Two new brown rot polypores from tropical China

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Abstract
Brown-rot fungi are types of fungi that selectively degrade cellulose and hemicellulose from wood and are perhaps the most important agents involved in the degradation of wood products and dead wood in forest ecosystem. Two new brown-rot species, collected from southern China, are nested within the clades of *Fomitopsis* sensu stricto and *Oligoporus* sensu stricto, respectively. Their positions are strongly supported in the Maximum Likelihood phylogenetic tree of the concatenated the internal transcribed spacer (ITS) regions, the large subunit of nuclear ribosomal RNA gene (nLSU), the small subunit of nuclear ribosomal RNA gene (nuSSU), the small subunit of mitochondrial rRNA gene (mtSSU), the largest subunit of RNA polymerase II (RPB1), the second largest subunit of RNA polymerase II (RPB2) and the translation elongation factor 1-α gene (TEF1) sequences. *Fomitopsis bambusae*, only found on bamboo, is characterised by its resupinate to effused-reflexed or pileate basidiocarps, small pores (6–9 per mm), the absence of cystidia, short cylindrical to oblong-ellipsoid basidiospores measuring 4.2–6.1 × 2–2.3 μm. *Oligoporus podocarpi* is characterised by white to pale cream pore surface, round or sometimes angular pores (5–6 per mm), broadly ellipsoid to reniform basidiospores measuring 3.8–4.2 × 2–2.3 μm and growing on *Podocarpus*. Illustrated descriptions of these two novel species, *Fomitopsis bambusae* and *Oligoporus podocarpi*, are provided.

Keywords
Brown-rot fungi, multi-gene phylogeny, phylogeny, taxonomy

Introduction
Wood-inhabiting basidiomycota can be grouped into two categories, white-rot and brown-rot fungi, according to their ability for decaying or decomposing wood. Brown-rot fungi selectively degrade cellulose and hemicellulose from wood and decayed mate-
rial becomes reddish-brown or tan, crisp, causing massive cracks in the middle of a longitudinal crisscross. However, white-rot fungi can degrade all the components of wood and decayed material, become white or pale-yellow or light reddish-brown and expose the fibrous structure. The number of brown rot fungi is remarkably smaller compared to white rot fungi (Zhang 2003; Wu et al. 2020). Gilbertson (1981) has estimated that approximately 6% of the wood-rotting basidiomycetes in North America give a brown rot. On the other hand, Dai (2012) demonstrated that 14% of Chinese polypores in northern China can cause a brown rot (Cui et al. 2019). Brown-rot fungi are perhaps the most important agents involved in the degradation of wood products and in the degradation of dead wood in forest ecosystems. It is worth emphasising that the diversity of brown rot fungi is higher in high-latitude areas than in low-latitude areas and the number of brown rot fungi decreases from north to south in China (Zhou and Dai 2012; Dai et al. 2015), so that brown-rot fungi are infrequent in tropical areas.

As a cosmopolitan brown-rot genus of polypores, *Fomitopsis* P. Karst., was established by Karsten, based on *F. pinicola* (Sw.) P. Karst. (Karsten 1881). The genus was classified in the Fomitopsidaceae morphologically (Jülich 1981) and belonged to the *Antrodia* clade phylogenetically (Binder et al. 2005; Ortiz-Santana et al. 2013; Han et al. 2016). Han et al. (2016) confirmed that species, previously belonging to *Fomitopsis* sensu lato, were embedded in seven lineages and eleven species form the core group of *Fomitopsis*. In addition, four species *Fomitopsis caribensis* B.K. Cui & Shun Liu, *F. eucalypticola* B.K. Cui & Shun Liu, *F. ginkgonis* B.K. Cui & Shun Liu and *F. roseoalba* A.M.S. Soares, Ryvarden & Gibertoni were introduced as new species and *F. bondartsevae* (Spirin) A.M.S. Soares & Gibertoni was proposed as a new combination (Soares et al. 2017; Tibpromma et al. 2017; Liu et al. 2019). In the latest study, ten species have been recognised in the *Fomitopsis pinicola* complex (Haight et al. 2019; Liu et al. 2021). So far, 25 species have been accepted in *Fomitopsis* sensu stricto (s. str.).

*Oligoporus* Bref. (Polyporales, Basidiomycetes) was typified with *O. farinosus* Bref., 1888 (Syn. *O. rennyi* (Berk. & Broome) Kotl.) (Brefeld 1888). Recent phylogenetic analyses have demonstrated that *Oligoporus* and *Tyromyces* belong to different clades and that they were grouped within families Dacryobolaceae Jülich and Incrustoporiaceae Jülich (Binder et al. 2013; Floudas and Hibbett 2015; Justo et al. 2017). Shen et al. (2019) have proved *Oligoporus* s. str. is different from *Postia* s. str. in morphology and molecular phylogenetic analysis. Meanwhile, species in *Postia* s. str. have a broad host range growing both on angiosperm and gymnosperm wood, but *Oligoporus* s. str. grows only on gymnosperm wood (Donk 1971; Ryvarden and Melo 2014; Shen et al. 2019). So far, only two species have been accepted in *Oligoporus* s. str. (Shen et al. 2019).

During our investigations of brown-rot fungi in China, eight specimens were collected from Hainan Province in tropical China. Morphological examination shows these collections to represent two brown-rot polypores, corresponding to *Fomitopsis* s.s.s. and *Oligoporus* s.s.s. After phylogenetic analyses of the internal transcribed spacer (ITS) regions, the large subunit of nuclear ribosomal RNA gene (nLSU), the small subunit of nuclear ribosomal RNA gene (nuSSU), the small subunit of mitochondrial rRNA gene (mtSSU), the largest subunit of RNA polymerase II (RPB1), the second largest
Two new brown rot polypores from tropical China

subunit of RNA polymerase II (RPB2) and the translation elongation factor 1-α gene (TEF1) sequences, two new species were confirmed as belonging to *Fomitopsis* s.s. and *Oligoporus* s.s.. In this paper, we describe and illustrate these two new species.

