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Distoseptispora dipterocarpi sp. nov. (*Distoseptisporaceae*), a lignicolous fungus on decaying wood of *Dipterocarpus* in Thailand

Afshari N[1,2], Gomes de Farias AR[2], Bhunjun CS[2,3], Phukhamsakda C[2,3], Hyde KD[2,3] and Lumyong S[1,4,5*]

[1]*Department of Biology, Faculty of Sciences, Chiang Mai University, Chiang Mai 50200, Thailand*
[2]*Center of Excellence in Fungal Research, Mae Fah Luang University, Chiang Rai 57100, Thailand*
[3]*School of Science, Mae Fah Luang University, Chiang Rai 57100, Thailand*
[4]*Research Center of Microbial Diversity and Sustainable Utilization, Faculty of Science, Chiang Mai University, Chiang Mai 50200, Thailand*
[5]*Academy of Science, The Royal Society of Thailand, Bangkok 10300, Thailand*

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Abstract

Distoseptispora (*Distoseptisporaceae*, *Distoseptisporales*) is considered lignicolous saprobes. Different taxa have been identified from diverse substrates and hosts in terrestrial and freshwater habitats. During a taxonomic study on woody litter, micro-fungi from dead wood specimens of *Dipeterocarpus* sp. in Chiang Rai, Thailand, a sporidesmium-like taxon was collected. Morphological features, such as large, cylindrical or obclavate conidia with 10–72 distosepta, and branched, septated conidiophores, and multi-gene phylogenetic analyses of the combined large subunit ribosomal rRNA (LSU), internal transcribed spacer (ITS) regions, translation elongation factor 1-alpha (*tef1-α*), and RNA polymerase II subunit (*rpb2*) gene, identified *Distoseptispora dipterocarpi* as a new species.

Keywords – Fungal taxonomy – hyphomycete – molecular phylogeny – new taxa – *Sordariomycetes*

Introduction

Dipterocarpaceae species are distributed in most Southeast Asia tropical rain forests (Brearley et al. 2017), contributing to the global carbon balance, biodiversity, species richness, and species abundance (Ghazoul 2016). Woody litter is a substantial component in many terrestrial and aquatic ecosystems, contributing significantly to detritus biomass and ecosystem biodiversity (Harmon et al. 1986, Zimmer 2019). Fungi are one of the main decomposing organisms of dead wood or living trees worldwide (Nordén et al. 2004).

Among the prevalent woody litter saprobes in terrestrial and freshwater ecosystems, dematiaceous sporidesmium-like hyphomycetes are dominant (Yang et al. 2021). *Distoseptisporaceae* (*Sordariomycetes*) was reported by Su et al. (2016) as a monotypic family with *Distoseptispora* as the type genus and *D. fluminicola* McKenzie, H.Y. Su, Z.L. Luo & K.D. Hyde as type species. In the last few years, thxere has been a remarkable increment in the number of new *Distoseptispora* species, with 33 species outlined by Wijayawardene et al. (2022) and 59

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Corresponding Author: Saisamorn Lumyong – e-mail – scboi009@gmail.com,
Kevin D. Hyde – e-mail – kdhyde3@gmail.com

listed in the Mycobank database (Robert et al. 2013, accessed on 15 February 2023) and Species fungorum (2023), of which most are saprobes in freshwater and terrestrial environment (Luo et al. 2018, 2019, Ma et al. 2022, Phukhamsakda et al. 2020, Su et al. 2016, Sun et al. 2020, Yang et al. 2018, 2021, Zhai et al. 2022, Zhang et al. 2022).

During a survey on the diversity of woody litter microfungi in a dipterocarp forest in Chiang Rai Province, Thailand, a specimen with sporidesmium-like structures was found. Morphological characterisation and multilocus phylogenetic analysis of large subunit ribosomal rRNA (LSU), internal transcribed spacer (ITS), translation elongation factor 1-alpha (*tef1-α*), and RNA polymerase II subunit (*rpb2*) sequences revealed *Distoseptispora dipterocarpi* as a novel taxon. The isolate represents the first report of *Distoseptispora* on *Dipterocarpus* from Thailand.

Materials & Methods

Sample collection, fungal isolation, and microscopic characterisation

Dead wood of *Dipterocarpus* sp. was collected in Chiang Rai Province, Thailand, in September 2021 and taken to the laboratory. The sample was examined using a Leica EZ4 stereo microscope, and the fruiting structures were placed by a needle on a drop of sterilised water on a slide. The micro-morphological features were examined and photographed using a Nikon ECLIPSE Ni compound microscope (Nikon, Japan) with a Canon 600 D digital camera (Nikon, Japan). Tarosoft (R) Image Frame Work program (Version 0.9.7) was used to measure specimen structures, and photo plates were prepared using Adobe Photoshop CS6 Extended version 10.0 software (Adobe Systems, United States). Single conidia isolation was used to obtain pure cultures on Difco™ potato dextrose agar (PDA) (39 $g.L^{-1}$), following the spore suspension method described in (Senanayake et al. 2020). The plates were incubated at 25 ± 1 °C in the dark for four weeks.

