Digitodesmium polybrachiatum sp. nov., a new species of Dictyosporiaceae from Brazil

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Abstract

Digitodesmium is a genus of saprobic fungi, generally associated with decaying wood in freshwater habitats or in the soil. As morphologic markers they produce cheiroid, euseptate conidia on sporodochia. During an exam of a necrotic robusta coffee stem sent from Nova Venécia, state of Espírito Santo, to the Plant Clinic at the Universidade Federal de Viçosa (Brazil), for disease diagnosis a fungus, recognized as having the typical features of *Digitodesmium* was observed. The fungus was isolated in pure culture and DNA was extracted. Sequences of the partial 18S ribosomal RNA gene, large subunit of the nrDNA, internal transcribed spacer and translation elongation factor 1-α were generated. The combination of results of the phylogenetic analysis with the exam of the morphology led to the conclusion that the fungus from coffee stem morphological data showed that this fungus represents a monophyletic distinct lineage within *Digitodesmium* and an undescribed species for the genus. The concatenate tree also revealed that *Digitodesmium* is divided in two distinct clades. The novel species can be differentiated morphologically from other species of *Digitodesmium* by the size of the conidia, the number of arms and the presence of appendages. The new species *Digitodesmium polybrachiatum* is hence proposed herein. A comparative table of conidial morphology for the species in the genus is also included.

Introduction

The family Dictyosporiaceae was introduced by Boonmee et al. (2016) to accommodate a group of fungi belonging to the Dothideomycetes that are saprobes on decaying wood and plant debris in terrestrial and freshwater habitats typically having cheiroid, digitate, palmate and/or dictyosporous conidia. *Dictyosporium*, the type genus of the family, has been reported as saprobic on dead or decaying wood worldwide (Hyde and Goh 1998, Ho et al. 2002, Pinnoi et al. 2006, Pinruan et al. 2007). Corda (1836) established the genus with *D. elegans* as the type species. A phylogenetic analysis based on ITS sequence data has shown that the family Dictyosporiaceae comprise 44 distinct lineages that correspond to ten genera (Boonmee et al. 2016). More recently, three new genera were added to this family (Li et al. 2017; Liu et al. 2017; Iturrieta-González et al. 2018).

The genus *Digitodesmium* was proposed in 1981 to accommodate the species *D. elegans*, isolated from rotten wood (*Taxus baccata*) in the United Kingdom (Kirk 1981). After that, six more species were described within this genus, namely: *D. recurvum* recorded from freshwater habitats in Hong Kong, China (Ho et al. 1999); *D. bambusicola* on bamboo culms submerged in river from Philippines (Cai et al. 2002); *D. heptasporum* found on wood submerged in forest stream, from Yunnan, China (Cai et al. 2003); *D. intermedium* and *D. macrosporum*, obtained respectively from plant debris and from a soil sample, both collected in Spain (Silvera-Simón et al. 2010); and *D. chiangmaiense* isolated from dead wood in Thailand (Hyde et al. 2019).

The members of *Digitodesmium* are morphological characterized by punctiform, sporodochial conidiomata and acrogenous, euseptate, cheiroid, digitate conidia, with an apical gelatinous cap (Kirk 1981; Hyde et al. 2019). Conidia produced by species of *Digitodesmium* and *Dictyosporium* have a similar shape and can be easily confused. But there are some useful distinguishing differences. In *Dictyosporium* the conidial secession is rhexolytic and the conidial arms remain closely appressed at maturity, whereas in *Digitodesmium* the conidial secession is schizolytic and the conidial arms are divergent at maturity (Silvera-Simón et al. 2010).

During the examination of samples of necrotic robusta coffee (*Coffea canephora*) stems sent for diagnosis at the Plant Clinic (Clinica de Doenças de Plantas, Departamento de Fitopatologia, Universidade Federal de Viçosa, state of Minas Gerais, Brazil) from Nova Venécia, state of Espírito Santo, Brazil, a dematiaceous anamorphic fungus was found growing on decaying parts of the sample. This prompted a study aimed at elucidating the taxonomy of this fungus. Results of this investigation are presented here.

Material And Methods

Isolation

Samples of stem, taken from diseased robusta coffee plants (*Coffea canephora*), were collected at a commercial plantation at Nova Venécia (state of Espírito Santo, Brazil). Numerous plants in that plantation were presenting a combination of bark flaking on stems, wilt and dieback of plants. This disease has been the cause of increasing worries for coffee growers of northern Espírito Santo and southern Bahia. Controversy surrounds the etiology of this disease with suspicions ranging from the *Fusarium* Wilt reported in Brazil (Belan et al. 2018) to the Coffee Bark Disease and Coffee Wilt Disease reporters only on the African continent (Siddiqi and Corbett, 1965; Geiser et al. 2005). An agronomist based at Nova Venécia forwarded us the samples composed of bare-rooted adult plants (part of stems with root system) The stem presented bark flaking. While analyzing the sample in search of the possible causal agent of the disease, it was noticed that in parts of well advanced necrotic tissued colonies of a conidial fungus was present. These appeared to have no relation with the disease, but examined in detail, nonetheless.

