

New records and taxonomic notes on *Fomitiporia* (Hymenochaetaceae) in Taiwan

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ABSTRACT

Two species of *Fomitiporia*, *F. subtropica* and *F. torreyae*, are newly recorded in Taiwan based on morphological examinations and phylogenetic analyses of combined ITS and 28S rDNA sequences. Taxonomic notes on *F. bannaensis* and *F. punctata* are also provided, along with an identification key to the six species of *Fomitiporia* known in Taiwan.

Key words: Basidiomycota, Hymenochaetales, phylogeny, taxonomy, wood-decay fungi

Introduction

The genus *Fomitiporia* Murrill, typified by *F. langloisii* Murrill, is a polyporoid genus in the family Hymenochaetaceae (Hymenochaetales, Basidiomycota) (Murrill 1907; Wu et al. 2022b). It is characterized by resupinate to pileate basidiomata, a dimitic hyphal system with simple-septate generative hyphae, and thick-walled, smooth basidiospores that are dextrinoid and cyanophilous. The presence of cystidioles and hymenial setae varies among species. Members of *Fomitiporia* cause white rot on both living and dead woody hosts (Chen et al. 2025; Dai 2010; Dai et al. 2007; Fischer 2002; Yang et al. 2019; Yuan et al. 2023).

Species of *Fomitiporia* play important roles in

forest nutrient cycling, and some are economically significant plant pathogens. *Fomitiporia mediterranea* M. Fisch. and *F. torreyae* Y.C. Dai & B.K. Cui, for example, are known to cause severe trunk and root rot in various orchard and coniferous hosts (Chen et al. 2025; Dai et al. 2007; Fischer 2002; Yang et al. 2019; Yuan et al. 2023). In addition, several species, including *F. ellipsoidea* B.K. Cui & Y.C. Dai and *F. robusta* (P. Karst.) Fiasson & Niemelä, have been reported to possess medicinal or bioactive properties (Chen et al. 2025; Dai et al. 2009; Świdorski et al. 2025; Zan et al. 2015).

Traditionally, *Fomitiporia* was treated within *Phellinus* s.l., but molecular phylogenetic studies later supported its recognition as a distinct mon-

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ophyletic genus (Fischer and Binder 2004; Wagner and Fischer 2001). Recent studies have revealed high species diversity within the genus, particularly in subtropical and tropical regions (Chen and Cui 2017; Dai et al. 2021). Currently, 76 species are recognized worldwide, with South America harboring the highest species richness, with 24 reported species, followed by Asia with 22 documented species (Zhao et al. 2025).

In Taiwan, four species have previously been recorded: *Fomitiporia apiahyna* (Speg.) Robledo, Decock & Rajchenb. (Chang 1995) [as *Phellinus apiahynus* (Speg.) Rajchenb. & J.E. Wright], *F. bannaensis* Y.C. Dai (Shih et al. 2012), *F. punctata* (P. Karst.) Murrill (Ann et al. 2005; Chang et al. 1999) [as *Phellinus punctatus* (P. Karst.) Pilát], and *F. robusta* (P. Karst.) Fiasson & Niemelä (Sawada 1959) [as *Fomes robustus* P. Karst.]. In the present study, *F. subtropica* B.K. Cui & Hong Chen and *F. torreyae* Y.C. Dai & B.K. Cui are newly recorded in Taiwan. In addition, taxonomic notes on *F. bannaensis* and *F. punctata* are provided, together with an identification key to the six species of *Fomitiporia* known in Taiwan.

Materials and Methods

Morphological studies

The specimens examined in this study are deposited at the herbarium of the National Museum of Natural Science (TNM), Taichung, Taiwan. Basidiomata were photographed using a Canon EOS R digital camera. Free-hand thin sections of basidiomata were prepared and mounted in 5% potassium hydroxide (KOH) with 1% phloxine for microscopic observation and measurements. Microscopic observations were carried out using

a ZEISS Axioscope 5 microscope (Carl Zeiss, Germany) at magnifications up to 1000×. Melzer's reagent was used to test for amyloid and dextrinoid reactions (Shih et al. 2012).

DNA extraction, amplification, and sequencing

Genomic DNA was extracted from dried specimens using the Plant Genomic DNA Extraction Miniprep System (Viogene, Taiwan). The internal transcribed spacer (ITS) region was amplified with primer pairs ITS1/ITS4 or ITS1F/ITS4B (Gardes and Bruns 1993; White et al. 1990). The nuclear ribosomal large subunit (nLSU, 28S) region was amplified with the primer pair LR0R/LR5 (Cubeta et al. 1991; Vilgalys and Hester 1990). PCR amplification was performed under the following conditions: initial denaturation at 94°C for 5 min; 35 cycles of 94°C for 30 s, 55°C for 30 s, and 72°C for 1 min; and a final extension at 72°C for 7 min. Unpurified PCR products were sent to Genomics BioSci & Tech Co., Ltd. (New Taipei, Taiwan) for Sanger sequencing.

Phylogenetic analysis

Sequence alignments were performed using the G-INS-i algorithm in MAFFT v7 (Kato et al. 2019). Ambiguously aligned regions were removed using Gblocks 0.91b (Castresana 2000) implemented on the Phylogeny.fr platform, and the resulting alignments were manually adjusted in AliView v1.27 (Larsson 2014). The selection of reference sequences for *Fomitiporia* primarily followed Chen et al. (2025). Representative sequences were retrieved from GenBank, and *Neophellinus uncisetus* (Robledo, Urcelay & Rajchenb.) Y.C. Dai, F. Wu, L.W. Zhou, Vlasák & B.K.

Table 1. Species and sequences used in phylogenetic analyses. Newly generated sequences are shown in bold.

Species	Sample no.	GenBank accession no.		Location	References
		ITS	28S		
<i>Fomitiporia aethiopica</i>	MUCL 44777	GU478341	AY618204	Ethiopia	Amalfi et al. (2010)
<i>Fomitiporia aethiopica</i>	MUCL 44806	GU461944	AY618202	Ethiopia	Amalfi et al. (2010)
<i>Fomitiporia alpina</i>	Dai 15735	KX639627	KX639645	China	Wu et al. (2022a)
<i>Fomitiporia apiahyna</i>	MUCL 51485	GU461962	GU461996	Ecuador	Amalfi et al. (2010)
<i>Fomitiporia atlantica</i>	FLOR 47591	KU557529	–	Brazil	Li et al. (2016)
<i>Fomitiporia atlantica</i>	FLOR 58554	KU557528	KU557526	Brazil	Li et al. (2016)
<i>Fomitiporia australiensis</i>	VPRI 22859	AY624997	GU462001	Australia	Chen et al. (2021)
<i>Fomitiporia baccharidis</i>	MUCL 47756	JQ087886	JQ087913	Argentina	Amalfi et al. (2012)
<i>Fomitiporia baccharidis</i>	MUCL 47757	JQ087887	JQ087914	Argentina	Amalfi et al. (2012)
<i>Fomitiporia bakeri</i>	MUCL 51098	JQ087874	JQ087901	USA	Amalfi et al. (2012)
<i>Fomitiporia bambusarum</i>	ICN 200563	MN918544	MN918537	Brazil	Alves-Silva et al. (2020a)
<i>Fomitiporia bambusarum</i>	ICN 200564	MN918545	MN918538	Brazil	Alves-Silva et al. (2020a)
<i>Fomitiporia bambusipileata</i>	ICN 200559	MN918546	MN918539	Brazil	Alves-Silva et al. (2020a)
<i>Fomitiporia bambusipileata</i>	ICN 200557	MN918548	MN918541	Brazil	Alves-Silva et al. (2020a)
<i>Fomitiporia bannaensis</i>	MUCL 46926	KF444682	KF444705	China	Amalfi and Decock (2014)
<i>Fomitiporia bannaensis</i>	MUCL 46930	KF444683	KF444706	China	Amalfi and Decock (2014)
<i>Fomitiporia bannaensis</i>	WEI 17-355	PZ179826	PZ185140	Taiwan	This study
<i>Fomitiporia calkinsii</i>	MUCL 51099	KF444686	KF444709	USA	Amalfi and Decock (2014)
<i>Fomitiporia calkinsii</i>	MUCL 51398	KF444687	KF444710	USA	Amalfi and Decock (2014)
<i>Fomitiporia capensis</i>	MUCL 53009	JQ087890	JQ087917	South Africa	Amalfi et al. (2012)
<i>Fomitiporia capensis</i>	CMW 48613	MH599112	MH599122	South Africa	Tchoumi et al. (2020)
<i>Fomitiporia carpineae</i>	Dai 18023	MH930812	MH930810	China	Wu et al. (2022b)
<i>Fomitiporia castilloi</i>	MUCL FG10282	JQ087889	JQ087916	Guyana	Amalfi et al. (2012)
<i>Fomitiporia castilloi</i>	MUCL 53980	JX093786	JX093830	French Guiana	Amalfi and Decock (2013)
<i>Fomitiporia chilensis</i>	BAFC 52942	NR_164591	NG_068862	Chile	Rajchenberg et al. (2019)
<i>Fomitiporia chilensis</i>	CIEFAPcc586	MK131090	MK193751	Chile	Rajchenberg et al. (2019)
<i>Fomitiporia chilensis</i>	CIEFAPcc587	MK131094	MK193752	Chile	Rajchenberg et al. (2019)
<i>Fomitiporia conyana</i>	FLOR 58547	KU663298	KU663270	Brazil	Alves-Silva et al. (2020b)
<i>Fomitiporia conyana</i>	FLOR 58548	KU663299	KU663271	Brazil	Alves-Silva et al. (2020b)
<i>Fomitiporia cupressicola</i>	MUCL 52489	JQ087879	JQ087906	Mexico	Amalfi et al. (2012)
<i>Fomitiporia cupressicola</i>	MUCL 52490	JQ087880	JQ087907	Mexico	Amalfi et al. (2012)
<i>Fomitiporia deserticola</i>	JV 1209/40-J	KT381634	–	USA	Vlasák and Vlasák (2016)
<i>Fomitiporia deserticola</i>	JV 1209/41-J	KT381633	–	USA	Vlasák and Vlasák (2016)
<i>Fomitiporia deserticola</i>	JV 1209/46	KT381632	–	USA	Vlasák and Vlasák (2016)
<i>Fomitiporia dryophila</i>	MUCL 46380	EF429238	EF429219	USA	Decock et al. (2007)
<i>Fomitiporia dryophila</i>	MUCL 51144	KF444689	KF444712	USA	Amalfi and Decock (2014)
<i>Fomitiporia elegans</i>	FURB 44484	KU663320	–	Brazil	Alves-Silva et al. (2020b)
<i>Fomitiporia elegans</i>	FLOR 58556	KU663319	KU663293	Brazil	Alves-Silva et al. (2020b)
<i>Fomitiporia erecta</i>	MUCL 49871	GU461939	GU461976	France	Amalfi et al. (2010)
<i>Fomitiporia eucalypti</i>	Dai 18586A	MH971172	MH971217	Australia	Wu et al. (2022b)
<i>Fomitiporia eucalypti</i>	Dai 18682	MH971171	MH971216	Australia	Wu et al. (2022b)
<i>Fomitiporia expansa</i>	MUCL 55026	KJ401031	KJ401032	French Guiana	Amalfi and Decock (2014)
<i>Fomitiporia fissurata</i>	JV 1305/4-J	KT381629	–	USA	Vlasák and Vlasák (2016)
<i>Fomitiporia fissurata</i>	JV 1305/5-J	KT381630	–	USA	Vlasák and Vlasák (2016)
<i>Fomitiporia fissurata</i>	JV 1307/5-J	KT381631	–	USA	Vlasák and Vlasák (2016)
<i>Fomitiporia gabonensis</i>	MUCL 47576	GU461971	GU461990	Gabon	Amalfi et al. (2010)
<i>Fomitiporia gaoligongensis</i>	Cui 8261	KX639624	KX639642	China	Chen and Cui (2017)
<i>Fomitiporia gatesiae</i>	Dai 18680	MH971169	MH971214	Australia	Wu et al. (2022b)
<i>Fomitiporia gatesiae</i>	Dai 18681	MH971170	MH971215	Australia	Wu et al. (2022b)
<i>Fomitiporia hartigii</i>	MUCL 53551	JX093789	JX093833	Estonia	Amalfi and Decock (2013)

