

Morphology and multigene phylogeny reveal three new species of *Distoseptispora* (Distoseptisporales, Distoseptisporaceae) on palms (Arecaceae) from peat swamp areas in southern Thailand

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Abstract

Peat swamp forest is a unique habitat that supports high biodiversity, particularly fungal diversity. The current study collected submerged and dead plant parts from *Eleiodoxa conferta*, *Eugeissona tristis* and *Licuala paludosa* from a peat swamp forest in Narathiwat Province, Thailand. Morphological features coupled with multigene phylogenetic analyses of ITS, LSU, *rpb2* and *tef1-α* sequence data identified our isolates as new *Distoseptispora* species (viz. *D. arecacearum* **sp. nov.**, *D. eleiodoxae* **sp. nov.** and *D. narathiwatensis* **sp. nov.**). Morphological descriptions, illustrations and notes are provided.

Key words: asexual morph, molecular phylogeny, novel taxa, saprobic fungi, Sordariomycetes, taxonomy



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Introduction

Most peat swamp forests can be found in tropical rainforests where peat is submerged for most of the year and characterised by low nutrient contents and high acidity due to lack of fully decomposed plant materials (Page et al. 1999, 2011; Jackson et al. 2009; Lampela et al. 2016; Ratnayake 2020). Peat swamp forests are unique ecosystems due to their high species diversity and significant role in maintaining a stable global climate. They function as carbon sinks, storing twice as much carbon as all global forest biomass (Hakim et al. 2017; Fujimoto et al. 2019; Shuhada et al. 2020). Beyond carbon storage, peatlands offer valuable benefits. They play vital roles in the water cycle, storing and filtering water and mitigating floods by slowing peak flows. Home to diverse plants and animals, these wetlands support millions of people. Additionally, they hold archaeological relics and provide insights into past environmental conditions

through their peat layers, aiding predictions about the future climate (Parish et al. 2008; Posa et al. 2011; Minayeva and Sirin 2012; UNEP 2022). Asian peatlands are amongst the most diverse and geographically extensive in the world, with over 160 million hectares and the majority of tropical peatlands are found in Southeast Asia (e.g. Brunei, Indonesia, Malaysia, Papua New Guinea and Thailand) (UNEP 2022).

These habitats support many flora, including an extensive number of bryophytes, ferns and palms (Arecaceae) (Prentice 2011; Rieley 2016). Arecaceae comprises iconic monocotyledonous flowering plants belonging to 188 genera and 2,585 species that are distributed throughout tropical and subtropical areas of the world. However, they are most diverse in highly threatened moist tropical forest habitats (Dransfield et al. 2008; Palmweb 2023; POWO 2023). In peat swamp forests, many palm species, such as *Areca macrocalyx* Zipp. ex Blume, *Calamus concinnus* Mart, *Cyrtostachys renda* Blume, *Eugissona tristis* Griff, *Eleiodoxa conferta* (Griff.) Burret, *Licuala longicalycata* Furtado, *L. paludosa* Griff, *Metroxylon sagu* Rottb and *Nenga pumila* (Blume) H.Wendl. ex Schaedtler can be found (Calabon et al. 2022), exerting different biological functions.

Several studies on palm fungi have focused on saprobic, endophytic and plant pathogenic life modes from different habitats worldwide (Hyde 1988; Taylor et al. 1999; Fröhlich and Hyde 2000; Fröhlich et al. 2000; Hyde et al. 2000; Taylor and Hyde 2003; Pilantanapak et al. 2005; Lumyong et al. 2009; Liu et al. 2010; Wikee et al. 2013; Konta et al. 2016a, 2016b, 2016c, 2017, 2020a, 2020b, 2020c, 2021a, 2021b, 2023; Chou et al. 2019; El Meleigi et al. 2019; Kinge et al. 2019; Marin-Felix et al. 2019; Chen et al. 2020; Mapook et al. 2020; Zhang et al. 2020; Tian et al. 2022). Even though many palm trees grow in peat swamp forests, there are few records of fungal studies in these environments, mostly reported from Thailand (Pinruan et al. 2002, 2004a, 2004b, 2004c, 2004d, 2007, 2008, 2010a, 2010b, 2014; Pinnoi et al. 2003a, 2003b, 2004, 2006, 2009, 2010; Voglmayr and Yule 2006; Sivichai and Boonyuen 2010; Boonyuen et al. 2012), of which many lack molecular data. Pinnoi et al. (2006) studied saprobic fungi on dead palm material in the Sirindhorn peat swamp forest, Narathiwat Province, Thailand and listed 462 ascomycetous and basidiomycetous taxa from various parts of palm materials (such as dry, damp and submerged palm materials), based on morphological identification and also recorded five sporidesmium-like taxa. Pinnoi et al. (2009) identified 88 fungal species from 212 collections of *Calamus* sp. in Thailand, with six records resembling sporidesmium-like taxa.

Distoseptispora K.D. Hyde, McKenzie & Maharachch belongs to Distoseptisporaceae, Distoseptisporales, Sordariomycetes, Ascomycota and comprises sporidesmium-like taxa (Wijayawardene et al. 2022). Su et al. (2016) proposed Distoseptisporaceae to accommodate sporidesmium-like taxa with *Distoseptispora* as the type genus and *D. fluminicola* McKenzie, Hong Y. Su, Z.L. Luo & K.D. Hyde as the type species. Subsequently, Luo et al. (2019) introduced Distoseptisporales to accommodate Distoseptisporaceae, based on multigene phylogenetic analyses of LSU, SSU, *rpb2* and *tef1-a* sequence data. *Distoseptispora* is characterised by short, septate, olivaceous to brown conidiophores. The conidiogenous cells are monoblastic and determinate, bearing acrogenous conidia that are brown, euseptate, distoseptate or muriform and cut off by cross

walls at the basal cell with a basal scar (Yang et al. 2018). The genus exhibits morphology similar to *Sporidesmium*, but can be distinguished by having shorter conidiophores and darker conidia with pale round apices (Su et al. 2016). To date, *Distoseptispora* comprises 65 species listed in the MycoBank database (<https://www.mycobank.org/>; Accessed in August 2023), with molecular data available for all reported species in the GenBank. The estimated divergence time for Distoseptisporaceae is approximately 44.21 million years ago (MYA), after the Tertiary–Cretaceous extinction event (Hyde et al. 2020), which could have created conducive conditions for *Distoseptispora* to thrive as a saprobe on various hosts (Phukhamsakda et al. 2022).

Peatswamp forests are unique, endangered ecosystems and their fungal biodiversity is little known. Therefore, in the current study, we aimed to study fungal species on different palm materials from peatswamp forests in Thailand, based on morphology and phylogeny. This study introduces three new species, *Distoseptispora arecacearum*, *D. eleiodoxae* and *D. narathiwatensis*, associated with *Eleiodoxa conferta*, *Eugeissona tristis* and *Licuala paludosa* from a peatswamp forest in Narathiwat Province, Thailand, based on morphological characteristics coupled with multigene phylogenetic analyses (ITS, LSU, *rpb2* and *tef1-a*).

Materials and methods

Sample collection, morphological study and isolation

Decaying leaves of *Eleiodoxa conferta*, *Eugeissona tristis* and *Licuala paludosa* were collected from a peatswamp forest in Narathiwat Province, Thailand, in April 2022. Wet (submerged) and dry (aerial part) palm specimens were placed in plastic bags and brought to the laboratory. The submerged materials were kept moist and examined periodically for fungal fruiting structures and the dry materials were examined immediately or incubated in moisture chambers. Small pieces of the collected specimens were examined under a Leica EZ4 stereomicroscope and isolated into axenic culture using a single spore technique (Choi et al. 1999) in the Difco potato dextrose agar (PDA) media supplemented with Streptomycin 0.5 g/l. Germinating spores were transferred to new PDA and incubated at 25 ± 1 °C in dark conditions for two weeks. The micro-morphological characters were examined and photographed using a digital camera (Canon 600D, Japan) fitted to a compound microscope (Nikon ECLIPSE Ni, Japan) and the measurements were obtained using the Tarosoft (R) Image Frame Work programme version 0.9.7 (Tarosoft, Thailand). The ex-type living cultures were deposited at the Mae Fah Luang University Culture Collection (MFLUCC) and the herbarium specimens at the Mae Fah Luang University Herbarium (MFLU). The Facesoffungi (FoF) and Index Fungorum numbers were obtained, as explained in Jayasiri et al. (2015) and Index Fungorum (<http://www.indexfungorum.org>), respectively.

DNA extraction, PCR amplification and sequencing

Genomic DNA was extracted from fresh fungal mycelia using the Biospin Fungus Genomic DNA Extraction Kit (BioFlux, P.R. China), according to the

Table 1. Primers and PCR protocols.

Gene regions	Primers	PCR conditions	References
ITS	ITS5/ITS4	95 °C for 4 min, 40 cycles of 94 °C for 45 s, 56 °C for 1 min and 72 °C for 2 min, 72 °C for 10 min	White et al. (1990)
LSU	LR0R/LR5	94 °C for 3 min, 40 cycles of 94 °C for 30 s, 50 °C for 45 s and 72 °C for 2 min, 72 °C for 10 min	Vilgalys and Hester (1990), Rehner and Samuels (1994)
<i>rpb2</i>	fRPB2-5f/fRPB2-7cR	95 °C for 5 min, 35 cycles of 95 °C for 1 min, 55 °C for 1.25 min and 72 °C for 2 min, 72 °C for 10 min	Liu et al. (1999)
<i>tef1-a</i>	EF1-983F/EF1-2218R	94 °C for 3 min, 40 cycles of 94 °C for 30 s, 54 °C for 50 s and 72 °C for 2 min, 72 °C for 10 min	Rehner (2001)

manufacturer's standard protocol. Polymerase chain reactions (PCR) were conducted to amplify the internal transcribed spacer region rDNA (ITS), 28S large subunit rDNA (LSU), RNA polymerase II second largest subunit (*rpb2*) and translation elongation factor 1-alpha (*tef1-a*) using primers and conditions listed in Table 1. The PCR products were visualised on 1% agarose gels, stained with 4S Green Stain and sequenced at SolGent Co., Ltd (South Korea).

Sequence alignment and Phylogenetic analyses

The obtained sequences of ITS, LSU, *rpb2* and *tef1-a* were assembled using SeqMan software version 7.1.0 (DNASTAR Inc., WI) and subjected to BLASTn search against the GenBank nucleotide database at National Center for Biotechnology Information (NCBI) to identify closely-related sequences. Sequence data of related taxa were obtained from previous publications (Su et al. 2016; Yang et al. 2018, 2021; Crous et al. 2019; Hyde et al. 2019; Luo et al. 2019; Monkai et al. 2020; Phukhamsakda et al. 2020; Sun et al. 2020; Ma et al. 2022; Zhai et al. 2022; Zhang et al. 2022; Afshari et al. 2023) and downloaded from the GenBank database (Table 2). The sequences were aligned using MAFFT v.7 online web server (<http://mafft.cbrc.jp/alignment/server/index.html>, Katoh et al. 2019) under default settings and the alignments were trimmed in NGPhylogeny online web server (<https://ngphylogeny.fr/workflows/wkmake/3a4ab-1bef8e7ff3c>, Lemoine et al. 2019). The sequence datasets were combined using SequenceMatrix software version 1.9 (Vaidya et al. 2011). The Maximum Likelihood (ML) phylogenetic analysis was run in the CIPRES Science Gateway platform (Miller et al. 2010), using RAXMLHPC2 on the XSEDE (v. 8.2.10) tool (Stamatakis 2014) under the GTRCAT substitution model and 1,000 non-parametric bootstrap replicates. For Bayesian Inference (BI) analysis, the optimal substitution model of each region was determined using jModelTest2 on the CIPRES Science Gateway under the Akaike Information Criterion (AIC) (Darriba et al. 2012). Bayesian analysis was performed using MrBayes v. 3.2.6 on XSEDE at the CIPRES Science Gateway with four simultaneous Markov Chain runs for 1,000,000 generations. The resulting trees were visualised in FigTree v. 1.4.0 (Rambaut 2012) and edited in Microsoft PowerPoint 2019 (Forethought, Inc., The United States).

Table 2. GenBank accession numbers used in the phylogenetic analyses.