Herbarium material was deposited in the Mae Fah Luang University Fungarium (MFLU), Chiang Rai, Thailand, and ex-type pure living cultures in the Mae Fah Luang University Culture Collection (MFLUCC). Faces of fungi numbers (FoF) (Jayasiri et al. 2015) and Index Fungorum numbers (http://www.indexfungorum.org) were acquired.

DNA extraction, PCR amplification, and sequencing

Genomic DNA was extracted from the fresh fungal mycelium using the Forensic DNA Kit–D3591-01 (OMEGA Bio-Tek Inc) following the manufacturer's protocol. Polymerase chain reaction (PCR) amplifications were performed using the primers and conditions demonstrated in Table 1, in a total volume of 50 µl (25 µl of 10 × PCR Master Mix, 1 µl of 10 picomolar forward and reverse primers, 2 µl DNA template, and 21 µl ddH_2O). PCR amplification products were surveyed on agarose gel (1%) and sequenced by Biogenomed Co., Ltd (South Korea).

Alignments and phylogenetic analysis

Consensus sequences were assembled using SeqMan software version 7.1.0 (DNASTAR Inc., WI). The sequences of 59 *Distoseptispora* species and two *Aquapteridospora* species (Crous et al. 2019, Hyde et al. 2019, Luo et al. 2018, Ma et al. 2022, Monkai et al. 2020, Phukhamsakda et al. 2020, Su et al. 2016, Sun et al. 2020, Yang et al. 2018, 2021, Zhai et al. 2022, Zhang et al. 2022) were obtained from NCBI GenBank database (Sayers et al. 2019) (Table 2). The dataset of the LSU, ITS, *tef1-α* and *rpb2* were aligned using MAFFT v.7 online web server (http://mafft.cbrc.jp/alignment/server/index.html (Katoh et al. 2019), and the alignments were trimmed using trimAl v 1.2 under the *gappyout* (*-gt 0.5*) (Capella-Gutierrez et al. 2009).

Maximum likelihood (ML) analysis was carried out with RAxML-HPC2 on XSEDE (8.2.12) using a GTR-GAMMA model of evolution (Stamatakis 2014) and 1,000 non-parametric bootstrap replicates. Bayesian Inference (BI) analysis was performed in MrBayes (version) on XSEDE in CIPRES Science Gateway (Miller et al. 2015), using the GTR+I+G nucleotide substitutions models for each dataset, selected according to the Akaike Information Criterion (AIC) implemented in jModelTest (2.1.6) (Darriba et al. 2012) in the CIPRES Science Gateway web portal (Miller et al.

2010). Four Markov chains for 20,000,000 generations with trees were sampled every 1,000th generation for calculating the Bayesian Posterior Probabilities (BYPP). The first 25% of the trees, representing the burn-in phase, were excluded, and the remaining trees were applied for calculating posterior probabilities of recovered branches (Larget & Simon 1999). The resulting trees were visualised in FigTree v. 1.4.0 (Rambaut 2012), and the layout was created in Inkspace 1.2. The obtained sequences were deposited in GenBank (Table 2).

Table 1 Primers and PCR protocols.

Locus	Primer (Forward and Reverse)	PCR protocol	Reference
ITS	ITS5/ ITS4	94 ℃: 3 min, (94 ℃: 30 s, 55 ℃: 50 s, 72 ℃ :1 min) × 35 cycles 72 ℃: 10 min 4 ℃ on hold	White et al. (1990)
LSU	LR0R/ LR5	95 ℃: 3 min, (95 ℃: 30 s, 55 ℃: 50 s, 72 ℃: 30 s) × 35 cycles 72 ℃: 10 min 4 ℃ on hold	Vilgalys & Hester (1990), Rehner et al. (1994)
rpb2	fRPB2–5F/ fRPB2–7cR	95 °C: 5 min, (95 °C: 15 s, 56 °C: 50 s, 72 °C: 2 min) × 37 cycles 72 °C: 10 min 4 °C on hold	Liu et al. (1999)

Genealogical concordance phylogenetic species recognition analysis

A pairwise homoplasy index (PHI) test was carried out in Split Tree version 4.18.2 (Huson & Bryant 2006) to assess the recombination level within phylogenetically related species using single and multilocus genes (LSU, ITS, *tef1-α*, and *rpb2*), including gaps. The results were demonstrated by constructing a split diagram using the splits decomposition and LogDet transformation possibility.