<i>Fomitiporia hesleri</i>	01-712/2	AY340031	–	USA	Fischer and Binder (2004)
<i>Fomitiporia hesleri</i>	01-77/4	AY340026	–	USA	Fischer and Binder (2004)
<i>Fomitiporia hippophaëicola</i>	MUCL 31746	GU461945	AY618207	Belgium	Amalfi et al. (2010)
<i>Fomitiporia hippophaëicola</i>	MUCL 31747	GU461946	GU461977	Belgium	Amalfi et al. (2010)
<i>Fomitiporia ignea</i>	TX15	MN108101	MN113927	USA	Brown et al. (2020)
<i>Fomitiporia ignea</i>	TX16	MN108102	MN113928	USA	Brown et al. (2020)
<i>Fomitiporia ivindoensis</i>	MUCL 51311	GU461952	GU461979	Gabon	Amalfi et al. (2010)
<i>Fomitiporia ivindoensis</i>	MUCL 51312	GU461951	GU461978	Gabon	Amalfi et al. (2010)
<i>Fomitiporia lagerstroemiae</i>	Dai 18335	MH930813	MH930811	Vietnam	Hyde et al. (2019)
<i>Fomitiporia langloisii</i>	MUCL 46375	EF429242	EF429225	USA	Decock et al. (2007)
<i>Fomitiporia maxonii</i>	MUCL 46017	EF433559	EF429230	Cuba	Decock et al. (2007)
<i>Fomitiporia maxonii</i>	MUCL 46037	EF433560	EF429231	Cuba	Decock et al. (2007)
<i>Fomitiporia nubicola</i>	FLOR 57850	KU663303	NG_073602	Brazil	Alves-Silva et al. (2020b)
<i>Fomitiporia nubicola</i>	FLOR 57857	KU663309	KU663282	Brazil	Alves-Silva et al. (2020b)
<i>Fomitiporia neotropica</i>	MUCL 53114	JX093792	JX093836	French Guiana	Amalfi and Decock (2013)
<i>Fomitiporia nobilissima</i>	MUCL 47580	GU461966	GU461985	Gabon	Amalfi et al. (2010)
<i>Fomitiporia nobilissima</i>	MUCL 51289	GU461965	GU461984	Gabon	Amalfi et al. (2010)
<i>Fomitiporia norbulingka</i>	Cui 9722	KU364419	KU364429	China	Chen et al. (2016)
<i>Fomitiporia norbulingka</i>	Cui 9770	KU364420	KU364430	China	Chen et al. (2016)
<i>Fomitiporia norbulingka</i>	Cui 9766	KU364417	KU364427	China	Chen et al. (2016)
<i>Fomitiporia ovoidospora</i>	Dai 18283	MH971167	MH971212	Vietnam	Wu et al. (2022b)
<i>Fomitiporia ovoidospora</i>	Dai 18349	MH971168	MH971213	Vietnam	Wu et al. (2022b)
<i>Fomitiporia pentaphylaxis</i>	Yuan 6012	JQ003900	JQ003901	China	Zhou and Xue (2012)
<i>Fomitiporia polymorpha</i>	MUCL 46166	GU461955	DQ122393	USA	Amalfi et al. (2010)
<i>Fomitiporia polymorpha</i>	MUCL 46167	GU461956	EF429233	USA	Amalfi et al. (2010)
<i>Fomitiporia pseudopunctata</i>	MUCL 38514	GU461953	AY618201	Italy	Amalfi et al. (2010)
<i>Fomitiporia pseudopunctata</i>	MUCL 45670	GU461954	GU461980	Italy	Amalfi et al. (2010)
<i>Fomitiporia pseudopunctata</i>	MUCL 51325	GU461948	GU461981	Czech Republic	Amalfi et al. (2010)
<i>Fomitiporia pseudopunctata</i>	MUCL 46168	JQ087891	JQ087918	France	Amalfi et al. (2012)
<i>Fomitiporia punctata</i>	MUCL 47629	GU461950	GU461982	Japan	Amalfi et al. (2010)
<i>Fomitiporia punctata</i>	Dai 15772	KX639629	KX639647	China	Wu et al. (2022b)
<i>Fomitiporia punctata</i>	GC 1604-95	PZ179827	PZ185141	Taiwan	This study
<i>Fomitiporia punicata</i>	Cui 26	GU461975	GU461992	China	Amalfi et al. (2010)
<i>Fomitiporia punicata</i>	Dai 7175	KX639632	KX639650	China	Wu et al. (2022b)
<i>Fomitiporia punicata</i>	Dai 10640	KX663825	KX639653	China	Wu et al. (2022b)
<i>Fomitiporia rhamnoides</i>	Dai 17369	MH234388	MH234391	China	Liu et al. (2018)
<i>Fomitiporia rhamnoides</i>	GL-2016	KT861405	KY697187	China	Liu et al. (2018)
<i>Fomitiporia rhamnoides</i>	Dai 18091	MH234389	MH234392	China	Liu et al. (2018)
<i>Fomitiporia robusta</i>	MUCL 51297	JQ087892	JQ087919	Estonia	Amalfi et al. (2012)
<i>Fomitiporia robusta</i>	MUCL 51327	GU461949	GU461993	Czech Republic	Amalfi et al. (2010)
<i>Fomitiporia subtilissima</i>	FURB 47557	NR_148098	NG_060426	Brazil	Unpublished
<i>Fomitiporia subtilissima</i>	FURB 47437	KU557530	–	Brazil	Unpublished
<i>Fomitiporia sonorae</i>	MUCL 47689	JQ087893	JQ087920	USA	Amalfi et al. (2012)
<i>Fomitiporia</i> sp.	MUCL 53993	JX093807	JX093851	Mexico	Amalfi and Decock (2013)
<i>Fomitiporia</i> sp.	MUCL 53994	JX093808	JX093852	Mexico	Amalfi and Decock (2013)
<i>Fomitiporia</i> sp.	MUCL 53798	JX093811	JX093855	French Guiana	Amalfi and Decock (2013)
<i>Fomitiporia spinescens</i>	ICN 200566	MN918549	–	Brazil	Alves-Silva et al. (2020a)
<i>Fomitiporia subhippophaëicola</i>	Cui 12096	KU364421	KU364426	China	Chen et al. (2016)
<i>Fomitiporia subhippophaëicola</i>	Cui 12102	KU364423	KU364424	China	Chen et al. (2016)
<i>Fomitiporia subrobusta</i>	Dai 13576	KX639617	KX639635	China	Wu et al. (2022b)
<i>Fomitiporia subrobusta</i>	Dai 13577	KX639618	KX639636	China	Wu et al. (2022b)
<i>Fomitiporia subtropica</i>	Cui 9122	KX639622	KX639640	China	Wu et al. (2022b)
<i>Fomitiporia subtropica</i>	Cui 9115	KX639623	KX639641	China	Wu et al. (2022b)
<i>Fomitiporia subtropica</i>	WEI 18-074	PZ185126	PZ185144	Taiwan	This study

