Pleocatenata chiangraensis gen. et. sp. nov. (Pleosporales, Dothideomycetes) from medicinal plants in northern Thailand

Ya-Ru Sun¹,2,3, Ning-Guo Liu²,5, Kevin D. Hyde²,3,4, Ruvishika S. Jayawardena²,3, Yong Wang¹

¹ Department of Plant Pathology, College of Agriculture, Guizhou University, Guiyang 550025, China  
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 Innovative Institute of Plant Health, Zhongkai University of Agriculture and Engineering, Haizhu District, Guangzhou 510000, China  
⁵ School of Life Science and Technology, Center for Informational Biology, University of Electronic Science and Technology of China, Chengdu 611731, China

Corresponding author: Yong Wang (yongwangbis@aliyun.com)

Academic editor: Nalin Wijayawardene | Received 16 December 2021 | Accepted 19 January 2022 | Published 11 February 2022

Citation: Sun Y-R, Liu N-G, Hyde KD, Jayawardena RS, Wang Y (2022) Pleocatenata chiangraensis gen. et. sp. nov. (Pleosporales, Dothideomycetes) from medicinal plants in northern Thailand. MycoKeys 87: 77–98. https://doi.org/10.3897/mycokeys.87.79433

Abstract

Pleocatenata, a new genus, is introduced with its type species, Pleocatenata chiangraensis, which was isolated from withered twigs of two medicinal plants, Clerodendrum quadriloculare (Blanco) Merr (Verbenaceae) and Tarenna stellulata (Hook.f.) Ridl (Rubiaceae) in northern Thailand. The genus is characterized by mononematous, septate, brown or dark brown conidiophores, monotretic conidiogenous cells and catenate, obclavate, olivaceous to blackish brown conidia. Phylogenetic analysis of combined LSU, SSU, tef1-α, rpb2 and ITS sequence data showed Pleocatenata forms a distinct phylogenetic lineage in Pleosporales, Dothideomycetes. Therefore, we treat Pleocatenata as Pleosporales genera incertae sedis based on morphology and phylogenetic analyses. Descriptions and illustrations of the new taxa are provided, and it is compared with morphologically similar genera.

Keywords

Genera incertae sedis, hyphomycetes, multi-gene phylogeny, taxonomy
Introduction

Medicinal plants are a rich source of natural products with biological and chemical properties. They are used in health care or treatment of human ailments and have been used since prehistoric times worldwide (Rasool-Hassan 2012). Many fungi have been found on medicinal plants and are members of Dothideomycetes and Sordariomycetes (Bhagat et al. 2012; Long et al. 2019; Ma et al. 2019; Hyde et al. 2020; Tennakoon et al. 2021). They form important associations with medicinal plants and as pathogens or saprobes (Long et al. 2019; Tennakoon et al. 2021), sources of medicines (Strobel et al. 1993; Huang et al. 2008; Hyde et al. 2019), involved in nutrient recycling (Bonnardeaux et al. 2007) and some are used in biological control (Hyde et al. 2019).

Pleosporales is the largest order in Dothideomycetes, which accounts for about a quarter of the class (Zhang et al. 2012; Hyde et al. 2013; Hongsanan et al. 2020a). They have a worldwide distribution with diverse lifestyles, including saprobes, pathogens of plants and humans, endophytes, epiphytes and hyperparasites (Ramesh 2003; Kirk et al. 2008; Zhang et al. 2012; Hyde et al. 2013; Sun et al. 2019; Ferdinandez et al. 2021). Many species in Alternaria Nees, Curvularia Boedijn and Corynespora Güßow, can invade medicinal plants and cause leaf spots and other diseases, as economically important plant pathogens (Mathiyazhagan et al. 2004; Abtahi and Nourani 2017; Zhang et al. 2020), and some also pose a threat to human health (Hyde et al. 2018; Iturrieta-González et al. 2020). Endophytes in Pleosporales also show important biocontrol value (Su et al. 2014; De Silva et al. 2019; Hyde et al. 2019), for example, an extract from Cochliobolus spicifer R.R. Nelson has mosquito-larvicidal activity (Abutaha et al. 2015).

