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Taxonomy & Inventories

A new species of *Dictyochaeta* (Sordariomycetes, Chaetosphaeriales, Chaetosphaeriaceae) from freshwater habitats in China

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Abstract

Background

Freshwater fungi refer to the fungi that depend on the freshwater habitats for the whole life cycle or part of their life cycle. In this context, a new aquatic hyphomycete was isolated from decaying wood in a freshwater habitat in Jiangxi Province, China.

New information

Dictyochaeta jiangxiensis sp. nov., a new aquatic hyphomycete, is characterised by its unbranched, septate, base-fertile conidiophores with multisepta and single phialide at the

apex, brown, sterile seta, monophialidic, subcylindrical conidiogenous cells narrowing below the funnel-shaped collarette, hyaline, unicellular, thin-walled, smooth, guttulate, falcate to subclavate conidia narrowly rounded at both ends with hair-like appendages. Phylogenetically, the new species *Dictyochaeta jiangxiensis* clustered together with *Dictyochaeta brevis* MFLU 19-0216 in a well-supported clade, but formed a separate branch. In order to better define the taxonomic status of the new species, a phylogenetic tree of most closely-related taxa in Chaetosphaeriaceae was established, based on multi-locus sequences (ITS and LSU). The novel species is described and illustrated. Newly-generated molecular data of *Dictyochaeta jiangxiensis* is also provided.

Keywords

dematiaceous hyphomycete, new species, taxonomy, phylogeny

Introduction

Spegazzini (1923) established the genus *Dictyochaeta* with *D. fuegiana* as type species, which was isolated from fallen leaves of *Nothofagus betuloides* (Mirb.) Oerst. Gamundí et al. (1977) and Godeas et al. (1977) verified the holotype and redescribed it. Later, Réblová (2004) re-examined the type species and gave more detailed description about the genus *Dictyochaeta*, as two-layer conidiophores, the upper layer setiform, when sterile, monophialidic or rarely polyphialidic, the lower layer always fertile, monophialidic, rarely polyphialidic, collarette on conidiogenous cells and aseptate, hyaline, falcate conidia without setulae. Since then, more and more species have been discovered and classified as or transferred to *Dictyochaeta* and its molecular and morphological data have been expanded. According to literature and herbarium records, the *Dictyochaeta*-like fungi are globally distributed in the Holarctic Region and the Tropics and grow on decaying plant, such as bark, wood, bamboo culms, palm fronds, fallen leaves and petioles in freshwater and terrestrial environments. They also occur as plant pathogens or endophytes in living plants. (Agnihothrudu 1968, Lunghini et al. 1971, Shearer and Crane 1971, Sutton and Hodges 1975, Hewings and Crane 1981, Holubová-Jechová 1984, Kuthubutheen 1987, Kuthubutheen and Nawawi 1990, Kuthubutheen and Nawawi 1991a, Kuthubutheen and Nawawi 1991b, Réblová et al. 1999, Kirschner and Chen 2002, Crous et al. 2014, Crous et al. 2015, Maharachchikumbura et al. 2016).

There are always different opinions on the classification of *Dictyochaeta*, which is considered as a synonym of several genera, such as *Codinaea* Maire., *Menispora* Pers. and *Menisporopsis* S. Hughes. Previously, *Dictyochaeta* was usuallly regarded as a synonym of *Codinaea* (Maire 1937), because they share greatly similar features on phialidic conidiogenous cells and setae, but differ mainly in the conidia without setulae (Cai et al. 2006). Crous et al. (2018) thought that priority should be given to the older name, *Dictyochaeta*. Réblová (2000) recommended that species with setulae should be classified into *Codinaea* and those without setulae into *Dictyochaeta*. Réblová et al. (2021a) re-evaluated the concept of *Dictyochaeta* and revised species delimitation, based on six loci

(ITS, LSU, SSU, RPB2, TEF1-α, TUB2) along with comparative morphological and cultivation studies. In their study, some species of *Dictyochaeta*, such as *D. siamensis*, *D. simplex* etc. clustered within the clade *Codinaea* with a high support. As for the demarcation between *Dictyochaeta* and *Codinaea*, Réblová et al. (2021a) supported using conidial appendages as a classification criterion to distinguish *Dictyochaeta* from *Codinaea* (Réblová and Winka 2000). Based on revised species, morphological characteristics of conidia (shape, septation, absence or presence of setulae), collarettes (shape) and setae (presence or absence) and extension of the conidiogenous cell proved to be important at the generic level. To date, *Dictyochaeta*-like fungi, together with *Codinaea*-like fungi, were divided into five lineages in the phylogenetic analyses (Réblová et al. 2021b). Dual DNA barcoding and ancestral reconstruction of ecological and geographic distribution facilitated re-assessment of *Dictyochaeta*-like fungi. Réblová et al. (2021b) introduced five genera (*Codinaeella*, *Nimesporella*, *Stilbochaeta*, *Tainosphaeriella* and *Xyladelphia*) to accommodate *Codinaea*-like fungi and retained the taxonomic status of *Dictyochaeta* sensu stricto.

