Two new species of *Jalapriya* and a new record, *Dictyocheirospora vinaya* from freshwater habitats in China

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Abstract

Background

*Pleosporales* is the largest order of Dothideomycetes. In recent years, systematics of *Pleosporales* have undergone considerable revisions. Dictyosporiaceae is one of the newly established families within this order proposed to accommodate holomorphic saprobic Dothideomycetes. Currently 18 genera are recognised in Dictyosporiaceae.

New information

The new species, *Jalapriya aquaticum* sp. nov. and *J. apicalivaginatum* sp. nov. were collected from freshwater habitats in Gansu and Yunnan Provinces, China, respectively and are introduced, based on morphology and molecular analysis of combined ITS, LSU, SSU and TEF1-α sequence data. We also recovered one fresh collection of *Dictyocheirospora vinaya* D’souza, Bhat & K.D. Hyde, which is a new record for China. *Jalapriya aquaticum* differs from extant species of *Jalapriya* in rows converging at the apex.
and apical cells with spherical-like appendages. *Jalapriya apicalivaginatum* differs from extant species of *Jalapriya* in having the rows of conidia mostly arranged in a plane. The phylogenetic analysis place the new collections within Dictyosporiaceae (*Pleosporales*). Descriptions and illustrations of *Jalapriya aquaticum*, *J. apicalivaginatum* and *Dictyocheirospora vinaya* are provided. A synopsis of characters of species of *Jalapriya* is also provided.

**Keywords**

asexual morphs, Dictyosporiaceae, freshwater fungi, phylogeny, taxonomy

**Introduction**

*Pleosporales* is the largest order of Dothideomycetes. In recent years, various families and genera in the *Pleosporales* have undergone considerable revisions (Goh and Hyde 1999, Cai et al. 2008, Tanaka et al. 2009, Zhang et al. 2009, Zhang et al. 2012, Hyde et al. 2013, Ariyawansa et al. 2015, Wang et al. 2016). *Boonmee et al. (2016)* accepted eleven genera in the family Dictyosporiaceae (*Pleosporales*) to accommodate most cheiroid hyphomycetous genera that are saprobes on decaying wood and plant debris in terrestrial and freshwater habitats. One of the diagnostic characteristics of Dictyosporiaceae is their multicellular cheiroid conidia and this morphological feature distinguishes it from other families in the suborder Massarineae (Hyde et al. 2016). *Liu et al. (2017)* and *Yang et al. (2018)* updated the phylogenetic tree for Dictyosporiaceae and introduced two new genera *Aquadictyospora* and *Dendryphiella* in the family. Subsequently, three additional genera, *Neodendryphiella*, *Pseudoconiothyrium* and *Paradictyocheirospora* were added (Iturrieta-González et al. 2018, Crous et al. 2019, Rajeshkumar et al. 2021). Currently, 18 genera are accepted in Dictyosporiaceae (Boonmee et al. 2016, Li et al. 2017, Iturrieta-González et al. 2018, Yang et al. 2018, Crous et al. 2019, Hyde et al. 2020, Dong et al. 2020, Rajeshkumar et al. 2021).

The genus *Jalapriya* was introduced by *Boonmee et al. (2016)* with *Jalapriya pulchra* D'souza, Su, Luo & K.D. Hyde as type species; It is characterised by dark brown to black colonies, acrogenous, solitary and cheiroid conidia (Boonmee et al. 2016). Presently, three species are accepted in the genus, *Jalapriya inflata*, *J. pulchra* and *J. toruloides*.

*Dictyocheirospora* was established by *Boonmee et al. (2016)* to accommodate three new species, *Dictyocheirospora bannica*, *D. rotunda* and *D. vinaya* and four new combinations, *D. gigantica*, *D. heptaspora*, *D. pseudomusae* and *D. subramanianii*. *Dictyocheirospora* is characterised by non-complanate conidia with arms arising from the basal cell and closely gathered at the apex and compact (Wang et al. 2016). The species of *Dictyocheirospora* have been reported from freshwater and terrestrial habitats in China, Japan and Thailand (Jayasiri et al. 2015, Boonmee et al. 2016, Wang et al. 2016, Hyde et al. 2017, Li et al. 2017, Yang et al. 2018, Tibpromma et al. 2018, Phookamsak et al. 2019, Phukhamsakda
et al. 2020). Currently, 23 species are accepted in the genus (Boonmee et al. 2016, Yang et al. 2018, Index Fungorum - Search Page).

