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Fomitiporia expansa, an undescribed species from French Guiana

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Abstract – During the revision of the Neotropical *Fomitiporia* species, a collection from French Guiana was found to represent an undescribed species, on the basis of both morphological and molecular (DNA sequence) data. This taxon is described and illustrated as *Fomitiporia expansa* sp. nov. It is characterized by widely effused basidiomata, extending over 1 m long, with a variable greyish to light brownish grey pore surface, and microscopically in having basidiospores averaging 6.0 × 5.5 µm. It is known for the time being from a single specimen originating in the western edge of French Guiana, in rainforest. The species belongs to the *Fomitiporia langloisii* lineage. This lineage contains for the time being species with resupinate basidiomata spanning over the Neotropics.

Hymenochaetaceae / Neotropics / Phylogeny / Taxonomy

INTRODUCTION

Fomitiporia Murrill (Hymenochaetales) is typified by *F. langloisii* (Decock *et al.* 2007, Murrill 1907). The genus is above all characterized by subglobose to globose, thick-walled, hyaline, cyanophilous, and dextrinoid basidiospores, in addition to a dimitic (pseudodimitic) hyphal system. Cystidioles, hymenial and extra-hymenial setae are variably present (Campos Santana *et al.* 2014, Fischer 1996, Pieri & Rivoire 2000). Basidiomata are resupinate to pileate.

Numerous studies have dealt with the genus in the last 20 years, evidencing a much larger than presumed taxonomic/phylogenetic diversity (*e.g.* Amalfi and Decock 2013, Amalfi *et al.* 2010, 2012, Campos Santana *et al.* 2014, Cloete *et al.* 2013, Decock *et al.* 2005, 2007, Fischer *et al.* 2005, Vlasák and Kout 2011, Zhou and Xue 2012).

Pursuing the revision of the New World *Fomitiporia* (Amalfi *et al.* 2012, Amalfi and Decock 2013, Campos Santana *et al.* 2014, Decock *et al.* 2007, Raymundo *et al.* 2012), a collection from the lowland rainforest of French Guiana drew the attention by a remarkable combination of morphological features of which resupinate, widely effused basidiomata, extending over 1 m long, with a bright greyish to greyish brown pore surface when fresh. Multilocus phylogenetic inferences, based on DNA sequence data of 4 loci (5' end of the LSU, ITS-5.8S,

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partial *tef1* and partial *rpb2*) resolved this specimen as an isolated branch, within the *F. langloisii*, type lineage.

It is interpreted as belonging to a distinct species, for which no name could be found that could apply to it (Decock *et al.* 2007); hence it is described and illustrated below as *Fomitiporia expansa* sp. nov.

MATERIALS AND METHODS

Collection localities of the new taxa. – The specimens from French Guiana were collected in the Marouini river valley, western French Guiana, approx. 02.73103° N-054.01610° W, alt. approx. 130 masl and in the CNRS "inselberg" research plots, Nouragues Natural Reserve (approx. 04°05.5'N-52°40.6'W, http://www.nouragues.cnrs.fr/F-inselberg.html). Voucher herbarium specimens of the collections from French Guiana are preserved at MUCL, CAY, and NY (herbarium acronyms are according to Thiers, continuously updated). The senior author isolated strains in pure culture during fieldwork, from fresh basidiomata tissues, plated on malt extract agar supplemented by 2 ppm benomyl (benlate) and 50 ppm chloramphenicol. The living strains are preserved at MUCL with a duplicate at the CBS (The Netherlands).

Morphology and anatomy. – Basidiomata colours are described according to Kornerup and Wanscher (1981). Basidiomata sections were examined in Melzer's reagent, lactic acid Cotton blue (Kirk *et al.* 2001), and KOH 4%. All microscopic measurements were done in Melzer's reagent. In presenting the size range of the microscopic elements, 5% of the measurements were excluded from each end and are given in parentheses, ave = arithmetical mean, Q = ratio of length/width of basidiospores, and ave_Q = arithmetical mean of the ratio Q. As a rule, 30 elements (pores, hyphae, basidiospores) were measured, when sufficiently abundant.

Sequencing. – One hundred and nine specimens and cultures representing 40 species (or potential species clades) were included in the phylogenetic analysis. Materials and sequences used in this study are listed in Table I. As a rule, DNA was extracted from pure culture, except when noted (Table I). DNA extraction, amplification and sequencing of the 5' end of the nuclear ribosomal LSU rRNA gene, the ITS regions (including 5.8S), partial *tef1-α* gene, and the region between domains 6 and 7 of the second largest subunit of the *rpb2* (Frøslev *et al.* 2005, Matheny 2005) were as described in Decock *et al.* (2007) and Amalfi *et al.* (2010, 2012) and Amalfi and Decock (2013).

Phylogenetic analysis. – The nucleotide alignment deposited at TreeBASE under study accession number "http://purl.org/phylo/treebase/phylows/study/TB2:S12874" (Campos Santana *et al.* 2014) was used as starting data set to align the additional sequence obtained from the strain MUCL55026. Ambiguously aligned segments were detected with the Gblocks 0.91b program (Castresana 2000; http://molevol.cmima.csic.es/castresana/ Gblocks.html) with settings "ALLOW SMALLER FINAL BLOCKS", "ALLOW GAPS WITHIN BLOCKS". The alignment was screened visually to detect additional ambiguously aligned regions. Indels present within our datasets, especially in the ITS1 region (Decock *et al.* 2007), were recoded as binary characters with the simple indel coding method (SIC, Simmons and Ochoterena 2000) as implemented in SeqState software (Müller 2005).