<i>Fomitiporia subtropica</i>	Chen 3974	PZ185127	PZ185145	Taiwan	This study
<i>Fomitiporia tabaquilio</i>	MUCL 46230	GU461940	DQ122394	Argentina	Amalfi et al. (2010)
<i>Fomitiporia tabaquilio</i>	MUCL 47754	GU461941	GU461994	Argentina	Amalfi et al. (2010)
<i>Fomitiporia tasmanica</i>	Dai 18793	MH971173	MH971218	Australia	Wu et al. (2022b)
<i>Fomitiporia tasmanica</i>	Dai 18799	MH971174	MH971219	Australia	Wu et al. (2022b)
<i>Fomitiporia tenuis</i>	MUCL 44802	GU461957	AY618206	Ethiopia	Amalfi et al. (2010)
<i>Fomitiporia tenuis</i>	MUCL 49948	GU461958	GU461998	Uganda	Amalfi et al. (2010)
<i>Fomitiporia tenuitubus</i>	Dai 16204	KX639619	KX639637	China	Wu et al. (2022b)
<i>Fomitiporia tenuitubus</i>	Yuan 5736	JQ003902	JQ003903	China	Wu et al. (2022b)
<i>Fomitiporia texana</i>	MUCL 47690	JQ087894	JQ087921	USA	Amalfi et al. (2012)
<i>Fomitiporia texana</i>	MUCL 51143	JQ087895	JQ087922	USA	Amalfi et al. (2012)
<i>Fomitiporia torreyae</i>	MUCL WC31	JQ087897	JQ087924	China	Amalfi et al. (2012)
<i>Fomitiporia torreyae</i>	PES0201	LC333728	–	Japan	Unpublished
<i>Fomitiporia torreyae</i>	AP170	LC339480	–	Japan	Unpublished
<i>Fomitiporia torreyae</i>	WD2639	LC651678	–	Japan	Torii et al. (2021)
<i>Fomitiporia torreyae</i>	MUCL 47628	JQ087896	JQ087923	Japan	Amalfi et al. (2012)
<i>Fomitiporia torreyae</i>	GC 1412-2	PZ179828	PZ185142	Taiwan	This study
<i>Fomitiporia torreyae</i>	WEI 17-681	PZ179829	PZ185143	Taiwan	This study
<i>Fomitiporia torreyae</i>	GC 2109-14	PZ179830	–	Taiwan	This study
<i>Fomitiporia tsitsikamensis</i>	CMW 47881	MH599111	MH599121	South Africa	Tchoumi et al. (2020)
<i>Fomitiporia tsitsikamensis</i>	CMW 48058	MH599109	MH599120	South Africa	Tchoumi et al. (2020)
<i>Fomitiporia tsitsikamensis</i>	CMW 48621	MH599110	MH599123	South Africa	Tchoumi et al. (2020)
<i>Fomitiporia tsugina</i>	MUCL 52702	JQ087898	JQ087925	USA	Amalfi et al. (2012)
<i>Fomitiporia tsugina</i>	MUCL 52703	JQ087899	JQ087926	USA	Amalfi et al. (2012)
<i>Fomitiporia uncinata</i>	ICN 200561	–	MN918542	Brazil	Alves-Silva et al. (2020a)
<i>Neophellinus uncisetus</i>	MUCL 46231	GU461960	EF429235	Argentina	Amalfi et al. (2010)
<i>Neophellinus uncisetus</i>	MUCL 47061	GU461972	GU462000	Argentina	Amalfi et al. (2010)

Cui was used as the outgroup. All sequences included in this study are listed in Table 1.

Phylogenetic relationships were inferred using Maximum Likelihood (ML) and Bayesian Inference (BI) methods (Wu et al. 2022b). ML and BI analyses were conducted on the CIPRES Science Gateway platform (Miller et al. 2010) using RAxML-HPG BlackBox (Stamatakis 2014) and MrBayes v3.2.7a (Huelsenbeck and Ronquist 2001; Ronquist and Huelsenbeck 2003), respectively. For BI analyses, the best-fit substitution model for each locus was selected using jModel-Test2 (Guindon and Gascuel 2003; Posada 2008) based on the Akaike Information Criterion (AIC). The substitution models HKY+I+G and GTR+I+G were applied to the ITS and 28S partitions, respectively.

RESULTS AND DISCUSSION

Phylogenetic analyses

We generated 13 new sequences, including seven ITS and six 28S sequences, from seven specimens representing four species: *F. bannaensis* (WEI 17-355), *F. punctata* (GC 1604-95), *F. subtropica* (Chen 3974, WEI 18-074), and *F. torreyae* (GC 1412-2, GC 2109-14, WEI 17-681) (Table 1).

Phylogenetic analyses based on the combined ITS and 28S dataset (131 samples, 1,378 bp; ITS: 528 bp; 28S: 850 bp) recovered the major lineages of *Fomitiporia*, with generally congruent topologies between ML and BI analyses (Fig. 1). Therefore, only the ML tree is presented.

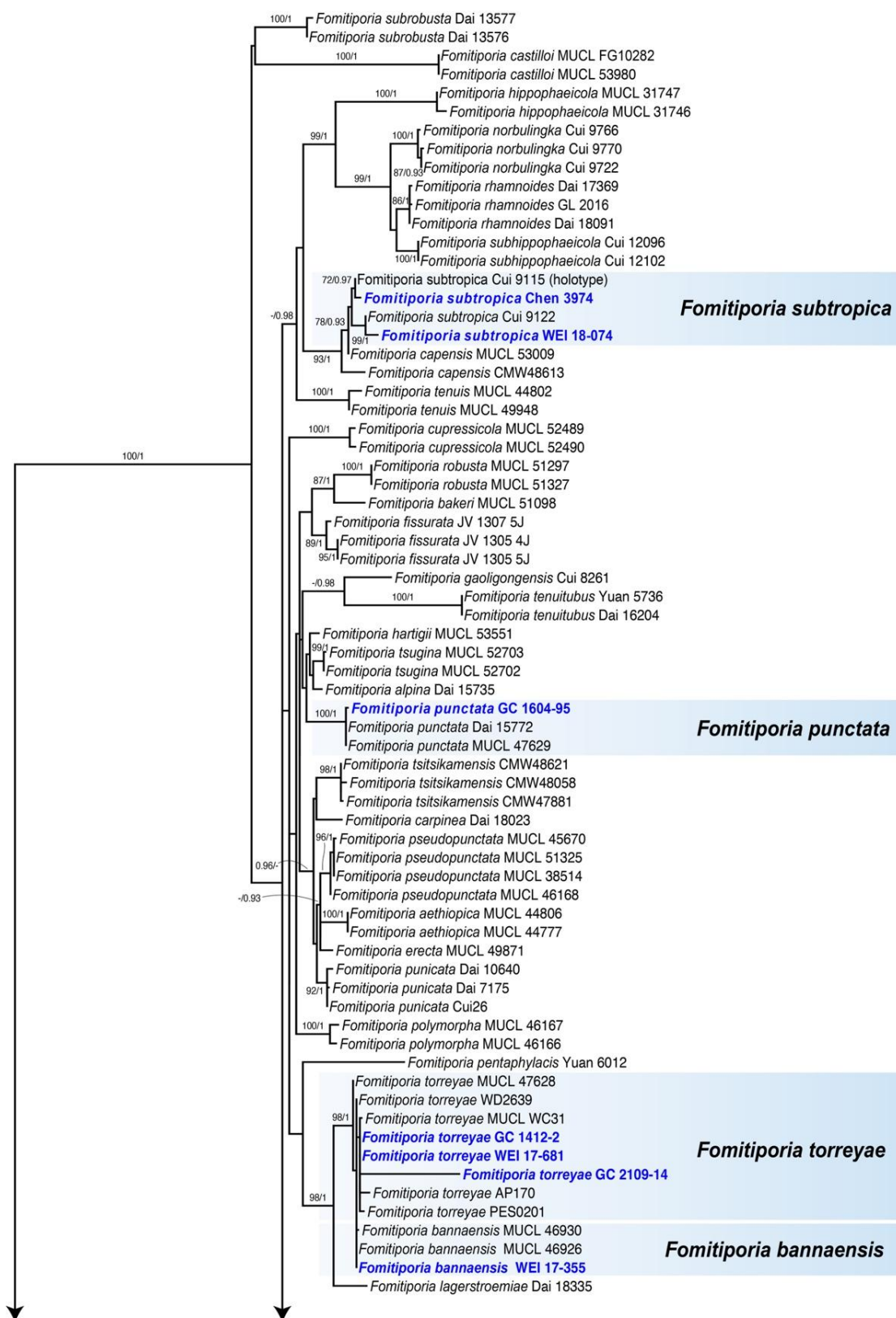


Fig. 1. Maximum likelihood phylogeny of *Fomitiporia* based on a combined ITS and 28S dataset. Branch support values are indicated by maximum likelihood bootstrap support (BS ≥ 70%) and Bayesian posterior probabilities (PP ≥ 0.9). Sequences newly generated in this study are shown in blue, bold italics. *Neophellinus uncisetus* was used as the outgroup. Scale bar = substitutions per site.