Materials and methods

Sample collection and specimen examination

Submerged wood samples were collected in a stream from Jishui County, Ji'an City, Jiangxi Province, China on 9 April 2018. The samples were taken to the laboratory in ziplock bags and placed in plastic boxes. The microscopic analysis was performed by a stereomicroscope to observe the fungal fruiting body on a natural substrate. Micro-examination and photomicrographs were taken under a compound microscope (Nikon Ni). The specimens were deposited in the Herbarium of Fungi, Jiangxi Agricultural University (HFJAU), Nanchang, China.

DNA extraction, PCR amplification and sequencing

Cultures were grown at room temperature on potato-dextrose agar (PDA). Mycelia were directly scraped off from plates and transferred into centrifugal tube after fragmentation. DNA was extracted with the CTAB method following Doyle and Doyle (1987). Approximately 500 mg of mycelium was mixed with ca. 0.2 g of white quartz sand and ground with preheated (ca. 65°C) 2 × CTAB buffer [2% (w/v) CTAB; 100 mM Tris-HCl; 1.4 M NaCl; 20 mM EDTA, pH 8.0]. DNA was extracted by chloroform:isoamyl alcohol (24:1) and precipitated by isopropanol at -20°C. The DNA precipitation was purified by 70% ethanol to remove remaining impurities. Approximately 50-100 µl TE buffer or deionised water were added and stored at -20°C. Dried DNA was dissolved in deionised water at 37°C and stored at -20°C.

DNA amplification was performed by polymerase chain reaction (PCR). LSU, TUB2, EF1-α and ITS regions were amplified using primers LR0R and LR5 (Vilgalys and Hester 1990, Rehner and Samuels 1995), EF1-983F and EF1-2218R (van den Brink et al. 2012), ITS1 and ITS4 (White et al. 1990) and T1 & Bt2b (Glass and Donaldson 1995, O'Donnell and

Cigelnik 1997) with 25 µl of the final volume including 9.5 µl ddH_2O, 12.5 µl 2 ×Taq PCR MasterMix (Qingke, Changsha, China), 1 µl of DNA template and 1 µl of each primer (10 µM). The PCR reaction was under the following conditions: 94°C for 4 min, then 35 cycles of 94°C for 60 s, 53°C (ITS, LSU, TEF1-a), 55°C (RPB2) for 60 s and 72°C for 80 s, followed by a final extension step of 72°C for 8 min (Wu et al. 2014). PCR products were checked on 2% agarose electrophoresis gels stained with GelRed. DNA sequencing was performed using the primers mentioned above by Tsingke, Changsha, China.

Phylogenetic analyses

The novel sequences and reference sequences collected from GenBank were aligned with MAFFT v.7.036 (http://mafft.cbrc.jp/alignment/server, Katoh et al. (2019)). The multilocus sequences were concatenated by PhyloSuite v.1.2.2 (Zhang et al. 2020). The concatenated aligned datasets were analysed separately using Maximum Likelihood (ML) and Bayesian Inference (BI). The best-fit models of evolution for the two loci tested were estimated by PhyloSuite v.1.2.2 (Zhang et al. 2020). The ML analyses were conducted with RAxML v.7.2.6 (Stamatakis and Alachiotis 2010) using a GTRGAMMA substitution model with 1000 bootstrap replicates. The robustness of the analyses was evaluated by bootstrap support (MLBS). Markov Chain Monte Carlo (MCMC) methods in MrBayes was used to estimate the posterior probabilities (PP) (Zhaxybayeva and Gogarten 2002). Trees were sampled every 100 generations. The MCMC sampling was set as four chains (three hot chains and one cold chain) running 2,000,000 generations simultaneously, resulting in 20001 total trees.

The first 25% of trees were discarded as burn-in trees and the remaining trees were used to calculate posterior probabilities. Posterior probabilities values of the BI analyses (BPP) over 0.95 were regarded to be important. Sequences generated in this study were displayed in GenBank (Table 1).

Table 1.

Strains used in this study and their GenBank numbers. Note: Type strains are in bold. The underlined species indicated the new taxa in this study. The sequences of new species are indicated as underlined and unavailable sequences in GenBank are indicated by hyphen "-".