Table 1. List of species, specimens/cultures, and sequences accession number (GenBank) included in the phylogenetic analyses

Genus/species names		*GenBank accession number*			
Voucher specimens/cultures reference	*Locality*	*nLSU*	*ITS*	*tef1-α*	*rpb2*
Fomitiporia aethiopica Decock *et al.*					
MUCL 44777 (T) [c, h]	Ethiopia	AY618204	GU478341	GU461893	JQ087956
MUCL 44806 [c, h]	Ethiopia	AY618202	GU461944	GU461892	JQ087955
F. apiahyna (Speg.) Robledo *et al.*					
MUCL 51451 [c, h]	Ecuador	GU461997	GU461963	GU461896	JQ087958
MUCL 51485 [c, h]	Ecuador	GU461996	GU461962	GU461895	JQ087957
MUCL 53042 [c, h]	French Guiana	JX093817	JX093773	JX093730	JX093861
F. australiensis M. Fisch. *et al.*					
VPRI 22451a (MUCL 49406) PT [c, 8]	Australia	GU462001	AY624997	GU461897	JQ087959
Fomitiporia bakeri (Murrill) Vlasák & Kout					
FP-134784-Sp (MUCL 51098) [c, 1]	USA	JQ087901	JQ087874	JQ087928	JQ087960
F. bannaensis Y.C. Dai					
MUCL 45926 [c, h]	Thailand	EF429217	GU461942	GU461898	JQ087961
MUCL 46926 [c, h]	China	KF444705	KF444682	KF444751	KF444728
MUCL 46930 [c, h]	China	KF444706	KF444683	KF444752	KF444729
MUCL 46948 [c, h]	China	KF444707	KF444684	KF444753	KF444730
MUCL 46950 [c, h]	China	EF429218	GU461943	GU461899	JQ087962
Fomitiporia calkinsii (Murrill) Vlasák & Kout					
FP-106252-Sp (MUCL 51095) [c, 1]	USA	KF444708	KF444685	KF444754	KF444731
FP-53385-T (MUCL 51099) [c, 1]	USA	KF444709	KF444686	KF444755	KF444732
FP-71907-T (MUCL 51100) [c, 1]	USA	JQ087902	JQ087875	JQ087929	JQ087963
CBS 175.34 (MUCL 51398) [c, 1]	USA	KF444710	KF444687	KF444756	KF444733
MUCL 52346 [c, h]	Mexico	JQ087903	JQ087876	JQ087930	JQ087964
MA-MX0945 [c, h]	Mexico	KF444711	KF444688	KF444757	KF444734
F. capenses M. Fisch. *et al.*					
MUCL 53009 [c, 5]	South Africa	JQ087917	JQ087890	JQ087944	JQ087997
F. castilloi Amalfi & Decock					
MUCL 53481 (T) [c, h]	French Guiana	JQ087916	JQ087889	JQ087943	JQ087996
MUCL 53980 (PT) [c, h]	French Guiana	JX093830	JX093786	JX093743	JX093874
F. cupressicola Amalfi *et al.*					
MUCL 52486 (T) [c, h]	Mexico	JQ087904	JQ087877	JQ087931	JQ087965
MUCL 52488 [c, h]	Mexico	JQ087905	JQ087878	JQ087932	JQ087966
MUCL 52489 [c, h]	Mexico	JQ087906	JQ087879	JQ087933	JQ087967
MUCL 52490 [c, h]	Mexico	JQ087907	JQ087880	JQ087934	JQ087968
F. dryophila Murrill					
TJV-93-232 (MUCL 46379) [c, 1]	USA	EF429221	EF429240	GU461902	JQ087969
TJV-93-234 (MUCL 46380) [c, 1]	USA	EF429219	EF429238	GU461900	JQ087970
TJV-93-259 (MUCL 46381) [c, 1]	USA	EF429220	EF429239	GU461901	KF444735
FP-104030-T (MUCL 51144) [c, 1]	USA	KF444712	KF444689	KF444758	KF444736
F. erecta (A. David *et al.*) Fiasson					
MUCL 49871 [c, h]	France	GU461976	GU461939	GU461903	JQ087971
MA-PA03 [c, h]	Italy	KF444713	KF444690	KF444759	ND
F. expansa Decock & Amalfi sp. nov.					
MUCL 55026 (T) [c, h]	French Guiana	KJ401031	KJ401032	KJ401033	KJ401034
F. gabonensis Amalfi & Decock					
MUCL 47576 (T) [c, h]	Gabon	GU461990	GU461971	GU461923	JQ087972
MUCL 51291 [c, h]	Gabon	GU461986	GU461967	GU461924	JQ087973
Fomitiporia hartigii (Allesch. & Schnabl) Fiasson & Niemelä					
MAFF 11-20016 (MUCL 31400) [c]	Japan	JQ087909	JQ087882	JQ087936	JQ087975
75-2 562 (MUCL 53549) [c, 4]	Estonia	JX093831	JX093787	JX093744	JX093875
71-25 464 (MUCL 53550) [c, 4]	Estonia	JX093832	JX093788	JX093745	JX093876
75-3 563 (MUCL 53551) [c, 4]	Estonia	JX093833	JX093789	JX093746	JX093877

