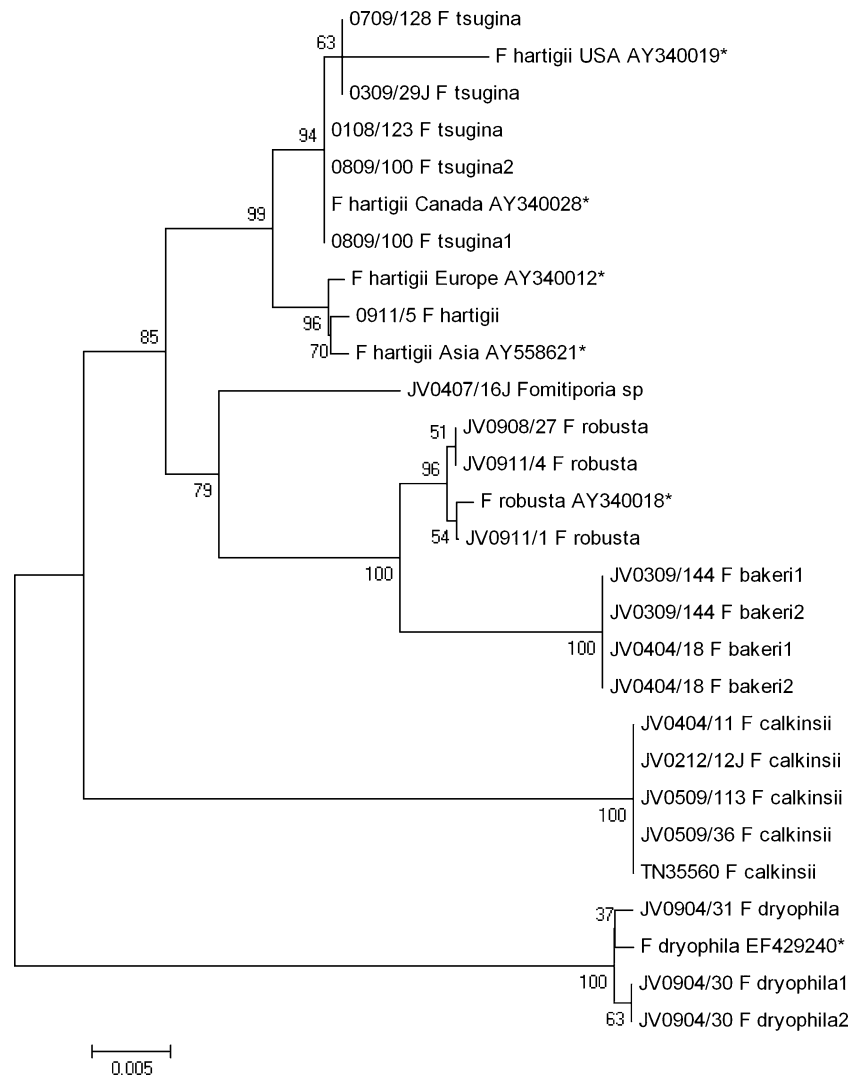
### ITS sequence analysis

All five sequenced *Quercus/Carya*-growing *F. robusta*-like collections from the Great Smoky Mountains and Northern Florida (Table 1) gave a very similar sequence of 694-bases-long ITS-5.8S region with only one variable position. Preliminary BLAST search at GenBank (Altschul et al. 1990) demonstrated rather low homology with other *Fomitiporia* species (*F. robusta* in particular). Recently described European *F. mediterranea* M. Fisch. (Fischer 2002) and *F. punicata* Y.C. Dai, et al. (Dai et al. 2008) from China came through as the closest relatives in BLAST

search, but with only 89% similitude. Therefore, we also sequenced our own collections of European *F. robusta* as well as American *F. robusta*-like polypore growing on birch, *Phellinus bakeri*, both from Pennsylvania and the Great Smoky Mt., and *F. dryophila* Murrill, another oak-growing, pseudopileate species from Florida (Decock et al. 2007) (Table 1). Phylogenetic analyses of the sequences obtained and of others retrieved from the GenBank were conducted in MEGA4 (Tamura et al. 2007). The results demonstrated that *Quercus/Carya*-growing, pileate *F. robusta*-like collections from eastern USA form a well-separated clade (Fig. 1) that justifies the establishment of *Fomitiporia calkinsii* (Murrill) comb. nov.