In this study, two new species Jalapriya aquaticum and J. apicalivaginatum and a new geographic record, Dictyocheirospora vinaya are introduced, based on morphology and phylogenetic analyses. Detailed descriptions and illustrations are provided.

Materials and methods
Isolation and morphological examination
Submerged woody substrates were collected from dynamic waters, Gansu and Yunnan Provinces and taken back to the laboratory in Zip-lock plastic bags. The samples were incubated in plastic boxes lined with moistened tissue paper at room temperature for one week. Methods of morphological observation and isolation follow Luo et al. (2018) and Senanayake et al. (2020).

The pure cultures were developed by single spore isolation following the method provided by Chomnunti et al. (2014). The cultures are deposited in Kunming Institute of Botany, Chinese Academy of Sciences (KUMCC) and China General Microbiological Culture Collection Center (CGMCC). Herbarium specimens are deposited at the Herbarium of Cryptogams Kunming Institute of Botany Academia Sinica (Herb. HKAS). Facesoffungi and Index Fungorum numbers were obtained as in Jayasiri et al. (2015) and Index Fungorum - Search Page.

DNA extraction, PCR amplification and sequencing
Genomic DNA was extracted from fresh mycelia grown on PDA at room temperature. The EZ geneTM Fungal gDNA kit (GD2416) was used to extract DNA according to the manufacturer’s instructions. ITS, LSU, TEF1-α, SSU gene regions were amplified using the primer pairs ITS5/ITS4, LROR/LR5, EF1-983F/EF1-2218R and NS1/NS4. The final volume of the PCR reaction was 25 µl and contained 12.5 µl of 2 × Power Taq PCR MasterMix (a premix and ready-to-use solution, including 0.1 Units/µl Taq DNA Polymerase, 500 µM dNTP Mixture each (dATP, dCTP, dGTP, dTTP), 20 mM Tris– HCl pH 8.3, 100 mM KCl, 3 mM MgCl₂, stabiliser and enhancer), 1 µl of each primer (10 µM), 1 µl genomic DNA extract and 9.5 µl deionised water. The PCR thermal cycle programme for ITS, LSU, TEF1α and SSU amplification was as follows: initial denaturation of 94°C for 3 minutes, followed by 35 cycles of denaturation at 94°C for 45 seconds, annealing at 56°C for 50 seconds, elongation at 72°C for 1 minute and the final extension at 72°C for 10 minutes. PCR products were purified using minicolumns, purification resin and buffer according to the manufacturer’s protocols (Amershamproduct code: 27–9602–01). The sequencing works were carried by Tsingke Biological Engineering Technology and Services Co. Ltd (Yunnan, P.R. China).
Phylogenetic analysis

Sequence data for relevant strains were downloaded from GenBank following recent publications (Boonmee et al. 2016, Li et al. 2017, Wang et al. 2016). The consensus sequences were initially aligned using MAFFT v.7 (http://mafft.cbrc.jp/alignment/server/) (Katoh and Standley 2013) and optimised manually when needed. The aligned dataset was analysed by Maximum Likelihood (ML) and Bayesian Inference (BI).

Maximum Likelihood analysis was performed using RAxMLGUI v.1.3 (Silvestro and Michalak 2011). The optimal ML tree search was conducted with 1,000 separate runs using
the default algorithm of the programme from a random starting tree for each run. The final tree was selected amongst suboptimal trees from each run by comparing the likelihood scores using the GTR+GAMMA substitution model. Maximum Likelihood bootstrap values equal to or greater than 75% were given as the first set of numbers above the nodes in the resulting ML tree (Fig. 1).

Bayesian analysis was conducted with MrBayes v.3.1.2 (Ronquist and Huelsenbeck 2003) to evaluate posterior probabilities (Rannala and Yang 1996) by Markov Chain Monte Carlo sampling (MCMC). The best-fit models of evolution were estimated by MrModeltest V.2.2 (Nylander and Uppsala University 2004). ITS, LSU and TEF selected the GTR+I+G model with inverse gamma-distributed rate in Bayesian analyses. SSU selected the GTR+G model with inverse gamma-distributed rate in Bayesian analyses. 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). Six simultaneous Markov chains were run for 10 million generations and trees were sampled every 100th generation and 100,000 trees were obtained. The first 20,000 trees, representing the burn-in phase of the analyses, were discarded, while the remaining 80,000 trees were used to calculate posterior probabilities in the majority rule consensus tree (the critical value for the topological convergence diagnostic was 0.01). Through the posterior probabilities (PP) to reflect visually the reliability of each branch without the test for bootstrap method.