Table 1. List of species, specimens/cultures, and sequences accession number (GenBank) included in the phylogenetic analyses *(continued)*

Genus/species names		*GenBank accession number*			
Voucher specimens/cultures reference	*Locality*	*nLSU*	*ITS*	*tef1-α*	*rpb2*
F. hippophaeicola (H. Jahn) Fiasson & Niemelä					
MUCL 31746 [c, h]	Belgium	AY618207	GU461945	GU461904	JQ087976
MUCL 31747 [c, h]	Belgium	GU461977	GU461946	GU461905	JQ087977
F. ivindoensis Decock *et al.*					
MUCL 51311 [c, h]	Gabon	GU461979	GU461952	GU461907	JQ087978
MUCL 51312 (T) [c, h]	Gabon	GU461978	GU461951	GU461906	JQ087979
F. langloisii Murrill					
FP-94347-R (MUCL 46375) [c, 1]	USA	EF429225	EF429242	GU461908	JQ087980
01-77/4 (MUCL 46165), (T of *F. hesleri*) [c, 5]	USA	EF429223	AY340026	GU461909	JQ087981
FP-105-816-T (MUCL 46373) [c, 1]	USA	EF429226	EF429243	KF444760	ND
HHB-9868-Sp (MUCL 46377) [c, 1]	USA	EF429224	EF429241	KF444761	ND
01-712/2 (MUCL 46164) [c, 5]	USA	EF429222	AY340031	KF444762	ND
FP-105818-R (MUCL 46374) [c, 1]	USA	EF429227	EF429244	KF444763	ND
F. maxonii Murrill					
MUCL 46017 [c, h] (= CRGF 182)	Cuba	EF429230	EF433559	GU461910	JQ087983
MUCL 46037 [c, h] (= CRGF 183)	Cuba	EF429231	EF433560	GU461911	JQ087982
MUCL 51331 [c, h]	Argentina	KF444714	KF444691	KF444764	KF444737
MUCL 51540 [c, h]	Cuba	KF444715	KF444692	KF444765	KF444738
MUCL 51399 [c, h]	Cuba	KF444716	KF444693	KF444766	KF444739
MUCL 52340 [c, h]	Mexico	KF444717	KF444694	KF444767	KF444740
MUCL 53364 [c, h]	Mexico	KF444718	KF444695	KF444768	KF444741
F. mediterranea M. Fisch.					
AFTOL ID 688	ND	AY684157	AY854080	AY885149	AY803748
MUCL 38514	Italy	AY618201	GU461953	GU461912	JQ087984
MUCL 45670 [c, h]	France	GU461980	GU461954	GU461913	JQ087985
Fomitiporia neotropica Campos Santana *et al.*					
MUCL 53114 [c, h]	French Guiana	JX093836	JX093792	JX093749	JX093880
MUCL 49549 [c, h, 7]	Argentina	KF444719	KF444696	KF444769	KF444742
MUCL 54246 [c, h]	Brazil	KF444720	KF444697	KF444770	KF444743
MUCL 51335 (T) [c, h]	Argentina	KF444721	KF444698	KF444771	KF444744
MUCL 51336 [c, h]	Argentina	KF444722	KF444699	KF444772	KF444745
MUCL 54206 [c, h]	Brazil	KF444723	KF444700	KF444773	KF444746
MUCL 54196 [c, h]	Brazil	KF444724	KF444701	KF444774	KF444747
MUCL 54212 [c, h]	Brazil	KF444725	KF444702	KF444775	KF444748
F. nobilissima Decock & Yombiyeni					
MUCL 47580 [c, h]	Gabon	GU461985	GU461966	GU461921	JQ087986
MUCL 51289 (T) [c, h]	Gabon	GU461984	GU461965	GU461920	JQ087987
F. polymorpha M. Fisch.					
91-42/3 (MUCL 46166) (PT) [c, 5]	USA	DQ122393	GU461955	GU461914	JQ087988
91-42/1 (MUCL 46167) (PT) [c, 5]	USA	EF429233	GU461956	GU461915	JQ087989
F. pseudopunctata (A. David *et al.*) Fiasson					
MUCL 51325 [c, 2]	Czech Rep.	GU461981	GU461948	GU461916	JQ087998
MUCL 46168 [c, h]	France	JQ087918	JQ087891	JQ087945	JQ087999
Fomitiporia PS 4					
MUCL 53993	Mexico	JX093851	JX093807	JX093764	JX093893
MUCL 53994	Mexico	JX093852	JX093808	JX093765	JX093894
Fomitiporia PS 5					
MUCL 51555 [c, h]	Martinique	JX093853	JX093809	JX093766	JX093895
MUCL 53797 [c, h]	French Guiana	JX093854	JX093810	JX093767	JX093896
Fomitiporia PS 6					
MUCL 53798 [c, h]	French Guiana	JX093855	JX093811	JX093768	JX093897

Table 1. List of species, specimens/cultures, and sequences accession number (GenBank) included in the phylogenetic analyses *(continued)*

