

Article

Exploring More on *Dictyosporiaceae*: The Species Geographical Distribution and Intriguing Novel Additions from Plant Litter

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Abstract: Five fungal taxa collected from plant litter in Chiang Mai province, Thailand, are described with illustrations. The maximum likelihood, maximum parsimony, and Bayesian analyses of combined loci of the internal transcribed spacer (ITS), large subunit nuclear ribosomal DNA (LSU), and translation extension factor 1- α (*tef1- α*) region were used for phylogeny analyses. *Dictyocheirospora acaciae* is introduced as a new species from *Acacia dealbata*. Based on size differences in conidiomata, conidia, and DNA sequence data, it is separated from the other species in the genus. Four new host records, *Dictyocheirospora garethjonesii*, *Di. taiwanense*, *Dictyosporium digitatum*, and *Pseudocoleophoma zingiberacearum* are also reported from *Bismarkia nobilis*, *Ficus benjamina*, *Cyperus aggregatus*, and *Hedychium spicatum*, respectively. Detailed descriptions, microphotographs, and phylogenetic information were provided, and all the species were compared to similar taxa. It is noted that there is still a necessity for a collective worldwide account of the distribution of *Dictyosporiaceae* species. Therefore, we compiled the geographical distributions and host species associations of all the so far known *Dictyosporiaceae* species and discussed them here.

Keywords: diversity; morphology; new host records; phylogeny; taxonomy; Thailand



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1. Introduction

Plant litter decomposition is one of the most important processes of the global carbon budget [1,2]. In particular, it signifies a crucial pathway for nutrient recycling in any ecosystem [3,4]. The decomposition of plant litter mainly refers to a variety of complicated processes involving chemical, physical, and biological components [4–7]. The breakdown of plant litter is affected by a wide range of aspects, such as environmental variables (e.g., temperature, rainfall, moisture condition, seasonal variations, and soil characteristics), plant litter quality (e.g., toughness, surface properties, and chemical components), and decomposer communities (e.g., bacteria, fungi, and detritivores) [6,8,9]. Particularly with a greater than 75% capacity to reduce organic matter than other microbes, fungi are among the top-level decomposers [10]. Thus, saprobic fungal species surveys in various host species and regions are crucial to understanding the fungal diversity in plant litter.

Boonmee et al. [11] introduced *Dictyosporiaceae* to include species having brown, cheiroid, digitate, multi-septate, palmate, and/or dictyosporous conidia. The sexual morphs have dark brown to black, superficial ascomata, bitunicate, fissitunicate asci, and hyaline, septate ascospores with a mucilaginous sheath [11–13]. Most known *Dictyosporiaceae* species occur as saprobes and pathogenicity seems doubtful since infected

host records are not known so far [11,13]. There is an astounding global distribution of *Dictyosporiaceae* species, reported from plant litter in terrestrial and aquatic habitats [11,14–17]. Numerous novel *Dictyosporiaceae* genera were discovered in recent studies. For instance, five new genera, such as *Pseudoconiothyrium* [18], *Sajamaea* [19], *Paradictyocheirospora* [16], *Verrucoccum* [20], and *Neodigitodesmium* [21] were established in just three years. However, Tian et al. [21] reanalyzed the morphological characteristics of the type of *Paradictyocheirospora* (*P. tectonae*) and demonstrated that *Paradictyocheirospora* and *Digitodesmium* are congeneric. Thus, to date there are 20 accepted genera in *Dictyosporiaceae*: viz. *Aquadictyospora*, *Aquaticheirospora*, *Cheirosporium*, *Dendryphiella*, *Dictyocheirospora*, *Dictyopalmispora*, *Dictyosporium*, *Digitodesmium*, *Gregarithecium*, *Immotthia*, *Jalapriya*, *Neodendryphiella*, *Neodigitodesmium*, *Pseudocoleophoma*, *Pseudoconiothyrium*, *Pseudocyclothyriella*, *Pseudodictyosporium*, *Sajamaea*, *Verrucoccum*, and *Vikalpa* [22].

We study the plant litter inhabiting fungal diversity in Thailand. In this paper, we aimed to introduce *Dictyocheirospora acaciae*, a new species isolated from *Acacia dealbata* and four new host records: *Di. garethjonesii*, *Di. taiwanense*, *Dictyosporium digitatum*, and *Pseudocoleophoma zingiberacearum* from *Bismarkia nobilis*, *Ficus benjamina*, *Cyperus aggregatus*, and *Hedychium spicatum*, respectively. Phylogenetic placements were confirmed based on the maximum likelihood (ML), maximum parsimony (MP), and Bayesian inference (BYPP) analyses using combined ITS, LSU, and *tef1- α* sequence data. We also discovered that there is still a need for an updated checklist of *Dictyosporiaceae* species. Thus, we listed all the so far known *Dictyosporiaceae* species' geographic distribution and host associations. We expect that this comprehensive list will be helpful for coming studies in understanding the distribution of *Dictyosporiaceae* species.

2. Materials and Methods

2.1. Samples Collection, Fungal Isolation, and Examination

Plant litter samples (dead leaves and stems) were collected from Chiang Mai province in Thailand. Five samples were subjected to one-day incubation at room temperature (25 °C) in plastic boxes lined with wet tissue paper. Specimens were inspected following the methods described by Tennakoon et al. [9]. Squash mount preparations were prepared to determine micro-morphology (*Dictyocheirospora acaciae*, *Di. garethjonesii*, *Di. taiwanense*, and *Dictyosporium digitatum*) and sections were obtained to check the conidiomata shapes and conidial wall (*Pseudocoleophoma zingiberacearum*). A razor blade was used to manually cut thin sections of conidiomata (*P. zingiberacearum*). Fungal fruiting bodies were examined using a stereomicroscope (AXIOSKOP 2 PLUS Series, Göttingen, Germany). Morphological characteristics (e.g., conidia and conidiogenous cells) were examined and photographed using the Axioskop 2 Plus (Göttingen, Germany) compound microscope equipped with a Canon Axiocam 506 color digital camera (Hanover, Germany). The Tarosoft (R) Image Frame Work application was used to obtain all the measurements. Fungal material was mounted in lactoglycerol to prepare permanent slides, and the cover slip edges were sealed with nail polish. Adobe Photoshop CS3 Extended version 10.0 software (Adobe Systems, San Jose, CA, USA) was used to construct the photo plates.

Using the method outlined by Senanayake et al. [23], single spore isolation was conducted to produce pure cultures. Type specimens and living cultures were deposited in the Herbarium of the Department of Biology (CMUB) and Sustainable Development of Biological Resources Laboratory (SDBR), Faculty of Science, Chiang Mai University. The Faces of Fungi (FOF) and Index Fungorum (IF) numbers were obtained following Jayasiri et al. [24] and the Index Fungorum [25], respectively.

2.2. DNA Extraction, PCR Amplification, and Sequencing

Axenic mycelium (50–100 mg) grown on Potato Dextrose Agar (PDA) for four weeks at room temperature (25 °C) was used to extract the total genomic DNA. The Biospin Fungus Genomic DNA Extraction Kit (BioFlux®) (Hangzhou, China) was used to extract fungal DNA following the manufacturer's instructions. For DNA amplification, the DNA

product was stored at 4 °C and for long-term storage it was kept at –20 °C. Polymerase chain reaction (PCR) was used to amplify the DNA using three genes: the large subunit (28S, LSU), internal transcribed spacers (ITS1, 5.8S, ITS2), and translation extension factor 1- α gene region (*tef1- α*). The LSU gene was amplified using LR0R and LR5 primers [26] and nuclear ITS was amplified using ITS4 and ITS5 primers [27]. The *tef1- α* gene was amplified using EF1-983F and EF1-2218R primers [28]. The final volume of PCR was prepared as described in Tennakoon et al. [29], including 1 μ L of DNA template, 1 μ L of each forward and reverse primers, 12.5 μ L of 2 \times SanTaq PCR Master Mix (with Blue Dye), and 9.5 μ L of double-distilled water. The PCR thermal cycle program for LSU, ITS, and *tef1- α* gene amplifications was provided as mentioned in Tennakoon et al. [9]. Agarose gel electrophoresis (1%) was used to check the quality of PCR products. The PCR products were purified and subjected for sequencing at Sangon Biotech (Shanghai) Co., Ltd., China. All generated new sequences were deposited in the GenBank and accession numbers were listed (Table 1).

Table 1. GenBank and culture collection accession numbers of species included in the phylogenetic study. The newly generated sequences are shown in bold.

Fungal Species	Strain/Voucher No.	GenBank Accession Number		
		ITS	LSU	<i>tef1-α</i>
<i>Aquadictyospora lignicola</i>	MFLUCC 17-1318 T	MF948621	MF948629	MF953164
<i>Aquaticheirospora lignicola</i>	HKUCC 10304 T	AY864770	AY736378	–
<i>Cheiosporium triseriale</i>	HMAS 180703 T	EU413953	EU413954	–
<i>Dendryphiella eucalyptorum</i>	CBS 137987 T	KJ869139	KJ869196	–
<i>D. fasciculata</i>	MFLUCC 17-1074 T	MF399213	MF399214	–
<i>D. paravinos</i>	CBS 141286 T	KX228257	KX228309	–
<i>Dictyocheirospora acaciae</i>	SDBR-CMU454 T	OP965332	OP965372	OQ000838
<i>Di. acaciae</i>	SDBR-CMU455	OP965333	OP965373	OQ000839
<i>Di. acaciae</i>	SDBR-CMU456C	OP965334	OP965374	OQ000840
<i>Di. aquadulcis</i>	MFLUCC 17-2571 T	MK634545	MK634542	–
<i>Di. aquadulcis</i>	MFLUCC 22-0095	OP526634	OP526644	OP542236
<i>Di. aquatica</i>	KUMCC 15-0305 T	KY320508	KY320513	–
<i>Di. bannica</i>	KH 332 T	LC014543	AB807513	AB808489
<i>Di. bannica</i>	MFLUCC 16-0874	MH381765	MH381774	–
<i>Di. cheirospora</i>	KUMCC 17-0035 T	MF177035	–	–
<i>Di. chiangmaiensis</i>	MFLUCC 22-0097 T	OP526630	OP526640	OP542232
<i>Di. clematidis</i>	MFLUCC 17-2089 T	MT310593	MT214546	MT394728
<i>Di. garethjonesii</i>	MFLUCC 16-0909 T	KY320509	KY320514	–
<i>Di. garethjonesii</i>	DLUCC 0848	MF948623	MF948631	MF953166
<i>Di. garethjonesii</i>	MFLUCC 20-0028	MW063152	MW063213	–
<i>Di. garethjonesii</i>	SDBR-CMU457	OP965335	OP965375	–
<i>Di. giganticum</i>	BCC 11346	DQ018095	–	–
<i>Di. heptaspora</i>	CBS 396.59	DQ018090	–	–
<i>Di. heptaspora</i>	DLUCC 1992	MT756244	MT756243	MT776563
<i>Di. heptaspora</i>	MFLUCC 22-0096	OP526635	OP526645	OP542237
<i>Di. indica</i>	MFLUCC 15-0056	MH381763	MH381772	MH388817
<i>Di. lithocarpi</i>	MFLUCC 17-2537 T	MK347781	MK347999	–
<i>Di. metroxylonis</i>	MFLUCC 15-0282a T	MH742321	MH742313	–
<i>Di. metroxylonis</i>	MFLUCC 15-0282b	MH742322	MH742314	MH764303
<i>Di. metroxylonis</i>	MFLUCC 15-0282c	MH742323	MH742315	MH764302
<i>Di. metroxylonis</i>	MFLUCC 15-0282d	MH742324	MH742316	MH764301
<i>Di. multiappendiculata</i>	KUNCC 22-10734 T	OP526632	OP526642	OP542234
<i>Di. multiappendiculata</i>	KUNCC 22-10736	OP526633	OP526643	OP542235
<i>Di. nabanheensis</i>	KUMCC 16-0152 T	MH388340	MH376712	MH388375
<i>Di. pandanicola</i>	MFLUCC 16-0365 T	MH388341	MH376713	MH388376
<i>Di. pseudomusae</i>	yone 234 T	LC014550	AB807520	AB808496

Table 1. Cont.