**Materials and methods**

**Morphological studies**

The examined specimens were deposited in the herbarium of the Institute of Microbiology, Beijing Forestry University (BJFC) in Beijing, China. Macro-morphological descriptions were based on the field notes and measurements of herbarium specimens. Colour terms followed Petersen (1996). Micro-morphological data were obtained from the dried specimens and observed under a light microscope following Chen et al. (2017) and Shen et al. (2019). Sections were studied at a magnification up to 1000× using a Nikon Eclipse 80i microscope with phase contrast illumination (Nikon, Tokyo, Japan). Drawings were made with the aid of a drawing tube. Microscopic features, measurements and drawings were made from slide preparations stained with Cotton Blue and Melzer’s Reagent. Spores were measured from sections cut from the tubes. To present the variation of spore size, 5% of measurements were excluded from each end of the range and are given in parentheses. The following abbreviations are used: IKI = Melzer’s Reagent, IKI– = neither amyloid nor dextrinoid, KOH = 5% potassium hydroxide, CB = Cotton Blue, CB– = acyanophilous, L = mean spore length (arithmetic average of all spores), 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.

**DNA extraction and sequencing**

A cetyltrimethylammonium bromide rapid plant genome extraction kit (Aidlab Biotechnologies Co., Ltd, Beijing, China) was used to extract the total genomic DNA from dried specimens according to the manufacturer’s instructions with some modifications (Song and Cui 2017; Xing et al. 2018). The ITS regions were amplified with the primer pairs ITS5 (GGA AGT AAA AGT CGT AAC AAG G) and ITS4 (TCC TCC GCT TAT TGA TAT GC) (White et al. 1990). The nLSU regions were amplified with the primer pairs LR0R (ACC CGC TGA ACT TAA GC) and LR7 (TAC TAC CAC CAA GAT CT) (http://www.biology.duke.edu/fungi/mycolab/primers.htm). The nuSSU regions were amplified with the primer pairs NS1 (CCG GAG AGG GAG CCT GAG AAA C) and NS4 (CCC GTG TTG AGT CAA ATT A) (White et al. 1990). The mtSSU regions were amplified with the primer pairs MS1 (CAG CAG TCA AGA ATA TTA GTC AAT G) and MS2 (GCG GAT TAT CGA ATT AAA TAA C) (White et al. 1990). RPB1 was amplified with the primer pairs RPB1-Af (GAR TGY CCD GGD CAY TTY GG) and RPB1-Cr (CCN GCD ATN TCR TTR TCC
ATR TA) (Matheny et al. 2002). RPB2 was amplified with the primer pairs fRPB2-5F (GAY GAY MGW GAT CAY TTY GG) and fRPB2-7CR (CCC ATR GCT TGY TTR CCC AT) (Matheny 2005). TEF1 was amplified with the primer pairs EF1-983F (GCY CCY GGH CAY CGT GAY TTY AT) and EF1-1567R (ACH GTR CCR ATA CCA CCR ATC TT) (Rehner and Buckley 2005). The PCR procedure followed that of Liu et al. (2019). The PCR products were purified with a Gel Extraction and PCR Purification Combo Kit (Spin-column) in Beijing Genomics Institute, Beijing, P.R. China. The purified products were then sequenced on an ABI-3730-XL DNA Analyzer (Applied Biosystems, Foster City, CA, USA) using the same primers as in the original PCR amplifications. The sequence quality was checked following Nils-son et al. (2012). All newly-generated sequences were submitted to GenBank and were listed in Tables 1 and 2.

Phylogenetic analyses

New sequences, deposited in GenBank (http://www.ncbi.nlm.nih.gov/genbank/) (Table 1), were aligned with additional sequences retrieved from GenBank (Table 1) using BioEdit 7.0.5.3 (Hall 1999) and ClustalX 1.83 (Thompson et al. 1997), followed by manual adjustment. Sequence alignment was deposited at TreeBase (http://purl.org/phylo/treebase/; submission ID 28131). In phylogenetic reconstruction, sequences of *Laetiporus zonatus* B.K. Cui & J. Song, obtained from GenBank, were used as outgroups in the phylogeny of *Fomitopsis* (Fig. 1) while sequences of *Antrodia serpens* (Fr.) P. Karst. were used as outgroups in the phylogeny of *Oligoporus* (Fig. 2).

Maximum Parsimony (MP) analysis was applied to those two phylogenies and trees construction procedure were performed in PAUP* version 4.0b10 (Swofford 2002). Settings for phylogenetic analyses in this study followed the approach of Zhu et al. (2019) and Song and Cui (2017). 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 5000, branches of zero length were collapsed and all parsimonious trees were saved. Clade robustness was assessed using a bootstrap (BT) analysis with 1000 replicates (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 (MPT) generated.

Maximum Likelihood (ML) analysis was conducted with RAxML-HPC252 on Abe through the CIPRES Science Gateway (www.phylo.org) and involved 100 ML searches. All model parameters were estimated by the programme. Only the best Maximum Likelihood tree from all searches was kept. The Maximum Likelihood bootstrap values (ML-BS) were performed using a rapid bootstrapping with 1000 replicates. The phylogenetic tree was visualised using Treeview (Page 1996).

MrModeltest 2.3 (Posada and Crandall 1998; Nylander 2004) was used to determine the best-fit evolution model for two combined matrices to reconstruct phylogenetic analyses as a 6-gene dataset (ITS+nLSU+nuSSU+mtSSU+RPB2+TEF1) and a 7-gene dataset
Two new brown rot polypores from tropical China

Table 1. A list of species, specimens and GenBank accession numbers of sequences used in the phylogeny of *Fomitopsis*.