Table 2 GenBank accession numbers used in the phylogenetic analyses.

Taxon	Gene bank accession number				
	Strain Code	**LSU**	**ITS**	***tef1-α***	***rpb2***
Distoseptispora adscendens	HKUCC 10820	DQ408561	–	–	DQ435092
D. amniculi	**MFLUCC 17–2129**	MZ868761	MZ868770	–	MZ892982
D. appendiculata	**MFLUCC 18–0259**	MN163023	MN163009	MN174866	_
D. aqualignicola	**KUNCC 21–10729**	ON400845	OK341186	OP413480	OP413474
D. aquamyces	**KUNCC 21–10732**	OK341199	OK341187	OP413482	OP413476
D. aquatica	**MFLUCC 15–0374**	KU376268	MF077552		–
D. aquatica	MFLUCC 16–0904	MK849794	MK828649	MN194053	–
D. aquatica	MFLUCC 18–0646	MK849793	MK828648	MN194052	–
D. aquatica	S–965	MK849792	MK828647	MN194051	MN124537
D. aquisubtropica	**GZCC 22–0075**	ON527941	ON527933	ON533677	ON533685
D. atroviridis	**GZCC 20–0511**	MZ868763	MZ868772	MZ892978	MZ892984
D. atroviridis	GZCC 19–0531	MZ227223	MW133915	–	–
D. bambusae	**MFLUCC 20–0091**	NG074430	NR170068	MT232880	MT232881
D. bambusae	MFLU 17–1653	MT232717	MT232712	–	MT232882
D. bangkokensis	**MFLUCC 18–0262**	MZ518206	MZ518205	–	–
D. cangshanensis	**MFLUCC 16–0970**	MG979761	MG979754	MG988419	–
D. caricis	**CPC: 36498**	MN567632	NR166325	–	MN556805

Table 2 Continued.

Taxon	Gene bank accession number				
	Strain Code	**LSU**	**ITS**	***tef1-α***	***rpb2***
D. caricis	CPC: 36442	–	MN562125	–	MN556806
D. chinensis	GZCC 21–0665	MZ474867	MZ474871	MZ501609	–
D. clematidis	**MFLUCC 17–2145**	MT214617	MT310661	–	MT394721
D. clematidis	KUN–HKAS:112708	MW879523	MW723056	–	–
D. crassispora	**KUMCC 21–10726**	OK341196	OK310698	OP413479	OP413473
D. curvularia	**KUMCC 21–10725**	OK341195	OK310697	OP413478	OP413472
D. cylindricospora	**KUN–HKAS:115796**	OK513523	OK491122	OK524220	–
D. dehongensis	**KUMCC 18–0090**	MK079662	MK085061	MK087659	–
D. dipterocarpi	**MFLUCC 22–0104 ***	**OP600052**	**OP600053**	–	**OP595140**
D. effuse	**GZCC 19–0532**	MZ227224	MW133916	–	–
D. euseptata	**MFLUCC 20–0154**	MW081544	MW081539	–	MW151860
D.euseptata	MFLU 20–0568	MW081545	MW081540	MW084994	MW084996
D. fasciculata	**KUMCC 19–0081**	NG075417	NR172452	MW396656	–
D. fluminicola	**MFLUCC 15–0417**	KU376270	MF077553	–	–
D. fusiformis	**GZCC 20–0512**	MZ868764	MZ868773	MZ892979	MZ892985
D. guizhouensis	**GZCC 21–0666**	MZ474869	MZ474868	MZ501610	MZ501611
D. guttulate	**MFLUCC 16–0183**	MF077554	MF077543	MF135651	–
D. hyaline	**MFLUCC 17–2128**	MZ868760	MZ868769	MZ892976	MZ892981
D. hydei	**MFLUCC 20–0115**	MT742830	MT734661	–	MT767128
D. lancangjiangensis	**DLUCC 1864**	MW879522	MW723055	–	–
D. leonensis	HKUCC 10822	DQ408566	_	–	DQ435089
D. lignicola	**MFLUCC 18–0198**	MK849797	MK828651	–	–
D. longispora	**HFJAU 0705**	MH555357	MH555359	–	–
D. martini	CGMCC 3.18651	KX033566	KU999975	–	–
D. meilingensis	JAUCC 4728	OK562397	OK562391	OK562409	–
D. multiseptata	**MFLUCC 15–0609**	KX710140	KX710145	MF135659	–
D. neorostrata	**MFLUCC 18–0376**	MN163017	MN163008	–	–
D. nonrostrata	**KUNCC 21–10730**	OK341198	OK310699	OP413481	OP413475
D. obclavate	**MFLUCC 18–0329**	MN163010	MN163012	–	–
D. obpyriformis	**MFLUCC 17–1694**	MG979764	–	MG988422	MG988415
D. obpyriformis	DLUCC 0867	MG979765	MG979757	MG988423	MG988416
D. pachyconidia	**KUMCC 21–10724**	OK341194	OK310696	OP413477	OP413471
D. palmarum	**MFLUCC 18–1446**	MK079663	MK085062	MK087660	MK087670
D. palmarum	MFLU 18–0588	NG067856	NR165897	–	–
D. phangngaensis	**MFLUCC 16–0857**	–	NR166230	MF135653	–
D. rayongensis	**MFLUCC 18–0415**	NG073624	NR171938	MH463253	–
D. rayongensis	MFLU 18–1045	MH457137	MH457172	–	MH463255
D. rostrata	**MFLUCC 16–0969**	MG979766	MG979758	MG988424	MG988417
D. rostrata	DLUCC 0885	MG979767	MG979759	MG988425	–
D. rostrata	MFLU 18–0479	NG064513	NR157552	_	–
D. saprophytica	**MFLUCC 18–1238**	NG075419	NR172454	MW396651	MW504069
D. septate	**GZCC 22–0078**	ON527947	ON527939	ON533683	ON533690
D. songkhlaensis	**MFLUCC 18–1234**	MW287755	MW286482	MW396642	–
D. submersa	MFLUCC 16–0946	MG979768	MG979760	MG988426	MG988418
D. suoluoensis	**MFLUCC 17–0224**	NG068552	NR168764	MF135654	–
D. tectonae	**MFLUCC 12–0291**	KX751713	KX751711	KX751710	KX751708
D. tectonigena	**MFLUCC 12–0292**	KX751714	NR154018	–	KX751709
D. thailandica	**MFLUCC 16–0270**	MH260292	MH275060	MH412767	–
D. thysanolaenae	KUN–HKAS: 112710	MW879524	MW723057	MW729783	–
D. thysanolaenae	KUMCC 18–0182	MK064091	MK045851	MK086031	–
D. tropica	**GZCC 22–0076**	ON527943	ON527935	ON533679	ON533687
D. verrucosa	**GZCC 20–0434**	MZ868762	MZ868771	MZ892977	MZ892983