Species	Strain number	GenBank accession numbers	
		ITS	LSU
Achrochaeta talbotii	ICMP 15161	MT454480	MT454495
Adautomilanezia caesalpiniae	CCLAMIC	KX821777	KU170671
Arcuatospora novae-zelandiae	CBS 109474	MW984569	MW984552
Arcuatospora novae-zelandiae	CBS 109476	MW984570	MW984553
Arcuatospora seorsa	CBS 147509	MW984571	MW984554
Arcuatospora seorsa	CBS 147510	MW984572	MW984555
Brunneodinemasporium brasiliense	CBS 112007	JQ889272	JQ889288

Species	Strain number	GenBank accession numbers	
		ITS	LSU
Cacumisporium capitulatum	FMR 11339	HF677176	——
Calvolachnella guaviyunis	CBS 134695	KJ834524	KJ834525
Catenularia cubensis	S.M.H. 3258	MW987826	——
Chaetosphaeria catenulat	S891	——	MK835838
Chaetosphaeria curvispora	CBS 113644	——	GU180636
Chaetosphaeria dilabens	CBS 712.88	AF178557	AF178557
Chaetosphaeria hebetiseta	CBS 102340	AF178549	AF178549
Chaetosphaeria inaequalis	MR 1450	AF178564	AF178564
Chaetosphaeria innumera	MenisporaR. 1175	AF178551	AF178551
Chaetosphaeria mangrovei	MCD 069	MG813821	MG813820
Chaetosphaeria myriocarpa	CBS 264.76	AF178552	AF178552
Chaetosphaeria pygmaea	MenisporaR. 1365	AF178545	AF178545
Chaetosphaeria submersa	MFLUCC 181342	MK828634	MK835835
Chloridium lignicola	CBS 143.54	AF178544	AF178544
Codinaea acaciae	CBS 139907	KR476732	——
Codinaea lambertiae	CBS 143419	MG386052	MG386105
Codinaea paniculata	CBS 145098	MT118230	MT118201
Codinaea pini	CBS 138866	KP004465	KP004493
Codinaea yunnanensis	MFLU:18-1611	MK828623	MK835823
Codinaeopsis gonytrichodes	CBS 593.93	AF178556	AF178556
Conicomyces pseudotransvaalensis	GS20	LC001710	LC001708
Cryptophiale hamulata	MFLU 17-1975	——	MG386756
Cryptophiale udagawae	MFLU:18-1497	MH758198	MH758211
Cryptophialoidea fasciculata	MFLU 18-1499	MH758195	MH758208
Dendrophoma cytisporoides	CBS 223.95	JQ889273	JQ889289
Dictyochaeta aquatica	MFLU 152691	MH476572	MH476569
Dictyochaeta assamica	CBS 242.66	MH858788	MH870426
Dictyochaeta brevis	MFLU 190216	MN104614	MN104625
Dictyochaeta callimorpha	ICMP 15155	MT454484	MT454499
Dictyochaeta callimorpha	ICMP 15170	MT454485	MT454500
Dictyochaeta callimorpha	ICMP 15130	MT454483	MT454498
Dictyochaeta cangshanensis	MFLU:181614	MK828632	MK835832
Dictyochaeta curvispora	CBS 114070	MH862954	——
Dictyochaeta detriticola	ICMP 14948	MT454486	MT454501
Dictyochaeta detriticola	EXP0560F	DQ914666	——

Species	Strain number	GenBank accession numbers	
		ITS	LSU
Dictyochaeta ellipsoidea	MFLU:181612	MK828628	MK835828
Dictyochaeta ellipsoidea	S304	MK828627	MK835827
Dictyochaeta fuegiana	ICMP 15153	MT454487	EF063574
Dictyochaeta fuegiana	FMR_13126	KY853440	KY853500
Dictyochaeta jiangxiensis	JAUCC 2824	MN619652	MN607224
Dictyochaeta lignicola	MFLU:181613	MK828630	MK835830
Dictyochaeta mimusopis	CBS 143435	MH107888	MH107935
Dictyochaeta montana	CBS 145342	MT454488	MT454502
Dictyochaeta pandanicola	KUMCC 160153	MH388338	MH376710
Dictyochaeta querna	CBS 146103	MT454490	MT454504
Dictyochaeta querna	CBS 145503	MT454489	MT454503
Dictyochaeta septata	CBS 143386	MH107889	MH107936
Dictyochaeta siamensis	MFLUCC 160371	MH388339	MH376711
Dictyochaeta siamensis	MFLUCC 150614	KX609955	KX609952
Dictyochaeta simplex	CBS 966.69	AF178559	AF178559
Dictyochaeta simplex	MFLU 190202	MN104609	MN104620
Dictyochaeta sp.	CBS 138684	MT454493	MT454507
Dictyochaeta stratosa	CBS 138739	MT454491	MT454505
Dictyochaeta stratosa	FMR 11228	MT454492	MT454506
Dictyochaeta submersa	MFLU:182321	MK828631	MK835831
Dictyochaeta terminalis	GZCC 180085	MN104613	MN104624
Dinemasporium americanum	CBS 127127	JQ889274	JQ889290
Dinemasporium decipiens	CBS 592.73	JQ889275	JQ889291
Dinemasporium morbidum	CBS 129.66	JQ889280	JQ889296
Dinemasporium morbidum	CBS 995.97	JQ889281	JQ889297
Dinemasporium nelloi	MFLUCC 130482	KP711358	KP711363
Dinemasporium polygonum	CBS516.95	JQ889276	JQ889292
Dinemasporium pseudoindicum	CBS 127402	JQ889277	JQ889293
Ellisembia aurea	CBS 144403	MH836375	MH836376
Ellisembia brachypus	HKUCC10555	——	DQ408563
Endoxyla operculata	UAMH 11085	——	JX460992
Ericiosphaeria spinosa	S.M.H. 2754	MW984575	AF466079
Eucalyptostroma eucalypti	CBS 142074	KY173408	KY173500
Exserticlava vasiformis	TAMA450	——	AB753846
Flectospora laminata	CBS 112964	MW984576	MW984558