Fungal Species	Strain/Voucher No.	GenBank Accession Number		
		ITS	LSU	tef1- α
<i>Di. rotunda</i>	MFLUCC 14-0293 T	KU179099	KU179100	—
<i>Di. rotunda</i>	MFLUCC 17-0222	MH381764	MH381773	MH388818
<i>Di. rotunda</i>	MFLUCC 17-1313	MF948625	MF948633	MF953168
<i>Di. suae</i>	KUNCC 22-12424 T	OP526631	OP526641	OP542233
<i>Di. subramanianii</i>	BCC 3503	DQ018094	—	—
<i>Di. taiwanense</i>	MFLUCC 17-2654 T	MK495821	MK495820	—
<i>Di. taiwanense</i>	SDBR-CMU458	OP965336	OP965376	—
<i>Di. thailandica</i>	MFLUCC 18-0987 T	MT627734	MN913743	—
<i>Di. vinaya</i>	MFLUCC 14-0294 T	KU179102	KU179103	—
<i>Di. xishuangbannaensis</i>	KUMCC 17-0181 T	MH388342	MH376714	MH388377
<i>Dictyosporium</i> sp.	MFLUCC 15-0629	MH381766	MH381775	MH388819
<i>Dic. alatum</i>	ATCC 34953 T	NR_077171	DQ018101	—
<i>Dic. aquaticum</i>	MF 1318 T	KM610236	—	—
<i>Dic. bulbosum</i>	yone 221	LC014544	AB807511	AB808487
<i>Dic. digitatum</i>	KH 401	LC014545	AB807515	AB808491
<i>Dic. digitatum</i>	yone 280	LC014547	AB807512	AB808488
<i>Dic. digitatum</i>	KUMCC 17-0269 T	MH388344	MH376716	MH388378
<i>Dic. digitatum</i>	SDBR-CMU459	OP965337	OP965377	OQ000841
<i>Di. elegans</i>	NBRC 32502 T	DQ018087	DQ018100	—
<i>Di. hughesii</i>	KT 1847	LC014548	AB807517	AB808493
<i>Dic. meiosporum</i>	MFLUCC 10-0131 T	KP710944	KP710945	—
<i>Dic. nigroapice</i>	BCC 3555	DQ018085	—	—
<i>Dic. nigroapice</i>	MFLUCC 17-2053	MH381768	MH381777	MH388821
<i>Dic. olivaceosporum</i>	KH 375 T	LC014542	AB807514	AB808490
<i>Dic. sexualis</i>	MFLUCC 10-0127 T	KU179105	KU179106	—
<i>Dic. stellatum</i>	CCFC 241241 T	NR_154608	JF951177	—
<i>Dic. strelitziae</i>	CBS 123359 T	NR_156216	FJ839653	—
<i>Dic. tetrasporum</i>	KT 2865	LC014551	AB807519	AB808495
<i>Dic. thailandicum</i>	MFLUCC 13-0773 T	KP716706	KP716707	—
<i>Dic. tratense</i>	MFLUCC 17-2052 T	MH381767	MH381776	MH388820
<i>Dic. tubulatum</i>	MFLUCC 15-0631 T	MH381769	MH381778	MH388822
<i>Dic. tubulatum</i>	MFLUCC 17-2056	MH381770	MH381779	—
<i>Dic. wuyiense</i>	CGMCC 3.18703 T	KY072977	—	—
<i>Dic. zhejiangense</i>	MW-2009a T	FJ456893	—	—
<i>Digitodesmium aquaticum</i>	MFLU 22-0203 T	OP749872	OP749877	—
<i>Dig. bambusicola</i>	CBS 110279 T	DQ018091	DQ018103	—
<i>Dig. chiangmaiense</i>	KUN HKAS 102163 T	—	MK571766	—
<i>Dig. polybrachiatum</i>	COAD 3174 T	MW879318	MW879316	—
<i>Dig. polybrachiatum</i>	COAD 3175	MW879319	MW879317	—
<i>Gregaritheciun curvisporum</i>	KT 922	AB809644	AB807547	—
<i>Immotthia bambusae</i>	KUN-HKAS 112012AI T	MW489455	MW489450	MW504646
<i>I. bambusae</i>	KUN-HKAS 112012AII	MW489456	MW489451	MW504647
<i>I. bambusae</i>	KUN-HKAS 112012B	MW489457	MW489452	—
<i>Jalapriya inflata</i>	NTOU 3855	JQ267362	JQ267363	—
<i>J. pulchra</i>	MFLUCC 15-0348 T	KU179108	KU179109	—
<i>J. pulchra</i>	MFLUCC 17-1683	MF948628	MF948636	MF953171
<i>J. toruloides</i>	CBS 209.65	DQ018093	DQ018104	—
<i>Neodendryphiella michoacanensis</i>	FMR 16098 T	LT906660	LT906658	—
<i>N. tarraconensis</i>	GZCC20-0002	MN999922	MN999927	—
<i>Neodigitodesmium cheirosporum</i>	HKAS 124014 T	ON595714	ON595713	—
<i>Periconia igniaria</i>	CBS 379.86	LC014585	AB807566	AB808542
<i>P. igniaria</i>	CBS 845.96	LC014586	AB807567	AB808543
<i>Pseudocoleophoma bauhiniae</i>	MFLUCC 17-2280	—	—	MK360075
<i>Ps. bauhiniae</i>	MFLUCC 17-2586 T	—	—	MK360076

Table 1. Cont.

Fungal Species	Strain/Voucher No.	GenBank Accession Number		
		ITS	LSU	tef1- α
<i>Ps. calamagrostidis</i>	KT 3284 T	LC014592	LC014609	LC014614
<i>Ps. flavescent</i>	CBS 178.93	—	GU238075	—
<i>Ps. polygonicola</i>	KT 731 T	AB809634	AB807546	AB808522
<i>Ps. typhicola</i>	MFLUCC 16-0123	KX576655	KX576656	—
<i>Ps. zingiberacearum</i>	NCYUCC 19-0052 T	MN615939	MN616753	MN629281
<i>Ps. zingiberacearum</i>	NCYUCC 19-0053	MN615940	MN616754	MN629282
<i>Ps. zingiberacearum</i>	NCYUCC 19-0054	MN615941	MN616755	MN629283
<i>Ps. zingiberacearum</i>	SDBR-CMU460	OP965338	OP965378	OQ000841
<i>Pseudoconiothyrium broussonetiae</i>	CBS 145036 T	MK442618	MK442554	MK442709
<i>Pseudocyclothyriella clematidis</i>	MFLU 16-0280	MT310596	MT214549	—
<i>Pse. clematidis</i>	MFLUCC 17-2177A T	MT310595	MT214548	MT394730
<i>Pseudodictyosporium elegans</i>	CBS 688.93 T	DQ018099	DQ018106	—
<i>Pseu. thailandica</i>	MFLUCC 16-0029 T	KX259520	KX259522	KX259526
<i>Pseu. wauense</i>	NBRC 30078 T	DQ018098	DQ018105	—
<i>Pseu. wauense</i>	DLUCC 0801	MF948622	MF948630	MF953165
<i>Verrucoccum coppinsii</i>	E 00814291 T	MT918785	MT918770	—
<i>V. spribillei</i>	SPO 1154	MT918781	MT918764	—
<i>Vikalpa australiensis</i>	HKUCC 8797 T	DQ018092	—	—
<i>Vi. grandispora</i>	KUNCC 22-12425 T	OP526638	OP526648	OP542240
<i>Vi. sphaerica</i>	CGMCC3.20682 T	OP526639	OP526649	OP542241

Note: All the type strains are indicated with "T".

2.3. Phylogenetic Analyses

The data of LSU, ITS, and *tef1- α* sequences were used for a BLAST search in the GenBank to identify the strains which have high similarities. Based on BLAST similarities and associated recent articles [9,12,21], closely relevant sequences were downloaded from the GenBank. The phylogenetic analyses included a total of 110 isolates. Isolates of *Periconia igniaria* (CBS 379.86 and CBS 845.96) were selected as the out-group taxa. SeqMan v. 7.0.0 was used to combine consensus sequences (DNASTAR, Madison, WI, USA). The multi-gene datasets were automatically performed by online MAFFT version 7 (<https://mafft.cbrc.jp/alignment/server/index.html/> accessed on 12 December 2022) [30]. In addition, BioEdit v.7.2.5 [31] was used for manual improvements of the alignment. Trimal v1.2 [32] was used to remove ambiguously aligned regions.

The online source CIPRES Science Gateway v. 3.3 [33] was used to conduct the maximum likelihood (ML) analysis, with the RAxML-HPC v.8 on XSEDE (8.2.12) tool [34,35]. The following default settings were selected: the GAMMA nucleotide substitution model and 1000 rapid bootstrap replicates. PAUP (Phylogenetic Analysis Using Parsimony) version 4.0b10 was used to perform the maximum parsimony analysis (MP) [36]. The statistics for the MP descriptive trees were calculated such as the Tree Length (TL), Consistency Index (CI), Retention Index (RI), Relative Consistency Index (RC), and Homoplasy Index (HI).

Bayesian inference phylogenies were inferred using MrBayes 3.2.1 [37]. Analysis was run with four chains of 3,000,000 generations, and trees were sampled every 100th generation. The initial 20% of the sampled data were discarded as burn-in. Using MrModeltest v. 3.7 [38] and the Akaike Information Criterion (AIC), evolutionary models for phylogenetic studies were determined individually for each locus. Each locus in MrModeltest provided the GTR+I+G model as the best-fit model for Bayesian analysis. The FigTree v1.4.0 tool [39] was used to show phylogenograms and was modified using Microsoft PowerPoint (2010) and Adobe Illustrator® CS5 (Version 15.0.0, Adobe®, San Jose, CA, USA). All the newly obtained sequences were deposited in the GenBank and the alignments in TreeBASE, submission ID:29917 (<http://www.treebase.org/> (accessed on 15 December 2022)).

3. Results

3.1. Phylogenetic Analyses

The combined data set of LSU, ITS, and *tef1-α* sequences comprised 2582 characters including gaps. All the characters have equal weight and there were 1596 constant characters, 773 parsimony-informative characters, and 213 parsimony-uninformative characters. The descriptive tree statistics were TL = 3420, CI = 0.416, RI = 0.770, RC = 0.321, and HI = 0.584. All the gaps are treated as missing data. The RAxML analysis of the combined dataset yielded a best-scoring tree (Figure 1). The final ML optimization likelihood value was -20228.278033. There were 35.83% undetermined characters or gaps and 1201 distinct alignment patterns. The estimated base frequencies were A = 0.235995, C = 0.255959, G = 0.268880, and T = 0.239166; the substitution rates were AC = 1.442221, AG = 3.055486, AT = 2.089879, CG = 0.773046, CT = 7.317661, and GT = 1.000; the proportion of invariable sites I = 0.419763; and the gamma distribution shape parameter was α = 0.587026. The Bayesian analysis resulted in 30,000 trees after 3,000,000 generations.

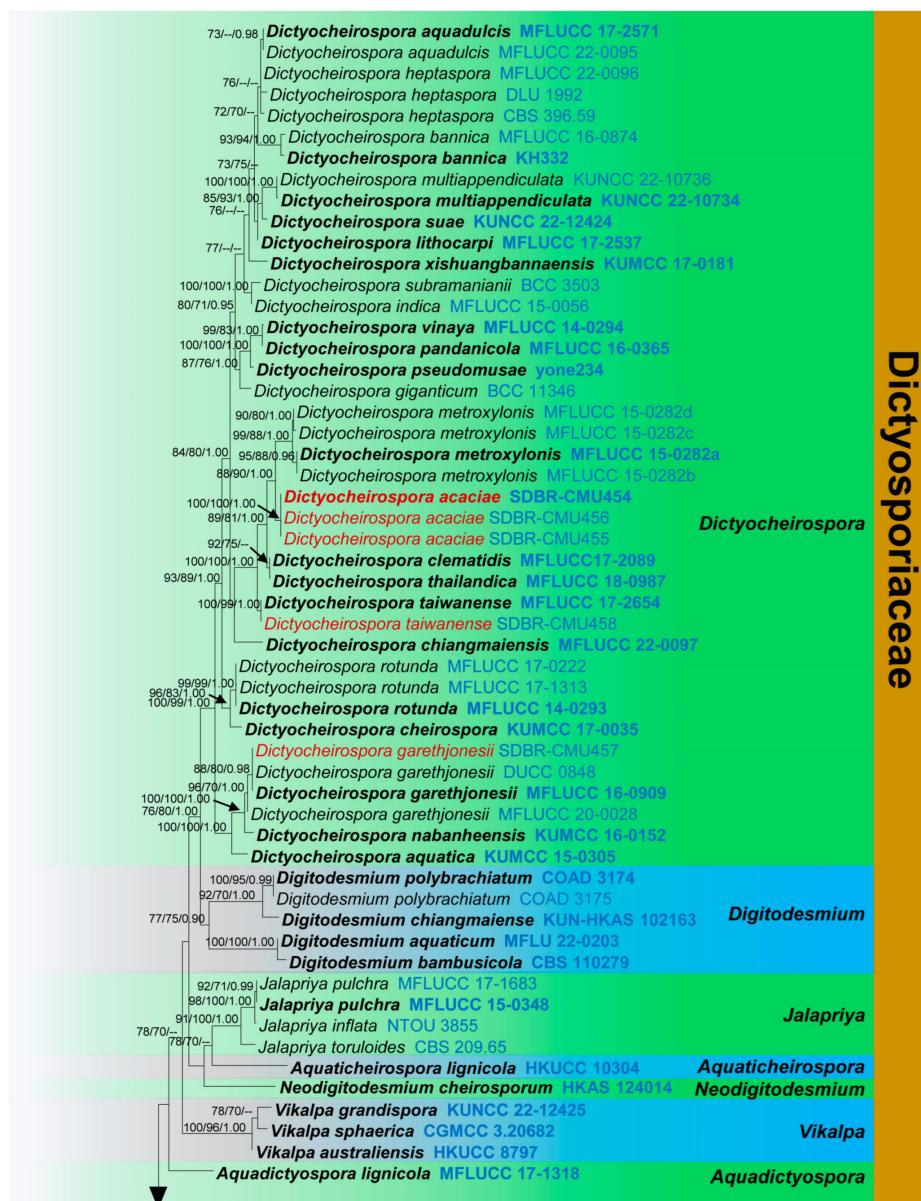


Figure 1. Cont.

