



<https://doi.org/10.11646/phytotaxa.459.2.1>

## *Distoseptispora hydei* sp. nov. (Distoseptisporaceae), a novel lignicolous fungus on decaying bamboo in Thailand

JUTAMART MONKAI<sup>1,8</sup>, SARANYAPHAT BOONMEE<sup>1,2,9</sup>, GUANG-CONG REN<sup>1,2,10</sup>, DE-PING WEI<sup>1,3,4,11</sup>, RUNGTIWA PHOOKAMSAK<sup>4,5,6,7,12\*</sup> & PETER E. MORTIMER<sup>4,13</sup>

<sup>1</sup>Center of Excellence in Fungal Research, Mae Fah Luang University, Chiang Rai 57100, Thailand

<sup>2</sup>School of Science, Mae Fah Luang University, Chiang Rai 57100, Thailand

<sup>3</sup>Department of Entomology and Plant Pathology, Faculty of Agriculture, Chiang Mai University, Chiang Mai, 50200, Thailand

<sup>4</sup>CAS Key Laboratory for Plant Diversity and Biogeography of East Asia, Kunming Institute of Botany, Chinese Academy of Sciences, Kunming 650201, Yunnan, People's Republic of China

<sup>5</sup>East and Central Asia Regional Office, World Agroforestry Centre (ICRAF), Kunming 650201, Yunnan, People's Republic of China

<sup>6</sup>Honghe Center for Mountain Futures, Kunming Institute of Botany, Chinese Academy of Sciences, Honghe County, Yunnan, People's Republic of China

<sup>7</sup>Research Center of Microbial Diversity and Sustainable Utilization, Faculty of Sciences, Chiang Mai University, Chiang Mai 50200, Thailand

<sup>8</sup>✉ [mjutamart@gmail.com](mailto:mjutamart@gmail.com); <https://orcid.org/0000-0001-6043-0625>

<sup>9</sup>✉ [saranyaphat.khag2@gmail.com](mailto:saranyaphat.khag2@gmail.com); <https://orcid.org/0000-0001-5202-2955>

<sup>10</sup>✉ [guangcong.ren@gmail.com](mailto:guangcong.ren@gmail.com); <https://orcid.org/0000-0001-9923-2626>

<sup>11</sup>✉ [dp.wei.elina@qq.com](mailto:dp.wei.elina@qq.com); <https://orcid.org/0000-0002-3740-0142>

<sup>12</sup>✉ [jomjam.rp2@gmail.com](mailto:jomjam.rp2@gmail.com); <https://orcid.org/0000-0002-6321-8416>

<sup>13</sup>✉ [petermortimer@mac.com](mailto:petermortimer@mac.com); <https://orcid.org/0000-0003-3188-9327>

\*Corresponding Author: ✉ [jomjam.rp2@gmail.com](mailto:jomjam.rp2@gmail.com)

### Abstract

In this paper, we described and illustrated a new species of lignicolous fungi, *Distoseptispora hydei*, found on decaying bamboo in Phitsanulok Province, Thailand. According to the phylogenetic results from combined sequence data (LSU, ITS and RPB2), the new species is distinct from other *Distoseptispora* species. *Distoseptispora hydei* is characterized by obpyriform to fusiform conidia with 7–9 distosepta and a hyaline, gelatinous sheath around the tip. Phylogenetic analyses and morphological comparisons with other species of *Distoseptispora* are provided in this study.

**Key words:** 1 new species, Distoseptisporales, phylogeny, Sordariomycetes, taxonomy

### Introduction

An upswell in research on taxonomy and phylogeny of saprobic fungi in Thailand has occurred over the last decade (Liu *et al.* 2011, Monkai *et al.* 2013, Phookamsak *et al.* 2015, Wanasinghe *et al.* 2016, 2017, Doilom *et al.* 2017, Promputtha *et al.* 2017, Tibpromma *et al.* 2018, Jayasiri *et al.* 2019, Mapook *et al.* 2020, Phookamsakda *et al.* 2020). In terrestrial habitats, several taxa have been reported from different lignicolous substrates and hosts (Kodsueb *et al.* 2008a, b, Boonmee *et al.* 2011, 2014, 2016, Shang *et al.* 2017, Lu *et al.* 2018, Lin *et al.* 2019, Liu *et al.* 2019). Among them, bamboo is an important host for saprobic fungi in need of more research (Hyde *et al.* 2002a, b, Morakotkarn *et al.* 2007, Tanaka *et al.* 2009, 2015, Phookamsak *et al.* 2014, 2015, Dai *et al.* 2017, 2018). A review of the literature revealed that up to 1300 species of fungi associated with bamboo have so far been described globally (Dai *et al.* 2018). Many of these fungi growing on decaying bamboo feature diverse and novel taxonomic placements (Dai *et al.* 2012, 2014, 2017, Jaklitsch *et al.* 2015, Liu *et al.* 2015, Phookamsak *et al.* 2015, Tanaka *et al.* 2015, Wang *et al.* 2018, Jiang *et al.* 2018, 2019, 2020).

The genus *Distoseptispora* (Distoseptisporaceae, Distoseptisporales) was introduced and typified with *D. fluminicola* by Su *et al.* (2016). This genus is known only for its asexual morph, which is mainly characterized by hyphomycetous, macronematous conidiophores, percurrent, elongate conidiogenous cells, olivaceous, brown or yellowish or reddish brown, euseptate or distoseptate conidia, and occasionally muriform conidia (Su *et al.* 2016, Xia

*et al.* 2017, Luo *et al.* 2018, Tibpromma *et al.* 2018, Yang *et al.* 2018, Hyde *et al.* 2020). *Distoseptispora* is regarded as saprobic lignicolous fungal genus and presently comprises 28 species, 16 of which were found from freshwater and 12 from terrestrial habitats (Yang *et al.* 2015, 2018, Hyde *et al.* 2016, 2020, Su *et al.* 2016, Xia *et al.* 2017, Luo *et al.* 2018, 2019, Tibpromma *et al.* 2018, Crous *et al.* 2019, Phookamsak *et al.* 2019, Phukhamsakda *et al.* 2020, Sun *et al.* 2020). Many new species of *Distoseptispora* have been discovered in Thailand in recent years; *D. rayongensis* was introduced by Hyde *et al.* (2020) from submerged wood; and *D. clematidis* was introduced by Phukhamsakda *et al.* (2020) from dead stem of *Clematis sikkimensis*. Sun *et al.* (2020) introduced *D. bambusae* from dead bamboo in Guizhou, China and also reported this species from Chiang Rai, Thailand while also reporting *D. tectonae* from dead wood in Thailand.

This paper aims to describe the new species of *Distoseptispora* with morphological descriptions and illustrations, and to evaluate their molecular phylogenetic relationships in Distoseptisporaceae using molecular analyses. We introduce a new species, *Distoseptispora hydei*, found on decaying bamboo, with evidence from morphology and phylogenetic analyses. A synopsis of the morphological characters of *Distoseptispora* species is also provided.

## Materials and methods

### *Specimen collection, morphological observation and isolation*

A collection of decaying bamboo was carried out in a disturbed forest in Phitsanulok Province, Thailand. Fungi was examined using a Motic SMZ 168 Series microscope (Motic Incorporation Ltd., Hong Kong). Micro-morphological characteristics were observed and captured using a Nikon ECLIPSE 80i compound microscope equipped with a Canon EOS 600D digital camera. All measurements were calculated using the Tarosoft (R) Image Frame Work program, and figures were processed using Adobe Photoshop CS6 Extended version 10.0 software (Adobe Systems, USA). The single spore isolation method was used to obtain a pure culture according to the protocol described in Chomnunti *et al.* (2014). The germinating conidia were transferred to potato dextrose agar (PDA) and incubated at 25–28°C for four weeks. The fungal culture was deposited in the Mae Fah Luang University Culture Collection (MFLUCC), and the holotypic specimen was deposited in the herbarium of Mae Fah Luang University (MFLU). The Faces of Fungi number was registered as outlined in Jayasiri *et al.* (2015), and the Index Fungorum number was registered as outlined in Index Fungorum (2020).

