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New species and records of *Dictyocheirospora* from submerged wood in north-western Yunnan, China

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Abstract

Two new species of *Dictyocheirospora*, *D. aquatica* and *D. garethjonesii*, isolated from submerged wood in aquatic habitats in north-western Yunnan, China, are introduced in this paper. The introductions are based on morphology and molecular analysis of DNA sequence data. We also recovered two fresh isolates of *Dictyocheirospora rotunda* D' Souza, Bhat & K.D. Hyde, which is a first record for China. Descriptions and illustrations of *D. aquatica*, *D. garethjonesii* and *D. rotunda* are provided. The phylogenetic analysis of combined ITS and LSU sequence data place the isolates within the family *Dictyosporiaceae* (Pleosporales). A synopsis of characters of the accepted species of *Dictyocheirospora* is provided.

Key words – Asexual morphs – *Dictyosporiaceae* – Phylogeny – Taxonomy

Introduction

The order Pleosporales has been of great research interest in recent years and has undergone considerable revision (Zhang et al. 2009, 2012, Hyde et al. 2013, Ariyawansa et al. 2015). Boonmee et al. (2016) introduced the family *Dictyosporiaceae* (Pleosporales) to accommodate most cheirosporous hyphomycete genera that are saprobes on decaying wood and plant debris in terrestrial and freshwater habitats. One of the diagnostic characteristics of *Dictyosporiaceae* is their multicellular cheiroid conidia, and these morphological features separate it from other families in the suborder Massarineae (Hyde et al. 2016a).

The genus *Dictyocheirospora* D' Souza, Bhat & K.D. Hyde, introduced by Boonmee et al. (2016) with *Dictyocheirospora rotunda* D' Souza, Bhat & K.D. Hyde as the type species, is characterized by dark sporodochial colonies that produce aero-aquatic, cheiroid, dictyosporous conidia (Boonmee et al. 2016). Presently, there are seven species accepted in the genus.

We are studying the freshwater lignicolous fungi in three rivers, viz. Jinsha, Lancang and Dulong, in north-western Yunnan Province, China (Hyde et al. 2016b, Luo et al. 2016). In this

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study, five fresh collections of cheirosporous hyphomycetous taxa were made from submerged wood. Descriptions and illustrations are provided for two new species, *D. aquatica* and *D. garethjonesii* and for *D. rotunda*, which is a new record for China.

Material & methods

Isolation and morphology

Specimens of submerged decaying wood were collected from Jinsha, Lancang and Dulong rivers, in north-western Yunnan, China and brought to the laboratory in plastic bags. The samples were incubated in plastic boxes lined with moistened tissue paper at room temperature for one week and processed and examined following the methods described in Taylor & Hyde (2003). Morphological observations were made using a Motic SMZ 168 Series stereomicroscope and photographed by an OLYMPUS BX51 microscope imaging system. The fungal structures were measured using Image-Pro-Express software.

Single spore isolations were made to obtain the pure cultures as described in Chomnunti et al. (2014). The cultures are deposited in Mae Fah Luang University Culture Collection (MFLUCC), Culture collection of Kunming Institute of Botany (KUMCC) and Dali University (DLUCC). Herbarium specimens are deposited at the herbarium of Mae Fah Luang University (MFLU), the Herbarium of Cryptogams Kunming Institute of Botany Academia Sinica (HKAS) and Dali University (DLU). Facesoffungi and Index Fungorum numbers were obtained as in Jayasiri et al. (2015) and Index Fungorum (2016).

DNA extraction, PCR amplification and sequencing

Total genomic DNA was extracted from fresh fungal mycelium grown on PDA at room temperature. The EZ geneTM Fungal gDNA kit (GD2416) was used to extract DNA according to the manufacturer's instructions. ITS and LSU gene regions were amplified using the primer pairs ITS5/ITS4 and LROR/LR5. The final volume of the PCR reaction was 25 µL and contained 12.5 µL of 2×Power Taq PCR MasterMix (a premix and ready to use solution, including 0.1 Units/µL Taq DNA Polymerase, 500 µM dNTP Mixture each (dATP, dCTP, dGTP, dTTP), 20 mM Tris–HCl pH 8.3, 100 mM KCl, 3 mM MgCl2, stabilizer and enhancer), 1 µL of each primer (10 µM), 1 µL genomic DNA extract and 9.5 µL deionised water. The PCR thermal cycleprogram for ITS amplification was as follows: initially 95 ℃ for 3 minutes, followed by 35 cycles of denaturation at 95 ℃ for 1 minutes, annealing at 53 ℃ for 30 seconds, elongation at 72 ℃ for 1 min. The PCR thermal cycle program for LSU was followed as initially 95 ℃ for 3 minutes, followed by 35 cycles of denaturation at 95 ℃ for 30 seconds, annealing at 52 ℃ for 40 seconds, elongation at 72 ℃ for 90 seconds. PCR products were purified using minicolumns, purification resin and buffer according to the manufacturer's protocols (Amershamproduct code: 27–9602–01). The sequences were carried by Beijing Tsingke Biological Engineering Technology and Services Co., Ltd (Beijing, P.R. China).

Phylogenetic analysis

Raw sequences were assembled with Sequencher 4.9 for Windows (Gene Codes Corp., Ann Arbor, Michigan). The consensus sequences were initially aligned using MAFFTv.7 (http://mafft.cbrc.jp/alignment/server/) (Katoh & Standley 2013) and optimised manually when needed.