Species	Strain number	GenBank accession numbers	
		ITS	LSU
Infundibulomyces cupulata	BCC 11929	EF113976	EF113979
Infundibulomyces oblongisporus	BCC 13400	EF113977	EF113980
Kionochaeta castaneae	MFLU 19-0204	MN104610	MN104621
Kionochaeta microspora	MFLU 19-0206	MN104607	MN104618
Kionochaeta ramifera	MUCL 39164	MW144421	MW144404
Lecythothecium duriligni	CBS 101317	——	AF261071
Melanochaeta aotearoae	SMH 3551	——	AF466082
Melanochaeta hemipsila	SMH 2125	——	AY346292
Melanochaeta taitensis	GKM156N	——	EU583220
Melanochaeta taitensis	GKM150N	——	EU583219
Melanopsammella gonytrichii	SMH 3785	——	AF466085
Melanopsammella vermicularioides	FC 404	——	AF466087
Menispora caesia	M.R. 1120	AF178543	——
Menispora caesia	CBS 144659	MW984578	MW984560
Menispora ciliata	ICMP 18253	——	GU180637
Menispora ciliata	CBS 122131	EU488736	——
Menispora tortuosa	DAOM 231154	KT225527	AY544682
Menisporopsis anisospora	CBS 109475	MH862827	MH874421
Menisporopsis breviseta	MFLU 19-0212	MN104612	MN104623
Menisporopsis dushanensis	GZCC 180084	MN104615	MN104626
Menisporopsis pirozynskii	MUCL 47217	MW984579	MW984561
Menisporopsis theobromae	MFLUCC 150055	KX609957	KX609954
Menisporopsis theobromae	MUCL 41079	MW984580	MW984562
Menisporopsis theobromae	MUCL 40984	MW984581	MW984563
Multiguttulispora dimorpha	CBS 140002	MW984582	MW984564
Multiguttulispora triseptata	CBS 487.92	MW984583	MW984565
Multiguttulispora triseptata	IMI 353690	MW984584	MW984566
Nawawia filiformis	MFLUCC 17-2394	MH758196	MH758209
Neopseudolachnella magnispora	MAFF 244359	AB934066	AB934042
Neopseudolachnella uniseptata	MAFF 244360	AB934067	AB934043
Paliphora intermedia	CBS 896.97	MH862682	MH874289
Paragaeumannomyces garethjonesii	MFLUCC 15-1012	KY212751	KY212759
Paragaeumannomyces longisporus	ILLS00121385	MT118237	MT118211
Paragaeumannomyces raciborskii	S.M.H. 3119	AY906953	AY436402
Paragaeumannomyces rubicundus	S.M.H. 3221	MT118242	MT118224