The phylogenetic trees were viewed and optimised in FigTree v.1.2.2 (Rambaut and Drummond 2008) and edited further using Microsoft Office PowerPoint. Newly-generated sequences in this study were deposited in GenBank (Table 1).

| Taxon                   | Voucher/culture | GenBank accession numbers |
|-------------------------|-----------------|---------------------------|
|                         |                 | ITS | LSU | TEF1α  | SSU  |
| A. lignicola            | HKUCC 10304T    | AY864770 | AY736378 |       | AY736377 |
| Aquadictyospora clematidis | MFLUCC 17-2080T | NR171871 |       | MT394727 | NG070646 |
| A. lignicola            | MFLUCC 17-1318T | MF948621 | MF948629 | MF953164 |     |
| Cheirosporium triseriale | MB 506570       | EU413953 | EU413954 |       |     |
| Dendryphiella eucalyptorum | CBS 137987T    | KJ869139 | KJ869196 |       |     |
| Den. fasciculata        | MFLUCC 17-1074T | MF399213 | MF399214 |       |     |
| Den. paravinosa         | CBS 141286T     | KX228257 | KX228309 |       |     |
| Dictyocheirospora aquadulcis | MFLU 18-1088T | MK634545 | MK634542 |       |     |
| Di. aquatica            | KUMCC 15-0305T  | KY320508 | KY320513 |       |     |
| Di. aquatica            | HKAS 92714T     | NR154030 |       |       |     |