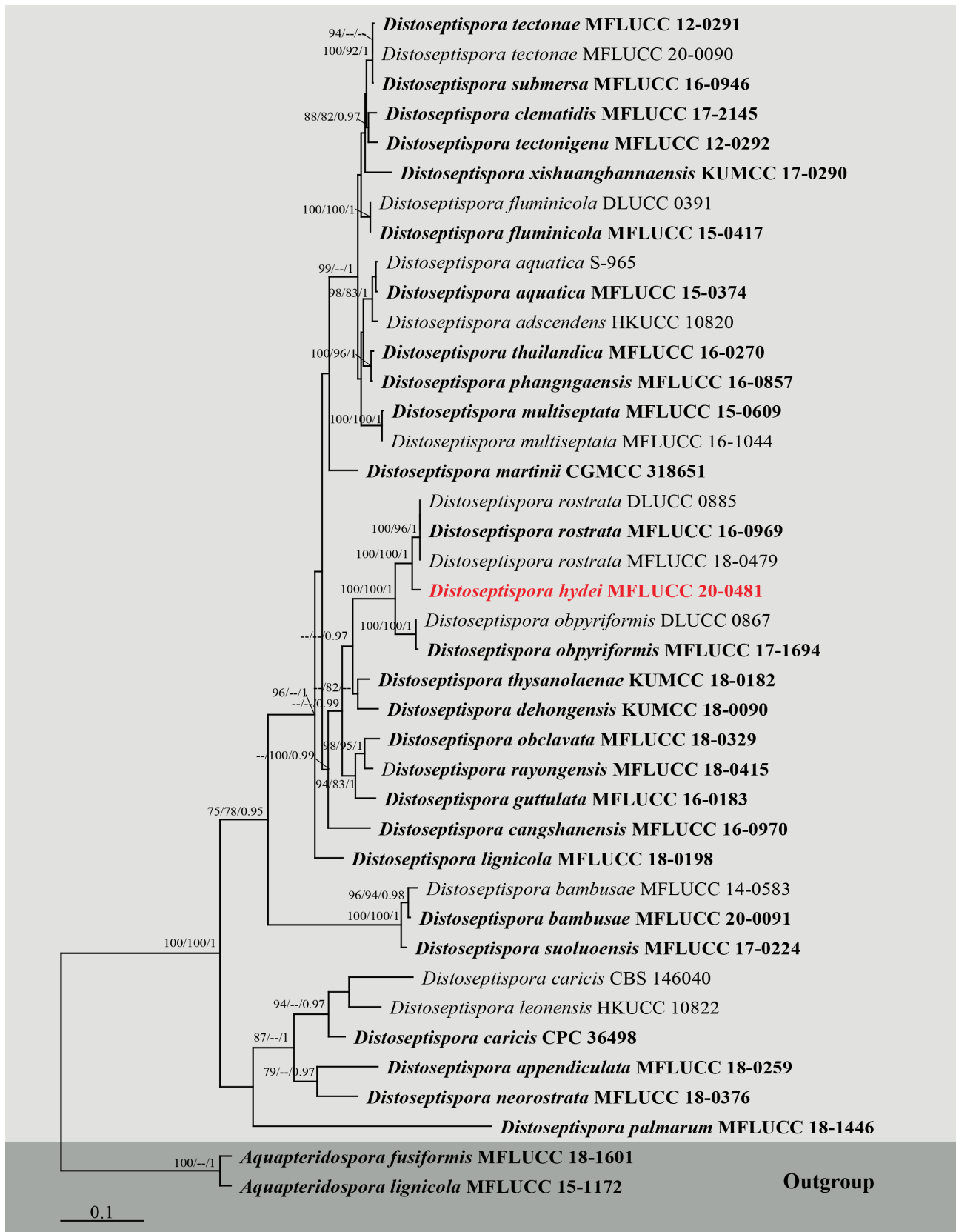
### *DNA extraction, PCR amplification and sequencing*

Fungal isolates were grown on PDA at 25–28°C for four weeks, and fresh mycelium was scraped from the margin of a colony for DNA extraction. DNA extraction was conducted using a Biospin Fungus Genomic DNA Extraction Kit (BioFlux®, Hangzhou, P.R. China) following the manufacturer's protocol. Polymerase chain reaction (PCR) amplification was processed for three gene regions, including the partial 28S large subunit nuclear ribosomal DNA (LSU) using primer pairs LR0R and LR5 (Vilgalys & Hester 1990); the internal transcribed spacers region of ribosomal DNA (ITS) using primer pairs ITS5 and ITS4 (White *et al.* 1990); and the RNA polymerase II second largest subunit (RPB2) using primers fRPB2-5F and fRPB2-7cR (Liu *et al.* 1999). The final volume of PCR reaction is 25 µL, composed of 2 µL template DNA (50 ng/µL), 12.5 µL of PCR Master Mix (0.5 mM of each primer, 50 U *Taq* DNA polymerase 400 mM of each dNTP, and 3 mM MgCl<sub>2</sub>) 1 µL of each primer and 8.5 µL of double distilled water (ddH<sub>2</sub>O). The PCR thermal cycling programs were set for LSU and ITS with an initial denaturation at 94 °C for 3 minutes, followed by 40 cycles of denaturation at 94 °C for 45 seconds, annealing at 56 °C for 50 seconds, extension at 72 °C for 1 minute and a final extension step at 72 °C for 10 minutes. The PCR amplification of RPB2 was set at initial denaturation at 95 °C for 5 minutes, followed by 40 cycles of denaturation at 95 °C for 1 minute, annealing at 52 °C for 2 minutes and extension at 72 °C for 90 seconds, and a final extension step at 72 °C for 10 minutes. PCR products were sent for purification and sequencing to TsingKe Biological Technology, Kunming City, Yunnan Province, China (Kunming, P.R. China).

### *Phylogenetic analysis*

The sequences generated in this study were blasted to search for preliminary identification with GenBank database ([www.ncbi.nlm.nih.gov/blast/](http://www.ncbi.nlm.nih.gov/blast/)). The dataset composed of LSU, ITS and RPB2 sequences of the closely related taxa to the new isolate were compiled based on the blastn results from GenBank and recent publications (Luo *et al.* 2018, 2019, Yang *et al.* 2018; Phookamsak *et al.* 2019, Phukhamsakda *et al.* 2020, Hyde *et al.* 2020, Sun *et al.* 2020). Detailed information on fungal strains used in this paper are provided in TABLE 1. Consensus sequences were aligned

by MAFFT v.7 via online web portal (<http://mafft.cbrc.jp/alignment/server/index.html>; Katoh *et al.* 2019) using the default settings and adjusted manually using BioEdit v. 7.0.9.1. (Hall *et al.* 1999).



**FIGURE 1.** Phylogenetic tree obtained from RAxML analyses of a combined LSU, ITS and RPB2 sequence data. Bootstrap support values for ML, MP equal or greater than 75% and Bayesian posterior probabilities greater than 0.95 PP are indicated at the nodes. The ex-type strains are in bold and the new isolate of this study is in red bold. The tree is rooted to *Aquapteridospora fusiformis* (MFLUCC 18-1601) and *A. lignicola* (MFLUCC 15-1172).

Maximum likelihood (ML) analysis was performed by raxmlGUI v.1.3 (Silvestro & Michalak 2012) using the GTRGAMMAI model of nucleotide substitution with 1000 replicates. Maximum parsimony (MP) analysis was carried out with the heuristic search option in PAUP (Phylogenetic Analysis Using Parsimony) v.4.0b 10 (Swofford 2002) with 1000 sequence additions. The branches of zero length were collapsed, and gaps were treated as missing data. Descriptive tree statistics for parsimony; Tree Length [TL], Consistency Index [CI], Retention Index [RI], Relative Consistency Index [RC] and Homoplasy Index [HI] were analyzed for the maximum parsimonious tree.

Bayesian inference (BI) analysis was conducted by MrBayes v3.1.2 (Ronquist *et al.* 2012) using Markov chain Monte Carlo sampling (BMCMC) (Huelsenbeck & Ronquist 2001, Zhaxybayeva & Gogarten 2002). Parameters of BI analysis in MrBayes were set up on six simultaneous Markov chains, run for 1000000 generations, and sampled every 100<sup>th</sup> generations. The initial trees were checked for the effective sampling size (ESS) using Tracer v. 1.6 (Rambaut & Drummond 2007). The first 10% of the generated trees were discarded, and the remaining trees were used to evaluate the posterior probabilities (PP) of the 50% majority rule consensus tree. Phylograms were visualized using FigTree v1.4.0 (Rambaut, 2012) and rearranged in Adobe Photoshop CS6 software (Adobe Systems, USA).

**TABLE 1.** List of the taxa used in the analyses and their GenBank accession numbers. Newly generated sequences are indicated with asterisk (\*) after collection number. The ex-type strains are indicated in bold. “N/A” sequence is unavailable.