Genus/species names *Voucher specimens/cultures reference*		*GenBank accession number*			
	Locality	*nLSU*	*ITS*	*tef1-α*	*rpb2*
Fomitiporia PS 8					
MUCL 47756 $^{c, h, 7}$	Argentina	JQ087913	JQ087886	JQ087940	JQ087993
MUCL 47757 $^{c, h, 7}$	Argentina	JQ087914	JQ087887	JQ087941	JQ087994
MUCL 47758 $^{c, h, 7}$	Argentina	JQ087915	JQ087888	JQ087942	JQ087995
Fomitiporia PS 10					
CBS 386.66 = MUCL 46181 $^{c, 6}$	Argentina	EF429234	EF433563	GU461930	JQ088007
MUCL 53675 $^{c, h}$	French Guiana	JX093835	JX093791	JX093748	JX093879
F. punctata (Fr.) Murrill					
MUCL 34101 $^{c, h}$	Germany	AY618200	GU461947	GU461917	JQ088000
WD-2055 (MUCL 47629) $^{c, 3}$	Japan	GU461982	GU461950	GU461918	JQ088001
71-8 298 (MUCL 53548) $^{c, 4}$	Europe	JX093834	JX093790	JX093747	JX093878
F. punicata Y.C. Dai et *al.*					
Cui 23	China	GU461991	GU461974	GU461927	JQ088002
Cui 26	China	GU461992	GU461975	GU461928	JQ088003
F. robusta (P. Karst.) Fiasson & Niemelä					
CBS 389.72 (MUCL 51297) $^{c, 6}$	Estonia	JQ087919	JQ087892	JQ087946	JQ088004
Tomšovský 1013 (MUCL 51327) $^{c, 2}$	Czech Rep.		GU461993	GU461949	GU461929
Fomitiporia sonorae (Gilb.) Y.C. Dai					
RLG-10862-Sp (MUCL 47689) (T) $^{c, 1}$	USA	JQ087920	JQ087893	JQ087947	JQ088006
Fomitiporia "sp."					
FP-98505-T (MUCL 51105) $^{c, 1}$	USA	JQ087911	JQ087884	JQ087938	JQ087991
RLG-10827 (MUCL 51106) $^{c, 1}$	USA	JQ087910	JQ087883	JQ087937	JQ087990
F. tabaquilio (Urcelay *et al.*) Decock & Robledo					
MUCL 46230 $^{c, h, 7}$	Argentina	DQ122394	GU461940	GU461931	JQ088008
MUCL 47754 $^{c, h, 7}$	Argentina	GU461994	GU461941	GU461932	JQ088009
F. tenuis Decock *et al.*					
MUCL 44802 (T) $^{c, h}$	Ethiopia	AY618206	GU461957	GU461934	JQ088010
MUCL 49948 $^{c, h}$	Gabon	GU461998	GU461958	GU461935	JQ088011
MUCL 49971 $^{c, h}$	Uganda	GU461998	GU461958	GU461935	JQ088012
Fomitiporia texana (Murrill) Nuss					
RLG-7763-T (MUCL 47690) $^{c, 1}$	USA	JQ087921	JQ087894	JQ087948	JQ088013
FP-89674-R (MUCL 51143) $^{c, 1}$	USA	JQ087922	JQ087895	JQ087949	JQ088014
Fomitiporia torreyae Y.C. Dai & B.K. Cui					
WD-199 (MUCL 47628) $^{c, 3}$	Japan	JQ087923	JQ087896	JQ087950	JQ088015
WC31 ^{h}	Chine	JQ087924	JQ087897	JQ087951	JQ088016
Fomitiporia tsugina Murrill					
Ft_San (MUCL 52702)	USA	JQ087925	JQ087898	JQ087952	JQ088017
Ft_T2-1 (MUCL 52703)	USA	JQ087926	JQ087899	JQ087953	JQ088018
CBS125.40 (MUCL 51295) $^{c, 6}$	USA	JQ087908	JQ087881	JQ087935	JQ087974
Phellinus juniperinus Bernicchia & S. Curreli					
MUCL 51757 $^{c, h}$	Tunisia	JQ087927	JQ087900	JQ087954	JQ088019
MA-PA01 $^{c, h}$	Italy	KF444726	KF444703	KF444776	KF444749
MA-PA02 $^{c, h}$	Italy	KF444727	KF444704	KF444777	KF444750
P. uncisetus Robledo et al.					
MUCL 46231 $^{c, h}$	Argentina	EF429235	GU461960	GU461937	JQ088020
MUCL 47061 $^{c, h}$	Argentina	GU462000	GU461972	GU461938	JQ088021

T, PT = type, paratype.

^{c} = culture available; ^{h} = voucher herbarium specimen corresponding to the culture available at the MUCL herbarium; ^{1} cultures from CFMR, USDA, USA, courtesy of Dr. K. Nakasone); ^{2} cultures from Faculty of Forestry and Wood Technology, Mendel University of Agriculture and Forestry in Brno, Czech Republic, courtesy of Dr. M. Tomšovský; ^{3} cultures from Microbial Ecology Lab Forestry and Forest Products Research Institute, courtesy of Prof. T. Hattori, Japan; ^{4} cultures from National History Museum, University of Tartu, Estonia, courtesy of K. Põldmaa; ^{5} cultures courtesy of Dr. M. Fischer, Germany; ^{6} cultures from the CBS, The Netherlands, courtesy of Prof. P. Crous; ^{7} cultures from Colección de Cultivos Córdoba, Instituto Multidisciplinario de Biología Vegetal, Córdoba, Argentina, courtesy of Dr. G. Robledo; ^{8} cultures courtesy of Dr. I. Pascoe, Primary Industries Research Victoria, VPRI, Australia.