A Maximum likelihood (ML) analysis was performed using RAxMLGUI v. 1.3 (Silvestro & Michalak 2011). The optimal ML tree search was conducted with 1000 separate runs, using the default algorithm of the program from a random starting tree for each run. The final tree was selected among suboptimal trees from each run by comparing likelihood scores under the GTR+GAMMA substitution model. Maximum parsimony analyses were performed using the heuristic search option with 1000 random taxa additions and tree bisection and reconnection (TBR) as the branch-swapping algorithm. All characters were unordered and of equal weight and gaps

were treated as missing data. Maxtrees were unlimited, branches of zero length were collapsed and all multiple, equally parsimonious trees were saved. Clade stability was assessed using a bootstrap (BT) analysis with 1000 replicates, each with 10 replicates of random stepwise addition of taxa (Hillis & Bull 1993).

Bayesian analyses were performed by using PAUP v.4.0b10 (Swofford 2002) and MrBayes v3.1.2 (Ronquist & Huelsenbeck 2003). The model of evolution was estimated by using MrModeltest 2.2 (Nylander 2004). Posterior probabilities (PP) (Rannala & Yang 1996) were performed by Markov Chain Monte Carlo Sampling (BMCMC) in MrBayes v. 3.0b4 (Liu et al. 2012). Six simultaneous Markov Chains were run for 1 million generations and trees were sampled every 100th generation (Resulting 10000 total trees) (Cai et al. 2006). The first 2000 trees representing the burn-in phase of the analyses were discarded and the remaining 8000 (post burning) trees used for calculating posterior probabilities (PP) in the majority rule consensus tree (Cai et al. 2006, Liu et al. 2012).

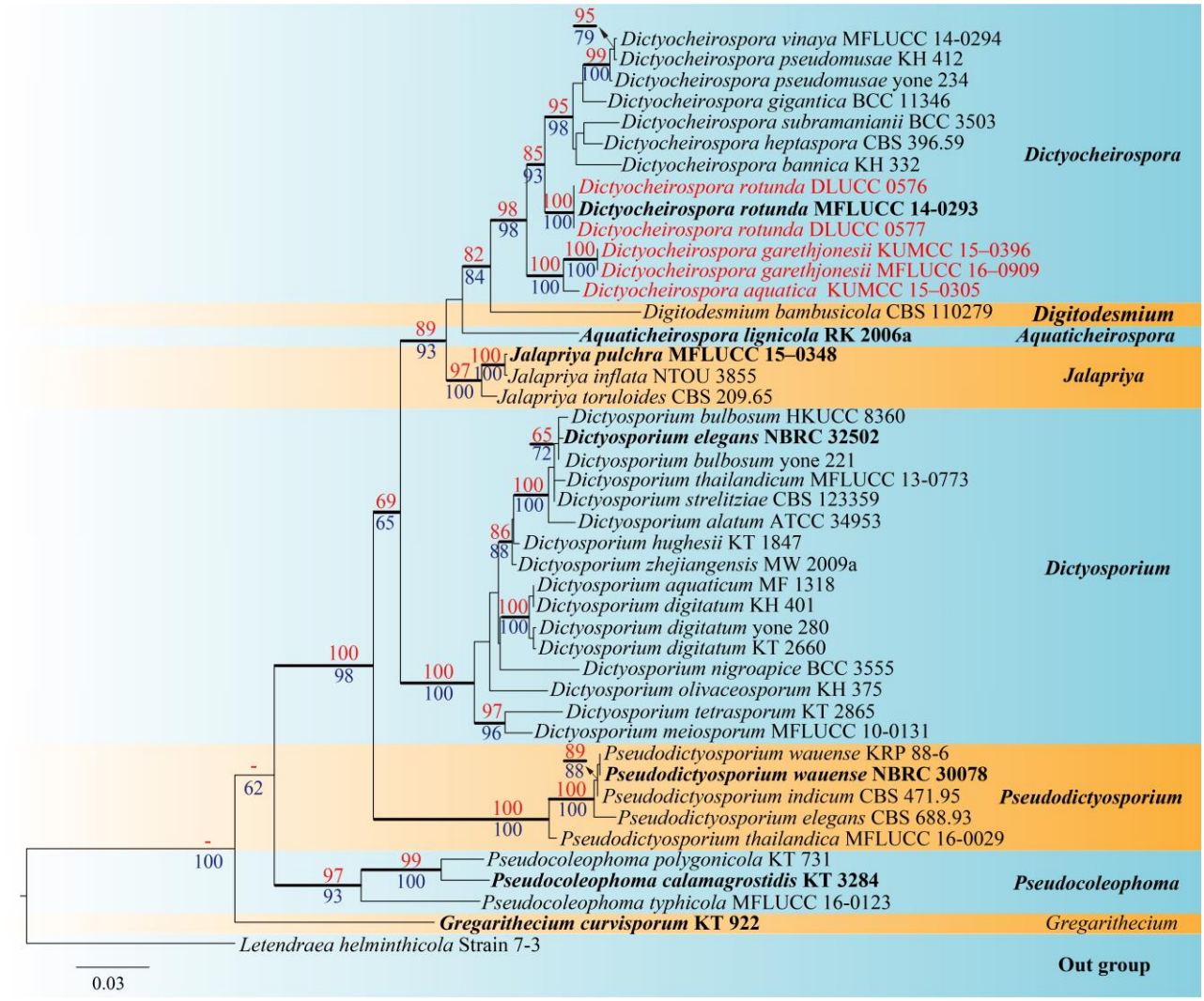

Fig. 1 Phylogram generated from Maximum likelihood analysis (RAxML) based on combined ITS and LSU sequence data for the family *Dictyosporiaceae*. Bootstrap support values for maximum likelihood (red) equal to or greater than 60% are given above the nodes. Bootstrap support values for maximum parsimony (blue) equal to or greater than 60% are given below the nodes. Branches with Bayesian posterior probabilities greater than 0.95 are in bold. The tree is rooted to *Letendraea helminthicola* (strain 7–3). Newly generated sequences are indicated in red and generic types are highlighted in bold.