Species	Culture accession no.	GenBank accession no.		
		LSU	ITS	RPB2
<i>Aquapteridospora lignicola</i>	<b>MFLUCC 15-1172</b>	<b>KU221018</b>	N/A	N/A
<i>A. fusiformis</i>	<b>MFLUCC 18-1601</b>	<b>MK849798</b>	<b>MK828652</b>	N/A
<i>Distoseptispora adscendens</i>	HKUCC 10820	DQ408561	N/A	DQ435092
<i>D. appendiculata</i>	<b>MFLUCC 18-0259</b>	<b>MN163023</b>	<b>MN163009</b>	N/A
<i>D. aquatica</i>	<b>MFLUCC 15-0374</b>	<b>KU376268</b>	<b>MF077552</b>	N/A
<i>D. aquatica</i>	S-965	MK849792	MK828647	MN124537
<i>D. bambusae</i>	<b>MFLUCC 20-0091</b>	<b>MT232718</b>	<b>MT232713</b>	<b>MT232881</b>
<i>D. bambusae</i>	MFLUCC 14-0583	MT232717	MT232712	MT232882
<i>D. cangshanensis</i>	<b>MFLUCC 16-0970</b>	<b>MG979761</b>	<b>MG979754</b>	N/A
<i>D. caricis</i>	<b>CPC 36498</b>	<b>MN567632</b>	<b>NR_166325</b>	N/A
<i>D. caricis</i>	CBS 146040	N/A	N/A	MN556806
<i>D. clematidis</i>	<b>MFLUCC 17-2145</b>	<b>MT214617</b>	<b>MT310661</b>	<b>MT394721</b>
<i>D. dehongensis</i>	<b>KUMCC 18-0090</b>	<b>MK079662</b>	<b>MK085061</b>	N/A
<i>D. fluminicola</i>	<b>MFLUCC 15-0417</b>	<b>KU376270</b>	<b>MF077553</b>	N/A
<i>D. fluminicola</i>	DLUCC 0391	MG979762	MG979755	N/A
<i>D. guttulata</i>	<b>MFLUCC 16-0183</b>	<b>MF077554</b>	<b>MF077543</b>	N/A
<i>D. hydei</i>	<b>MFLUCC 20-0481*</b>	<b>MT742830</b>	<b>MT734661</b>	<b>MT767128</b>
<i>D. leonensis</i>	HKUCC 10822	DQ408566	N/A	DQ435089
<i>D. lignicola</i>	<b>MFLUCC 18-0198</b>	<b>MK849797</b>	<b>MK828651</b>	N/A
<i>D. martinii</i>	<b>CGMCC 318651</b>	<b>KX033566</b>	<b>KU999975</b>	N/A
<i>D. multiseptata</i>	<b>MFLUCC 15-0609</b>	<b>KX710140</b>	<b>KX710145</b>	N/A
<i>D. multiseptata</i>	MFLUCC 16-1044	MF077555	MF077544	MF135644
<i>D. neurostrata</i>	<b>MFLUCC 18-0376</b>	<b>MN163017</b>	<b>MN163008</b>	N/A
<i>D. obclavata</i>	<b>MFLUCC 18-0329</b>	<b>MN163010</b>	<b>MN163012</b>	N/A
<i>D. obpyriformis</i>	DLUCC 0867	MG979765	MG979757	MG988416
<i>D. obpyriformis</i>	<b>MFLUCC 17-1694</b>	<b>MG979764</b>	N/A	<b>MG988415</b>
<i>D. palmarum</i>	<b>MFLUCC 18-1446</b>	<b>MK079663</b>	<b>MK085062</b>	<b>MK087670</b>
<i>D. phangngaensis</i>	<b>MFLUCC 16-0857</b>	<b>MF077556</b>	<b>MF077545</b>	N/A
<i>D. rayongensis</i>	<b>MFLUCC 18-0415</b>	<b>MH457137</b>	<b>MH457172</b>	<b>MH463255</b>
<i>D. rostrata</i>	<b>MFLUCC 16-0969</b>	<b>MG979766</b>	<b>MG979758</b>	<b>MG988417</b>

... Continued on the next page

TABLE 1. (Continued)

Species	Culture accession no.	GenBank accession no.		
		LSU	ITS	RPB2
<i>D. rostrata</i>	DLUCC 0885	MG979767	MG979759	N/A
<i>D. rostrata</i>	MFLUCC 18-0479	NG_064513	NR_157552	N/A
<i>D. submersa</i>	MFLUCC 16-0946	MG979768	MG979760	MG988418
<i>D. suoluoensis</i>	MFLUCC 17-0224	MF077557	MF077546	N/A
<i>D. tectonae</i>	MFLUCC 12-0291	KX751713	KX751711	KX751708
<i>D. tectonae</i>	MFLUCC 20-0090	MT232719	MT232714	N/A
<i>D. tectonigena</i>	MFLUCC 12-0292	KX751714	KX751712	KX751709
<i>D. thailandica</i>	MFLUCC 16-0270	MH260292	MH275060	N/A
<i>D. thysanolaenae</i>	KUMCC 18-0182	MK064091	MK045851	N/A
<i>D. xishuangbannaensis</i>	KUMCC 17-0290	MH260293	MH275061	MH412754

## Results

### Phylogenetic analyses

The combined dataset composed of LSU, ITS and RPB2 sequences comprised 40 strains in Distoseptisporaceae and other related taxa, including two outgroup taxa (FIGURE 1). The RAxML analysis of the combined dataset yielded a best scoring tree with a final ML optimization likelihood value of -11870.204445. The aligned sequence matrix comprises 796 distinct alignment patterns, with 31.93% undetermined characters or gaps. Estimated base frequencies were as followed; A = 0.238984, C = 0.246561, G = 0.298618, T = 0.215836; substitution rates AC = 1.551456, AG = 3.282721, AT = 1.068920, CG = 0.713411, CT = 7.921686, GT = 1.000000; gamma distribution shape parameter  $\alpha = 0.209797$ . The maximum parsimonious dataset consisted of 2213 characters of which 1423 were constant, 622 parsimony-informative and 168 parsimony-uninformative. The parsimony analysis of the data matrix resulted in a single most parsimonious tree (TL = 1924, CI = 0.619, RI = 0.731, RC = 0.452, HI = 0.381). Bayesian analysis indicated that the average standard deviation of split frequencies at the end of total MCMC generations was less than 0.01. Phylogenetic analyses retrieved from ML, MP and BI analyses were not significantly different and show similar topologies. The new species, *Distoseptispora hydei* sp. nov., formed a sister clade to *D. rostrata* with strong statistical support (100% ML, 100% MP and 1.00 PP, FIGURE 1).

## Taxonomy

### *Distoseptispora hydei* Monkai & Phookamsak, sp. nov. FIGURE 2

*Index Fungorum* number: IF557858; *Facesoffungi* number: FoF 08845

*Etymology* – Named in honor of Kevin D. Hyde for his excellent contributions to mycology and to commemorate his 65<sup>th</sup> birthday.

*Holotype* – MFLU 20-0481

*Saprobic* on decaying bamboo culm. **Sexual morph:** Undetermined. **Asexual morph:** Colonies effuse, dark brown, hairy or velvety. *Mycelium* mostly immersed, consisting of branched, septate, smooth, subhyaline to pale brown hyphae. *Conidiophores* macronematous, mononematous, solitary, dark brown, paler at apical part, 4–9-septate, straight or slightly flexuous, unbranched, smooth, cylindrical, 87–145 × 3–7  $\mu\text{m}$  ( $\bar{x}$  = 126 × 5  $\mu\text{m}$ , n = 20), rounded at the apex. *Conidiogenous cells* monoblastic, integrated, terminal, brown, cylindrical. *Conidia* acrogenous, solitary, obpyriform to fusiform, straight or slightly curved, 7–9-distoseptate, olivaceous to brown, truncate at base, narrow at apex, 32–58 × 10–15  $\mu\text{m}$  ( $\bar{x}$  = 49 × 12  $\mu\text{m}$ , n = 20), smooth-walled, guttulate, with a hyaline, globose, gelatinous sheath around tip, 5.3–8 × 6.4–8  $\mu\text{m}$  ( $\bar{x}$  = 6.7 × 7.2  $\mu\text{m}$ , n = 5).

**Known distribution:**—Thailand



**Culture characteristics:**—Conidia germinated on PDA within 24 hours and germ tubes were produced from both ends. Colony on PDA reached at 5–10 mm diam. in two weeks at 28°C, circular, with fluffy, dense, dark brown mycelium in the center, becoming sparse and paler at the entire margin and in reverse pale brown.

**Material examined:**—Thailand, Phitsanulok Province, Amphoe Nakhon Thai, Tambon Huai Hia, saprobic on decaying bamboo culm, 25 July 2019, E. Yasanthika, E3-4 (MFLU 20-0481, **holotype**), ex-type living culture, MFLUCC 20-0115.

Notes:—Phylogenetic analyses of a concatenated LSU, ITS and RPB2 sequence dataset revealed that the new species clustered within *Distoseptispora* with high statistical support in a sister clade of *D. rostrata* (100% ML, 100% MP and 1.00 PP, FIGURE 1). The new species resembles *D. appendiculata* in having a gelatinous sheath around the tip; however, the latter has obclavate conidia with a higher number of septa and longer size (32–58 µm vs 67–89 µm) (Luo *et al.* 2019). *Distoseptispora hydei* differs from *D. rostrata* in having obpyriform and shorter conidia (32–58 µm vs 115–155 µm) (Luo *et al.* 2018). *Distoseptispora hydei* shares similar characteristics with *D. obpyriformis* in having obpyriform conidia (Luo *et al.* 2018). However, *D. obpyriformis* has longer conidia (53–71 µm vs 32–58 µm) (Luo *et al.* 2018). *Distoseptispora bambusae*, also found on bamboo, is distinguished from *D. hydei* by its obclavate conidia (Sun *et al.* 2020). A comparison of morphological features of species in *Distoseptispora* is provided in TABLE 2.



**FIGURE 2.** *Distoseptispora hydei* (MFLU 20-0481, **holotype**). **a** Colonies on substrate. **b** Conidiophore with attached conidium. **c, d** Conidiophores showing conidial production. **e–h** Conidia. **i** Germinating conidium. **j, k** Culture on PDA after 21 days (j = from above, k = from below). Scale bars: b–i = 20 µm.