Taxon	Identifier	GenBank accession number			
		ITS	LSU	<i>rpb2</i>	<i>tef1-a</i>
<i>Aquapteridospora aquatica</i>	MFLUCC 17-2371*	NR172447	NG075413	–	–
<i>A. fusiformis</i>	MFLU 18-1601*	MK828652	MK849798	–	MN194056
<i>Distoseptispora adscendens</i>	HKUCC 10820	–	DQ408561	DQ435092	–
<i>D. amniculi</i>	MFLUCC 17-2129*	MZ868770	MZ868761	MZ892982	–
<i>D. appendiculata</i>	MFLUCC 18-0259*	MN163009	MN163023	–	MN174866
<i>D. aqualignicola</i>	KUNCC 21-10729*	OK341186	ON400845	OP413474	OP413480
<i>D. aquamyces</i>	KUNCC 21-10732*	OK341187	OK341199	OP413476	OP413482
<i>D. aquatica</i>	MFLUCC 15-0374*	MF077552	KU376268	–	–
<i>D. aquatica</i>	MFLUCC 16-0904	MK828649	MK849794	–	MN194053
<i>D. aquatica</i>	MFLUCC 18-0646	MK828648	MK849793	–	MN194052
<i>D. aquatica</i>	S-965	MK828647	MK849792	MN124537	MN194051
<i>D. aquisubtropica</i>	GZCC 22-0075*	ON527933	ON527941	ON533685	ON533677
<i>D. areacearum</i>	MFLUCC 23-0211*	OR234707	OR510857	OR250439	OR250442
<i>D. areacearum</i>	MFLUCC 23-0212	OR354399	OR510860	OR481048	OR481045
<i>D. atroviridis</i>	GZCC 20-0511*	MZ868772	MZ868763	MZ892984	MZ892978
<i>D. atroviridis</i>	GZCC 19-0531	MW133915	MZ227223	–	–
<i>D. bambusae</i>	MFLUCC 20-0091*	NR170068	NG074430	MT232881	MT232880
<i>D. bambusae</i>	MFLU 17-1653	MT232712	MT232717	MT232882	–
<i>D. bangkokensis</i>	MFLUCC 18-0262*	MZ518205	MZ518206	–	–
<i>D. cangshanensis</i>	MFLUCC 16-0970*	MG979754	MG979761	–	MG988419
<i>D. caricis</i>	CPC: 36498*	NR166325	MN567632	MN556805	–
<i>D. caricis</i>	CPC: 36442	MN562125	–	MN556806	–
<i>D. chinensis</i>	GZCC 21-0665	MZ474871	MZ474867	–	MZ501609
<i>D. clematidis</i>	MFLUCC 17-2145*	MT310661	MT214617	MT394721	–
<i>D. clematidis</i>	KUN-HKAS:112708	MW723056	MW879523	–	–
<i>D. crassispora</i>	KUMCC 21-10726*	OK310698	OK341196	OP413473	OP413479
<i>D. curvularia</i>	KUMCC 21-10725*	OK310697	OK341195	OP413472	OP413478
<i>D. cylindricospora</i>	KUN-HKAS:115796*	OK491122	OK513523	–	OK524220
<i>D. dehongensis</i>	KUMCC 18-0090*	MK085061	MK079662	–	MK087659
<i>D. dipteroearpi</i>	MFLUCC 22-0104 *	OP600053	OP600052	OP595140	–
<i>D. effusa</i>	GZCC 19-0532*	MW133916	MZ227224	–	–
<i>D. eleiodoxae</i>	MFLUCC 23-0213*	OR234706	OR510856	OR250438	OR250441
<i>D. eleiodoxae</i>	MFLUCC 23-0214	OR354398	OR510859	OR481047	OR481044
<i>D. euseptata</i>	MFLUCC 20-0154*	MW081539	MW081544	MW151860	–
<i>D. euseptata</i>	MFLU 20-0568	MW081540	MW081545	MW084996	MW084994
<i>D. fasciculata</i>	KUMCC 19-0081*	NR172452	NG075417	–	MW396656
<i>D. fluminicola</i>	MFLUCC 15-0417*	MF077553	KU376270	–	–
<i>D. fusiformis</i>	GZCC 20-0512*	MZ868773	MZ868764	MZ892985	MZ892979
<i>D. guizhouensis</i>	GZCC 21-0666*	MZ474868	MZ474869	MZ501611	MZ501610
<i>D. guttulata</i>	MFLUCC 16-0183*	MF077543	MF077554	–	MF135651
<i>D. hyalina</i>	MFLUCC 17-2128*	MZ868769	MZ868760	MZ892981	MZ892976
<i>D. hydei</i>	MFLUCC 20-0115*	MT734661	MT742830	MT767128	–
<i>D. lancangjiangensis</i>	DLUCC 1864*	MW723055	MW879522	–	–
<i>D. leonensis</i>	HKUCC 10822	–	DQ408566	DQ435089	–

Taxon	Identifier	GenBank accession number			
		ITS	LSU	<i>rpb2</i>	<i>tef1-a</i>
<i>D. licualae</i>	MFLUCC 14-1163*	ON650686	ON650675	–	ON734007
<i>D. lignicola</i>	MFLUCC 18-0198*	MK828651	MK849797	–	–
<i>D. longispora</i>	HFJAU 0705*	MH555359	MH555357	–	–
<i>D. martinii</i>	CGMCC 3.18651	KU999975	KX033566	–	–
<i>D. meilingensis</i>	JAUCC 4728	OK562391	OK562397	–	OK562409
<i>D. mengsongensis</i>	HJAUP C2126*	OP787876	OP787874	–	OP961937
<i>D. multiseptata</i>	MFLUCC 15-0609*	KX710145	KX710140	–	MF135659
<i>D. nabanheensis</i>	HJAUP C2003*	OP787877	OP787873	–	OP961935
<i>D. narathiwatensis</i>	MFLUCC 23-0215*	OR234708	OR510858	OR250440	OR250443
<i>D. narathiwatensis</i>	MFLUCC 23-0216	OR354400	OR510861	OR481049	OR481046
<i>D. neorostrata</i>	MFLUCC 18-0376*	MN163008	MN163017	–	–
<i>D. nonrostrata</i>	KUNCC 21-10730*	OK310699	OK341198	OP413475	OP413481
<i>D. obclavata</i>	MFLUCC 18-0329*	MN163012	MN163010	–	–
<i>D. obpyriformis</i>	MFLUCC 17-1694*	–	MG979764	MG988415	MG988422
<i>D. obpyriformis</i>	DLUCC 0867	MG979757	MG979765	MG988416	MG988423
<i>D. pachyconidia</i>	KUMCC 21-10724*	OK310696	OK341194	OP413471	OP413477
<i>D. palmarum</i>	MFLUCC 18-1446*	MK085062	MK079663	MK087670	MK087660
<i>D. palmarum</i>	MFLU 18-0588	NR165897	NG067856	–	–
<i>D. phangngaensis</i>	MFLUCC 16-0857*	NR166230	–	–	MF135653
<i>D. rayongensis</i>	MFLUCC 18-0415*	NR171938	NG073624	–	MH463253
<i>D. rayongensis</i>	MFLU 18-1045	MH457172	MH457137	MH463255	–
<i>D. rostrata</i>	MFLUCC 16-0969*	MG979758	MG979766	MG988417	MG988424
<i>D. rostrata</i>	DLUCC 0885	MG979759	MG979767	–	MG988425
<i>D. rostrata</i>	MFLU 18-0479	NR157552	NG064513	–	–
<i>D. saprophytica</i>	MFLUCC 18-1238*	NR172454	NG075419	MW504069	MW396651
<i>D. septata</i>	GZCC 22-0078*	ON527939	ON527947	ON533690	ON533683
<i>D. sinensis</i>	HJAUP C2044*	OP787878	OP787875	–	OP961936
<i>D. songkhlaensis</i>	MFLUCC 18-1234*	MW286482	MW287755	–	MW396642
<i>D. submersa</i>	MFLUCC 16-0946	MG979760	MG979768	MG988418	MG988426
<i>D. suoluensis</i>	MFLUCC 17-0224*	NR168764	NG068552	–	MF135654
<i>D. tectonae</i>	MFLUCC 12-0291*	KX751711	KX751713	KX751708	KX751710
<i>D. tectonigena</i>	MFLUCC 12-0292*	NR154018	KX751714	KX751709	–
<i>D. thailandica</i>	MFLUCC 16-0270*	MH275060	MH260292	–	MH412767
<i>D. thysanolaenae</i>	KUN-HKAS: 112710	MW723057	MW879524	–	MW729783
<i>D. thysanolaenae</i>	KUMCC 18-0182	MK045851	MK064091	–	MK086031
<i>D. tropica</i>	GZCC 22-0076*	ON527935	ON527943	ON533687	ON533679
<i>D. verrucosa</i>	GZCC 20-0434*	MZ868771	MZ868762	MZ892983	MZ892977
<i>D. wuzhishanensis</i>	GZCC 22-0077*	ON527938	ON527946	–	ON533682
<i>D. xishuangbannaensis</i>	KUMCC 17-0290*	MH275061	MH260293	MH412754	MH412768
<i>D. yongxiensis</i>	JAUCC 4725	OK562388	OK562394	–	OK562406
<i>D. yongxiensis</i>	JAUCC 4726	OK562389	OK562395	–	OK562407
<i>D. yunjushanensis</i>	JAUCC 4723	OK562392	OK562398	–	OK562411
<i>D. yunjushanensis</i>	JAUCC 4724	OK562393	OK562399	–	OK562410
<i>D. yunnanensis</i>	MFLUCC 20-0153*	MW081541	MW081546	MW151861	MW081541

Ex-type strains are indicated with an asterisk (*) after the collection number; “–” indicates unavailable sequences; sequences produced in the current study are in bold.

Abbreviations

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

Results

Phylogenetic analyses

The combined ITS, LSU, *rpb2* and *tef1- α* dataset consisted of 83 strains, with *Aquapteridospora aquatica* X.D. Yu, W. Dong & H. Zhang (MFLUCC 17-2371) and *A. fusiformis* Z.L. Luo, D.F. Bao, H.Y. Su & K.D. Hyde (MFLU 18-1601) as outgroup taxa (Table 2). The final alignment comprised 3,383 characters (ITS: 567 bp, LSU: 855 bp, *rpb2*: 1,051 bp, *tef1- α* : 909 bp), including gaps. The final ML optimisation likelihood value of the best RAxML tree was -33894.57 and the matrix had 1,637 distinct alignment patterns, with 29.85% undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.240315, C = 0.262752, G = 0.283175, T = 0.213758; substitution rates AC = 1.324179, AG = 3.427671, AT = 1.239665, CG = 0.914354, CT = 6.950002, GT = 1.0; gamma distribution shape parameter α = 0.273123. The RAxML and Bayesian analyses yielded a similar tree topology.

The topology of our phylogenetic tree is nearly identical to previous publications, but there are some differences, which may be due to different taxon sampling. As new species are introduced into this genus frequently, taxon sampling conducted for different studies varies. In our phylogenetic analyses, two strains of the new species *Distoseptispora areacearum* (MFLUCC 23-0211 and MFLUCC 23-0212) formed a robust subclade (100% ML, 1.00 PP) independently. The species has close relationships with *D. amniculi* (MFLUCC 17-2129), *D. bangkokensis* (MFLUCC 18-0262), *D. cangshanensis* (MFLUCC 16-0970) and *D. cylindricospora* (KUN-HKAS:115796) with 82% ML bootstrap support. The other two new species, *D. eleiodoxae* and *D. narathiwatensis*, clustered with *D. saprophytica* (MFLUCC 18-1238), *D. palmarum* (MFLU 18-0588 and MFLUCC 18-1446) and *D. tropica* (GZCC 22-0076) with 0.96 PP support. *Distoseptispora eleiodoxae* (strains MFLUCC 23-0213 and MFLUCC 23-0214) formed a robust subclade (100% ML, 1.00 PP) basal to *D. narathiwatensis* (MFLUCC 23-0215 and MFLUCC 23-0216), *D. saprophytica* (MFLUCC 18-1238) and *D. palmarum* (MFLU 18-0588 and MFLUCC 18-1446) with 90% ML and 1.00 PP support. *Distoseptispora narathiwatensis* (MFLUCC 23-0215 and MFLUCC 23-0216) formed a sister clade with *D. saprophytica* (MFLUCC 18-1238) with 100% ML and 1.00 PP support (Fig. 1).