Conidia were transferred to the center of a potato dextrose-agar (PDA) plates supplemented with 0.1 g/L streptomycin sulfate and maintained in a controlled temperature room at 25°C under a 12-h daily light /12-h dark regime (light provided by two white and one near-UV lamps placed 35 cm above the plates) with a sterile fine poited needle. These were spread over the surface of the medium with a sterile loop and, after 12 hs incubation, individual germinated single conidia were transferred to text tubes containing potato carot-agar (PCA). Long-term preservation was performed on silica gel and also at -80 ° C in cryogenic microtubes containing a 10% glycerol solution as described in Dhingra and Sinclair (1995). Two representative cultures were selected and deposited in the local culture collection – Coleção Octávio de Almeida Drumond of the University Federal of Viçosa (COAD).

Morphological characterization

Fungal structures formed on sporulating colonies in vegetable broth-agar (VBA), as described in Pereira et al. (2003), were mounted in lactoglycerol. Observations of fungal structures were made under an Olympus BX53 light microscope adapted with differential interference contrast lighting and fitted with a digital image capture system (Olympus Q-Color 3 ™). Biometric data was obtained from the measurement of at least 30 representative fungal structures.

Colony description was based on the observation of fungal colonies on malt extract-agar (MEA) and VBA (Pereira et al. 2003), after 40 days under a daily 12 h light regime at 25C^{o}. Color terminology followed Rayner (1970).

Molecular characterization and multilocus phylogenetic analysis

Genomic DNA was extracted from each of the isolates grown in potato-dextrose (PD) – liquid medium – in the dark for one week. Mycelium of each isolate was dried on sterile filter paper for 2 days and transferred to a sterile plastic tube containing zirconium spheres and placed in a grinder (L-Beader-3, Loccus Biotecnologia). After 20 seconds grinding, the resulting suspension was drained into a sterile plastic tube and used for DNA extraction. This was performed with the Wizard Genomic DNA Purification Kit following the manufacturer's protocol.

Target regions of the partial 18S ribosomal RNA gene (SSU), large subunit of the nrDNA (LSU), internal transcribed spacer (ITS) and translation elongation factor 1-α (*TEF1*) were amplified using fungal specific primers NS1 and NS4 for partial SSU rDNA (White et al. 1990), LROR and LR5 for partial LSU rDNA (Vilgalys and Hester 1990), ITS4 and ITS5 (White et al. 1990) for ITS region and EF1-983 and EF1-2218R for *TEF1* region (Rehner 2001). PCR products were analyzed on GelRed ™ (Biotium Inc., Hayward, CA, E.U.A.) and visualized under UV light to verify the size and purity of amplificons. The PCR products were sequenced by Macrogen Inc., South Korea (http://www.macrogen.com). The nucleotide sequences were edited with software SeqAssem ver. 07/2008 (Hepperle 2004).

The consensus sequences were compared with others deposited in the GenBank database using the MegaBLAST program. Sequences from GenBank were aligned using MUSCLE (Edgar 2004) and built in MEGA X 10.1 software (Kumar et al. 2018). All of the ambiguously aligned regions within the dataset were excluded from the analyses. Gaps (insertions/deletions) were treated as missing data.

Bayesian inference (BI) analyses employing a Markov Chain Monte Carlo method were performed with all sequences, first with each locus separately and then with the concatenated sequences. The alignments consisted of 22 parsimony-informative positions/1024 bp for SSU, 104/1315 bp for LSU, 252/638 for ITS and 200/987 bp for *TEF1*. Before launching the BI, the best nucleotide substitution models were determined for each gene with MrMODELTEST 2.3 (Posada and Buckley 2004). Once the likelihood scores were calculated, the models were selected according to the Akaike Information Criterion (AIC). The GTR + I + G model of evolution was used for SSU and LSU regions, SYM + I + G was used for ITS and GTR + G was used for *TEF1*. One concatenated tree with the four regions was generated with Sequence Matrix (Vaidya et al. 2011) and estimated on the CIPRES web portal using MrBayes on XSEDE 3.2.6 (Miller et al. 2011).

Additionally, a Maximum likelihood (ML) tree was generated with the Nearest-Neighbor-Interchange (NNI) ML heuristic method and the Tamura-Nei substitution model as tree inference options, using CIPRES web portal. The chain stabilities of the phylogenetic tree were assessed by using the bootstrap re-sampling strategy with 1000 bootstrap test replicates. The resulting tree topologies using the two methods (ML and BI) were then compared and the phylogram layout was edited with CorelDRAW Graphics Suite 2017.

Sequences derived from this study were deposited in GenBank (http://www.ncbi.nlm.nih.gov/genbank) (Table 1).