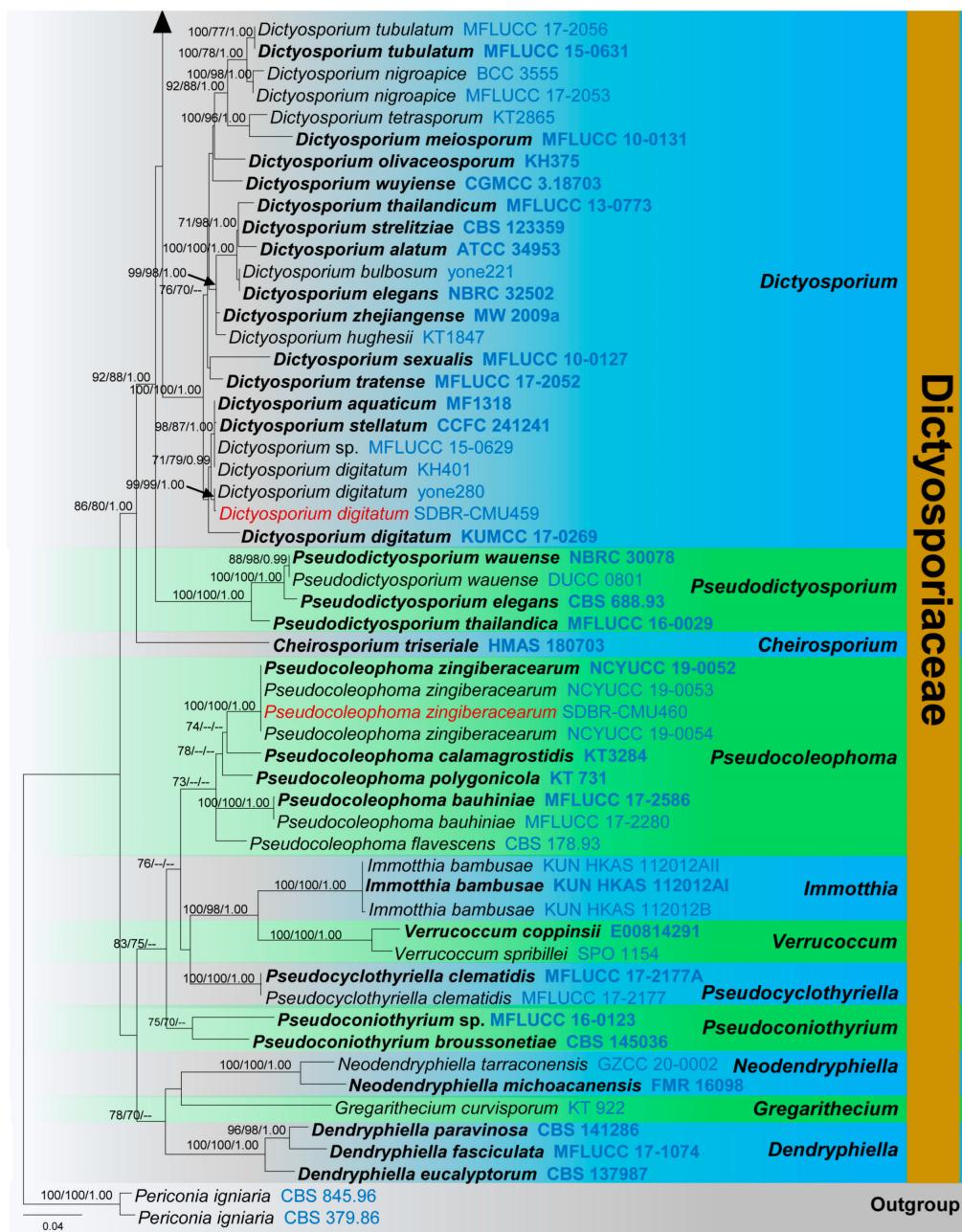


Figure 1. The phylogram generated from maximum likelihood analysis is based on combined LSU, ITS, and *tef1- α* sequence data. The tree is rooted with *Periconia igniaria* (CBS 379.86 and CBS 845.96). The new isolates are in red, and ex-type strains are bold. All the strain numbers are in blue. Bootstrap support values $\geq 70\%$ from the maximum likelihood (ML) and maximum parsimony (MP) and Bayesian posterior probabilities (BYPP) values ≥ 0.90 are given above the nodes, respectively.

Multigene phylogeny showed strong statistically supportive values within the clades (Figure 1). Bootstrap support values for ML, MP higher than 70%, and BYPP greater than 0.90 are given above each branch, respectively (Figure 1). All the analyses (ML, MP, and BYPP) generated similar findings and concurred with previous studies based on multi-gene analyses [9,12,21,40]. Our isolates, namely SDBR-CMU454, SDBR-CMU455, and SDBR-CMU456, cluster within *Dictyochirospora* and provide an independent lineage sister to *Di. metroxili* with solid support (88% ML, 90% MP, and 1.00 BYPP). As well as grouping together in 100% ML, 100% MP, and 1.00 BYPP statistical support (Figure 1), the isolates SDBR-CMU458 and SDBR-CMU457 also group within the *Dictyochirospora* and provide

close phylogeny relationships with the type strains of *Di. taiwanense* (MFLUCC 17-2564) and *Di. garethjonesii* (MFLUCC 16-0909), respectively. In addition, isolate SDBR-CMU459 groups with *Dictyosporium* species and shows a close phylogeny relationship with *Dic. digitatum* (yone 280) with 99% ML, 99% MP, and 1.00 BYPP support. The isolate SDBR-CMU460 clusters within *Pseudocoleophoma zingiberacearum* isolates (NCYUCC 19-0052, NCYUCC 19-0053, and NCYUCC 19-0054) in a statistically well-supported clade (100% ML, 100% MP, and 1.00 BYPP).

3.2. Taxonomy

3.2.1. *Dictyocheirospora* M.J. D’souza, Boonmee, and K.D. Hyde, Fungal Divers. 80: 465 (2016)

Dictyocheirospora is a speciose genus introduced by Boonmee et al. [11] with *Di. rotunda* as the type. This has unique morphological characteristics, such as dark sporodochial colonies and aero-aquatic cheiroid dictyospores [11]. The species are distributed worldwide as saprobes on decaying stems, leaves, and branches [11,12,40,41]. To date, there are 26 species listed in the Index Fungorum [25]. Here, we present *Di. acaciae* as a novel species and *Di. garethjonesii* and *Di. taiwanense* as two new host records on *Bismarkia nobilis* and *Ficus benjamina*.

Dictyocheirospora acaciae Tennakoon and S. Lumyong, sp. nov.

Index Fungorum number: IF900168; Facesoffungi number: FoF13616; Figure 2

Etymology: Named after the host genus where this fungus was collected.

Holotype: CMUB 39980

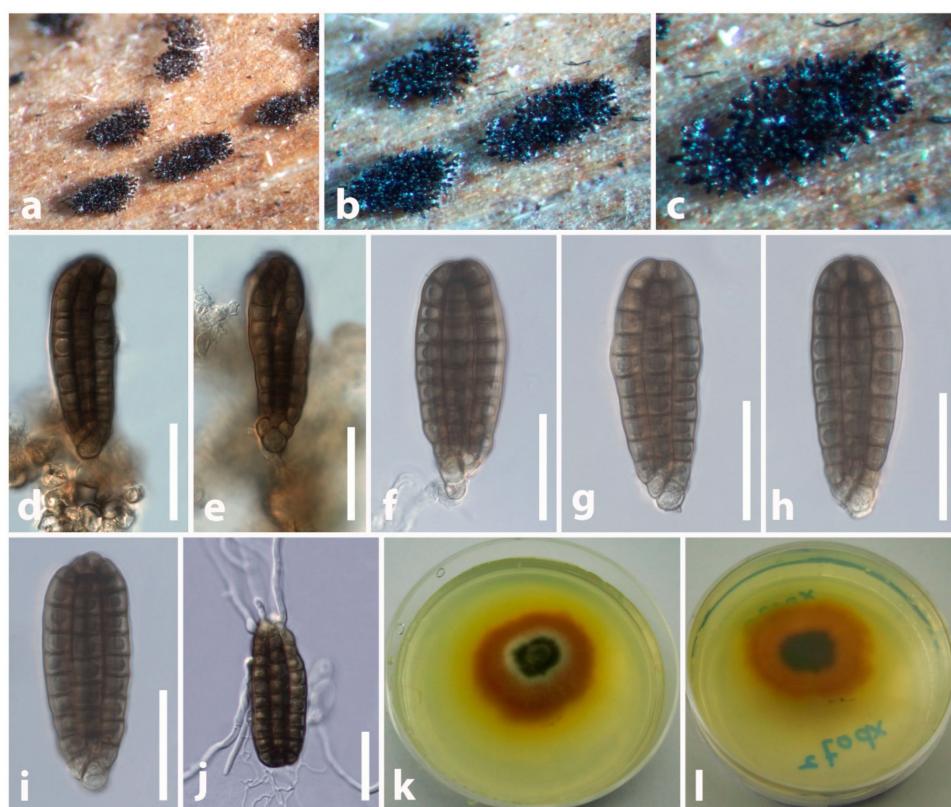


Figure 2. *Dictyocheirospora acaciae* (CMUB 39980, holotype). (a,b) Sporodochia on dead stem of *Acacia dealbata*. (c) Close-up of sporodochium. (d,e) Conidiogenous cells with developing conidia. (f-i) Conidia. (j) A germinating conidium. (k) Colonies from above (on PDA/4 weeks). (l) Colonies from below (on PDA/4 weeks). Scale bars: (d–j) = 25 μ m.

Saprobic on the decaying stem of *Acacia dealbata* Link (Fabaceae). **Sexual morph:** Undetermined. **Asexual morph:** Hyphomycetous. Colonies 170–300 μ m in diameter (\bar{x} = 250 μ m,

$n = 20$), on natural substrate forming sporodochial conidiomata, punctiform, velvety, superficial, scattered, and dark brown to black. *Conidiophores* micronematous, pale brown, smooth, and thin-walled. *Conidiogenous cells* $4\text{--}8 \times 3\text{--}6 \mu\text{m}$ holoblastic, hyaline or pale brown, cylindrical, and smooth-walled. *Conidia* $42\text{--}60 \times 15\text{--}18 \mu\text{m}$ ($\bar{x} = 52 \times 17 \mu\text{m}$, $n = 30$), solitary, cheiroid, light brown to dark brown, consisting of 5–6 vertical rows of cells, with a basal connecting cell, separated when mounted in water, with each row composed of 9–11 cells, constricted at septa, with a large guttule in each cell, without appendages.

Culture characteristics: *Colonies* on PDA reaching 8–10 mm in diameter after 4 weeks at 25°C . Colonies viewed from above were medium dense, circular, flat, surface smooth, entire margin, yellowish at the outer margin, light brown and whitish at the middle, and dark brown to black at the center. Colonies observed in the reverse view were yellowish at the margin, light brown at the middle, and dark brown to black at the center. *Mycelium* white to cream.

Materials examined: Thailand, Chiang Mai ($18^\circ 47' 12'' \text{ N } 98^\circ 57' 26'' \text{ E}$), on decaying stem of *Acacia dealbata* (Fabaceae), 24 January 2017, D.S. Tennakoon, DXP072A, (CMUB 39980, holotype), ex-type living culture (SDBR-CMU454), ibid., 27 March 2017, DXP072B (SDBR-CMU455), DXP072C (SDBR-CMU456).

Notes: The morphology of our collection (CMUB 39980) tally well with those species described under *Dictyocheirospora* by having punctiform, velvety, superficial, dark brown to black sporodochial conidiomata and cheiroid, and light brown to dark brown conidia [11,12,41,42]. The multi-gene phylogeny generated herein indicates that *Dictyocheirospora* is sister to *Digitodesmium* (Figure 1). In particular, our collection constitutes an independent lineage sister to *Di. metroxyli* with statistical solid support (88% ML, 90% MP, 1.00 BYPP). Our collection can be distinguished from *Di. metroxyli* by having larger sporodochial conidiomata (170–300 vs. 100–200 μm in diameter) and cheiroid, light brown to dark brown smaller conidia ($52 \times 17 \mu\text{m}$ vs. $61 \times 20 \mu\text{m}$) [42]. In addition, we compared the ITS (+5.8S) and *tef1- α* base pair differences between *D. metroxyli* (MFLUCC 15-0282b) and our collection (CMUB 39980). A comparison of the 565 nucleotides of ITS (+5.8S) and 786 nucleotides of *tef1- α* gene regions shows 12 (2.1%) and 25 (3.1%) differences between them, respectively. Hence, we introduce *Di. acaciae* from *Acacia dealbata* in Thailand. A synopsis of the morphological distinctiveness of species of *Dictyocheirospora* is provided (Table 2).

Table 2. A synopsis of all the known species of *Dictyocheirospora*.