Table 2 Continued.

Taxon	Gene bank accession number				
	Strain Code	**LSU**	**ITS**	***tef1-α***	***rpb2***
D. wuzhishanensis	**GZCC 22–0077**	ON527946	ON527938	ON533682	–
D. xishuangbannaensis	**KUMCC 17–0290**	MH260293	MH275061	MH412768	MH412754
D. yongxiuensis	JAUCC 4725	OK562394	OK562388	OK562406	–
D. yongxiuensis	JAUCC 4726	OK562395	OK562389	OK562407	–
D. yunjushanensis	JAUCC 4723	OK562398	OK562392	OK562411	–
D. yunjushanensis	JAUCC 4724	OK562399	OK562393	OK562410	–
D. yunnansis	**MFLUCC 20–0153**	MW081546	MW081541	MW081541	MW151861
Aquapteridospora aquatica	**MFLUCC 17–2371**	NG075413	NR172447	–	–
A. fusiformis	**MFLU 18–1601**	MK849798	MK828652	MN194056	–

Ex–type strains are denoted in bold; "_" sequence is unavailable; the current study sequence is indicated with an asterisk (*) after the collection number.

Abbreviations: CGMCC: China General Microbiological Culture Collection Center, Institute of Microbiology, Chinese Academy of Sciences, Beijing, China; CPC: Collection of P.W. Crous; DLUCC: Dali University Culture Collection, Yunnan, GZCC: Guizhou Culture Collection China; HFJAU: Herbarium of Fungi, Jiangxi Agricultural University; HKUCC: The University of Hong Kong Culture Collection, Hong Kong, China; JAUCC: Jiangxi Agricultural University Culture Collection; KUMCC: Kunming Institute of Botany Culture Collection; KUN HKAS: Kunming Institute of Botany Academia Sinica, Yunnan, China; MFLU: the herbarium of Mae Fah Luang University, Chiang Rai, Thailand; MFLUCC: Mae Fah Luang University Culture Collection, Chiang Rai, Thailand.