Table 1.
Isolates and sequences used in this study (newly-generated sequences are indicated in bold, strains isolated from the holotype and reference specimens are indicated in with a T, without GenBank accession numbers are indicated in "_").
| Taxon            | Voucher/culture | GenBank accession numbers |
|------------------|-----------------|---------------------------|
|                  |                 | ITS | LSU | TEF1α | SSU |
| Di. bannica      | HHUF 30126<sup>T</sup> | NR154039 | NG059061 | AB808489 | NG064841 |
|                  | MFLU 18-1040    | MH381765 | MH381774 | _ | MH381759 |
| Di. cheirospora  | KUMCC 17-0035<sup>T</sup> | MF177035 | MF177036 | _ | MF928073 |
| Di. clematidis   | MFLUCC 17-2089<sup>T</sup> | MT310593 | MT214546 | MT394728 | MT226665 |
| Di. garethjonesii| MFLUCC 16-0909<sup>T</sup> | KY320509 | KY320514 | _ | _ |
| Di. gigantica    | BCC 11346       | _ | _ | _ | _ |
| Di. heptaspora   | DLU 1992        | MT756244 | MT756243 | _ | _ |
| Di. indica       | MFLUCC 15-0056<sup>T</sup> | MH381763 | MH381772 | MH388817 | MH381757 |
| Di. lithocarpi   | MFLUCC 17-2537<sup>T</sup> | NR163345 | NG070074 | _ | NG065783 |
| Di. metroxylonis | MFLUCC 15-0028b<sup>T</sup> | MH742322 | MH742314 | MH764303 | MH742318 |
| Di. nabanheensis | MFLUCC 17-2291  | MK347748 | MK347965 | MK360050 | _ |
| Di. nabanheensis | MFLUCC 17-2296  | MK347756 | MK347973 | MK360051 | _ |
| Di. pandanicola  | MFLUCC 16-0365<sup>T</sup> | MH388341 | MH376713 | MH388376 | _ |
| Di. pseudomusae  | Yone 234<sup>T</sup> | LC014550 | AB807520 | AB808496 | AB797230 |
| Di. rotunda      | MFLUCC 17-0222  | MH381764 | MH381773 | MH388818 | MH381758 |
| Di. rotunda      | MFLUCC 140293a<sup>T</sup> | KU179099 | KU179010 | _ | _ |
| Di. rotunda      | MFLUCC 17-1313  | MF948625 | MF948633 | MF953168 | _ |
| Di. subramanianii| BCC 3503        | DQ018094 | AB807520 | _ | _ |
| Di. taiwanense   | MFLUCC 17-2654<sup>T</sup> | MK495821 | MK495820 | _ | _ |
| Di. thailandica  | MFLUCC 18-0987<sup>T</sup> | NR171885 | MN913743 | _ | _ |
| Di. vinaya       | MFLUCC140294d<sup>T</sup> | KU179102 | KU179103 | _ | KU179104 |
| Di. vinaya       | HKAS 115802     | MZ618659 | MZ618660 | MZ851994 | _ |
| Di. xishuangbannaensis | MFLUCC 17-2267<sup>T</sup> | MH388342 | MH376714 | MH388377 | _ |
| Dictyosporium appendiculatum | MFLUCC 17-2259 | MH388343 | MH376715 | _ | _ |
| Dictyos. aquaticum | MF1318<sup>T</sup> | KM610236 | _ | _ | _ |
| Dictyos. digitatum | MFLUCC 17-0635 | MH388344 | MH376716 | MH388378 | _ |
| Dictyos. guttulatum | MFLUCC 16-0258 | MH388345 | MH376717 | MH388379 | MH388312 |
| Dictyos. hongkongensis | MFLUCC 17-0633 | MH388346 | MH376718 | MH388380 | NG068388 |
| Dictyos. meiosporum | MFLUCC 10-0131<sup>T</sup> | KP710944 | KP710945 | _ | _ |
| Dictyos. nigroapice | MFLUCC 17-2053 | MH381768 | MH381777 | MH388821 | _ |
| Dictyos. krabiense | MFLU 16-1890   | _ | MH376719 | MH388381 | _ |
| Dictyos. palmae  | CBS H-22129    | _ | KX555648 | _ | _ |
| Dictyos. pandanicola | MFLU 16-1886 | MH388347 | MH376720 | MH388382 | _ |
| Dictyos. stellatum | CCFC 241241<sup>T</sup> | NR154608 | JF951177 | _ | _ |
| Taxon                                      | Voucher/culture | GenBank accession numbers |
|--------------------------------------------|-----------------|---------------------------|
|                                            |                 | ITS          | LSU          | TEF1α | SSU          |
| Dictyos. streitiziae                       | CBS 123359      | NR156216     | FJ839653     |       |              |
| Dictyos. tetrasporum                       | KT 2865         | LC014551     | AB807519     | AB808495 |              |
| Dictyos. tubulatum                         | MFLUCC 15-0631T | MH381769     | MH381778     | MH388822 |              |
|Dictyos. wuyiense                           | CMGC 3-1870T   | KY072977     |              |       |              |
|Dictyos. zhejiangense                       | MW-2009aT       | FJ456893     |              |       |              |
|Dictyos. bambusicola                        | CBS 110279      | DQ018091     | DQ018103     |       |              |
|Gregarithecium curvisporum                  | KT 92T          | AB809644     | AB807547     |       | AB797257     |
|Gregarithecium sp.                          | MFLUCC 13-0853  | KX364281     | KX364282     |       | KX364283     |
|Jalapriya apicalivaginatum                  | HKAS 102163     | _            | MK571766     |       | MK571775     |
|J. aquaticum (2101)                         | HKAS 115807T    | MZ621152     | MZ621169     | MZ851995 | MZ621170     |
|J. aquaticum (2351)                         | DLUCC 2351      | MZ621151     | MZ621165     |       | MZ621166     |
|J. inflata                                  | NTOU 3855       | JQ267362     | JQ267363     |       | JQ267361     |
|J. pulchra                                  | MFLUCC 15-0348T | KU179108     | KU179109     |       | KU179110     |
|J. pulchra                                  | MFLUCC 17-1683  | MF948628     | MF948636     | MF953171 |              |
|Jalapriya sp.                               | 19VA07          | JX270548     |              |       |              |
|J. toruloides                               | CBS 209.65      | DQ018093     | DQ018104     |       | DQ018081     |
|Neodendryphiella mali                       | CBS 139.95T     | LT906655     | LT906657     |       |              |
|N. michoacanensis                           | FMR 16098T      | LT906660     | LT906658     |       |              |
|N. tarraconensis                            | FMR 16234T      | LT906659     | LT906656     |       |              |
|Periconia igniaria                          | CBS 379.86      | LC014585     | AB807566     | AB808542 | AB797276     |
|P. igniaria                                 | CBS 845.96      | LC014586     | AB807567     | AB808543 | GU296171     |
|Pseudocoleophoma bauhiniae                  | MFLUCC 17-2228  | MK347735     | MK347952     | MK360075 | MK347843     |
|Pseudoc. bauhiniae                          | MFLUCC 17-2586  | MK347736     | MK347953     | MK360076 | MK347844     |
|Pseudoc. calamagrostidis                    | KT 3284T        | LC014592     | LC014609     | LC014614 | LC014604     |
|Pseudoc. polygonicola                       | KT 731T         | AB809634     | AB807546     | AB808522 | AB797256     |
|Pseudoc. tychicola                          | MFLUCC 16-0123T | KX576655     | KX576656     |       |              |
|Pseudocoaniothyrium broussonetiae           | CBS 145036      | MK442618     | MK442554     | MK442709 |              |
|Pseudodictyosporum elegans                  | CBS 688.93T     | MH862454     | MH874101     |       | DQ018084     |
|Pseudodi. indicum                           | CBS 471.95      | DQ018097     |              |       |              |
|Pseudodi. thailandica                       | MFLUCC 16-0029T | KX259520     | KX259522     | KX259526 | KX259524     |
|Pseudodi. wauense                           | NBRC 30078      | DQ018098     | DQ018105     |       | DQ018083     |
|Pseudodi. wauense                           | DUCC 0801       | MF948622     | MF948630     | MF953165 |              |
|Vikalpa australiensis                       | HKUCC 8797T     | DQ018092     |              |       |              |
Taxon treatments

