Multi-gene phylogenetic evidence suggests *Dictyoarthrinium* belongs in Didymosphaeriaceae (Pleosporales, Dothideomycetes) and *Dictyoarthrinium musae* sp. nov. on *Musa* from Thailand

Binu C. Samarakoon\(^1,2,3\), Dhanushka N. Wanasinghe\(^4,5,6\), Milan C. Samarakoon\(^1,2\), Rungtiwa Phookamsak\(^1,4,5,6,9\), Eric H. C. McKenzie\(^8\), Putarak Chomnunti\(^2,3\), Kevin D. Hyde\(^2,7\), Saisamorn Lumyong\(^1,9,10\), Samantha C. Karunarathna\(^1,4,5,6,9\)

\(^1\) Department of Biology, Faculty of Science, Chiang Mai University, Chiang Mai 50200, Thailand \(^2\) Center of Excellence in Fungal Research, Mae Fah Luang University, Chiang Rai 57100, Thailand \(^3\) School of Science, Mae Fah Luang University, Chiang Rai 57100, Thailand \(^4\) CAS Key Laboratory for Plant Biodiversity and Biogeography of East Asia (KLPB), Kunming Institute of Botany, Chinese Academy of Sciences, Kunming 650201, Yunnan, China \(^5\) World Agro Forestry Centre, East and Central Asia, 132 Lanhei Road, Kunming 650201, Yunnan, China \(^6\) Centre for Mountain Futures (CMF), Kunming Institute of Botany, Kunming 650201, Yunnan, China \(^7\) Innovative Institute of Plant Health, Zhongkai University of Agriculture and Engineering, Guangdong Province, People's Republic of China \(^8\) Manaaki Whenua-Landcare Research, Private Bag 92170, Auckland, New Zealand \(^9\) Research Center of Microbial Diversity and Sustainable Utilization, Faculty of Sciences, Chiang Mai University, Chiang Mai 50200, Thailand \(^10\) Academy of Science, The Royal Society of Thailand, Bangkok 10300, Thailand

Corresponding authors: S. C. Karunarathna (samanthakarunarathna@gmail.com); S. Lumyong (schoi009@gmail.com)

Academic editor: Huzefa Raja | Received 16 June 2020 | Accepted 12 July 2020 | Published 5 August 2020

Citation: Samarakoon BC, Wanasinghe DN, Samarakoon MC, Phookamsak R, McKenzie EHC, Chomnunti P, Hyde KD, Lumyong S, Karunarathna SC (2020) Multi-gene phylogenetic evidence suggests *Dictyoarthrinium* belongs in Didymosphaeriaceae (Pleosporales, Dothideomycetes) and *Dictyoarthrinium musae* sp. nov. on *Musa* from Thailand. MycoKeys 71: 101–118. https://doi.org/10.3897/mycokeys.71.55493

Abstract

Dead leaves of *Musa* sp. (banana) were collected in northern Thailand during an investigation of saprobic fungi. Preliminary morphological observations revealed that three specimens belong to *Dictyoarthrinium*. Phylogenetic analyses of combined SSU, LSU, ITS and *tef1*-α sequence data revealed that *Dictyoarthrinium* forms a clade in Didymosphaeriaceae (Massarineae, Pleosporales, Dothideomycetes) sister to *Spegazzinia*. Based on contrasting morphological features with the extant taxa of *Dictyoarthrinium*, coupled with the multigene analyses, *Dictyoarthrinium musae* sp. nov. is introduced herein. Our study
provides the first detailed molecular investigation for *Dictyoarthrinium* and supports its placement in Didymosphaeriaceae (Massarinaceae, Pleosporales, Dothideomycetes). Previously, *Dictyoarthrinium* was classified in Apiosporaceae (Xylariales, Sordariomycetes).

**Keywords**
Banana, *Dictyoarthrinium sacchari*, DNA sequences, Musaceae, one new species, saprobes, taxonomy

**Introduction**

Hughes (1953) documented seven hyphomycete genera (*Arthrinium*, *Catenospegazzinia*, *Cordella*, *Dictyoarthrinium*, *Endocalyx*, *Pteroconium* and *Spegazzinia*) that had unique basauxic conidiogenous cell development. Hyde et al. (1998) accommodated *Dictyoarthrinium*, *Endocalyx*, *Scyphospora* (= *Arthrinium*) and *Spegazzinia* in Apiosporaceae (Xylariales, Sordariomycetes), based on morphological characteristics. Based on molecular phylogenetic data (LSU and ITS), *Cordella* and *Pteroconium* were synonymised under *Arthrinium* by Crous and Groenewald (2013) and *Arthrinium* was confirmed as the asexual morph of *Apiospora*. With the availability of molecular data (SSU, LSU, ITS and *tef1*-α), Tanaka et al. (2015) transferred *Spegazzinia* to Didymosphaeriaceae. Wijayawardene et al. (2018) and Hyde et al. (2020) accommodated *Arthrinium*, *Dictyoarthrinium* and *Endocalyx*, all with basauxic conidiogenous cell development, in Apiosporaceae.

*Dictyoarthrinium* was introduced by Hughes (1952) with *D. quadratum* as the type species. *Dictyoarthrinium africanum* was simultaneously introduced. Damon (1953) re-examined the type material, descriptions and illustrations of *Tetracoccosporum sacchari* (Johnston and Stevenson 1917) and mentioned that *T. sacchari* was congeneric with *Dictyoarthrinium quadratum*. Therefore, Damon (1953) combined *T. sacchari* as *Dictyoarthrinium sacchari*. Damon (1953) also named *D. quadratum* as the heterotypic synonym of *D. sacchari*. Rao and Rao (1964) introduced *D. lilliputeum* and *D. microsporum*, while Kobayasi et al. (1971) introduced *D. rabaulense* as novel taxa to the genus. Somrithipol (2007) introduced *D. synnematicum* and currently seven epithets of *Dictyoarthrinium* are listed in Index Fungorum (2020). All *Dictyoarthrinium* species were introduced, based only on morphological data. Vu et al. (2019) sequenced *D. sacchari* (CBS 529.73) and submitted LSU data to GenBank as the only valid molecular record for the genus.

*Dictyoarthrinium* is characterised by basauxic conidiogenous cell development (Hughes 1952; Damon 1953; Matsushima 1971). Basauxic development is demonstrated by conidiogenous cells in which elongation occurs at a basal growing point after formation of a single, terminal blastic conidium at its apex (Cole 1976). Conidiophores of *Dictyoarthrinium* are minutely verruculose, subhyaline and transversely septate (Ellis 1971). Usually, the septa are dark brown and appear as thick stripes on the conidiophore. Conidiophore mother cells are often hyaline or pale brown and cup-shaped (Hughes 1952) or subspherical (Ellis 1971). The length of conidiophores
Dictyoarthrinium belongs in Didymosphaeriaceae (Pleosporales, Dothideomycetes)

varies within the genus, but in some species, the dimensions are more or less similar. Conidia of Dictyoarthrinium arise from the conidiophore at terminal or lateral parts. Conidiogenesis is monoblastic or polyblastic and integrated (Ellis 1971). Conidia are simple, solitary, dematiaceous and often four-celled. Some taxa (e.g. D. africanum) have 16-celled conidia (Hughes 1952). The surface of conidia is verruculose and most species have warts on the surface. However, the conidia of D. rabaulense are densely echinulate with long spines (Kobayasi 1971). The conidia vary in shape from square to spherical, subspherical or oblong. Most conidia appear flattened on one side. As a specific feature, only D. synnematicum possesses synnemata with filaments (Somrithipol 2007). Stroma, setae and hyphopodia have not been observed in Dictyoarthrinium.

