



Dendryphiella fasciculata sp. nov. and notes on other *Dendryphiella* species

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Abstract

Dendryphiella is an asexual morph genus placed in the family Dictyosporiaceae. During our study on brown-spored hyphomycetes, a new taxon *D. fasciculata* was found on decaying wood collected in Chiang Mai Province, Thailand. The new species is characterized by mononematous, fasciculate conidiophores with polytretic, terminal and intercalary conidiogenous cells. Conidia are fusiform to ellipsoidal, pale brown and aseptate when young, becoming brown or dark brown, verrucose and 3-septate when mature. The phylogenetic analysis of combined ITS and LSU sequence data showed that isolates of *Dendryphiella* form a well-supported clade in Dictyosporiaceae, and *Dendryphiella fasciculata* is phylogenetically distinct from other species. *Dendryphiella fasciculata* is therefore introduced here with a description and morphological illustrations. Taxonomic notes and a key to *Dendryphiella* species are provided.

Key words – asexual morph – Dictyosporiaceae – Phylogeny – Pleosporales

Introduction

The family Dictyosporiaceae was first mentioned in Liu et al. (2015) and Boonmee et al. (2016) validly introduced the family based on type genus, *Dictyosporium* Corda. The asexual morph genera in Dictyosporiaceae are characterized by sporodochial, punctiform or effuse colonies, mononematous, hyaline to brown conidiophores, with reduced to standard and blastic or tretic conidiogenous cells, and cheiroid or fusiform conidia with or without appendages (Goh et al. 1999, Cai et al. 2002, Liu et al. 2015, Boonmee et al. 2016). Some genera have been linked to their sexual morphs, such as *Dictyosporium* and *Pseudocoleophoma* Kaz. Tanaka & K. Hiray (Liu et al. 2015, Tanaka et al. 2015).

The genus *Dendryphiella* was established by Ranojevic (1914) with the type species *D. interseminata* (Berk. & Ravenel) Bubák. The genus is characterized by macronematous conidiophores with polytretic, integrated conidiogenous cells at the swollen tip and at intercalary

swellings and catenate or solitary conidia (Ellis 1971, Matsushima 1971, Rai & Kamal 1986, Guo & Zhang 1999, Crous et al. 2014, 2016). Reisinger (1968) introduced *D. vinosa* (Berk. & Curt.) Reisinger and Matsushima (1971) synonymized *D. interseminata* under this species based on morphology. Hughes (1953) treated *Dendryphiella* as a synonym of *Dendryphion* Wallr. as he considered that the looser and longer branched conidiophores are not sufficient characters for keeping this genus as distinct. Nicot (1958) described a new species, *Dendryphiella arenaria* Nicot and re-established *Dendryphiella* as a distinct genus. Ellis (1971) agreed with this viewpoint. Currently no *Dendryphiella* species have been linked with their sexual morphs (Wijayawardene et al. 2012).

Two marine species, *Dendryphiella arenaria* and *D. salina* (G.K. Sutherl.) Pugh & Nicot were described as conspicuous, cosmopolitan dematiaceous hyphomycete taxa which commonly occur in sea-water foam and marine sediments, as well as on macro-algae and decaying plant debris (Kohlmeyer 1966, Kirk 1983, Jones et al. 2015). Ellis (1976) transferred *Dendryphiella* to the genus *Scolecobasidium* Abbott apparently based on the character of polyblastic, denticulate, conidiogenous cells that appear as denticles when the conidia become detached (Ellis 1976). However, subsequent mycologists (Kohlmeyer & Kohlmeyer 1979, Jones et al. 2008) did not observe this distinct morphology in this genus. Woudenberg et al (2013) provided a phylogenetic analysis based on SSU, LSU and RPB2 sequence data. In their study, *Dendryphiella salina* was equated with *Embellisia annulata* de Hoog, Seigle-Mur., Steiman & K.-E. Erikss. Moreover, *Dendryphiella arenaria* and *D. salina* formed a well-supported clade in Pleosporaceae, while the type species *D. vinosa* was placed in the family Dictyosporiaceae (Woudenberg et al. 2013, Boonmee et al. 2016). Thus, a new genus *Paradendryphiella* Woudenb. & Crous, typified by *P. salina* (G.K. Sutherl.) Woudenb. & Crous, was established to accommodate these two species (Woudenberg et al. 2013, Jones et al. 2015). Another two species, *D. eucalyptorum* Crous & E. Rubio and *D. paravinosa* Crous & Guarnaccia were introduced based on distinct morphology and phylogenetic evidence in the recent studies (Crous et al. 2014, Crous et al. 2016). In this study, eleven species are compiled in this genus.