*Jalapriya apicalivaginatum* D.F. Bao, X. Fu, H.Y. Su & Z.L. Luo, 2021, sp. nov.

- IndexFungorum 558682
- Species-ID Facesoffungi number: FoF 10257

**Material**

**Holotype:**

- scientificName: *Jalapriya apicalivaginatum*
- phylum: Ascomycota
- class: Dothideomycetes
- order: Pleosporales
- family: Dictysporiaceae
- genus: *Jalapriya*
- locationRemarks: China, Gansu Province, Gannan City, Xiahe County, Sangke Town, on decaying wood submerged in stream, July 2020
- habitat: decaying wood submerged in stream
- collectionID: SK 1-21-1 H
- collectionCode: L-78

**Description**

Saprobic on decaying wood submerged in stream. **Asexual morph:** Hyphomycetous (Fig. 2). Colonies effuse, scattered, dark brown or black. Mycelium mostly immersed, partly superficial, composed of smooth, septate, branched, hyaline to pale brown hyphae. Conidiophores micronematous, reduced, hyaline to pale brown, unbranched, thin-walled, smooth. Conidiogenous cells holoblastic, integrated, terminal. Conidia acrogenous, solitary, cheiroid, pale brown, the shape of conidia like a "U", with 3–5 rows of cells. The rows in the middle are little bit longer than the outer rows and each row of cells with an apical hyaline, inflated, gelatinous subglobose, cap-like appendage, the rows of conidia mostly arranged in a plane and 2 outer rows arising from a basal cell, rows not separating, each row consisting of 6–12 cells, the size of outer rows 15–52 × 3–6 µm (x = 36 × 5 µm, n = 30), excluding apical hyaline gelatinous appendages, the size of inner rows 24–47 × 4–7 µm (x = 40 × 5.5 µm, n = 30). The size of conidia 24–47 × 17–31.5 µm (x = 40 × 23 µm, n = 30). **Sexual morph:** Undetermined.

**Culture characteristics:** Conidia germinating on PDA within 24 h, germ tubes arising from the outermost cells of the conidium. Colonies on MEA covering 9 cm diam., in 4 weeks at 28°C. On the obverse, the edges are white and the middle is greyish-white. On the reverse, colonies appear pale yellow. Sporulation not observed in culture.

**Material examined:** CHINA, Gansu Province, Gannan City, Xiahe County, Sangke Town, 35°8'9"N, 102°27'11"E, on decaying wood submerged in stream, July 2020, Z.L. Luo, SK 1–21–1 H (HKAS 115801, holotype), ex-type living culture, KUNCC 21-10704 = CGMCC 3.20612.

**Etymology**

Referring to the conidia with an apical mucilaginous sheath.
Notes

In the phylogenetic analysis, *J. apicalivaginatum* formed a distinct lineage within *Jalapriya* and close to *Jalapriya* sp. (19VA07); However, the morphology of *Jalapriya* sp. (19VA07) was not available, but phylogeny of *J. apicalivaginatum* and *Jalapriya* sp. are distinct. *Jalapriya apicalivaginatum* resembles *J. pulchra* and *J. inflata* in having each conidial row of cells with an apical hyaline, inflated, gelatinous subglobose, cap-like appendage. However, *Jalapriya inflata* is characterised by branched conidiophores, whereas conidiophores of *J. apicalivaginatum* are not differentiated. *Jalapriya apicalivaginatum* has fewer number of rows than those of *J. pulchra* (3–5 rows vs. 5–7 rows) and conidia are smaller than those of *J. pulchra* (24–47 × 17–31.5 µm vs. 32–46 × 23.5–31.5 µm) (Boonmee et al. 2016) (Table 2).