**TABLE 2.** Synopsis of morphological characteristics, habitats and hosts compared across *Distoseptispora* species.

Species	Conidiophores (µm)	Conidia (µm)	Conidia septation	Conidia characteristics	Habitat	Host	References
<i>Distoseptispora hydei</i>	87–145 × 3–7	32–58 × 10–15	7–9-distoseptate	Obpyriform to fusiform, olivaceous to brown, with gelatinous sheath around tip	Terrestrial	Dead bamboo culm	This study
<i>D. adscendens</i>	28–46 × 8–10	(80–)350–500 × 15–18	80-distoseptate	Cylindrical, hemispherical apex, hyaline	Terrestrial	Decaying wood of <i>Fagus sylvatica</i>	Shoemaker & White (1985), Réblová (1999)
<i>D. appendiculata</i>	62–86 × 4.5–5.5	67–89 × 10–16	13–17-distoseptate	Obpyriform or obclavate, olivaceous or dark brown, with gelatinous sheath around tip	Freshwater	Unidentified submerged wood	Luo <i>et al.</i> (2019)
<i>D. aquatica</i>	29–41 × 7–9	110–157 × 13.5–16.5	15–28-distoseptate	Obclavate, dark brown with bluish green to malachite green tinge	Freshwater	Unidentified submerged wood	Su <i>et al.</i> (2016)
<i>D. bambusae</i>	40–96 × 4–5.5	45–74 × 5.5–9.5	5–10-distoseptate	Obclavate, olivaceous or brown	Terrestrial	Dead bamboo culms	Sun <i>et al.</i> (2020)
<i>D. cangshanensis</i>	44–68 × 4–8	58–166(–287) × 10–14	Multi-distoseptate	Obclavate or lanceolate, olivaceous or brown	Freshwater	Unidentified submerged wood	Luo <i>et al.</i> (2018)
<i>D. caricis</i>	35–90 × 6–7	(55–)65–85(–100) × 15–16(–17)	5–10-distoseptate	Obclavate, brown	Terrestrial	Leaves of <i>Carex</i> sp.	Crous <i>et al.</i> (2019)
<i>D. clematidis</i>	22–40 × 4–10	120–210 × 12–20	28–35-distoseptate	Obclavate, cylindrical or rostrate, brown with green tinge	Terrestrial	Dried branches of <i>Clematis sikkimensis</i>	Phukhamsakda <i>et al.</i> (2020)
<i>D. dehongensis</i>	45–80 × 4–5	17–30 × 7.5–10	3–5-distoseptate	Obpyriform to obclavate, broad cylindrical	Freshwater	Unidentified submerged wood	Hyde <i>et al.</i> (2019)
<i>D. fluminicola</i>	21–33 × 5.5–6.5	125–250 × 13–15	17–34-distoseptate	Oblong to obclavate or cylindrical, brown with green tinge	Freshwater	Unidentified submerged wood	Su <i>et al.</i> (2016)

...Continued on the next page

TABLE 2. (Continued)

Species	Conidiophores ( $\mu\text{m}$ )	Conidia ( $\mu\text{m}$ )	Conidia septation	Conidia characteristics	Habitat	Host	References
<i>D. leonensis</i>	Up to $175 \times 6-7$	$(38-50-75(-85) \times 11-15$	7-12-distoseptate	Obclavate, rostrate, brown	Terrestrial	Dead culms of <i>Pennisetum purpureum</i> on <i>Freycinetia</i> sp.	Ellis (1958), McKenzie (1995)
<i>D. guttulata</i>	$55-90(-145) \times 3.5-5.5$	$75-130(-165) \times 7-11$	11-14(-20)-euseptate	Obclavate or lanceolate, rostrate, mid to dark brown or olivaceous	Freshwater	Unidentified submerged wood	Yang <i>et al.</i> (2018)
<i>D. lignicola</i>	$84-124 \times 4-5$	$60-108 \times 7-9$	5-9-euseptate	Obclavate, brown	Freshwater	Unidentified submerged wood	Luo <i>et al.</i> (2019)
<i>D. martini</i>	$50-110 \times 3.5-4.5$	$15-20 \times 11-16$	Transversal septa	Transversal ellipsoid, oblate or subglobose, muriform, pale brown to brown	Terrestrial	Unidentified dead branches	Xia <i>et al.</i> (2017)
<i>D. multiseptata</i>	$29-47 \times 4-6$	$147-185 \times 12-14$	Multi-distoseptate	Obclavate, rostrate, dark olivaceous green	Freshwater	Unidentified submerged wood	Hyde <i>et al.</i> (2016)
<i>D. neurostrata</i>	$93-117 \times 5.5-6.5$	$109-147 \times 13-15$	Multi-distoseptate	Obclavate, rostrate, dark olivaceous to mid or dark brown	Freshwater	Unidentified submerged wood	Luo <i>et al.</i> (2019)
<i>D. obclavata</i>	$117.5-162.5 \times 5-7$	$46-66 \times 9-11$	9-11-distoseptate	Obclavate, olivaceous to pale or dark brown	Freshwater	Unidentified submerged wood	Luo <i>et al.</i> (2019)
<i>D. obpyriformis</i>	$97-119 \times 5-7$	$53-71 \times 12-16$	9-11-distoseptate	Obpyriform, olivaceous to pale or dark brown	Freshwater	Unidentified submerged wood	Luo <i>et al.</i> (2018)
<i>D. palmarum</i>	$75-125 \times 3.5-5.5$	$35-180 \times 7-11$	7-27-distoseptate	Oblong, obclavate, cylindrical or rostrate	Terrestrial	Rachis of <i>Cocos nucifera</i> (Arecaceae)	Hyde <i>et al.</i> (2019)
<i>D. phangngaensis</i>	$18-30(-40) \times 4.3-6.5$	$165-350 \times 14-19$	Multi-distoseptate	Elongate, obclavate, rostrate, dark olivaceous to mid or dark brown	Freshwater	Unidentified submerged wood	Yang <i>et al.</i> (2018)

... Continued on the next page



TABLE 2. (Continued)

Species	Conidiophores ( $\mu\text{m}$ )	Conidia ( $\mu\text{m}$ )	Conidia septation	Conidia characteristics	Habitat	Host	References
<i>D. rayongensis</i>	75–125 $\times$ 3.5–5.5	(36–)60–106(–120) $\times$ 9–14.5	Mostly 9–13- euseptate, rarely 14–15-septate	Obclavate or obspathulate, rostrate, pale brown or pale olivaceous	Freshwater	Unidentified submerged wood	Hyde <i>et al.</i> (2020)
<i>D. rostrata</i>	82–126 $\times$ 5–7	115–155 $\times$ 9–11	(15–)18–23- distoseptate	Obclavate or lanceolate, rostrate, olivaceous to pale brown	Freshwater	Unidentified submerged wood	Luo <i>et al.</i> (2018)
<i>D. submersa</i>	55–73 $\times$ 7–9	95–123 $\times$ 15–19	17–23(–28)- distoseptate	Obclavate, lanceolate or obpyriform, mid olivaceous to brown	Freshwater	Unidentified submerged wood	Luo <i>et al.</i> (2018)
<i>D. suoluensis</i>	80–250 $\times$ 4.5–5.8	(65–)80–125(–145) $\times$ 8–13	8–10-euseptate	Narrowly obclavate or obspathulate, yellow brown or dark olivaceous	Freshwater	Unidentified submerged wood	Yang <i>et al.</i> (2018)
<i>D. tectonae</i>	Up to 40 $\times$ 4–6	(90–)130–140(–170) $\times$ 13–14	20–28-distoseptate	Cylindric-obclavate, dark reddish brown	Terrestrial	Dead twig of <i>Tectona</i> <i>grandis</i>	Hyde <i>et al.</i> (2016)
<i>D. tectonigena</i>	Up to 110 $\times$ 5–11	148–225(–360) $\times$ 11–12	20–46-distoseptate	Cylindric-obclavate, dark reddish brown	Terrestrial	Dead twig of <i>Tectona</i> <i>grandis</i>	Hyde <i>et al.</i> (2016)
<i>D. thailandica</i>	15–26 $\times$ 3–6	130–230 $\times$ 13.5–17	35–52-distoseptate	Oblong, obclavate, cylindrical or rostrate, reddish brown to brown	Terrestrial	Dead leave of <i>Pandanus</i> sp.	Tibpromma <i>et al.</i> (2018)
<i>D. thysanolaenae</i>	30–80 $\times$ 3.5–5.5	21.5–80 $\times$ 6.5–12.8	8–14-distoseptate	Elongated obclavate, slightly curved, light to dark brown, paler at the apex	Terrestrial	Dead culms of <i>Thysanolaena maxima</i>	Phookamsak <i>et al.</i> (2019)
<i>D. xishuangbannaensis</i>	12–17 $\times$ 2–5	160–305 $\times$ 8–15	Up to 40- distoseptate	Cylindric-obclavate, tapering towards apex, green-brown to brown	Terrestrial	Dead leave of <i>Pandanus</i> <i>utilis</i>	Tibpromma <i>et al.</i> (2018)

## Discussion

Luo *et al.* (2019) raised Distoseptisporaceae to the order Distoseptisporales based on evidence from morphological and phylogenetic analyses of combined LSU, SSU, RPB2 and TEF1- $\alpha$  sequence data, and also treated the genus *Aquapteridospora* in the Distoseptisporales genera *incertae sedis*. However, Wijayawardene *et al.* (2020) placed *Aquapteridospora* in the Diaporthomycetidae genera *incertae sedis* following Yang *et al.* (2015). The phylogenetic status of *Aquapteridospora* is thus uncertain. We follow the latest treatment of Distoseptisporales in Wijayawardene *et al.* (2020), and accordingly, the order Distoseptisporales currently only accommodates the family Distoseptisporaceae, whereas *Aquapteridospora* is treated in the Diaporthomycetidae genera *incertae sedis* pending further study.

Su *et al.* (2016) included two species in *Distoseptispora* and also included two taxa in *Ellisembia* (Sordariomycetes genera *incertae sedis*): *Ellisembia adscendens* and *E. leonensis* in *Distoseptispora* as *D. adscendens* and *D. leonensis* based on phylogenetic support. However, these two species are invalidly introduced as new combinations in *Distoseptispora*. Thus, the generic types *E. adscendens* and *E. leonensis* are in need of clarification to be validly introduced into *Distoseptispora*. Many subsequent authors followed Su *et al.*'s (2016) treatment, and accordingly, 28 species are currently accommodated in this genus (Luo *et al.* 2019, Phookamsak *et al.* 2019, Phukhamsakda *et al.* 2020, Sun *et al.* 2020).