During ongoing surveys of brown-spored hyphomycetes, a new species of *Dendryphiella* was collected. Detailed morphological study and molecular analysis of combined ITS and LSU sequence data indicated that *Dendryphiella fasciculata* was a phylogenetically distinct species and clustered together with three other *Dendryphiella* species. All reside in Dictyosporiaceae. In this study, we introduce a new species and provide notes on *Dendryphiella* species with an updated taxonomic key.

Materials & Methods

Collections and examination of specimens

Specimens of decaying woody litter were collected from Chiang Mai Province, Thailand in September 2016 and taken to the laboratory in Ziplock plastic bags. The samples were incubated in plastic boxes with sterile and moist tissue at 25–30 °C for 3 days. The samples were examined following the methods described in Phookamsak et al. (2014) under a Motic SMZ 168 Series dissecting microscope. The morphological characters were studied with the fruiting bodies mounted in a drop of water and photographed by a Nikon ECLIPSE 80i compound microscope fitted with a Cannon 600D digital camera. Measurements were performed using the Tarosoft (R) Image Frame Work software and photo plate was made using Adobe Photoshop CS3 software (Adobe Systems, USA).

Fungal isolation was performed using the single spore isolation method described in Chomnunti et al. (2014). Specimens are deposited in the herbarium of Mae Fah Luang University (MFLU), Chiang Rai, Thailand and the herbarium of Cryptogams Kunming Institute of Botany Academia Sinica (HKAS), Kunming, China. Pure cultures are deposited in the Mae Fah Luang University Culture Collection (MFLUCC), Chiang Rai, Thailand. Faces of fungi (FOF) numbers and Index Fungorum numbers are acquired as in Jayasiri et al. (2015) and Index Fungorum (2017).

DNA extraction, PCR amplification and sequencing

Fresh mycelia were scraped from the pure cultures growing on PDA after one month at 25 °C. DNA was extracted using DNA Extraction Kit (Sangon Biotech) from fresh fungal mycelia. Two gene fragments, internal transcribed spacer (ITS) and large subunit rDNA (28S, LSU), were amplified by the primer pairs ITS5 and ITS4 (White et al. 1990), and LROR and LR5 (Vilgalys & Hester 1990) respectively. Polymerase chain reaction (PCR) was carried out in 25 µl reaction volume containing 12.5 µl 2 × PCR Master Mix (TIANGEN Co., China), 9.5 µl ddH₂O, 1 µl of each primer and 1 µl DNA template. The amplification condition for both ITS and LSU regions followed Yang et al. (2015) The PCR products are examined using 1% agarose electrophoresis gel stained with ethidium bromide. Purified PCR products were sequenced by commercial company Invitrogen Biotechnology Co., Ltd (Shanghai, P. R. China).

Phylogenetic analysis

Related strains in Dictyosporiaceae for phylogenetic analyses listed in Table 1 were obtained using the Blast process at NCBI (National Center for Biotechnology Information) and from recent relevant publications (Jones et al. 2008, Crous et al. 2014, Boonmee et al. 2016, Crous et al. 2016, Wang et al. 2016). Sequences were aligned using online MAFFT version 7 (Kato & Standley 2013). Single gene analyses were performed and trees were used to check the conflict of these two gene regions, and then two genes were combined using BioEdit (Hall 1999). The alignments were checked visually and optimized manually using AliView (Larsson 2014) and BioEdit (Hall 1999) where necessary.

Table 1 DNA sequences used for the phylogenetic tree (newly generated sequences are indicated in bold, ex-type strains are indicated in * after collection number)

Species name	Strain number	GenBank Accession Numbers	
		ITS	LSU
<i>Aquaticheirospora lignicola</i>	RK 2006a*	AY864770	AY736378
<i>Dendryphiella eucalyptorum</i>	CPC 22927*	KJ869139	KJ869196
<i>Dendryphiella paravinosa</i>	CPC 26176*	KX228257	KX228309
<i>Dendryphiella vinosa</i>			EU848590
<i>Dendryphiella fasciculata</i>	MFLUCC 17-1074	MF399213	MF399214
<i>Dictyocheirospora aquatica</i>	KUMCC 15-0305*	KY320508	KY320513
<i>Dictyocheirospora bannica</i>	KH 332*	LC014543	AB807513
<i>Dictyocheirospora garethjonesii</i>	MFLUCC 16-0909*	KY320509	KY320514
<i>Dictyocheirospora pseudomusae</i>	KH 412	LC014549	AB807516
<i>Dictyocheirospora pseudomusae</i>	yone 234*	LC014550	AB807520
<i>Dictyocheirospora rotunda</i>	MFLUCC 14-0293*	KU179099	KU179100
<i>Dictyosporium alatum</i>	ATCC34953*	NR077171	DQ018101
<i>Dictyosporium elegans</i>	NBRC 32502*	DQ018087	DQ018100
<i>Dictyosporium meiosporum</i>	MFLUCC 10-0131*	KP710944	KP710945
<i>Dictyosporium olivaceosporum</i>	KH 375*	LC014542	AB807514
<i>Dictyosporium sexualis</i>	MFLUCC 10-0127*	KU179105	KU179106
<i>Dictyosporium stellatum</i>	CCFC 241241*	JF951154	JF951177
<i>Dictyosporium thailandicum</i>	MFLUCC 13-0773*	KP716706	KP716707
<i>Digitodesmium bambusicola</i>	CBS 110279*	DQ018091	DQ018103
<i>Gregarithecium curvisporum</i>	KT 922*	AB809644	AB807547