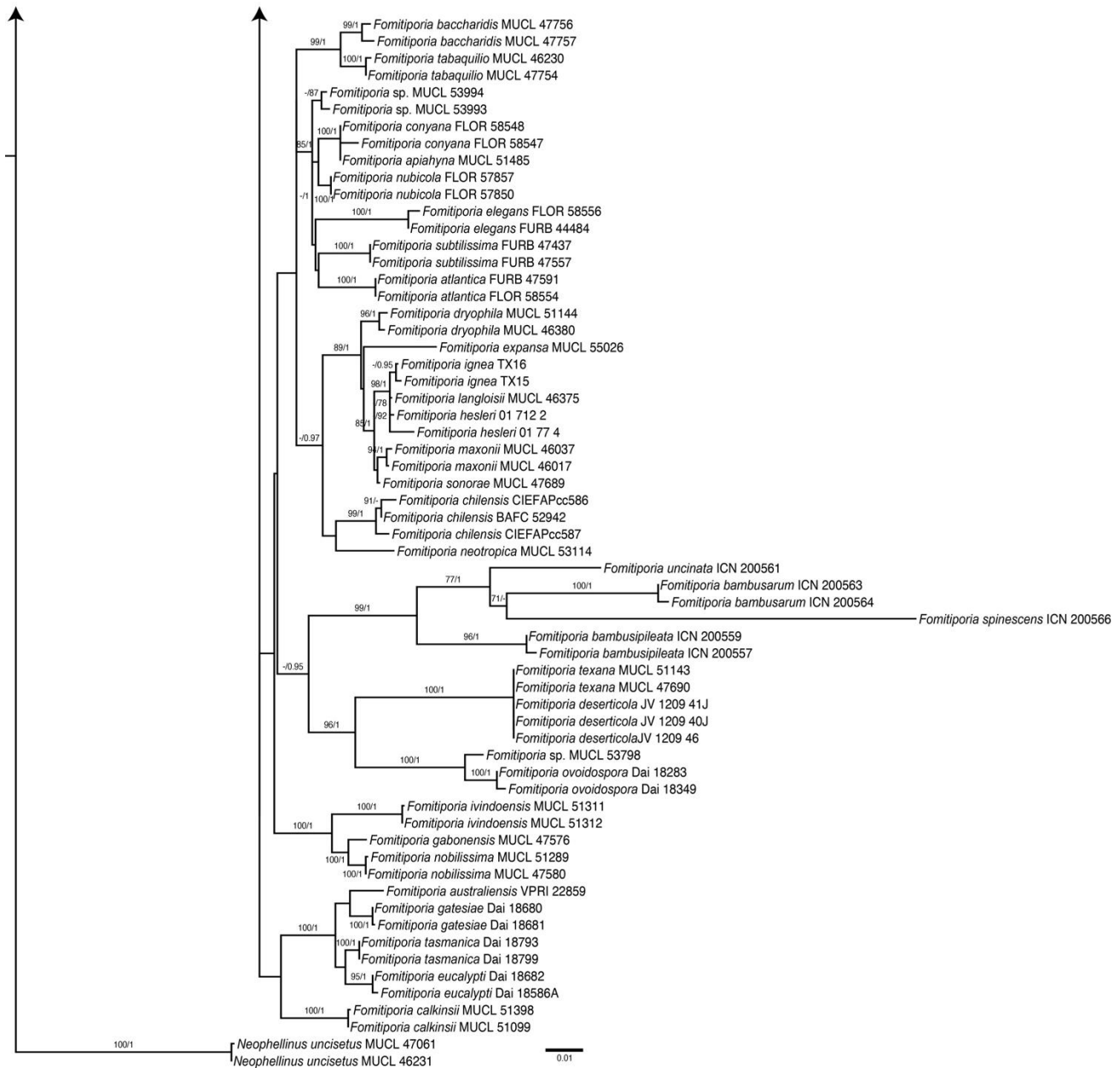


Fig. 1. (continued)

The Taiwanese specimens of *Fomitiporia subtropica* (WEI 18-074 and Chen 3974) clustered with the type strain of *F. subtropica* (Cui 9115, China) and an additional Chinese strain (Cui 9122, China). This lineage formed a clade with *F. capensis* M. Fisch., Cloete, L. Mostert & Halleen (MUCL 53009) (BS = 78%, PP = 0.93). In contrast, *F. punctata* (GC 1604-95) grouped with representative sequences from China (Dai 15772)

and Japan (MUCL 47629) in a well-supported clade (BS = 100%, PP = 1).

Fomitiporia torreyae (GC 1412-2, GC 2109-14, and WEI 17-681) clustered with sequences from China (MUCL WC31) and Japan (PES0201, AP 170, WD2639, and MUCL 47628), whereas *F. bannaensis* (WEI 17-355) grouped with sequences from China (MUCL 46926 and MUCL

46930). These two species formed a well-supported clade (BS = 98%, PP = 1) (Fig. 1), but were not recovered as distinct monophyletic lineages in the ITS-28S phylogeny, suggesting limited resolution of these loci at the species level.

Previous studies based on multilocus datasets, including ITS, 28S, translation elongation factor 1- α (*TEF1*), and the second largest subunit of RNA polymerase II (*RPB2*), have demonstrated that *F. torreyae* and *F. bannaensis* formed distinct, well-supported monophyletic lineages, supporting their recognition as separate species (Alves-Silva et al. 2020a; Amalfi and Decock 2013; Chen and Cui 2017; Ota et al. 2014). Similarly, *Fomitiporia subtropica* and *F. capensis*, although unresolved in the present study, have been shown to represent distinct species based on multilocus phylogenetic analyses (Chen and Cui 2017).

These results suggest that additional loci are required to fully resolve species boundaries within *Fomitiporia*. Despite the limited resolution of ITS and 28S, the species examined in this study can be reliably distinguished based on morphological characters.

Key to the species of *Fomitiporia* in Taiwan

1. Basidiomata resupinate 2
1. Basidiomata pileate or effused-reflexed..... 5
2. Basidiomata usually at mid to high elevations in Taiwan; pores 4–5 per mm; basidiospores $7-8 \times 6.5-7.5 \mu\text{m}$ *F. punctata*
2. Basidiomata usually at low elevations in Taiwan; pores 6–10 per mm; basidiospores $< 7 \mu\text{m}$ in length 3
3. Pores 8–10 per mm; hymenial setae present;

basidiospores $4.5-5.5 \times 4-5.5 \mu\text{m}$

..... *F. bannaensis*

3. Pores 6–8 per mm; hymenial setae present, rare, or absent 4

4. Basidiospores $5-6 \times 4.5-5.5 \mu\text{m}$; hymenial setae occasionally present *F. torreyae*

4. Basidiospores $5.5-6.5 \times 5-6 \mu\text{m}$; hymenial setae rare or absent *F. subtropica*

5. Basidiospores $6-8.5 \times 5.5-7 \mu\text{m}$; hymenial setae occasionally present (Núñez and Ryvar-den 2000)..... *F. robusta*

5. Basidiospores $5-6 \times 4.5-5 \mu\text{m}$; hymenial setae absent (Chang 1995)..... *F. apiahyna*

Taxonomy

Fomitiporia bannaensis Y.C. Dai, in Dai, Zhang & Zhou, Mycosystema 20: 17. 2001. Fig. 2

Description. See Ota et al. (2014).

Specimen examined. TAIWAN. Kaohsiung City, Maolin District, Shan-Ping Forest Ecological Garden, 730 m, on gymnosperm branch, 29 Jun 2017, C.C. Chen, C.L. Wei, W.C. Chen & Y.P. Chen, *WEI 17-355* (TNM F0032468).

Ecology and distribution. Causes white rot on dead or living angiosperm (e.g., *Ficus*) and gymnosperm wood from China (Fujian, Yunnan), Thailand, and Taiwan (Ota et al. 2014; Shih et al. 2012; Wu et al. 2022b; this study).