Many Dictyoarthrinium species are saprobes that colonise dead plant materials, although D. rabaulense was recorded even from soil and air (Kobayasi et al. 1971; Ellis 1976). Most Dictyoarthrinium species occur on monocotyledonous plants. The genus is widely distributed across the tropics, mainly in terrestrial environments (Ellis 1971; 1976). The sexual morph of Dictyoarthrinium is unknown. Hosts, substrates and geographical distributions of extant Dictyoarthrinium species are listed in Table 1.

A study was undertaken to determine the saprobic fungi associated with Musa sp. (banana) in Thailand, during the dry season. Three hyphomycetous taxa that morpho-

| Table 1. Hosts, substrates and geographical distribution of Dictyoarthrinium species. |
|---------------------------------------------------------------|
| **Species** | **Hosts/substrates** | **Geographical distribution** | **References** |
|---------------|-------------------|-------------------------------|---------------|
| Dictyoarthrinium africanum S. Hughes | Miscanthus, Panicum, Parpalum virgatum, Saccharum, leaf litter of Typha latifolia | Argentina, Ghana, Solomon Islands, Venezuela | Hughes (1952); Ellis (1971); McKenzie and Jackson (1986); Urtiaga (1986); Tarda et al. (2019) |
| D. lilliputum P. Rag. Rao and D. Rao | Leaf litter of Bambusa | India | Rao and Rao (1964); Sushma et al. (2020) |
| D. microsporum P. Rag. Rao and D. Rao | Dead leaves of Borassus flabellifer | India | Rao and Rao (1964) |
| D. rabaulense Matsush. | Brassica campestris, Dendrocalamus strictus, Gossypium, Xyla xylocarpa, air and soil | Bismarck Archipelago, Britain, Congo, India, New Caledonia, Nigeria, Tanzania. | Kobayasi et al. (1971); Ellis (1976); Bhat (2010) |
| D. sacchari (J.A. Stev.) Damon = D. quadratum S. Hughes | Dead stems and leaves of Ananais, Bambusa, Borassus, Cassia, Cosmos bipinnatus, Cymbopogon, Dendronema elata, Dactylaria, Erythrina, Lithochene pauciflora, Musa acuminata, M. paradisiaca, Neolitsea scrobiculata, Pandanus, Persea meehrantha, Phragmites, Prunus amygdalus, Saccharum sp., S. officinarum, S. spontaneum, Zinnia, leaf litter of Typha latifolia, decaying plant materials of dicots | Brazil, Cuba, Federated Ghana, India, Malaysia, Pakistan, Puerto Rico, Solomon Islands, Spain, States of Micronesia, Thailand, Venezuela, Zambia. | Hughes (1952); Subramanian (1952); Nair and Tyagi (1961); Srivastava et al. (1964); Dennis (1970); Ellis (1971); Matsushima (1971); Stevenson (1975); Srivastava and Gupta (1981); Arnold (1986); McKenzie and Jackson (1986); Paul and Singh (1986); Gene et al. (1990); McKenzie and Jackson (1990); Ahmad et al. (1997); Pande and Rao (1998); Lumyong et al. (2003); Saravanan and Virtal (2007); Leão-Ferreira et al. (2010); Tarda et al. (2019) |
| D. synnematicum Somrith. | Decaying leaves of Musa sp. | India, Thailand | Somrithipol (2007) |
logically resembled *Dictyoarthrinium* were examined. According to our phylogenetic analyses of combined SSU, LSU, ITS and tef1-α sequence data, *Dictyoarthrinium* clustered in Didymosphaeriaceae (Pleosporales, Dothideomycetes) with strong statistical support, sister to *Spegazzinia*. Hence, we propose to transfer *Dictyoarthrinium* from Apiosporaceae (Xylariales, Sordariomycetes) to Didymosphaeriaceae (Pleosporales, Dothideomycetes) and introduce *Dictyoarthrinium musae* sp. nov. as a saprobe recorded from *Musa* sp. We also provide detailed morphological illustrations, descriptions and DNA sequence data for *D. sacchari*, recorded on *Musa* sp. from Thailand, which further validates the novel taxonomic placement of *Dictyoarthrinium* in Didymosphaeriaceae.

**Materials and methods**

**Sample collection, morphological studies and isolation**

Dead leaves of *Musa* sp. were collected from Thailand during the dry season (December to August) of 2018 and 2019. Specimens were transferred to the laboratory in cardboard boxes. Samples were examined with a Motic SMZ 168 Series microscope. Powder-like masses of fungal conidia were mounted in water for microscopic studies and photomicrography. The specimens were examined using a Nikon ECLIPSE 80i compound microscope and photographed with a Canon 550D digital camera fitted to the microscope. Measurements were made with the Tarosoft (R) Image Frame Work programme and images used for figures were processed with Adobe Photoshop CS3 Extended v. 10.0 software (Adobe Systems, USA).

Single spore isolation was carried out following the method described in Chomnunti et al. (2014). Germinated spores were individually transferred to potato dextrose agar (PDA) plates and incubated at 25 °C in daylight. Colony characteristics were observed and measured after 3 weeks at 25 °C. Herbarium specimens were deposited in the Mae Fah Luang University (MFLU) Herbarium, Chiang Rai, Thailand. Living cultures were deposited in the Culture Collection of Mae Fah Luang University (MFLUCC). Faces of fungi numbers (Jayasiri et al. 2015) and MycoBank numbers ([http://www.MycoBank.org](http://www.MycoBank.org)) were obtained for the respective taxa.

**DNA extraction, PCR amplification and sequencing**

Fungal isolates grown on potato dextrose agar (PDA) for 4 weeks at 25 °C were used to extract total genomic DNA. DNA was extracted from 50 to 100 mg of axenic mycelium of the 4-weeks-old growing cultures. The mycelium was ground to a fine powder in liquid nitrogen and fungal DNA was extracted using the Biospin Fungus Genomic DNA Extraction Kit-BSC14S1 (BioFlux, P.R. China) according to the manufacturer's instructions. Four gene regions, the internal transcribed spacer (ITS), partial 18S small sub unit (SSU), partial 28S large sub unit (LSU) and partial translation elongation fac-
Dictyoarthrinium belongs in Didymosphaeriaceae (Pleosporales, Dothideomycetes). The 1-alpha gene (tefl-α) were amplified using ITS5/ITS4 (White et al. 1990), NS1/NS4 (White et al. 1990), LR0R/LR5 (Vilgalys and Hester 1990) and EF1-983F /EF1-2218R (Rehner 2001) primers, respectively.