Phylogenetic analyses were performed separately for each locus and concatenated with Bayesian inference as implemented in MrBayes 3.1.2 (Ronquist and Huelsenbeck 2003), and Maximum likelihood (ML) as implemented in RAxML 7.0.4 (Stamatakis *et al*. 2008). *Phellinus uncisetus* was designated as outgroup (Decock *et al.* 2007). Models of evolution for Bayesian inference were estimated with the Akaike information criterion (AIC) as implemented in Modeltest 3.7 (Posada and Crandall 1998). The dataset was subdivided into 10 data partitions: ITS1, 5.8S, ITS2, nucLSU, *tef1* 1st and 2nd codon position, *tef1* 3rd codon position, *tef1* introns, *rpb2* 1st and 2nd codon position, *rpb2* 3rd codon position, and the recoded indels (Table II). The best-fit models for each partition were implemented as partition-specific models within partitioned mixed-model analyses of the combined dataset. Three optimal models of nucleotide substitution were selected for ITS regions, the GTR + G model was used for ITS1 and the HKY + G model for ITS2 while the K80 model was used for 5.8S. The GTR + I + G model was used for the nucLSU dataset, for the *rpb2* region (for the first and second codon and for the third codon position) and for the first and second codon position of the *tef1* region, while the GTR + G model was used for the third codon position and HKY + I for the *tef1* introns dataset. For analysis of SIC data under Bayesian inference, we used the MrBayes restriction site model (F81-like) as recommended by Ronquist *et al*. (2005). All parameters were unlinked across partitions. Bayesian analyses were implemented with two independent runs, each with four simultaneous independent chains for 6000000 generations, starting from random trees, and keeping one tree every 1000th generation. Before combining the data partitions, topological incongruence between the datasets was assessed using 1000 replicates of ML BS under the same models described above, on each locus separately. Paired trees were examined for conflicts only involving nodes with ML BS > 75% and Bayesian posterior probabilities (PP) > 95% (Lutzoni *et al.* 2004, Mason-Gamer and Kellogg 1996, Reeb *et al.* 2004). A conflict was assumed to be significant if two different relationships for the same set of taxa (one being monophyletic and the other non-monophyletic) were observed in rival trees.

Maximum likelihood (ML) searches conducted with RAxML involved 1000 replicates under the GTRGAMMAI model, with all model parameters estimated by the program. In addition 1000 bootstrap (ML BS) replicates were run with the same GTRGAMMAI model. We provided an additional alignment partition file to force RAxML software to search for a separate evolution model for each dataset including the recoded indels.

RESULTS

DNA sequence comparisons. – Sequence length and parsimony data for each dataset (length of aligned sequences, variable parsimony uninformative positions, parsimony informative positions, excluded characters) are summarized in Table II. As already evidenced by Decock *et al*. (2007) and confirmed by Amalfi *et al*. (2012) and Campos Santana *et al*. (2014), the species forming the *F. langloisii* lineage, namely *F. dryophila*, *F. langloisii*, *F. maxonii*, *F. neotropica*, *F. sonorae*, and an unnamed *Fomitiporia sp.* (MUCL 46181 and MUCL 53675) present a 31 bps long deletion near the 5' end of the ITS1 region. An identical deletion (in terms of length and position) is present in the ITS1 region of *Fomitiporia sp.* MUCL 55026. This deletion seems to be a plesiomorphic character inherited by all species of the *F. langloisii* lineage.

Table 2. Summary of data sets of ITS rDNA, LSU rDNA, *tef1* and *rpb2*

	Datasets									
Properties	*ITS 1*	*5.8S*	*ITS 2*	*nLSU*	*tef1 1st/2nd*	*tef1 3rd*	*tef1introns*	*rpb2 1st/2nd*	*rpb2 3rd*	*Indels*
Alignment size	508	159	348	970	663	331	231	542	271	449
Variable parsimony uninformative positions	30	12	18	32	10	29	12	12	8	115
Parsimony informative positions	197	9	122	119	26	209	122	41	226	282
Excluded characters	36	–	–	–	–	–	–	–	–	–
Model selected	GTR+G	K80	HKY+G	GTR+I+G	GTR+I+G	GTR+G	HKY+G	GTR+I+G	GTR+I+G	F81-like
Likelihood score	–3192.5922	–358.0664	–2097.8201	– 3013.7699	–1308.5839	–3387.6094	–1921.3866	–1372.9069	–5234.7168	–
Base frequencies										
Freq. A =	0.2682	Equal	0.2512	0.2670	0.3079	0.1497	0.2754	0.2922	0.2306	–
Freq. C =	0.1845	Equal	0.1783	0.1993	0.2212	0.3127	0.1980	0.2138	0.1870	–
Freq. G =	0.1953	Equal	0.2014	0.2897	0.2629	0.2333	0.1561	0.2767	0.2960	–
Freq. T =	0.3520	Equal	0.3691	0.2440	0.2080	0.3043	0.3705	0.2173	0.2863	–
Proportion of invariable sites	–	–	–	0.4760	0.8604	–	–	0.7746	0.0787	–
Gamma shape	0.6470	–	0.4620	0.3330	0.8073	1.5346	3.9120	0.7535	2.1687	–

Individual dataset comparisons. – Sequence data and statistical analysis for each dataset and combined analysis are provided (Table II).

By comparing the tree topologies obtained for the individual datasets, no conflict involving significantly supported nodes was found using the reciprocal 75% ML BS and 95% PP criterion; the datasets were therefore combined.