Notes. Shih et al. (2012) reported this species in Taiwan based on specimen *SYS 110807-3* (TNM F0026062). However, our re-examination indicates that this specimen does not correspond to *F. bannaensis*, although the description and illustrations provided by Shih et al. (2012) are generally

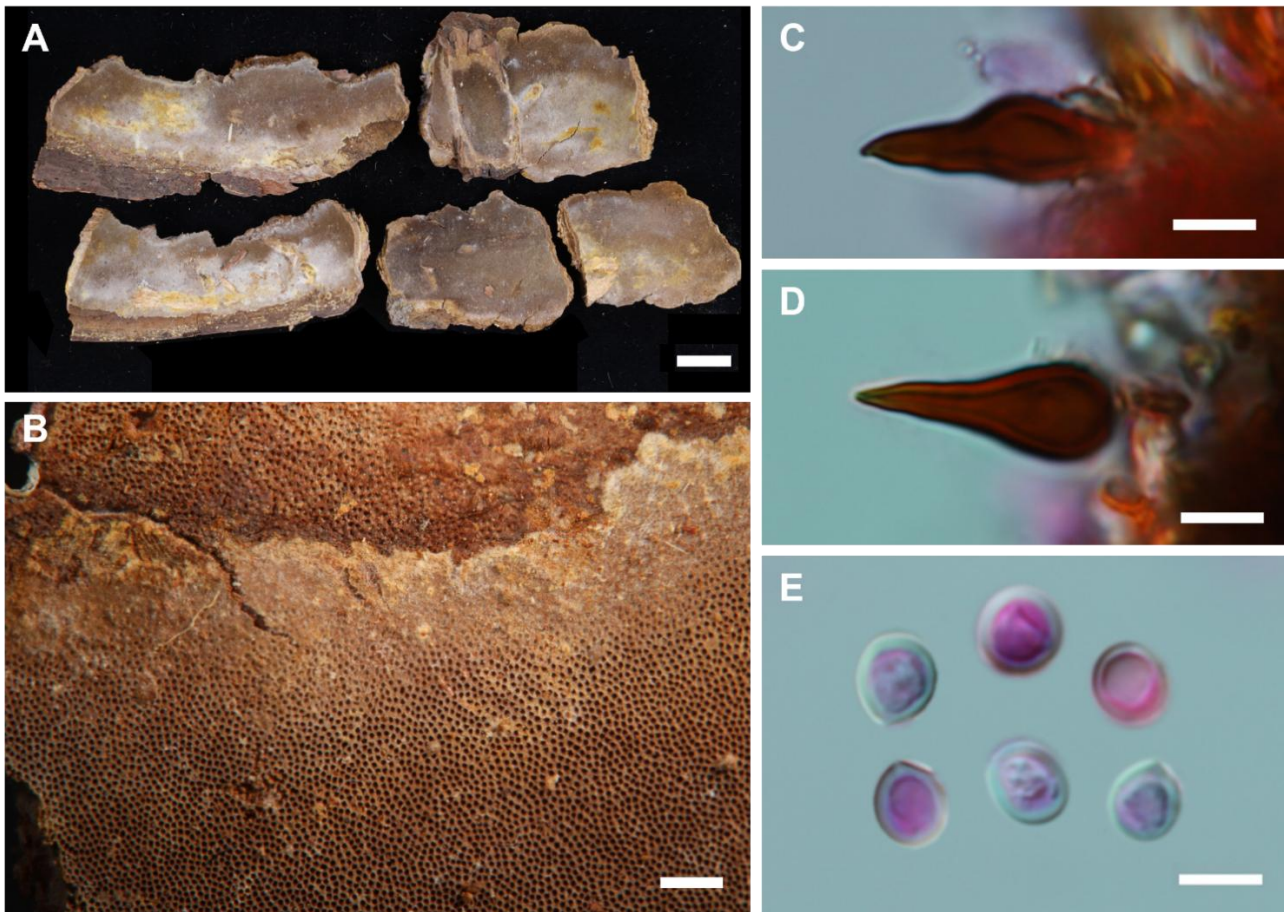


Fig. 2. *Fomitiporia bannaensis*. A–B. Dried basidiomata of *F. bannaensis* (WEI 17-355). C–D. Setae. E. Basidiospores. Scale bars: A = 10 mm; B = 1 mm; C–E = 5 μ m.

consistent with the species. The specimen has effused-reflexed basidiomata with 6–8 pores per mm, a dimitic hyphal system, numerous hymenial setae, and ellipsoid, thin-walled basidiospores lacking a dextrinoid reaction, measuring $3.5\text{--}5 \times 2\text{--}2.5 \mu\text{m}$. Based on these morphological features, it may represent a species of *Phellinus* s.s.

In Taiwan, *F. bannaensis* is characterized by resupinate basidiomata with a light brown pore surface (8–10 pores per mm), a dimitic hyphal system with simple-septate generative hyphae, hymenial setae $13\text{--}18 \times 5\text{--}8 \mu\text{m}$, and sub-globose, thick-walled basidiospores $4.5\text{--}5.5 \times 4\text{--}5.5 \mu\text{m}$, with a dextrinoid reaction. This species is similar

to *F. torreyae*; a detailed comparison is provided in the notes on *F. torreyae*.

Fomitiporia punctata (P. Karst.) Murrill, Lloydia 10: 254. 1947. Fig. 3

Description. See Decock et al. (2007).

Specimens examined. TAIWAN. Hsinchu County, Jianshi Township, Beidelaman-Neini-aozuishan Trail, 1300–1700 m, on angiosperm trunk, 1 Jan 2022, C.C. Chen, GC 2201-16 (TNM F0039125). Hualien County, Hsiulin Township, Taroko National Park, between 121–122 km of Provincial Highway No.8, $24^{\circ}11'N$, $121^{\circ}21'E$, 2460 m, on living trunk of *Salix taiwanalpina*, 23 Apr 2016, C.C. Chen, GC 1604-95 (TNM

F0030446, culture TNM V01061).

Ecology and distribution. Known to cause white rot on dead or living angiosperm wood in subtropical to temperate and boreal regions of the Northern Hemisphere (Asia, Europe, North America) (Decock et al. 2007; this study).

Notes. Ann et al. (2005) and Chang et al. (1999) reported this species as *Phellinus punctatus* from lowland areas in Taiwan, where it caused stem and root rot on *Juniperus chinensis* var. *kaizuka*, *Prunus mume*, and *Eriobotrya japonica*. According to Chang et al. (1999), the specimens were characterized by resupinate, yellowish-brown basidiomata up to 2 cm thick, a dimitic hyphal system with simple-septate generative hyphae, and ellipsoid to subglobose basidiospores measuring $5\text{--}6.5 \times 5\text{--}6.5 \mu\text{m}$ with a dextrinoid reaction. These features differ from the concept of Decock et al. (2007) of *F. punctata*, which has larger basidiospores $6.5\text{--}8.5 \times 5.5\text{--}7 \mu\text{m}$.

In the present study, *Fomitiporia torreyae* is confirmed to occur in lowland areas of Taiwan, where it causes stem rot on *J. chinensis* var. *kaizuka* (Figs. 5A–B). The morphological features of *Fomitiporia* reported by Chang et al. (1999) are consistent with those of *F. torreyae*, suggesting that their specimens likely represent this species.

In Taiwan, *Fomitiporia punctata* occurs in mid- to high-elevation regions and is characterized by resupinate basidiomata with 4–5 pores per mm, the absence of hymenial setae, and basidiospores measuring $7\text{--}8 \times 6.5\text{--}7.5 \mu\text{m}$ (Fig. 3).

Fomitiporia subtropica B.K. Cui & Hong Chen,

in Chen & Cui, Mycol. Progr. 16:697. 2017.

Fig. 4

Description. See Chen and Cui (2017).

Specimens examined. TAIWAN. Nantou County, Yuchih Township, Lienhuachih, $23^{\circ}56'N$, $120^{\circ}53'E$, 700 m, on angiosperm branch, 2 Jun 2018, S.Z. Chen, *Chen 3974* (TNM F0034515, culture TNM V01062). New Taipei City, Linkou District, Linkou Forest Trail, $121^{\circ}21'30"E$, $25^{\circ}5'28"N$, 200 m, on fallen angiosperm trunk, 1 May 2018, C.L. Wei, *WEI 18-074* (TNM F0033523).

Ecology and distribution. Causes white rot on dead or living angiosperm wood in subtropical regions of southern China (Guangdong) (Chen and Cui 2017) and Taiwan (this study).

Notes. In Taiwan, *Fomitiporia subtropica* is characterized by resupinate basidiomata with a yellowish-brown to pale brown pore surface (6–8 pores per mm) and subglobose to obovoid basidiospores ($5.5\text{--}6.5 \times 5\text{--}6 \mu\text{m}$) with a dextrinoid reaction. These measurements are slightly smaller than those reported in the protologue (6–10 pores per mm; basidiospores $5.2\text{--}6 \times 4.4\text{--}5 \mu\text{m}$) (Chen and Cui 2017), likely reflecting intra-specific variation.

Although *F. subtropica* was originally described as lacking hymenial setae, a few setae were occasionally observed in one Taiwanese specimen (*WEI 18-074*), measuring $23\text{--}28 \times 4.5 \mu\text{m}$ (Fig. 4C).