![Figure 2. *Jalapriya apicalivaginatum* (HKAS 115801, holotype). a Colonies on submerged wood; b-l Conidia; m Germinating conidium; n-o Culture on PDA from above and reverse. Scale bars: b, f-g, 20 µm; c, 30 µm; d-e, h-m, 15 µm.](doi)
| Species            | Conidia                                                                 | Shape                                    | Size (µm)       | Colour          | Number of rows | Distribution                              | Reference                                           |
|--------------------|--------------------------------------------------------------------------|------------------------------------------|-----------------|-----------------|----------------|-------------------------------------------|----------------------------------------------------|
| Jalapriya inflata  | Euseptate, thin-walled and staurosporous, composed of an apically inflated basal cell | 28.5–38 × 14.5–21.5                      | Brown           | 3–4 rows        | UK, Ontario, On rotten wood               | Matsushima 1983, Kirschner et al. 2013, Boonmee et al. 2016, Iturrieta-González et al. 2018 |
| J. pulchra         | Acrogenous, solitary, each row of cells with an apical hyaline, inflated, gelatinous subglobose, cap-like appendage | 32–46 × 23.5–31.5                        | Uniform pale to medium reddish-brown | 5–7 rows | CHINA, Yunnan Province, on decaying wood submerged in stream | Boonmee et al. 2016, Iturrieta-González et al. 2018 |
| J. aquaticum       | Acrogenous, solitary, rows converging at apex, apical cells with spherical-like appendages | 22–53 × 16–24                           | Pale to medium brown | 3–4 rows | CHINA, Yunnan Province, on decaying wood submerged in stream | This study                                           |
| J. apicalivaginatum| Acrogenous, solitary, thin-walled, each row of cells with an apical hyaline, inflated, gelatinous subglobose, cap-like appendage | 24–47 × 17–31.5                         | Pale brown      | 3–5 rows        | CHINA, Gansu Province, on decaying wood submerged in stream | This study                                           |

**Jalapriya aquaticum** D.F. Bao, X. Fu, H.Y. Su & Z.L. Luo, 2021, sp. nov.

- IndexFungorum [558683](#)
- Species-ID [Facesoffungi number: FoF 10258](#)

**Material**

**Holotype:**

- scientificName: *Jalapriya aquaticum*; phylum: Ascomycota; class: Dothideomycetes; order: Pleosporales; family: Dictyosporiaceae; genus: *Jalapriya*; locationRemarks: China, Yunnan Province, Dali, Cangshan Mountain, Lingquan stream, on decaying wood submerged in stream, April 2019; habitat: Saprobic on decaying wood submerged in stream; collectionID: 1LQX III H Z-7-1; collectionCode: S-2101
Description

Saprobic on decaying wood submerged in stream. Asexual morph: Hyphomycetous (Fig. 3). Colonies punctiform, sporodochial, velvety, dark brown to black. Conidiophores micronematous, subhyaline to pale brown hyphae, unbranched, thin-walled, smooth. Mycelium immersed, composed of brown, smooth, thin-walled, septate. Conidiogenous cells holoblastic, integrated, terminal. Conidia acrogenous, solitary, cheiroid, pale to medium brown, with 3–4 rows of cells, rows converging at apex, apical cells with spherical-like appendages, the immature conidia are slightly curved and become straight after maturity. Two outer rows arising from a basal cell, rows not separating, each row consisting of 6–12 cells, the size of outer rows 29–53 × 6–8 μm (x̄ =45 × 5 μm, n = 30), excluding apical hyaline gelatinous appendages, the size of inner rows 22–44 × 4–8 μm (x̄ = 38 ×6 μm, n = 30). The size of conidia 22–53 × 16–24 μm. Sexual morph: Undetermined.

Culture characteristics: Conidia germinating on PDA within 24 h, germ tubes arising from the outermost cells of the conidium. Colonies on MEA covering 9 cm diam., in 4 weeks, at 28°C, white to cream. Sporulation not observed in culture.

Material examined: CHINA, Yunnan Province, Dali, Cangshan Mountain, Lingquan stream, 25.747501°N, 100.090989°E, on decaying wood submerged in stream, April 2019, Z.Q. Zhang, 1LQX III H Z-7-1 (S-2101) (HKAS 115807, holotype), ex-type living culture, KUNCC 21-10705 = DLUCC 2101 = CGMCC 3.20613; ibid. July 2019, Zhengquan Zhang, 2LQX III Z-56-1 H (S-2351), living culture, KUNCC 21-10706 = DLUCC 2101.