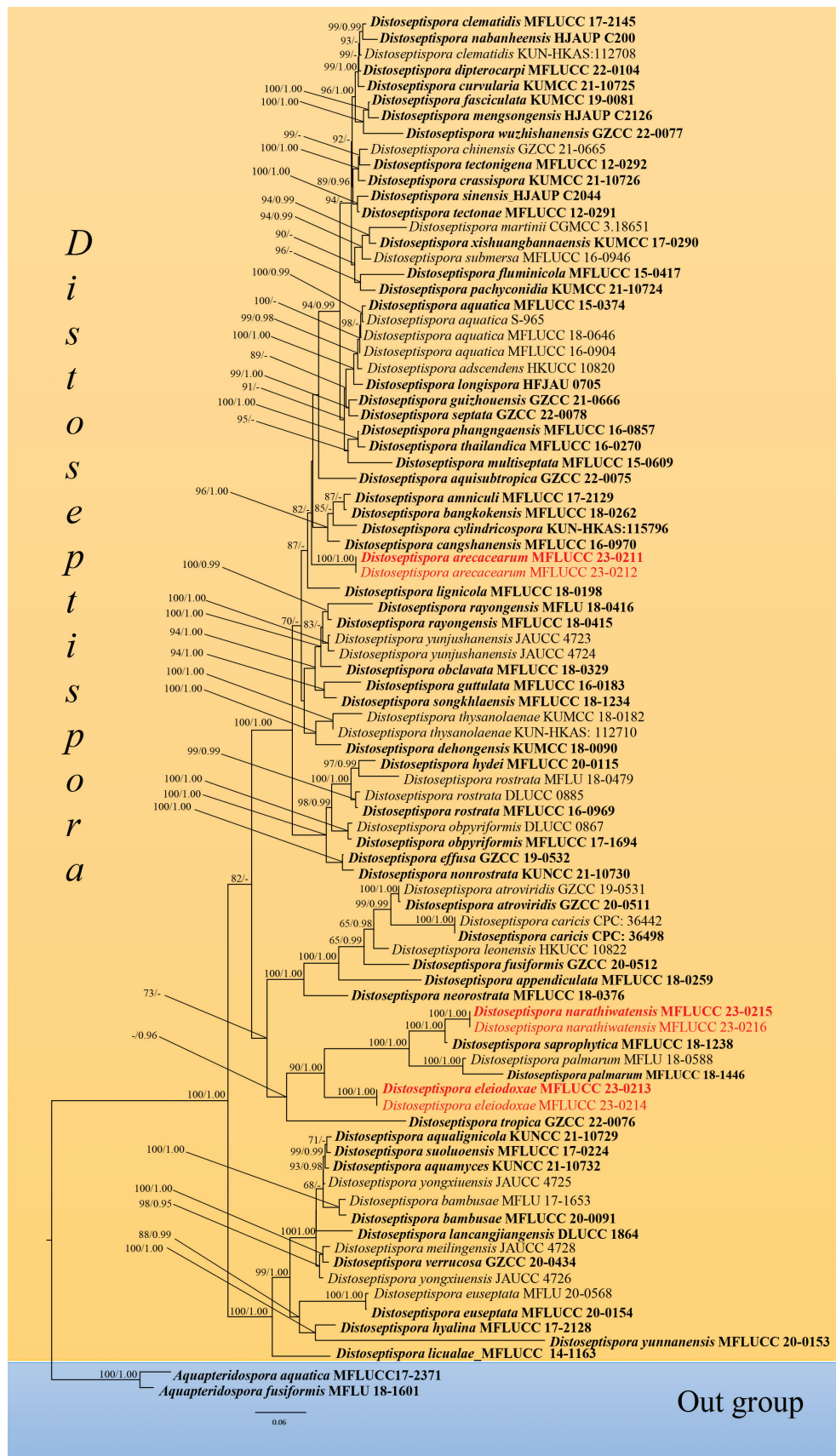


Figure 1. Maximum Likelihood tree generated from combined ITS, LSU, *rpb2* and *tef1-α* sequence data. Bootstrap support values $\geq 65\%$ and Bayesian posterior probabilities ≥ 0.95 are demonstrated at the nodes. The new taxa are indicated in red bold. Ex-type strains are in black bold.

Taxonomy

***Distoseptispora areacearum* O. Karimi, Q.R. Li & K.D. Hyde, sp. nov.**

Index Fungorum number: IF900843

Facesoffungi number: FoF14756

Fig. 2

Etymology. The epithet “*areacearum*” refers to host family, Aceraceae.

Holotype. MFLU 23-0276.

Description. **Saprobic** on submerged rachis of *Licuala paludosa* in peat swamp forest. **Sexual morph:** Undetermined. **Asexual morph:** Hyphomycetous. Colonies gregarious or scattered, effuse, hairy, dark brown to black. **Mycelium** mostly immersed, composed of branched, septate, smooth hyphae. **Conidiophores** 70–140 × 5.1–6.3 µm ($\bar{x}$ = 110 × 5.5 µm, n = 20), macronematous, mononematous, unbranched, erect, straight or flexuous, cylindrical, smooth, thick-walled, brown, 4–7 septa, sometimes consists a swollen cell in the middle or towards the apex. **Conidiogenous cells** 13–25 × 4.5–6 µm ($\bar{x}$ = 17 × 5 µm, n = 20), monoblastic or polyblastic, terminal or subterminal, determinate, cylindrical, brown. **Conidia** 25–60 × 7–17 µm ($\bar{x}$ = 44 × 10 µm, n = 30), acrogenous, solitary, cylindrical, obclavate to obpyriform or irregular, straight or curved, 4–10-distoseptate, brown, thick-walled, smooth, round apex, truncated base, sometimes with percurrent regeneration forming a secondary conidium from the conidial apex.

Culture characteristics. Colonies grown on PDA, reaching 50 mm in diameter after 15 days at 25 °C, under dark conditions, circular, fimbriate edge, flat, dull surface, radiating outwards, felted, medium dense, without pigment diffusion and sporulation, brown on the top, reverse dark brown to black.

Material examined. Thailand. Narathiwat Province: Yi-ngo District, peat swamp forest, on submerged rachis of *Licuala paludosa*, 06 April 2022, Omid Karimi, S5PP3SG (MFLU 23-0276, **holotype**); ex-type culture MFLUCC 23-0211, additional living culture MFLUCC 23-0212.

Notes. Morphologically, our proposed new species is similar to *Distoseptispora dehongensis* W. Dong, H. Zhang & K.D. Hyde and *D. obpyriformis* Z.L. Luo & H.Y. Su in having macronematous, mononematous, unbranched, erect, straight or flexuous, cylindrical, septate conidiophores, terminal, determinate, cylindrical, brown conidiogenous cells and acrogenous, distoseptate, straight or curved conidia (Luo et al. 2018; Hyde et al. 2019). However, our isolate differs from *D. dehongensis* (HKAS 101738) in having longer and wider conidiophores (70–140 × 5.1–6.3 µm vs. 45–80 × 4–5 µm), with swollen cells, longer and wider conidia (25–60 × 7–17 µm vs. 17–30 × 7.5–10 µm) and more distosepta (4–10-distoseptate vs. 3–5-distoseptate). *Distoseptispora areacearum* (MFLU 23-0276) differs from *D. obpyriformis* (MFLU 18-0476) in having conidiophores with swollen cells and shorter conidia (25–60 µm vs. 53–71 µm) (Luo et al. 2018). The BLASTn searches of the ITS sequence of *D. areacearum* (MFLUCC 23-0211) resulted in *D. aquatica* Z.L. Luo, H.Y. Su & K.D. Hyde (MFLUCC 18-0646) with 92.21% similarity across 100% of the query sequence coverage, while the LSU sequence of *D. areacearum* has 99.09% similarity across 100% of the sequence coverage with *D. phangngaensis* J. Yang, Maharachch. & K.D. Hyde (MFLUCC 16-0857). *Distoseptispora areacearum* (MFLU 23-0276) is easily distinguishable from *D. aquatica* (HKAS 83991) in having longer



Figure 2. *Distoseptispora areacearum* (MFLU 23-0276, holotype) **a** host material **b** colonies on the substrate **c–e** conidiophores and conidia **f–i** conidia **j, k** culture on PDA. Scale bars: 200 µm (**b**); 50 µm (**c–e**); 10 µm (**f–i**).

conidiophores (70–140 µm vs. 29–41 µm) and shorter conidia (25–60 µm vs. 110–157 µm) with less distosepta (4–10-distoseptate vs. 15–28-distoseptate) (Su et al. 2016). *Distoseptispora areacearum* (MFLU 23-0276) differs from *D. phangngaensis* (MFLU 17-0855) in having longer conidiophores (70–140 µm vs. 18–30(–40) µm) and shorter conidia (25–60 µm vs. 165–350 µm) (Yang et al. 2018). Therefore, we introduced *D. areacearum* (MFLU 23-0276) as a novel species, based on morphological and phylogenetic analyses.

***Distoseptispora eleiodoxae* O. Karimi, Q.R. Li & K.D. Hyde, sp. nov.**

Index Fungorum number: IF900844

Facesoffungi number: FoF14757

Fig. 3

Etymology. The epithet “*eleiodoxae*” refers to the name of the host genus, *Eleiodoxa conferta*.

Holotype. MFLU 23-0277.

Description. *Saprobic* on submerged rachis of *Eleiodoxa conferta* in peatswamp forest. **Sexual morph:** Undetermined. **Asexual morph:** Hyphomycetous. **Mycelium** immersed to superficial, septate, smooth, brown to dark brown. **Colonies** on submerged rachis, solitary, scattered, dark brown to black. **Conidiophores** 71–161 × 5–6.5 µm ($\bar{x}$ = 110 × 5.7 µm, n = 20), macronematous, mononematous, cylindrical, erect, straight to flexuous, unbranched, smooth or finely verrucose, thick-walled, dark brown, 5–10-septate with lobed basal cells, percurrent proliferations at the apex. **Conidiogenous cells** 13.5–18.8 × 5–6.8 µm ($\bar{x}$ = 15.96 × 5.6 µm, n = 20), holoblastic, monoblastic, terminal, integrated, cylindrical to ampulliform, percurrent, brown to dark brown, smooth. **Conidia** 31.5–48 × 13.5–15.8 µm ($\bar{x}$ = 40.8 × 14.8 µm, n = 30), secession schizolytic, solitary, obpyriform, rostrate, truncated base, 6–7-euseptate, verrucose, thick-walled, brown with dark brown to black cells in the middle, paler towards the apex.

Culture characteristics. Colonies grown on PDA, reaching 30 mm in diameter after 15 days at 25 °C, under dark conditions, circular, entire to radially with lobate edge, well-defined margin, low convex, dull surface, felted, dense, mycelium superficial to immersed, without pigment diffusion and sporulation, greyish-brown on the top with dark brown margin, reverse brown with dark brown centre and margin.

Material examined. Thailand. Narathiwat Province: Yi-ngo District, peatswamp forest, on submerged rachis of *Eleiodoxa conferta*, 06 April 2022, Omid Karimi, S5PP8N1SG (MFLU 23-0277, **holotype**); ex-type culture MFLUCC 23-0213, additional living culture MFLUCC 23-0214.

Notes. *Distoseptispora eleiodoxae* (MFLU 23-0277) shares similar characteristics with *D. tropica* J. Ma & Y.Z. Lu (HKAS 123761), in having macronematous, mononematous, cylindrical, erect, straight, unbranched conidiophores with holoblastic, monoblastic, terminal, cylindrical, thick-walled conidiogenous cells and verrucose, rostrate conidia (Ma et al. 2022). However, *D. eleiodoxae* (MFLU 23-0277) differs from *D. tropica* (HKAS 123761) in having shorter and wider obpyriform conidia (31.5–48 × 13.5–15.8 µm vs. 39–75 × 7.5–10.5 µm), with broad and darker middle cells, no guttules and lacking conspicuous hyphae attachment to conidia. The BLAST search against GenBank showed that the