| Species | Sample no. | GenBank accessions | References |
|---------|------------|--------------------|------------|
| *Astrodia* heteromorpha | Dai 12755 | KP715306 KP715322 KR605908 KR606009 KP715536 KR610828 | Chen and Cui (2015) |
| *Astrodia* serpen | Dai 14850 | MG787582 MG787624 MG787731 MG787674 MG787849 MG787798 | Chen et al. (2018) |
| *Bulgosporus* quercinus | JV 1406/1 | KR605801 KR605740 KR605899 KR606002 KR610730 KR610820 | Han et al. (2016) |
| *Bulgosporus* quercinus | LY BR 2030 | KR605799 KR605738 KR605897 KR606000 KR610728 KR610818 | Han et al. (2016) |
| *Daedalea* quercina | Dai 2260 | KR605792 KR605731 KR605885 KR605988 KR610718 KR610808 | Han et al. (2016) |
| *Daedalea* quercina | Dai 12659 | KP171208 KP171230 KR605887 KR605990 KR610719 KR610810 | Han et al. (2015) |
| *Fomitopsis* bambusae | Dai 22110 | MW937874 MW937881 MW937867 MW937888 MZ082980 MZ082974 | Present study |
| *Fomitopsis* bambusae | Dai 22114 | MW937875 MW937882 MW937868 MW937889 MZ082981 MZ082975 | Present study |
| *Fomitopsis* bambusae | Dai 22116 | MW937876 MW937883 MW937869 MW937890 — — | Present study |
| *Fomitopsis* bambusae | Dai 21942 | MW937873 MW937880 MW937866 MW937887 MZ082979 — | Present study |
| *Fomitopsis* betulina | Cai 10756 | KR605797 KR605756 KR605894 KR605997 KR610725 KR610815 | Han et al. (2016) |
| *Fomitopsis* betulina | Dai 11449 | KR605798 KR605737 KR605895 KR605998 KR610726 KR610816 | Han et al. (2016) |
| *Fomitopsis* bondartseae | X 1207 | JQ700277 JQ700277 — — — — | Soares et al. (2017) |
| *Fomitopsis* bondartseae | X 1059 | JQ700275 JQ700275 — — — — | Soares et al. (2017) |
| *Fomitopsis* caena | Cai 6239 | JX435777 JX435777 KR605826 KR605934 KR610661 KR610761 | Li et al. (2013) |
| *Fomitopsis* caena | Dai 9611 | JX435776 JX435774 KR605825 KR605935 KR610660 KR610762 | Li et al. (2013) |
| *Fomitopsis* caribenensis | Cai 16871 | MK852559 MK860108 MK860124 MK860116 MK900482 MK900474 | Liu et al. (2019) |
| *Fomitopsis* durescens | Overhols 4215 | KP937299 KP937295 KR605835 KR605941 — — | Han et al. (2014) |
| *Fomitopsis* durescens | O 10796 | KP937292 KP937294 KR605834 KR605940 KR610669 KR610766 | Han et al. (2014) |
| *Fomitopsis* eucalypticola | Cai 16594 | MK852560 MK860110 MK860126 MK860118 MK900483 MK900476 | Liu et al. (2019) |
| *Fomitopsis* eucalypticola | Cai 16598 | MK852562 MK860113 MK860129 MK860121 MK900484 MK900479 | Liu et al. (2019) |
| *Fomitopsis* ghignonis | Cai 17170 | MK852563 MK860114 MK860130 MK860122 MK900485 MK900480 | Liu et al. (2019) |
| *Fomitopsis* ghignonis | Cai 17171 | MK852564 MK860115 MK860131 MK860123 MK900486 MK900481 | Liu et al. (2019) |
| *Fomitopsis* hemiepiphrpha | O 10808 | KR605770 KR605709 KR605841 KR605947 KR610675 — | Han et al. (2016) |
| *Fomitopsis* ibericus | O 10810 | KR605771 KR605710 KR605842 KR605948 KR610676 KR610771 | Han et al. (2016) |
| *Fomitopsis* ibericus | O 10811 | KR605772 KR605711 KR605843 — KR610677 KR610772 | Han et al. (2016) |
| *Fomitopsis* meliae | Dai 10035 | KR605774 KR605713 KR605847 KR605952 KR610683 — | Han et al. (2016) |
| *Fomitopsis* mounceae | Ryvarden 16893 | KR905776 KR905715 KR605849 KR605954 KR610681 KR610775 | Han et al. (2016) |
| *Fomitopsis* mounceae | DR-366 | KF160624 — — — KF178349 KF160903 | Haight et al. (2019) |
| *Fomitopsis* mounceae | JAG-08-19 | KF160626 — — — KF178351 KF160905 | Haight et al. (2019) |
| *Fomitopsis* niveus | JV 0509/52 X | KR605779 KR605718 KR605853 KR605957 KR610686 KR610777 | Han et al. (2016) |
| *Fomitopsis* niveus | Man 09 | MF589766 MF590166 — — — — | Liu et al. (2019) |
| *Fomitopsis* ochracea | ss5 | KF160609 — — — KF178334 KF160678 | Haight et al. (2016) |
| *Fomitopsis* ochracea | ss7 | KF160910 — — — KF178335 KF160679 | Haight et al. (2016) |
| *Fomitopsis* ostreiformis | IRET 22 | KY449363 — — — — — | Thangamalai et al. (2018) |
| *Fomitopsis* ostreiformis | LDCMY 21 | KY111252 — — — — — | Thangamalai et al. (2018) |
Bayesian Inference was calculated with MrBayes 3.2.6 (Ronquist et al. 2012), with a general time reversible (GTR) model of DNA substitution and a gamma distribution rate variation across sites. Four Markov chains were run for two runs from random starting trees for one million generations and trees were sampled every 100 generations. The burn-in was set to discard 25% of the trees. A majority rule consensus tree of all remaining trees was calculated. Branches that received bootstrap support for Maximum Parsimony (MP), Maximum Likelihood (ML) and Bayesian Posterior Probabilities (BPP) greater than or equal to 75% (MP and ML) and 0.95 (BPP) were considered as significantly supported.