Table 1
DNA sequences used for the phylogenetic tree

Species name	Strain number	GenBank accession numbers			
		ITS	*TEF1*	nc LSU rDNA	SSU
Aquaticheirospora lignicola	HKUCC 10304^{T}	AY864770	–	AY736378	AY736377
Aquadictyospora lignicola	MFLUCC 17-1318^{T}	MF948621	MF953164	MF948629	–
Cheirosporium triseriale	HMAS 180703^{T}	EU413953	–	EU413954	–
Dendryphiella eucalyptorum	CBS 137987^{T}	KJ869139	–	KJ869196	–
Dendryphiella fasciculata	MFLUCC 17-1074^{T}	MF399213	–	MF399214	–
Dendryphiella paravinosa	CBS 141286^{T}	KX228257	–	KX228309	–
Dendryphiella variabilis	CBS 584.96 ^{T}	LT963453	–	LT963454	–
Dictyocheirospora aquatica	KUMCC 15-0305^{T}	KY320508	–	KY320513	–
Dictyocheirospora bannica	KH 332^{T} = JCM 19406 = MAFF 243828	LC014543	AB808489	AB807513	AB797223
Dictyocheirospora garethjonesii	MFLUCC 16-0909^{T}	KY320509	–	KY320514	–
Dictyocheirospora garethjonesii	DLUCC 0848	MF948623	MF953166	MF948631	–
Dictyocheirospora gigantica	BCC 11346	DQ018095	–	–	–
Dictyocheirospora heptaspora	CBS 396.59	DQ018090	–	–	DQ018082
Dictyocheirospora indica	MFLUCC 15–0056/ YJ-2018a voucher MFLU:15-1169	MH381763	MH388817	MH381772	–
Dictyocheirospora pseudomusae	KH 412 = JCM 19408 = MAFF 243831	LC014549	AB808492	AB807516	AB797226
Dictyocheirospora pseudomusae	yone 234 = CBS 139686 = JCM 19409 = MAFF 243836	LC014550	AB808496	AB807520	AB797230
Dictyocheirospora rotunda	MFLUCC 14–0293^{T}	KU179099	–	KU179100	KU179101
Dictyocheirospora subramanianii	BCC 3503	DQ018094	–	–	–
Dictyocheirospora vinaya	MFLUCC 14–0294^{T}	KU179102	–	KU179103	KU179104
Dictyosporium alatum	ATCC 34953^{T}	DQ018088	–	DQ018101	DQ018080
Dictyosporium aquaticum	MF1318^{T}	KM610236	–	–	–
Dictyosporium bulbosum	HKUCC 8360	DQ018086	AB808487	–	–
Dictyosporium bulbosum	yone 221 = MAFF 243835	LC014544	–	AB807511	AB797221

Sequences obtained in this study are highlighted in bold. Ex-type strains are indicated in T after collection number.

Species name	Strain number	GenBank accession numbers			
Dictyosporium cf. heptasporum	HKUCC 5572	DQ018096	–	–	–
Dictyosporium digitatum	KH 401 = JCM 19404 = MAFF 243830	LC014545	AB808491	AB807515	AB797225
Dictyosporium digitatum	KT 2660 = JCM 19405 = MAFF 243833	LC014546	AB808494	AB807518	AB797228
Dictyosporium digitatum	yone 280 = MAFF 243837	LC014547	AB808488	AB807512	AB797222
Dictyosporium elegans	NBRC 32502^{T}	DQ018087	–	DQ018100	DQ018079
Dictyosporium hughesii	KT 1847 = JCM 19407 = MAFF 243832	LC014548	AB808493	AB807517	AB797227
Dictyosporium meiosporum	MFLUCC 10–0131	KP710944	–	KP710945	KP710946
Dictyosporium nigroapice	BCC 3555	DQ018085	–	–	–
Dictyosporium nigroapice	MFLUCC 17-2053/MFLU:18-1043	MH381768	MH388821	MH381777	–
Dictyosporium olivaceosporum	KH 375 ^{T}= JCM 19403 = MAFF 243829	LC014542	AB808490	AB807514	AB797224
Dictyosporium sexualis	MFLUCC 10–0127^{T}	KU179105	–	KU179106	KU179107
Dictyosporium stellatum	CCFC 241241^{T}	NR_154608	–	JF951177	–
Dictyosporium strelitziae	CBS 123359^{T}	FJ839618	–	FJ839653	–
Dictyosporium tetrasporum	KT 2865 = JCM 19410 = MAFF 243834	LC014551	AB808495	AB807519	AB797229
Dictyosporium thailandicum	MFLUCC 13–0773^{T}	KP716706	–	KP716707	–
Dictyosporium tratense	MFLUCC 17-2052^{T}	MH381767	MH388820	MH381776	–
Dictyosporium tubulatum	MFLUCC 15-0631^{T}/ MFLU15_1166	MH381769	MH388822	MH381778	–
Dictyosporium tubulatum	MFLUCC 17-2056/ YJ-2018a voucher MFLU:18-1044	MH381770	–	MH381779	–
Dictyosporium wuyiense	CGMCC 3.18703^{T}	KY072977	–	–	–
Dictyosporium zhejiangensis	MW-2009a^{T}	FJ456893	–	–	–
Digitodesmium bambusicola	CBS 110279	DQ018091	–	DQ018103	–
Digitodesmium chiangmaiense	KUN-HKAS 102163	–	–	MK571766	MK571775
Digitodesmium polybrachiatum sp. nov	COAD 3174^{T}	**MW879318**	**MW890262**	**MW879316**	**MW879325**
Digitodesmium polybrachiatum sp. nov	COAD 3175	**MW879319**	**MW890263**	**MW879317**	**MW879326**

Sequences obtained in this study are highlighted in bold. Ex-type strains are indicated in T after collection number.