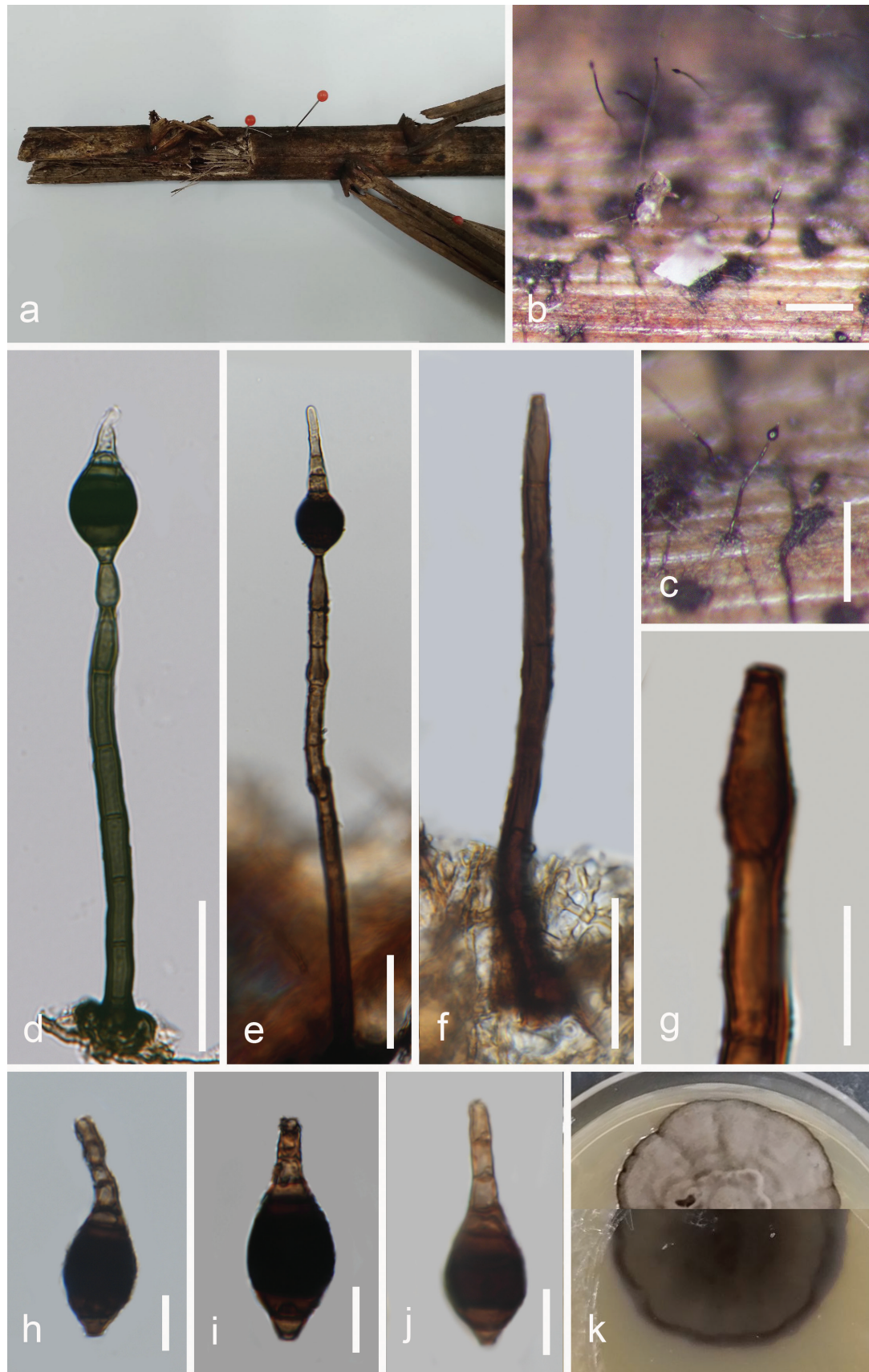


Figure 3. *Distoseptispora eleiodoxae* (MFLU 23-0277, holotype) **a** host material **b, c** colonies on the substrate **d–f** conidiophores and conidia **g** conidiogenous cell **h–j** conidia **k** culture on PDA (top and reverse). Scale bars: 100 μ m (**b, c**); 30 μ m (**d–f**); 10 μ m (**g–j**).

ITS and LSU sequences of the new isolate, *D. eleiodoxae* (MFLUCC 23-0213), share 84.25% similarity across 100% sequence coverage with *D. tropica* (GZCC 22-0076) and 96.09% similarity across 100% sequence coverage with *D. effusa* L.L. Liu & Z.Y. Liu, respectively. *Distoseptispora eleiodoxae* (MFLU 23-0277) differs from *D. effusa* (GZAAS 20-0427) in having shorter conidia (31.5–48 vs. 35.5–113 µm) (Yang et al. 2021). Based on a pairwise comparison of ITS, LSU, *rpb2* and *tef1-α* nucleotides, *D. eleiodoxae* (MFLUCC 23-0213) differs from *D. tropica* (GZCC 22-0076) in 70/536 bp (13.05%) for ITS, 50/834 bp (5.99%) for LSU, 141/1052 bp (13.40%) for *rpb2* and 96/888 bp (10.8%) for *tef1-α* (without including gaps). Therefore, we introduced *D. eleiodoxae* (MFLU 23-0277) as a novel species, based on the morphological evidence and according to the species delimitation guidelines proposed by Chethana et al. (2021) and Maharachchikumbura et al. (2021).

***Distoseptispora narathiwatensis* O. Karimi, Q.R. Li & K.D. Hyde, sp. nov.**

Index Fungorum number: IF900845

Facesoffungi number: FoF14758

Fig. 4

Etymology. The epithet “*narathiwatensis*” refers to Narathiwat Province, where the holotype was collected.

Holotype. MFLU 23-0278.

Description. *Saprobic* on dead petiole of *Eugeissona tristis* in peatswamp forest. **Sexual morph:** Undetermined. **Asexual morph:** Hyphomycetous. **Colonies** superficial, effuse, hairy, gregarious, brown. **Mycelium** immersed to superficial, composed of septate, branched, pale brown hyphae. **Conidiophores** 27–155 × 3–6.5(–7) µm ($\bar{x}$ = 104 × 5 µm, n = 50), macronematous, mononematous, cylindrical, straight or flexuous, occasionally slightly curved in the middle and near the base and the apex, up to 10 septa, slightly constricted at septa, unbranched, brown, thin-walled, smooth, often containing inflated or constricted cells at the apex or middle, sometimes percurrent with annellations. **Conidiogenous** cells 7–17 × 4–5.5 µm ($\bar{x}$ = 12.5 × 5 µm, n = 30), holoblastic, mono- to polyblastic, integrated, determinate, terminal and intercalary, subcylindrical, brown, smooth. **Conidia** 12–38 × 4.5–8 µm ($\bar{x}$ = 27 × 6.5 µm, n = 30), secession schizolytic, solitary or occasionally catenate, dry, thin-walled, smooth, subcylindrical to obclavate to conical, straight or curved, 1–7-distoseptate, slightly constricted at septa, olivaceous to brown, apex rounded, truncated base with slightly pigmented scar, often the primary cells of conidia are narrower than the second ones which are often inflated.

Culture characteristics. Colonies grown on PDA, reaching 50 mm in diameter after 15 days at 25 °C, under dark conditions, circular, entire margin, well-defined margin, low convex, dull surface, felted, dense, mycelium mostly superficial, without pigment diffusion and sporulation, medium brown to reddish-brown with dark brown edge on the top, reverse-side dark brown to black.

Material examined. Thailand. Narathiwat Province: Yi-ngo District, peatswamp forest, on dead petiole of *Eugeissona tristis*, 06 April 22, Omid Karimi, 35Y (MFLU 23-0278, **holotype**); ex-type culture MFLUCC 23-0215, additional living culture MFLUCC 23-0216.



Figure 4. *Distoseptispora narathiwatensis* (MFLU 23-0278, holotype) **a** host material **b** colonies on the substrate **c–e** conidiophores and conidia **f** conidiogenous cell **g–j** conidia **k, l** culture on PDA. Scale bars: 100 µm (**b**); 50 µm (**c–e**); 10 µm (**f–j**).

Notes. *Distoseptispora narathiwatensis* (MFLU 23-0278) is similar to *D. saprophytica* (MFLU 18-1568), but it can be distinguished in having longer and wider conidiophores ($27\text{--}155 \times 3\text{--}6.5$ (-7) μm vs. $50\text{--}140 \times 3.2\text{--}4.2$ μm) and conidiogenous cells ($7\text{--}17 \times 4\text{--}5.5$ μm vs. $5\text{--}11.5 \times 3\text{--}4.5$ μm). In *D. narathiwatensis* (MFLU 23-0278), the conidiophore is slightly curved at the base, middle and near the top in contrast to *D. saprophytica* (MFLU 23-0278), which is characterised by sharp curving near the base; also in *D. narathiwatensis*, the conidiophore cells are often inflated or constricted at the apex or middle which is not observed in *D. saprophytica* (Dong et al. 2021). Conidiogenous cells of *D. narathiwatensis* are terminal and intercalary and their conidia are not acrogenous as in *D. saprophytica*. The primary cell in the conidium is often narrower than the second one and the second cell is often inflated, which is not observed in *D. saprophytica*. The BLAST search against the GenBank showed that the ITS and *rpb2* sequences of the new isolate, *D. narathiwatensis* (MFLUCC 23-0215), share 98.33% similarity across 100% sequence coverage and 98.63% similarity across 78% sequence coverage with *D. saprophytica* (MFLUCC 18-1238), respectively. In a BLAST search against GenBank, the LSU and *tef1-a* sequences of *D. narathiwatensis* (MFLUCC 23-0215) share 99.3% similarity across 85% sequence coverage and 94.12% similarity across 94% sequence coverage with *D. palmarum* (MFLU 18-0588), respectively. However, *D. palmarum* is distinguished in having longer ($12\text{--}38$ μm vs. $35\text{--}180$ μm), elongated, greenish-black to brown conidia (Hyde et al. 2019). Based on a pairwise comparison of ITS and LSU nucleotides, *D. narathiwatensis* (MFLUCC 23-0215) differs from *D. saprophytica* (MFLUCC 18-1238) by 22/580 bp (3.8%), 16/870 bp (1.8%) differences, respectively (without including gaps). Therefore, we introduced *D. narathiwatensis* (MFLU 23-0278) as a novel species, based on the morphological evidence and according to the species delimitation guidelines proposed by Chethana et al. (2021) and Maharachchikumbura et al. (2021).

Discussion

Peat swamp forests are unique habitats found in only a few regions worldwide (Jackson et al. 2009). The destruction caused by humans threatens them; hence more extensive studies on fungal identification are needed before the extinction of fungal species. Pinnoi et al. (2006, 2009) recorded sporidesmium-like taxa on the palm species *Eleiodoxa conferta* and *Calamus* sp. in Sirindhorn peat swamp forest, Narathiwat, Thailand, based on morphological data. In this study, three new *Distoseptispora* species (*D. areacearum*, *D. eleiodoxae* and *D. narathiwatensis*) from peat swamp forest in Thailand are introduced, based on multilocus phylogenetic analysis (ITS, LSU, *rpb2* and *tef1-a*) (Fig. 1) and morphology (Figs 2–4).

The fungal diversity in peat swamp forest has not been well studied and a few previously studies (Pinruan et al. 2002, 2004a, 2004b, 2007, 2008, 2010a, 2010b, 2014; Pinnoi et al. 2003a, 2003b, 2004, 2006, 2009, 2010; Voglmayr and Yule 2006; Sivichai and Boonyuen 2010; Boonyuen et al. 2012) show a high fungal diversity in this habitat, especially in Thailand, but some of the previous studies (Pinruan et al. 2002, 2007, 2014; Pinnoi et al. 2003a, 2003b, 2004, 2006, 2009; Sivichai and Boonyuen 2010) lack molecular data. As only morphological data are insufficient to identify a fungal species (Chethana et al. 2021; Maharachchikumbura et al.

2021), studying the fungal diversity by combining morphological and molecular data are required and this has been followed in this study.

Except for *Distoseptispora hyalina* J. Yang & K.D. Hyde and *D. licualae* Konta & K.D. Hyde, most *Distoseptispora* species have been recorded as having an asexual morph and their characters, such as size, shape, colour and the number of septa in conidiophores and conidia, are crucial for distinguishing species. Morphologically, *Distoseptispora* is similar to *Ellisembia* Subram and *Sporidesmium* Link; therefore, it is problematic to recognise *Distoseptispora* species by only morphological signatures (Su et al. 2016; Hyde et al. 2019; Luo et al. 2019; Yang et al. 2021). Different studies have explored the taxonomy of *Distoseptispora* using various combinations of gene regions, such as combined ITS, LSU (Tibpromma et al. 2018), combined LSU, ITS, *rpb2* (Monkai et al. 2020) or combined LSU, ITS, *tef1-a* and *rpb2* (Zhang et al. 2022). In our study, we constructed the phylogenetic tree using concatenated ITS, LSU, *rpb2* and *tef1-a*. In this study, *Distoseptispora clematidis* (MFLUCC 17-2145) and *D. nabanheensis* Jing W. Liu, X.G. Zhang & Jian Ma (HJAUP C2003) formed a sister clade, consistent with previous research (Liu et al. 2023). However, *D. clematidis* (KUN-HKAS:112708) appeared separated from these two taxa, presenting an unresolved relationship. The phylogenetic relationship amongst these three taxa is not comparable with the previous studies due to the lack of all these taxa together in their phylogenetic trees (Afshari et al. 2023; Liu et al. 2023). The unresolved clade's origin may stem from the lack of *rpb2* sequence data for *D. clematidis* (KUN HKAS:112708) in contrast to the other two taxa where this gene region is available. This suggests that different taxon sampling and protein-coding sequences can influence the topology of the tree. However, further studies are essential to validate this hypothesis.