Polymerase chain reactions (PCR) were conducted according to the following protocol. The total volume of the PCR reaction was 25 μl and consisted of 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 MgCl₂, stabiliser and enhancer), 1 μl of each primer (10 pM), 2 μl genomic DNA extract and 8.5 μl double distilled water (ddH₂O). The reaction was conducted by running for 40 cycles. The annealing temperature was 56 °C for ITS and LSU, 57.2 °C for tefl-α and 55 °C for SSU and initially 95 °C for 3 min, denaturation at 95 °C for 30 seconds, annealing for 1 min, elongation at 72 °C for 30 seconds and final extension at 72 °C for 10 min for all gene regions. PCR amplification was confirmed on 1% agarose electrophoresis gels stained with ethidium bromide. The amplified PCR fragments were sent to a commercial sequencing provider (TsingKe Biological Technology Co., Beijing, China). The nucleotide sequence data acquired were deposited in GenBank.

### Sequence alignment

Sequences obtained in this study were subjected to BLAST search in GenBank (https://blast.ncbi.nlm.nih.gov/Blast.cgi). BLAST search results and initial morphological studies supported that our isolates belong to Didymosphaeriaceae. Other sequences used in the analyses were obtained from GenBank based on recently published papers (Tanaka et al. 2015; Jayasiri et al. 2019) (Table 2) and BLAST search results. The single gene alignments were done by MAFFT v. 7.036 (http://mafft.cbrc.jp/alignment/server/large.html; Katoh et al. 2019) using the default settings and later refined, where necessary, using BioEdit v. 7.0.5.2 (Hall 1999).

| Taxa                               | Culture collection | ITS       | LSU       | SSU       | tefl-α   |
|------------------------------------|--------------------|-----------|-----------|-----------|----------|
| Alloconiothyrium aptrootii         | CBS 980.95T        | JX496121  | JX496234  | NA        | NA       |
| A. aptrootii                       | CBS 981.95T        | JX496122  | JX496235  | NA        | NA       |
| Austropleospora archidendri       | CBS 168.77T        | JX496049  | JX496162  | NA        | NA       |
| A. keteleeriae                     | MFLUCC 18-1551T    | NR_163349 | MK348021  | MK347910  | MK360045 |
| Bambusistroma didymosporum        | MFLU 15-0057T      | KP761733  | KP761730  | KP761737  | KP761727 |
| B. didymosporum                   | MFLU 15-0058       | KP761734  | KP761731  | KP761738  | KP761728 |
| Binuria novae zelandiae           | CBS 107.79T        | MH861181  | A016356   | A016338   | DQ471087 |
| Chromolaenicola lampangensis      | MFLUCC 17-1462T    | MN325016  | MN325004  | MN325010  | MN335649 |
| C. thailandensis                  | MFLUCC 17-1510T    | MN325018  | MN325006  | MN325012  | MN335651 |
| Cylindroasteptospora leucaenae    | MFLUCC 17-2424T    | NR_163333 | NG_066310 | MK347856  | MK360047 |
| Taxa                          | Culture collection | ITS   | LSU   | SSU   | ref1-α |
|------------------------------|--------------------|-------|-------|-------|--------|
| Deniquelata barrantingaiae   | MFLUCC 11-0422     | NR    | NG    | JX542656 | NA     |
| D. vittalii                  | NCFCI4249          | MF406218 | MF182395 | MF622059 | MF182398 |
| Dictyoarthrinium musaeae     | MFLUCC 20-0105     | MT482323 | MT482320 | MT482326 | MT495602 |
| D. musaeae                   | MFLUCC 20-0106     | MT482324 | MT482321 | MT482327 | MT495603 |
| D. sacchari                  | MFLUCC 20-0107     | MT482325 | MT482322 | MT482328 | NA     |
| D. sacchari                  | CBS 529.73         | NA    | MH872479 | NA     | NA     |
| Didymosphaeria sadasavianii  | CBS 438.65         | MH858658 | DQ384103 | NA     | NA     |
| Didymosphaeria rubi-ulmifolii| MFLUCC 14-0023     | NA    | KJ435856 | NG_063557 | NA     |
| D. rubi-ulmifolii            | MFLUCC 14-0024     | NA    | KJ435855 | KJ435857 | NA     |
| Kalmusia italicla            | MFLUCC 14-0560     | KP325440 | KP325441 | KP325442 | NA     |
| K. variisporum               | CBS 121.517        | NR     | JX469143 | NA     | NA     |
| Kalmusibambusa trisepata     | MFLUCC 13-0232     | KY682697 | KY682695 | KY682696 | NA     |
| Karstenula rhodostoma        | CBS 690.94         | NA    | GU301821 | GU296154 | GU349067 |
| K. rhodostoma                | CBS 691.94         | LC014559 | AB807531 | AB797241 | AB808506 |
| Laburnicola hauksworthii     | MFLUCC 13-0602     | KU743194 | KU743195 | KU743196 | NA     |
| L. muriformis                | MFLUCC 14-0921     | KU743200 | KU743201 | KU743202 | NA     |
| Letendrega cordylincola      | MFLUCC 11-0150     | KM213996 | KM213999 | KM214002 | NA     |
| L. cordylincola              | MFLUCC 11-0148     | NR     | NG_059530 | KM214001 | NA     |
| Montagnuma belleviae         | MFLUCC 14-0924     | KT443906 | KT443902 | KT443904 | KX949743 |
| M. crisii                    | MFLUCC 13-0680     | KX274234 | KX274234 | KX284707 | NA     |
| M. scabiosae                 | MFLUCC 14-0954     | KX443907 | KX443903 | KX443905 | NA     |
| Neokalmaia brevispora        | KT 1466           | LC014573 | AB524600 | AB524459 | AB591112 |
| N. scabrispora               | KT 1023           | LC014575 | AB524593 | AB524452 | AB59106 |
| N. aureus                    | CMG12             | MK912121 | NA     | NA     | MK948000 |
| N. auritus                   | CMG13             | MK912122 | NA     | NA     | MK948001 |
| Paracamaroporum fagi         | CPC 24890         | KR611886 | KR611904 | NA     | NA     |
| P. fagi                      | CPC 24891         | KR611887 | KR611905 | NA     | NA     |
| Paraconiothyrium cyclothyroides| CBS 972.95      | JX496119 | JX496232 | AY642524 | NA     |
| Paramusariophaeria anastomoides| CBS 615.86   | MH862005 | GU205223 | GU205246 | NA     |
| P. anastomoides              | MFLU 16-0172      | KU743206 | KU743207 | KU743208 | NA     |
| Paraphaeosphaeria roseae     | MFLUCC 17-2549     | MG828937 | MG829046 | MG829152 | MG829223 |
| P. rosicola                  | MFLUCC 15-0042     | NR_157528 | MG829047 | MG829153 | NA     |
| Phanodothri winteri          | CBS 182.58        | NA    | GU301857 | GU296183 | NA     |
| Pseudoacamaroporum propinquum| MFLUCC 13-0544    | KJ747049 | KJ813280 | KJ819949 | NA     |
| P. pteleae                   | MFLUCC 17-0724     | NR_157536 | MG829061 | MG829166 | MG829233 |
| Pseudopithomyces entadae      | MFLUCC 17-0917     | NA    | MG829064 | MG829168 | NA     |
| P. roseae                    | MFLUCC 15-0035     | MG82953 | MG829064 | MG829168 | NA     |
| Spegazzinia bromeliacearum    | URM 8084          | MK804501 | MK809513 | NA     | NA     |
| S. deightoni                 | MFLUCC 20-0002     | MN956768 | MN956772 | MN956770 | NA     |
| S. intermediia               | CBS 249.89        | MH862171 | MH873861 | NA     | NA     |
| S. lobulata                  | CBS 361.58        | MH857812 | MH869344 | NA     | NA     |
| S. musae                      | MFLUCC 20-0001    | MN930512 | MN930514 | MN930513 | NA     |
| S. neosundara                | MFLUCC 15-0456    | KX965728 | KX954397 | KX986341 | NA     |
| S. radermachenae             | MFLUCC 17-2285     | MK347740 | MK347957 | MK347848 | MK360088 |
| S. tesartha                  | SH 287            | JQ673429 | AB807584 | AB797249 | AB808560 |
| Tremeata arundicola          | MFLU 16-1275      | KX274241 | KX274248 | KX274254 | KX284706 |
| T. guiangensis               | GZAA5103         | KX274240 | KX274247 | KX274253 | KX284705 |
| T. musripora                 | GZC2 18-2787      | NR_165916 | MK972751 | MK972750 | MK986482 |
| Verrucoconiothyrium nitidae  | CBS119209         | EU552112 | NA     | NA     | NA     |
| Xenocamarosporium acacae      | CBS139895         | NR_137982 | NG_058163 | NA     | NA     |
| X. acacae                    | MFLUCC 17-2432     | MK347766 | MK347983 | MK347873 | MK360093 |