**Results**

**Molecular phylogeny**

The phylogeny of *Fomitopsis*, based on a combined 6-gene (ITS, nLSU, nuSSU, mtSSU, RPB2, TEF1) dataset, included sequences from 64 fungal samples repre-
Figure 1. Maximum Likelihood phylogenetic tree of the new *Fomitopsis* species, based on multi-genes sequences data. Branches are labelled with bootstrap values (MP/ML) higher than 50% and posterior probabilities (BI) more than 0.90, respectively. Bold names: New species.
| Species          | Sample no. | GenBank accessions | References                  |
|------------------|------------|--------------------|-----------------------------|
| *Amaropostia*    |            | ITS: nLSU nuSSU mtSSU TEF1 RPB2 RPB1 |                             |
| *stiptica*       | Cui 10043  | KX900906 KX900976 KX901119 KX901046 KX901219 KX901167 | Shen et al. (2019)          |
| *stiptica*       | Cui 10981  | KX900907 KX900977 KX901120 KX901047 KX901220 KX901168 | Shen et al. (2019)          |
| *Amylocystis*    | HHB-13400  | KC585237 KC585059 |                             |
| *lapponica*      | OKM-4118   | KC585238 KC585060 |                             |
| *Antrodia*       |            | FR605813 FR605752 FR605913 FR610742 FR610832 | Han et al. (2016)           |
| *serpens*        | Dai 7465   | MG787582 MG787624 MG787731 MG787849 MG787798 | Chen et al. (2018)          |
| *Calcipostia*    | Cui 10028  | KF727433 KJ684979 KX901139 KX901066 KX901237 KX901182 | Shen et al. (2019)          |
| *guttulata*      | KHL 11739(GB) | EU118650 EU118650 |                             |
| *Cyanosporus*    |            | KX900883 KX900953 KX901096 KX901021 KX901206 KX901159 | Shen et al. (2019)          |
| *caesius*        | Dai 12605  | KX900884 KX900954 KX901097 KX901022 KX901258 KX901207 KX901160 | Shen et al. (2019)          |
| *subcaesius*     | KA12-1375  | KR673585 |                             |
| *Cystidiopostia* |            | K(M)32713 AY599576 |                             |
| *hibernica*      | Cui 2658   | KX900905 KX900975 KX901118 KX901045 KX901218 | Shen et al. (2019)          |
| *Cystidiopostia* | K(M)17352  | AJ006665 |                             |
| *hibernica*      | Cui 5721   | KF699127 KX900960 KX901121 KX901049 KX901268 KX901221 KX901169 | Shen et al. (2019)          |
| *Cystidiopostia* | Cui 10034  | KX900908 KX900956 KX901122 KX901050 KX901269 KX901222 KX901170 | Shen et al. (2019)          |
| *pileata*        | Cui 10366  | KF699124 KJ684975 KR605927 KR606026 KR610755 KR610844 KX901173 | Han et al. (2016)           |
| *Fuscopostia*    | Dai 13411  | KF699125 KJ684976 KR605928 KR606027 KR610756 KR610845 KX901174 | Han et al. (2016)           |
| *duplicata*      | Cui 10020  | KX900912 KX900982 KX901126 KX901054 KX901270 KX901226 | Shen et al. (2019)          |
| *fragilis*       | Cui 10088  | KF699120 KJ684977 KX901127 KT893749 KT893745 | Han et al. (2016)           |
| *Oligoporus*     | Dai22042   | MW937877 MW937884 MW937870 MW937891 MZ082982 MZ082976 MZ005579 | Present study               |
| *podocarpi*      | Dai22043   | MW937878 MW937885 MW937871 MW937892 MZ082983 MZ082977 MZ005580 | Present study               |
| *Oligoporus*     | Dai22044   | MW937879 MW937886 MW937872 MW937893 MZ082984 MZ082978 MZ005581 | Present study               |
| *renyi*          | KEW 57     | AY218416 AF287876 |                             |
| *Oligoporus*     | MR 10497   | JX090117 |                             |
| *sericeomollis*  | Cui 9560   | KX900919 KX900989 KX901140 KX901067 KX901183 | Shen et al. (2019)          |
| *sericeomollis*  | Cui 9870   | KX900920 KX900990 KX901141 KX901068 KX901184 | Shen et al. (2019)          |
Two new brown rot polypores from tropical China

Senting 29 taxa. They were downloaded from GenBank and generated in the present study (Table 1). The dataset had an aligned length of 4718 characters, including gaps (680 characters for ITS, 1343 characters for nLSU, 1013 characters for nuSSU, 547 characters for mtSSU, 648 characters for RPB2, 487 characters for TEF1), of which 3346 characters were constant, 1860 were variable and parsimony-uninformative, and 1212 were parsimony-informative. Maximum parsimony analysis yielded one equally-parsimonious tree (TL = 3802, CI = 0.544, RI = 0.787, RC = 0.428, HI = 0.456) and the MP tree is shown in Fig. 1. The best model for the combined ITS+nLSU+nuSSU+mtSSU+RPB2+TEF1 sequence dataset was estimated and applied in the Bayesian analysis was GTR+I+G with equal frequency of nucleotides, lset nst = 6 rates = invgamma; prset statefreqpr = dirichlet (1,1,1,1). Bayesian analysis resulted in a concordant topology with an average standard deviation of split frequencies = 0.008975.

The phylogeny of Oligoporus, combined 7-gene (ITS, nLSU, nuSSU, mtSSU, RPB1, RPB2, TEF1) dataset, included sequences from 43 fungal samples representing 21 taxa. They were downloaded from GenBank and generated in the present study (Table 2). The dataset had an aligned length of 5772 characters,
including gaps (612 characters for ITS, 1302 characters for nLSU, 1009 characters for nuSSU, 491 characters for mtSSU, 1231 characters for RPB1, 648 characters for RPB2, 479 characters for TEF1), of which 4127 characters were constant, 129

Figure 2. Maximum Likelihood phylogenetic tree of the new Oligoporus species, based on multi-genes sequences data. Branches are labelled with bootstrap values (MP/ML) higher than 50% and posterior probabilities (BI) more than 0.90, respectively. Bold names: New species.
### Table 3. A comparison of species in the *Fomitopsis*.