Morphologically, some taxa that share similarities exhibit distinct phylogenies. For instance, *D. arecacearum* shares a morphological resemblance with *D. dehongensis*, although they are phylogenetically distinct. Similarly, *D. eleiodoxae* shows morphological similarities to *D. tropica*, but resides in a separate clade in the phylogenetic tree. *Distoseptispora narathiwatensis* forms a sister clade with *D. saprophytica* despite the differences highlighted by the pairwise comparison of ITS, LSU and other genetic markers. These encompass 22/580 bp (3.8%) and 16/870 bp (1.8%) differences for ITS and LSU, respectively, excluding gaps. Moreover, distinctions in the morphology of conidiophores and the absence of acrogenous conidia further contribute to the differentiation between *D. narathiwatensis* and *D. saprophytica*. Our study confirmed the necessity of associating molecular data with morphological characters to distinguish them, as previously demonstrated in other studies (Su et al. 2016; Hyde et al. 2019; Luo et al. 2019; Yang et al. 2021; Ma et al. 2022).

To date, the majority of *Distoseptispora* species have been reported from China (42 species) and Thailand (23 species), primarily on dead plant materials in freshwater (44 species) and terrestrial (21 species) habitats. In most cases, the hosts are unknown. Although in 19 cases, their hosts have been identified, two of which have been reported from palm, including *D. palmarum* from *Cocos nucifera* and *D. licualae* from dead leaves of *Licuala glabra* in terrestrial habitats (Hyde et al. 2016, 2021; Su et al. 2016; Xia et al. 2017; Tibpromma et al. 2018; Yang et al. 2018; Luo et al. 2019; Phookamsak et al. 2019; Monkai et al. 2020; Phukhamsakda et al. 2020, 2022; Song et al. 2020; Sun et al. 2020; Dong et al.

2021; Li et al. 2021; Shen et al. 2021; Jayawardena et al. 2022; Ma et al. 2022; Zhai et al. 2022; Zhang et al. 2022; Konta et al. 2023; Liu et al. 2023). *Distoseptispora* species have been recorded as saprophytes and their reported limited geographic distribution (China and Thailand) is most likely due to increased attention by mycologists in these areas on saprophytic fungi in aquatic and terrestrial habitats. This study shows that there is much to be done in this regard. Ongoing and future investigations will reveal the diversity and functions of these microorganisms in this ecosystem.

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Additional information

Conflict of interest

The authors have declared that no competing interests exist.

Ethical statement

No ethical statement was reported.

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Author contributions

Morphological identification, photo-plates, and phylogenetic analyzes were completed by Omid Karimi and Raheleh Asghari. The original draft was written by Omid Karimi, and K.W. Thilini Chethana, Antonio R.G. Farias, Saithong Kaewchai, Kevin D. Hyde, Qirui Li revised the paper.

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Data availability

All of the data that support the findings of this study are available in the main text.

References

- Afshari N, Gomes de Farias AR, Bhunjun CS, Phukhamsakda C, Hyde KD, Lumyong S (2023) *Distoseptispora dipterocarpi* sp. nov. (Distoseptisporaceae), a lignicolous fungus on decaying wood of *Dipterocarpus* in Thailand. *Current Research in Environmental & Applied Mycology* 13(1): 68–78. <https://doi.org/10.5943/cream/13/1/5>
- Boonyuen N, Sri-indrasutdhi V, Suetrong S, Sivichai S, Jones EBG (2012) *Annulatascus aquatorba* sp. nov., a lignicolous freshwater ascomycete from Sirindhorn Peat Swamp Forest, Narathiwat, Thailand. *Mycologia* 104(3): 746–757. <https://doi.org/10.3852/11-238>
- Calabon MS, Hyde KD, Jones EBG, Luo ZL, Dong W, Hurdeal VG, Gentekaki E, Rossi W, Leonardi M, Thiyagaraja V, Lestari AS, Shen HW, Bao DF, Boonyuen N, Zeng M (2022) Freshwater fungal numbers. *Fungal Diversity* 114(1): 3–235. <https://doi.org/10.1007/s13225-022-00503-2>
- Chen YJ, Jayawardena RS, Bhunjun CS, Harishchandra DL, Hyde KD (2020) *Pseudocercospora dypsidis* sp. nov. (Mycosphaerellaceae) on *Dypsis lutescens* leaves in Thailand. *Phytotaxa* 474(3): 218–234. <https://doi.org/10.11646/phytotaxa.474.3.2>
- Chethana KWT, Manawasinghe IS, Hurdeal VG, Bhunjun CS, Appadoo MA, Gentekaki E, Raspé O, Promputtha I, Hyde KD (2021) What are fungal species and how to delineate them? *Fungal Diversity* 109(1): 1–25. <https://doi.org/10.1007/s13225-021-00483-9>
- Choi YW, Hyde KD, Ho WWH (1999) Single spore isolation of fungi. *Fungal Diversity* 3: 29–38.
- Chou T, Xu W, Mukhtar I, Quan X, Jiang S, Huang R, Xie B, Xu W (2019) First report of leaf spot disease caused by *Colletotrichum siamense* on *Chrysalidocarpus lutescens* in China. *Plant Disease* 103(6): 1–5. <https://doi.org/10.1094/PDIS-11-18-2049-PDN>
- Crous PW, Wingfield MJ, Lombard L, Roets F, Swart WJ, Alvarado P, Carnegie AJ, Moreno G, Luangsaard J, Thangavel R, Alexandrova AV, Baseia IG, Bellanger JM, Bessette AE, Bessette AR, De la Peña-Lastra S, García D, Gené J, Pham THG, Heykoop M, Malysheva E, Malysheva V, Martín MP, Morozova OV, Noisripoom W, Overton BE, Rea AE, Sewall BJ, Smith ME, Smyth CW, Tasanathai K, Visagie CM, Adamčík S, Alves A, Andrade JP, Aninat MJ, Araújo RVB, Bordallo JJ, Bouffleur T, Baroncelli R, Barreto RW, Bolin J, Cabero J, Caboň M, Cafà G, Caffot MLH, Cai L, Carlavilla JR, Chávez R, de Castro RRL, Delgat L, Deschuyteneer D, Dios MM, Domínguez LS, Evans HC, Eyssartier G, Ferreira BW, Figueiredo CN, Liu F, Fournier J, Galli-Terasawa LV, Gil-Durán C, Glienke C, Gonçalves MFM, Gryta H, Guarro J, Himaman W, Hywel-Jones N, Iturrieta-González I, Ivanushkina NE, Jargeat P, Khalid AN, Khan J, Kiran M, Kiss L, Kochkina GA, Kolařík M, Kubátová A, Lodge DJ, Loizides M, Luque D, Manjón JL, Marbach PAS, Massola Jr NS, Mata M, Miller AN, Mongkolsamrit S, Moreau PA, Morte A, Mujic A, Navarro-Ródenas A, Németh MZ, Nóbrega TF, Nováková A, Olariaga I, Ozerskaya SM, Palma MA, Petters-Vandresen DAL, Piontelli E, Popov ES, Rodríguez A, Requejo Ó, Rodrigues ACM, Rong

- IH, Roux J, Seifert KA, Silva BDB, Sklenář F, Smith JA, Sousa JO, Souza HG, De Souza JT, Švec K, Tanchaud P, Tanney JB, Terasawa F, Thanakitpipattana D, Torres-Garcia D, Vaca I, Vaghefi N, van Iperen AL, Vasilenko OV, Verbeken A, Yilmaz N, Zamora JC, Zapata M, Jurjević Ž, Groenewald JZ (2019) Fungal Planet description sheets: 951–1041. *Persoonia* 43(1): 223–425. <https://doi.org/10.3767/persoonia.2019.43.06>
- Darriba D, Taboada GL, Doallo R, Posada D (2012) JModelTest 2: More models, new heuristics and parallel computing. *Nature Methods* 9(8): 772. <https://doi.org/10.1038/nmeth.2109>
- Dong W, Hyde HD, Jeewon R, Doilom M, Yu XD, Wang GN, Liu NG, Hu DM, Nalumpang S, Zhang H (2021) Towards a natural classification of annulatascaceae-like taxa II: Introducing five new genera and eighteen new species from freshwater. *Mycosphere: Journal of Fungal Biology* 12(1): 1–88. <https://doi.org/10.5943/mycosphere/12/1/1>
- Dransfield J, Uhl NW, Asmussen CB, Baker WJ, Harley MM, Lewis CE (2008) *Genera Palmarum – The evolution and classification of the palms*. Royal Botanic Gardens, Kew, UK, London, 732 pp.
- El Meleigi MA, Omar AF, Al Rokibah AA, Alsohim A, Al Jamhan KA, Sukar NA (2019) Molecular identification and pathogenicity of phytophthora nicotianae-caused bud rot disease of washingtonia palms in saudi arabia and use of Lysobacter enzymes as a bioagent in an in vitro study. *Egyptian Journal of Biological Pest Control* 29(1): 1–9. <https://doi.org/10.1186/s41938-019-0107-y>
- Fröhlich J, Hyde KD (2000) *Palm microfungi*. Fungal Diversity Press, Hong Kong, 1–393.
- Fröhlich J, Hyde KD, Petrini O (2000) Endophytic fungi associated with palms. *Mycological Research* 104(10): 1202–1212. <https://doi.org/10.1017/S095375620000263X>
- Fujimoto K, Miura M, Kobayashi S, Simbolon H (2019) Habitat evolution of a peat swamp forest and belowground carbon sequestration during the Holocene along the coastal lowland in Central Sumatra, Indonesia. *Progress in Earth and Planetary Science* 6(1): 1–13. <https://doi.org/10.1186/s40645-019-0288-8>
- Hakim SS, Yuwati TW, Nurulita S (2017) Isolation of peat swamp forest foliar endophyte fungi as biofertiliser. *Journal of Wetlands Environmental Management* 5(1): 10–17. <https://doi.org/10.20527/jwem.v5i1.111>
- Hyde KD (1988) The genus *Linocarpon* from the mangrove palm *Nypa fruticans*. *Nippon Kingakkai Kaiho* 29: 338–350.
- Hyde KD, Taylor JE, Fröhlich J (2000) *Genera of Ascomycetes from palm*. Fungal Diversity Press, Hong Kong, 247 pp.
- Hyde KD, Hongsanan S, Jeewon R, Bhat DJ, McKenzie EHC, Jones EBG, Phookamsak R, Ariyawansa HA, Boonmee S, Zhao Q, Abdel-Aziz FA, Abdel-Wahab MA, Banmai S, Chomnunti P, Cui BK, Daranagama DA, Das K, Dayarathne MC, de Silva NI, Dissanayake AJ, Doilom M, Ekanayaka AH, Gibertoni TB, Góes-Neto A, Huang SK, Jayasiri SC, Jayawardena RS, Konta S, Lee HB, Li WJ, Lin CG, Liu JK, Lu YZ, Luo ZL, Manawasinghe IS, Manimohan P, Mapook A, Niskanen T, Norphanphoun C, Papizadeh M, Perera RH, Phukhamsakda C, Richter C, André ALCM, Drechsler-Santos ER, Senanayake IC, Tanaka K, Tennakoon TMDS, Thambugala KM, Tian Q, Tibpromma S, Thongbai B, Vizzini A, Wanasinghe DN, Wijayawardene NN, Wu HX, Yang J, Zeng XY, Zhang H, Zhang JF, Bulgakov TS, Camporesi E, Bahkali AH, Amoozegar MA, Araujo-Neta LS, Ammirati JF, Baghela A, Bhatt RP, Bojantchev D, Buyck B, da Silva GA, de Lima CLF, de Oliveira RJV, de Souza CAF, Dai YC, Dima B, Duong TT, Ercole E, Mafalda-Freire F, Ghosh A, Hashimoto A, Kamolhan S, Kang JC, Karunarathna SC, Kirk PM, Kytövuori I, Lantieri A, Liimatainen K, Liu ZY, Liu XZ, Lücking R, Medardi G, Mortimer PE, Nguyen TTT, Promputtha I, Raj KNA, Reck MA, Lumyong S, Shahzadeh-Fazeli SA,