*Abbreviations of culture collections: CBS: Centraalbureau voor Schimmelcultures, Utrecht, The Netherlands. CPC: Working collection of Pedro Crous housed at CBS, GZAAS: Guizhou Academy of Agricultural Sciences Herbarium, China, KT: K. Tanaka, MFLU: Mae Fah Luang University, Chiang Rai, Thailand, MFLUCC: Mae Fah Luang University Culture Collection, Chiang Rai, Thailand, SH: Academia Sinica People's Republic of China. Shanghai, URM: Universidade Federal de Pernambuco.
Dictyoarthrinium belongs in Didymosphaeriaceae (Pleosporales, Dothideomycetes)

Phylogenetic analyses

Maximum Likelihood (ML) trees were generated using the RAxML-HPC2 on XSEDE (8.2.8) (Stamatakis et al. 2008; Stamatakis 2014) in the CIPRES Science Gateway platform (Miller et al. 2010) using GTR+I+G model of evolution. Bootstrap supports were obtained by running 1000 pseudo-replicates. Maximum Likelihood bootstrap values (ML) ≥ 60% are given above each node of the phylogenetic tree in blue (Fig. 1).

Bayesian analysis was conducted with MrBayes v. 3.1.2 (Huelsenbeck and Ronquist 2001) to evaluate posterior probabilities (PP) (Rannala and Yang 1996; Zhaxybayeva and Gogarten 2002) by Markov Chain Monte Carlo sampling (BMCMC). Two parallel runs were conducted, using the default settings, but with the following adjustments: four simultaneous Markov chains were run for 2,000,000 generations, trees were sampled every 100th generation and 20,001 trees were obtained. The first 4,000 trees, representing the burn-in phase of the analyses, were discarded. The remaining 16,001 trees were used for calculating PP in the majority rule consensus tree. Branches with Bayesian posterior probabilities (BYPP) ≥ 0.95 are indicated above each node of the phylogenetic tree (Fig. 1). Phylogenetic trees were visualised with the FigTree v1.4.0 programme (Rambaut 2011).

Results

The combined SSU, LSU, ITS and tefl-α matrix comprised 61 sequences that represents the genera in Didymosphaeriaceae. The best scoring RAxML tree is shown (Fig. 1) with a final ML optimisation likelihood value of -19278.64. The matrix had 1091 distinct alignment patterns, with 39.08% of undetermined characters or gaps. Estimated base frequencies were: A = 0.234095, C = 0.252628, G = 0.278053, T = 0.235224; substitution rates AC = 1.252730, AG = 2.198875, AT = 1.318760, CG = 0.953798, CT = 5.276095, GT = 1.000000; proportion of invariable sites I = 0.491333; gamma distribution shape parameter α = 0.446418. All trees (ML and BYPP) were similar in topology and did not differ at the generic relationships, which are in agreement with multi-gene phylogeny of Tanaka et al. (2015) and Jayasiri et al. (2019). All Dictyoarthrinium strains analysed herein clustered as a highly-supported monophyletic clade (ML = 100%, BYPP = 1.00) in Didymosphaeriaceae (Fig. 1) sister to Spegazzinia (ML = 75%, BYPP = 0.98). We have included LSU sequence data of D. sacchari (CBS 529.73) of Vu et al. (2019) in our phylogenetic analyses. According to GenBank, CBS 529.73 was classified in Apiosporaceae (Sordariomycetes). In our analyses, D. sacchari (CBS 529.73) clustered with MFLUCC 20-0105, MFLUCC 20-0106 and MFLUCC 20-0107 strains in Didymosphaeriaceae with a strong statistical support (ML = 100%, BYPP = 1.00). Our strain MFLUCC 20-0107 grouped with D. sacchari (CBS 529.73). The novel isolates of D. musae (MFLUCC 20-0105 and MFLUCC 20-0106) were sister to D. sacchari (CBS 529.73 and MFLUCC 20-0107) with strong statistical support (ML = 100%, BYPP = 1.00).
Figure 1. Maximum Likelihood tree revealed by RAxML from an analysis of SSU, LSU and ITS and tef 1-α sequence data of the genera of Didymosphaeriaceae, showing the phylogenetic position of Dictyoarthrinium musae (MFLUCC 20-0105, MFLUCC 20-0106) and D. sacchari (MFLUCC 20-0107). ML bootstrap supports (≥ 60%) and Bayesian posterior probabilities (≥ 0.95 BYPP) are given above the branches, respectively. The tree is rooted with Bambusistroma didymosporum (MFLU 15-0057 and MFLU 15-0058). Strains generated in this study are indicated in brown bold type. Ex-type strains are indicated in black bold. The scale bar represents the expected number of nucleotide substitutions per site.
**Dictyoarthrinium belongs in Didymosphaeriaceae (Pleosporales, Dothideomycetes)**

### Taxonomy

*Dictyoarthrinium musae* Samarakoon, Chomnunti & K.D. Hyde, sp. nov.