The phylogenetic analyses were carried out with combined ITS and LSU sequence data alignment to illustrate the placement of the isolates in Tubeufiaceae. All new sequence data generated in this study are deposited in GenBank (Table 1). All alignments are deposited in TreeBASE (www.treebase.org, submission number 20337). Phylogenetic trees were viewed in Treeview (Page 1996). The terminals of the tree (Fig. 1) are labelled with species and the isolates/culture collection codes as provided in GenBank.

Table: 1 Isolates and sequences used in this study (newly generated sequences are indicated in bold, ex-type strains are indicated in * after collection number).

Species	Collection/Isolate No.	GenBank Accession No.	
		ITS	LSU
Aquaticheirospora lignicola	RK 2006a*	AY864770	AY736378
Dictyocheirospora aquatica	**KUMCC 15–0305***	**KY320508**	**KY320513**
Dictyocheirospora bannica	KH 332	LC014543	AB807513
Dictyocheirospora garethjonesii	**MFLUCC 16–0909***	**KY320509**	**KY320514**
Dictyocheirospora garethjonesii	**KUMCC 15–0396**	**KY320510**	**KY320515**
Dictyocheirospora gigantica	BCC 11346	DQ018095	–
Dictyocheirospora heptaspora	CBS 396.59	DQ018090	–
Dictyocheirospora rotunda	MFLUCC 14–0293*	KU179099	KU179100
Dictyocheirospora rotunda	**DLUCC 0576**	**KY320511**	**KY320516**
Dictyocheirospora rotunda	**DLUCC 0577**	**KY320512**	**KY320517**
Dictyocheirospora vinaya	MFLUCC 14–0294*	KU179102	KU179103
Dictyocheirospora pseudomusae	KH 412	LC014549	AB807516
Dictyocheirospora pseudomusae	yone 234*	LC014550	AB807520
Dictyocheirospora subramanianii	BCC 3503	DQ018094	–
Dictyosporium alatum	ATCC34953*	NR077171	DQ018101
Dictyosporium aquaticum	MF1318*	KM610236	–
Dictyosporium bulbosum	HKUCC 8360	DQ018086	–
Dictyosporium bulbosum	yone 221	LC014544	AB807511
Dictyosporium digitatum	KH 401	LC014545	AB807515
Dictyosporium digitatum	KT 2660	LC014546	AB807518
Dictyosporium digitatum	yone 280	LC014547	AB807512
Dictyosporium elegans	NBRC 32502*	DQ018087	DQ018100
Dictyosporium hughesii	KT 1847	LC014548	AB807517
Dictyosporium meiosporum	MFLUCC 10–0131*	KP710944	KP710945
Dictyosporium nigroapice	BCC 3555	DQ018085	–
Dictyosporium olivaceosporum	KH 375	LC014542	AB807514
Dictyosporium strelitziae	CBS 123359*	FJ839618	FJ839653
Dictyosporium tetrasporum	KT 2865	LC014551	AB807519
Dictyosporium thailandicum	MFLUCC 13–0773*	KP716706	KP716707
Dictyosporium zhejiangensis	MW-2009a	FJ456893	–
Digitodesmium bambusicola	CBS 110279*	DQ018091	DQ018103
Gregarithecium curvisporum	KT 922*	AB809644	AB807547
Jalapriya inflata	NTOU 3855	JQ267362	JQ267363
Jalapriya pulchra	MFLUCC 15–0348	KU179108	KU179109
Jalapriya toruloides	CBS 209.65	DQ018093	DQ018104
Letendraea helminthicola	Strain 7-3	HM486428	AY016362
Pseudocoleophoma calamagrostidis	KT 3284*	LC014592	LC014609
Pseudocoleophoma polygonicola	KT 731*	AB809634	AB807546
Pseudocoleophoma typhicola	MFLUCC 16–0123*	KX576655	KX576656
Pseudodictyosporium elegans	CBS 688.93*	DQ018099	DQ018106
Pseudodictyosporium indicum	CBS 471.95	DQ018097	–
Pseudodictyosporium thailandica	MFLUCC 16–0029*	KX259520	KX259522
Pseudodictyosporium wauense	NBRC 30078	DQ018098	DQ018105
Pseudodictyosporium wauense	KRP88–6	HM036613	–

Results

Phylogenetic analyses

ITS and LSU sequence data were used to resolve the generic placement of the collections of *Dictyosporiaceae*. The alignment datasets included 44 taxa of which *Letendraea helminthicola* (strain 7–3) was used as the outgroup taxon. The combined datasets comprised 1265 characters including gaps. The best scoring RAxML tree was chosen as the backbone tree and is shown in Fig. 1.

The phylogenetic analyses show that all the new strains cluster in the genus *Dictyocheirospora* with high support (98% ML, 98% MP and 1.00 PP). Two isolates clustered with *Dictyocheirospora rotunda* with 100% ML, 100% MP and 1.00 PP. Three new isolates formed a distinct clade at the basal position of the genus *Dictyocheirospora* with strong support (100% ML, 100% MP and 1.00 PP), but *Dictyocheirospora garethjonesii* (MFLUCC 16–0909 and KUMCC 15–0396) clustered with *D. aquatica* (KUMCC 15–0305) in a sister group.