| Species          | Holotype | Basidiocarp | Pileal surface  | Pore surface  | Pore (per mm.) | Hyphal system | Cystidia/cystidioles | Basidiospores | Reference               |
|------------------|----------|-------------|-----------------|--------------|--------------|---------------|---------------------|---------------|------------------------|
| *F. abieticola*   | China    | Annual to perennial; pileate | Cream to pinkish buff | Cream to pinkish buff when fresh, becoming buff to curry-yellow when dry | Round to angular, 2–4 | Trimitic | Cystidia absent; fusoid cystidioles occasionally present, 17.5–50.2 × 4.3–9.5 μm | Oblong-ellipsoid to ellipsoid, 7–9 × 4–5 μm | Liu et al. (2021) |
| *F. bambusae*    | China    | Annual; resupinate to effused-reflexed or pileate | Plush grey to pale mouse-grey to greyish-sepia when dry | Blush-grey to pale mouse-grey to greyish-sepia when fresh, becoming mouse-grey to dark grey when dry | Round to angular, 6–9 | Dimitic | Cystidia absent; fusoid cystidioles present, 11–18 × 2.5–4 μm | Cylindrical to oblong ellipsoid, 4.2–6.1 × 2–2.3 μm | Present study |
| *F. betulina*    | Norway   | Annual; pileate | White to pale brownish | White to pale brownish | Round to angular, 3–5 | Di-trimitic | Absent | Cylindrical, slightly allantoid, 5–6 × 1.5–1.7 μm | Ryvarden and Melo (2014) |
| *F. bondartsevae* | Russia   | Annual; effused-reflexed to pileate | Pale mouse-grey to dark grey, azonate | Cream to straw coloured turning mouse-grey to dark grey | Angular, 5–8 | Trimitic | Cystidia absent; fusoid cystidioles present, 18–26 × 4.5–6 μm | Cylindrical, 6–7.2 × 2.2–2.5 μm | Spirin (2002) |
| *F. cana*        | China    | Annual; resupinate to effused-reflexed or pileate | Pale mouse-grey to dark grey, azonate | Cream to straw coloured turning mouse-grey to dark grey | Angular, 5–8 | Trimitic | Cystidia absent; fusoid cystidioles present, 9–16 × 3–5 μm | Cylindrical to oblong ellipsoid, 5–6.2 × 2.1–3 μm | Li et al. (2015) |
| *F. caribensis*  | Puerto Rico | Annual; pileate, sessile | White to cream buff when fresh, cream buff to curry-yellow at base | White to cream when fresh, becoming cream to pinkish-buff when dry | Round to angular, 6–9 | Dimitic | Cystidia absent; fusoid cystidioles occasional, hyaline, thin-walled, 12.5–23.5 × 2.5–4 μm | Cylindrical to oblong ellipsoid, 6–7.5 × 2.3–3.1 μm | Liu et al. (2019) |
| *F. durenmii*    | USA      | Annual; sessile | Cream coloured to pale buff, drying tan | White to cream coloured, ochraceous on drying | Round to angular, 4–5 | Trimitic | Cystidia absent; fusoid cystidioles present, 14–16 × 5–6 μm | Narrowly cylindrical, 6–8 × 1.5–2.5 μm | Gilbertson and Ryvarden (1986) |
| *F. eucalypticola* | Australia | Annual to biennial; effused-reflexed to pileate | Cream to salmon-coloured when young, straw yellow to clay-pink | Cream to yellow when fresh, buff to clay-buff when dry | Round to angular, 3–5 | Trimitic | Cystidia absent; fusoid cystidioles occasionally present, 15–36 × 2–5.3 μm | Cylindrical to oblong ellipsoid, 5.8–9.1 × 2.7–5 μm | Liu et al. (2019) |
| *F. gigasenii*   | China    | Annual; pileate, imbricate | Dirty greyish-brown to mouse-grey | Pinkish-buff to cinnamon-buff | Round to angular, 3–6 | Trimitic | Cystidia absent; fusoid cystidioles occasionally present, 12.5–27.6 × 2.8–4.1 μm | Cylindrical, 7.2–9 × 2.2–3 μm | Liu et al. (2019) |
| *F. hemitrapha*  | New Zealand | Perennial; solitary, attached by a broad lateral base | Tobacco brown or fuscous | White or straw to isabelline | Round or slightly angular, 6–7 | Trimitic | Cystidia absent; cystidioles, 6–8 × 3.5–4 μm | Elliptic-oblong, 4–6 × 2–2.5 μm | Cunningham (1965) |
| Species     | Holotype | Basidiocarps | Pileal surface | Pore surface | Pore (per mm.) | Hyphal system | Cystidia/cystidioles | Basidiospores | Radiospores | References                                      |
|-------------|----------|--------------|----------------|--------------|----------------|---------------|--------------------|---------------|-------------|------------------------------------------------|
| *F. bengduanensis* | China     | Annual to perennial; pileate | Pale dark grey to reddish-brown at base and cream to flesh-pink towards the margin | White to cream when fresh, becoming buff to straw-yellow | Round to angular, 6–8 | Trimitic | Cystidia absent; fusoid cystidioles occasionally present, 13.2–36.5 × 2.5–5.4 μm | Oblong-ellipsoid to ellipsoid, 5.2–6 × 3.2–3.6 μm | Liu et al. (2021) |
| *F. ibérica* | Portugal  | Annual; sessile, diminuate, single or imbricate | White to cream when young, drying honey-coloured to brown | Pale, white, cream to straw-coloured | Round to angular, 3–4 per mm | Trimitic | Cystidia absent; pointed cystidioles present, 20–27 × 4–5–5 μm | Cylindrical to distinctly fusoid, 6–8 × 2.8–3.7 μm | Melo and Ryvarden (1989) |
| *F. keizae* | Vietnam   | Annual; pileate | Buff yellow to orange-yellow buff | White to cream when fresh, cream to buff | Round to angular, 6–8 | Trimitic | Cystidia absent; fusoid cystidioles occasionally present, 11.5–30.4 × 2.6–6 μm | Oblong-ellipsoid, 4.8–5.3 × 3–3.5 μm | Liu et al. (2021) |
| *F. massoniana* | China     | Annual; effused-reflexed to pileate | Buff-yellow to apricot-orange | White to cream when fresh, olivaceous buff to cinnamon-buff when dry | Round, 5–7 | Dimitic | Cystidia absent; fusoid cystidioles occasionally present, 14.8–36 × 3.8–6 μm | Oblong-ellipsoid, 6.2–7.3 × 3–4 μm | Liu et al. (2021) |
| *F. meliae* | USA       | Annual or biennial; sessile, pilei single to imbricate, diminiate | Ivory to tan or cinerous | Ochraceous | Round to angular, 5–7 | Trimitic | Cystidia absent; fusoid cystidioles present, 15–23 × 4–5 μm | Cylindrical, slightly fusiform, tapering to the apex, 6–8 × 2.5–3 μm | Gilbertson (1981) |
| *F. mounceae* | Canada    | Perennial; pileate | Brownish-orange to black at base and pale orange to greyish-orange towards the margin | Yellowish-white, greyish-yellow, pale orange to light ochraceous buff, bright reddish-brown when dry | Round, 3–5 | Dimitic | Cystidia obclavate to sub fusiform with subacute or rounded apices, 16–35 × 3–6.5 μm | Ellipsoid to cylindrical, 5.8–6.6 × 3.4–4 μm | Haight et al. (2019) |
| *F. nitens* | Brazil    | Annual to biennial; sessile, diminiate, single to imbricate | Cream to pale sordid brown or tan | Cream to pale sordid brown or tan | Round to angular, 6–8 | Trimitic | Cystidia absent; cystidioles broadly rounded, subapically contracted, 12–15 × 4–5 μm | Cylindrical, 6–9 × 2–3 μm | Gilbertson and Ryvarden (1986) |
| *F. ochracea* | Canada    | Perennial; pileate | Brownish-grey to greyish-brown at base and orange white to pale orange towards the margin | Pale yellow, pale orange, light ochraceous buff, reddish-brown when dry | Round, 4–5 | Trimitic | Cystidia absent; fusoid cystidioles occasionally present, 20–40 × 4–6.5 μm | Broadly ellipsoid, 5.1–5.9 × 3.6–4 μm | Stokland and Ryvarden (2008); Haight et al. (2019) |
| *F. ostreiformis* | Singapore | Annual; sessile or effuse-reflexed | Greyish pileal surface | White or greyish-white | Round to angular, 3–4 | Trimitic | Cystidia absent; cystidioles present, 10–17 × 2.8–4 μm | Cylindrical, 4.2–5.6 × 1.4–2.6 pm | Do (1981); Hattori (2003) |
Two new brown rot polypores from tropical China