Dictyocheirospora Species	Conidiomata Size (μm diam)	Conidia			Reference
		Size (μm)	No. of Rows	No. of Cells/Row	
<i>D. acaciae</i>	170–300	$42\text{--}60 \times 15\text{--}18$	5–6	9–11	This study
<i>D. aquatica</i>	150–250	$34\text{--}42 \times 12.5\text{--}19.5$	5–6	6–8	[41]
<i>D. bannica</i>	100–260	$73\text{--}86 \times 21\text{--}26$	(5–)7	17–19	[11]
<i>D. cheirospora</i>	–	$54\text{--}63 \times 15\text{--}26$	5–7	8–12	[43]
<i>D. chiangmaiensis</i>	–	$42\text{--}46 \times 16\text{--}18$	4–6	9–10	[40]
<i>D. clematidis</i>	200–340	$42\text{--}60 \times 15\text{--}30$	6–7	10–12	[44]
<i>D. garethjonesii</i>	200–300	$45.5\text{--}54.5 \times 15.5\text{--}24.5$	6–7	7–10	[41]
<i>D. gigantica</i>	–	$105\text{--}121 \times 25\text{--}32$	7	19–22	[45]
<i>D. heptaspora</i>	–	$50\text{--}80 \times 20\text{--}30$	7	–	[45]
<i>D. hydei</i>	120–240	$30\text{--}33 \times 14\text{--}17$	7	5–6	[46]
<i>D. indica</i>	130–415	$36\text{--}46 \times 13\text{--}18$	6–7	8–10	[46]
<i>D. lithocarpi</i>	225–248	$35\text{--}40 \times 12\text{--}18$	6	10–16	[47]

Table 2. Cont.

Dictyocheirospora Species	Conidiomata Size (μm diam)	Conidia			Reference
		Size (μm)	No. of Rows	No. of Cells/Row	
<i>D. rotunda</i>	300–350	42–58 × 19–38	5–7	8–12	[11]
<i>D. suae</i>	—	72–79 × 20–25	5–7	12–15	[40]
<i>D. metroxyli</i>	100–200	45–69 × 15–29	4–6	9–14	[42]
<i>D. multiappendiculata</i>	—	55–62 × 19–22	(5–)7	9–13	[40]
<i>D. pandanicola</i>	—	60–75 × 18.5–35.5	5–7	13–18	[48]
<i>D. pseudomusae</i>	170–490	61–78 × 19–29	(6–)7	13–15	[49]
<i>D. taiwanense</i>	110–230	74–84 × 16–20	5	10–13	[50]
<i>D. thailandica</i>	—	42–65 × 20–45	6–7	9–12	[51]
<i>D. nabanheensis</i>	—	35–40 × 18–21	6	6–10	[48]
<i>D. subramanianii</i>	—	33–42 × 16–20	7	9–13	[52]
<i>D. vinaya</i>	200	58–67 × 15.5–26.5	6–7	9–13	[11]
<i>D. xishuangbannaensis</i>	—	35–50 × 17–25	6	6–12	[48]

Dictyocheirospora garethjonesii Z.L. Luo, Hong Y. Su, and K.D. Hyde, Mycosphere 7: 1361 (2017)

Index Fungorum number: IF552684; Facesoffungi number: FoF 02734; Figure 3.

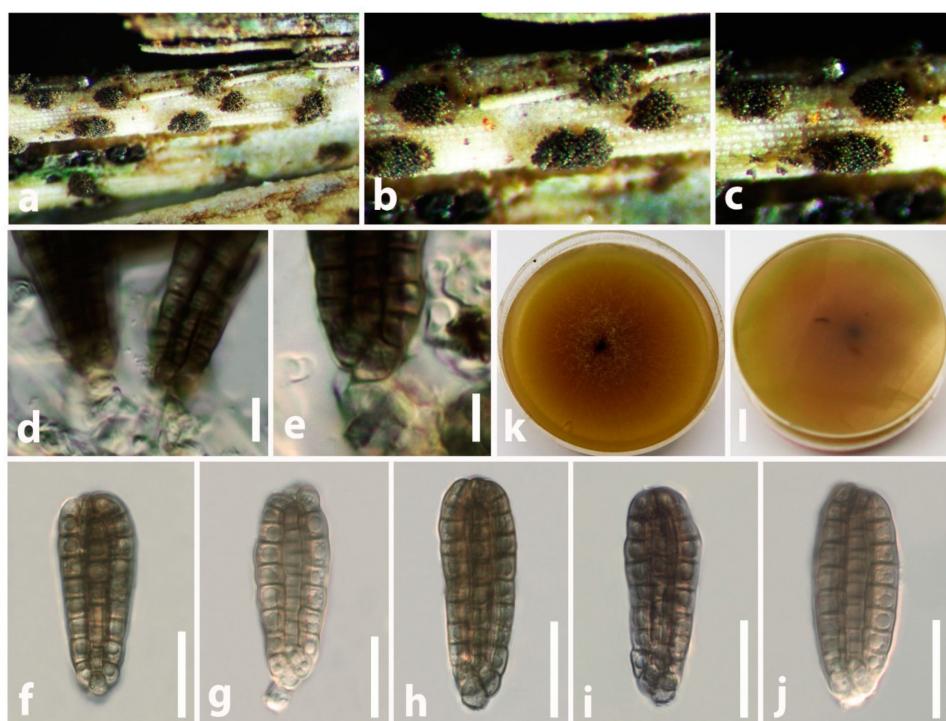


Figure 3. *Dictyocheirospora garethjonesii* (CMUB 39982, new host record). (a) Sporodochia on dead stem of *Bismarkia nobilis*. (b,c) Close-up of Sporodochia. (d,e) Conidiogenous cells with developing conidia. (f–j) Conidia. (k) Colonies from above (on PDA/4 weeks). (l) Colonies from below (on PDA/4 weeks). Scale bars: (d,e) = 4 μm and (f–j) = 20 μm .

Saprobic on the decaying stem of *Bismarkia nobilis* Hildebr. and H.Wendl. (Arecaceae). Sexual morph: Undetermined. Asexual morph: Hyphomycetous. Colonies 130–270 μm in diameter ($\bar{x} = 210 \mu\text{m}$, $n = 20$), on natural substrate forming sporodochial conidiomata,

punctiform, velvety, superficial, scattered, and dark brown to black. *Conidiophores* micronematous, undifferentiated from vegetative hyphae, pale brown, smooth, and thin-walled. *Conidiogenous cells* $4\text{--}6 \times 3\text{--}5 \mu\text{m}$ holoblastic, hyaline or pale brown, cylindrical, and smooth-walled. *Conidia* $35\text{--}70 \times 10\text{--}20 \mu\text{m}$ ($\bar{x} = 48 \times 18 \mu\text{m}$, $n = 30$), solitary, cheiroid, light brown to dark brown, consisting of 5–7 vertical rows of cells, with a basal connecting cell, slightly inwardly curved at the apex, separated when mounted in water, each row composed of 7–10 cells, constricted at septa, with a large guttule in each cell, without appendages.

Culture characteristics: *Colonies* on PDA reaching 9–10 mm in diameter after 4 weeks at 25°C . Colonies viewed from above were medium dense, circular, flat, surface smooth, entire margin, yellowish at the margin, and light brown at the center. Colonies observed in the reverse view were yellowish at the margin and light brown at the center. *Mycelium* white to cream.

Known hosts: *Bismarkia nobilis* (Arecaceae) and *Macaranga tanarius* (Euphorbiaceae) [9,41,53].

Known distribution: China and Thailand [9,41,53].

Material examined: Thailand, Chiang Mai ($18^\circ 47' 34''$ N $98^\circ 57' 41''$ E), on decaying stem of *Bismarkia nobilis* (Arecaceae), 24 January 2017, D.S. Tennakoon, DXP01 (CMUB 39982), living culture (SDBR-CMU457).

Notes: Wang et al. [41] introduced *Dictyocheirospora garethjonesii* from China. The morphological characteristics of our collection (CMUB 39982) are similar to the type specimen (MFLUCC 16-0909) by having dark brown to black, superficial, sporodochial conidiomata, holoblastic, and cylindrical conidiogenous cells, and light brown to dark brown, ellipsoid to cylindrical, and cheiroid conidia with 5–7 rows of cells, each composed of 7–10 cells [9,41]. Phylogeny also shows that our collection (CMUB 39982) group with *Di. garethjonesii* isolates (DUCC 0848 and MFLUCC 16-0909) in a solidly supported clade (88% ML, 80% MP, and 0.98 BYPP). Thus, our collection is identified as a new host record of *Di. garethjonesii* from *Bismarkia nobilis* (Arecaceae) in Thailand.

Dictyocheirospora taiwanense Tennakoon, C.H. Kuo, and K.D. Hyde, Fungal Divers. 96: 27 (2019)

Index Fungorum number: IF556309; Facesoffungi number: FoF 05964; Figure 4

Saprobic on the decaying stem of *Ficus benjamina* L. (Moraceae). **Sexual morph:** Undetermined. **Asexual morph:** Hyphomycetous. *Colonies* 100–150 μm in diameter ($\bar{x} = 130 \mu\text{m}$, $n = 20$), on natural substrate forming sporodochial conidiomata, punctiform, velvety, superficial, scattered, and dark brown to black. *Conidiophores* micronematous, pale brown, smooth, and thin-walled. *Conidiogenous cells* $4\text{--}7 \times 3\text{--}5 \mu\text{m}$ holoblastic, hyaline or pale brown, cylindrical, and smooth-walled. *Conidia* $70\text{--}80 \times 15\text{--}20 \mu\text{m}$ ($\bar{x} = 76 \times 18 \mu\text{m}$, $n = 30$), solitary, cheiroid, light brown to dark brown, consisting of 5–6 vertical rows of cells, with a basal connecting cell, separated when mounted in water, each row composed of 10–13 cells, constricted at septa, with a large guttule in each cell, without appendages.

Culture characteristics: *Colonies* on PDA reaching 8–9 mm in diameter after 4 weeks at 25°C . Colonies viewed from above were medium dense, circular, flat, with a surface smooth, entire margin, yellowish at the margin, and light brown at the center. Colonies observed in the reverse view were yellowish at the margin, and light brown to dark brown at the center. *Mycelium* white to cream.

Known hosts: *Ficus benjamina* (Moraceae) and *Macaranga tanarius* (Euphorbiaceae) [9,53].

Known distribution: Taiwan and Thailand [9,53].

Material examined: Thailand, Chiang Mai ($18^\circ 47' 26''$ N $98^\circ 57' 56''$ E), on the decaying stem of *Ficus benjamina* (Moraceae), 24 January 2017, D.S. Tennakoon, DXP02, (CMUB 39981), living culture (SDBR-CMU458).

Notes: The morphological characteristics of our collection (CMUB 39981) are similar to the type of *Dictyocheirospora taiwanense* (MFLUCC 17-2654) by having overlapping size ranges of conidiomata (110–230 μm vs. 100–150 μm in diameter) and conidia (74–84 \times 16–20 μm vs. 70–80 \times 15–20 μm). The conidial characteristics (e.g., cheiroid, light brown to dark brown, 5–6 rows of cells, and each composed of 10–13 cells) are also similar in both species [50]. According to multi-gene phylogeny, our collection (CMUB 39981)

clusters with the type of *Di. taiwanense* by statistical solid support (100% ML, 99% MP, 1.00 BYPP).

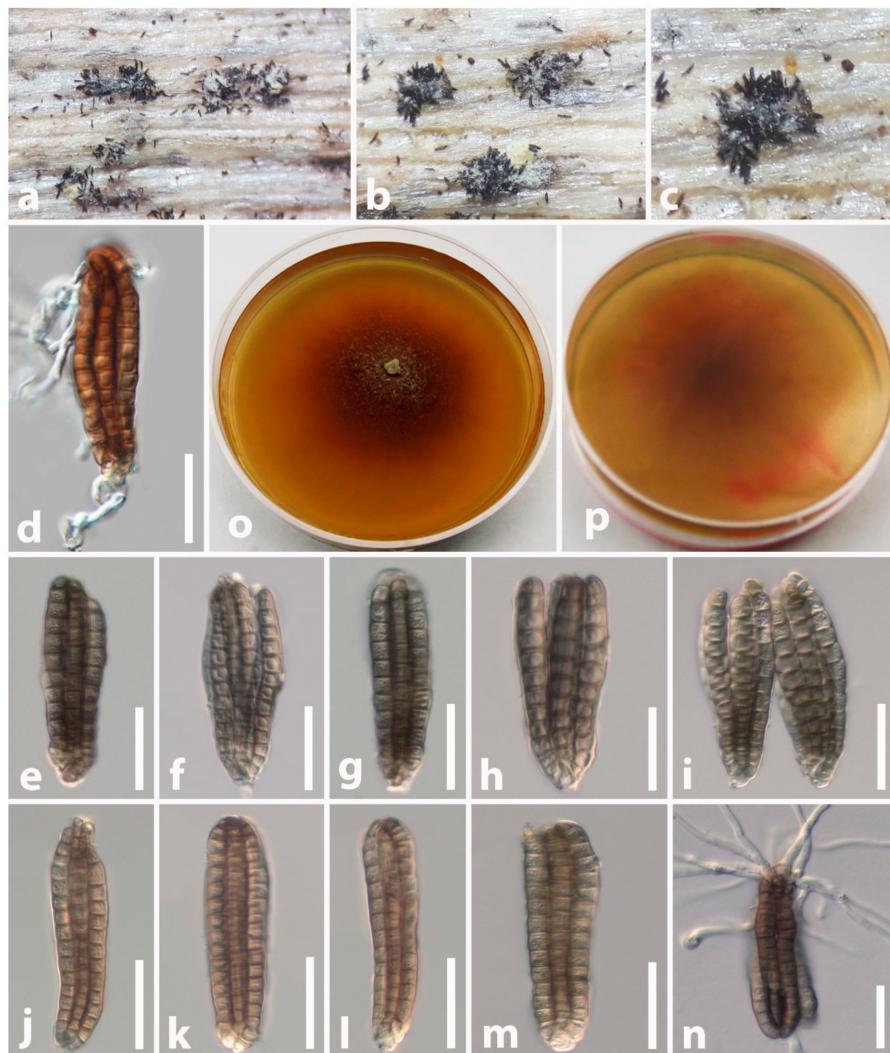


Figure 4. *Dictyochirospora taiwanense* (CMUB 39981, new host record). (a,b) Sporodochia on dead stem of *Ficus benjamina*. (c) Close-up of Sporodochium. (d) Conidiogenous cell with a conidium. (e–m) Conidia. (n) A germinating conidium. (o) Colonies from above (on PDA/4 weeks). (p) Colonies from below (on PDA/4 weeks). Scale bars: (d–n) = 30 μ m.