The generic concept of *Distoseptispora* is based on the characteristics of asexual morph (Su *et al.* 2016, Luo *et al.* 2018, Hyde *et al.* 2020). Conidial characteristics include septate types (distoseptate vs euseptate), septate number, size, shape and color, all of which are mainly used to identify species in *Distoseptispora* (Su *et al.* 2016, Luo *et al.* 2018, Tibpromma *et al.* 2018, Yang *et al.* 2018, Hyde *et al.* 2020). However, these characteristics are not significantly correlated with the phylogenetic relationship. Some species, including *D. guttulata*, *D. lignicola*, *D. rayongensis* and *D. suoluensis*, produced euseptate conidia (Yang *et al.* 2018, Luo *et al.* 2019, Hyde *et al.* 2020). Phylogenetic analysis showed that they form distinct subclades, clustering with other *Distoseptispora* species that produced distoseptate conidia (FIGURE 1), and this has led to *Distoseptispora* possessing a broad generic concept. Therefore, it is necessary to combine both morphological characteristics and multi-gene phylogenetic analyses to clarify their taxonomic placement (Luo *et al.* 2018, 2019).

*Distoseptispora* is one genus of many lignicolous fungi encountered in aquatic and terrestrial habitats (Luo *et al.* 2019, Hyde *et al.* 2020). Species of *Distoseptispora* are not restricted to any particular hosts and have been recorded from a diverse range of plants, including both monocotyledons and dicotyledons, e.g., *Carex* sp., *Pandanus* sp., *Tectona grandis* (Hyde *et al.* 2016, Tibpromma *et al.* 2018, Crous *et al.* 2019). *Distoseptispora hydei* is the second species of *Distoseptispora* to occur on bamboo. In addition, *Distoseptispora* species are almost exclusively distributed in Thailand and China (Yang *et al.* 2015, 2018, Hyde *et al.* 2016, 2020, Su *et al.* 2016, Xia *et al.* 2017, Luo *et al.* 2018, 2019, Tibpromma *et al.* 2018, Crous *et al.* 2019, Phookamsak *et al.* 2019, Phukhamsakda *et al.* 2020, Sun *et al.* 2020). Only two species, *D. adscendens* and *D. leonensis*, have been found from Hungary and Malaysia, respectively (Shoemaker & White 1985, McKenzie 1995). Therefore, more collections of *Distoseptispora* and related taxa are needed, from a range of geographic regions and hosts, to investigate their sexual morphs and better resolve their phylogenetic relationships and taxonomic placements.

## Acknowledgments

Jutamart Monkai would like to thank Mae Fah Luang University (project no. 631A15001) for supporting this research. The authors thank Areerat Manowong for her assistance in culture work. The authors would like to thank the Thailand Research Fund "Impact of climate change on fungal diversity and biogeography in the Greater Mekong Subregion" (project no. RDG6130001). Rungtiwa Phookamsak thanks CAS President's International Fellowship Initiative (PIFI) for young staff (grant no. Y9215811Q1), the National Science Foundation of China (NSFC) project code 31850410489 (grant no. Y811982211) and Chiang Mai University for support this research work. Shaun Pennycook from Landcare Research, Auckland, New Zealand is thanked for advising on the taxon name.

## References

- Boonmee, S., D'souza, M.J., Luo, Z., Pinruan, U., Tanaka, K., Su, H., Bhat, D.J., McKenzie, E.H.C., Jones, E.B.G., Taylor, J.E. & Phillips, A.J. (2016) Dictyosporiaceae fam. nov. *Fungal Diversity* 80: 457–482.  
<https://doi.org/10.1007/s13225-016-0363-z>
- Boonmee, S., Rossman, A.Y., Liu, J.K., Li, W.J., Dai, D.Q., Bhat, J.D., Jones, E.B.G., McKenzie, E.H.C., Xu, J.C. & Hyde, K.D. (2014) Tubeufiales, ord. nov., integrating sexual and asexual generic names. *Fungal Diversity* 68: 239–298.  
<https://doi.org/10.1007/s13225-014-0304-7>
- Boonmee, S., Zhang, Y., Chomnunti, P., Chukeatirote, E., Tsui, C.K., Bahkali, A.H. & Hyde, K.D. (2011) Revision of lignicolous Tubeufiaceae based on morphological reexamination and phylogenetic analysis. *Fungal Diversity* 51: 63–102.  
<https://doi.org/10.1007/s13225-011-0147-4>
- Chomnunti, P., Hongsanan, S., Aguirre-Hudson, B., Tian, Q., Peršoh, D., Dhimi, M.K., Alias, A.S., Xu, J., Liu, X., Stadler, M. & Hyde, K.D. (2014) The sooty moulds. *Fungal Diversity* 66: 1–36.  
<https://doi.org/10.1007/s13225-014-0278-5>
- Crous, P.W., Wingfield, M.J., Lombard, L., Roets, F., Swart, W.J., Alvarado, P., Carnegie, A.J., Moreno, G., Luangsaard, J., Thangavel, R. & Alexandrova, A.V. (2019) Fungal Planet description sheets: 951–1041. *Persoonia: Molecular Phylogeny and Evolution of Fungi* 43: 223.  
<https://doi.org/10.3767/persoonia.2019.43.06>
- Dai, D.Q., Bhat, D.J., Liu, J.K., Chukeatirote, E., Zhao, R.L. & Hyde, K.D. (2012) *Bambusicola*, a new genus from bamboo with asexual and sexual morphs. *Cryptogamie Mycologie* 33: 363–379.  
<https://doi.org/10.7872/crym.v33.iss3.2012.363>
- Dai, D.Q., Phookamsak, R., Wijayawardene, N.N., Li, W.J., Bhat, D.J., Xu, J.C., Taylor, J.E., Hyde, K.D. & Chukeatirote, E. (2017) Bambusicolous fungi. *Fungal Diversity* 82: 1–105.  
<https://doi.org/10.1007/s13225-016-0367-8>
- Dai, D.Q., Wijayawardene, N.N., Bhat, D.J., Chukeatirote, E., Bahkali, A.H., Zhao, R.L., Xu, J.C. & Hyde, K.D. (2014) *Pustulomyces* gen. nov. accommodated in Diaporthaceae, Diaporthales, as revealed by morphology and molecular analyses. *Cryptogamie, Mycologie* 35: 63–72.  
<https://doi.org/10.7872/crym.v35.iss1.2014.63>
- Dai, D.Q., Tang, L.Z. & Wang, H.B. (2018) A review of bambusicolous ascomycetes. *Bamboo-Current and future prospects. IntechOpen*: 165–183.  
<https://doi.org/10.5772/intechopen.76463>
- Doilom, M., Dissanayake, A.J., Wanasinghe, D.N., Boonmee, S., Liu, J.K., Bhat, D.J., Taylor, J.E., Bahkali, A.H., Mckenzie, E.H.C. & Hyde, K.D. (2017) Microfungi on *Tectona grandis* (teak) in Northern Thailand. *Fungal Diversity* 82: 107–182.  
<https://doi.org/10.1007/s13225-016-0368-7>
- Ellis, M.B. & Ellis, J.P. (1985) *Microfungi on land plants. An identification handbook*. Macmillan, London.
- Hall, T.A. (1999) BioEdit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. *Nucleic Acids Symposium Series* 41: 95–98.  
[http://doi.org/10.14601/Phytopathol\\_Mediterr-14998u1.29](http://doi.org/10.14601/Phytopathol_Mediterr-14998u1.29)
- Huelsenbeck, J.P. & Ronquist, F. (2001) MRBAYES: Bayesian inference of phylogenetic trees. *Bioinformatics* 17: 754–755.  
<https://doi.org/10.1093/bioinformatics/17.8.754>
- Hyde, K.D., Hongsanan, S., Jeewon, R., Bhat, D.J., McKenzie, E.H.C., Jones, E.B.G., Phookamsak, R., Ariyawansa, H.A., Boonmee, S., Zhao, Q., Abdel-Aziz, F.A., Abdel-Wahab, M.A., Banmai, S., Chomnunti, P., Cui, B.K., Daranagama, D.A., Das, K., Dayarathne, M.C., de Silva, N.I., Dissanayake, A.J., Doilom, M., Ekanayaka, A.H., Gibertoni, T.B., Góes-Neto, A., Huang, S.K., Jayasiri, S.C., Jayawardena, R.S., Konta, S., Lee, H.B., Li, W.J., Lin, C.G., Liu, J.K., Lu, Y.Z., Luo, Z.L., Manawasinghe, I.S., Manimohan, P., Mapook, A., Niskanen, T., Norphanphoun, C., Papizadeh, M., Perera, R.H., Phukhamsakda, C., Richter, C., de A Santiago, A.L.C.M., Drechsler-Santos, E.R., Senanayake, I.C. & Tanaka, K. (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, K.D., Norphanphoun, C., Maharachchikumbura, S.S.N., Bhat, D.J., Jones, E.B.G., Bundhun, D., Chen, Y.J., Bao, D.F., Boonmee, S., Calabon, M.S., Chaiwan, N., Chethana, K.W.T., Dai, D.Q., Dayarathne, M.C., Devadatha, B., Dissanayake, A.J., Dissanayake, L.S., Doilom, M., Dong, W., Fan, X.L., Goonasekara, I.D., Hongsanan, S., Huang, S.K., Jayawardena, R.S., Jeewon, R., Karunarathna, A., Konta, S., Kumar, V., Lin, C.G., Liu, J.K., Liu, N.G., Luangsaard, J., Lumyong, S., Luo, Z.L., Marasinghe, D.S., McKenzie, E.H.C., Niego, A.G.T., Niranjana, M., Perera, R.H., Phukhamsakda, C., Rathnayaka, A.R., Samarakoon, M.C., Samarakoon, S.M.B.C., Sarma,