Combined dataset analysis. – Thirty six characters in the ITS1 region were judged too ambiguous to be aligned. The two Bayesian runs converged to stable likelihood values after 645000 generations. 5355 stationary trees from each analysis were used to compute a 50% majority rule consensus tree in PAUP* 4.0b10 (Swofford 2003) and to calculate posterior probabilities (PP). In the ML searches with RAxML the combined dataset alignment had 2008 distinct patterns with a proportion of gaps and undetermined characters of 12.41%.

The topologies obtained analysing the individual dataset are highly congruent with published trees (Amalfi *et al.* 2010, 2012, Amalfi and Decock 2013, Campos Santana *et al*. 2014) and almost identical to the Bayesian consensus tree and to the optimal tree inferred under the Maximum likelihood criterion (-lnL = -27093.377, Fig. 1). The results of the phylogenetic inferences, independently of analyzing the data sets individually or combined, were highly congruent and resolve the same clades and lineages as previously reported (Amalfi and Decock 2013, Amalfi *et al*. 2010, 2012, Campos Santana *et al*. 2013).

The collection MUCL 55026, originating from French Guiana, formed a new lineage within the *F. langloisii* clade (Fig. 1, PS 9).

Morphological analysis. – The collection MUCL 55026 shows a singular combination of morphological features, thereby defining also one morphospecies. This includes especially a widely effused basidiomata, extending over 1 m long and a bright greyish to pale brownish grey pore surface. There are no known *Fomitiporia* species developing such extended, effused basidiomata and a greyish pore surface when actively growing. The basidiospores are typical of *Fomitiporia*, subglobose to obovoid, slightly thick-walled, dextrinoid, and cyanophilous. Their size range is mainly 5.5-6.3 × 5.0-5.7 µm (ave = 6.0 × 5.5 µm).

Given the results of the phylogenetic inferences that identify our collection as a phylogenetic species (Fig. 1, PS 9), and the morphological data that define a unique morphotype, PS 9 is considered as representing a distinct species. The search for a possible epithet within the synonyms of *F. punctata* (Decock *et al.* 2007, Robert *et al.* 2005) yielded no name that could apply to it. We therefore propose below this species as *Fomitiporia expansa sp. nov.*

TAXONOMY

Fomitiporia expansa Decock & Amalfi, *sp. nov.* Figs 2-4

MYCOBANK: MB 807669

Etymology: "*expansa*" refers to the extended, effused basidiomata.

Basidiomata perennial, resupinate, widely effused, following the substrate, adnate, extending up to > 100 cm long in the longest extension, 30 cm wide, 1.5-5 mm in the thickest part, with a corky consistency, fibrous, coriaceous texture when fresh, drying corky, light in weight; *margin* narrow, thin or slightly rounded in upper part, densely and very minutely velutinous, reddish to ferruginous brown (7D7, brick red, 8[D-E]6, reddish brown); *pore surface* bright greyish (4[B-C]1,