Species name	Strain number	GenBank accession numbers			
Digitodesmium sp.	TBRC 10038	MK405235	MK405231	MK405233	–
Digitodesmium sp.	TBRC 10037	MK405234	MK405230	MK405232	–
Gregarithecium curvisporum	KT 922^{T} = CBS 139688 = JCM 19411 = MAFF 243838	AB809644	AB808523	AB807547	AB797257
Jalapriya inflata	NTOU 3855	JQ267362	–	JQ267363	JQ267361
Jalapriya pulchra	LQXM47	KU179108	–	KU179109	KU179110
Jalapriya toruloides	CBS 209.65	DQ018093	–	DQ018104	DQ018081
Neodendryphiella mali	CBS 139.95 ^{T}	LT906655	–	LT906657	–
Neodendryphiella mali	FMR 17003	LT993734	–	LT993735	–
Neodendryphiella michoacanensis	FMR 16098 ^{T}	LT906660	–	LT906658	–
Neodendryphiella tarraconensis	FMR 16234 ^{T}	LT906659	–	LT906656	–
Periconia igniaria	CBS 379.86	LC014585	AB808542	AB807566	–
Periconia igniaria	CBS 845.96	LC014586	AB808543	AB807567	–
Pseudocoleophoma calamagrostidis	KT 3284^{T} = CBS 139700	LC014592	LC014614	LC014609	LC014604
Pseudocoleophoma polygonicola	KT 731^{T} = CBS 139701 = JCM 19412 = MAFF 239468	AB809634	AB808522	AB807546	AB797256
Pseudocoleophoma typhicola	MFLUCC 16-0123^{T}	KX576655	–	KX576656	–
Pseudodictyosporium elegans	CBS 688.93^{T}	DQ018099	–	DQ018106	DQ018084
Pseudodictyosporium indicum	CBS 471.95	DQ018097	–	–	–
Pseudodictyosporium wauense	NBRC 30078	DQ018098	–	DQ018105	DQ018083
Pseudodictyosporium wauense	KRP88–6	HM036613	–	–	–
Vikalpa australiensis	HKUCC 8797	DQ018092	–	–	–

Sequences obtained in this study are highlighted in bold. Ex-type strains are indicated in T after collection number.

Results

Phylogeny

The alignment to construct phylogenetic trees included 62 strains (Table 1) representative of GenBank, representing the family Dictyosporiaceae and two isolates of *Periconia igniaria* used with outgroup taxon. The combined matrix consisted of 3964

characters including alignment gaps (SSU: 1024, LSU: 1315, ITS: 638 and *TEF1*: 987). The trees obtained with ML and BI had an equivalent topology. The phylogenetic analyses inferred from the combined dataset (Fig. 1) indicated that the two strains of the fungus COAD 3174 and COAD 3175 clustered together with 100% (ML) and 1.0 (BI) support. This clade formed a distinct lineage within the genus *Digitodesmium*, forming a sister clade of the species *D. chiangmaiense.* The genus *Digitodesmium* is clearly divided into two distinct lineages highly supported: the first (100% ML and 1.0 BI support) including *D. bambusicola* CBS 110279, *Digitodesmium* sp. TBRC 10037 and *Digitodesmium* sp. TBRC 10038 and the second (99% ML and 1.0 BI support) including *D. chiangmaiense* KUN-HKAS 102163 and the two strains obtained in this study.

Taxonomy

Digitodesmium polybrachiatum T.F. Nóbrega, B.W. Ferreira and R.W. Barreto, **sp. nov.** (Fig. 2)

MycoBank: MB839275

Holotype: BRAZIL: ESPÍRITO SANTO, NOVA VENÉCIA: on dead wood of *Coffea canephora*, July 09, 2020, T. F. Nóbrega (**holotype** VIC 47492).

Ex-holotype cultures COAD 3174 and COAD 3175. DNA sequences of ex-holotype strain: MW879325 (SSU), MW879316 (LSU), MW879318 (ITS), MW890262 *TEF1.*

Etymology

In reference to its numerous conidial arms.

Description:

Saprobic on dead wood of *Coffea canephora*. Sexual morph Unknown. Colonies punctiform, scattered, glistening dark brown to black. Conidiomata sporodochial, scattered, dark brown. Conidiophores micronematous, subcylindrical, 4–8 × 4–5 µm, unbranched, thin walled, hyaline to pale brown, smooth. Conidiogenous cells monoblastic, integrated, terminal, determinate, hyaline to pale brown, smooth. Conidia acrogenous, solitary, cheiroid-ellipsoid, 35–54 × 15–19 µm, consisting of 6–9 closely compacted arms, side arms longer than middle arms, arms 7–9-euseptate, septal pores inconspicuous; arms cylindrical, 35–49 × 5–7 µm, straight (inner arms) or slightly curved (outer arms), unbranched, brown to dark brown, smooth, occasionally bearing cellular appendages attached to one of the inner arms. Appendages globose to subglobose, 10–15 × 8–14 µm, either fhin-walled and hyaline or light brown and as thick-walled as conidia, smooth.