Species	Strain number	GenBank accession numbers	
		ITS	LSU
Phaeostalagmus cyclosporus	CBS 663.70	MH859892	MH871680
Phialogeniculata guadalcanalensis	CBS:346.76	MH860986	MH872756
Phialosporostilbe scutiformis	MFLUCC 17-0227	MH758194	MH758207
Phialoturbella aseptata	MFLU 19-0208	MN104611	MN104622
Phialoturbella calva	ICMP 23826	MW984585	MW984567
Phialoturbella lunata	MFLUCC 18-0642	MK828624	MK835824
Polynema podocarpi	CPC:32761	MH327797	MH327833
Pseudodinemasporium fabiforme	MAFF 244361	AB934068	AB934044
Pseudolachnea fraxini	CBS 113701	JQ889287	JQ889301
Pseudolachnea hispidula	MFLU:19-2863	MT185550	MT183515
Pseudolachnella asymmetrica	MAFF 244366	AB934073	AB934049
Pseudolachnella botulispora	MAFF 244367	AB934074	AB934050
Pyrigemmula aurantiaca	CBS 126743	HM241692	HM241692
Pyrigemmula aurantiaca	CBS 126744	HM241693	HM241693
Rattania setulifera	GUFCC 15501	GU191794	HM171322
Sporidesmium minigelatinosa	NN 47497	——	DQ408567
Sporidesmium parvum	HKUCC 10836	——	DQ408558
Sporoschisma longicatenatum	MFLUCC 160180	KX505871	KX358077
Sporoschisma mirabile	FMR 11247	HF677174	HF677183
Striatosphaeria castanea	CBS 145352	MT118244	MT118229
Striatosphaeria codinaeophora	M.R. 1230	AF178546	AF178546
Striatosphaeria codinaeophora	S.M.H. 1524	MT118245	AF466088
Tainosphaeria cecropiae	CBS 101687	MW984586	MW984568
Tainosphaeria crassiparies	S.M.H. 1934	MW984587	AF466089
Tainosphaeria jonesii	GZCC 160065	KY026060	KY026057
Tainosphaeria jonesii	GZCC 16-0053	MN121305	KY026056
Tainosphaeria siamensis	MFLUCC 150607	KX609956	KX609953
Thozetella fabacearum	MFLU 16-1021	KY212754	KY212762
Thozetella nivea	EU825201	EU825201	EU825200
Thozetella tocklaiensis	CBS 378.58	MH857817	MH869349
Tracylla aristata	CPC 25500	KX306770	KX306795
Tracylla eucalypti	CPC:31806	MH327810	MH327846
Umbrinosphaeria caesariata	CBS 102664	——	AF261069
Zanclospora iberica	CBS 130426	KY853480	KY853544
Zanclospora novae-zelandiae	ICMP 15781	MW144429	MW144411

Species	Strain number	GenBank accession numbers	
		ITS	LSU
Zanclospora xylophila	ICMP 22737	MW144437	MW144417
Zignoëlla pulviscula	MUCL 15710	——	AF466090
Zignoëlla pulviscula	SMH 3289	——	AF466091

Taxon treatment

Dictyochaeta jiangxiensis J.E. Huang, X.Y. Yan, H.Y. Song & D.M. Hu, sp. nov.

- MycoBank 846403

Material

Holotype:

a. scientificName: ***Dictyochaeta jiangxiensis***; acceptedNameUsage: ***Dictyochaeta jiangxiensis*** J.E. Huang, X.Y. Yan & D.M. Hu; kingdom: Fungi; phylum: Ascomycota; class: Sordariomycetes; order: Chaetosphaeriales; family: Chaetosphaeriaceae; taxonRank: species; verbatimTaxonRank: species; genus: ***Dictyochaeta***; specificEpithet: ***jiangxiensis***; scientificNameAuthorship: J.E. Huang, X.Y. Yan & D.M. Hu; continent: Asia; country: China; stateProvince: Jiangxi Province; county: Jishui county; locality: Dingjiang; verbatimLatitude: 27.127397 N; verbatimLongitude: 115.276527 E; identifiedBy: J.E Huang, X.Y. Yan; type: PhysicalObject; language: en; rightsHolder: Dian-Ming Hu; institutionID: HFJAU 3175; collectionID: HJ0108-1; institutionCode: the Herbarium of Fungi, Jiangxi Agricultural University (HFJAU); collectionCode: Fungi; ownerInstitutionCode: the Herbarium of Fungi, Jiangxi Agricultural University (HFJAU); basisOfRecord: PreservedSpecimen; occurrenceID: B23E3165-B465-54BD-ADAE-FB318AEB9F70

Description

Saprobic on decaying submerged wood. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Colonies* effuse, aggregate, spreading very widely, glistening white to transparent spots and short dark brown hairs. *Mycelium* composed of partly immersed and partly superficial, brown to dark brown, septate. *Setae* of the upper layer sterile, brown to black, usually associated with the conidiophores and together these can form small clusters originating from a knot of superficial hyphae, 200–420 × 4.6–7.2 µm, cylindrical, straight or slightly flexuous, septate, smooth, thick-walled, base swollen 9–12 µm wide, tapering to terminal. *Conidiophores* of the lower layer always fertile, mononematous, macronematous, erect or flexuous, unbranched, 26–60 × 3.5–5 µm (av. = 48.3 × 4.0 µm, n = 20), 3–8-septate, smooth, thin-walled, base brown 4.8–7.5 µm, apex pale brown with single phialide. *Conidiogenous cells* monophialidic (15–) 24–34 × 3.6–5 µm (av. = 27.6 × 4 µm, n = 20), subcylindrical, light brown, narrowing below the collarette. Collarettes light brown, funnel-shaped, 2.2–4.9 µm at the opening, 0.8–1.1 µm at deep. *Conidia* accumulating at the heads white, 23–32 × 2.5–3.2 µm (av. =