| Species            | Holotype  | Basidiocarps          | Pileal surface                                      | Pore surface                                      | Pore (per mm) | Hyphal system  | Cystidia/cystidioles          | Basidiospores       | Radiospores | References                      |
|--------------------|-----------|-----------------------|-----------------------------------------------------|---------------------------------------------------|---------------|----------------|-------------------------------|---------------------|-------------|--------------------------------|
| *F. palustris*     | USA       | Perennial; sessile, horizontal, applanate | Dimgy ochraceous to ochraceous buff, suffused dimgy brownish-vinaceous | Vinaceous drab to brownish-vinaceous but pallid ochraceous near the margin | Angular, 7–9 | Dimitic | absent | Cylindrical, 3.7–4.7 × 2–2.5 μm. | Corner (1989); Hattori (2003) |
| *F. pinicola*     | Europe    | Perennial; pileate    | Brownish-orange to black at base and buff-yellow to cinnamon towards the margin | Cream coloured becoming citric yellow when bruised | Round, 4–6 | Trinitic | Cystidia present, 18–90 × 3–9 μm | Cyldrical-ellipsoid, 6–9 × 3–4.5 μm | Ryyvarden and Mello (2014); Haight et al. (2019) |
| *F. rosenalba*    | Brazil    | Annual; pileate, resupinate to effused-reflexed | White to pink when fresh, cream to greyish when dry | White to cream when fresh and ochraceous when dried | Round to angular, 4–6 | Trinitic | absent | Ellipsoid to sub-cylindrical, 3–4.9 × 1.8–2 μm | Tibpromma et al. (2017) |
| *F. schrenkii*    | USA       | Perennial; effused-reflexed to pileate | Greyish-orange to olive brown at base and greyish-orange to greyish-yellow towards the margin | Pale yellow, pale orange, cream buff, reddish-brown when dry | Round, 3–4 | Dimitic | Cystidia cylindrical, subulate, or subfusiform with subacutes, 16–30 × 3–8 μm | Ellipsoid to broadly cylindrical, 5.7–6.7 × 3.7–4.2 μm | Haight et al. (2019) |
| *F. subtropic*    | China     | Annual; pileate       | Apricot-orange, scarlet to fuscous | White to cream when fresh, turning buff yellow to buff when dry | Round, 6–8 | Dimitic | Cystidia absent; fusoid cystidioles occasionally present, 14.5–34.6 × 3.2–7.2 μm | Oblong-ellipsoid to ellipsoid, 4.3–5.5 × 2.7–3.3 μm | Liu et al. (2021) |
| *F. tianshanensis* | China     | Annual to perennial; effused-reflexed to pileate | Straw-yellow when young, becoming pale mouse-grey to flesh-pink with age | Cream to straw coloured or pale pinkish | Angular, 6–9 | Trinitic | Cystidia absent; fusoid cystidioles occasionally present, 9–15 × 3–4 μm | Cylindrical to oblong-ellipsoid, 3.2–4 × 1.8–2.1 μm | Li and Cui (2013) |

Bayesian analysis resulted in a concordant topology with an average standard deviation of split frequencies = 0.008567.
In our phylogenies (Figs 1 and 2), five samples on bamboo formed an independent lineage in the *Fomitopsis* s.s. clade with strong support (100% ML, 100% MP, 1.00 BPPs) and are distant from other taxa in the genus. Both morphology and rDNA sequence data confirmed that the five samples represent a new species in *Fomitopsis*. Meanwhile, three samples on *Podocarpus* were nested in the *Oligoporus* s.s. clade and formed an independent lineage with a robust support (100% ML, 100% MP, 1.00 BPPs). Both morphology and rDNA sequence data confirmed that the three samples represent a new species in *Oligoporus*.

**Taxonomy**

*Fomitopsis bambusae* Y.C. Dai, Meng Zhou & Yuan Yuan, sp. nov.

MycoBank No: 839359

Figs 3, 4

**Diagnosis.** *Fomitopsis bambusae* is characterised by resupinate to effused-reflexed or pileate, soft corky basidiocarps with bluish-grey pores, small pores measuring 6–9 per mm, cylindrical to oblong ellipsoid basidiospores measuring 4.2–6.1 × 2–2.3 μm and growing on dead bamboo.

**Type.** China. Hainan, Haikou, Jinniuling Park, on dead bamboo, 18.XI.2020, Yu-Cheng Dai leg., Dai 22116 (holotype BJFC036008).

**Etymology.** *Bambusae* (Lat.): refers to the species growing on bamboo.

**Fruiting body.** Basidiocarps annual, resupinate to effused-reflexed or pileate, separable from the substrate, without odour or taste and soft corky when fresh, corky and light in weight when dry. Pilei semicircular, projecting up to 1 cm, 1.5 cm wide and 5 mm thick at base; resupinate part up to 14 cm long, 6 cm wide and 2 mm thick at centre. Pileal surface bluish-grey when fresh, pale mouse-grey to greyish-sepia when dry, glabrous to slightly velutinate, rough, azonate; margin acute, incurved when dry. Pore surface bluish-grey to pale mouse-grey when fresh, becoming mouse-grey to dark grey when dry; sterile margin up to 1 mm wide; pores round to angular, 6–9 per mm; dissepiments thin, entire. Context white to cream, corky, up to 3.5 mm thick. Tubes paler than pore surface, corky, up to 1.5 mm long.