Taxonomy

Dictyocheirospora aquatica Z.L. Luo, D.J. Bhat & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF 552683; Facesoffungi number: FoF 02733; Fig. 2

Etymology – Referring to aquatic habitat of this fungus.

Holotype – HKAS 92714

Saprobic on decaying, submerged wood in freshwater. ***Sexual morph***: Undetermined. ***Asexual morph***: Hyphomycetous. Colonies on natural substrate superficial, scattered. *Mycelium* immersed, composed of pale brown, smooth, septate, branched hyphae. *Conidiomata* sporodochial, 150–250 μm wide, dark brown to black. *Conidiophores* micronematous, undifferentiated from vegetative hyphae, short. *Conidiogenous cells* holoblastic, integrated, terminal, pale brown, smooth-walled. *Conidia* 34–42 × 12.5–19.5 μm ($\overline{x}$ = 38 × 16 μm, n = 35), solitary, acrogenous, cheiroid, pale brown to brown, consisting of 5–6 rows of cells, with rows cylindrical, palmately divergent, inwardly curved at the tip, arising from a basal cell, without appendages, with each row composed of 8–10 cells, euseptate, slightly constricted at septa, smooth-walled.

Material examined – CHINA, Yunnan Province, Dulong River, on decaying submerged wood, 6 May 2015, Z.L. Luo, S-395 (HKAS 92714, **holotype**); ex-type living culture, KUMCC 15–0305.

Notes – *Dictyocheirospora aquatica* morphologically resembles *D. subramanianii* in having a similar conidial size and cylindrical, palmately divergent rows of cells, without appendages. However, *D. aquatica* differs from *D. subramanianii* in conidial shape with 5–6 separable rows, having 6–8 cells in each row, whereas the conidia in the latter has seven tightly appressed rows with each having 9–13 cells (Sutton 1985). Phylogenetic analysis also showed that *D. aquatica* is distinct from *D. subramanianii* (Fig. 1).

Dictyocheirospora garethjonesii Z.L. Luo, H.Y. Su & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF 552684; Facesoffungi number: FoF 02734; Fig. 3

Etymology – In honour of Professor E.B.G. Jones for his major contributions to mycology.

Holotype – HKAS 92836

Saprobic on decaying, submerged wood in freshwater. ***Sexual morph***: Undetermined. ***Asexual morph***: Hyphomycetous. Colonies on natural substrate superficial, scattered. *Mycelium* immersed, composed of brown, smooth, septate hyphae. *Conidiomata* sporodochial, dark brown, 200–300 μm wide. *Conidiophores* micronematous, undifferentiated from vegetative hyphae, short. *Conidiogenous cells* holoblastic, integrated, terminal, pale brown, cylindrical, smooth-walled. *Conidia* 45.5–54.5 × 15.5–24.5 μm ($\overline{x}$ = 50 × 20 μm, n = 25), solitary, acrogenous, cheiroid, brown, consisting of 6–7 rows of cells, with rows digitate, cylindrical, inwardly curved at apex, arising from a basal cell, without appendages, with each row composed of 7–10 cells, euseptate, slightly constricted at septa.

Material examined – CHINA, Yunnan Province, Lancang River, on submerged wood, 25 April 2015, Z.L. Luo, S-310 (HKAS 92836, **holotype**), ex-type living culture MFLUCC 16–0909;

ibid. Jinsha River, on submerged wood, 18 April 2015, S.M. Tang, S-422 (DLU 0422); living culture, KUMCC 15–0396.

Notes – *Dictyocheirospora garethjonesii* is morphologically similar to *D. rotunda* and *D. aquatica*. However, *D. garethjonesii* differs from *D. rotunda* in having conidia with 6–7 rows with each row composed of 7–10 cells, whereas the conidia of *D. rotunda* have 5–7 rows with each row composed of 8–12 cells (Boonmee et al. 2016). *Dictyocheirospora garethjonesii* differs from *D. aquatica* in having larger conidia (45.5–54.5 × 15.5–24.5 µm vs 34–42 × 12.5–19.5 µm) and conidia with 6–7 rows and each row composed of 7–10 cells, whereas the conidia of *D. aquatica* have 5–6 rows and each row composed of 6–8 cells (Table 2). Phylogenetic analysis also showed that *D. garethjonesii* is distinct from *D. subramanianii* (Fig. 1).