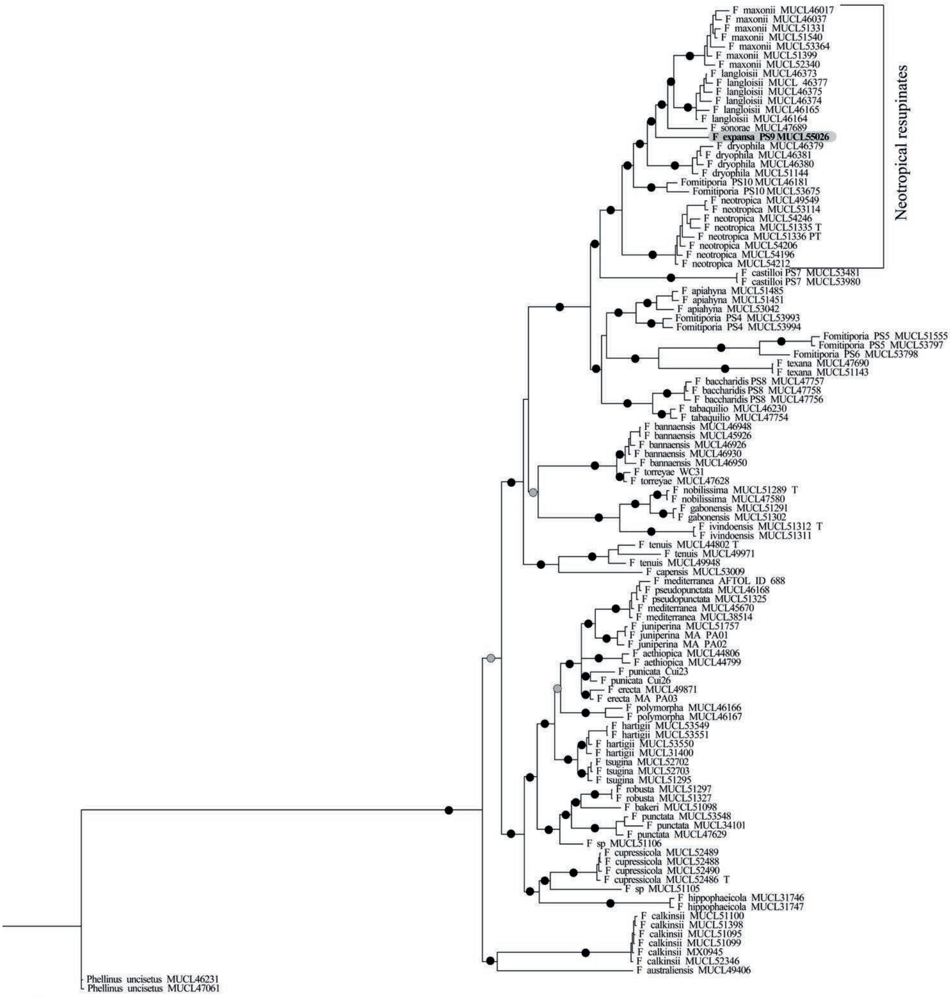

Fig. 1. The 50% majority-rule consensus tree from Bayesian inference of the combined ITS, LSU, *tef1* and *rpb2* sequences. Black dots on branches represent PP and ML BS of 99% or higher; grey dots on branches denote PP greater than 85% and ML BS greater than 75%.

greyish white to light grey), orange grey to brownish grey when actively growing (5B[2-4], 5C2, marble white, greyish orange, birch grey), drying cork to light brown, with sterile patches light reddish brown to ferruginous brown (7D7, brick red, 8[D-E]6, reddish brown); *pores* round to mostly ellipsoid, elongated, strongly stretched in most parts, mostly 5-6/mm, (100-) 135-175 µm diam (ave = 148 µm); *dissepiments* entire, with free hyphal tips, occasionally pruinose due to crystal cover, thin to thick, 120-240 µm diam; *subiculum* indistinct fusing with the underneath decaying wood or when discernible 100-500 µm thick, homogeneous, densely fibrous, light brown (6D[6-7], cinnamon, autumn leaf); *tubes* up to 5 mm thick, probably multilayered but layers mostly indistinct, darker than the pore surface, greyish brown to brown, the oldest parts mottled with white stuff.

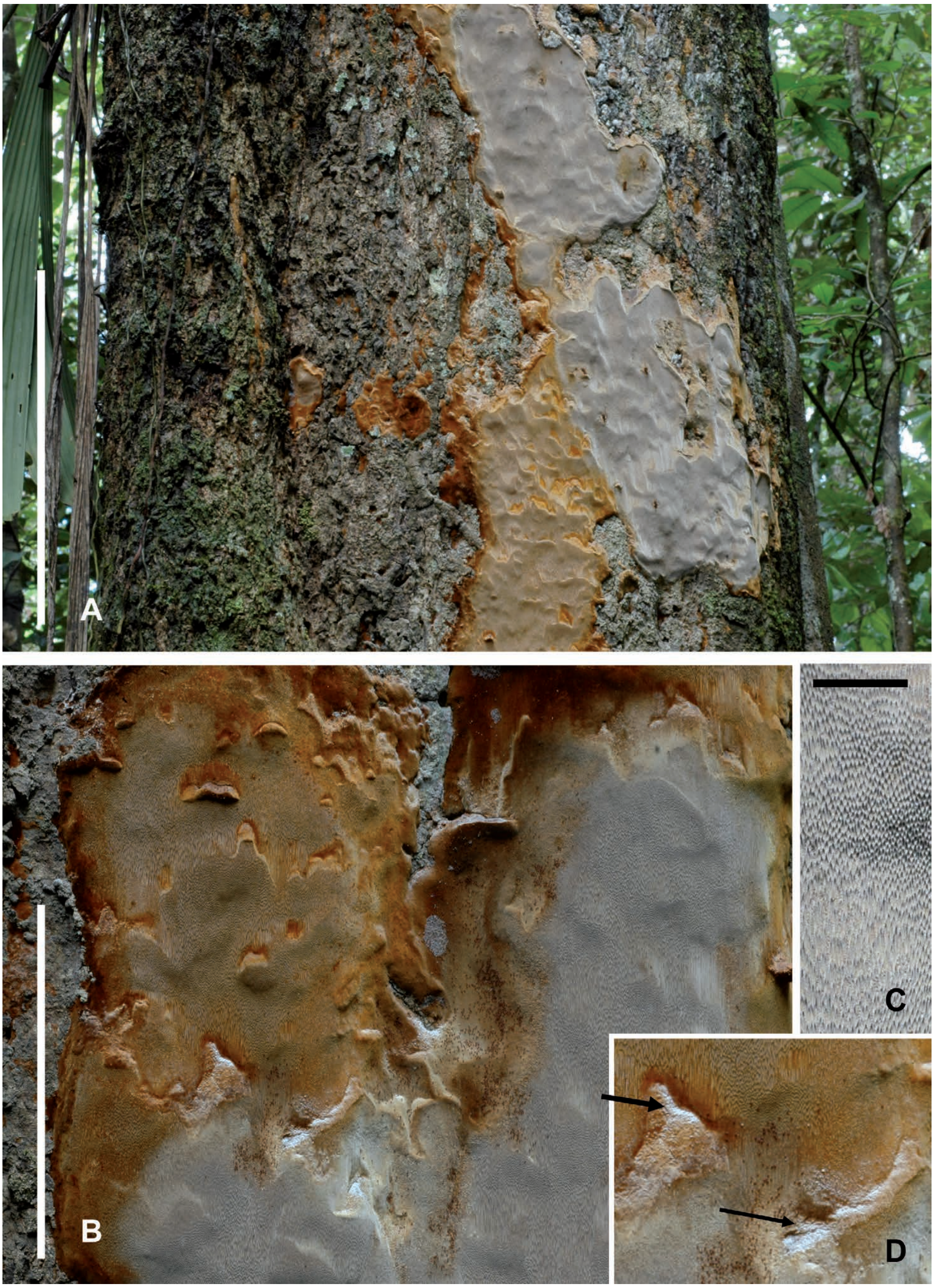

Fig. 2. *Fomitiporia expansa*, basidiomata *in situ* (MUCL 55026). A, B. Actively growing basidiomata (A, scale bar = 5 cm; B, scale bar = 2 cm). C. Detail of the pore surface (scale bar = 5 cm). D. White basidiospores print (arrow).