- V.V., Senanayake, I.C., Shang, Q.J., Stadler, M., Tibpromma, S., Wanasinghe, D.N., Wei, D.P., Wijayawardene, N.N., Xiao, Y.P., Yang, J., Zeng, X.Y., Zhang, S.N. & Xiang, M.M. (2020) Refined families of Sordariomycetes. *Mycosphere* 11: 305–1059. <https://doi.org/10.5943/mycosphere/11/1/7>
- Hyde, K.D., Zhou, D. & Dalisay, T. (2002a) Bambusicolous fungi: a review. *Fungal Diversity* 9: 1–14.
- Hyde, K.D., Zhou, D., McKenzie, E.H.C., Ho, W.H. & Dalisay, T. (2002b) Vertical distribution of saprobic fungi on bamboo culms. *Fungal Diversity* 11: 109–118.
- Index Fungorum (2020) Available from: <http://www.indexfungorum.org/names/Names.asp> (accessed 21 June 2020)
- Jaklitsch, W.M., Fournier, J., Dai, D.Q., Hyde, K.D. & Voglmayr, H. (2015) *Valsaria* and the Valsariales. *Fungal diversity* 73: 159–202. <https://doi.org/10.1007/s13225-015-0330-0>
- Jayasiri, S.C., Hyde, K.D., Jones, E.B.G., McKenzie, E.H.C., Jeewon, R., Phillips, A.J.L., Bhat, D.J., Wanasinghe, D.N., Liu, J.K., Lu, Y.Z. & Kang, J.C. (2019) Diversity, morphology and molecular phylogeny of Dothideomycetes on decaying wild seed pods and fruits. *Mycosphere* 10: 1–186. <https://doi.org/10.5943/mycosphere/10/1/1>
- Jayasiri, S.C., Hyde, K.D., Abd-Elsalam, K.A., Abdel-Wahab, M.A., Ariyawansa, H.A., Bhat, J., Buyck, B., Dai, Y.C., Ertz, D., Hidayat, I., Jeewon, R., Jones, E.B.G., Karunarathna, S.C., Kirk, P., Lei, C., Liu, J.K., Maharachchikumbura, S.S.N., McKenzie, E.H.C., Ghobad Nejhad, M., Nilsson, H., Pang, K.L., Phookamsak, R., Rollins, A.W., Romero, A.I., Stephenson, S., Suetrong, S., Tsui, C.K.M., Vizzini, A., Wen, T.C., de Silva, N.I., Promputtha, I. & Kang, J.C. (2015) The faces of fungi database: fungal names linked with morphology, molecular and human attributes. *Fungal Diversity* 74: 18–357. <https://doi.org/10.1007/s13225-015-0351-8>
- Jiang, H.B., Hyde, K.D., Doilom, M., Karunarathna, S.C., Xu, J.C. & Phookamsak, R. (2019) *Arthrinium setostromum* (Apiosporaceae, Xylariales), a novel species associated with dead bamboo from Yunnan, China. *Asian Journal of Mycology* 2: 254–268. <https://doi.org/10.5943/ajom/2/1/16>
- Jiang, H.B., Phookamsak, R., Bhat, D.J., Khan, S., Bahkali, A.H., Elgorban, A.M. & Hyde, K.D. (2018) *Vamsapriya yunnana*, a new species of *Vamsapriya* (Xylariaceae, Xylariales) associated with bamboo from Yunnan, China. *Phytotaxa* 356: 61–70. <http://dx.doi.org/10.11646/phytotaxa.356.1.5>
- Jiang, H.B., Phookamsak, R., Xu, J., Karunarathna, S.C., Mortimer, P.E. & Hyde, K.D. (2020) Taxonomic and phylogenetic characterizations reveal three new species of *Mendogia* (Myriangiaceae, Myriangiales). *Mycological Progress* 19: 41–51. <https://doi.org/10.1007/s11557-019-01540-z>
- Katoh, K., Rozewicki, J. & Yamada, K.D. (2019) MAFFT online service: multiple sequence alignment, interactive sequence choice and visualization. *Briefings in Bioinformatics* 20: 1160–1166. <https://doi.org/10.1093/bib/bbx108>
- Kodsueb, R., McKenzie, E.H.C., Lumyong, S. & Hyde, K.D. (2008a) Diversity of saprobic fungi on Magnoliaceae. *Fungal Diversity* 30: 37–53.
- Kodsueb, R., McKenzie, E.H.C., Lumyong, S. & Hyde, K.D. (2008b) Fungal succession on woody litter of *Magnolia liliifera* (Magnoliaceae). *Fungal Diversity* 30: 55–72.
- Lin, C.G., McKenzie, E.H.C., Liu, J.K., Jones, E.B.G. & Hyde, K.D. (2019) Hyaline-spored chaetosphaeriaceous hyphomycetes from Thailand and China, with a review of the family Chaetosphaeriaceae. *Mycosphere* 10: 655–700. <https://doi.org/10.5943/mycosphere/10/1/14>
- Liu, J.K., Hyde, K.D., Jones, E.B.G., Ariyawansa, H.A., Bhat, D.J., Boonmee, S., Maharachchikumbura, S.S.N., McKenzie, E.H.C., Phookamsak, R., Phukhamsakda, C., Shenoy, B.D., Abdel-Wahab, M.A., Buyck, B., Chen, J., Chethana, K.W.T., Singtripop, C., Dai, D.Q., Dai, Y.C., Daranagama, D.A., Dissanayake, A.J., Doilom, M., D'souza, M.J., Fan, X.L., Goonasekara, I.D., Hirayama, K., Hongsanan, S., Jayasiri, S.C., Jayawardena, R.S., Karunarathna, S.C., Li, W.J., Mapook, A., Norphanphoun, C., Pang, K.L., Perera, R.H., Peršoh, D., Pinruan, U., Senanayake, I.C., Somrithipol, S., Suetrong, S., Tanaka, K., Thambugala, K.M., Tian, Q., Tibpromma, S., Udayanga, D., Wijayawardene, N.N., Wanasinghe, D., Wisitrasameewong, K., Zeng, X.Y., Abdel-Aziz, F.A., Adamčík, S., Bahkali, A.H., Boonyuen, N., Bulgakov, T., Callac, P., Chomnunti, P., Greiner, K., Hashimoto, A., Hofstetter, V., Kang, J.C., Lewis, D., Li, X.H., Liu, X.Z., Liu, Z.Y., Matsumura, M., Mortimer, P.E., Rambold, G., Randrianjohany, E., Sato, G., Sri-Indrasudhi, V., Tian, C.M., Verbeken, A., von Brackel, W., Wang, Y., Wen, T.C., Xu, J.C., Yan, J.Y., Zhao, R.L. & Camporesi, E. (2015) Fungal diversity notes 1–110: taxonomic and phylogenetic contributions to fungal species. *Fungal Diversity* 72: 1–197. <https://doi.org/10.1007/s13225-015-0324-y>
- Liu, J.K., Phookamsak, R., Jones, E.B.G., Zhang, Y., Ko-Ko, T.W., Hu, H.L., Boonmee, S., Doilom, M., Chukeatirote, E., Bahkali, A.H. & Wang, Y. (2011) *Astrosphaeriella* is polyphyletic, with species in *Fissuroma* gen. nov., and *Neoastrosphaeriella* gen. nov. *Fungal Diversity* 51: 135–154.
- Liu, N.G., Lu, Y.Z., Bhat, D.J., McKenzie, E.H.C., Lumyong, S., Jumpathong, J. & Liu, J.K.J. (2019) *Kevinhydea brevistipitata* gen. et sp. nov. and *Helicoma hydei* sp. nov., (Tubeufiaceae) from decaying wood habitats. *Mycological Progress* 18: 671–682.