3.2.2. *Dictyosporium* Corda, Weitenwe'er's Beitr. Nat. 1: 87 (1837)

Dictyosporium is considered the type genus of *Dictyosporiaceae* and *Dic. elegans* Corda is the type species [54]. *Dictyosporium* species are distributed worldwide as saprobes in terrestrial and aquatic habitats. The Index Fungorum [25] currently lists 63 species under *Dictyosporium*. This genus is quite attractive in terms of morphological traits (e.g., sporodochial colonies and cheiroid, digitate complanate conidia with several parallel rows of cells). Their sexual morph has dark brown, superficial ascomata, cylindrical ascii, and fusiform, hyaline, and uniseptate ascospores with or without a mucilaginous sheath [12].

Dictyosporium digitatum J.L. Chen, C.H. Hwang, and Tzean, Mycol. Res. 95: 1145 (1991)
Index Fungorum number: IF355284; Facesoffungi number: FoF 04487; Figure 5.

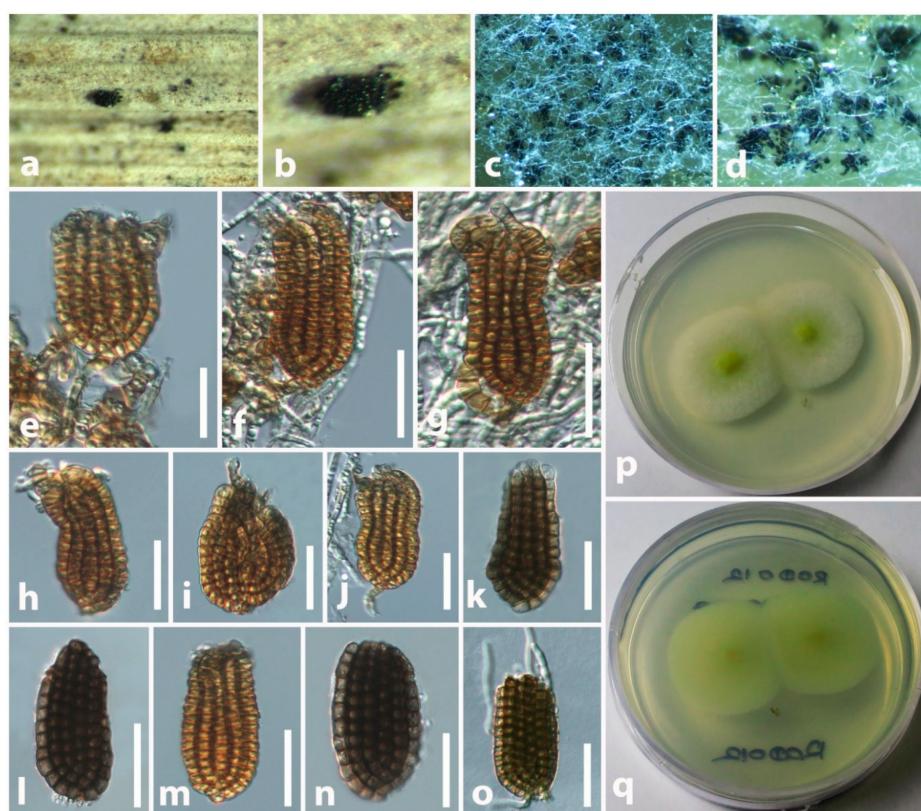


Figure 5. *Dictyosporium digitatum* (CMUB 39981, new host record). (a) Sporodochia on a dead leaf of *Cyperus aggregatus*. (b) Close-up of Sporodochium. (c,d) Sporodochia on the culture. (e–g) Conidiogenous cells with conidia. (h–n) Conidia. (o) A germinating conidium. (p) Colonies from above (on PDA/7 days). (q) Colonies from below (on PDA/7 days). Scale bars: (e–o) = 30 μ m.

Saprobic on the dead leaf of *Cyperus aggregatus* (Willd.) Endl. (Cyperaceae). **Sexual morph:** Undetermined. **Asexual morph:** Hyphomycetous. Colonies 150–200 μ m in diameter ($\bar{x} = 170 \mu\text{m}$, $n = 20$), on natural substrate forming sporodochial conidiomata, punctiform, velvety, superficial, scattered, and dark brown to black. Conidiophores micronematous, simple or branched, hyaline or pale brown, smooth, and thin-walled. Conidiogenous cells 4–6 \times 3–5 μ m holoblastic, hyaline or pale brown, cylindrical, and smooth-walled. Conidia 45–70 \times 26–35 μ m ($\bar{x} = 63 \times 32 \mu\text{m}$, $n = 30$), solitary, cheiroid, oval to ellipsoid, and greyish orange to reddish brown, consisting of 5–7 vertical rows of cells, with a basal connecting cell, separated when mounted in water, each row is composed of 7–13 cells, cells 3–6 μ m wide, with the terminal cell distinctly thin-walled, constricted at the septa, subhyaline at the tip of peripheral rows, with a large guttule in each cell, without appendages.

Culture characteristics: Colonies on PDA reached 5–7 mm in diameter after 7 days at 25 °C. Colonies viewed from above were medium dense, circular, raised, velvety, surface smooth, entire margin, white to cream at the margin and yellowish green at the center. Colonies observed in the reverse view were white to yellowish at the margin and yellowish at the center. Mycelium white to cream.

Known hosts: *Anisoptera oblonga* (Dipterocarpaceae), *Archontophoenix alexandrae* (Arecaceae), *Castanopsis sieboldii* (Fagaceae), *Cyperus aggregatus* (Cyperaceae), *Licuala longicalycata* (Arecaceae), *Machilus velutina* (Lauraceae), *Pandanus* spp. (Pandanaceae), *Phoenix hanceana* (Arecaceae), and *Pinus massoniana* (Pinaceae) [45,48,49,53,55–57].

Known distribution: Australia, Brunei, Japan, Mauritius, Philippines, Seychelles, Taiwan, and Thailand [45,48,49,53,55–57].

Material examined: Thailand, Chiang Mai (18°47'22" N 98°57'36" E), on the dead leaf of *Cyperus aggregatus* (Cyperaceae), 26 February 2017, D.S. Tennakoon, DROD012, (CMUB 39983), living culture (SDBR-CMU459).

Notes: Multi-gene phylogenetic analyses indicated that the new collection (MFLU 19-2809) groups with *Dictyosporium digitatum* (yone 280) with a solid support (99% ML, 99% MP, 1.00 BYPP). Morphology is also similar to the type (PPH 12) and the isolate (yone 280) by having punctiform, velvety, superficial, dark brown to black, sporodochial conidiomata, hyaline or pale brown, cylindrical, holoblastic conidiogenous cells (4–6 × 3–5 µm vs. 4.2–10 × 3.3–7.5 µm) and cheiroid, oval to ellipsoid, greyish orange to reddish brown conidia (45–70 × 26–35 µm vs. 46.7–74.2 × 22.5–36.7 µm) with 5–7 vertical rows of cells which are each composed of 7–13 cells [49,55]. *Dictyosporium digitatum* has previously been recorded from *Castanopsis sieboldii*, *Machilus velutina*, *Pandanus* spp., *Phoenix hanceana*, *Pinus massoniana*, and numerous unidentified herbaceous host species [48,49,53,55]. Interestingly, this is the first *Dic. digitatum* was recorded on Cyperaceae.

3.2.3. *Pseudocoleophoma* Kaz. Tanaka and K. Hiray., Stud. Mycol. 82: 89 (2015)

Pseudocoleophoma was established by Tanaka et al. [49] to include two species, namely *P. calamagrostidis* Kaz. Tanaka, and K. Hiray. (type) from *Calamagrostis matsumurae* and *P. polygonicola* from a polygonaceous plant. The sexual morph of this genus has immersed to semi-immersed or erumpent, ostiolate ascomata, cylindrical to clavate ascospores and hyaline, fusiform, and uniseptate ascospores with a conspicuous sheath [49]. The asexual morph is characterized by having pycnidial, semi-immersed to superficial conidiomata and hyaline or pale brown, aseptate, oval, or oblong to cylindrical conidia with obtuse ends [17,29,49]. Currently, there are nine *Pseudocoleophoma* species listed in the Index Fungorum [25].

Pseudocoleophoma zingiberacearum Tennakoon, D.J. Bhat, C.H. Kuo, and K.D. Hyde, Kavaka, Phytotaxa 53: 3 (2019)

Index Fungorum number: IF556893. Facesoffungi number: FoF 06719. Figure 6.

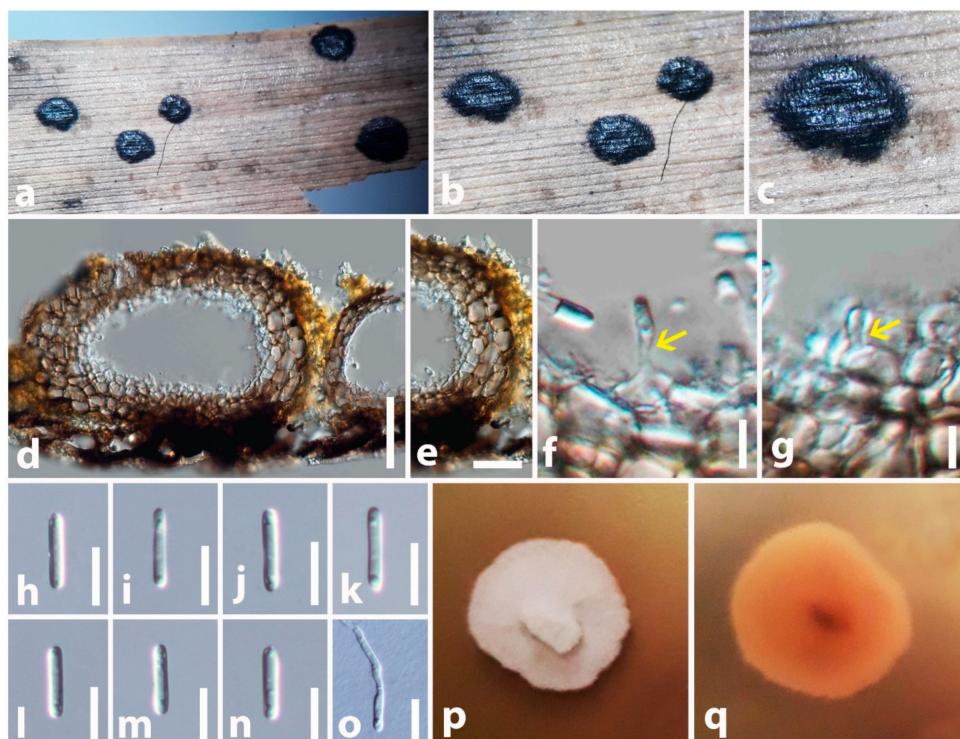


Figure 6. *Pseudocoleophoma zingiberacearum* (CMUB 39984, new host record). (a,b) Conidiomata on dead leaf of *Hedychium spicatum*. (c) Close-up of conidioma. (d) Vertical section through conidioma (e) Conidioma wall. (f,g) Conidiogenous cells with developing conidia (yellow arrows show the conidiogenous cells). (h–n) Conidia. (o) A germinating conidium. (p) Colonies from above (on PDA/4 weeks). (q) Colonies from below (on PDA/4 weeks). Scale bars: (d) = 50 µm, (e) = 12 µm, (f,g) = 3 µm, and (h–o) = 10 µm.