Culture characteristics: i) on MEA – very slow-growing, 3.5 cm diam after 40 days; flat, margin strongly lobate outline with immersed dendritic borders, aerial mycelium velvety, umber centrally, bay towards the edge, pigmenting the medium with a luteous taint; no sporulation.; ii) On VBA, very slow-growing, 7 cm diam after 40 days; umbonate with strongly lobate margins. cottony center, white, followed by a ring of felty pale mouse gray mycelium and an external halo of white sparse mycelium, dark with pockets of intense sporulation; reverse sienna centrally with amber margins.

Notes

The isolates obtained in this study had a distinct morphology from the other species described in *Digitodesmium* (Table 2). *Digitodesmium polybrachiatum* sp. nov. differs from *D. macrospora*, *D. intermedium* and *D. heptasporum* by having smaller and narrower conidia (35–54 x 15–19 µm *vs*. 130–145 × 19–26 µm; 39–76 × 25–35 µm and 50–75 × 32.5–70 µm, respectively). *Digitodesmium bambusicola*, *D. chiangmaiense* and *D. elegans*, despite having conidia with similar dimensions to the newly proposed species, have few arms in their conidia as compared to *D. polybrachiatum*. In addition, in the phylogenetic tree, the isolates of *D. bambusicola* and *D. chiangmaiense* were in separate clades to that of *D. polybrachiatum*. Other characteristics that also help distinguishing *D. polybrachiatum* from other species in the genus are the occasional presence of isolate globoid appendages on its conidia, which are either hyaline and thin-walled or pale brown and thicker-walled, and the presence of

inconspicuous septal pores. Appendices are only known for *D. bambusicola* and inconspicuous septal pores is only found in *D. elegans.*

Table 2
Comparison of conidial morphology in species of *Digitodesmium*

Taxa	Colour	Dimension (µm)	Appendages	Septal pores	Number of arms	Number of septa per arm	Origin	Reference
D. bambusicola	Pale brown	24–32.5 × 12.5–23	Yes	Conspicuous	3	4–7	Philippines	Cai et al. (2002)
D. chiangmaiense	Brown to dark brown	(25–)30–45(–44) × (13–)12–21(–21)	No	Conspicuous	3	5–7	Thailand	Hyde et al. (2019)
D. elegans	–	45–60 × 12–21	No	Inconspicuous	(2–)3–4(–6)	9–12	UK	Kirk. (1981)
D. heptasporum	Pale brown	50–75 × 32.5–70	No	Conspicuous	6–7	11–17	China	Cai et al. (2003)
D. intermedium	Brown to dark brown	39–76 × 25–35	No	Conspicuous	3–11	7–13	Spain	Silvera-Simo´net al. (2010)
D. macrosporum	Brown to dark brown	130–145 × 19–26	No	Conspicuous	5–8	17–19	Spain	Silvera-Simo´net al. (2010)
D. recurvum	Pale brown	30–45 × 12.5–23	No	Conspicuous	(2–)4–6(–7)	6–10	China	Ho et al. (1999)
D. polybrachiatum sp. nov.	Brown to dark brown	35–54 x 15–19	Yes	Inconspicuous	6–9	7–9	Brazil	This study

Discussion

In the present study the new species *Digitodesmium polibracchium* was described and recognized as distinct based on the combination of a multilocus phylogenetic analysis using SSU, LSU rDNA, ITS and *TEF1* sequences – which indicated it to represent a novel monophyletic lineage and a morphological study that indicated it to be morphologically different from other species in the same genus. However, the combined phylogenetic tree showed that there is a taxonomic inconsistency in this genus. The sequences available for previously described *Digitodesmium* are grouped into two different highly supported clades. The great phylogenetic distance between these clades strongly suggests that *D. bambusicola* belongs to a different genus from *D. chiangmaiense* and *D. polybrachiatum.* Nevertheless, in order to fully clarify this situation and elucidate which of these two clades represents *Digitodesmium* sensu stricto it is necessary to compare the available sequences with those of the type for the genus – *D. elegans* IMI 238430e (Kirk, 1981). Unfortunately, there seem to be no pure cultures of this fungus available for study and there are no sequences of this species available in databases. Therefore, we decided not to propose any nomenclatural changes for *Digitodesmium* at this stage and to wait for *D. elegans* to be recollected and reexamined in the future allowing the clarification of the status for the species in the two clades.

Until then, the *Digitodesmium* genus has been reported only from Europe and Asia (Kirk 1981; Ho et al. 1999; Cai et al. 2002; Cai et al. 2003; Silvera-Simón et al. 2010; Hyde et al. 2019), so this is the first time that a species of *Digitodesmium* has been found in the Americas.

Declarations

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Contributions

TFN conducted the isolation of strains, DNA extractions, PCR amplifications, phylogenetic analyses and wrote the manuscript. BWF prepared the morphological characterization and participated in writing of the manuscript. RWB is the research leader. He corrected the text and guided throughout the development of the study.