**Hyphal structure.** Hyphal system dimitic; generative hyphae bearing clamp connections; skeletal hyphae IKI–, CB–; tissue unchanged in KOH.

**Context.** Generative hyphae hyaline, thin- to slightly thick-walled, occasionally branched, 1.5–3 μm in diam.; skeletal hyphae dominant, hyaline, thick-walled with a narrow lumen to subsolid, occasionally branched, interwoven, 2–4.5 μm in diam.

**Tubes.** Generative hyphae hyaline, thin- to slightly thick-walled, rarely branched, 1.5–2.5 μm in diam.; skeletal hyphae dominant, hyaline, thick-walled with a narrow lumen to subsolid, occasionally branched, flexuous, interwoven, 2–3 μm in diam. Cystidia absent; fusoid cystidioles present, hyaline, thin-walled, 11–18 × 2.5–4 μm. Basidia short clavate to barrel-shaped, bearing four sterigmata and a basal clamp connection, 13–19 × 4.5–5.5 μm; basidioles dominant, in shape similar to basidia, but smaller.
Spores. Basidiospores cylindrical to oblong ellipsoid, hyaline, thin-walled, smooth, IKI–, CB–, (4–)4.2–6.1(–6.5) × (1.9–)2–2.3(–2.6) μm, L = 4.917 μm, W = 2.109 μm, Q = 2.26–2.41 (n = 90/3).
Type of rot. Brown rot.

Additional specimens (paratypes) examined. China. Hainan, Haikou, Jinniuling Park, on dead bamboo, 7.XI.2020, Yu-Cheng Dai leg., Dai 21942 (BJFC035841), 18.XI.2020, Dai 22104 (BJFC035996), Dai 22110 (BJFC036002) and Dai 22114 (BJFC036006).

Figure 4. Microscopic structures of *Fomitopsis bambusae* (drawn from the holotype) a basidiospores b basidia c basidioles d cystidioles e hyphae from context f hyphae from trama.
Two new brown rot polypores from tropical China

**Table 4.** A comparison of species in the *Oligoporus.*

| Species                  | Basidiocarps | Pore (per mm) | Pore surface               | Cystidia                           | Cystidiales | Basidiospores size (μm) | Basidiospores shape | Reference                      |
|--------------------------|--------------|---------------|----------------------------|------------------------------------|-------------|------------------------|---------------------|--------------------------------|
| *Oligoporus podocarpi*   | Resupinate   | Round to angular, 5–6 | White to pale cream         | Thick-walled with apically encrusted | Absent      | 3.8–4.2 x 2–2.5         | Allantoid to oblong ellipsoid | Present study               |
| *O. rennyi*              | Resupinate   | Angular, 2–4   | White or cream, then pale brown | Absent                              | Absent      | 4.8–6 x 2.5–3.5         | Oblong ellipsoid        | Ryvarden and Melo (2014); Shen et al. (2019) |
| *O. sericeomollis*       | Resupinate   | Round and angular, 4–6 | White or discoloured yellowish or tan | Thick-walled with apically encrusted | Present, thin-walled | 4–5 x 2–2.5 | Oblong cylindrical to ellipsoid | Ryvarden and Melo (2014); Shen et al. (2019) |

**Oligoporus podocarpi** Y.C. Dai, Chao G. Wang & Yuan Yuan, sp. nov.
MycoBank No: 839360
Figs 5, 6

**Diagnosis.** *Oligoporus podocarpi* is characterised by soft fresh basidiocarps, becoming rigid upon drying, a monomitic hyphal system with hyaline clamped generative hyphae, the presence of apically encrusted cystidia, broadly ellipsoid to reniform, dextrinoid, cyanophilous basidiospores measuring 3.8–4.2 x 2–2.3 μm, and growing on rotten wood of *Podocarpus.*

**Type.** China. Hainan, Changjiang, Hainan Tropical Rainforest National Park, Bawangling, rotten wood of *Podocarpus imbricatus*, 10.XI.2020, Yu-Cheng Dai leg., Dai 22042 (holotype BJFC035938).

**Etymology.** *Podocarp* (Lat.): referring to the species growing on wood of *Podocarpus imbricatus.*

**Fruiting body.** Basidiocarps annual, resupinate, adnate, soft corky, with mushroom odour when fresh, becoming rigid when dry, mild taste, up to 3 cm long, 2 cm wide and 2.3 mm thick at the centre. Pore surface snow white when fresh, becoming cream to buff upon drying, somewhat glancing; sterile margin indistinct, thinning out, up to 0.3 mm wide; pores round to angular, 5–6 per mm; dissepi-ments thin, entire. Subiculum white, fibrous to soft corky when dry, up to 0.3 mm thick. Tubes concolorous with the pore surface, hard corky to brittle when dry, up to 2 mm long.

**Hyphal structure.** Hyphal system monomitic; generative hyphae with clamp connections, smooth, hyaline, IKI–, CB–; tissues unchanged in KOH.

**Subiculum.** Generative hyphae thick-walled with a wide lumen, occasionally branched, flexuous, interwoven, 2.5–3.8 μm in diam.

**Tubes.** Generative hyphae thin- to thick-walled, occasionally branched, subparallel along the tubes to loosely interwoven, 2–3.1 μm in diam. Cystidia present, ventricose, very thick-walled, some apically encrusted. Basidia short clavate, sometimes with an intermediate constriction, with four sterigmata and a basal clamp connection, 12.5–16 x 4–5 μm; basidioloe in shape similar to basidia, but smaller.
**Spores.** Basidiospores broadly ellipsoid to reniform, hyaline, thin- to slightly thick-walled, smooth, often with one guttule, dextrinoid, CB+, (3.5–)3.8–4.2(–4.5) × 2–2.3(–2.5) μm, L = 3.98 μm, W = 2.14 μm, Q = 1.82–1.90 (n = 90/3).