Etymology

Referring to the species collected from aquatic habitats.

Notes

In the phylogenetic analysis, J. aquaticum nested in Jalapriya and sister to J. toruloides. Morphologically, J. aquaticum is similar to J. inflata in having 3–4 rows of conidia, but differs from J. inflata in the shape of the conidia, the cells of J. inflata are fuller and more three-dimensional. J. inflata arranged more loosely in the rows of conidia and J. aquaticum packed more tightly. J. aquaticum has larger conidia than those of J. inflata (22–53 × 16–24 vs. 28.5–38 × 14.5–21.5 μm). Jalapriya quaticum similar to J. pulchra in having appendages on the apical cells of the conidia, but differs in the rows of J. aquaticum not being separable without manual force.

Dictyocheirospora vinaya D’souza, Bhat & K.D. Hyde, 2016, Fungal Diversity 80: 465

- Species-ID Facesoffungi number: FoF 01263
Material

Holotype:

- **scientificName:** *Dictyocheirospora vinaya*; **phylum:** Ascomycota; **class:** Dothideomycetes; **order:** Pleosporales; **family:** Dictyocheirosporaceae; **genus:** *Dictyocheirospora*; **locationRemarks:** Thailand. Chiang Mai, Mushroom Research Centre, on submerged wood in a freshwater stream, 24 November 2013; **habitat:** submerged wood in a freshwater stream; **identifiedBy:** D’souza, Bhat & K.D. Hyde; **type:** MFLU 14–0264; **collectionCode:** MJD-26; **source:** [https://doi.org/10.1007/s13225-016-0363-z](https://doi.org/10.1007/s13225-016-0363-z)

Description

Saprobic on decaying wood in streams. **Asexual morph:** Hyphomycetous (Fig. 4). Colonies punctiform, sporodochial, velvety, dark brown. Mycelium immersed, composed of pale brown, smooth, thin-walled septate, branched, 1–2 μm wide hyphae. Conidiophores 9–27 × 3–6 μm (x = 15 × 5 μm, n = 18), micronematous to semi-macronematous, pale brown, smooth, thin-walled. Conidiogenous cells holoblastic, integrated, terminal, determinate, pale brown. Conidia solitary, terminal, cheiroid, 48–110 × 14–32 μm (x = 73 × 22 μm, n = 30), pale brown, consisting of 7 rows of cells; rows digitate, arising from a basal cell, each arm consisting of 10–20 cells, distoseptate, constricted at septa, rows appressed when young, inwardly curved at the tip, palmately divergent when squashed, smooth-walled, guttulate. **Sexual morph:** Undetermined.

Culture characteristics: Conidia germinating on water agar within 24 h, germ tubes emerging from the basal cells of the conidium. Colonies on PDA covering 9 cm diam., in 4 weeks, at 28°C, with wavy margins, at first white, later becoming orange. Sporulating regions scattered, but mostly confined to the centre of the culture.

Material examined: CHINA, Yunnan Province, Nanpanjiang River, 24°33’57.48”N, 103°06’44.44”E, on decaying wood submerged in stream, 23 February 2018, X. He, NPJ H 3–2–1 (HKAS 115802); living culture KUNCC 21-10707.

Notes

*Dictyocheirospora vinaya*, the type species of *Dictyocheirospora*, was introduced by Boonmee et al. (2016). *Dictyocheirospora vinaya* is characterised by punctiform, dark brown colonies, pale brown, solitary, terminal, cheiroid conidia. Our fresh collection fits perfectly with the original description of *D. vinaya* (Boonmee et al. 2016). Phylogenetic analyses showed that our strain (DLUCC 1674) clustered with the ex-type strain of *D. vinaya* with high bootstrap support (93% ML and 1.00 PP). ITS comparison between our strain and MFLUCC 14–0294 revealed that there is no difference in a total of 499 bp, comparison of LSU between our strain and MFLUCC 14–0294 revealed 3 bp differences in a total of 1252 bp. Thus, we identified our new collection as *D. vinaya*, based on both phylogeny and morphology. *Dictyocheirospora vinaya* MFLUCC 14–0294 collected from freshwater habitats in Thailand, while our new collection was collected from freshwater habitats in China. It is a new record for China.
Figure 4. *Dictyocheirospora vinaya* (HKAS 115802). a Colonies on submerged wood; b Squash mount of conidioma; c-k Conidia; l Germinating conidium; m-n Culture on PDA from above and reverse. Scale bars: b, 50 μm; c-d, h-k, 40 μm; e-g, l, 30 μm.