Results

Phylogenetic analysis

Partial nucleotide sequences of the LSU, ITS, *tef1-α*, and *rpb2* were used to assess the phylogenetic relationships of 78 strains, representing 59 *Distoseptispora* species and the outgroup taxa *Aquapteridospora aquatica* (MFLUCC 17–2371) and *A. fusiformis* (MFLU18–1601) (Table 2). The final alignment comprised 2,800 bases (ITS: 1–556; LSU: 557–1,420; *rpb2*: 1,421–2,469; *tef1-α*: 2,470–3,376), including gaps. The matrix had distinct alignment patterns with 34.03% of gaps and the estimated base frequencies of A = 0.239923, C = 0.263467, G = 0.282718, T = 0.213892; substitution rates AC = 1.314262, AG = 3.320157, AT = 1.294707, CG = 0.931325, CT = 7.086725, and GT = 1.000000. The RAxML and Bayesian analyses resulted in trees with congruent topology. The RAxML tree with the best score had the final value of the ML optimisation likelihood: -31779.501476 (Fig 1). The newly obtained isolate clustered sister of *Distoseptispora fasciculata* (KUMCC 19–0081) and *D. wuzhishanensis* (GZCC 22–0077), with 83% ML and 0.98 BYPP support.

Taxonomy

Distoseptispora dipterocarpi N. Afshari, K.D. Hyde & S. Lumyong, sp. nov. Fig. 3

Index Fungorum number: IF558392; Facesoffungi number: FoF 13099

Etymology – the epithet refers to the host genus, *Dipterocarpus*.

Holotype – MFLU 22–0151

Saprobic on woody litter of *Dipterocarpus* sp. Sexual morph: Undetermined. Asexual morph: *Hyphomycetous. Colonies* on the substratum are superficial, effuse, gregarious, hairy, erect, dark brown to black. *Mycelium* superficial on host substrate, composed of septa, branched, dark brown, thick-walled hyphae. *Conidiophores* 14–72 × 5–7 μm ($\bar{x}$ = 32.5 × 6 μm, n = 20), macronematous, mononematous, erect, straight or slightly flexuous, 1–7-septate, unbranched, single or in groups, brown, thick-walled, robust at the base. *Conidiogenous cells* 4–13.5 × 4–6.5 μm ($\bar{x}$ = 8 × 5 μm,

n = 20), monoblastic, terminal, determinate, cylindrical, brown. *Conidia* 31.5–350 × 6.5–12 µm ($\bar{x}$ = 146 × 9 µm, n = 20), solitary, cylindrical or obclavate, elongated, straight or slightly curved, truncate at the base, rounded at the apex, 10–72-distoseptate, smooth, olivaceous when young, brown tinge when mature, mostly lighter towards the apex, thick-walled, and scars or pigmented disjunction present in the attachment site.