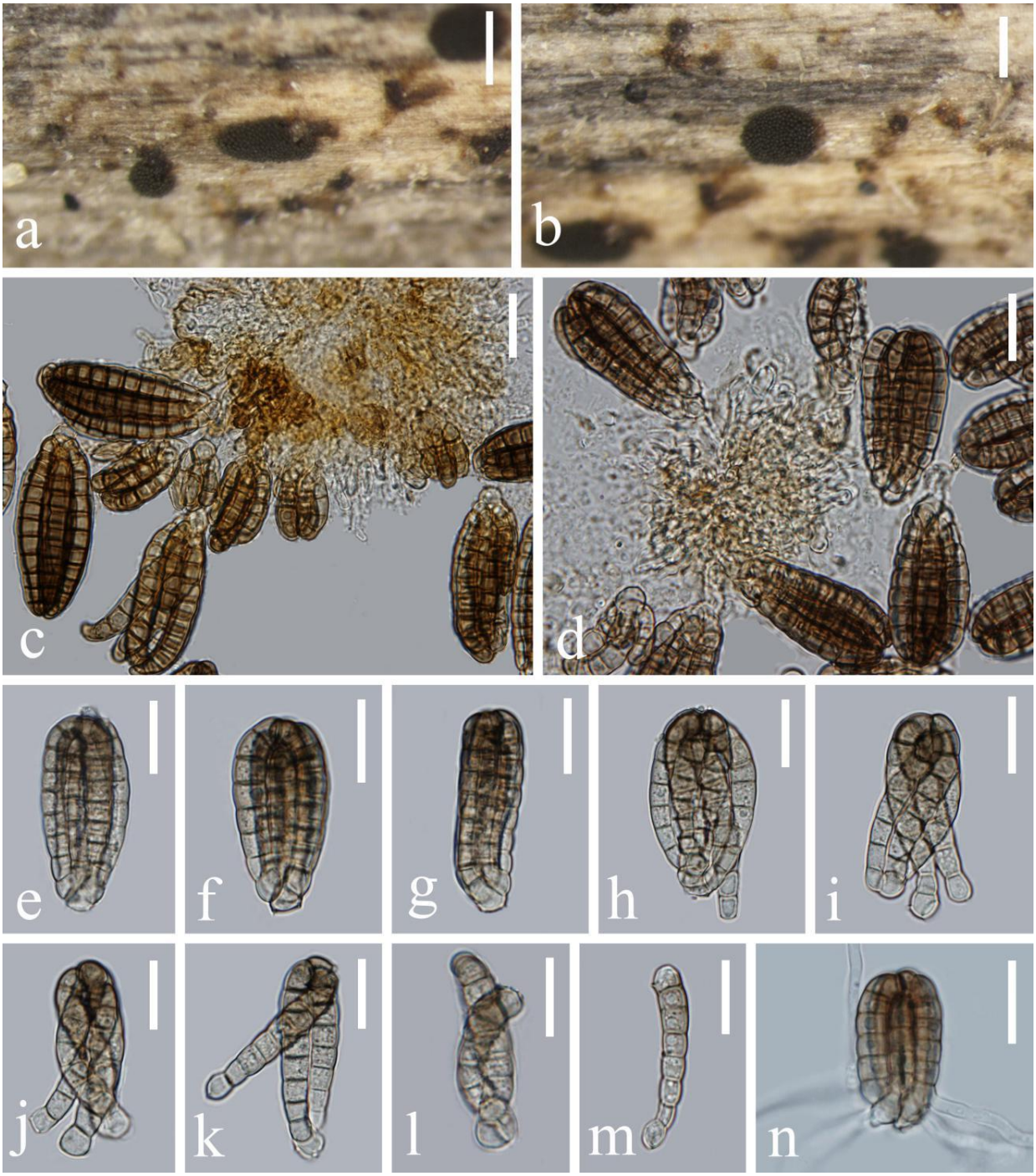

Fig. 2 – ***Dictyocheirospora aquatica*** (HKAS 92714, **holotype**) **a–b** Conidiomata on the substrate. **c–d** Squash mount of conidioma with conidiogenous cells. **e–g** Conidia. **h–m** Separable rows. **n** Germinating conidium. – **Scale bars**: **a–b** = 200 µm, **c–d** = 20 µm, **e–n** = 10 µm.