Mycobank No: 835764
Facesoffungi Number: FoF08467

**Figure 2**

**Etymology.** Name reflects the host genus, *Musa* (Musaceae).

**Holotype.** MFLU 20-0437

**Description.** *Saprobic* on dead leaves of *Musa* sp. **Sexual morph:** Undetermined. **Asexual morph:** Colonies compact or effuse, black, often pulvinate. *Mycelium* superficial, a close network of branched and anastomosing hyphae. *Stromata* none. *Setae* and *hyphopodia* absent. *Conidiophores* 30–140 × 1–2 μm (x̄ = 81.5 × 1.6 μm, n = 25), basaustic, arising usually singly from subspherical, subhyaline to light brown conidiophore mother cells, 4.5–4.8 × 4.3–4.5 μm (x̄ = 4.6 × 4.4 μm, n = 10), macronematous, mononematous, straight or flexuous, narrow, cylindrical, rough, subhyaline to pale brown, with thick brown or dark brown transverse septa that appear as stripes with distances of 6.3–5.8 μm at apex and 2.3–3 μm at base of the conidiophore. *Conidiogenous cells* 4.1–4.5 × 4.3–4.7 μm (x̄ = 4.4 × 4.5 μm, n = 10), blastic, integrated, terminal and intercalary, cylindrical, smooth, denticles absent, hyaline. *Conidia* 7–11.5 × 6.5–9 μm (x̄ = 8.7 × 7.9 μm, n = 40), solitary, dry, acropleurogenous, simple, square, rounded at the corners, 4-celled, spherical or subspherical, often flattened in one plane, pale to dark brown at maturity, verrucose, with light brown to dark brown warts, immature conidia often 1-celled and subhyaline. Terminal conidium with four cells, sometimes absent or fallen before lateral conidia, mature conidia split along one line of the septa, most conidia arranged obliquely downwards on the conidiophore, conidial formation observed as a bunch starting after conidiophore 1–3 septate.

**Culture characteristics.** Conidia germinating on PDA within 18 hrs. Colonies on PDA reaching a diameter of 50 mm after 14 days at 25 °C, slightly raised, hairy, filamentous, moderately dense, middle light grey, periphery white; reverse white to greyish-white.

**Material examined.** THAILAND. Chiang Rai. On dead leaves of *Musa* sp. (Musaceae), 7 December 2018, M. C. Samarakoon, BNS265 (MFLU 20-0437, holotype), ex-type living culture (MFLUCC 20-0105); *ibid*. 20 February 2019, B. C. Samarakoon BNS2239 (MFLU 20-0438, paratype), ex-paratype living culture (MFLUCC 20-0106).

**Notes.** Based on BLAST search results of SSU, LSU, ITS and *tef1–α* sequence data, *Dictyoarthrinium musae* (MFLUCC 20-0105 and MFLUCC 20-0106) showed high similarity as follows: SSU = 99.15% to *Paraconiothyrium hawaiiense* (CBS 120025), LSU = 95.57% to *Cylindroaseptospora siamensis* (MFLUCC 17-2527), ITS = 98.24% to *Kalmusia italica* (isolate 5), *tef1–α* = 97.75% to *Spegazzinia neosundara* (MFLUCC 13-0211) with 100%, 100%, 87% and 99% query covers, respectively. In the multigene phylogeny, the *Dictyoarthrinium* clade was sister to *Spegazzinia* (ML = 75%, BYPP = 0.98). Within the *Dictyoarthrinium* clade, *D. musae* (MFLUCC 20-0105 and MFLUCC 20-0106) separated from the sister taxon, *D. sacchari* with strong statisti-
cal support (ML = 100%, BYPP = 1.00). ITS sequence comparison revealed 7.84% base pair differences between *D. musae* and *D. sacchari* (MFLUCC 20-0107), which is in agreement with the new species concept outlined by Jeewon and Hyde (2016). *Dictyoarthrinium musae* differs from *D. sacchari* by its unique conidial development in the apex. The terminal conidia of *D. musae* are always 4-celled and similar in colour.

Figure 2. *Dictyoarthrinium musae* (MFLU 20-0437, holotype) a conidia on the host b conidiophore and conidia with conidiophore mother cell c–f conidia with conidiophores on stalk g developmental stage of an immature lateral conidium h four-celled terminal conidium i conidiophore j conidiophores and conidia with terminal conidium k, l conidiophores without terminal conidium m attachment of a mature lateral conidium n–q warty four-celled mature conidia r, s mature conidia that split at septa t colony on PDA after 21 days. Scale bars: 500 μm (a); 50 μm (b, c); 20 μm (d–g, i); 10 μm (h); 5 μm (j–s).
Dictyoarthrinium belongs in Didymosphaeriaceae (Pleosporales, Dothideomycetes) to mature lateral conidia. In addition, the terminal conidia of *D. musae* are sometimes absent or fallen before the lateral conidia. In contrast, the terminal conidia of *D. sacchari* can be 2-celled or 4-celled, pale brown with respect to lateral mature conidia and always persist on the conidiophore. In addition, the mature conidia of *D. musae* split along one line of the septa and this specific feature is absent in *D. sacchari*. *Dictyoarthrinium musae* has a subhyaline, spherical conidiophore mother cell while *D. sacchari* has a distinct cup-shaped, brown conidiophore mother cell. Therefore, based on contrasting morphological differences to *D. sacchari* and strong statistical support from our molecular phylogeny, *D. musae* is herein introduced as a new species.

*Dictyoarthrinium sacchari* (J.A. Stev.) Damon, Bull. Torrey bot. Club 80: 164 (1953)
Facesoffungi Number: FoF08468
Figure 3

**Description.** Saprobic on dead leaves of *Musa* sp. **Sexual morph:** Undetermined. **Asexual morph:** **Colonies** compact or effuse, black, often pulvinate. **Mycelium** superficial, a close network of branched and anastomosing hyphae. **Stromata** none. **Setae** and **hyphopodia** absent. **Conidiophores** 50–110 × 1–2 μm (μ̄ = 72.0 × 1.6 μm, n = 15), basauxic, arising from cup-shaped, brown, distinct conidiophore mother cells, 3.4–4.4 × 2.9–4.7 μm (μ̄ = 4 × 3.7 μm, n = 10), macronematous, mononematous, usually straight or flexuous, narrow, cylindrical, rough-walled, subhyaline to pale brown, with dark brown transverse septa as stripes with distances of 6.3–5.8 μm at apex and 2.3–3 μm at base of the conidiophore. **Conidiogenous cells** 4–4.5 × 4.3–4.7 μm (μ̄ = 4.4 × 4.5 μm, n = 10), blastic, integrated, terminal and intercalary, cylindrical, smooth, hyaline. **Conidia** at maturity 8.5–11.5 × 8.5–10 μm (μ̄ = 9.9 × 9.3 μm, n = 40), solitary, dry, acropleurogenous, simple, square, rounded at the corners, 4-celled, but difficult to distinguish the cells due to their blackish-brown nature, spherical or subspherical, often flattened in one plane, blackish-brown at maturity, with brown warts on surface of the cells, terminal conidium always 4-celled or 2-celled, light brown when compared with lateral conidia, most conidia arranged perpendicular to the conidiophore, some directed obliquely upwards.