Fomitiporia subtropica resembles *F. capensis* but differs by its smaller pores (6–8 per mm vs. 4–6 per mm), thinner dissepiments, and smaller

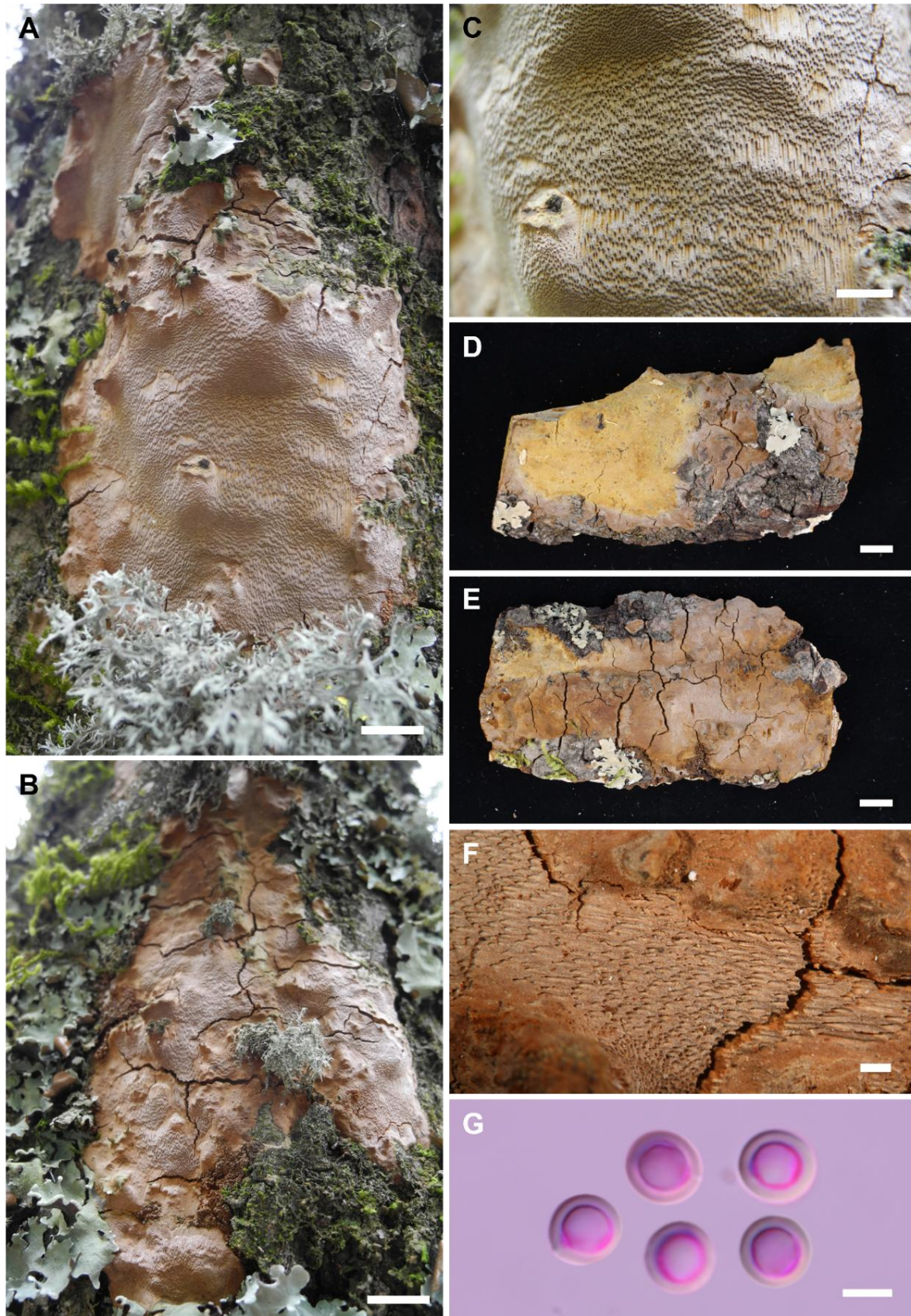


Fig. 3. *Fomitiporia punctata*. A–F. Basidiomata of *F. punctata* (GC 1604-95). A–C, in situ; D–F, dried specimens. G. Basidiospores. Scale bars: A–B, D–E = 10 mm; C = 5 mm; F = 1 mm; G = 5 μ m.

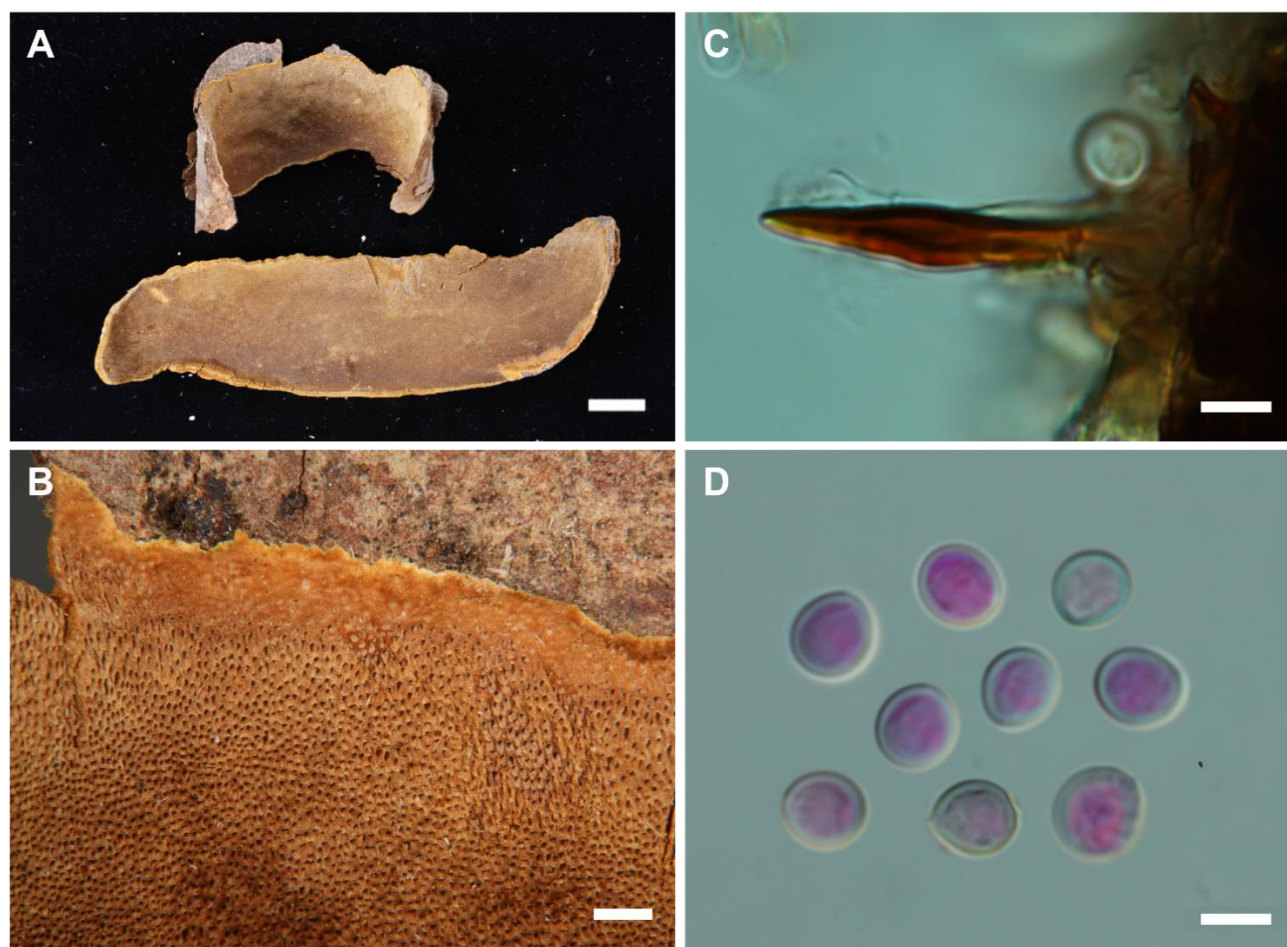


Fig. 4. *Fomitiporia subtropica*. A–B. Dried basidiomata of *F. subtropica* (WEI 18-074). C. Seta. D. Basidiospores. Scale bars: A = 10 mm; B = 1 mm; C–D = 5 μ m.

basidiospores ($5.5\text{--}6.5 \times 5\text{--}6 \mu\text{m}$ vs. $6.5\text{--}7.5 \times 5.5\text{--}7 \mu\text{m}$ in *F. capensis*). Furthermore, the two species differ in host preference: *F. capensis* is almost exclusively associated with *Vitis* spp., whereas *F. subtropica* occurs on a broader range of angiosperm hosts (Cloete et al. 2014; Chen and Cui 2017).

Fomitiporia torreyae Y.C. Dai & B.K. Cui, Mycotaxon 94:344. 2006. Fig. 5

Description. See Dai and Cui (2005) and Ota et al. (2014).

Specimens examined. TAIWAN. New Taipei City, Linkou District, Linkou Forest Trail, 200 m,

on living angiosperm trunk, 1 Oct 2017, C.L. Wei, C.T. Wei & M.Y. Huang, WEI 17-681 (TNM F0032623). Taichung City, Tungshih District, Huangcaogang, 470 m, on trunk of *Citrus* sp., 14 Dec 2014, C.C. Chen, GC 1412-2 (TNM F0028943, culture TNM V01064). Taipei City, Nangang District, Academia Sinica, $25^{\circ}02'34''\text{N}$, $121^{\circ}36'51''\text{E}$, 12 m, on living trunk of *Juniperus chinensis* var. *kaizuka*, 8 Sep 2021, C.C. Chen, GC 2109-14 (TNM F0039109).