Ribosomal RNA sequence of birch-growing *Phellinus robustus* (*bakeri*) is much more similar to the European *F. robusta*. Yet, two sequenced specimens (Table 1) from distant and very different localities and different substrates show typical sequence features, not present in *F. robusta*: four insertions/deletions 1–4 bases long and four

**Fig. 1** Evolutionary relationships of 28 *Fomitiporia* species based on sequence comprising ITS1, 5.8S and ITS2. The optimal tree with the sum of branch length=0.15814583 is shown. The bootstrap consensus tree inferred from 1,000 replicates is taken to represent the evolutionary history of the taxa analyzed. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1,000 replicates) are shown next to the branches. The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances are in the units of the number of base substitutions per site. Accession numbers with \* represent sequences retrieved from GenBank. Other GenBank accession numbers are in Table 1





transitions/transversions in ITS2, where all sequenced *F. robusta* have identical sequence, and four insertions/deletions 1–5 bases and also four other changes in ITS1, where *F. robusta* sequenced specimens show only transitions/transversions in five other positions. The sequence difference in BLAST search of about 8–9% in ITS1 and 6–7% in ITS2 between *P. robustus (bakeri)* and *F. robusta* is the same as between, for example, *Fomitiporia hartigii* and *F. mediterranea* (Fig. 1). Taking into consideration that in the distribution area of *P. robustus (bakeri)* the oak-growing *F. robusta* does not occur at all, we approve the notion of Larsen and Cobb-Pouille (1990) that the birch-growing fungus should be considered a good species for which we suggest the name *Fomitiporia bakeri* (Murrill) comb. nov.

For the comparison, we have also sequenced four of our collections, semipileate or resupinate, of American conifer-growing *Fomitiporia robusta (tsugina, hartigii?)* from different conifer substrates in the east and the west of USA. All these sequences are essentially identical with the previously published two sequences of American *F. hartigii* (Fischer and Binder 2004) and make a very homogeneous group with only one variable site in ITS1 and one in ITS2. They represent a distinct clade, well separated from the hardwood-growing collections. Surprisingly, though, Asian and European *F. hartigii* (including a specimen growing in Europe on introduced *Tsuga* sp.) show several very constant mutations: 1b and 3b deletions in ITS1, 3b insertion in ITS2 and a few transitions/transversions. This represents only 3–4% sequence difference in BLAST search, but causes distinct clustering of American conifer collections, separately from European *F. hartigii*.

#### Taxonomy

***Fomitiporia calkinsii* (Murrill) Vlasák & Kout, comb. nov.** — MycoBank MB518864

Figs. 2, 3 and 4.

**Basionym** *Pyropolyporus calkinsii* Murrill, The Polyporaceae of North America. II. The genus *Pyropolyporus*. B. Torrey Bot. Club 30:109–120, 1903.

**Description** *Basidiomes* perennial, sessile, unguate to applanate, up to 10×8×5 cm, woody hard; upper surface glabrous but somewhat grainy on touch, sulcate, making up to seven broad, seasonal zones, later becoming incrustated and slightly rimose, marginal zone yellowish brown, the older zones stepwise more and more dark reddish to blackish brown, sometimes with a silvery cover. *Pore surface* dark reddish- or grayish-brown, the pores circular, very regular, 6–8 per mm, with



**Fig. 2** *Fomitiporia calkinsii*, spec. PRM915979 (JV 0509/36), Maddron Trail, Great Smoky Mt., in situ

thick, entire dissepiments; young context yellowish brown, later reddish brown, zonate, up to 2 cm thick; tubes in many year layers, sometimes indistinctly stratified, brown, becoming whitish within, woody, up to 5 mm long.

**Hyphal system** dimitic in the context and hymenophoral trama, *generative hyphae* simple-septate, hyaline to pale yellowish, thin-walled, 1.5–3 μm wide, *skeletal hyphae* yellowish brown, thick-walled, nonseptate, 2.5–3.5 μm wide. *Setae* lacking. *Cystidioles* present in hymenium, hyaline, thin-walled, ventricose, ending in an elongated hyphoid apex, 13–16 μm long and 5–7 μm wide at the base, narrow apical part 1.5–2 μm wide. *Basidia* subglobose, 4-sterigmate, 10–12×8–10 μm. *Basidiospores* subglobose, hyaline, thick-walled, dextrinoid in Melzer's reagent, 5–6.5 (7)×5–6 μm. On living oaks and hickory.