Ethics declarations

Conflict of interest

The authors declare that they have no conflict of interest.

Data availability

The datasets generated and analysed during the current study are available either in GenBank at NCBI (National Center for Biotechnology Information), as indicated in the text, or available from the corresponding author.

References

1. Belan LL, Belan LL, Rafael AM, Lorenzoni RM et al (2018) First report of *Fusarium* species associated with *Fusarium* wilt in *Coffea canephora* plants in Brazil. Plant Dis 102:1859–1859. https://doi.org/10.1094/PDIS-01-18-0186-PDN
2. Boonmee S, D'souza MJ, Luo Z, Pinruan U et al (2016) Dictyosporiaceae fam. nov. Fungal Divers 80:457–482. https://doi.org/10.1007/s13225-016-0363-z
3. Cai L, Zhang K, McKenzie EHC, Ho WH, Hyde KD (2002) *Acrodictys liputii* sp. nov. and *Digitodesmium bambusicola* sp. nov. from bamboo submerged in Liput River in the Philippines. Nova Hedwigia 75:525–532. https://doi.org/10.1127/0029-5035/2002/0075-0525
4. Cai L, Zhang K, McKenzi EHC, Hyde KD (2003) New species of *Dictyosporium* and *Digitodesmium* from submerged wood in Yannan, China. Sydowia 55:129–135

5. Corda AC (1836) Mykologische Beobachtungen. Weitenweber's Beitrage zur gesammtem Natur-und Heilwissenschaften Prague
6. Dhingra OD, Sinclair JB (1995) Basic Plant Pathology Methods. CRC Press, Boca Raton
7. Edgar RC (2004) MUSCLE: multiple sequence alignment with high accuracy and high throughput. Nucleic Acids Res 32:1792–1797. https://doi.org/10.1093/nar/gkh340
8. Geiser DM, Lewis Ivey ML, Hakiza G, Juba JH et al (2005) *Gibberella xylarioides* (anamorph: *Fusarium xylarioides*), a causative agent of coffee wilt disease in Africa, is a previously unrecognized member of the *G. fujikuroi* species complex. Mycologia 97:191–201. https://doi.org/10.1080/15572536.2006.11832853
9. Goh TK, Hyde KD (1996) Biodiversity of freshwater fungi. J Ind Microbiol Biotechnol 17:328–345. https://doi.org/10.1007/BF01574764
10. Hepperle D (2004) SeqAssem©. Win32–Version. A sequence analysis tool contig assembler and trace data visualization tool for molecular sequences. Available at: http://www.sequentix.de
11. Ho WH, Hyde KD, Hodgkiss IJ (1999) *Digitodesmium recurvum*, a new species of chirosporous hyphomycete from Hong Kong. Mycologia 91:900–904. https://doi.org/10.1080/00275514.1999.12061096
12. Ho WH, Hyde KD, Hodgkiss IJ (2002) Seasonality and sequential occurrence of fungi on wood submerged in Tai Po Kau Forest Stream, Hong Kong. Fungal Divers 10:21–43
13. Hyde KD, Tennakoon DS, Jeewon R, Bhat DJ et al (2019) Fungal diversity notes 1036–1150: taxonomic and phylogenetic contributions on genera and species of fungal taxa. Fungal Divers 96:1–242. https://doi.org/10.1007/s13225-019-00429-2
14. Iturrieta-González I, Gené J, Guarro J, Castañeda-Ruiz RF et al (2018) *Neodendryphiella*, a novel genus of the Dictyosporiaceae (Pleosporales). MycoKeys 19–38. https://doi.org/10.3897/mycokeys.37.27275
15. Kirk PM (1981) New or interesting microfungi II. Dematiaceous hyphomycetes from Esher Common, Surrey. Trans Brit Mycol Soc 77:279–297. https://doi.org/10.1016/S0007-1536(81)80031-9
16. Kumar S, Stecher G, Li M, Knyaz C et al (2018) MEGA X: molecular evolutionary genetics analysis across computing platforms. Mol Biol Evol 35:1547–1549. https://doi.org/10.1093/molbev/msy096
17. Li WL, Luo ZL, Liu JK, Bhat DJ et al (2017) Lignicolous freshwater fungi from China I: *Aquadictyospora lignicola* gen. et sp. nov. and new record of *Pseudodictyosporium wauense* from northwestern Yunnan Province. Mycosphere 8:1587–1597. https://doi.org/10.5943/mycosphere/8/10/1
18. Liu NG, Hongsanan S, Yang J, Lin CG et al (2017) *Dendryphiella fasciculata* sp. nov. and notes on other *Dendryphiella* species. Mycosphere 8:1575–1586. https://doi.org/10.5943/mycosphere/8/9/12
19. Miller MA, Pfeiffer W, Schwartz T (2011) The CIPRES science gateway: a community resource for phylogenetic analyses. In Proceedings of the 2011 TeraGrid Conference: extreme digital discovery, pp 1–8. https://doi.org/10.1145/2016741.2016785
20. Pereira JM, Barreto RW, Ellison CA, Maffia LA (2003) *Corynespora cassiicola* f. sp. *lantanae*: a potential biocontrol agent for *Lantana camara* from Brazil. Biol Control 26:21–31. https://doi.org/10.1016/S1049-9644(02)00112-3
21. Pinnoi A, Lumyong S, Hyde KD, Jones EG (2006) Biodiversity of fungi on the palm *Eleiodoxa conferta* in Sirindhorn peat swamp forest, Narathiwat, Thailand. Fungal Divers 22:205–218
22. Pinruan U, Hyde KD, Lumyong S, McKenzie EHC et al (2007) Occurrence of fungi on tissues of the peat swamp palm *Licuala longicalycata*. Fungal Divers 25:157–173
23. Posada D, Buckley TR (2004) Model selection and model averaging in phylogenetics: advantages of Akaike information criterion and Bayesian approaches over likelihood ratio tests. Syst Biol 53:793–808. https://doi.org/10.1080/10635150490522304
24. Rayner RW (1970) A Mycological Colour Chart. CMI and British Mycological Society, Kew
25. Rehner S (2001) Primers for elongation factor 1-α (EF1-α). Available at: http://ocid.NACSE.ORG/research/deephyphae/EF1primer.pdf