26.1 × 2.9 µm, n = 30), hyaline, unicellular, thin-walled, smooth, abundant guttulate, falcate to subclavate, rarely straight, narrowly rounded at the both ends, with 6–11 µm long hair-like appendages at both ends, smooth (Fig. 2).

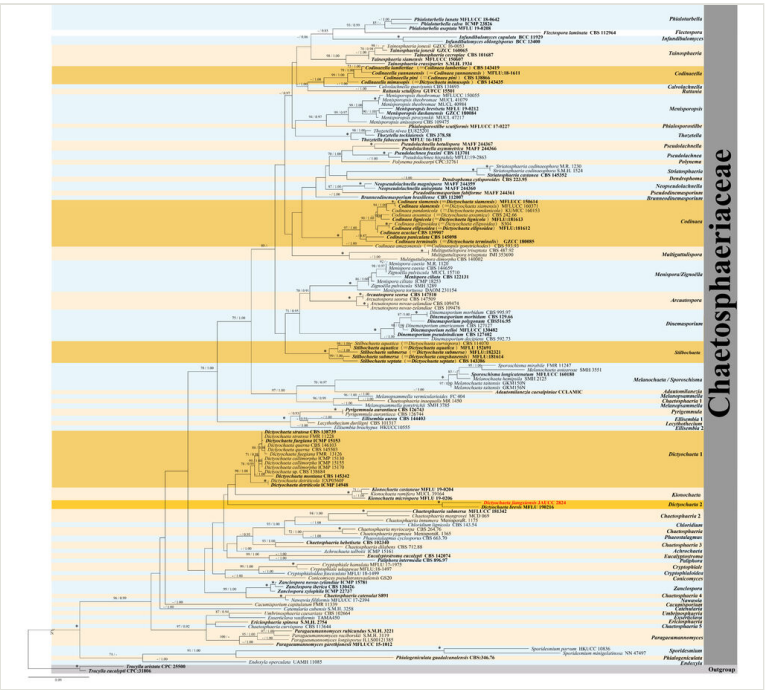

Figure 1. doi

Phylogenetic tree based on combined ITS, LSU sequences of most taxa of the Chaetosphaeriaceae. Species name given in bold red is a new taxon in this study; species name given in bold indicates a type strain, respectively. Asterisk (*) indicates branches with MLBS = 100% and PP value = 1.0. The ML bootstrap support values and Bayesian posterior probabilities are given above the branches (MLBS/BPP). The tree is rooted to *Tracylla aristata* CPC 25500 and *Tracylla eucalypti* CPC:31806.

Culture characteristics: Conidia germinating on PDA within 12 h. *Colonies* growing on PDA, reaching 20–30 mm diam. after 3 weeks at 28°C, circular, white to pale grey mycelium with hyaline margin, centre lightly raised, pale brown to dark brown in reverse, with smooth margin.

Material examined: CHINA, Jiangxi Province, Jian, Dingjiang, on submerged wood in a stream, 9 April 2018, J.E. Huang (HFJAU 3175, **Holotype**); ex-type living culture (JAUCC 2824).

Etymology

'*jiangxiensis*' refering to the host location, Jiangxi Province, where the holotype was collected.