- Stadler M, Soudi MR, Su HY, Takahashi T, Tangthirasunun N, Uniyal P, Wang Y, Wen TC, Xu JC, Zhang ZK, Zhao YC, Zhou JL, Zhu L (2016) Fungal diversity notes 367–490: Taxonomic and phylogenetic contributions to fungal taxa. *Fungal Diversity* 80: 1–270. <https://doi.org/10.1007/s13225-016-0373-x>
- Hyde KD, Tennakoon DS, Jeewon R, Bhat DJ, Maharachchikumbura SSN, Rossi W, Leonardi M, Lee HB, Mun HY, Houbaken J, Nguyen TTT, Jeon SJ, Frisvad JC, Wanasinghe DN, Lücking R, Aptroot A, Cáceres MES, Karunarathna SC, Hongsanan S, Phookamsak R, de Silva NI, Thambugala KM, Jayawardena RS, Senanayake IC, Boonmee S, Chen J, Luo ZL, Phukhamsakda C, Pereira OL, Abreu VP, Rosado AWC, Bart B, Randrianjohany E, Hofstetter V, Gibertoni TB, Soares AM da S, Plautz Jr HL, Sotão HMP, Xavier WKS, Bezerra JDP, de Oliveira TGL, de Souza-Motta CM, Magalhães OMC, Bundhun D, Harishchandra D, Manawasinghe IS, Dong W, Zhang SN, Bao DF, Samarakoon MC, Pem D, Karunarathna A, Lin CG, Yang J, Perera RH, Kumar V, Huang SK, Dayarathne MC, Ekanayaka AH, Jayasiri SC, Xiao Y, Konta S, Niskanen T, Liimatainen K, Dai YC, Ji XH, Tian XM, Mešić A, Singh SK, Phutthacharoen K, Cai L, Sorvongxay T, Thiagaraja V, Norphanphoun C, Chaiwan N, Lu YZ, Jiang HB, Zhang JF, Abeywickrama PD, Aluthmuhandiram JVS, Brahmanage RS, Zeng M, Chethana T, Wei D, Réblová M, Fournier J, Nekvindová J, do Nascimento Barbosa R, dos Santos JEF, de Oliveira NT, Li G-J, Ertz D, Shang Q-J, Phillips AJL, Kuo C-H, Camporesi E, Bulgakov TS, Lumyong S, Jones EBG, Chomnunti P, Gentekaki E, Bungartz F, Zeng X-Y, Fryar S, Tkalčec Z, Liang J, Li G, Wen T-C, Singh PN, Gafforov Y, Promptutha I, Yasanthika E, Goonasekara ID, Zhao R-L, Zhao Q, Kirk PM, Liu J-K, Yan JY, Mortimer PE, Xu J, Doilom M (2019) Fungal diversity notes 1036–1150: Taxonomic and phylogenetic contributions on genera and species of fungal taxa. *Fungal Diversity* 96(1): 1–242. <https://doi.org/10.1007/s13225-019-00429-2>
- Hyde KD, de Silva NI, Jeewon R, Bhat DJ, Phookamsak R, Doilom M, Boonmee S, Jayawardena RS, Maharachchikumbura SSN, Senanayake IC, Manawasinghe IS, Liu NG, Abeywickrama PD, Chaiwan N, Karunarathna A, Pem D, Lin CG, Sysouphanthong P, Luo ZL, Wei DP, Wanasinghe DN, Norphanphoun C, Tennakoon DS, Samarakoon MC, Jayasiri SC, Jiang HB, Zeng XY, Li JF, Wijesinghe SN, Devadatha B, Goonasekara ID, Brahmanage RS, Yang EF, Aluthmuhandiram JVS, Dayarathne MC, Marasinghe DS, Li WJ, Dissanayake LS, Dong W, Huanraluek N, Lumyong S, Liu JK, Karunarathna SC, Jones EBG, Al-Sadi AM, Xu JC, Harishchandra D, Sarma VV, Bulgakov TS (2020) AJOM new records and collections of fungi: 1–100. *Asian Journal of Mycology* 3(1): 22–294. <https://doi.org/10.5943/ajom/3/1/3>
- Hyde KD, Suwannarach N, Jayawardena RS, Manawasinghe IS, Liao CF, Doilom M, Cai L, Zhao P, Buyck B, Phukhamsakda C, Su WX, Fu YP, Li Y, Zhao RL, He MQ, Li JX, Tibpromma S, Lu L, Tang X, Kang JC, Ren GC, Gui H, Hofstetter V, Ryoo R, Antonín V, Hurdeal VG, Gentekaki E, Zhang JY, Lu YZ, Senanayake IC, Yu FM, Zhao Q, Bao DF (2021) Mycosphere notes 325–344 – Novel species and records of fungal taxa from around the world. *Mycosphere* 12(1): 1101–1156. <https://doi.org/10.5943/mycosphere/12/1/14>
- Jackson CR, Liew KC, Yule CM (2009) Structural and functional changes with depth in microbial communities in a tropical malaysian peat swamp forest. *Microbial Ecology* 57(3): 402–412. <https://doi.org/10.1007/s00248-008-9409-4>
- Jayasiri SC, Hyde KD, Ariyawansa HA, Bhat J, Buyck B, Cai L, Dai YC, Abd-Elsalam KA, Ertz D, Hidayat I, Jeewon R, Jones EBG, Bahkali AH, Karunarathna SC, Liu JK, Luangsa-ard JJ, Lumbsch HT, Maharachchikumbura SSN, McKenzie EHC, Moncalvo JM, Ghobad-Nejhad M, Nilsson H, Pang KL, Pereira OL, Phillips AJL, Raspé O, Rollins AW,

- Romero AI, Etayo J, Selçuk F, Stephenson SL, Suetrong S, Taylor JE, Tsui CKM, Vizzini A, Abdel-Wahab MA, Wen TC, Boonmee S, Dai DQ, Daranagama DA, Dissanayake AJ, Ekanayaka AH, Fryar SC, Hongsanan S, Jayawardena RS, Li WJ, Perera RH, Phookamsak R, de Silva NI, Thambugala KM, Tian Q, Wijayawardene NN, Zhao RL, Zhao Q, Kang JC, Promputtha I (2015) The Faces of Fungi database: Fungal names linked with morphology, phylogeny and human impacts. *Fungal Diversity* 74(1): 3–18. <https://doi.org/10.1007/s13225-015-0351-8>
- Jayawardena RS, Hyde KD, Wang S, Sun YR, Suwannarach N, Sysouphanthong P, Abdel-Wahab MA, Abdel-Aziz FA, Abeywickrama PD, Abreu VP, Armand A, Aptroot A, Bao DF, Begerow D, Bellanger JM, Bezerra JDP, Bundhun D, Calabon MS, Cao T, Cantillo T, Carvalho JLVR, Chaiwan N, Chen CC, Courtecuisse R, Cui BK, Damm U, Denchev CM, Denchev TT, Deng CY, Devadatha B, de Silva NI, dos Santos LA, Dubey NK, Dumez S, Fernandez HS, Firmino AL, Gafforov Y, Gajanayake AJ, Gomdola D, Gunaseelan S, Shucheng-He, Htet ZH, Kaliyaperumal M, Kemler M, Kezo K, Kularathnaje ND, Leonardi M, Li J-P, Liao C, Liu S, Loizides M, Luangharn T, Ma J, Madrid H, Mahadevakumar S, Maharachchikumbura SSN, Manamgoda DS, Martín MP, Mekala N, Moreau P-A, Mu Y-H, Pahoua P, Pem D, Pereira OL, Phonrob W, Phukhamsakda C, Raza M, Ren G-C, Rinaldi AC, Rossi W, Samarakoon BC, Samarakoon MC, Sarma VV, Senanayake IC, Singh A, Souza MF, Souza-Motta CM, Spielmann AA, Su W, Tang X, Tian XG, Thambugala KM, Thongklang N, Tennakoon DS, Wannathes N, Wei DP, Welti S, Wijesinghe SN, Yang H, Yang Y, Yuan H-S, Zhang H, Zhang J, Balasuriya A, Bhunjun CS, Bulgakov TS, Cai L, Camporesi E, Chomnunti P, Deepika YS, Doilom M, Duan W-J, Han S-L, Huanraluek N, Jones EBG, Lakshmidhevi N, Li Y, Lumyong S, Luo Z-L, Khuna S, Kumla J, Manawasinghe IS, Mapook A, Punyaboon W, Tibpromma S, Lu Y-Z, Yan JY, Wang Y (2022) Fungal diversity notes 1512–1610: Taxonomic and phylogenetic contributions on genera and species of fungal taxa. *Fungal Diversity* 117(1): 1–272. <https://doi.org/10.1007/s13225-022-00513-0>
- Katoh K, Rozewicki J, Yamada KD (2019) MAFFT online service: Multiple sequence alignment, interactive sequence choice and visualisation. *Briefings in Bioinformatics* 20(4): 1160–1166. <https://doi.org/10.1093/bib/bbx108>
- Kinge TR, Moforcha ZL, Mih AM (2019) Cultural Variability of *Fusarium oxysporum* f. sp. *elaedis* Isolates from Oil Palm in South Western Cameroon and Sensitivity to Four Plant Extracts. *Plant Pathology & Quarantine Journal of Fungal Biology* 9(1): 116–127. <https://doi.org/10.5943/ppq/9/1/10>
- Konta S, Phillips AJ, Bahkali AH, Jones EBG, Eungwanichayapant DP, Hyde KD, Boonmee S (2016a) Botryosphaeriaceae from palms in Thailand-*Barriopsis archontophoenicis* sp. nov, from *Archontophoenix alexandrae*. *Mycosphere: Journal of Fungal Biology* 7(7): 921–932. <https://doi.org/10.5943/mycosphere/si/1b/1>
- Konta S, Hongsanan S, Phillips AJ, Jones EB, Boonmee S, Hyde KD (2016b) Botryosphaeriaceae from palms in Thailand II-two new species of *Neodeightonia*, *N. rattanica* and *N. rattanicola* from *Calamus* (rattan palm). *Mycosphere: Journal of Fungal Biology* 7(7): 950–961. <https://doi.org/10.5943/mycosphere/si/1b/6>
- Konta S, Hongsanan S, Tibpromma S, Thongbai B, Maharachchikumbura SSN, Bahkali AH, Hyde KD, Boonmee S (2016c) An advance in the endophyte story: *Oxydothidea* fam. nov. with six new species of *Oxydothis*. *Mycosphere: Journal of Fungal Biology* 7(9): 1425–1446. <https://doi.org/10.5943/mycosphere/7/9/15>
- Konta S, Hongsanan S, Liu JK, Eungwanichayapant PD, Jeewon R, Hyde KD, Maharachchikumbura SSN, Boonmee S (2017) *Leptospora* (Leptosporaceae fam. nov.) and *Linocarpon* and *Neolinocarpon* (Linocarpaceae fam. nov.) are accommodated

- in Chaetosphaeriales. *Mycosphere: Journal of Fungal Biology* 8(10): 1943–1974. <https://doi.org/10.5943/mycosphere/8/10/16>
- Konta S, Maharachchikumbura SSN, Senanayake IC, McKenzie EHC, Stadler M, Boonmee S, Phookamsak R, Jayawardena RS, Senwanna C, Hyde KD, Elgorban AM, Eungwanichayapant PD (2020a) A new genus *Allodiatrype*, five new species and a new host record of diatrypaceous fungi from palms (Arecaceae). *Mycosphere: Journal of Fungal Biology* 11(1): 239–268. <https://doi.org/10.5943/mycosphere/11/1/4>
- Konta S, Hyde KD, Eungwanichayapant PD, Doilom M, Tennakoon DS, Senwanna C, Boonmee S (2020b) *Fissuroma* (Aigialaceae: Pleosporales) appears to be hyperdiverse on Arecaceae: evidence from two new species from Southern Thailand. *Acta Botanica Brasiliica* 34(2): 384–393. <https://doi.org/10.1590/0102-33062020abb0021>
- Konta S, Hyde KD, Phookamsak R, Xu JC, Maharachchikumbura SSN, Daranagama DA, McKenzie EHC, Boonmee S, Tibpromma S, Eungwanichayapant PD, Samarakoon MC (2020c) Polyphyletic genera in Xylariaceae (Xylariales): *Neoxylaria* gen. nov. and *Stilbohypoxyton*. *Mycosphere: Journal of Fungal Biology* 11(1): 2629–2651. <https://doi.org/10.5943/mycosphere/11/1/17>
- Konta S, Hyde KD, Karunarathna SC, Mapook A, Senwanna C, Dauner LAP, Nanayakkara CM, Xu J, Tibpromma S, Lumyong S (2021a) Multigene phylogeny and morphology reveal *Haplohelminthosporium* gen. nov. and *Helminthosporiella* gen. nov. associated with palms in Thailand and a checklist for *Helminthosporium* reported worldwide. *Life (Basel, Switzerland)* 11(5): 454. <https://doi.org/10.3390/life11050454>
- Konta S, Hyde KD, Eungwanichayapant PD, Karunarathna SC, Samarakoon MC, Xu J, Dauner LAP, Aluthwattha ST, Lumyong S, Tibpromma S (2021b) Multigene phylogeny reveals *Haploanthostomella elaeidis* gen. et sp. nov. and familial replacement of *Endocalyx* (Xylariales, Sordariomycetes, Ascomycota). *Life (Basel, Switzerland)* 11(6): 486. <https://doi.org/10.3390/life11060486>
- Konta S, Tibpromma S, Karunarathna SC, Samarakoon MC, Steven LS, Mapook A, Boonmee S, Senwanna C, Balasuriya A, Eungwanichayapant PD, Hyde KD (2023) Morphology and multigene phylogeny reveal ten novel taxa in Ascomycota from terrestrial palm substrates (Arecaceae) in Thailand. *Mycosphere* 14(1): 107–152. <https://doi.org/10.5943/mycosphere/14/1/2>
- Lampela M, Jauhiainen J, Kämäri I, Koskinen M, Tanhuanpää T, Valkeapää A, Vasander H (2016) Ground surface microtopography and vegetation patterns in a tropical peat swamp forest. *Catena* 139: 127–136. <https://doi.org/10.1016/j.catena.2015.12.016>
- Lemoine F, Correia D, Lefort V, Doppelt-Azeroual O, Mareuil F, Cohen-Boulakia S, Gascuel O (2019) NGPhylogeny.fr: New generation phylogenetic services for non-specialists. *Nucleic Acids Research* 47(W1): W260–W265. <https://doi.org/10.1093/nar/gkz303>
- Li W-L, Liu Z-P, Zhang T, Dissanayake AJ, Luo Z-L, Su H-Y, Liu J-K (2021) Additions to *Distoseptispora* (Distoseptisporaceae) associated with submerged decaying wood in China. *Phytotaxa* 520(1): 75–86. <https://doi.org/10.11646/phytotaxa.520.1.5>
- Liu YJ, Whelen S, Hall BD (1999) Phylogenetic relationships among Ascomycetes: Evidence from an RNA polymerase II subunit. *Molecular Biology and Evolution* 16(12): 1799–1808. <https://doi.org/10.1093/oxfordjournals.molbev.a026092>
- Liu JK, Chomnunti P, Cai L, Phookamsak R, Chukeatirote E, Jones EBG, Moslem M, Hyde KD (2010) Phylogeny and morphology of *Neodeightonia palmicola* sp. nov. from palms. *Sydowia* 62: 261–276.
- Liu J, Hu Y, Luo X, Xu Z, Castañeda-Ruiz RF, Xia J, Zhang X, Zhang L, Cui R, Ma J (2023) Morphological and Phylogenetic Analyses Reveal Three New Species of