**Culture characteristics.** Conidia germinating on PDA within 18 hrs. Colonies on PDA reaching a diameter of 55 mm after 14 days at 25 °C, raised, moderately dense, entire margined, brownish-grey at maturity; reverse white to greyish-white.

**Material examined.** THAILAND, Chiang Mai. On mid-rib of a dead leaf of *Musa* sp. (Musaceae), S. Phongeun, 18 July 2018, BNS2287, (MFLU 20-0439), living culture MFLUCC 20-0107.

**Notes.** Based on BLAST search results of SSU, LSU, ITS and *tef1-α* sequence data, our strain (MFLUCC 20-0107) showed high similarity to the taxa in GenBank as follows (SSU = 99.26% to *Paraconiothyrium brasiliense* (isolate GF1), LSU = 96.14% to *Alloconiothyrium aptrooti* (CBS 981.95), ITS = 93.00% to *Kalmusia italica* (MFLUCC 13-0066). In the multigene phylogeny, MFLUCC 20-0107 groups with *Dictyoarthrinium sacchari*, sister to *D. musae* with strong statistical support (ML = 100%, BYPP =
Our strain shares similar morphological features with *D. sacchari* (Subramani 1952; Ellis 1971) and did not differ significantly. There are slight differences in conidial dimensions and the length of conidiophores of our collection and other *D. sacchari* collections by previous studies. Conidial dimensions and the length of conidiophores may differ due to diverse environmental effects and host associations. LSU sequence data of *D. sacchari* (CBS 529.73) are identical with our strain (MFLUCC 20-0107). Unfortunately, ITS, SSU and *tef1*-α sequence data of CBS 529.73 are not

**Figure 3.** *Dictyoarthrinium sacchari* (MFLU 20-0439) *a* conidia on the host *b* developmental stage of terminal conidium attached to the conidiophore *c–f* Conidiophores and conidia (*e*, with distinct mother cell) *g, h* mature conidiophores with four-celled terminal conidium *i* conidiophore with two celled terminal conidium *j* developmental stages of conidia on conidiophore *k* colony on PDA after 21 days *l–q* conidia. Scale bars: *a* = 1000 μm (*a*); 20 μm (*b, j*); 50 μm (*c–i*); 5 μm (*l–q*).
Dictyoarthrinium belongs in Didymosphaeriaceae (Pleosporales, Dothideomycetes) available in GenBank to compare with our strain. LSU data of Dictyoarthrinium musae have 2.24% of base pair difference with D. sacchari (CBS 529.73 and MFLUCC 20-0107). Dictyoarthrinium sacchari was reported on Musa sp. from Thailand in Lumyong et al. (2003) without morpho-molecular justifications. In this study, we document D. sacchari with detailed morphological illustrations, description, herbarium material and a living culture coupled with DNA sequence data (SSU, LSU, ITS) for a better taxonomic resolution.
Discussion

Both *Dictyoarthrinium* and *Spegazzinia* are characterised by basauxic conidiophores (Hughes 1952; Ellis 1971; Tanaka et al. 2015). *Spegazzinia* often has stellate (α) and disc-shaped (β) conidia (Ellis 1971; Tanaka et al. 2015). The conidia of *Dictyoarthrinium* (except *D. africanum*) share some similar characteristics with disc-shaped, β conidia of *Spegazzinia*. Both conidia are brown, 4-celled and constricted at the septa. Conidia of *Dictyoarthrinium* have characteristic hyaline or brown warts. Rarely, some taxa of *Spegazzinia*, for example, *S. deightonii*, also bear blunt ended spines. Most disc-shaped conidia of *Spegazzinia* are not warted. In addition, stellate conidia of *Spegazzinia* are always 4–5-celled and spinulose (Ellis 1971; Tanaka et al. 2015). There are contrasting morphological features of the basauxic conidiophores of both genera. The conidiophores of *Dictyoarthrinium* are hyaline to subhyaline with septa that appear as dark brown or light brown stripes throughout the conidiophore. The conidiophores (in stellate conidia) of *Spegazzinia* are more elongated, narrow, asceptate and dematiaceous.

*Dictyoarthrinium quadratum* (type of *Dictyoarthrinium*) is the heterotypic synonym of *D. sacchari*. *Dictyoarthrinium quadratum* has a terminal mature conidium with one to two cells. As described in Hughes (1952), these 2-celled conidia remain on the conidiophore, even when other conidia fall off. This feature is absent in *D. musae*. The terminal conidium of *D. musae* always ends up with four cells. The conidia of *D. quadratum* are obliquely upwardly directed, whereas the conidia of *D. musae* are obliquely downwardly directed (Fig. 2). The conidiophores of *D. quadratum* are erect and straight while *D. musae* has more curved conidiophores.

*Dictyoarthrinium africanum* differs significantly from *D. musae* by having 16-celled conidia. The conidia of *D. rabaulense* are completely black and densely echinulate with spines sometimes up to 4 μm long (Ellis 1976). However, *D. musae* has brown warts on the surface of conidia, while *D. lilliputeum* has hyaline warts. *Dictyoarthrinium microsporum* has longer conidiophores (250 μm) than *D. musae*. Morphological features of *Dictyoarthrinium* species are illustrated in Fig. 4. A key to the species of *Dictyoarthrinium* is provided below.

**Key to the species of Dictyoarthrinium**

1. Synnemata present .................................................. *D. synnematicum*
   – Synnemata absent ..................................................2

2. Conidia 2- or 4-celled .................................................3
   – Conidia 16-celled .................................................... *D. africanum*

3. Conidia with brown warts ...........................................4
   – Conidia with hyaline warts ....................................... *D. lilliputeum*

4. Conidiophores up to 130 μm long ................................ *D. microsporum *
   – Conidiophores up to 250 μm long
Dictyoarthrinium belongs in Didymosphaeriaceae (Pleosporales, Dothideomycetes)

5 Terminal conidium always 4-celled, mature conidia split along one line of the septa.......................................................... D. musae

– Terminal conidium 2- or 4-celled, mature conidia do not split along septa.......................................................... D. sacchari

To date, the taxonomy and phylogeny of most genera that have basauxic conidio-genesis (Hughes 1952) have been resolved with their correct taxonomic placements. Dictyoarthrinium and Endocalyx represented the sole unresolved genera. We transferred Dictyoarthrinium to Didymosphaeriaceae based on morphological and molecular evidence. This study uses multigene sequence data of SSU, LSU, ITS and tef1-α for the first time to confirm the taxonomic placement of Dictyoarthrinium in Didymosphaeriaceae.