<i>Jalapriya inflata</i>	NTOU 3855	JQ267362	JQ267363
<i>Jalapriya pulchra</i>	MFLUCC 15–0348*	KU179108	KU179109
<i>Jalapriya toruloides</i>	CBS 209.65	DQ018093	DQ018104
<i>Paradendryphiella arenariae</i>	CBS 181.58*	KF156010	KC793338
<i>Paradendryphiella salina</i>	CBS 142.60	DQ411540	KC793339
<i>Pseudocoleophoma calamagrostidis</i>	KT 3284*	LC014592	LC014609
<i>Pseudocoleophoma polygonicola</i>	KT 731*	AB809634	AB807546
<i>Pseudocoleophoma typhicola</i>	MFLUCC 16–0123*	KX576655	KX576656
<i>Pseudodictyosporium elegans</i>	CBS 688.93*	DQ018099	DQ018106
<i>Pseudodictyosporium wauense</i>	NBRC 30078	DQ018098	DQ018105

Maximum likelihood analysis was performed using CIPRES web portal (Miller et al. 2010) using RAxML-HPC BlackBox tool and the default GTRGAMMA + I model. The tree search included 1000 non-parametric bootstrap replicates and the best scoring tree was selected from suboptimal trees under the GTRGAMMA + I substitution model. The resulting replicates were plotted on to the best scoring tree obtained previously.

Maximum parsimony analysis was performed with the heuristic search in PAUP v. 4.0b10 (Swofford 2002). Gaps in the alignment were treated as missing characters and all characters were unordered. 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 carried out using MrBayes 3.2 (Ronquist et al. 2012). The best-fit evolutionary model was selected using MrModeltest 2.2 (Nylander 2004). Posterior probabilities (PP) (Rannala & Yang 1996) were performed by Markov Chain Monte Carlo sampling (MCMC) in MrBayes v. 3.0b4. Bayesian analyses of six simultaneous Markov chains were run for 1000000 generations and trees were sampled every 100th generation (resulting in 10000 total trees). The first 1000 trees, representing the burn-in phase of the analyses, were discarded and the remaining 9000 trees were used for calculating posterior probabilities (PP) in the majority rule consensus tree.

Trees were visualized with FigTree v1.4.2 (Page 1996) and the layout was edited using Adobe Illustrator CS5.

Results

Phylogenetic analyses

The alignment of combined ITS and LSU sequence data comprised a total of 1887 characters with gaps (590 for ITS, 1297 for LSU). The dataset composed 30 strains including one newly sequenced taxon and two outgroups, *Paradendryphiella arenariae* and *P. salina* (Pleosporaceae). In order to compare the topology of the tree and clade stability, single gene phylogenetic analyses were performed and yielded two trees. The tree topologies are similar between these two trees. Maximum likelihood, maximum parsimony and Bayesian analyses on combined data were performed separately. Tree topologies of these three analyses are similar. The best scoring RAxML tree with a final likelihood value of -8310.242789 is presented in Fig. 1. The matrix had 525 distinct alignment patterns with 23.61% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.244589, C = 0.231709, G = 0.277241, T = 0.246462; substitution rates AC = 1.531992, AG = 2.291657, AT = 2.224229, CG = 0.335383, CT = 6.072279, GT = 1.000000; gamma distribution shape parameter α = 0.145768. Maximum parsimony analysis had 343 parsimony informative, 1463 constant, 81 parsimony uninformative characters and yielded 6 most parsimonious trees (CI = 0.555, RI = 0.701, RC = 0.390, HI = 0.445).

The phylogenetic analyses generated by maximum likelihood (ML), maximum parsimony (MP), and Bayesian analysis indicate that *Dendryphiella fasciculata* is placed within the genus

Dendryphiella with high support (97%/89%/1.00, respectively). The 30 taxa represented nine genera of Dictyosporiaceae with two outgroups. The genus *Dendryphiella* showed a close phylogenetic relationship with *Pseudocoleophoma*. The isolate of *Dendryphiella fasciculata* clustered together with other three of *Dendryphiella* species. Additionally, *Dendryphiella fasciculata* formed a distinct lineage and was sister to strain of *D. paravinosa*.