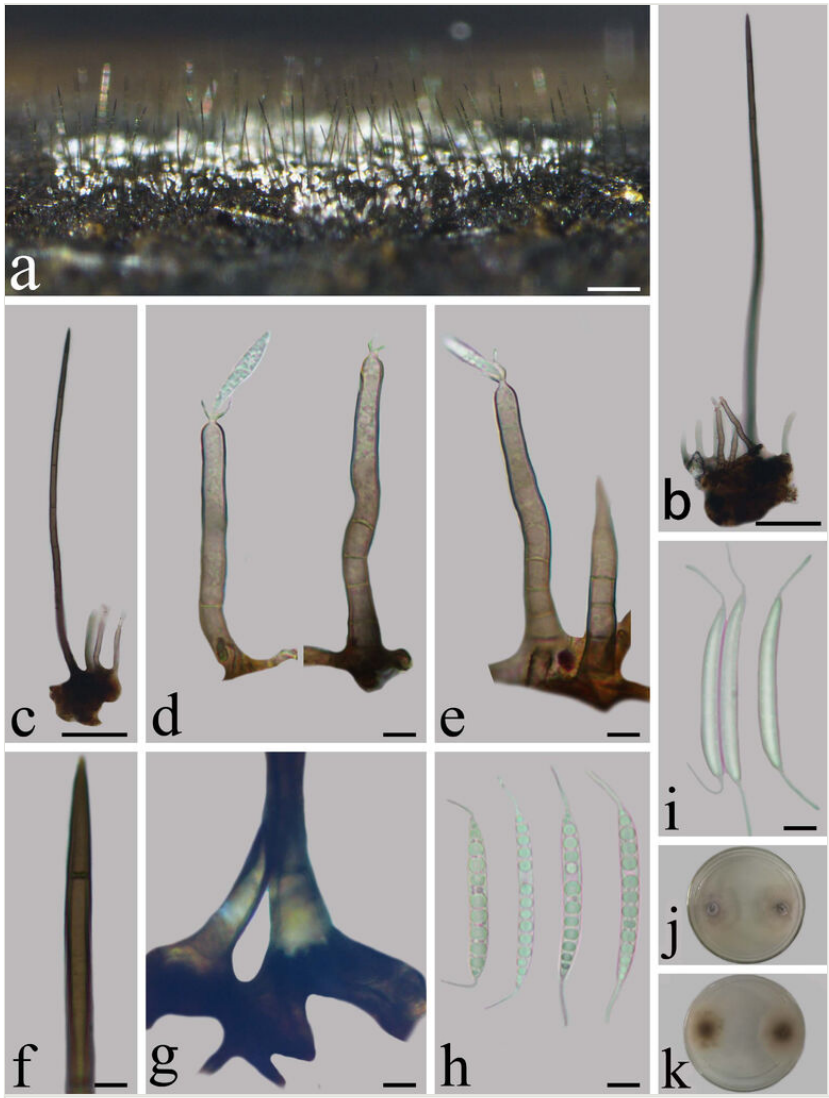

Figure 2. doi

Dictyochaeta jiangxiensis (HFJAU 3175, holotype). **a** Colonies on submerged wood; **b, c** Setae and conidiophores; **d, e** Conidiophores and phialides with a developing conidia; **f, g** Apex and base of setae; **h, i** Conidia; **j, k** Colony on PDA from above and below. Scale bars: a = 200 µm, b, c = 50 µm, d–h = 5 µm.

Notes

Dictyochaeta jiangxiensis is a distinct species in the genus as supported by molecular phylogenetic analysis and it clusters with *D. brevis*, but the latter has smaller conidia (7.5–11.4 µm long, 2.0–2.9 µm wide; Lin et al. (2019)). We found that there was 8% nucleotide difference of ITS sequences and about 2% nucleotide difference between

the LSU sequences of *Dictyochaeta jiangxiensis* sp. nov. JAUCC2824 and *Dictyochaeta brevis* MFLU 19-0216. Morphologically, *D. jiangxiensis* matches *Dictyochaeta* well, especially the setae surrounded by several conidiophores and conidia with setulae at both ends. *D. jiangxiensis* is similar to *D. fuegiana* (*Chaetosphaeria fuegiana*), *D. occidentalis*, *C. siamensis* (*Dictyochaeta siamensis*) and *C. lignicola* (*Dictyochaeta lignicola*) in having multi-septae and a single phialide at the apex, subcylindrical conidiogenous cells with funnel-shaped collarette and guttulate conidia with hair-like appendages. However, *D. fuegiana* (*Chaet. fuegiana*) has smaller conidia (15–23 × 2–2.5 µm) without hair-like appendages at both ends (Spegazzini 1923). *C. lignicola* also has smaller conidia (13–15 µm long, 4.5–5.5 µm wide) and has no setae (Luo et al. 2019). *D. occidentalis* has wider conidia (24–32 × 3–4 µm; Whitton et al. (2000)) with degenerated appendages. *C. siamensis* has mono- or polyphialidic conidiogenous cells and samller conidia (8–17 × 2–5 µm; Tibpromma et al. (2018)).

Analysis

Phylogenetic analyses

Based on ITS and LSU, a multi-locus phylogenetic tree was established to demonstrate the relationships between the new species and related taxa in Chaetosphaeriaceae (Fig. 1). The alignment has 1767 characters (including alignment gaps), with 715 characters for ITS and 1052 characters for LSU. The ML analysis result showed coincident topology with BI. Fig. 1 shows the ML tree based on the combined dataset, along with the fully supported bootstrap values and Bayesian posterior probabilities. All phylogenetic trees were similar in topologies.