Acknowledgements

Samantha C. Karunarathna would like to thank the CAS President’s International Fellowship Initiative (PIFI) young staff under the grant number: 2020FYC0002 for funding his postdoctoral research and the National Science Foundation of China (NSFC, project code 31851110759) for partially funding this work. Rungtiwa Phookamsak thanks CAS President’s International Fellowship Initiative (PIFI) for young staff (grant no. Y9215811Q1), the National Science Foundation of China (NSFC) project code 31850410489 (grant no. Y811982211) and Chiang Mai University for their partial support of this research work. Dhanushka Wanasinghe thanks CAS President’s International Fellowship Initiative (PIFI) for funding his postdoctoral research (number 2019PC0008), the National Science Foundation of China and Chinese Academy of Sciences for financial support under the grant 41761144055. K.D Hyde thanks Thailand research grants entitled “The future of specialist fungi in a changing climate: baseline data for generalist and specialist fungi associated with ants, Rhododendron species and Dracaena species (Grant No: DBG6080013) and “Impact of climate change on fungal diversity and biogeography in the Greater Mekong Sub region (Grant No: RDG6130001). Binu C. Samarakoon offers her sincere gratitude to S. Phongeun, G. Samarakoon, Seetha Malani, Thiue Samarakoon and A.J Gajanayake for the valuable support they have given.

References

Ahmad S, Iqbal SH, Khalid AN (1997) Fungi of Pakistan. Sultan Ahmad Mycological Society of Pakistan, 248 pp.

Arnold GRW (1986) Lista de Hongos Fitopatogenos de Cuba. Ministerio de Cultura Editorial Cientifico-Tecnica, 207 pp.

Bhat DJ (2010) Fascinating Microfungi (Hyphomycetes) of Western Ghats – India. Broadway Publishing House, 190–221.
Chomnunti P, Hongsanan S, Hudson BA, Tian Q, Peršoh D, Dhami MK, Alias AS, Xu J, Liu X, Stadler M, Hyde KD (2014) The sooty moulds. Fungal Diversity 66: 1–36. https://doi.org/10.1007/s13225-014-0278-5

Cole GT (1986) Models of cell differentiation in conidial fungi. Microbiological Reviews 50: 95–132. https://doi.org/10.1128/MMBR.50.2.95-132.1986

Crous PW, Groenewald JZ (2013) A phylogenetic re-evaluation of Arthrinium. IMA Fungus 4: 133–154. https://doi.org/10.5598/imafungus.2013.04.01.13

Damon SC (1953) Notes on the hyphomycetous genera, Spegazzinia Sacc. and Isthmospora. Bulletin of the Torrey Botanical Club: 155–165. https://doi.org/10.2307/2482189

Dennis RWG (1970) Fungus Flora of Venezuela and Adjacent Countries. Kew Bulletin Additional Series III. Verlag von J. Cramer, 531 pp.

Ellis MB (1971) Dematiaceous Hyphomycetes. Commonwealth Mycological Institute, Kew. Ellis MB (1976) More Dematiaceous Hyphomycetes. Commonwealth Mycological Institute, Kew. Gene J, Cano J, Guarro J (1990) [Contribution to the study of the Spanish hyphomycetes XI]. Revista Iberoamericana de Micología 7: 31–33.

Hall TA (1999) BioEdit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. Nucleic Acids Symposium Series 41: 95–98.

Huelsenbeck JP, Ronquist F (2001) MRBAYES: Bayesian inference of phylogenetic trees. Bioinformatics 17: 754–755. https://doi.org/10.1093/bioinformatics/17.8.754

Hughes SJ (1952) Fungi from the Gold Coast. 11. Mycological Papers 50: 1–104.

Hughes SJ (1953) Conidiophores, conidia, and classification. Canadian Journal of Botany 39: 577–679. https://doi.org/10.1139/b53-046

Hyde KD, Fröhlich J, Taylor JE (1998) Fungi from palms XXXVI Reflections on unitunicate ascomycetes with apiospores. Sydowia 50: 21–80.

Hyde KD, Norphanphoun C, Mahararchikumbura SSN, Bhat DJ, Jones EBG, Bundhun D, Chen YJ, Bao DF, Boonmee S, Calabon MS, Chaiwan N, Chethana KWT, Dai DQ, Dayaratne MC, Devadatha B, Dissanayake AJ, Dissanayake LS, Doilom M, Dong W, Fan XL, Goonasekara ID, Hongsanan S, Huang SK, Jayawardena RS, Jeewon R, Karunarathna A, Konta S, Kumar V, Lin CG, Liu JK, Liu NG, Luangs-a-ard J, Lumyong S, Luo ZL, Marasinghe DS, McKenzie EHC, Niego AGT, Niranjan M, Perera RH, Phukhamsakda C, Rathnayaka AR, Samarakoon MC, Samarakoon SMBC, Sarma VV, Senanayake IC, Shang QJ, Stadler M, Tibpromma S, Wanasighe DN, Wei DP, Wijayawardene NN, Xiao YP, Yang J, Zeng XY, Zhang SN, Xiang MM (2020) Refined families of Sordariomycetes. Mycosphere 11: 305–1059. https://doi.org/10.5943/mycosphere/11/17

Index Fungorum (2020) Index Fungorum. http://www.indexfungorum.org/Names/Names.asp [Retrieved 5 May 2020]

Jayasiri SC, Hyde KD, Ariyawansa HA, Bhat J, Buyck B, Cai L, Dai YC, Abd-Elsalam KA, Ertz D, Hidayat I, Jeewon R (2015) The Faces of fungi database: fungal names linked with morphology, molecular and human attributes. Fungal Diversity 74(1): 3–18. https://doi.org/10.1007/s13225-015-0351-8

Jayasiri SC, Hyde KD, Jones EBG, McKenzie EHC, Jeewon R, Phillips AJL, Bhat DJ, Wanasighe DN, Liu JK, Lu YZ, Kang JC, Xu J, Karunarathna SC (2019) Diversity, morphology and molecular phylogeny of Dothideomycetes on decaying wild seed pods and fruits. Mycosphere 10: 1–186. https://doi.org/10.5943/mycosphere/10/1/1
Dictyoarthrinium belongs in Didymosphaeriaceae (Pleosporales, Dothideomycetes)

Jeewon R, Hyde KD (2016) Establishing species boundaries and new taxa among fungi: recommendations to resolve taxonomic ambiguities. Mycosphere 7: 1669–1677. https://doi.org/10.5943/mycosphere/7/11/4

Johnston JR, Stevenson JA (1917) Sugar cane fungi and diseases of Porto Rico. Journal of the Department of Agriculture, Porto Rico 1: 177–264.