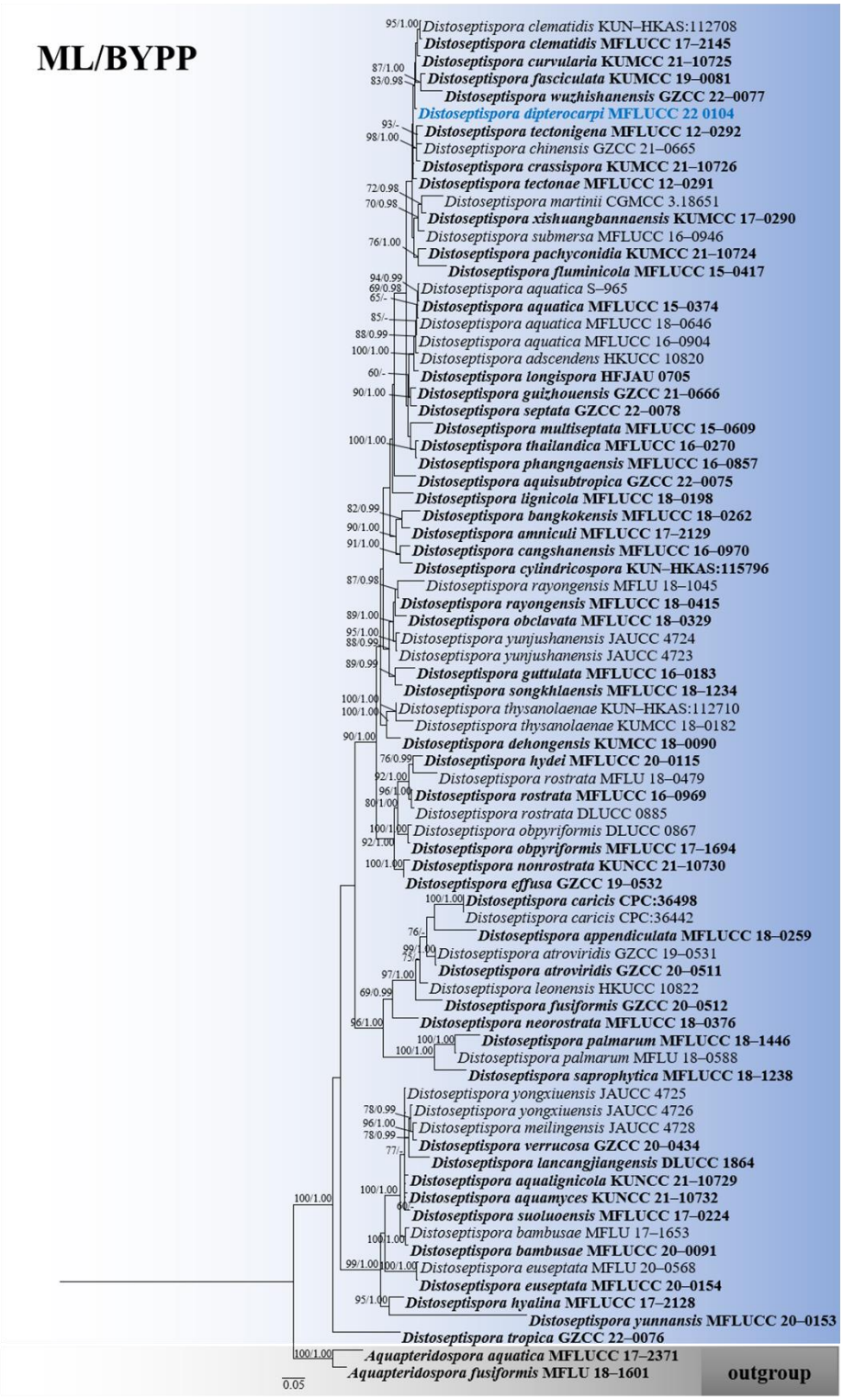

Fig. 1 – Maximum likelihood tree generated from combined ITS, LSU, *rpb2*, and *tef1-α* sequence data. Bootstrap support values ≥ 60% and Bayesian posterior probabilities ≥ 0.95 are demonstrated at the branches. The tree is rooted with *Aquapteridospora aquatic* (MFLUCC 17–2371) and

A. fusiformis (MFLU 18–1601). The new taxon (MFLUCC 22–0104) is indicated in bold and blue. Type species are in bold.

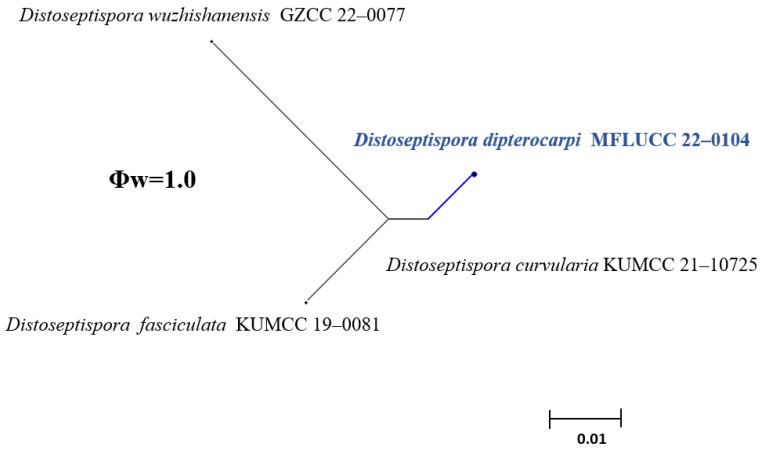

Fig. 2 – The splits diagram from the pairwise homoplasy index (PHI) test created from the combined ITS, LSU, *rpb2*, and *tef1-α* sequence data of closely related taxa. The PHI test (Φw) < 0.05 indicates significant recombination within the dataset. The novel taxon is in blue.

Culture characteristics – Colonies on PDA, circular, reaching 10 mm diam. at 7 days at 25 °C. Cultures from above hazel, dense mycelium, circular, surface smooth, dry, fluffy, undulate at the edge; reverse black at the center, radiating black outwardly.

Material examined – Thailand, Chiang Rai Province, on woody litter of *Dipterocarpus* sp. 27 September 2021, N. Afshari, S6NAD2 (MFLU 22–0151, holotype), ex-type living culture MFLUCC 22–0104.