Saprobic on the decaying leaves of *Hedychium spicatum* Sm. In A. Rees (Zingiberaceae). **Sexual morph:** Undetermined. **Asexual morph:** Coelomycetous. Conidiomata 80–150 µm high, 150–220 µm in diameter ($\bar{x} = 125 \times 180$ µm, $n = 10$), pycnidial, solitary, scattered, superficial or semi-immersed, visible as black dots, globose to sub-globose, multi-loculate, and non-ostiolate. Conidiomata wall 15–22 µm wide, thin walled, composed of 3–5 layers of brown pseudoparenchymatous cells, arranged in *textura angularis*, darker at the outside, fusing, and indistinguishable from the host tissues. Conidiophores reduced to conidiogenous cells. Conidiogenous cells 1–3 × 1–2 µm ($\bar{x} = 2 \times 1.5$ µm, $n = 10$), phialidic, doliiform to lageniform, hyaline, aseptate, and smooth-walled. Conidia 11–15 × 2–3 µm ($\bar{x} = 13 \times 2.5$ µm, $n = 30$), solitary, hyaline, aseptate, oblong to cylindrical, obtuse ends, guttulate, and smooth-walled.

Culture characteristics: Colonies on PDA reached 6–7 mm in diameter after 4 weeks at 25 °C. Colonies viewed from above were medium dense, circular, raised, with a surface smooth, entire margin, and white to cream at the margin and center whereas in the reverse view the colonies were white to light brown at the margin and light brown at the center. Mycelium white to cream.

Known hosts: *Hedychium coronarium* and *H. spicatum* (Zingiberaceae) [29,53].

Known distribution: Taiwan and Thailand [29,53].

Material examined: Thailand, Chiang Mai (18°47'23" N 98°57'46" E), on decaying leaves of *Hedychium spicatum* (Zingiberaceae), 28 January 2017, D.S. Tennakoon, DXP05, (CMUB 39984), living culture (SDBR-CMU460).

Notes: Multi-gene phylogeny indicates that our collection (CMUB 39984) clusters with *Pseudocoleophoma zingiberacearum* isolates (NCYUCC 19-0052, NCYUCC 19-0053, and NCYUCC 19-0054) in a strongly supportive clade (100% ML, 100% MP, and 1.00 BYPP, Figure 1). The morphology of the new collection also shares similarities with the type by having superficial or semi-immersed, pycnidial conidiomata, doliiform to lageniform, hyaline, aseptate conidiogenous cells (1–3 × 1–2 µm vs. 1.5–2.5 × 1–1.5 µm), and hyaline, aseptate, oblong to cylindrical conidia (11–15 × 2–3 µm vs. 12–14 × 2–3 µm) [29]. *Pseudocoleophoma zingiberacearum* was previously recorded from *Hedychium coronarium* and this time it was from *H. spicatum*. Undeniably, this opens the possibility that these fungi are generalists or specialists to the *Hedychium* species. Thus, to determine their host-specific status, additional ecological studies are essential.

3.2.4. Geographical Distribution and Host Associations of *Dictyosporiaceae* Species

In this study, we listed 154 *Dictyosporiaceae* species, belonging to 20 genera with their host associations and geographical distribution (Table 3). The information was gathered from published books, publications in reputable journals, Index Fungorum [25], the U.S. National Fungus Collections Fungus-Host Database [53], graduate student theses, and online sources. Each data source was identified in the list, along with appropriate references. Species Fungorum [58] was used to illustrate the nomenclature validity of the taxa.

Geographical findings indicate that *Dictyosporiaceae* species have a worldwide distribution including subtropical, tropical, and temperate regions (e.g., Australia, Brazil, China, Cuba, Egypt, India, Italy, Japan, Taiwan, Thailand, Sri Lanka, South Africa, and the United States) (Figure 7). The highest number of *Dictyosporiaceae* species were reported from the Asian region, in particular from Thailand (43 species) and China (39 species) (indicated by dark blue areas, Figure 7). This is primarily because extensive taxon samplings and critical studies were carried out in these two countries in the last one and a half decades, particularly following both morphological and phylogenetic analyses [11,12,40,41,44,51,59]. In contrast, few reports are available in some continents, such as Africa and Europe. This might be due to scanty taxonomic studies on *Dictyosporiaceae* species in those countries (indicated in light blue areas). Therefore, it would be worthwhile to collect more extensively, conduct additional taxonomic investigations, and identify the *Dictyosporiaceae* species in those less-known geographical regions and countries.

Table 3. Host association and geographical distribution of reported *Dictyosporiaceae* species.

Fungal Species	Host	Locality	Reference
<i>Aquadictyospora clematis</i> Phukhams., D.J. Bhat, and K.D. Hyde	<i>Clematis sikkimensis</i>	Thailand	[44]
<i>Aquadictyospora lignicola</i> Z.L. Luo, W.L. Li, K.D. Hyde, and H.Y. Su	Unidentified submerged wood	China	[60]
<i>Aquaticheirospora lignicola</i> Kodsuueb and W.H. Ho	Unidentified submerged wood	Thailand	[61]
<i>Cheirosporium triseriale</i> L. Cai and K.D. Hyde	Unidentified submerged wood	China	[62]
<i>Cheirosporium vesiculare</i> Abdel-Aziz	Unidentified decaying wood	Egypt	[14]
<i>Dendryphiella aspera</i> R.W. Barreto and J.C. David	<i>Lantana camara</i>	Brazil	[63]
<i>Dendryphiella broussonetiae</i> Y.L. Guo and Z.Y. Zhang	<i>Broussonetia papyrifera</i>	China	[64]
<i>Dendryphiella dregeae</i> A.N. Rai and Kamal	<i>Dregea volubilis</i>	India	[65]
<i>Dendryphiella eucalypti</i> Matsush.	<i>Eucalyptus</i> sp.	Chile and Taiwan	[53,66]
<i>Dendryphiella eucalyptorum</i> Crous and E. Rubio	<i>Eucalyptus globulus</i>	China, Spain, and South Africa	[53,67–69]
<i>Dendryphiella fasciculata</i> N.G. Liu, Z.Y. Liu, and K.D. Hyde	Unidentified decaying wood	Thailand	[70]
<i>Dendryphiella indica</i> V. Rao and Narania	<i>Aloe</i> sp.	India	[71]
<i>Dendryphiella infuscans</i> (Thüm.) M.B. Ellis	<i>Cassia tora</i> , <i>Cucumis sativus</i> , <i>Curcuma aromatica</i> , <i>Desmodium strictum</i> , <i>Eichhornia crassipes</i> , <i>Lablab purpureus</i> , <i>Leucadendron</i> sp., <i>Merremia umbellata</i> , and <i>Vitis coignetiae</i>	China, India, Japan, Taiwan, United States, and West Indies	[53]
<i>Dendryphiella lycopersicifolia</i> Bat. and Peres	<i>Lycopersicon esculentum</i>	Brazil	[72]
<i>Dendryphiella paravinosa</i> Crous and Guarnaccia	<i>Citrus limon</i> and <i>Citrus sinensis</i>	Italy	[53,73]
<i>Dendryphiella phitsanulokensis</i> N.G. Liu and K.D. Hyde	Unidentified decaying wood	Thailand	[59,74]
<i>Dendryphiella stromaticola</i> Cantillo, Gusmão, and Madrid	Unidentified wood	Brazil	[75]
<i>Dendryphiella trisepta</i> (J.J. Muchovej) B.W. Ferreira and R.W. Barreto	<i>Glycine max</i>	Brazil	[76]
<i>Dendryphiella uniseptate</i> Matsush.	<i>Ficus</i> sp. and <i>Pistacia lentiscus</i>	Italy and Papua New Guinea	[77,78]
<i>Dendryphiella variabilis</i> Iturrieta-González, Dania García, and Gené	Lauraceae sp.	Cuba	[15]
<i>Dictyocheirospora acaciae</i> Tennakoon and S. Lumyong	<i>Acacia dealbata</i>	Thailand	This study
<i>Dictyocheirospora aquadulcis</i> Sorvongxay, S. Boonmee, and K.D. Hyde	Unidentified submerged wood	Thailand	[40,50]
<i>Dictyocheirospora aquatica</i> Z.L. Luo, Bhat, and K.D. Hyde	Unidentified submerged wood	China	[41]
<i>Dictyocheirospora bannica</i> Kaz. Tanaka, K. Hiray., Boonmee, and K.D. Hyde	Unidentified submerged wood	Thailand	[11,12]
<i>Dictyocheirospora cheirospora</i> S.K. Huang and f K.D. Hyde	Unidentified decaying wood	China	[43]
<i>Dictyocheirospora chiangmaiensis</i> H.W. Shen, Boonmee, and Z.L. Luo	Unidentified submerged wood	Thailand	[40]

Table 3. Cont.

Fungal Species	Host	Locality	Reference
<i>Dictycheirospora clematidis</i> Phukhams., D.J. Bhat, and K.D. Hyde	<i>Clematis sikkimensis</i>	Thailand	[44]
<i>Dictycheirospora garethjonesii</i> Z.L. Luo, Hong Y. Su, and K.D. Hyde	Unidentified submerged wood, <i>Bismarkia nobilis</i> , and <i>Macaranga tanarius</i>	China, and Thailand	[9,41]
<i>Dictycheirospora gigantica</i> (Goh and K.D. Hyde) M.J. D'souza, Boonmee, and K.D. Hyde	<i>Anisoptera oblonga</i>	South Africa and Thailand	[45]
<i>Dictycheirospora heptaspora</i> (Garov.) M.J. D'souza, Boonmee, and K.D. Hyde	Unidentified submerged wood	China and Thailand	[40]
<i>Dictycheirospora hydei</i> (Prasher and R.K. Verma) J. Yang and K.D. Hyde	<i>Tecoma stans</i>	India	[46]
<i>Dictycheirospora indica</i> (Prasher and R.K. Verma) J. Yang and K.D. Hyde	<i>Phoenix rupicola</i>	India and Thailand	[12,46]
<i>Dictycheirospora lithocarpi</i> Jayasiri, E.B.G. Jones, and K.D. Hyde	<i>Lithocarpus</i> sp.	Thailand	[47]
<i>Dictycheirospora metroxyli</i> Konta. and K.D. Hyde	<i>Metroxylon sagu</i>	Thailand	[42]
<i>Dictycheirospora multiappendiculata</i> H.W. Shen and Z.L. Luo	Unidentified submerged wood	China	[40]
<i>Dictycheirospora musae</i> (Photita) J. Yang, K.D. Hyde, and Z.Y. Liu	<i>Musae acuminata</i>	Thailand	[79]
<i>Dictycheirospora nabanheensis</i> Tibpromma and K.D. Hyde	<i>Pandanus</i> sp.	China and Thailand	[40,48]
<i>Dictycheirospora pandanicola</i> Tibpromma and K.D. Hyde	<i>Pandanus</i> sp.	Thailand	[11,48]
<i>Dictycheirospora pseudomusae</i> (Kaz. Tanaka, G. Sato, and K. Hiray.) Kaz. Tanaka, K. Hiray., Boonmee, and K.D. Hyde	Unidentified decaying twigs	Japan	[49]
<i>Dictycheirospora rotunda</i> M.J. D'souza, Bhat, and K.D. Hyde	Unidentified decaying wood	China and Thailand	[11,12,41,50,51]
<i>Dictycheirospora suae</i> H.W. Shen and Z.L. Luo	Unidentified submerged wood	China	[40]
<i>Dictycheirospora subramanianii</i> (B. Sutton) M.J. D'souza, Boonmee, and K.D. Hyde	<i>Eucalyptus globulus</i>	India	[52]
<i>Dictycheirospora taiwanense</i> Tennakoon, C.H. Kuo, and K.D. Hyde	<i>Ficus benjamina</i> and <i>Macaranga tanarius</i>	Taiwan and Thailand	[50], this study
<i>Dictycheirospora tetraploides</i> (L. Cai and K.D. Hyde) J. Yang and K.D. Hyde	Unidentified submerged wood	China	[12,80]
<i>Dictycheirospora thailandica</i> X.D. Yu, W. Dong and H. Zhang	Unidentified submerged wood	Thailand	[51]
<i>Dictycheirospora vinaya</i> M.J. D'souza, Bhat, and K.D. Hyde	Unidentified submerged wood	China and Thailand	[11,81]
<i>Dictycheirospora xishuangbannaensis</i> Tibpromma and K.D. Hyde	<i>Clematis sikkimensis</i> and <i>Pandanus</i> sp.	Thailand	[44,48]
<i>Dictyopalmispora palmae</i> Pinruan and K.D. Hyde	<i>Licuala longicalycata</i>	Thailand	[11]
<i>Dictyosporium acroinflatum</i> Whitton, K.D. Hyde, and McKenzie	<i>Freyinetia banksii</i>	New Zealand	[56]
<i>Dictyosporium alatum</i> Emden	<i>Machilus velutina</i> , <i>Pinus massoniana</i> , and soil	China and Indonesia	[53,82–84]
<i>Dictyosporium amoenum</i> C.R. Silva, Gusmão, and R.F. Castañeda	<i>Calophyllum brasiliense</i>	Brazil	[85]

Table 3. Cont.