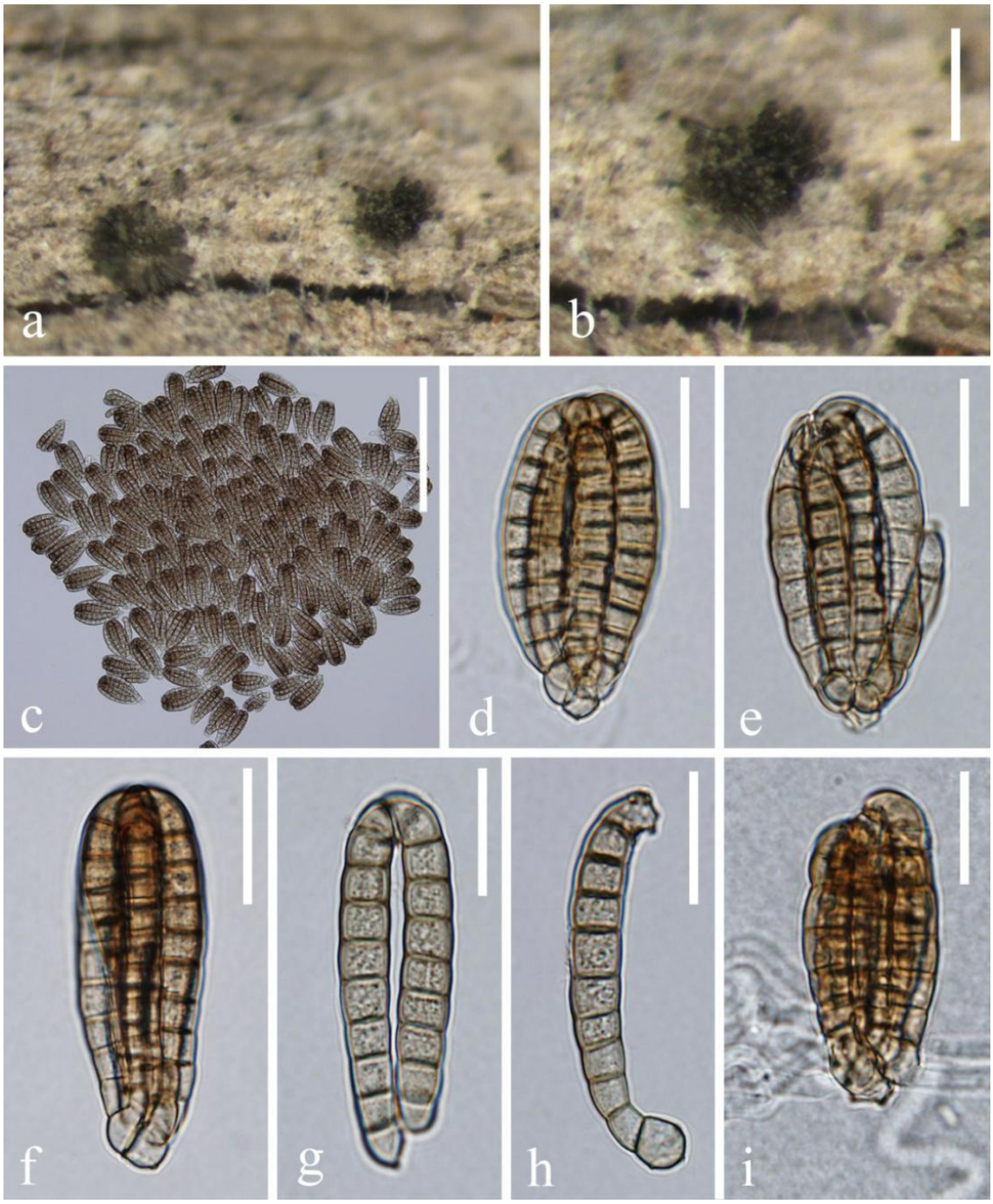

Fig. 3 – *Dictyocheirospora garethjonesii* (HKAS 92836, **holotype) a–b** Colonies on the substrate. **c** Squash mount of conidia. **d–f** Conidia. **g–h** Crushed conidia. **i** Germinating conidium. **– Scale bars**: **b** = 250 μm, **c** = 150 μm, **d–i** = 20 μm.

Dictyocheirospora rotunda D'Souza, D.J. Bhat & K.D. Hyde, Fungal Diversity 80: 465

Facesoffungi number: FoF 01262; Fig. 4

Saprobic on decaying, submerged wood in freshwater. ***Sexual morph***: Undetermined. ***Asexual morph***: Hyphomycetous. Colonies on natural substrate scattered. *Mycelium* immersed, composed of brown, smooth, septate hyphae. *Conidiomata* sporodochial, dark brown to black, 150–250 μm. *Conidiophores* micronematous, pale brown, smooth. *Conidiogenous cells* holoblastic, integrated, terminal, pale brown, cylindrical, smooth-walled. *Conidia* 49–55 × 19.5–22.5 μm ($\bar{x}$ = 52 × 21 μm, n = 35), solitary, acrogenous, cheiroid, pale brown to brown, consisting of 5–7 rows of cells, rows digitate, cylindrical, inwardly curved at the tip, arising from a basal cell, without

appendages, with each row composed of 8–12 cells, euseptate, guttulate, slightly constricted at septa.

Material examined – CHINA, Yunnan Province, Jinsha River, on submerged wood, 19 April 2015, Z.L. Luo, JSJ H 11–7–1 (HKAS 92883), living culture, DLUCC 0576; *ibid.* 21 April 2015, Q Dai, JSJ H 35–1–1 (HKAS 92994), living culture, DLUCC 0577.

Notes – *Dictyocheirospora rotunda*, the type species of *Dictyocheirospora*, was introduced by Boonmee et al. (2016). Two new collections were from submerged wood in Jinsha River, during our study of lignicolous freshwater fungi of three parallel rivers in northwestern Yunnan Province, China. Morphologically our fresh collections fit perfectly well with the description of *Dictyocheirospora rotunda* (Boonmee et al. 2016). The phylogenetic analyses of our strains (DLUCC 0576 and DLUCC 0577) clustered with *D. rotunda* with high bootstrap support (100% ML, 100% MP and 1.00 PP).