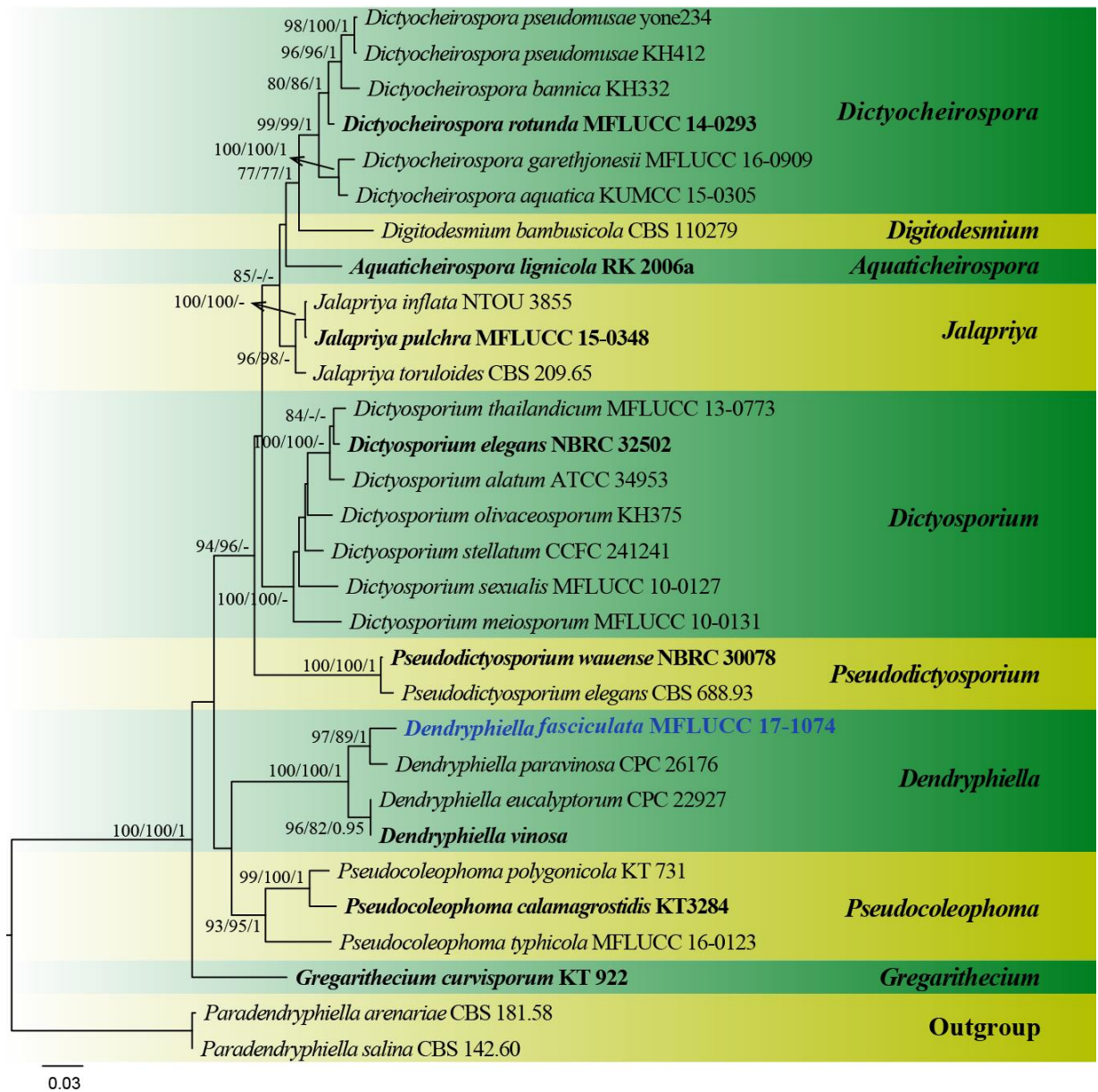


Figure 1 Maximum likelihood (RAxML) tree based on analysis of a combined dataset of ITS and LSU sequence data representing Dictyosporiaceae. Bootstrap support values for ML and MP greater than 75% and Bayesian posterior probabilities greater than 0.95 are given near nodes respectively. The tree is rooted with *Paradendryphiella arenariae* and *Paradendryphiella salina*. The genetic types are indicated in bold and the new isolate is in bold and blue.

Taxonomy

Dendryphiella fasciculata N.G. Liu, Z.Y. Liu & K.D. Hyde, sp. nov.

Index Fungorum number: IF553596; Facesoffungi number: FoF03525

Etymology – Name reflects the fasciculate conidiophores.