Ecology and distribution. Causes white rot on a wide range of living angiosperm hosts (e.g., *Cinnamomum*, *Citrus*, *Cyclobalanopsis*, *Morus*, *Rhododendron*, and *Vitex*) and gymnosperm hosts

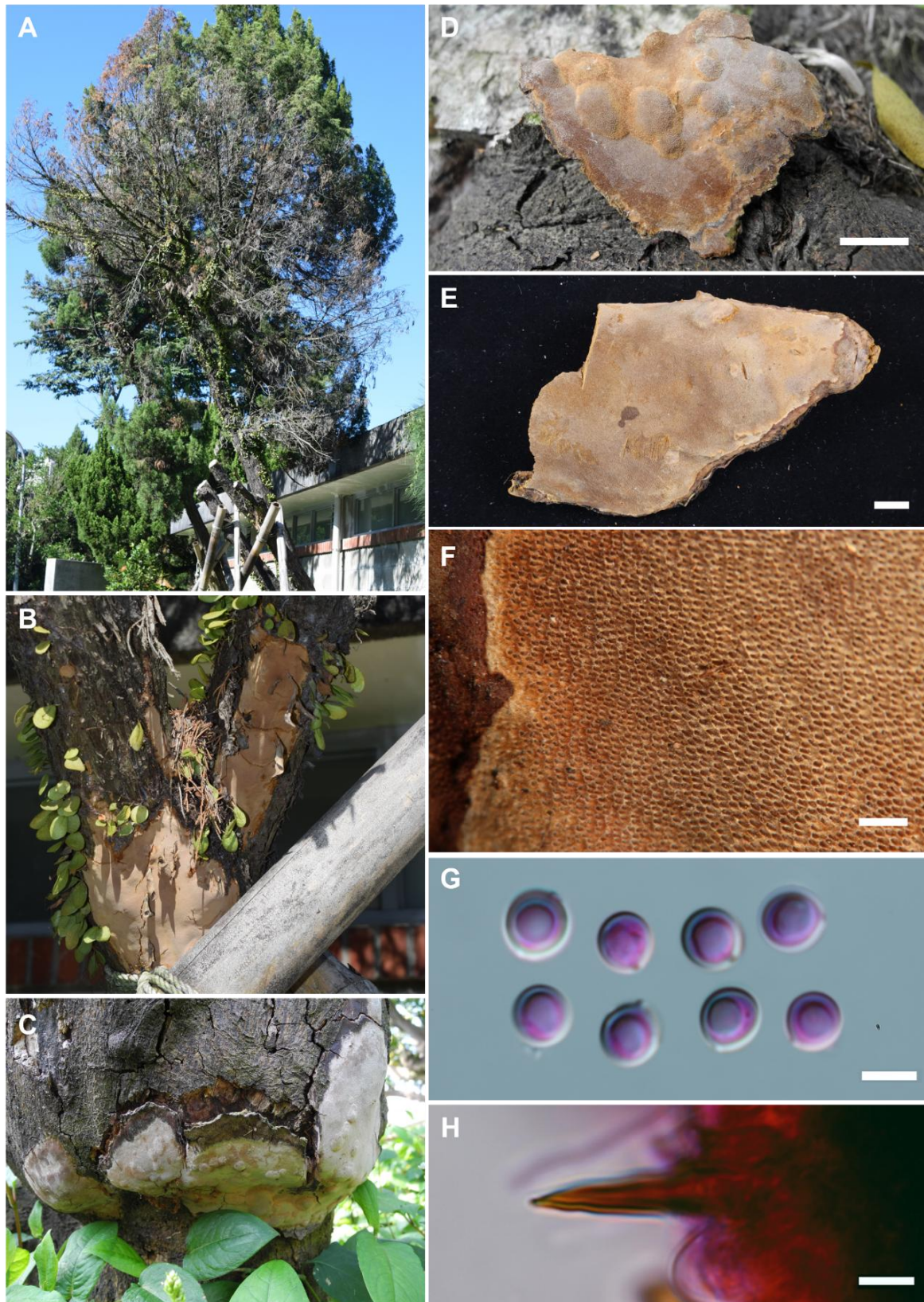


Fig. 5. *Fomitiporia torreyae*. A–B. Basidiomata on the trunk of *Juniperus chinensis* var. *kaizuka* (GC 2109-14), in situ. C–D. Basidiomata on the trunk of *Citrus* sp. (GC 1412-2), in situ. E–F. Dried basidiomata of *F. torreyae* (GC 2109-14). G. Basidiospores (GC 2109-14). H. Seta (WEI 17-681). Scale bars: D–E = 10 mm; F = 1 mm; G–H = 5 μ m.

(e.g., *Cryptomeria*, *Cunninghamia*, *Juniperus*, and *Torreya grandis*). This species is widely distributed in East Asia, including China (Anhui, Beijing, Fujian, Guangxi, Guizhou, Hubei, Hunan, Jiangxi, and Tianjin) (Dai and Cui 2005; Yang et al. 2019; Yuan et al. 2023), Japan (Honshu, Kyushu, and Okinawa) (Ota et al. 2014), Vietnam (Wu et al. 2022b), and Taiwan (this study).

Notes. In Taiwan, *Fomitiporia torreyae* is characterized by resupinate basidiomata with a light brown to yellowish-brown pore surface (6–8 per mm), a dimitic hyphal system with simple-septate generative hyphae, occasional presence of hymenial setae (14–23 × 5–7 µm), and subglobose, thick-walled basidiospores (5–6 × 4.5–5.5 µm) with a dextrinoid reaction. This species is similar to *F. bannaensis* but differs in having slightly larger basidiospores (5–6 × 4.5–5.5 µm vs. 4.5–5.5 × 4–5.5 µm in *F. bannaensis*) and larger pores (6–8 per mm vs. 8–10 per mm in *F. bannaensis*).

Although *F. torreyae* was originally described as lacking hymenial setae (Dai and Cui 2005), hymenial setae were observed in two Taiwanese specimens (*GC 1412-2* and *WEI 17-681*; Fig. 5H), consistent with the observations of Ota et al. (2014).

To our knowledge, this study represents the first report of *F. torreyae* associated with *Citrus* sp. and *Juniperus chinensis* var. *kaizuka*. The specimen from *Citrus* was collected from a stump in an orchard (Figs. 5C–D), and the original condition of the host could not be determined. In contrast, the infected *J. chinensis* var. *kaizuka* exhib-

ited dieback symptoms in the canopy, with resupinate basidiomata developing along the main trunk (Figs. 5A–B). However, pathogenicity tests on these hosts have not been conducted, and the pathogenic potential of *F. torreyae* requires further investigation.

Acknowledgements

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References

- Alves-Silva G, Drechsler-Santos ER, da Silveira RMB. 2020a. Bambusicolous *Fomitiporia* revisited: multilocus phylogeny reveals a clade of host-exclusive species. *Mycologia* 112:633–648.
- Alves-Silva G, Reck MA, da Silveira RMB, Bittencourt F, Robledo GL, Góes-Neto A, Drechsler-Santos ER. 2020b. The Neotropical *Fomitiporia* (Hymenochaetales, Basidiomycota): the redefinition of *F. api-hyna* ss allows revealing a high hidden species diversity. *Mycological Progress* 19: 769–790.
- Amalfi M, Decock C. 2013. *Fomitiporia castilloi* sp. nov. and multiple clades around *F. api-hyna* and *F. texana* in Meso- and South America evidenced by multiloci phylogenetic inferences. *Mycologia*, 105:873–887.
- Amalfi M, Decock C. 2014. *Fomitiporia expansa*, an undescribed species from French Guiana. *Cryptogamie. Mycologie* 35:73–85.

- Amalfi M, Raymundo T, Valenzuela R, Decock C. 2012. *Fomitiporia cupressicola* sp. nov., a parasite on *Cupressus arizonica*, and additional unnamed clades in the southern USA and northern Mexico, determined by multilocus phylogenetic analyses. *Mycologia* 104:880–893.
- Amalfi M, Yombiyeni P, Decock C. 2010. *Fomitiporia* in sub-Saharan Africa: morphology and multigene phylogenetic analysis support three new species from the Guineo-Congolian rainforest. *Mycologia* 102:1303–1317.
- Ann PJ, Tsai JN, Chang TT, Wang IT. 2005. Distribution of decline of fruit trees and ornamental woody plants in Taiwan. *Plant Pathology Bulletin* 14:203–210. (in Chinese)
- Brown A, Lawrence D, Baumgartner K. 2020. Role of basidiomycete fungi in the grapevine trunk disease esca. *Plant Pathology* 69:205–220.
- Castresana J. 2000. Selection of conserved blocks from multiple alignments for their use in phylogenetic analysis. *Molecular biology and evolution* 17:540–552.
- Chang TT. 1995. Diseases of cypress in Taiwan (II). *Forest Research Newsletter*, 2(1). (in Chinese)
- Chang TT, Hsieh HJ, Chang RJ, Fu CS. 1999. Common tree diseases in Taiwan. Taiwan Forestry Research Institute. Taipei. 202 pp. (in Chinese)
- Chen H, Cui BK. 2017. Multi-locus phylogeny and morphology reveal five new species of *Fomitiporia* (Hymenochaetaceae) from China. *Mycological Progress* 16:687–701.
- Chen H, Zhou JL, Cui BK. 2016. Two new species of *Fomitiporia* (Hymenochaetales, Basidiomycota) from Tibet, southwest China. *Mycologia* 108:1010–1017.
- Chen JJ, Wu YD, Ji XH, Gates G, Xu X. 2021. A new species of *Fomitiporia* (Hymenochaetales) from Australia. *Phytotaxa* 489:200–208.
- Chen J, Vlasák J, Luo KY, Yuan Y. 2025. Three new species of *Fomitiporia* (Hymenochaetales, Basidiomycota) from tropical dry forests in Ecuador and Peru. *MycKeys* 118:267–287.
- Cloete M, Fischer M, Mostert L, Halleen F. 2014. A novel *Fomitiporia* species associated with esca on grapevine in South Africa. *Mycological Progress* 13:303–311.
- Cubeta M, Echandi E, Abernethy T, Vilgalys R. 1991. Characterization of anastomosis groups of binucleate *Rhizoctonia* species using restriction analysis of an amplified ribosomal RNA gene. *Phytopathology* 81:1395–1400.
- Dai YC. 2010. Hymenochaetaceae (Basidiomycota) in China. *Fungal Diversity* 45:131–343.
- Dai YC, Cui BK. 2005. Two new species of Hymenochaetaceae from eastern China. *Mycotaxon* 94:341–347.
- Dai YC, Cui BK, Yuan HS, Li BD. 2007. Pathogenic wood-decaying fungi in China. *Forest Pathology* 37:105–120.
- Dai YC, Yang ZL, Cui BK, Wu G, Yuan HS, Zhou LW, He SH, Ge ZW, Wu F, Wei YL. 2021. Diversity and systematics of the important macrofungi in Chinese forests. *Mycosystema* 40:770–805.
- Dai YC, Yang ZL, Cui BK, Yu CJ, Zhou LW. 2009. Species diversity and utilization of