Fungal Species	Host	Locality	Reference
<i>Dictyosporium appendiculatum</i> Tibpromma and K.D. Hyde	<i>Pandanus</i> sp.	Thailand	[48]
<i>Dictyosporium aquaticum</i> Abdel-Aziz	Unidentified submerged wood	Egypt	[86]
<i>Dictyosporium araucariae</i> S.S. Silva, R.F. Castañeda, and Gusmão	<i>Araucaria angustifolia</i>	Brazil	[87]
<i>Dictyosporium biseriale</i> D.M. Hu, L. Cai, and K.D. Hyde	Unidentified submerged wood	China	[88]
<i>Dictyosporium boydii</i> A.L. Sm. and Ramsb.	Unidentified decaying wood	United Kingdom	[89]
<i>Dictyosporium brahmaswaroopii</i> M.D. Mehrotra	<i>Leucaena leucocephala</i>	India	[90]
<i>Dictyosporium bulbosum</i> Tzean and J.L. Chen	<i>Bucida palustris</i> , <i>Clusia melchiori</i> , <i>Freycinetia banksia</i> , and <i>Pandanus</i> sp.	Brazil, China, Japan, New Zealand, Spain, Taiwan, and West Indies	[45,49,53,91–94]
<i>Dictyosporium campaniforme</i> Matsush.	<i>Trachycarpus fortunei</i> and <i>Quercus myrsinaefolia</i>	Japan and Switzerland	[53,95,96]
<i>Dictyosporium canisporum</i> L. Cai and K.D. Hyde	Unidentified submerged wood	China	[80]
<i>Dictyosporium cocophylum</i> Bat.	<i>Butia yatay</i> , <i>Cocos nucifera</i> , and <i>Elaeis guineensis</i>	Argentina, Brazil, and Ghana	[53,97,98]
<i>Dictyosporium digitatum</i> J.L. Chen, C.H. Hwang, and Tzean	<i>Anisoptera oblonga</i> , <i>Archontophoenix alexandrae</i> , <i>Cyperus aggregatus</i> , <i>Licuala longicalycata</i> , <i>Machilus velutina</i> , <i>Pinus massoniana</i> , <i>Pandanus copelandii</i> , <i>P. furcatus</i> , and <i>Phoenix hanceana</i>	Australia, Brunei, China, Japan, Mauritius, Philippines, Seychelles, Taiwan, and Thailand	[45,48,49,53,55,56], this study
<i>Dictyosporium elegans</i> Corda	<i>Arenga engleri</i> , Bamboo sp., <i>Carpinus betulus</i> , <i>Chamaecyparis nootkatensis</i> , <i>Cistus</i> sp., <i>Cocos nucifera</i> , <i>Heritiera littoralis</i> , <i>Hordeum vulgare</i> , <i>Larix decidua</i> , <i>Livistona chinensis</i> , <i>Machilus velutina</i> , <i>Phillyrea angustifolia</i> , <i>Phoenix hanceana</i> , <i>Pinus massoniana</i> , <i>Pinus wallichiana</i> , <i>Pistacia lentiscus</i> , <i>Quercus ilex</i> , <i>Rhopalostylis</i> sp., and <i>Vitis</i> sp.	Alaska, Australia, China, Germany, Italy, New Zealand, Pakistan, Poland, South Africa, and Taiwan	[53,99]
<i>Dictyosporium foliicola</i> P.M. Kirk	<i>Ilex pernyi</i>	Scotland and United Kingdom	[100]
<i>Dictyosporium gauntii</i> Bhat and B. Sutton	Unidentified decaying wood	Ethiopia	[101]
<i>Dictyosporium guttulatum</i> Tibpromma and K.D. Hyde	<i>Pandanus</i> sp.	Thailand	[48]
<i>Dictyosporium hongkongensis</i> Tibpromma and K.D. Hyde	<i>Pandanus</i> sp.	Hong Kong	[48]
<i>Dictyosporium hughesii</i> McKenzie	<i>Rhopalostylis sapida</i> and <i>Stewartia monadelpha</i>	Japan and New Zealand	[49,102]
<i>Dictyosporium hymenaearum</i> Bat. and J.L. Bezerra	<i>Hymenaea</i> sp.	Brazil	[103]
<i>Dictyosporium krabiense</i> Tibpromma and K.D. Hyde	<i>Pandanus</i> sp.	Thailand	[48]
<i>Dictyosporium lakefuxianensis</i> L. Cai, K.D. Hyde, and McKenzie	<i>Freycinetia scandens</i>	Australia	[104]
<i>Dictyosporium manglietiae</i> Kodsuab and McKenzie	Unidentified decaying wood	Thailand	[105]
<i>Dictyosporium marinum</i> Dayar. and E.B.G. Jones	Unidentified submerged wood	United Kingdom	[106]

Table 3. Cont.

Fungal Species	Host	Locality	Reference
<i>Dictyosporium meiosporum</i> Boonmee and K.D. Hyde	Unidentified decaying wood	Thailand	[86]
<i>Dictyosporium minus</i> Sacc.	<i>Inga</i> sp.	Brazil	[53]
<i>Dictyosporium muriformis</i> N.G. Liu, K.D. Hyde, and J.K. Liu	Unidentified decaying wood	China	[74]
<i>Dictyosporium nigroapice</i> Goh, W.H. Ho, and K.D. Hyde	Unidentified decaying wood and <i>Machilus velutina</i>	China and Thailand	[12,45]
<i>Dictyosporium oblongum</i> (Fuckel) S. Hughes	<i>Phillyrea angustifolia</i> , <i>Phragmites australis</i> , and <i>Populus tremuloides</i>	Canada, Italy, and Netherlands	[53]
<i>Dictyosporium olivaceosporum</i> Kaz. Tanaka, K. Hiray., Boonmee, and K.D. Hyde	Unidentified submerged wood	Japan	[11]
<i>Dictyosporium palmae</i> Abdel-Aziz	<i>Licuala longicalycata</i> and <i>Phoenix dactylifera</i>	Egypt and Thailand	[14,53]
<i>Dictyosporium pandani</i> Whitton, K.D. Hyde, and McKenzie	<i>Pandanus</i> spp.	Australia, Brunei, China, Nepal, and Philippines	[56]
<i>Dictyosporium pandanicola</i> Tibpromma and K.D. Hyde	<i>Pandanus</i> spp.	Thailand	[48]
<i>Dictyosporium pelagicum</i> (Linder) G.C. Hughes ex E.B.G. Jones	Unidentified decaying wood	Canada and United States	[53,107]
<i>Dictyosporium prolificum</i> Damon	<i>Juncus</i> sp.	United States	[108]
<i>Dictyosporium rhopalostylidis</i> McKenzie	<i>Rhopalostylis sapida</i>	New Zealand	[102]
<i>Dictyosporium schizostachyfolium</i> Bat. and M.L. Farr	<i>Schizostachyum acutiflorum</i>	Philippines	[109]
<i>Dictyosporium sexualis</i> Boonmee and K.D. Hyde	Decaying wood	Thailand	[11]
<i>Dictyosporium sinense</i> H.M. Liu and T.Y. Zhang	Soil	China	[53]
<i>Dictyosporium solanii</i> A.D. Sharma, Munjal, and Jandaik	<i>Juglans regia</i> and <i>Trachycarpus fortunei</i>	China and India	[53]
<i>Dictyosporium splendidum</i> Alves-Barb., Malosso, and R.F. Castañeda	Unidentified decaying leaves	Brazil	[110]
<i>Dictyosporium stellatum</i> G.P. White and Seifert	Unidentified decaying wood	United States	[111]
<i>Dictyosporium strelitziae</i> Crous and A.R. Wood	<i>Strelitzia nicolai</i>	South Africa	[112]
<i>Dictyosporium taishanense</i> G.Z. Zhao and T.Y. Zhang	Unidentified decaying wood	China	[113]
<i>Dictyosporium tetraseriale</i> Goh, Yanna, and K.D. Hyde	<i>Livistona chinensis</i>	Hong Kong	[45]
<i>Dictyosporium tetrasporum</i> L. Cai and K.D. Hyde	Unidentified submerged wood	China and Japan	[49,114]
<i>Dictyosporium thailandicum</i> M.J. D'souza, Bhat, and K.D. Hyde	Unidentified submerged wood	Thailand	[86]
<i>Dictyosporium tratense</i> J. Yang and K.D. Hyde	Unidentified decaying wood	Thailand	[12]
<i>Dictyosporium triramosum</i> Aramb., Cabello, and Cazau	Unidentified decaying wood	Argentina	[115]
<i>Dictyosporium triseriale</i> Matsush.	<i>Phyllostachys</i> sp.	China and Taiwan	[53,116]
<i>Dictyosporium tubulatum</i> J. Yang, K.D. Hyde, and Z.Y. Liu	Unidentified decaying wood	China and Thailand	[12,40]
<i>Dictyosporium wuyiense</i> Y. Zhang ter and G.Z. Zhao	<i>Bamboo</i> sp.	China	[117]

Table 3. Cont.

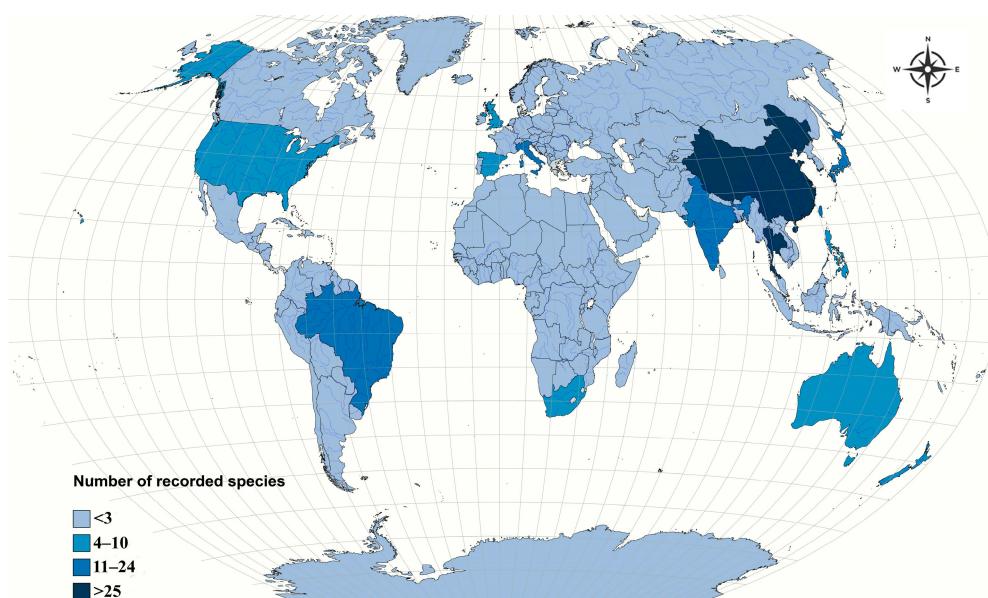
Fungal Species	Host	Locality	Reference
<i>Dictyosporium yerbae</i> Speg.	<i>Ilex paraguariensis</i>	Argentina	[118]
<i>Dictyosporium yunnanense</i> L. Cai, K.D. Hyde, and McKenzie	Unidentified submerged wood	China	[80]
<i>Dictyosporium zeylanicum</i> Petch	Unidentified decaying wood	Sri Lanka	[119]
<i>Dictyosporium zhejiangense</i> Wongs., H.K. Wang, K.D. Hyde, and F.C. Lin	Unidentified submerged wood	China	[120]
<i>Digitodesmium aquaticum</i> H.W. Shen, Boonmee, and Z.L. Luo	Unidentified submerged wood	Thailand	[40]
<i>Digitodesmium bambusicola</i> L. Cai, K.Q. Zhang, McKenzie, W.H. Ho, and K.D. Hyde	Bamboo sp.	Philippines	[121]
<i>Digitodesmium chiangmaiense</i> Q.J. Shang and K.D. Hyde	Unidentified decaying wood	Thailand	[50]
<i>Digitodesmium elegans</i> P.M. Kirk	<i>Fagus</i> sp. and <i>Quercus</i> sp.	United Kingdom	[122,123]
<i>Digitodesmium heptasporum</i> L. Cai and K.D. Hyde	Unidentified submerged wood	China	[80]
<i>Digitodesmium intermedium</i> J. Mena, Silvera, Gené, and Guarro	Plant debris	Spain	[124]
<i>Digitodesmium macrosporum</i> Silvera, Mercado, Gené, and Guarro	Soil	Spain	[124]
<i>Digitodesmium polybrachiatum</i> T.F. Nóbrega, B.W. Ferreira, and R.W. Barreto	<i>Coffea canephora</i>	Brazil	[125]
<i>Digitodesmium recurvum</i> W.H. Ho, K.D. Hyde, and Hodgkiss	<i>Machilus velutina</i>	Hong Kong	[53,126]
<i>Digitodesmium tectonae</i> (Rajeshk., Rajn. K. Verma, Boonmee, K.D. Hyde, Chandrasiri, and Wijayaw.) W.H. Tian and Maharanachch.	<i>Tectona grandis</i>	India	[16,21]
<i>Gregarithecium curvisporum</i> Kaz. Tanaka and K. Hiray.	<i>Sasa</i> sp.	Japan	[49]
<i>Immotthia atrograna</i> (Cooke and Ellis) M.E. Barr	<i>Aceri-Fraxinetum</i> , <i>Carya olivaeformis</i> , <i>Carya</i> sp., <i>Salix alba</i> , <i>Acer pseudoplatanus</i> , and <i>Fraxinus excelsior</i>	United States	[127,128]
<i>Immotthia atroseptata</i> (Piroz.) M.E. Barr	<i>Rhododendron maximum</i>	United States	[128,129]
<i>Immotthia bambusae</i> H.B. Jiang and Phookamsak	Bamboo sp.	Thailand	[128]
<i>Jalapriya apicalivaginata</i> D.F. Bao, X. Fu, H.Y. Su, and Z.L. Luo	Unidentified submerged wood	China	[81]
<i>Jalapriya aquatica</i> D.F. Bao, X. Fu, H.Y. Su, and Z.L. Luo	Unidentified submerged wood	China	[81]
<i>Jalapriya inflata</i> (Matsush.) M.J. D'souza, Hong Y. Su, Z.L. Luo, and K.D. Hyde	Unidentified decaying wood	Canada	[11,66]
<i>Jalapriya pulchra</i> M.J. D'souza, Hong Y. Su, Z.L. Luo, and K.D. Hyde	Unidentified submerged wood	China	[11]
<i>Jalapriya toruloides</i> (Corda) M.J. D'souza, Hong Y. Su, Z.L. Luo, and K.D. Hyde	<i>Laurus nobilis</i> and <i>Populus nigra</i>	Pakistan and Spain	[53,130,131]
Neodendryphiella mali Iturrieta-González, Gené, and Dania García	<i>Malus domestica</i>	Italy	[15]
Neodendryphiella michoacanensis Iturrieta-González, Dania García, and Gené	Soil	Mexico	[15]

Table 3. Cont.