Fig. 2

Holotype – MFLU 17-0748

Saprobic on decaying wood. **Asexual morph** Colonies on natural substrate superficial, effuse, greyish brown. *Mycelium* partly immersed, composed of septate, branched, brown, guttulate, 1.5–2.5 μm wide hyphae. *Conidiophores* 170–250 μm long, macronematous, mononematous, fasciculate, dark brown at base, slightly paler towards the apex, thick-walled, erect, straight or slightly flexuous, verruculose, septate, unbranched or occasionally branched, wider at the sub-section. *Conidiogenous cells* 17–33 μm long (\bar{x} = 23.86 μm , n = 22), polytretic, terminal, later becoming subterminal, proliferating asymmetrically, integrated, brown, verrucose, enlarged at vertex. *Conidia* 15–30 \times 4.3–7.4 μm (\bar{x} = 22.38 \times 5.54 μm , n = 25), solitary to catenate, when

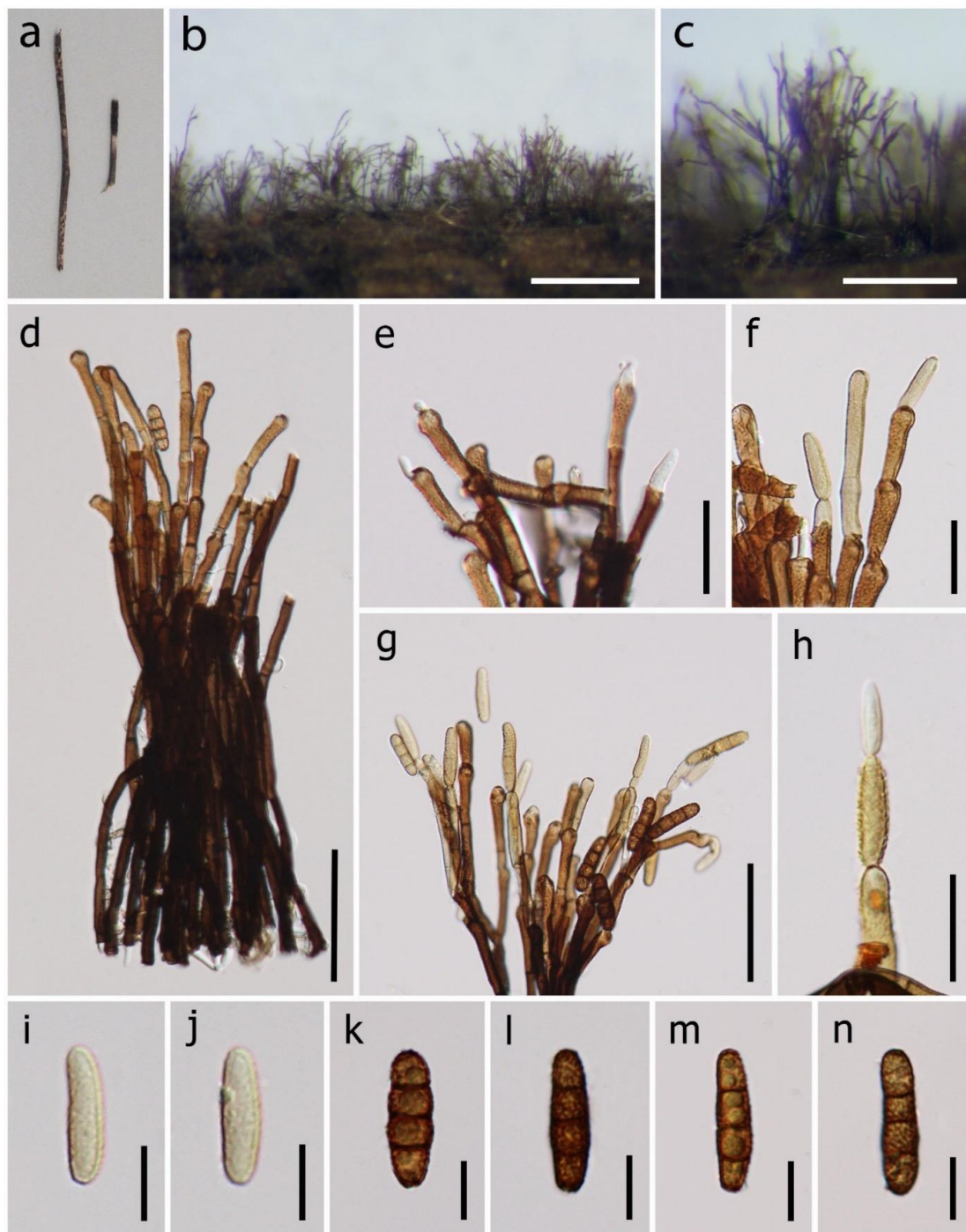


Figure 2 *Dendryphiella fasciculata* (MFLU 17-0748, **holotype**). a Specimens. b, c Colonies on substrate. d Conidiophores. e–g Conidiogenous cells and conidia. h–n Conidia. Scale bars: b = 400 μm , c = 200 μm , d = 50 μm , e = 25 μm , f, h = 20 μm , g = 50 μm , i–n = 10 μm .

catenate in acropetal chain, fusiform to ellipsoidal, rounded at apex, truncate at base, pale brown, aseptate when young, brown or dark brown, 3-septate when mature, slightly constricted at septa, thick-walled, verrucose. **Sexual morph:** Unknown.