**Holotypus** USA, Florida, on living live oak, Feb 1886, W. W. Calkins (NYBG742984).

**Specimens examined** USA, TN, Great Smoky Mountains, on living *Quercus rubra*, Sep 2005, collected by J. Vlasak, PRM915979 and PRM915980; USA, NC, Great Smoky Mountains, on living *Quercus* sp. Apr 2004, coll. J. Vlasak Jr., PRM915978; USA, FL, Bulow Creek State Park, *Carya* sp., Dec 2002, coll. J. Vlasak Jr., JV0212/12-J; USA, TN, Great Smoky Mountains, *Quercus falcata*, Jun 1970, coll. M.A. Donk, TN35560.

**Remarks** *Fomitiporia calkinsii* is very similar to European *Fomitiporia robusta* in both macro- and microscopic characteristics. Pileus surface is perhaps notably different. In *F. robusta*, it is usually green of algae except for the marginal zone; in rare cases of pilei without algae, the second or third zone from the margin is already dark blackish brown with a thick crust and the older zones more



**Fig. 3** *Fomitiporia calkinsii*, spec. PRM915979 (JV0509/36), dry basidiocarp

or less black. In *F. calkinsii*, the pileus surface is brown or rusty brown, indistinctly incrustated, in outer zones with lighter and brighter colors, in inner zones darker, but not just black (Figs. 1 and 2). Pores and spores are smaller in *F. calkinsii* and the contextual skeletal hyphae are distinctly narrower, as noted already by Lowe (1957).

*Fomitiporia bakeri* (Murrill) Vlasák & Kout, *comb. nov.* — MycoBank MB518865  
Photograph in <http://mykoweib.pr.f.jcu.cz/polypores>.

*Basionym* *Pyropolyporus bakeri* Murrill, *Polyporaceae*, Part 2. North American Flora 9:104, 1908.

**Description** *Basidiomes* perennial, sessile, unguulate, rarely applanate, often triquetrous in section, up to 13×15×8 cm, not so hard as other pileate species of *Fomitiporia*; upper surface tomentose to glabrous, sulcate, later becoming incrustated and slightly rimose, marginal zone yellowish brown, the older zones stepwise more and more dark reddish to blackish brown, margin thick, rounded. *Pore surface* pale brown to golden brown, the pores circular or somewhat irregular, 5–6 per mm, with thin to thick dissepiments; context yellowish brown, shining, zonate, up to 5 cm thick; tubes brown, in distinct year layers, up to 10 mm long each year.

*Hyphal system* dimitic in the context and hymenophoral trama, *generative hyphae* simple-septate, hyaline to pale yellowish, thin-walled, 1.5–3 µm wide, *skeletal hyphae* yellowish brown, thick-walled, nonseptate, 3–6 µm wide. *Setae* lacking. *Cystidioles* present in hymenium, hyaline, thin-walled, ventricose, ending in an elongated hyphoid apex. *Basidia* subglobose, 4-sterigmate, 10–11×8–10 µm. *Basidiospores* subglobose, hyaline, thick-walled, dextrinoid in Melzer's reagent, 6–8×5.5–6.5 µm.

*Holotypus* USA, WI, St. Croix Falls, *Betula lenta*, 1897, C. F. Baker (NYBG742981).

*Specimens examined* USA, PA, Norristown, Valley Forge, on living *Betula lenta*, Sep 2003, collected by J. Vlasak, PRM915948; USA, TN, Great Smoky Mountains, on living *Betula allegheniensis*, Apr 2004, coll. J. Vlasak Jr., JV0404/18-J.

**Remarks** The basidiome is roughly similar to *Fomitiporia calkinsii* although often larger, not so hard, with larger and sometimes somewhat irregular pores that also have a more yellowish, brighter color. The context is often very thick, more yellowish brown, distinctly shining. Growth on birch (*Betula* sp.) is the most important field characteristic. Basidiocarps develop on dead standing stems unlike to *F. calkinsii* and *F. robusta* that grow mostly on living trees.