Notes – In the phylogenetic tree, *Distoseptispora dipterocarpi* clusters as a sister taxon to *D. fasciculata* and *D. wuzhishanensis* with high support (GZCC 22–0077), with 83% ML/0.98 BYPP support. *Distoseptispora dipterocarpi* (MFLUCC 22–0104) shares several morphological characters with the phylogenetically related species *D. fasciculata* and *D. clematidis*, in terms of the shape and color of conidia. However, it can be distinguished from these two species by its wider range of conidial length (*D. fasciculata*: 46–200 µm; *D. clematidis*: 120–210 µm; *D. dipterocarpi*: 31.5–350 µm), and conidial septation, up to 72-distoseptate and having more conidiophore septa (up to 7) (Table 3), while conidia of *D. fasciculata* and *D. clematidis* have up to 40 and 35 septa, respectively (Phukhamsakda et al. 2020, Dong et al. 2021). *Distoseptispora dipterocarpi* and *D. clematidis* were both isolated from terrestrial environments. However, *D. fasciculata* was isolated from freshwater. A pairwise homoplasy index based on the combined gene of LSU, ITS, *rpb2*, and *tef1-α* sequence data of closely related taxa indicated no significant recombination (Φw = 1.0) (Fig. 2). *Distoseptispora dipterocarpi* is thus reported as a novel species based on morphological characters and high phylogenetic support.

Table 3 Comparison of conidial and conidiophores dimensions of *Distoseptispora clematidis*, *D. curvularia*, *D. fasciculata*, *D. wuzhishanensis*, and our isolate (*D. dipterocarpi*).

Isolate no.	Conidia	Conidiophore	Substrate	References
***D. dipterocarpi* (MFLUCC 22–0104)**	**31.5–350 × 6.5–12 µm 10–72-distoseptate**	**14–72 × 5–7 µm (1–7) septate**	**Dead wood of *Dipterocarpus* sp.**	**This study**
***D. clematidis* (MFLUCC 17–2145)**	120–210 × 12–20 µm 28–35-distoseptate	22–40 × 4–10 µm (3–5) septate	Dried branches of *Clematis sikkimensis*	Phukhamsakda et al. (2020)

Table 3 Continued.

Isolate no.	Conidia	Conidiophore	Substrate	References
***D. curvularia* (KUMCC 21–10725)**	(60–)100 × 200(–314) μm	11–28 μm –	Submerged wood in freshwater	Zhang et al. (2022)
***D. fasciculata* (KUMCC 19–0081)**	46–200 × 10–16.5 μm 10–40-distoseptate	12–16 × 5–6 μm (0–1) septate	Submerged wood in freshwater	Dong et al. (2021)
***D. wuzhishanensis* (GZCC 22–0077)**	76–143 × 11–17 μm	16–56 × 5–7 μm (1–4) septate	Submerged wood in freshwater	Ma et al. (2022)