- Distoseptispora* (Distoseptisporaceae, Distoseptisporales) from Yunnan, China. *Journal of Fungi* 9(4): 470. <https://doi.org/10.3390/jof9040470>
- Lumyong S, Techa W, Lumyong P, McKenzie EHC, Hyde KD (2009) Endophytic fungi from *calamus kerrianus* and *Wallichia caryotoides* (Arecaceae) at Doi Suthep-Pui National Park, Thailand. *Warasan Khana Witthayasat Maha Witthayalai Chiang Mai* 36: 158–167.
- Luo ZL, Hyde KD, Liu JK, Bhat DJ, Bao DF, Li WL, Su HY (2018) Lignicolous freshwater fungi from China II: Novel *Distoseptispora* (Distoseptisporaceae) species from northwestern Yunnan Province and a suggested unified method for studying lignicolous freshwater fungi. *Mycosphere* 9(3): 444–461. <https://doi.org/10.5943/mycosphere/9/3/2>
- Luo ZL, Hyde KD, Liu JK, Maharachchikumbura SSN, Jeewon R, Bao DF, Bhat DJ, Lin CG, Li WL, Yang J, Liu NG, Lu YZ, Jayawardena RS, Li JF, Su HY (2019) Freshwater Sordariomycetes. *Fungal Diversity* 99(1): 451–660. <https://doi.org/10.1007/s13225-019-00438-1>
- Ma J, Zhang JY, Xiao XJ, Xiao YP, Tang X, Boonmee S, Kang JC, Lu YZ (2022) Multi-gene Phylogenetic Analyses Revealed Five New Species and Two New Records of Distoseptisporales from China. *Journal of Fungi* (Basel, Switzerland) 8(11): 1202. <https://doi.org/10.3390/jof8111202>
- Maharachchikumbura SSN, Chen Y, Ariyawansa HA, Hyde KD, Haelewaters D, Perera RH, Samarakoon MC, Wanasinghe DN, Bustamante DE, Liu JK, Lawrence DP, Cheewangkoon R, Stadler M (2021) Integrative approaches for species delimitation in Ascomycota. *Fungal Diversity* 109(1): 155–179. <https://doi.org/10.1007/s13225-021-00486-6>
- Mapook A, Macabeo APG, Thongbai B, Hyde KD, Stadler M (2020) Polyketide-derived secondary metabolites from a Dothideomycetes fungus, *Pseudopalawania siamensis* gen. et sp. nov., (Muyocoprionales) with antimicrobial and cytotoxic activities. *Biomolecules* 10(4): 569. <https://doi.org/10.3390/biom10040569>
- Marin-Felix Y, Hernández-Restrepo M, Iturrieta-González I, García D, Gené J, Groenewald JZ, Cai L, Chen Q, Quaedvlieg W, Schumacher RK, Taylor PWJ, Ambers C, Bonthond G, Edwards J, Krueger-Hadfield SA, Luangsa-ard JJ, Morton L, Moslemi A, Sandoval-Denis M, Tan YP, Thangavel R, Vaghefi N, Cheewangkoon R, Crous PW (2019) Genera of phytopathogenic fungi: GOPHY 3. *Studies in Mycology* 94(1): 1–124. <https://doi.org/10.1016/j.simyco.2019.05.001>
- Miller MA, Pfeiffer W, Schwartz T (2010) Creating the CIPRES Science Gateway for inference of large phylogenetic trees. *Gateway Computing Environments Workshop, GCE 2010*: 1–8. <https://doi.org/10.1109/GCE.2010.5676129>
- Minayeva TY, Sirin AA (2012) Peatland biodiversity and climate change. *Biology Bulletin Reviews* 2(2): 164–175. <https://doi.org/10.1134/S207908641202003X>
- Monkai J, Boonmee S, Ren GC, Wei DP, Phookamsak R, Mortimer PE (2020) *Distoseptispora hydei* sp. nov. (Distoseptisporaceae), a novel lignicolous fungus on decaying bamboo in Thailand. *Phytotaxa* 459(2): 93–107. <https://doi.org/10.11646/phytotaxa.459.2.1>
- Page SE, Rieley JO, Shotyk ØW, Weiss D (1999) Interdependence of peat and vegetation in a tropical peat swamp forest. *Philosophical Transactions of the Royal Society of London, Series B, Biological Sciences* 354(1391): 1885–1897. <https://doi.org/10.1098/rstb.1999.0529>
- Page SE, Rieley JO, Banks CJ (2011) Global and regional importance of the tropical peatland carbon pool. *Global Change Biology* 17(2): 798–818. <https://doi.org/10.1111/j.1365-2486.2010.02279.x>

- Palmweb (2023) Palms of the World Online. <https://palmweb.org/node/4?q=node/5> [Accessed on 27 May 2023]
- Parish F, Sirin A, Charman D, Joosten H, Minayeva T, Silvius M, Stringer L (2008) Assessment on Peatlands, Biodiversity, and Climate Change: Main Report. Kuala Lumpur: Global Environment Centre & Wetlands International. http://www.imcg.net/media/download_gallery/books/assessment_peatland.pdf
- Phookamsak R, Hyde KD, Jeewon R, Bhat DJ, Jones EBG, Maharachchikumbura SSN, Raspé O, Karunarathna SC, Wanasinghe DN, Hongsanan S, Doilom M, Tennakoon DS, Machado AR, Firmino AL, Ghosh A, Karunarathna A, Mešić A, Dutta AK, Thongbai B, Devadatha B, Norphanphoun C, Senwanna C, Wei D, Pem D, Ackah FK, Wang G-N, Jiang H-B, Madrid H, Lee HB, Goonasekara ID, Manawasinghe IS, Kušan I, Cano J, Gené J, Li J, Das K, Acharya K, Raj KNA, Latha KPD, Chethana KWT, He M-Q, Dueñas M, Jadan M, Martín MP, Samarakoon MC, Dayarathne MC, Raza M, Park MS, Telleria MT, Chaiwan N, Matočec N, de Silva NI, Pereira OL, Singh PN, Manimohan P, Uniyal P, Shang Q-J, Bhatt RP, Perera RH, Alvarenga RLM, Nogal-Prata S, Singh SK, Vadthanarat S, Oh S-Y, Huang S-K, Rana S, Konta S, Paloi S, Jayasiri SC, Jeon SJ, Mehmood T, Gibertoni TB, Nguyen TTT, Singh U, Thiyagaraja V, Sarma VV, Dong W, Yu X-D, Lu Y-Z, Lim YW, Chen Y, Tkálčec Z, Zhang Z-F, Luo Z-L, Daranagama DA, Thambugala KM, Tibpromma S, Camporesi E, Bulgakov TS, Dissanayake AJ, Senanayake IC, Dai DQ, Tang L-Z, Khan S, Zhang H, Promputtha I, Cai L, Chomnunti P, Zhao R-L, Lumyong S, Boonmee S, Wen T-C, Mortimer PE, Xu J (2019) Fungal diversity notes 929–1035: Taxonomic and phylogenetic contributions on genera and species of fungi. *Fungal Diversity* 95(1): 1–273. <https://doi.org/10.1007/s13225-019-00421-w>
- Phukhamsakda C, McKenzie EHC, Phillips AJL, Jones EBG, Bhat DJ, Stadler M, Bhunjun CS, Wanasinghe DN, Thongbai B, Camporesi E, Ertz D, Jayawardena RS, Perera RH, Ekanayake AH, Tibpromma S, Doilom M, Xu J, Hyde KD (2020) Microfungi associated with *Clematis* (Ranunculaceae) with an integrated approach to delimiting species boundaries. *Fungal Diversity* 102(1): 1–203. <https://doi.org/10.1007/s13225-020-00448-4>
- Phukhamsakda C, Nilsson RH, Bhunjun CS, de Farias ARG, Sun YR, Wijesinghe SN, Raza M, Bao DF, Lu L, Tibpromma S, Dong W, Tennakoon DS, Tian XG, Xiong YR, Karunarathna SC, Cai L, Luo ZL, Wang Y, Manawasinghe IS, Camporesi E, Kirk PM, Promputtha I, Kuo CH, Su HY, Doilom M, Li Y, Fu YP, Hyde KD (2022) The numbers of fungi: contributions from traditional taxonomic studies and challenges of metabarcoding. *Fungal Diversity* 114: 327–386. <https://doi.org/10.1007/s13225-022-00502-3>
- Pilantanapak A, Jones EBG, Eaton RA (2005) Marine fungi on *Nypa fruticans* in Thailand. *Botanica Marina* 48(5–6): 365–373. <https://doi.org/10.1515/bot.2005.049>
- Pinnoi A, Jones EBG, McKenzie EHC, Hyde KD (2003a) Aquatic fungi from peat swamp palms: *Unisetosphaeria penguinoidea* gen. et sp. nov., and three new *Dactylaria* species. *Mycoscience* 44(5): 377–382. <https://doi.org/10.1007/S10267-003-0124-1>
- Pinnoi A, McKenzie EHC, Jones EBG, Hyde KD (2003b) Palm fungi from Thailand: *Custingophora undulatistipes* sp. nov. and *Vanakripa minutiellipsoidea* sp. nov. *Nova Hedwigia* 77(1–2): 213–219. <https://doi.org/10.1127/0029-5035/2003/0077-0213>
- Pinnoi A, Pinruan U, Hyde KD, McKenzie EHC, Lumyong S (2004) *Submersisphaeria palmae* sp. nov. with a key to species, and notes on *Helicoubisia*. *Sydowia* 56: 72–78.
- Pinnoi A, Lumyong S, Hyde KD, Jones EBG (2006) Biodiversity of fungi on the palm *Eleiodoxa conferta* in Sirindhorn peat swamp forest, Narathiwat, Thailand. *Fungal Diversity* 22: 205–218.
- Pinnoi A, Phongpaichit S, Hyde KD, Jones EBG (2009) Biodiversity of fungi on *Calamus* (Palmae) in Thailand. *Cryptogamie. Mycologie* 30: 181–190.