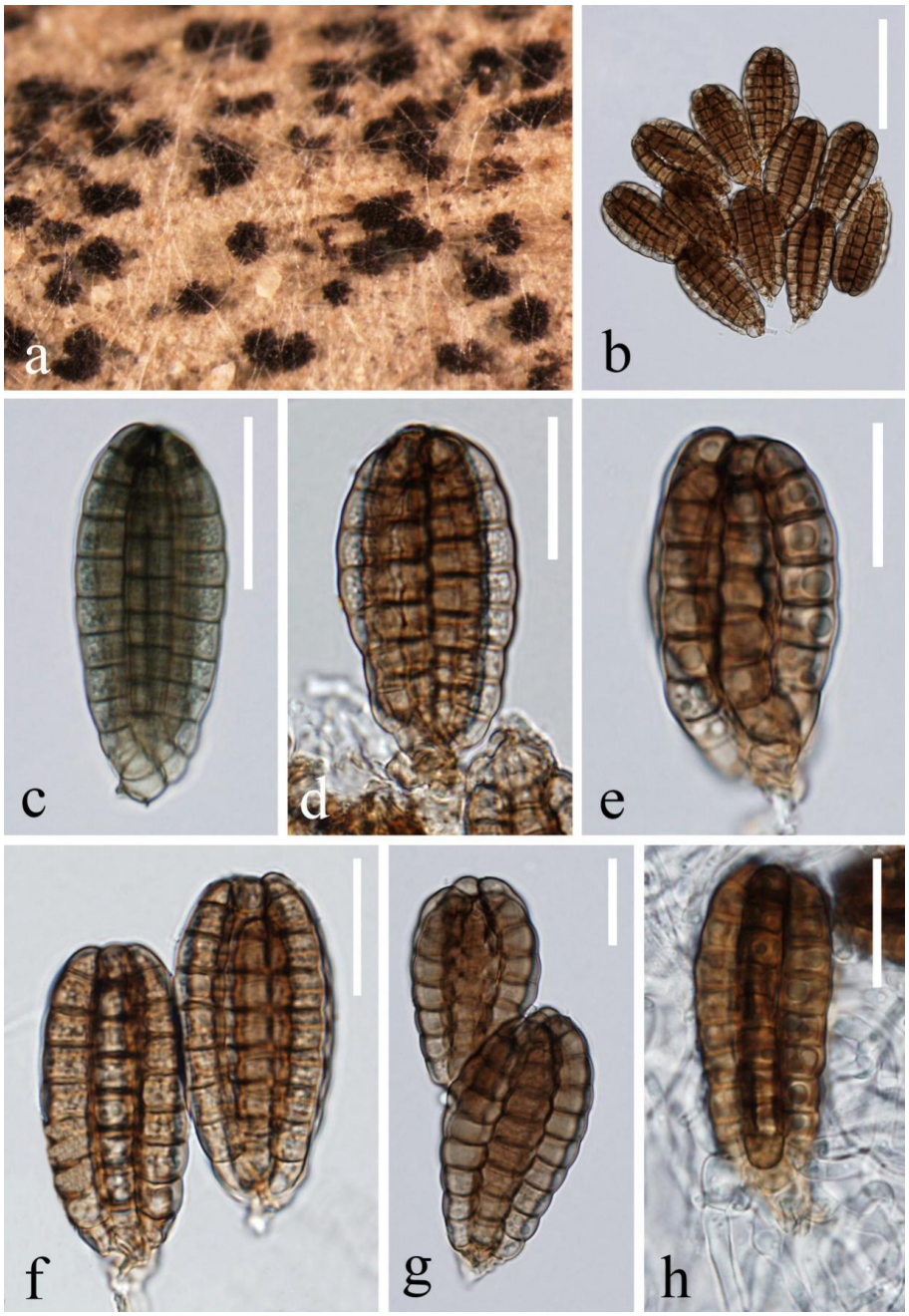

Fig. 4 – ***Dictyocheirospora rotunda*** (HKAS 92883) **a** Conidiomata on the substrate. **b** Squash mount of conidioma. **c–g** Conidia. **h** Germinating conidium. – **Scale bars**: **b** = 50 μm; **c–h** = 20 μm.

Table 2. A synopsis of characters of *Dictyocheirospora* species

Species	Colonies	Conidia				Substrate	Reference
		Size (μm)	Shape	No. of rows	No. of cells with each row		
Dictyocheirospora aquatica	Sporodochial	34–42 × 12.5–19.5	Cylindrical	5–6	6–8	Submerged decaying wood	This study
D. bannica	Punctiform	73–86 × 21–26	Ellipsoid to cylindrical	(5–) 7	17–19	Submerged twigs of woody plant	Boonmee et al. 2016
D. garethjonesii	Sporodochial	45.5–54.5 × 15.5–24.5	Cylindrical	6–7	7–10	Submerged decaying wood	This study
D. gigantica	Sporodochial	105–121 × 25–32	Cylindrical	7	19–22	Submerged decaying wood	Goh et al. 1999
D. heptaspora	Sporodochial	50–80 × 20–30	Cylindrical	7	No available	Palm and submerged wood	Goh et al. 1999
D. rotunda	Sporodochial	42–58 × 19–38	Cylindrical	5–7	8–12	Submerged decaying wood	Tanaka et al. 2015
D. rotunda	Sporodochial	49–55 × 19.5–22.5	Cylindrical	5–7	8–12	Submerged decaying wood	This study
D. pseudomusae	Sporodochial	61–78 × 19–29	Ellipsoid to cylindrical	(6–) 7	13–15	Submerged dead twigs of Bamboo	Tanaka et al. 2015
D. subramanianii	Sporodochial	33–42 × 16–20	Cylindrical	7	9–13	Palm	Sutton 1985
D. vinaya	Sporodochial	58–67 × 15.5–26.5	Cheiroid	6–7	9–13	Submerged decaying wood	Boonmee et al. 2016

Discussion

Freshwater taxa forming on the surface of wood, with multicellular, cheiroidconidia produced in sporodochia, were previously placed in the genus *Dictyosporium*. This fungal form is common in freshwater streams and swamps worldwide (Pinruan et al. 2007, Tsui et al. 2000, Ho et al. 2001, 2002). Boonmee et al. (2016), however revised the genus based on morphology and molecular analysis and accepted ten genera in Dictyosporiaceae. *Dictyocheirospora* is cosmopolitan in distribution and largely reported from freshwater habitats in Asia, Europe and Africa (Ellis 1971, Morris 1978, Mercado-Sierra 1981, Rao & de Hoog 1986, Matsushima 1993, Goh et al. 1999, Boonmee et al. 2016). The fresh collections used in this study are from submerged wood in freshwater lotic habitats in northwestern Yunnan Province, China.

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References

Ariyawansa HA, Phukhamsakda C, Thambugala KM, Bulgakov TS et al. 2015 – Revision and phylogeny of Leptosphaeriaceae. Fungal Diversity 74, 1–33.