The new species *Dictyochaeta jiangxiensis*, together with *Dictyochaeta brevis* MFLU 19-0216, formed a well-supported clade (BPP = 1.00; MLBS = 100%), but formed a separate branch and there were obvious differences between them. By comparing the ITS and LSU sequences of *Dictyochaeta jiangxiensis* sp. nov. JAUCC2824 and *Dictyochaeta brevis* MFLU 19-0216 respectively in NCBI, we found that there was 8% nucleotide difference of ITS sequences and about 2% nucleotide difference between the LSU sequences of *Dictyochaeta jiangxiensis* sp. nov JAUCC2824 and *Dictyochaeta brevis* MFLU 19-0216.

Discussion

Freshwater fungi refer to the fungi that rely on the freshwater habitats for the whole life cycle or part of the life cycle. Phylogenetic studies on freshwater ascomycetes have shown that some species cluster with terrestrial ascomycete lineages, while others cluster with exclusive aquatic lineages (Raja et al. 2018). However, Shearer (1993) defined freshwater fungi as “fungi that must rely on the freshwater environment to complete their life cycle”. The concept of aquatic fungi in a broad sense was adopted in this study. Chaetosphaeriaceae is a huge and diverse group with overwhelmingly phialidic fungi and

some members of Chaetosphaeriaceae possess known teleomorphs. The family has a world-wide distribution. They are predominantly isolated from soil and plant debris, some are endophytic and have been isolated from herbaceous plants (Hughes and Kendrick 1968, Réblová 2004, Fernández and Huhndorf 2005, Huhndorf and Fernández 2005, Crous et al. 2012, Yang et al. 2018, Lin et al. 2019, Luo et al. 2019). In this study, the new *Dictyochaeta* species in the family Chaetosphaeriaceae was isolated from a freshwater environment. Most known species in *Dictyochaeta* were reported from rotting parts of plants, such as decaying leaf, bark or stem and submerged wood, partly from soil. Previously, *Dictyochaeta* and *Codinaea* were hard to demarcate, not only because of their morphological and ecological similarities, but their closely-related phylogenetic relationship. The difference between *Dictyochaeta* and *Codinaea* lies in the presence or absence of setae. The taxonomy of these fungi has relied mainly on morphological criteria. However, it is hard to treat setae as a criterion for identification as setae are always irregular amongst these similar taxa as mentioned above. *Codinaea* was introduced to accommodate a single species, *C. aristata*. Since then, the type species of *Codinaea* has become a taxonomic bottleneck. This species has not been recorded in any literature since its initial description. The holotype material and molecular data could not be traced. That is why the phylogenetic statuses of the *Dictyochaeta*-like fungi are still ambiguous. Hughes and Kendrick (1968) made an attempt at using the name *Dictyochaeta* instead of *Codinaea* on account of the principle of priority and suggested to adopt the name *Codinaea* as the type material for *D. fuegiana* of *Dictyochaeta*. Since Gamundí et al. (1977) redescribed *D. fuegiana* from fresh material, *Dictyochaeta* became a precedently used name. Crous et al. (2018) accepted this treatment. Simultaneously, the name *Codinaea* was suggested to be treated as the type material for *D. fuegiana* of *Dictyochaeta* by Hughes and Kendrick (1968), but this view has great limitations. Shortage of abundant original descriptions and loss of the type material of *Codinaea* were the factors (Liu et al. 2016) which indicated that the molecular phylogeny of *Dictyochaeta* has not been solved due to the small number of sequences in GenBank. The species, thus, need recollecting, epitypifying and sequencing to establish which morphological characters are of taxonomic significance and generic boundaries.

Recently, *Dictyochaeta* has still not been classified as monophyletic even though most *Dictyochaeta*-like and *Codinaea*-like species were re-assessed and recognised as five genera: *Codinaeella*, *Nimesporella*, *Stilbochaeta*, *Tainosphaeriella* and *Xyladelphia* (Réblová et al. 2021b). Réblová et al. (2021b) indicated *Codinaea* is a highly polyphyletic taxon unrelated to *Dictyochaeta* and that its original delimitation, based on a single morphotype of *C. aristata*, is too narrow and unsustainable and they emphasise the importance of combination of microscopic morphological characters developed in culture and under a natural substrate for identification. In our analysis, the phylogenetic position of some taxa, such as *Zignoëlla* and *Menispora*, are unclear in the tree with low BS and PP values. *Kionochaeta* formed a sister clade with *Dictyochaeta* and they were clustered together, but with low BS and PP values. Quite a number of species have not been adopted to establish the phylogenetic tree on account of the absence of molecular data and type materials. The molecular database and materials of Chaetosphaeriaceae species needs to be supplemented and improved.

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