Culture characters – Conidia germinated on WA (Water Agar) within 24 hours. One or two germ tubes produced from both ends. Colonies reached about 5 cm diameter after 1 week on PDA at 25 °C. Mycelia are superficial, with entire edge, floccose at the center, white to light brown from above and light brown from below.

Material examined – Thailand, Chiang Mai Province, on decaying wood, 27 September 2016, Chuangen Lin, Lin 03-1 (MFLU 17-0748, **holotype**; HKAS 99519, **isotype**) – ex-type living culture MFLUCC 17-1074

Notes – *Dendryphiella fasciculata* resembles *D. aspera*, *D. broussonetiae*, and *D. lycopersicifolia* in having fasciculate conidiophores. However, *D. aspera* occasionally has fasciculate conidiophores and *D. fasciculata* differs from *D. broussonetiae* and *D. lycopersicifolia* in having 3-septate conidia when mature, while the latter two are mostly 1-septate and 0–1–3-septate respectively. *Dendryphiella fasciculata* has brown conidia, while those of *D. broussonetiae* and *D. lycopersicifolia* are olivaceous. Moreover, *D. lycopersicifolia* has larger conidiophores and conidia than those of *D. fasciculata* (up to 500 vs up to 250 µm and 12–58 × 4–8 vs 15–30 × 4.3–7.4 µm). Phylogenetic analysis showed that *D. fasciculata* is phylogenetically distinct from other *Dendryphiella* species.

Notes on currently accepted species of *Dendryphiella*

1. *Dendryphiella aspera* R.W. Barreto & J.C. David, Mycological Research 99 (7): 770 1995.

Description and illustrations – See Barreto et al. (1995)

Notes – *Dendryphiella aspera* was introduced by Barreto et al. (1995) on *Lantana camara* in Brazil. This species has rough-walled conidiophores which are distinct from other species. See note on *D. dregeae*. Type material of this species is IMI 345366.

2. *Dendryphiella broussonetiae* Y.L. Guo & Z.Y. Zhang, Mycosystema 18 (3): 236 1999.

Description and illustrations – See Guo & Zhang (1999)

Notes – This species was reported on *Broussonetia papyrifera* (Moraceae) by Guo & Zhang (1999). The conidiophores in *D. broussonetiae* are similar to those of *D. lycopersicifolia* and *D. fasciculata*, but conidia are mostly 1-septate, which in *D. lycopersicifolia* they are 0–1–3-septate and in *D. fasciculata* aseptate when young and 3-septate when mature. Type material of this species is MHYAU 03898.

3. *Dendryphiella dregeae* A.N. Rai & Kamal, Kavaka 14 (1–2): 31 1987.

Description and illustrations – See Rai & Kamal (1986)

Notes – Rai & Kamal (1986) reported this taxon on living leaves of *Dregea volubilis* (Asclepiadaceae). The conidia of *D. dregeae* share similar characters with *D. aspera*, but are distinct in conidial colour. Moreover basal cells of conidiophores in *D. dregeae* are peltate to irregularly lobed. Type material of this species is IMI 254686.

4. *Dendryphiella eucalypti* Matsush., Matsushima Mycological Memoirs 3: 9 1983.

Description and illustrations – See Matsushima (1983)

Notes – Matsushima (1983) introduced *Dendryphiella eucalypti* from leaf litter of *Eucalypti* sp. in Taiwan. *Dendryphiella eucalypti* and *D. infuscans* have pale brown conidia which distinctly differ in size. *Dendryphiella eucalypti* is (15–)17.5–25(–30) × (4–)4.5–6 µm and the latter is smaller and 9–16 × 4–7 µm. Moreover, *D. eucalypti* has mostly 3-septate conidia, while *D. infuscans* has 0–2-septate conidia. Type material of this species is MFC-6685.

5. *Dendryphiella eucalyptorum* Crous & E. Rubio, Persoonia 32: 231 2014.

Description and illustrations – See Crous et al. (2014)

Notes – Crous et al. (2014) introduced *D. eucalyptorum* on small branches of *Eucalyptus globulus* (Myrtaceae). *Dendryphiella eucalyptorum* and *D. paravinosa* share similar characters of conidiophores in being branched above and below and both conidiophores are verruculose. However, *D. eucalyptorum* has longer conidiophores than *D. paravinosa* (up to 500 vs up to 150 µm). Type material of this species is CBS H-21699.