<https://doi.org/10.1007/s11557-019-01480-8>

- Liu, Y.J., Whelen, S. & Hall, B.D. (1999) Phylogenetic relationships among ascomycetes: evidence from an RNA polymerase II subunit. *Molecular Biology and Evolution* 16: 1799–1808.
- Lu, Y.Z., Liu, J.K.J., Hyde, K.D., Jeewon, R., Kang, J.C., Fan, C., Boonmee, S., Bhat, D.J., Luo, Z.L., Lin, C.G. & Eungwanichayapant, P.D. (2018) A taxonomic reassessment of Tubeufiales based on multi-locus phylogeny and morphology. *Fungal Diversity* 92: 131–344.
- <https://doi.org/10.1007/s13225-018-0411-y>
- Luo, Z.L., Hyde, K.D., Liu, J.K., Bhat, D.J., Bao, D.F., Li, W.L. & Su, H.Y. (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: 444–461.
- <https://doi.org/10.5943/mycosphere/9/3/2>
- Luo, Z.L., Hyde, K.D., Liu, J.K.J., Maharachchikumbura, S.S., Jeewon, R., Bao, D.F., Bhat, D.J., Lin, C.G., Li, W.L., Yang, J., Liu, N.G., Lu, Y.Z., Jayawardena, R.S., Li, J.F. & Su, H.Y. (2019) Freshwater Sordariomycetes. *Fungal diversity* 99: 451–660.
- <https://doi.org/10.1007/s13225-019-00438-1>
- Mapook, A., Hyde, K.D., McKenzie, E.H.C., Jones, E.B.G., Bhat, D.J., Jeewon, R., Stadler, M., Samarakoon, M.C., Malaithong, M., Tanunchai, B. & Buscot, F. (2020) Taxonomic and phylogenetic contributions to fungi associated with the invasive weed *Chromolaena odorata* (Siam weed). *Fungal Diversity* 101: 1–175.
- <https://doi.org/10.1007/s13225-020-00444-8>
- Mckenzie, E.H.C. (1995) Dematiaceous Hyphomycetes on Pandanaceae. V. *Sporidesmium* sensu lato. *Mycotaxon* 56: 9–29.
- Monkai, J., Promputtha, I., Kodsueb, R., Chukeatirote, E., McKenzie, E.H.C. & Hyde, K.D. (2013) Fungi on decaying leaves of *Magnolia liliifera* and *Cinnamomum iners* show litter fungi to be hyperdiverse. *Mycosphere* 4: 292–301.
- <https://doi.org/10.5943/mycosphere/4/2/12>
- Morakotkarn, D., Kawasaki, H. & Seki, T. (2007) Molecular diversity of bamboo-associated fungi isolated from Japan. *FEMS microbiology letters* 266: 10–19.
- Phookamsak, R., Hyde, K.D., Jeewon, R., Bhat, D.J., Jones, E.B.G., Maharachchikumbura, S.S.N., Raspé, O., Karunarathna, S.C., Wanasinghe, D.N., Hongsanan, S., Doilom, M., Tennakoon, D.S., Machado, A.R., Firmino, A.L., Ghosh, A., Karunarathna, A., Mešić, A., Dutta, A.K., Thongbai, B., Devadatha, B., Norphanphoun, C., Senwannana, C., Wei, D., Pem, D., Ackah, F.K., Wang, G., Jiang, H-B., Madrid, H., Lee, H.B., Goonasekara, I.D., Manawasinghe, I.S., Kušan, I., Cano, J., Gené, J., Li, J., Das, K., Acharya, K., Raj, K.N.A., Latha, K.P.D., Chethana, K.W.T., He, M-Q., Dueñas, M., Jadan, M., Martín, M.P., Samarakoon, M.C., Dayarathne, M.C., Raza, M., Park, M.S., Telleria, M.T., Chaiwan, N., Matočec, N., de Silva, N.I., Pereira, O.L., Singh, P.N., Manimohan, P., Uniyal, P., Shang, Q-J., Bhatt, R.P., Perera, R.H., Alvarenga, R.L.M., Nogal-Prata, S., Singh, S.K., Vadthananat, S., Oh, S-Y, Huang, S-K., Rana, S., Konta, S., Paloi, S., Jayasiri, S.C., Jeon, S.J., Mehmood, T., Gibertoni, T.B., Nguyen, T.T.T., Singh, U., Thiagaraja, V., Sarma, V.V., Dong, W., Yu, X-D., Lu, Y-Z., Lim, Y.W., Chen, Y., Tkalčec, Z., Zhang, Z-F., Luo, Z-L., Daranagama, D.A., Thambugala, K.M., Tibpromma, S., Camporesi, E., Bulgakov, T.S., Dissanayake, A.J., Senanayake, I.C., Dai, D.Q., Tang, L-Z., Khan, S., Zhang, H., Promputtha, I., Cai, L., Chomnunti, P., Zhao, R-L., Lumyong, S., Boonmee, S., Wen, T-C., Mortimer, P.E. & Xu, J.C. (2019) Fungal diversity notes 929–1035: taxonomic and phylogenetic contributions on genera and species of fungal taxa. *Fungal Diversity* 95: 1–273.
- <https://doi.org/10.1007/s13225-019-00421-w>
- Phookamsak, R., Liu, J.K., Manamgoda, D.S., Wanasinghe, D.N., Ariyawansa, H., Mortimer, P.E., Chukeatirote, E., Mckenzie, E.H.C. & Hyde, K.D. (2014) Epitypification of two bambusicolous fungi from Thailand. *Cryptogamie Mycologie* 35: 239–256.
- <https://doi.org/10.7872/crym.v35.iss3.2014.239>
- Phookamsak, R., Norphanphoun, C., Tanaka, K., Dai, D.Q., Luo, Z.L., Liu, J.K., Su, H.Y., Bhat, D.J., Bahkali, A.H., Mortimer, P.E. & Xu, J.C. (2015) Towards a natural classification of *Astrosphaeriella*-like species; introducing *Astrosphaeriellaceae* and *Pseudoastrosphaeriellaceae* fam. nov. and *Astrosphaeriellopsis*, gen. nov. *Fungal Diversity* 74: 143–197.
- <https://doi.org/10.1007/s13225-015-0352-7>
- Phukhamsakda, C., McKenzie, E.H.C., Phillips, A.J.L., Jones, E.B.G., Bhat, D.J., Stadler, M., Bhunjun, C.S., Wanasinghe, D.N., Thongbai, B., Camporesi, E., Jayawardena, R.S., Perera, R.H., Ekanayake, A.H., Tibpromma, S., Doilom, M., Xu, J.C. & Hyde, K.D. (2020) Study of fungi associated with *Clematis* L. (Ranunculaceae) and integrated approach to delimiting species boundaries. *Fungal diversity* (in press).
- Promputtha, I., Mckenzie, E.H.C., Tennakoon, D.S., Lumyong, S. & Hyde, K.D. (2017) Succession and natural occurrence of saprobic fungi on leaves of *Magnolia liliifera* in a tropical forest. *Cryptogamie Mycologie* 38: 213–225.
- <https://doi.org/10.7872/crym/v38.iss2.2017.213>
- Rambaut, A. (2012) *FigTree, version 1.4. 2*. University of Edinburgh, Edinburgh.