**Type of rot.** Brown rot.

**Additional specimens (paratypes) examined.** China. Hainan, Changjiang, Hainan Tropical Rainforest National Park, Bawangling; rotten wood of *Podocarpus imbricatus*, 10.XI.2020, Yu-Cheng Dai leg., Dai 22043 (BJFC035939) and Dai 22044 (BJFC035940).

**Discussion**

In this study, two new species, *Fomitopsis bambusae* and *Oligoporus podocarpi*, are described, based on morphological features and molecular data. The phylogenetic analysis of *Fomitopsis* (Fig. 1), inferred from ITS+nLSU+nuSSU+mtSSU+PRB2+TEF1 sequences, provides strong support (100% ML, 100% MP, 1.00 BPPs) for the placement of *F. bambusae* in *Fomitopsis* s.s. Besides, *Fomitopsis bambusae* formed a distinct and independent lineage, which is clearly distinguishable phylogenetically from all other known species of the genus. *Fomitopsis roseoalba* A.M.S. Soares and *F. subtropica* B.K. Cui & Hai J. Li are potentially the most closely related. Meanwhile, *F. roseoalba* is distinguished from *F. bambusae* by its larger pores (4–6 per mm vs. 6–9 per mm) and smaller basidiospores (3–4.9 × 1.8–2 μm vs. 4.2–6.1 × 2–2.3 μm, Tibpromma et al. 2017); *F. subtropica* is different from *F. bambusae* by smaller basidiospores (3.2–4 × 1.8–2.1 μm vs. 4.2–6.1 × 2–2.3 μm, Li et al. 2013).

Morphologically, *Fomitopsis bambusae*, *F. cana* (Blume & T. Nees) Imazeki, *F. caribenensis*, *F. hemitephra* (Berk.) G. Cunn. and *F. nivosa* (Berk.) Gilb. & Ryvarden share approximately the same-sized pores (6–9 per mm). However, *Fomitopsis cana* differs from *F. bambusae* by its trimitic hyphal system, slightly larger basidiospores (5–6.2 × 2.1–3 μm, L = 5.81 μm, W = 2.6 μm vs. 4.2–6.1 × 2–2.3 μm, L = 4.917 μm, W = 2.109 μm) and grows on angiosperm wood rather than bamboo (Li et al. 2013). *Fomitopsis caribenensis* differs from *F. bambusae* by larger basidiospores (6–7.5 × 2.3–3.1 μm vs. 4.2–6.1 × 2–2.3 μm, Liu et al. 2019). *Fomitopsis hemitephra* is distinguished from *F. bambusae* by its perennial habitat, woody hard basidiocarps (Cunningham 1965). *Fomitopsis nivosa* differs from *F. bambusae* by having longer basidiospores (6–9 × 2–3 μm vs. 4.2–6.1 × 2–2.3 μm, Gilbertson and Ryvarden 1986). In addition, *Fomitopsis bambusae* may be confused with *F. ostreiformis* (Berk.) T. Hatt. in having similar-sized basidiospores and also growing on bamboo, but *F. ostreiformis* differs from *F. bambusae* by the larger pores (3–4 per mm vs. 6–9 per mm) and trimitic hyphal system (De 1981).

Our phylogeny of *Oligoporus* (Fig. 2), based on ITS+nLSU+nuSSU+mtSSU+PRB1+PRB2+TEF1 sequence, demonstrated *Oligoporus* s.s. formed a monophyletic lineage with a robust rating (100% ML, 100% MP, 1.00 BPPs), which is distant from *Postia* s.s. Though *Oligoporus* and *Postia* are similar to each other in morphological characteristics, some significant differences remain. For instance, *Postia* s.s. has effuse-
Two new brown rot polypores from tropical China

reflexed to pileate basidiocarps, thin-walled and acyanophilous basidiospores (Donk 1971; Ryvarden and Melo 2014; Shen et al. 2019), while *Oligoporus* s.s. has resupinate basidiocarps, slightly thick-walled and cyanophilous basidiospores (Shen et al. 2019). Figure 5. Basidiocarps of *Oligoporus podocarpi* (holotype Dai 22042). Scale bar: 1.0 cm.
2019). Phylogenetically, *Oligoporus podocarpi* is nested in the *Oligoporus* s.s. clade with a strong support (100% ML, 100% MP, 1.00 BPPs) and related to *O. rennyi* (Berk. & Broome) Donk and *O. sericeomollis* (Romell) Bondartseva (Fig. 2). These three species, representing *Oligoporus* s.s., have resupinate basidiocarps, white to cream pore

**Figure 6.** Microscopic structures of *Oligoporus podocarpi* (drawn from the holotype) a basidiospores b Basidia and basidioles c cystidia d hyphae from subiculum e hyphae from trama.
Two new brown rot polypores from tropical China

surface and thick-walled, dextrinoid, cyanophilous basidiospores. However, Oligoporus rennyi differs from O. podocarpi in the very fragile dry basidiocarps, the lack of cystidia and the presence of chlamydospores (Donk 1971; Ryvarden and Melo 2014). Oligoporus sericeomollis is different from O. podocarpi by fragile dry basidiocarps, longer basidiospores (4–5 × 2–2.5 μm vs. 3.8–4.2 × 2–2.3 μm) and the extremely bitter taste (Núñez and Ryvarden 2001; Ryvarden and Melo 2014). Morphologically, Oligoporus podocarpi is similar to Postia simanii (Pilát) Jülich, Cystidiopostia hibernica (Berk. & Broome) B.K. Cui, L.L. Shen & Y.C. Dai and Rhodonia rancida (Bres.) B.K. Cui, L.L. Shen & Y.C. Dai by resupinate basidiocarps, white to cream pore surface (Jülich 1982; Núñez and Ryvarden 2001; Ryvarden and Melo 2014; Shen et al. 2019). However, Postia simanii has smaller pores (6–8 per mm) and allantoid, thin-walled basidiospores measuring 4–5.3 × 0.8–1.2 μm (Jülich 1982; Ryvarden and Melo 2014). Cystidiopostia hibernica and Rhodonia rancida are different from Oligoporus podocarpi by larger pores (2–3 per mm in C. hibernica, 2–4 per mm in R. rancida) and allantoid, thin-walled basidiospores (4.3–6 × 1.4–1.9 μm in C. hibernica, 5–7 × 2–2.5 μm in R. rancida) (Ryvarden and Melo 2014; Shen et al. 2019).

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