26. Siddiqi MA, Corbett DCM (1965) *Fusarium* Bark Diseases of Coffee. East African Agricultural Forestry Journal 31:11–15. https://doi.org/10.1080/00128325.1965.11662018
27. Silvera-Simón C, Mercado-Sierra A, Mena-Portales J, Gene J et al (2010) Two new species of *Digitodesmium* from Euskadi (Spain). Cryptogamie 31:211–218
28. Vilgalys R, Hester M (1990) Rapid genetic identification and mapping of enzymatically amplified ribosomal DNA from several *Cryptococcus* species. J Bacteriol Res 172:4238–4246. https://doi.org/10.1128/jb.172.8.4238-4246.1990
29. White TJ, Bruns T, Lee S, Taylor J (1990) Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In: Innis GelfandM, Shinsky D, White T (eds) PCR protocols: a guide to methods and applications. Academic, New York, pp 315–322

Figures

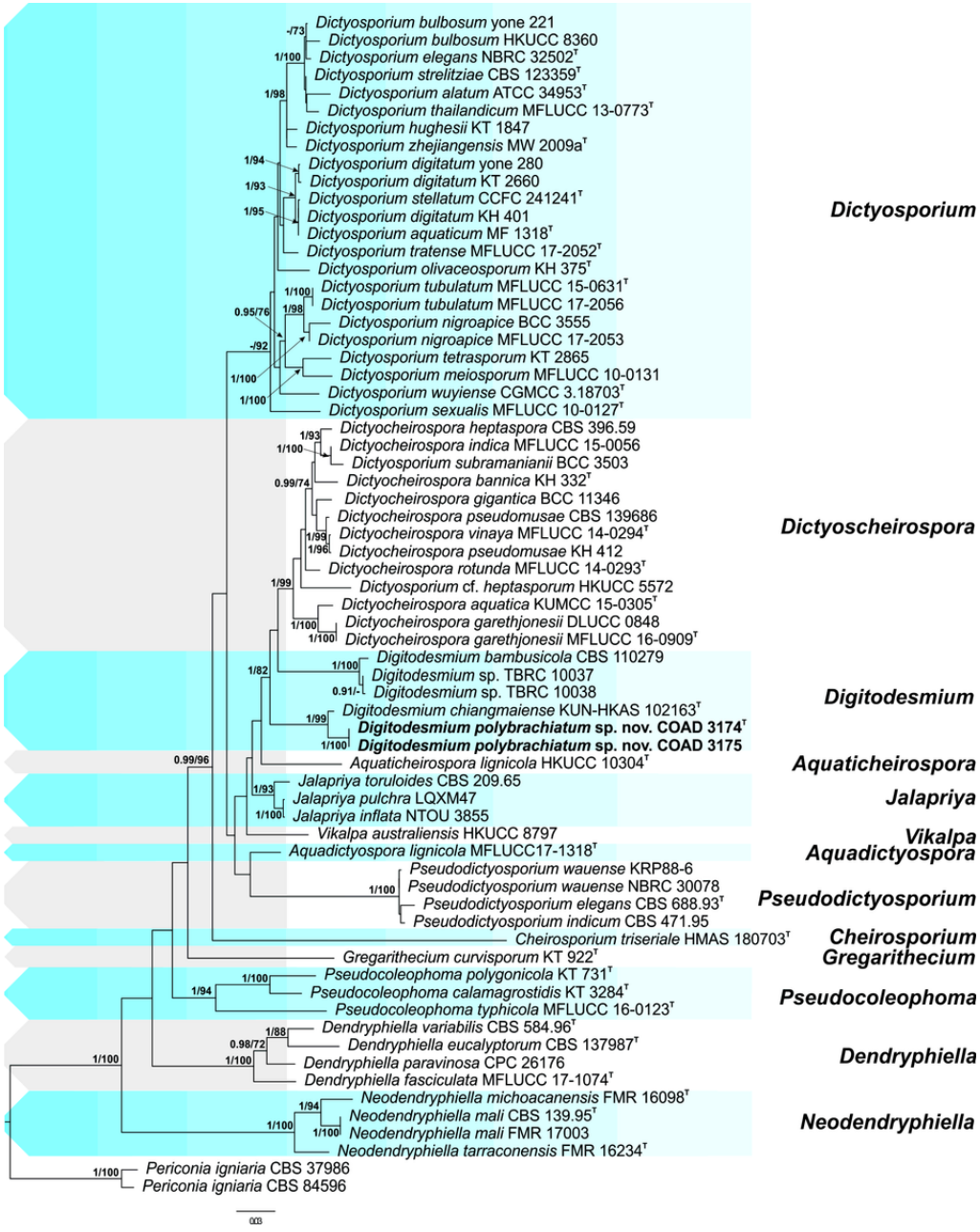

Figure 1