Hyphal system dimitic, identical in the context and hymenophoral trama; *generative hyphae* hyaline to faintly yellow, thin-walled, sparsely branched 1.5-2.5 (-3) µm wide (ave = 2.0 µm), *skeletal hyphae* pale yellow brown to golden brown, thick-walled but with an open lumen, 2.5-4.0 µm wide (ave = 3.2 µm), tightly packed in the hymenophoral trama.

Hymenium: *basidia* pyriform to subglobose, 7.0-10 × 6.0-9.0 µm, with four small sterigmata; *basidioles* identical in shape but slightly smaller; *hymenial setae* absent; *basidiospores* subglobose to broadly obovoid, 5.5-6.3 (- 6.6) × 5.0-5.7 µm (ave = 6.0 × 5.5 µm) Q = 1.0-1.2 (ave_Q = 1.1), thick-walled, the wall hyaline, cyanophilous, strongly dextrinoid; *basidiospores print* white; *chlamydospore* absent.

Type of rot: white rot.

Substrate and host: known from a dead standing trunk, unidentified angiosperm.

Specimen examined: FRENCH GUIANA, MUNICIPALITY OF MARIPASOULA: rainforest along the Marouini river valley, approx. 02,73103° N, 054.01610° W, elev. approx. 130 masl, on a dead standing trunk, approx. 70-80 cm diam. at 1 m high, broken at about 4 m high, unidentified angiosperm, 07 Jul. 2013, *C. Decock*, *FG-13-658* (HOLOTYPE NY, Isotype MUCL 55026, CAY; culture ex-holotype MUCL 55026; CBS).

Commentary: The combination of a resupinate, effused, extended basidiomata, a greyish to light greyish brown pore surface, 5-6 pores/mm, absence of setae, and basidiospores averaging 6.0 × 5.5 µm characterized *F. expansa*.

In a phylogenetic perspective, *F. expansa* nests within the *F. langloisii* lineage as defined first by Decock *et al*. (2007) and repeatedly confirmed (Amalfi *et al*. 2012, Amalfi and Decock 2013, Campos Santana *et al*. 2014. This lineage contains in addition to *F. langloisii* the species *F. dryophila*, *F. maxonii*, *F. neotropica*, *F. sonorae*, and a still unnamed taxon (PS 10, Fig. 1). The latter is known from two cultures, which voucher specimens originated from Argentina and French Guiana. The *F. langloisii* lineage is composed of species with resupinate basidiomata. This lineage is more likely endemic to the Neotropics; its distribution extends from the subtropical belt of south-eastern USA down to Argentina and Southern Brazil.

Morphologically and ecologically, *F. expansa* should be compared to *F. neotropica*; both species are likely to occur sympatrically in French Guiana. It could be also compared to *F. maxonii*, which has a wide distribution range in the Neotropics.

Campos Santana *et al.* (2014) described *F. neotropica* on the basis of a set of South American specimens, including collections from French Guiana. *Fomitiporia neotropica* differs from *F. expansa* in having much less extended basidiomata, with a distinctly brown pore surface and smaller pores, mostly 6-9/mm (75-145 µm diam) (Campos Santana *et al*. 2014). *Fomitiporia neotropica* also presents, although very occasionally, hymenial setae (Campos Santana *et al.* 2014).

Fomitiporia neotropica and *F. expansa* both inhabit the same rainforest ecosystem in French Guiana but they might differ by some autecological features, or niche specialization. The specimen of *F. expansa* was found on a large (70-80 cm diam at 1 m high), dead but standing trunk (Fig. 2). In French Guiana, *F. neotropica* was found repeatedly on fallen, decayed branches or liana of a diam < to approximately 10 cm diam. It may grow initially on branches (living or dead) still attached to the tree, somewhere in the intermediate canopy; basidiomata are found on the ground when the rotten branches (or liana) are fallen down, but should be looked for in the intermediate canopy.

Fomitiporia maxonii was originally described by Murrill (1907) and redescribed by Decock *et al.* (2007). In comparison to *F. expansa*, *F. maxonii* has a much darker, commonly brown to dark brown pore surface and small pores (7-9 (-10)/mm, (80-) 90-120 (-130) µm) (Decock *et al.* 2007). It has not been found so far in the rainforest of French Guiana.

For the time being, three species of *Fomitiporia* with resupinate basidiomata are known from French Guiana: in addition to *F. neotropica* (Campos Santana *et al.* 2014) and *F. expansa*, a third unnamed species (PS 10, Fig. 1) is known from two cultures (of which one, MUCL 53675, is originating from the Nouragues Nature Reserve, French Guiana). For the time being, the voucher herbarium specimens are not available for phenotypic characterization. These species occurs sympatrically, in the rainforest, but might have distinct habitat specialization.

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