Boonmee S, D'souza MJ, Luo ZL, Pinruan U et al. 2016 – Dictyosporiaceae fam. nov. Fungal Diversity 80, 457–482.

Cai L, Jeewon R, Hyde KD. 2006 − Phylogenetic investigations of Sordariaceae based on multiple gene sequences and morphology. Mycological Research 110, 137–150.

Chomnunti P, Hongsanan S, Aguirre-Hudson B, Tian Q et al. 2014 – The sooty moulds. Fungal Diversity 66, 1−36.

Ellis MB 1971 − Dematiaceous hyphomycetes. Commonwealth Mycological Institute, Kew.

Goh TK, Hyde KD, Ho WH, Yanna. 1999 − A revision of the genus *Dictyosporium*, with descriptions of three new species. Fungal Diversity 2, 65–100.

Hillis DM, Bull JJ. 1993 − An empirical test of bootstrapping as a method for assessing confidence in phylogenetic analysis. Systematic Biology 42, 182.

Ho WH, Hyde KD, Hodgkiss IJ, Yanna. 2001 − Fungal communities on submerged wood from streams in Brunei, Hong Kong and Malaysia. Mycological Research 105, 1492–1501.

Ho WH, Yanna, Hyde KD, Hodgkiss IJ. 2002 − Seasonality and sequential occurrence of fungi on wood submerged in Tai Po Kau Forest Stream, Hong Kong. Fungal Diversity 10, 21–43.

Hyde KD, Jones EBG, Liu JK, Ariyawansa H et al. 2013 – Families of Dothideomycetes. Fungal Diversity 63, 1–313.

Hyde KD, Hongsanan S, Jeewon R, Bhat DJ et al. 2016a – Fungal diversity notes 367–492: taxonomic and phylogenetic contributions to fungal taxa. Fungal Diversity 80, 1–270.

Hyde KD, Fryar S, Tian Q, Bahkali AH, Xu JC. 2016b – Lignicolous freshwater fungi along a north-south latitudinal gradient in the Asian/Australian region; can we predict the affects of global warming on biodiversity and function? Fungal Ecology 19, 190–200.

Jayasiri SC, Hyde KD, Ariyawansa HA, Bhat DJ et al. 2015 – The Faces of Fungi database: fungal names linked with morphology, phylogeny and human impacts. Fungal Diversity 74, 3–18.

Katoh K, Standley DM 2013 − MAFFT multiple sequence alignment software version 7: improvements in performance and usability. Molecular Biology & Evolution 30, 772–780.

Liu JK, Phookamsak R, Doilom M, Wikee S et al. 2012 − Towards a natural classification of Botryosphaeriales. Fungal Diversity 57, 149–210

Luo ZL, Bao DF, Bhat DJ, Yang J et al. 2016 – *Sporoschisma* from submerged wood in Yunnan, China. Mycological Progress 15, 1145–1155.
Matsushima T. 1993 − Matsushima Mycological Memoirs 7. Matsushima: Kobe, Japan. Mercado
Sierra A. 1981 − Lista preliminar de hifomicetes demaci, keos de la Estacion Eco1ogica de Sierra del Rosarioy zonas adyacentes. Acta Botanica Cubana 6, 1–6.
Morris EP. 1978 − Belizean hyphomycetes. Mycotaxon 7, 265–274.
Nylander JAA. 2004 − MrModeltest v2.2 Program distributed by the author. Evolutionary Biology Centre, Uppsala University, Uppsala
Page RD 1996 − TREEVIEW: an application to display phylogenetic trees on personal computers. Computer Applications in the Biosciences 12, 357–358.
Rannala B, Yang Z. 1996 − Probability distribution of molecular evolutionary trees: a new method of phylogenetic inference. Journal of Molecular Evolution 43, 304–311.
Rao V, Hoog GS de 1986 − New or critical hyphomycetes from India. Studies in Mycology 28, 1–84.
Ronquist F, Huelsenbeck JP. 2003 − MrBayes 3: Bayesian phylogenetic inference under mixed models. Bioinformatics 19, 1572.
Silvestro D, Michalak I. 2011 − RAxML-GUI: a graphical front-end for RAxML. Organisms Diversity & Evolution 12, 335–337.
Sutton BC 1985 − Notes on some deuteromycete genera with cheiroid or digitate brown conidia. Proceedings of the National Academy of Sciences, India Section B 94, 229–244.
Swofford DL. 2002 − PAUP 4.0b10: phylogenetic analysis using parsimony. Sinauer Associates, Sunderland.
Tanaka K, Hirayama K, Yonezawa H, Sato G, Toriyabe A, Kudo H, Hashimoto A, Matsumura M, Harada Y, Kurihara Y, Shirouzu T, Hosoya T. 2015 – Revision of the Massarineae (Pleosporales, Dothideomycetes). Studies in Mycology 82, 75–136.
Taylor JE, Hyde KD. 2003 – Microfungi on Tropical and Temperate Palms. In: Fungal Diversity Research Series 12, 1–459.
Tsui CKM, Hyde KD, Hodgkiss IJ. 2000 – Biodiversity of fungi on submerged wood in Hong Kong streams. Aquatic Microbial Ecology 21, 289–298.
Zhang Y, Schoch CL, Fournier J, Crous PW et al. 2009 – Multi-locus phylogeny of Pleosporales: a taxonomic, ecological and evolutionary re-evaluation. Studies in Mycology 64, 85–102.
Zhang Y, Crous PW, Schoch CL, Hyde KD. 2012 – Pleosporales. Fungal Diversity 53, 1–221.