- Pinnoi A, Phongpaichit P, Jeewon R, Tang AMC, Hyde KD, Jones EBG (2010) Phylogenetic relationships of *Astrocystis eleiodoxae* sp. nov. (Xylariaceae). *Mycosphere* 1: 1–9.
- Pinruan U, Jones EBG, Hyde KD (2002) Aquatic fungi from peat swamp palms: *Jahnula appendiculata* sp. nov. *Sydowia* 54: 242–247.
- Pinruan U, Sakayaroj J, Jones EBG, Hyde KD (2004a) Aquatic fungi from peat swamp palms: *Phruensis brunneispora* gen. et sp. nov. and its hyphomycete anamorph. *Mycologia* 96(5): 1163–1170. <https://doi.org/10.1080/15572536.2005.11832916>
- Pinruan U, Sakayaroj J, Jones EBG, Hyde KD (2004b) *Flammispora* gen. nov., a new freshwater ascomycete from decaying palm leaves. *Studies in Mycology* 50: 381–386.
- Pinruan U, McKenzie EHC, Jones EBG, Hyde KD (2004c) Two new species of *Stachybotrys*, and a key to the genus. *Fungal Diversity* 17: 145–157.
- Pinruan U, Lumyong S, McKenzie EHC, Jones EBG, Hyde KD (2004d) Three new species of *Craspedodidymum* from palm in Thailand. *Mycoscience* 45(3): 177–180. <https://doi.org/10.1007/S10267-003-0173-5>
- Pinruan U, Hyde KD, Lumyong S, McKenzie EHC, Jones EBG (2007) Occurrence of fungi on tissues of the peat swamp palm *Licuala longicalycata*. *Fungal Diversity* 25: 157–173.
- Pinruan U, Sakayaroj J, Hyde KD, Jones EBG (2008) *Thailandiomyces bisetulosus* gen. et sp. nov. (Diaporthales, Sordariomycetidae, Sordariomycetes) and its anamorph *Craspedodidymum*, is described based on nuclear SSU and LSU rDNA sequences. *Fungal Diversity* 29: 89–98.
- Pinruan U, Rungjindamai N, Choeyklin R, Lumyong S, Hyde KD, Jones EBG (2010a) Occurrence and diversity of basidiomycetous endophytes from the oil palm, *Elaeis guineensis* in Thailand. *Fungal Diversity* 41(1): 71–88. <https://doi.org/10.1007/s13225-010-0029-1>
- Pinruan U, Rungjindamai N, Sakayaroj J, Lumyong S, Hyde KD, Jones EBG (2010b) *Baipadisphaeria* gen. nov., a freshwater ascomycete (Hypocreales, Sordariomycetes) from decaying palm leaves in Thailand. *Mycosphere* 1: 53–63.
- Pinruan U, Pinnoi A, Hyde KD, Jones EBG (2014) Tropical peat swamp fungi with special reference to palms. *Freshwater Fungi and Fungal-like Organisms*, Dee Gruyter Press, Berlin, 371–386. <https://doi.org/10.1515/9783110333480.371>
- Posa MRC, Wijedasa LS, Corlett RT (2011) Biodiversity and conservation of tropical peat swamp forests. *Bioscience* 61(1): 49–57. <https://doi.org/10.1525/bio.2011.61.1.10>
- POWO (2023) Plants of the World Online. Facilitated by the Royal Botanic Gardens, Kew. <http://www.plantsoftheworldonline.org/> [Accessed on 27 May 2023]
- Prentice RC (2011) The Peatland Biodiversity Management Toolbox: A Handbook for the Conservation and Management of Peatland Biodiversity in Southeast Asia. A Compilation. ASEAN Peatland Forests Project: Rehabilitation and Sustainable Use of Peatland Forests in Southeast Asia. Association of Southeast Asian Nations (ASEAN) and the Global Environment Centre. http://www.aseanpeat.net/ebook/toolbox/The_Peatland_Biodiversity_Management_Toolbox.Pdf
- Rambaut A (2012) FigTree, version 1.4.2. University of Edinburgh, Edinburgh.
- Ratnayake AS (2020) Characteristics of Lowland Tropical Peatlands: Formation, Classification, and Decomposition. *Journal of Tropical Forestry and Environment* 10(1): 1–16. <https://doi.org/10.31357/jtfe.v10i1.4685>
- Rehner SA (2001) Primers for elongation factor 1- α (EF1- α).
- Rehner SA, Samuels GJ (1994) Taxonomy and phylogeny of *Gliocladium* analysed from nuclear large subunit ribosomal DNA sequences. *Mycological Research* 98(6): 625–634. [https://doi.org/10.1016/S0953-7562\(09\)80409-7](https://doi.org/10.1016/S0953-7562(09)80409-7)

- Rieley JO (2016) Biodiversity of Tropical Peatland in Southeast Asia. 15th International Peat Congress, 707–711. <https://peatlands.org/assets/uploads/2019/06/ip-c16p707-711a213rieley.pdf>
- Shen H-W, Bao D-F, Hyde KD, Su H-Y, Bhat DJ, Luo Z-L (2021) Two novel species and two new records of *Distoseptispora* from freshwater habitats in China and Thailand. *MycKeys* 84: 79–101. <https://doi.org/10.3897/mycokeys.84.71905>
- Shuhada SN, Salim S, Nobilly F, Lechner AM, Azhar B (2020) Conversion of peat swamp forest to oil palm cultivation reduces the diversity and abundance of macrofungi. *Global Ecology and Conservation* 23: e01122. <https://doi.org/10.1016/j.gecco.2020.e01122>
- Sivichai S, Boonyuen N (2010) *Jahnula morakotii* sp. nov. and *J. appendiculata* from a peat swamp in Thailand. *Mycotaxon* 112(1): 475–481. <https://doi.org/10.5248/112.475>
- Song H, El Sheikh AF, Zhai Z, Zhou J-P, Chen M-H, Huo G-H, Huang X-G, Hu D-M (2020) *Distoseptispora longispora* sp. nov. from freshwater habitats in China. *Mycotaxon* 135(3): 513–523. <https://doi.org/10.5248/135.513>
- Stamatakis A (2014) RAxML version 8: A tool for phylogenetic analysis and post-analysis of large phylogenies. *Bioinformatics (Oxford, England)* 30(9): 1312–1313. <https://doi.org/10.1093/bioinformatics/btu033>
- Su HY, Hyde KD, Maharachchikumbura SSN, Ariyawansa HA, Luo Z, Promputtha I, Tian Q, Lin C, Shang Q, Zhao Y, Chai H, Liu XY, Bahkali AH, Bhat DJ, McKenzie EHC, Zhou D (2016) The families Distoseptisporaceae fam. nov., Kirschsteinioteliaceae, Sporormiaceae and Torulaceae, with new species from freshwater in Yunnan Province, China. *Fungal Diversity* 80(1): 375–409. <https://doi.org/10.1007/s13225-016-0362-0>
- Sun Y, Goonasekara ID, Thambugala KM, Jayawardena RS, Wang Y, Hyde KD (2020) *Distoseptispora bambusae* sp. nov. (Distoseptisporaceae) on bamboo from China and Thailand. *Biodiversity Data Journal* 8: e53678. <https://doi.org/10.3897/BDJ.8.e53678>
- Taylor JE, Hyde KD (2003) Microfungi of tropical and temperate palms. Fungal Diversity Press, Hong Kong, 459 pp.
- Taylor JE, Hyde KD, Jones EBG (1999) Endophytic fungi associated with the temperate palm, *Trachycarpus fortunei*, within and outside its natural geographic range. *The New Phytologist* 142(2): 335–346. <https://doi.org/10.1046/j.1469-8137.1999.00391.x>
- Tian X, Tibpromma S, Karunarathna SC, Dai D, Lu Y, Mapook A, Jayawardena RS (2022) A new species and a new host record of *Pseudoberkleasium* (Pseudoberkleasmiaceae, Dothideomycetes) from *Cocos nucifera* and *Zea mays* in northern Thailand. *Phytotaxa* 547(3): 232–242. <https://doi.org/10.11646/phytotaxa.547.3.2>
- Tibpromma S, Hyde KD, McKenzie EHC, Bhat DJ, Phillips AJL, Wanasinghe DN, Samarakoon MC, Jayawardena RS, Dissanayake AJ, Tennakoon DS, Doilom M, Phookamsak R, Tang AMC, Xu J, Mortimer PE, Promputtha I, Maharachchikumbura SSN, Khan S, Karunarathna SC (2018) Fungal diversity notes 840–928: Micro-fungi associated with Pandanaceae. *Fungal Diversity* 93(1): 1–160. <https://doi.org/10.1007/s13225-018-0408-6>
- UNEP (2022) Global Peatlands Assessment – The State of the World’s Peatlands: Evidence for action toward the conservation, restoration, and sustainable management of peatlands. Main Report. Global Peatlands Initiative. United Nations Environment Programme, Nairobi.
- Vaidya G, Lohman DJ, Meier R (2011) SequenceMatrix: Concatenation software for the fast assembly of multigene datasets with character set and codon information. *Cladistics* 27(2): 171–180. <https://doi.org/10.1111/j.1096-0031.2010.00329.x>

- Vilgalys R, Hester M (1990) Rapid genetic identification and mapping of enzymatically amplified ribosomal DNA from several *Cryptococcus* species. *Journal of Bacteriology* 172(8): 4238–4246. <https://doi.org/10.1128/jb.172.8.4238-4246.1990>
- Voglmayr H, Yule CM (2006) *Polyancora globosa* gen. sp. nov., an aeroaquatic fungus from Malaysian peat swamp forests. *Mycological Research* 110(10): 1242–1252. <https://doi.org/10.1016/j.mycres.2006.07.001>
- White TJ, Bruns T, Lee S, Taylor J (1990) Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In: Innis MA, Gelfand DH, Sninsky JJ, White TJ (Eds) *PCR protocols: a guide to methods and applications*. Academic Press, San Diego, 315–322. <https://doi.org/10.1016/B978-0-12-372180-8.50042-1>
- Wijayawardene NN, Hyde KD, Dai DQ, Sánchez-García M, Goto BT, Saxena RK, Erdoğdu M, Selçuk F, Rajeshkumar KC, Aptroot A, Błaszczowski J, Boonyuen N, da Silva GA, de Souza FA, Dong W, Ertz D, Haelewaters D, Jones EBG, Karunarathna SC, Kirk PM, Kukwa M, Kumla J, Leontyev DV, Lumbsch HT, Maharachchikumbura SSN, Marguno F, Martínez-Rodríguez P, Mešić A, Monteiro JS, Oehl F, Pawłowska J, Pem D, Pfliegler WP, Phillips AJL, Pošta A, He MQ, Li JX, Raza M, Sruthi OP, Suetrong S, Suwannarach N, Tedersoo L, Thiyagaraja V, Tibpromma S, Tkáčec Z, Tokarev YS, Wanasinghe DN, Wijesundara DSA, Wimalasekera SDMK, Madrid H, Zhang GQ, Gao Y, Sánchez-Castro I, Tang LZ, Stadler M, Yurkov A, Thines M (2022) Outline of Fungi and fungus-like taxa – 2021. *Mycosphere: Journal of Fungal Biology* 13(1): 53–453. <https://doi.org/10.5943/mycosphere/13/1/2>
- Wikee S, Lombard L, Nakashima C, Motohashi K, Chukeatirote E, Cheewangkoon R, McKenzie EHC, Hyde KD, Crous PW (2013) A phylogenetic re-evaluation of *Phyllosticta* (Botryosphaerales). *Studies in Mycology* 76: 1–29. <https://doi.org/10.3114/sim0019>
- Xia JW, Ma YR, Li Z, Zhang XG (2017) Acrodictys-like wood decay fungi from southern China, with two new families Acrodictaceae and Junewangiaceae. *Scientific Reports* 7(1): 7888. <https://doi.org/10.1038/s41598-017-08318-x>
- Yang J, Maharachchikumbura SSN, Liu JK, Hyde KD, Jones EBG, Al-Sadi AM, Liu ZY (2018) *Pseudostanjehughesia aquitropica* gen. et sp. nov. and *Sporidesmium* sensu lato species from freshwater habitats. *Mycological Progress* 17(5): 591–616. <https://doi.org/10.1007/s11557-017-1339-4>
- Yang J, Liu LL, Gareth Jones EBG, Li WL, Hyde KD, Liu ZY (2021) Morphological variety in *Distoseptispora* and introduction of six novel species. *Journal of Fungi* (Basel, Switzerland) 7(11): 945. <https://doi.org/10.3390/jof7110945>
- Zhai ZJ, Yan JQ, Li WW, Gao Y, Hu HJ, Zhou JP, Song HY, Hu DM (2022) Three novel species of *Distoseptispora* (Distoseptisporaceae) isolated from bamboo in Jiangxi Province, China. *Mycosphaerella* 88: 35–54. <https://doi.org/10.3897/mycokeys.88.79346>
- Zhang SN, Hyde KD, Jones EBG, Cheewangkoon R, Liu JK (2020) Additions to *Fissuroma* and *Neoastrosphaeriella* (Aigialaceae, Pleosporales) from palms. *Mycosphere* 11(1): 269–284. <https://doi.org/10.5943/mycosphere/11/1/5>
- Zhang H, Zhu R, Qing Y, Yang H, Li C, Wang G, Zhang D, Ning P (2022) Polyphasic Identification of *Distoseptispora* with Six New Species from Fresh Water. *Journal of Fungi* (Basel, Switzerland) 8(10): 1036. <https://doi.org/10.3390/jof8101063>