6. *Dendryphiella indica* V. Rao & Naranja, Current Science 43 (16): 525 1974.

Description and illustrations – See Rao & Naranja (1974)

Notes – Rao & Naranja (1974) reported this taxon on dead leaves of *Aloe* spp. Conidia of *D. indica* are morphologically similar to those of type species *D. vinosa*, but differs in conidiophores. Conidiophores of *D. indica* are branched, while the type species are simple or branched. Type collection of this species is in Herb. V.V.C.B.L. No. 1301.

7. *Dendryphiella infuscans* (Thüm.) M.B. Ellis, Dematiaceous Hyphomycetes: 500 1971.

= *Cladosporium infuscans* Thüm., Revue mycol., 1: 59 1879.

Description and illustrations – See Ellis (1971)

Notes – see note on *D. eucalypti*.

8. *Dendryphiella lycopersicifolia* Bat. & Peres, Memórias da Sociedade Broteriana 14: 83 1961.

Description and illustrations – See Batista & Peres (1961)

Notes – see notes on *D. fasciculata* and *D. broussonetiae*. Type material of this species is IMUR 17333

9. *Dendryphiella paravinosa* Crous & Guarnaccia, Persoonia 36: 337 2016.

Description and illustrations – See Crous et al. (2016)

Notes – Crous et al. (2016) introduced this species on leaves of *Citrus sinensis* (Rutaceae). See note on *D. eucalyptorum*. Type material of this species is CBS H-22595.

10. *Dendryphiella uniseptata* Matsush., Microfungi of the Solomon Islands and Papua-New Guinea: 23 1971.

Description and illustrations – See Matsushima (1971)

Notes – Matsushima (1971) introduced this taxon on *Fici* sp. *Dendryphiella uniseptata* have branched or unbranched conidiophores, which are similar than *D. dregeae*, *D. infuscans* and *D. vinosa*. However they differ in conidial septa and colour. Type material of this species is MFC-2879.

11. *Dendryphiella vinosa* (Berk. & M.A. Curtis) Reisinger, Bull. trimest. Soc. mycol. Fr.84: 27 1968.

= *Helminthosporium vinosum* Berk. & Curt., in Berkeley, Jl. Linn. Soc. (Bot.), 10: 361 1869.

= *Dendryphiella interseminata* (Berk. & Rav.) Bubak & Ranojevic, Ann. mycol., Berl., 12: 417 1914.

= *Dendrophion nodulosum* Saccardo, Michelia, 1: 81 1877.

Description and illustrations – See Ellis (1971) and Matsushima (1971)

Notes – *D. vinosa* is the type species of *Dendryphiella* that occur commonly on the lower parts of dead or old herbaceous stems (Ellis 1971). Ellis (1971) described the species having 3-septate conidia, while Matsushima (1971) described the conidia as (0–)3(–5)-septate. The conidia of *D. vinosa* are morphologically similar to *D. fasciculata* in conidial size (17–30 × 5–8 µm vs. 15–30 × 4.3–7.4 µm). However, *D. vinosa* develops light brown conidia and conidia are formed in simple or branched chains, while *D. fasciculata* has conidia pale brown, aseptate when young, brown or dark brown, 3-septate when mature and conidia are formed in simple chains. Moreover, they differ

distinctly in conidiophores. The type species has simple or branched conidiophores, while the latter's are unbranched and fasciculate in loose. Type material of this species is MFC-2830.

Notes on currently excluded species of *Dendryphiella*

1. *Paradendryphiella arenariae* (Nicot) Woudenb. & Crous, comb. nov. Studies in Mycology 75: 208 2013.

- ≡ *Dendryphiella arenariae* Nicot, [as “arenaria”] Rev. Mycol. (Paris) 23: 93, 1958.
- ≡ *Scolecobasidium arenarium* (Nicot) M.B. Ellis, More dematiaceous hyphomycetes (Kew): 194, 1976.

Description and illustrations – See Pugh & Nicot (1964) and Woudenberg et al. (2013)
 Notes – Woudenberg et al. (2013) proposed *Dendryphiella arenariae* as a synonym of *Paradendryphiella arenaria*, and this species is currently residing in Pleosporaceae.

2. *Paradendryphiella salina* (G.K. Sutherl.) Woudenb. & Crous, comb. nov. Studies in Mycology 75: 207 2013.