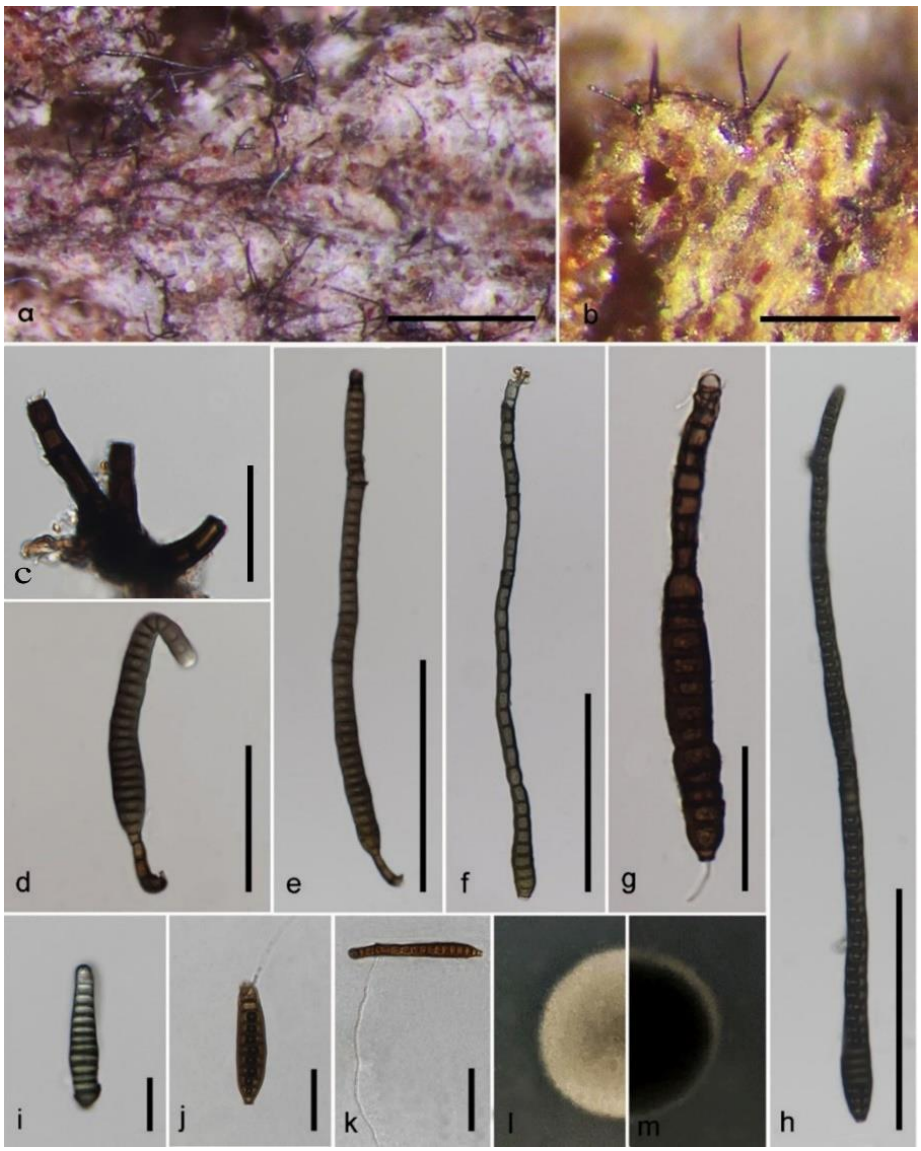

Fig. 3 – *Distoseptispora dipterocarpi*. a, b Colonies on *Dipterocarpus* sp. woody litter. c conidiophores. d, e conidiophores with conidia. f-j Conidia. k Germinating conidium. l, m Colony on PDA (front, reverse). Scale bars: a, b, e–h = 100 μm, k = 50 μm, c, d, i, j = 20 μm.

Discussion

Distoseptisporaceae was raised to the order *Distoseptisporales* based on morphological and molecular phylogenetic evidence of concatenated LSU, SSU, *rpb2*, and *tef1-α* sequence data (Luo et al. 2019). *Distoseptispora* was introduced to accommodate *D. aquatica* and *D. fluminicola* based on morphology and phylogenetic analysis. This monophyletic genus differs from other

sporidesmium-like taxa, such as *Sporidesmium aquaticum* (*Sporidesmiaceae*), *Morrisiella indica* (*Sordariomycetidae*), and *Sporidesmina malabarica* (*Xylariomycetidae*), by its phylogenetic placement and distinguishable morphological features (Su et al. 2016). Although *Distoseptispora*, *Ellisembia*, and *Sporidesmium* share similar morphological characteristics, it is challenging to recognise some *Distoseptispora* species by morphological signatures alone. Still, it is possible to distinguish them by molecular data (Hyde et al. 2016, Tibpromma et al. 2018, Yang et al. 2021). The asexual morph of *Distoseptispora* is critical to distinguish species based on the size, shape, colour, and the number of septate of the conidia (Su et al. 2016, Luo et al. 2018, Yang et al. 2021, Hyde et al. 2019). Therefore, species boundary delimitation should follow the polyphasic approaches (Chethana et al. 2021, Maharachchikumbura et al. 2021, Manawasinghe et al. 2021, Jayawardena et al. 2021). Based on that, we introduce *D. dipterocarpi* as a new taxon.

Most *Distoseptispora* species were collected from submerged wood in freshwater ecosystems (Su et al. 2016, Dong et al. 2021, Yang et al. 2018, 2021, Phukhamsakda et al. 2022, Zhang et al. 2022), but some have been isolated from the terrestrial environment (Monkai et al. 2020, Phukhamsakda et al. 2020, Sun et al. 2020, Zhai et al. 2022); therefore, they are unlikely to have a particular habitat preference. Besides, species in this genus have been reported only in China and Thailand, where fungal surveys in different habitats are continuous. This may be due to the lack of geographical sampling or specificity (Phukhamsakda et al. 2022). Besides, *Distoseptispora* species are not host-specific and have been isolated from a variety of plants, including *Carex* sp., *Clematis sikkimensis*, *Pandanus* sp., *Tectona grandis* and *Bambuseae* (Hyde et al. 2016, Tibpromma et al. 2018, Crous et al. 2019, Phukhamsakda et al. 2020, Sun et al. 2020).

In this study, *D. dipterocarpi* was found on decaying wood of *Dipterocarpus* sp. from terrestrial habitat in Chiang Rai, Thailand. Since *Distoseptispora* species are mostly isolated from freshwater in Thailand and China, different hosts and geographical regions need to be surveyed to reveal this genus diversity and contribute to increasing the fungal species number curve.

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