- Rambaut, A. & Drummond, A.J. (2007) *Tracer v1, 4*. Available from: <http://beast.bio.ed.ac.uk/Tracer> (accessed 1 June 2020)
- Réblová, M. (1999) Studies in *Chaetosphaeria* sensu lato III. *Umbrinosphaeria* gen. nov. and *Miyoshiella* with *Sporidesmium* anamorphs. *Mycotaxon* 71: 13–43.
- Ronquist, F., Teslenko, M., van der Mark, P., Ayres, D.L., Darling, A., Höhna, S., Larget, B., Liu, L., Suchard, M.A. & Huelsenbeck, J.P. (2012) MrBayes 3.2: efficient Bayesian phylogenetic inference and model choice across a large model space. *Systematic Biology* 61: 539–542.
- Shoemaker, R.A. & White, G.P. (1985) *Lasiosphaeria caesariata* with *Sporidesmium hormiscioides* and *L. triseptata* with *S. adscendens*. *Sydowia* 38: 278–283
- Silvestro, D. & Michalak, I. (2012) raxmlGUI: a graphical front-end for RAxML. *Organisms Diversity and Evolution* 12: 335–337.
- Su, H.Y., Hyde, K.D., Maharachchikumbura, S.S.N., Ariyawansa, H.A., Luo, Z.L., Promputtha, I., Tian, Q., Lin, C.G., Shang, Q.J., Zhao, Y.C., Chai, H.M., Liu, X.Y., Bahkali, A.H., Bhat, J.D., McKeenzie, E.H.C. & Zhou, D.Q. (2016) The families Distoseptisporaceae fam. nov., Kirschsteinioteliaceae, Sporormiaceae and Torulaceae, with new species from freshwater in Yunnan Province, China. *Fungal Diversity* 80: 375–409.  
<https://doi.org/10.1007/s13225-016-0362-0>
- Sun, Y., Goonasekara, I.D., Thambugala, K.M., Jayawardena, R.S., Wang, Y. & Hyde, K.D. (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>
- Swofford, D.L. (2002) PAUP: phylogenetic analysis using parsimony, version 4.0 b10. Sinauer Associates, Sunderland.  
<https://doi.org/10.1111/j.0014-3820.2002.tb00191.x>
- Tanaka, K., Hirayama, K., Yonezawa, H., Hatakeyama, S., Harada, Y., Sano, T., Shirouzu, T. & Hosoya, T. (2009) Molecular taxonomy of bambusicolous fungi: Tetraplosphaeriaceae, a new pleosporalean family with *Tetraploa*-like anamorphs. *Studies in Mycology* 64: 175–209.  
<https://doi.org/10.3114/sim.2009.64.10>
- Tanaka, K., Hirayama, K., Yonezawa, H., Sato, G., Toriyabe, A., Kudo, H., Hashimoto, A., Matsumura, M., Harada, Y., Kurihara, Y. & Shirouzu, T. (2015) Revision of the Massariaceae (Pleosporales, Dothideomycetes). *Studies in Mycology* 82: 75–136.  
<https://doi.org/10.1016/j.simyco.2015.10.002>
- Tibpromma, S., Hyde, K.D., Jeewon, R., Maharachchikumbura, S.S.N., Liu, J.K., Bhat, D.J., Jones, E.B.G., McKenzie, E.H.C., Camporesi, E., Bulgakov, T.S., Doilom, M., de Azevedo, S.A., Das, K., Manimohan, P., Gibertoni, T.B., Lim, Y.W., Ekanayaka, A.H., Thongbai, B., Lee, H.B., Yang, J.B., Kirk, P.M., Sysouphanthong, P., Singh, S.K., Boonmee, S., Dong, W., Raj, K.N.A., Latha, K.P.D., Phookamsak, R., Phukhamsakda, C., Konta, S., Jayasiri, S.C., Norphanphoun, C., Tennakoon, D.S., Li, J.F., Dayarathne, M.C., Perera, R.H., Xiao, Y., Wanasinghe, D.N., Senanayake, I.C., Goonasekara, I.D., de Silva, N.I., Mapook, A., Jayawardena, R.S., Dissanayake, A.J., Manawasinghe, I.S., Chethana, K.W.T., Luo, Z.L., Hapuarachchi, K.K., Baghela, A., Soares, A.M., Vizzini, A., Meiras-Ottoni, A., Mešić, A., Dutta, A.K., de Souza, C.A.F., Richter, C., Lin, C.G., Chakrabarty, D., Daranagama, D.A., Lima, D.X., Chakraborty, D., Ercole, E., Wu, F., Simonini, G., Vasquez, G., da Silva, G.A., Plautz, J.H., Ariyawansa, H.A., Lee, H., Kušan, I., Song, J., Sun, J., Karmakar, J., Hu, K., Semwal, K.C., Thambugala, K.M., Voigt, K., Acharya, K., Rajeshkumar, K.C., Ryvarden, L., Jadan, M., Hosen, M.I., Mikšik, M., Samarakoon, M.C., Wijayawardene, N.N., Kim, N.K., Matočec, N., Singh, P.N., Tian, Q., Bhatt, R.P., de Oliveira, R.J.V., Tulloss, R.E., Aamir, S., Kaewchai, S., Svetasheva, S.T.Y., Nguyen, T.T.T., Antonín, V., Li, W.J., Wang, Y., Indoliya, Y., Tkalčec, Z., Elgorban, A.M., Bahkali, A.H., Tang, A.M.C., Su, H.Y., Zhang, H., Promputtha, I., Luangsa-ard, J., Xu, J.C., Yan, J., Chuan, K.J., Stadler, M., Mortimer, P.E., Chomnunti, P., Zhao, Q., Phillips, A.J.L., Nontachaiyapoom, S., Wen, T.C. & Karunarathna, S.C. (2017) Fungal diversity notes 491–602: taxonomic and phylogenetic contributions to fungal taxa. *Fungal Diversity* 83: 1–261.  
<https://doi.org/10.1007/s13225-017-0378-0>
- Vilgalys, R. & Hester, M. (1990) Rapid genetic identification and mapping of enzymatically amplified ribosomal DNA from several *Cryptococcus* species. *Journal of Bacteriology* 172: 4238–4246.
- Wanasinghe, D.N., Jeewon, R., Jones, E.B.G., Tibpromma, S. & Hyde, K.D. (2017) Saprobic Dothideomycetes in Thailand: *Muritestudina* gen. et sp. nov. (Testudinaceae) a new terrestrial pleosporalean ascomycete, with hyaline and muriform ascospores. *Studies in Fungi* 2: 219–234.  
<https://doi.org/10.5943/sif/2/1/26>
- Wanasinghe, D.N., Jones, E.B.G., Dissanayake, A.J. & Hyde, K.D. (2016) Saprobic Dothideomycetes in Thailand: *Vaginatisspora appendiculata* sp. nov. (Lophiostomataceae) introduced based on morphological and molecular data. *Studies in Fungi* 1: 56–68.  
<https://doi.org/10.5943/sif/1/1/5>
- Wang, M., Tan, X.M., Liu, F. & Cai, L. (2018) Eight new *Arthrinium* species from China. *MycKeys* 34: 1–24.  
<https://doi.org/10.3897/mycokeys.34.24221>
- White, T.J., Bruns, T., Lee, J. & Taylor, S.B. (1990) Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics.

In: Innis, M.A., Gelfand, D.H., Sninsky, J.J., White, T.J. (eds), *PCR protocols: a guide to methods and applications* Academic Press, San Diego, California, USA. pp. 315–322.

<https://doi.org/10.1016/B978-0-12-372180-8.50042-1>

- Wijayawardene, N.N., Hyde, K.D., Al-Ani, L.K.T., Tedersoo, L., Haelewaters, D., Rajeshkumar, K.C., Zhao, R.L., Aptroot, A., Leontyev, D.V., Saxena, R.K., Tokarev, Y.S., Dai, D.Q., Letcher, P.M., Stephenson, S.L., Ertz, D., Lumbsch, H.T., Kukwa, M., Issi, I.V., Madrid, H., Phillips, A.J.L., Selbmann, L., Pfliegler, W.P., Horváth, E., Bensch, K., Kirk, P., Kolaříková, Z., Raja, H.A., Radek, R., Papp, V., Dima, B., Ma, J., Malosso, E., Takamatsu, S., Rambold, G., Gannibal, P.B., Triebel, D., Gautam, A.K., Avasthi, S., Suetrong, S., Timdal, E., Fryar, S.C., Delgado, G., Réblová, M., Doilom, M., Dolatabadi, S., Pawłowska, J., Humber, R.A., Kodsueb, R., Sánchez-Castro, I., Goto, B.T., Silva, D.K.A., De Souza, F.A., Oehl, F., Da Silva, G.A., Silva, I.R., Błaszowski, J., Jobim, K., Maia, L.C., Barbosa, F.R., Fiuza, P.O., Divakar, P.K., Shenoy, B.D., Castañeda-Ruiz, R.F., Somrithipol, S., Karunarathna, S.C., Tibpromma, S., Mortimer, P.E., Wanasinghe, D.N., Phookamsak, R., Xu, J., Wang, Y., Fenghua, T., Alvarado, P., Li, D.W., Kušan, I., Matočec, N., Maharachchikumbura, S.S.N., Papizadeh, M., Heredia, G., Wartchow, F., Bakhshi, M., Boehm, E., Youssef, N., Hustad, V.P., Lawrey, J.D., Santiago, A.L.C.M.A., Bezerra, J.D.P., Souza-Motta, C.M., Firmino, A.L., Tian, Q., Houbraken, J., Hongsanan, S., Tanaka, K., Dissanayake, A.J., Monteiro, J.S., Grossart, H.P., Suija, A., Weerakoon, G., Etayo, J., Tsurykau, A., Kuhnert, E., Vázquez, V., Mungai, P., Damm, U., Li, Q.R., Zhang, H., Boonmee, S., Lu, Y.Z., Becerra, A.G., Kendrick, B., Brearley, F.Q., Motiejūnaitė, J., Sharma, B., Khare, R., Gaikwad, S., Wijesundara, D.S.A., Tang, L.Z., He, M.Q., Flakus, A., Rodriguez-Flakus, P., Zhurbenko, M.P., McKenzie, E.H.C., Stadler, M., Bhat, D.J., Liu, J.K., Raza, M., Jeewon, R., Nassonova, E.S., Prieto, M., Jayalal, R.G.U., Yurkov, A., Schnittler, M., Shchepin, O.N., Novozhilov, Y.K., Liu, P., Cavender, J.C., Kang, Y., Mohammad, S., Zhang, L.F., Xu, R.F., Li, Y.M., Dayarathne, M.C., Ekanayaka, A.H., Wen, T.C., Deng, C.Y., Lateef, A.A., Pereira, O.L., Navathe, S., Hawksworth, D.L., Fan, X.L., Dissanayake, L.S. & Erdođdu, M. (2020) Outline of Fungi and fungi-like taxa. *Mycosphere* 11: 1060–1456.  
<http://doi.org/10.5943/mycosphere/11/1/8>
- Xia, J.W., Ma, Y.R., Li, Z. & Zhang, X.G. (2017) *Acrodictys*-like wood decay fungi from southern China, with two new families Acrodictyaceae and Junewangiaceae. *Scientific Reports* 7: 7888.  
<https://doi.org/10.1038/s41598-017-08318-x>
- Yang, J., Maharachchikumbura, S.S.N., Liu, J.K., Hyde, K.D., Jones, E.B.G., Al-Sadi, A.M. & Liu, Z.Y. (2018) *Pseudostanjehughesia aquitropica* gen. et sp. nov. and *Sporidesmium* sensu lato species from freshwater habitats. *Mycological Progress* 17: 591–616.  
<https://doi.org/10.1007/s11557-017-1339-4>
- Yang, J., Maharachchikumbura, S.S.N., Bhat, D.J., McKenzie, E.H.C., Bahkali, A.H., Jones, E.B.G. & Liu, Z.Y. (2015) *Aquaapteridospora lignicola* gen. et sp. nov., a new hyphomycetous taxon (Sordariomycetes) from wood submerged in a freshwater stream. *Cryptogamie Mycologie* 36: 469–478.  
<https://doi.org/10.7872/crym/v36.iss4.2015.469>
- Zhaxybayeva, O. & Gogarten, J.P. (2002) Bootstrap, Bayesian probability and maximum likelihood mapping: exploring new tools for comparative genome analyses. *BMC Genomics* 3: 4.  
<https://doi.org/10.1186/1471-2164-3-4>