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

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Research Article

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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 tissue 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 test 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 25°C. 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, Locus 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).
| 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 | –    | –    | –           | –     |
| *Cheirosorium 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 32502T                    | 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 10–0127T               | KU179105 – KU179106 KU179107 |
| Dictyosporium stellatum         | CCFC 241241T                  | NR_154608 – JF951177 –  |
| Dictyosporium strelitzae        | CBS 123359T                   | FJ839618 – FJ839653 –   |
| Dictyosporium tetrasporum       | KT 2865 = JCM 19410 = MAFF 243834 | LC014551 AB808495 AB807519 AB797229 |
| Dictyosporium thailandicum      | MFLUCC 13–0773T               | KP716706 – KP716707 –   |
| Dictyosporium tratense          | MFLUCC 17-2052T               | MH381767 MH388820 MH381776 – |
| Dictyosporium tubulatum         | MFLUCC 15-0631T/ MFLU15_1166  | MH381769 MH388822 MH381778 – |
| Dictyosporium tubulatum         | MFLUCC 17-2056/ YJ-2018a voucher MFLU:18-1044 | MH381770 – MH381779 – |
| Dictyosporium wuyiense          | CGMCC 3.18703T                | KY072977 – – – –        |
| Dictyosporium zhejiangensis     | MW-2009aT                     | FJ456893 – – – –        |
| Digitodesmium bambusicola       | CBS 110279                    | DQ018091 – DQ018103 –   |
| Digitodesmium chiangmaiensense  | KUN-HKAS 102163               | – – MK571766 MK571775  |
| Digitodesmium polybrachiatum sp. nov | COAD 3174T                   | 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<sup>T</sup> = 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<sup>T</sup> | LT906655, –, LT906657 –                     |
| *Neodendryphiella mali*     | FMR 17003      | LT993734, –, LT993735 –                      |
| *Neodendryphiella michoacanensis* | FMR 16098<sup>T</sup> | LT906660, –, LT906658 –                   |
| *Neodendryphiella tarracensis* | FMR 16234<sup>T</sup> | LT906659, –, LT906656 –                 |
| *Periconia igniaria*        | CBS 379.86     | LC014585, AB808542, AB807566 –               |
| *Periconia igniaria*        | CBS 845.96     | LC014586, AB808543, AB807567 –               |
| *Pseudocoleophoma calamagrostidis* | KT 3284<sup>T</sup> = CBS 139700 | LC014592, LC014614, LC014609, LC014604 |
| *Pseudocoleophoma polygonicola* | KT 731<sup>T</sup> = CBS 139701 = JCM 19412 = MAFF 239468 | AB809634, AB808522, AB807546, AB797256 |
| *Pseudocoleophoma typicola* | MFLUCC 16-0123<sup>T</sup> | KX576655, –, KX576656 –             |
| *Pseudodictyosporium elegans* | CBS 688.93<sup>T</sup> | DQ018099, –, DQ018106, DQ018084             |
| *Pseudodictyosporium indicum* | –             | 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 thin-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 × 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

| 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-Simón et al. (2010)  |
| *D. macrosporum*         | Brown to dark brown | 130–145 × 19–26       | No         | Conspicuous  | 5–8              | 17–19                  | Spain   | Silvera-Simón et 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 × 15–19          | Yes        | Inconspicuous | 6–9              | 7–9                    | Brazil  | This study                    |

## Discussion

In the present study the new species *Digitodesmium polibrachium* 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.

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**Figures**

![Figure 1](image_url)
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.