- medicinal mushrooms and fungi in China. *International Journal of Medicinal Mushrooms* 11:287–302.
- Decock C, Figueroa SH, Robledo G, Castillo G. 2007. *Fomitiporia punctata* (Basidiomycota, Hymenochaetales) and its presumed taxonomic synonyms in America: taxonomy and phylogeny of some species from tropical/subtropical areas. *Mycologia* 99: 733–752.
- Fischer M. 2002. A new wood-decaying basidiomycete species associated with esca of grapevine: *Fomitiporia mediterranea* (Hymenochaetales). *Mycological Progress* 1: 315–324.
- Fischer M, Binder M. 2004. Species recognition, geographic distribution and host-pathogen relationships: a case study in a group of lignicolous basidiomycetes, *Phellinus* sl. *Mycologia* 96:799–811.
- Gardes M, Bruns TD. 1993. ITS primers with enhanced specificity for basidiomycetes-application to the identification of mycorrhizae and rusts. *Molecular Ecology* 2: 113–118.
- Guindon S, Gascuel O. 2003. A simple, fast, and accurate algorithm to estimate large phylogenies by maximum likelihood. *Systematic Biology* 52:696–704.
- Huelsenbeck JP, Ronquist F. 2001. MRBAYES: Bayesian inference of phylogenetic trees. *Bioinformatics* 17:754–755.
- Hyde KD, Tennakoon DS, Jeewon R, et al. 2019. Fungal diversity notes 1036–1150: taxonomic and phylogenetic contributions on genera and species of fungal taxa. *Fungal Diversity* 96:1–242.
- Katoh K, Rozewicki J, Yamada KD. 2019. MAFFT online service: multiple sequence alignment, interactive sequence choice and visualization. *Briefings in Bioinformatics* 20:1160–1166.
- Larsson A. 2014. AliView: a fast and lightweight alignment viewer and editor for large datasets. *Bioinformatics* 30:3276–3278.
- Li GJ, Hyde KD, Zhao RL, Hongsan S, Abdel-Aziz FA, Abdel-Wahab MA, Alvarado P, Alves-Silva G, Ammirati JF, Ariyawansa HA et al. 2016. Fungal diversity notes 253–366: taxonomic and phylogenetic contributions to fungal taxa. *Fungal Diversity* 78:1–237.
- Liu TZ, Chen Q, Han ML, Wu F. 2018. *Fomitiporia rhamnoides* sp. nov. (Hymenochaetales, Basidiomycota), a new polypore growing on Hippophae from China. *Mycology Keys* 36:35–43.
- Miller MA, Pfeiffer W, Schwartz T. Creating the CIPRES Science Gateway for inference of large phylogenetic trees. 2010 gateway computing environments workshop (GCE) 2010:1–8.
- Murrill WA. 1907. Polyporaceae. *North American Flora* 9:1–131.
- Núñez, M., Ryvarden, L. 2000. East Asian Polypores. Vol. 1. *Fungiflora*, Oslo. 144 pp.
- Ota Y, Hattori T, Nakamura H, Terashima Y, Lee SS, Miyuki Y, Sotome K. 2014. Taxonomy and phylogenetic position of *Fomitiporia torreyae*, a causal agent of trunk rot on Sanbu-sugi, a cultivar of Japanese cedar (*Cryptomeria japonica*) in Japan. *Mycologia* 106:66–76.
- Posada D. 2008. jModelTest: phylogenetic model averaging. *Molecular Biology and Evolution* 25:1253–1256.

- Rajchenberg M, Pildain MB, Madriaga DC, de Errasti A, Riquelme C, Becerra J. 2019. New poroid Hymenochaetaceae (Basidiomycota, Hymenochaetales) from Chile. *Mycological Progress* 18:865–877.
- Ronquist F, Huelsenbeck JP. 2003. MrBayes 3: Bayesian phylogenetic inference under mixed models. *Bioinformatics* 19:1572–1574.
- Sawada K. 1959. Descriptive catalogue of Taiwan (Formosan) fungi. Part XI.
- Shih SY, Wu SH, Chen CY. 2012. Five new records of *Phellinus* s.l. in Taiwan. *Fungal Science* 27:153–163.
- Stamatakis A. 2014. RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. *Bioinformatics* 30:1312–1313.
- Świdorski G, Kalinowska M, Zapora E, Wołkowiński M, Stocki M, Ciszakowicz E, Bocian A, Jaromin M, Tyrka M, Lecka-Szlachta K, et al. 2025. Bioactive properties of selected European *Phellinus* species: A comprehensive study. *International Journal of Molecular Sciences* 26:8013.
- Tchoumi JMT, Coetzee MPA, Rajchenberg M, Roux J. 2020. Poroid Hymenochaetaceae associated with trees showing wood-rot symptoms in the Garden Route National Park of South Africa. *Mycologia* 112:722–741.
- Torii M, Masuya H, Hattori T. 2021. Temperature characteristics of two *Fomitiporia* fungi determine their geographical distributions in Japan. *Forests* 12:1580.
- Vilgalys R, Hester M. 1990. Rapid genetic identification and mapping of enzymatically amplified ribosomal DNA from several *Cryptococcus* species. *Journal of Bacteriology* 172:4238–4246.
- Vlasák J, Vlasák J. 2016. Two new polypore species from the southwestern USA: *Fomitiporia fissurata* and *F. deserticola*. *Mycotaxon* 131:193–203.
- Wagner T, Fischer M. 2001. Natural groups and a revised system for the European poroid Hymenochaetales (Basidiomycota) supported by 28S rDNA sequence data. *Mycological Research* 105:773–782.
- White TJ, Bruns T, Lee S, Taylor J. 1990. Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. *PCR protocols: a guide to methods and applications* 18:315–322.
- Wu F, Man XW, Tohtirjap A, Dai YC. 2022a. A comparison of polypore fungi and species composition in forest ecosystems of China, North America, and Europe. *Forest Ecosystems* 9:100051.
- Wu F, Zhou LW, Vlasák J, Dai YC. 2022b. Global diversity and systematics of Hymenochaetaceae with poroid hymenophore. *Fungal Diversity* 113:1–192.
- Yang X, Gu CY, Zang HY, Chen Y. 2019. First report of *Fomitiporia torreyae* causing trunk rot on Chinese torrey (Torreya grandis) in Anhui Province of China. *Journal of Plant Pathology* 101:1297–1297.
- Yuan Y, Bian LS, Wu YD, Chen JJ, Wu F, Liu HG, Zeng GY, Dai YC. 2023. Species diversity of pathogenic wood-rotting fungi (Agaricomycetes, Basidiomycota) in China. *Mycology* 14:204–226.
- Zan LF, Bao HY, Bau T, Li Y. 2015. A new antioxidant pyrano [4, 3-c][2] benzopyran-1, 6-dione derivative from the medicinal

- mushroom *Fomitiporia ellipsoidea*. Natural Product Communications 10:315–316.
- Zhou LW, Xue HJ. 2012. *Fomitiporia pentaphyllacis* and *F. tenuitubus* spp. nov. (Hymenochaetales, Basidiomycota) from Guangxi, southern China. Mycological Progress 11: 907–913.
- Zhao H, Cui YJ, Guan QX, Wang K, Zhuang L, Zeng GY, Wei YL, Wu F, Yuan HS. 2025. Global species diversity and distribution patterns within the order Hymenochaetales (Agaricomycetes, Basidiomycota). Mycosphere 16: 3257–3280.

臺灣嗜藍孢孔菌屬真菌之新紀錄及分類備註

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摘 要

本研究經由形態特徵觀察及 ITS 與 28S rDNA 序列之親緣關係分析，確認亞熱帶嗜藍孢孔菌(*Fomitiporia subtropica*)與榿樹嗜藍孢孔菌(*F. torreyae*)為臺灣新紀錄種；此外，亦提供版納嗜藍孢孔菌(*F. bannaensis*)與斑嗜藍孢孔菌(*F. punctata*)之分類備註，以及臺灣產 6 種嗜藍孢孔菌屬真菌之檢索表。

關鍵詞：擔子菌門、刺革菌目、親緣關係、分類學、木材腐朽菌