Katoh K, Rozewicki J, Yamada KD (2019) MAFFT online service: multiple sequence alignment, interactive sequence choice and visualization. Briefings in Bioinformatics 20: 1160–1166. https://doi.org/10.1093/bib/bbx108

Kobayasi Y (1971) Mycological reports from New Guinea and the Solomon Islands. Bulletin of the National Museum of Nature and Science, 1–11.

Leão-Ferreira SM, Gusmão LFP (2010) Conidial fungi from the semi-arid Caatinga biome of Brazil. New species of Endophragmiella and Spegazzinia with new records for Brazil, South America, and Neotropica. Mycotaxon 111: 1–10. https://doi.org/10.5248/111.1

Lumyong P, Photita W, McKenzie EHC, Hyde KD, Lumyong S (2003) Saprobic fungi on dead wild banana. Mycotaxon 85: 345–346.

Matsushima T (1971) Microfungi of the Solomon Islands and Papua-New Guinea. Nippon Printing Publishing Company, Osaka, 78 pp.

McKenzie EHC, Jackson GVH (1986) The fungi, bacteria and pathogenic algae of Solomon Islands. Strengthening Plant Protection and Root Crops Development in the South Pacific. RAS/83/001, Field Document 11. Suva, Fiji. 282 pp. https://trove.nla.gov.au/version/42503674

McKenzie EHC, Jackson GVH (1990) The fungi, bacteria and pathogenic algae of the Federated States of Micronesia. SPC Technical Paper 199. 67 pp.

Miller MA, Pfeiffer W, Schwartz T (2010) Creating the CIPRES science gateway for inference of large phylogenetic trees. Proceedings of the Gateway Computing Environments Workshop (GCE), November 14, 2010, New Orleans, Louisiana 1–8. https://doi.org/10.1109/GCE.2010.5676129

Nair MC, Tyagi PD (1961) Notes on some hyphomycetes-I. Proceedings of the Indian Academy of Sciences 54: 269–275.

Pande A, Rao VG (1998) A Compendium of Fungi on Legumes from India. Scientific Publishers (India), Jodhpur, 188 pp.

Paul YS, Singh BM (1986) Addition to fungi of India. Indian Phytopathology 39: 748–751.

Rambaut A (2011) FigTree Tree figure drawing tool version 131, Institute of Evolutionary Biology, University of Edinburgh. Available from: http://treebioedacuk/software/figtree/ [accessed 24 May 2020]

Rannala B, Yang Z (1996) Probability distribution of molecular evolutionary trees: a new method of phylogenetic inference. Journal of Molecular Evolution 43: 304–311. https://doi.org/10.1007/BF02338839

Rao PR, Rao D (1964) Some allied dematiaceae-dictyosporae from India. Mycopathologia 23: 23–28. https://doi.org/10.1007/BF02049180

Rehner S (2001) Primers for Elongation Factor 1-alpha (EF1-alpha). Insect Biocontrol Laboratory: USDA, ARS, PSI.

Saravanan T, Vittal BPR (2007) Some rare and interesting hyphomycetes from eastern Ghats in Tamil Nadu, India. Kavaka 35: 21–44.
Somrithipol S (2007) A synnematous species of *Dictyoarthrinium* from Thailand. Mycologia 99: 792–796. https://doi.org/10.1080/15572536.2007.11832542

Srivastava MP, Tandon RN, Bilgrami KS, Ghosh AK (1964) Study on fungal diseases of some tropical fruits–I. A list of fungi isolated from fruits and fruit trees. Phytopathology 50: 250–251. https://doi.org/10.1111/j.1439-0434.1964.tb02923.x

Srivastava RN, Gupta JS (1981) Seed mycoflora from Indian seed lots of *Cosmos bipinnatus* and their control. Indian Phytopathology 34: 383–385.

Stamatakis A (2014) RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. Bioinformatics 30: 1312–1313. https://doi.org/10.1093/bioinformatics/btu033

Stamatakis A, Hoover P, Rougemont J (2008) A rapid bootstrap algorithm for the RAxML web servers. Systematic Biology 57: 758–771. https://doi.org/10.1080/10635150802429642

Stevenson JA (1975) Fungi of Puerto Rico and the American Virgin Islands. Contribution of Reed Herbarium 23: 743 pp.

Subramanian CV (1952) Fungi imperfecti from Madras–IIi. Proceedings of the Indian Academy of Sciences Section B 34: 160–168.

Sushma, Prasher IB, Verma RK (2020) Some interesting hyphomycetous fungi from India. Vegetos 33: 74–82. https://doi.org/10.1007/s42535-019-00083-8

Tanaka K, Hirayama K, Yonezawa H, Sato G, Toriyabe A, Kudo H, Hashimoto A, Matsumura M, Harada Y, Kurihara Y, Shirouzu T (2015) Revision of the Massarineae (Pleosporales, Dothideomycetes). Studies in Mycology 82: 75–136. https://doi.org/10.1016/j.simyco.2015.10.002

Tarda AS, Saparrat MCN, Gómez N (2019) Assemblage of dematiaceous and Ingoldian fungi associated with leaf litter of decomposing *Typha latifolia* L. (Typhaceae) in riverine wetlands of the Pampean plain (Argentina) exposed to different water quality. Journal of Environmental Management 250: 109–409. https://doi.org/10.1016/j.jenvman.2019.109409

Urtiaga R (1986) Indice de enfermedades en plantas de Venezuela y Cuba. Impresos en Impresos Nuevo Siglo. S.R.L., Barquisimeto, Venezuela, 202 pp.

Vilgalys R, Hester M (1990) Rapid genetic identification and mapping of enzymatically amplified ribosomal DNA from several *Cryptococcus* species. Journal of Bacteriology 172: 4238–4246. https://doi.org/10.1128/JB.172.8.4238-4246.1990

Vu D, Groenewald M, De Vries M, Gehrmann T, Stielow B, Eberhardt U, Al-Hatmi A, Groenewald JZ, Cardinali G, Houbreken J, Boekhout T (2019) Large-scale generation and analysis of filamentous fungal DNA barcodes boosts coverage for kingdom fungi and reveals thresholds for fungal species and higher taxon delimitation. Studies in Mycology 92: 135–154. https://doi.org/10.1016/j.simyco.2018.05.001

Wijayawardene NN, Hyde KD, Lumbsch T, Liu JK, Maharachchikumbura SSN, Ekanayaka AH, Tian Q, Phookamsak R (2018) Outline of Ascomycota – 2017. Fungal Diversity 88: 167–263. https://doi.org/10.1007/s13225-018-0394-8

White TJ, Bruns T, Lee SJWT, Taylor JL (1990) Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. PCR protocols: a guide to methods and applications 18: 315–322. https://doi.org/10.1016/B978-0-12-372180-8.50042-1

Zhaxybayeva O, Gogarten JP (2002) Bootstrap, Bayesian probability and maximum likelihood mapping: exploring new tools for comparative genome analyses. BMC genomics 3: 1–4. https://doi.org/10.1186/1471-2164-3-4