Maximum Likelihood (ML) tree constructed with the SSU, LSU rDNA, ITS and TEF1 sequences of strains representatives of different taxa in Dictyosporiaceae. The phylogenetic tree was rooted with Periconia igniaria. Bootstrap support values for ML greater than 70% and Bayesian posterior probabilities greater than 0.95 are given near nodes, respectively. Names of species newly described here are indicated in bold. Branch lengths are proportional to distance. T Ex-type strain.

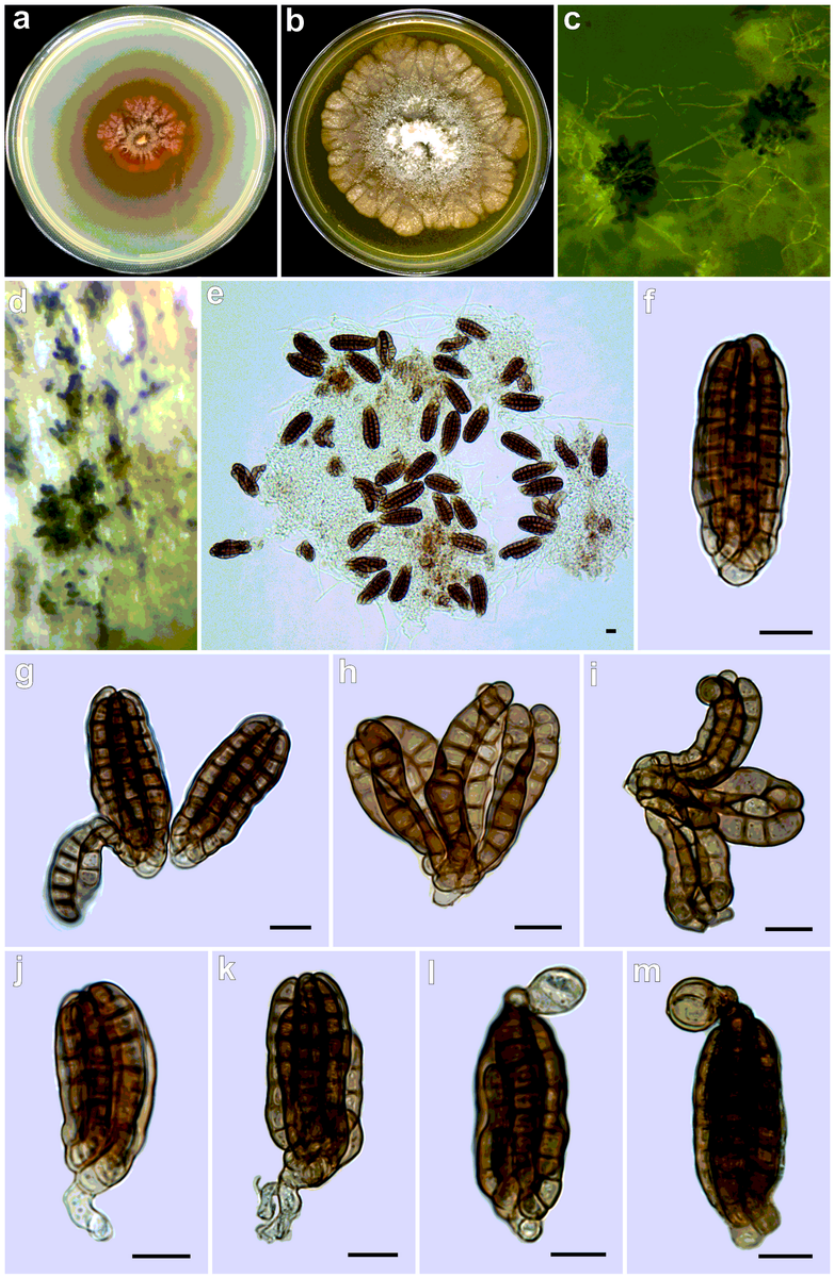

Figure 2

Digitodesmium polybrachiatum (COAD 3174). a Colony on malt extract-agar after 40-days. b Colony on vegetable broth-agar (VBA) after 40-days. c Spores produced on VBA colonies. d Colonies on coffee stem. e Squash mount of a sporodochium. f-i Conidium. j-k Conidia with conidiophores. l-m Conidia with appendages. Bars = 10 µm.