## Discussion

In the second half of the 20th century, the pragmatic approach to mycological systematics, based on the assumption that different species must show clear microanatomical differences, enabled to reduce the number of described synonymous species several times and restored the basic order in polyporology. Unfortunately, the extensive study of herbarium specimens, often misshaped and untypical, collected in different stages of development and without notes about their ecology, had a consequence, sometimes, in dispraising some external morphological traits and important ecological characteristics in species delimitation.

Prominent American polyporologists, L.O. Overholts and J.L. Lowe, were particularly careful in describing new species, and American polypores without conspicuous



**Fig. 4** *Fomitiporia calkinsii*, spec. PRM915980 (JV0509/113), dry basidiocarp



differences in spore shape and/or size were usually identified as their European relatives. This is probably why they included all American pileate hymenochaetoid fungi, microscopically similar to *Phellinus robustus*, in this species. A similar approach was used by Gilbertson and Ryvarden (1987) who only separated species with strikingly different ecology: *Phellinus texanus* (Murrill) A. Ames. growing only in the southwest on non-oak, desert plants, and *Phellinus hartigii* (Allesch. & Schnabl) Pat., growing on conifers. In the latter combination, they again identified all American conifer-growing *Phellinus robustus* as the European species. Yet, *P. hartigii* is distinctly pileate in Europe and semipileate with sloping pileus or more often resupinate in the USA (Overholts 1953, p. 89). Murrill (1907) named this common American fungus *Fomitiporia tsugina* Murr., and Lowe (1957) also did not regard this American fungus as conspecific with European *P. hartigii*. Fischer and Binder (2004) in their ITS sequencing study of *Phellinus* s.l. found that American *P. hartigii* collections cluster separately of *P. hartigii* from Europe and Asia and we could only confirm this. The sequence difference is rather low (3–4% in the ITS region), but because of the very constant sequence of all American collections and different morphology, we believe that the American fungus should also be considered a good species even if closely related to *F. hartigii*. Some comments on *Fomitiporia tsugina* taxonomic status were also published by Decock et al. (2007).

According to Gilbertson and Ryvarden (1987), oak-growing *Phellinus robustus*-like fungi are distributed along the USA southern border from east to west. We believe that this distribution pattern describes the occurrence of *Fomitiporia calkinsii* and *F. dryophila*, another common and thermophilic, but semipileate, species from oaks (Decock et al. 2007). Yet, another oak-growing species probably occurs in this area, at least in the west. Overholts (1953) noted that specimens of *Phellinus robustus* from Pacific Coast are “less developed and usually nodulose-sessile”. We have only a small slice of this western species at hand, from a very large, thick and typically nodulose basidiocarp (according to collector's comments), growing in Santa Cruz, CA, on an oak stump, and its ribosomal RNA sequence is different from all other described species (*Fomitiporia* sp. in Table 1 and Fig. 1). Having no more material at present and no field knowledge of this species, we leave this problem open. Fischer and Binder (2004), who studied American *Fomitiporia* species collected in California using ribosomal RNA sequencing, described a new species *F. polymorpha* M. Fisch., collected on *Salix* and several other non-oak hosts, with effused-reflexed to bulbous basidiocarps that is nevertheless not related to our *Fomitiporia* sp. by its sequence. It may be identical with also bulbous and *Salix*-collected *Pyropolyporus abramsianus*

(Murrill) Sacc. & Trotter that is also mentioned by Overholts (1953) and Decock et al. (2007) as *Phellinus robustus*-like species.

In summary, according to our results and literature data, hardwood-growing, pileate *Fomitiporia* species in the eastern USA include *Fomitiporia bakeri* having an exclusive preference for birch in the mid-west and east, *Fomitiporia calkinsii* on oak, beech and hickory, south of 35° parallel, and pseudopileate *Fomitiporia dryophila* on live oak in the very south. The occurrence of *Fomitiporia robusta* is very improbable, in our opinion, as we could not find any such fungus during years of exploring many ideal localities in the eastern USA. Fischer and Binder (2004) came to the same conclusion studying *Fomitiporia* species in California.

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