Fungal Species	Host	Locality	Reference
<i>Neodendryphiella tarragonensis</i> Iturrieta-González, Gené, and Dania García	Unidentified decaying wood and Soil	China and Spain	[15,69]
<i>Neodigitodesmium cheirosporum</i> W.H. Tian and Maharachch.	Unidentified submerged wood	China	[21]
<i>Pseudocoleophoma bauhiniae</i> Jayasiri, E.B.G. Jones, and K.D. Hyde	<i>Bauhinia</i> sp.	Thailand	[47]
<i>Pseudocoleophoma calamagrostidis</i> Kaz. Tanaka and K. Hiray.	<i>Calamagrostis matsumurae</i>	Japan	[49]
<i>Pseudocoleophoma flavescens</i> (Gruyter, Noordel. & Boerema) W.J. Li and K.D. Hyde	Soil	Netherlands	[132,133]
<i>Pseudocoleophoma polygonicola</i> Kaz. Tanaka and K. Hiray.	Polygonaceae sp.	Japan	[49]
<i>Pseudocoleophoma puerensis</i> L. Lu & Tibpromma	<i>Coffea arabica</i>	China	[134]
<i>Pseudocoleophoma rhipidis</i> Kular. and K.D. Hyde	<i>Rhapis excelsa</i>	China	[17]
<i>Pseudocoleophoma rusci</i> W.J. Li, Camporesi, and K.D. Hyde	<i>Ruscus aculeatus</i>	Italy	[133]
<i>Pseudocoleophoma typhicola</i> Kamolhan, Banmai, Boonmee, E.B.G. Jones, and K.D. Hyde	<i>Typha latifolia</i>	United Kingdom	[135]
<i>Pseudocoleophoma yunnanensis</i> L. Lu and Tibpromma	<i>Coffea</i> sp.	China	[134]
<i>Pseudocoleophoma zingiberacearum</i> Tennakoon, D.J. Bhat, C.H. Kuo, and K.D. Hyde	<i>Hedychium coronarium</i> and <i>H. spicatum</i>	Taiwan and Thailand	[29], this study
<i>Pseudoconiothyrium broussonetiae</i> Crous and R.K. Schumach.	<i>Broussonetia papyrifera</i>	Italy	[18]
<i>Pseudocyclothyriella clematidis</i> (Phukhams. and K.D. Hyde) Phukhams. and Phookamsak	<i>Clematis vitalba</i>	Italy	[44,128]
<i>Pseudodictyosporium elegans</i> (Tzean and J.L. Chen) R. Kirschner	Unidentified decaying wood	Taiwan	[136,137]
<i>Pseudodictyosporium indicum</i> (V.G. Rao and Subhedar) Boonmee and K.D. Hyde	<i>Schleichera trijuga</i>	India	[11,138]
<i>Pseudodictyosporium thailandicum</i> C.G. Lin, Yong Wang bis, and K.D. Hyde	Bamboo sp.	Thailand	[135]
<i>Pseudodictyosporium wauense</i> Matsush.	<i>Bambusa vulgaris</i> , <i>Caesalpinia echinata</i> , <i>Phillyrea angustifolia</i> , <i>Pistacia lentiscus</i> , and <i>Quercus ilex</i>	Brazil, China, Cuba, Italy, Papua New Guinea, and Venezuela	[53,60]
<i>Sajamaea mycophile</i> Flakus, Piątek, and Rodr. Flakus	<i>Leptosphaeria polylepidis</i> and <i>Polyepis tarapacana</i>	Bolivia	[19]
<i>Verrucoccum coppinsii</i> V. Atienza, D. Hawksw., and Pérez-Ort.	<i>Lobaria pulmonaria</i>	United Kingdom	[20]
<i>Verrucoccum hymeniicola</i> (Berk. & Broome) D. Hawksw., V. Atienza, and Pérez-Ort.	<i>Sticta</i> sp.	United States	[20]
<i>Verrucoccum spribilei</i> V. Atienza, D. Hawksw., and Pérez-Ort.	<i>Lobaria linita</i>	Alaska	[20]
<i>Vikalpa australiensis</i> (B. Sutton) M.J. D'souza, Boonmee, and K.D. Hyde	<i>Eucalyptus</i> sp.	Australia	[11,52]

Table 3. Cont.

Fungal Species	Host	Locality	Reference
<i>Vikalpa freycinetiae</i> (McKenzie) M.J. D'souza, Boonmee, and K.D. Hyde	<i>Freycinetia banksii</i>	New Zealand	[11,139]
<i>Vikalpa grandispora</i> H.W. Shen, Boonmee, and Z.L. Luo	Unidentified submerged wood	China	[40]
<i>Vikalpa lignicola</i> M.J. D'souza, Bhat, Hong Y. Su, and K.D. Hyde	Unidentified submerged wood	China	[11]
<i>Vikalpa micronesiaca</i> (Matsush.) M.J. D'souza, Bhat, and K.D. Hyde	<i>Calophyllum inophyllum</i> , <i>Cocos nucifera</i> , <i>Drymophloeus pachycladus</i> , and <i>Theobroma cacao</i>	Brazil, Cuba, United States, and Venezuela	[53]
<i>Vikalpa sphaerica</i> H.W. Shen and Z.L. Luo	Unidentified submerged wood	China	[40]

**Figure 7.** Distribution of so far reported *Dictyosporiaceae* species worldwide. Color gradient shows the number of recorded species from lowest (light blue) to highest (dark blue).

Considering the host association of the *Dictyosporiaceae* species reported so far, numerous species have been discovered in decaying wood or submerged woody substrates (e.g., *Dictyocheirospora tetraploides* (L. Cai and K.D. Hyde) J. Yang and K.D. Hyde; *Di. thailandica* X.D. Yu, W. Dong, and H. Zhang; *Dictyosporium zeylanicum* Petch; *Dic. zhejiangense* Wongs., H.K. Wang, K.D. Hyde, and F.C. Lin; *Digitodesmium aquaticum* H.W. Shen, Boonmee, and Z.L. Luo; *Jalapriya apicalivaginata* D.F. Bao, X. Fu, H.Y. Su, and Z.L. Luo; *J. aquatica* D.F. Bao, X. Fu, H.Y. Su, and Z.L. Luo; and *Neodigitodesmium cheirosporum* W.H. Tian and Maharachch). Some have been recorded from decaying leaves (e.g., *Di. nabaneensis* Tibpromma and K.D. Hyde; *Di. pandanicola* Tibpromma and K.D. Hyde; *Di. xishuangbannaensis* Tibpromma and K.D. Hyde; *Dic. splendidum* Alves-Barb., Malosso, and R.F. Castañeda) and soil (e.g., *Dic. alatum* Emder; *Dic. sinense* H.M. Liu, and T.Y. Zhang; *Digitodesmium macrosporum* Silvera, Mercado, Gené, and Guarro; *Neodendryphiella michoacanensis* Iturrieta-González, Dania García, and Gené; *N. tarraconensis* Iturrieta-González, Gené, and Dania García; *Pseudocoleophoma flavescens* (Gruyter, Noordel, and Boerema) W.J. Li and K.D. Hyde). However, the emerging concern is that the majority of these described species have been introduced from unidentified host species (Table 3). For instance, out of the 154 species listed, 55 were identified from unidentified host species. Thus, there is scant evidence of rigid host specialization in these species. Future taxonomical studies on *Dictyosporiaceae* are essen-

tially needed to concentrate on determining the host specificity and check whether they are generalists or specialists to respective host species.

4. Discussion

Thailand is located between Indochinese and Sundaic regions and has a rich biodiversity [140,141]. This is an astonishing home to numerous tropical forests, mountains, rivers, and suitable climatic conditions, which has led to tremendous biodiversity [141–144]. In particular, tropical forests represent 33% of the total area, with over 18% being protected forests. Thus, this country showcases luxuriant vegetation (15,000 plant species, 600 ferns, of which over 1000 endemic species), 1000 bird species, over 300 mammal species, 490 species of amphibians and reptiles, 2800 fish species, and a vast range of microorganisms [144,145]. With enormous biodiversity, Thailand is a magnet for all kinds of taxonomists, and new species are continuously being discovered. For instance, fungal taxonomists in Thailand have collected, observed, and introduced a great deal of fungal species in the last two decades [43,48,59,74,135,141,146,147]. Prior to this period, most of the Thailand fungal taxonomy studies were merely based on morphological characteristics. However, in recent years this has been improved vastly with the usage of modern molecular phylogeny [148–151]. In addition, Hyde et al. [152] revealed that 96% of the fungal species described in northern Thailand were novel to science. Therefore, it is worth continuing the investigation and research of fungi in Thailand with broader scientific aspects.

The *Dictyosporiaceae* species have been well-documented during the last two decades with the advancement of molecular data [11,12,40,48,51]. For instance, out of 154 species, 99 *Dictyosporiaceae* species were introduced between 2000 and 2022 [25]. Of them, most have been confined to two genera: *viz.* *Dictyosporium* (37 species) and *Dictyocheirospora* (20 species). Geographically, *Dictyosporiaceae* members are widely distributed in temperate, tropical, and subtropical regions [11,13,53]. Nevertheless, geographical specificity of *Dictyosporiaceae* species is still understudied. Host specificity of the *Dictyosporiaceae* also has yet to be investigated, despite having been collected from various plant families [53]. However, although *Dictyosporiaceae* species have been found all over the world, most of them are lack molecular data. For example, only 24 species of *Dictyosporium* have molecular data out of the 63 species listed in the Index Fungorum [25]. Some genera are highly diverse (e.g., *Dictyocheirospora*: 23 species and *Dictyosporium*: 63 species), while some have fewer species (e.g., *Aquadictyospora*: 2 species, *Cheirosporium*: 2 species, *Jalapriya*: 5 species, *Neodendryphiella*: 3 species, *Pseudodictyosporium*: 4 species, and *Verrucoccum*: 3 species) or monotypic genera (e.g., *Aquaticheirospora*, *Gregarithecium*, *Pseudoconiothyrium*, *Sajamaea*, and *Neodigitodesmium*) [13]. Furthermore, to define the phylogenetic position of some genera in *Dictyosporiaceae*, there is currently a lack of molecular data (e.g., *Sajamaea*). Most of the previous studies have used LSU, ITS, and *tef1- α* genes for phylogenetic classification [7,11,12,44,74,153]. However, additional genes are needed to determine the phylogenetic status of some taxa (e.g., *Dictyocheirospora clematidis* vs. *Di. thailandica*, *Di. pandanicola* vs. *Di. inaya*, and *Dictyosporium bulbosum* vs. *Dic. elegans*), whose morphological characteristics are nearly identical and there are minor size differences.

5. Conclusions

In this study, we provided taxonomic details for five species, which included a new species (*Dictyocheirospora acaciae*) and four new host records (*Di. garethjonesii*, *Di. taiwanense*, *Dictyosporium digitatum*, and *Pseudocoleophoma zingiberacearum*) from Thailand. All of them are members of the *Dictyosporiaceae* and were described based on both morphology and phylogeny. Thus, these findings have facilitated our understanding of the fungal diversity in plant litter substrates and the vast geographical distribution of *Dictyosporiaceae* species. Further collections are essential to understand the circumscription of some *Dictyosporiaceae* genera which have few or single species (e.g., *Aquaticheirospora*, *Gregarithecium*, *Pseudoconiothyrium*, *Sajamaea*, and *Neodigitodesmium*).

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