- ≡ *Cercospora salina* G.K. Sutherl., New Phytol. 15: 43 1916.
- ≡ *Dendryphiella salina* (G.K. Sutherl.) Pugh & Nicot, Trans. Brit. Mycol. Soc. 47(2): 266 1964.
- ≡ *Scolecobasidium salinum* (G.K. Sutherl.) M.B. Ellis, More dematiaceous hyphomycetes (Kew): 192 1976.
- = *Embellisia annulata* de Hoog, Seigle-Mur., Steiman & K.-E. Erikss., Antonie van Leeuwenhoek J. Microbiol. Serol. 51: 409 1985.

Description and illustrations – See Pugh and Nicot (1964) and Woudenberg et al. (2013)
 Notes – Woudenberg et al. (2013) synonymized *Dendryphiella salina* under *Paradendryphiella* (as a current name *Paradendryphiella salina*) based on morphological and molecular evidence. It is morphologically distinct from *Dendryphiella* species in having conidiogenous cells with denticles aggregated at the apex. Phylogenetic analysis places it in the family Pleosporaceae.

Key to *Dendryphiella* species

- 1. Conidiophores are fasciculate..... 2
- 1. Conidiophores mostly are solitary 3
- 2. Conidia 0-septate and pale brown when young, 3-septate and brown when mature.. *D. fasciculata*
- 2. Conidia 0–3-septate, mostly 1-septate, conidiophores 129–303 µm long..... *D. broussonetiae*
- 2. Conidia 0–1–3-septate, conidiophores 100–500 µm long..... *D. lycopersicifolia*
- 3. Conidiophores are occasionally in loose groups *D. aspera*
- 3. Conidiophores are solitary 4
- 4. Conidiophores are branched or unbranched 5
- 4. Conidiophores are unbranched 6
- 4. Conidiophores are branched 7
- 5. Conidia are 0–3-septate, subhyaline to light olivaceous, basal cells of conidiophores peltate to irregularly lobed..... *D. dregeae*
- 5. Conidia are 0–2-septate, pale brown *D. infuscans*
- 5. Conidia are 1(–2)-septate, pale olivaceous..... *D. uniseptata*
- 5. Conidia are (0–)3(–5)-septate, light brown *D. vinosa*
- 6. Conidia are 1–4-septate, mostly 3-septate, pale brown..... *D. eucalypti*
- 7. Conidiophores branched above and below, verruculose, up to 500 µm long, conidia (1–)3(–5)-septate, (19–)20–23(–25) × 5(–7) µm..... *D. eucalyptorum*
- 7. Conidiophores branched above and below, verruculose, up to 150 µm long, conidia (1–)3-septate, (10–)24–27(–33) × (6–)7(–7.5) µm..... *D. paravinosa*
- 7. Conidiophores smooth or verruculose, conidia 1–3-septate, 15–30 × 5–9 µm..... *D. indica*

Discussion

In this study, a new *Dendryphiella* species is introduced and all eleven hitherto accepted species and two excluded species in the genus are provided with notes. *Dendryphiella* is a distinct genus in Dictyosporiaceae (Boonmee et al. 2016). Other asexual morph genera in this family form blastic conidiogenous cells, while *Dendryphiella* forms tretic conidiogenous cells. Boonmee et al. (2016) performed phylogenetic analyses based on DNA sequence data for three loci (SSU, LSU, TEF1- α). The result showed that *Dendryphiella* is a distinct genus in Dictyosporiaceae. In our phylogenetic tree, *D. vinosa* and *D. eucalyptorum* can phylogenetically represent the same species. This might be because only LSU gene data is available for these two species, and in NCBI blast result on LSU, sequences of *D. eucalyptorum* is 821/821 (100%) similar to *D. vinosa* without gaps. This situation is common in phylogenetic studies (Crous et al. 2014). Additional molecular sequence data is needed for resolve for these two species. However, morphologically they can be distinguished from each other. *Dendryphiella vinosa* formed simple or branched conidiophores, while those of *D. eucalyptorum* are branched above and below. Additionally, the conidiophores of *D. eucalyptorum* are longer and narrower (up to 500 μm long, 3–5 μm wide), than those of *D. vinosa* (up to 450 μm long, 4.5–7 μm wide).

Dendryphiella and *Dendryphion* are distinguishable from each other. *Dendryphion* is characterized by usually apically branched conidiophores, terminal and intercalary, tretic conidiogenous cells and simple or branched, cylindrical or obclavate, sometimes cheiroid conidia formed in chains (Ellis 1971, Ellis 1976, Seifert et al. 2011, Su et al. 2016). In addition, phylogenetic study based on DNA sequence data places *Dendryphion* in Torulaceae (Crous et al. 2015, Su et al. 2016, Li et al. 2017), while *Dendryphiella* formed a distinct clade in Dictyosporiaceae (Boonmee et al. 2016).

In conclusion, this study serves as an update for future taxonomic studies of *Dendryphiella*. There is only sequence data available for four species. Additional sequence data is therefore required.

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