### Identification keys

| Key to *Jalapriya* species | 1 | Conidia without appendages | *J. toruloides* |
|----------------------------|---|----------------------------|----------------|
| –                          | 2 | Conidia composed of 5–7 rows| *J. pulchra*    |
| –                          | 3 | Conidia composed of 3–5 rows|                |

Two new species of Jalapriya and a new record, *Dictyocheirospora vinaya* ...
3 Conidia 28.5–38 × 14.5–21.5 μm  
\[ J. \text{ inflata} \]

4 The size of conidia not as above  
\[ J. \text{ aquaticum} \]

4 Apical cell of conidia with spherical-like appendages  
\[ J. \text{ apicalivaginatum} \]

Analysis

Phylogenetic analysis

The combined ITS, LSU, TEF1-α and SSU dataset consisted 78 sequences representing all genera of the Dictyosporiaceae with Periconia igniaria (CBS 379.86 and CBS 845.96) as outgroup taxon. The best scoring RaxML tree with the final ML optimisation likelihood value of −20943.450686 is shown here (Fig. 1). The alignment comprised 4309 characters including gaps. The matrix had 1309 distinct alignment patterns, with 51.74% undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.241918, C = 0.244332, G = 0.269566, T = 0.244184; substitution rates AC = 1.667496, AG = 3.298982, AT = 2.345910, CG = 0.903092, CT = 8.345950, GT = 1.000000; Tree-Length = 1.761576.

Two newly-collected Jalapriya aquaticum isolates grouped with species of Jalapriya and basal to the genus with highly-supported value (100 ML/1.00 PP). Jalapriya apicalivaginatum formed a distinct lineage between J. toruloides and Jalapriya sp. (19VA07) with high bootstrap (97 ML/1.00 PP). Dictyocheirospora vinaya (HKAS 115802) clustered with its ex-type strains with high support (93 ML/1.00 PP).

Discussion

Dictyosporiaceae accommodates a holomorphic group of Dothideomycetes, including 18 genera (Hyde et al. 2019, Rajeshkumar et al. 2021). Dictyocheirospora is the second largest genus of Dictyosporiaceae, followed by Dictyosporium. Dictyocheirospora is morphologically similar to Dictyosporium in having cheiroid, cylindrical conidia; However, Dictyocheirospora differs from Dictyosporium in having non-complanate conidia with arms arising from the basal cell and closely gathered at the apex and compact, while Dictyosporium has complanate conidia without separating arms. Thus, eight species were transferred from Dictyosporium to Dictyocheirospora, based on themorphological characters and phylogenetic analyses. (Boonmee et al. 2016, Yang et al. 2018). Dictyocheirospora is cosmopolitan in distribution and commonly reported from freshwater habitats in China, India, Japan and Thailand. Nine species of Dictyocheirospora were found on submerged decaying wood, others were found in terrestrial habitats. Currently, nine species have been discovered in China including Dictyocheirospora vinaya, which is mentioned in this article. (Boonmee et al. 2016, Wang et al. 2016, Hyde et al. 2017, Li et
al. 2017, Yang et al. 2018, Tibpromma et al. 2018, Jayasiri et al. 2015, Phookamsak et al. 2019, Phukhamsakda et al. 2020, Rajeshkumar et al. 2021).

Currently, three species are accepted in Jalapriya, of which, *J. toruloides* (Corda) is a terrestrial species discovered by Hennigsson (1974) in Sweden; Afterwards it has been found in subtropical to temperate areas of both hemispheres, seemingly more often reported from coastal localities, considered an euryhaline species (Tibell et al. 2020), but our fresh collections are all from submerged wood in freshwater lotic habitats. In addition, both *J. pulchra* and *J. aquaticum* were all found in Yunnan Province, China on decaying wood submerged in a stream (Table 2). The morphological differences between *J. apicalivaginatum* and *J. pulchra* are not significant, but they are phylogenetically distinct. Morphology of *J. toruloides* is not available; However, the new species *J. aquaticum* forms a distinct clade from *J. toruloides*. *Jalapriya aquaticum* is different from other species in *Jalapriya* and forms a separate branch with high support value (100% ML and 1.00 BYPP).

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