The sexual morph of Pleosporales is characterized by uniloculate ascomata typically with papillae, ostioles and pseudoparaphyses, generally fissitunicate asci bearing mostly septate ascospores of different colours and shapes (Ramesh 2003; Kirk et al. 2008; Zhang et al. 2012; Hyde et al. 2013). Coelomycetes and hyphomycetes are the asexual morphs of pleosporalean taxa (Zhang et al. 2012; Hongsanan et al. 2020a). Recent comprehensive studies on Dothideomycetes treated 91 families in Pleosporales (Hongsanan et al. 2020a). More than 40 genera are recognized as genera incertae sedis in Pleosporales (Hongsanan et al. 2020a; Wijayawardene et al. 2020, 2021). This uncertainty in genetic placement occurs for the following reasons: 1) some genera lack sufficient collections even though molecular data is available, they are not included in any families in phylogenetic analyses, eg. Aegeanispora E.B.G. Jones & Abdel-Wahab, Antealophiotrema A. Hashim. & Kaz. Tanaka and Perthomyces Crous (Li et al. 2016; Abdel-Wahab et al. 2017; Crous et al. 2017); 2) due to the diverse morphology of hyphomycetous asexual morphs, it is difficult to determine their familial placement without the sexual morph and molecular data. Examples are Briansuttonia R.F. Castañeda, Minter & Saikawa, Cheiromoniliophora Tzean & J.L. Chen, Dangeardiella Sacc. & P. Syd and Pleosphaerellula Naumov & Czerepan (Obrist 1959; Tóth 1975; Tzean and Chen 1990; Castañeda-Ruiz et al. 2004).

During the examination of collections from medicinal plants in northern Thailand (Sun et al. 2021), two isolates representing a new species were obtained from
A new genus from medicinal plants in northern Thailand

Cladotremum quadriloculare and Tarenna stellulata. Morphology and phylogenetic analyses confirmed that it was distinct in Pleosporales, but its familial placement was uncertain. Thus, we introduced a new genus, Pleocatenata (Pleosporales, genera incertae sedis) to accommodate the new species, P. chiangraiensis.

Materials and methods

Collection, examination and isolation

The isolates used in this study were collected from decaying twigs of Cladotremum quadriloculare and Tarenna stellulata from Mae Fah Luang University, Chiang Rai, Thailand during June to July 2020 in terrestrial habitat. The samples were packaged in envelopes and returned to the laboratory as described in Senanayake et al. (2020). The fruiting bodies on natural substrates were observed and photographed using a stereo-microscope (SteREO Discovery, V12, Carl Zeiss Microscopy GmBH, Germany). Morphological characters were observed using a Nikon ECLIPSE Ni compound microscope (Nikon, Japan) and photographed with a Nikon DS-Ri2 digital camera (Nikon, Japan). The Adobe Photoshop CS6 Extended v. 13.0 software was used to make photo-plates. Measurements were done with the Tarosoft (R) Image Frame Work software.

Single spore isolations were used to obtain pure cultures following the methods described by Senanayake et al. (2020). Germinated conidia were transferred to new potato dextrose agar (PDA) plates and incubated at 26 °C for four weeks. The pure cultures obtained were deposited in Mae Fah Luang University Culture Collection (MFLUCC), Chiang Rai, Thailand. Herbaria materials were deposited in the herbarium of Mae Fah Luang University (MFLU), Chiang Rai, Thailand. Facesoffungi (FoF) and Index Fungorum numbers were acquired as described in Jayasiri et al. (2015) and Index Fungorum (2022).

DNA extraction, PCR amplification and sequencing

Fresh fungal mycelia grown on PDA medium for 4 weeks at 26 °C were scraped with a sterile scalpel. Genomic DNA was extracted from scraped mycelia using the BIOMIGA Fungus Genomic DNA Extraction Kit (GD2416, BIOMIGA, San Diego, California, USA) following the manufacturer’s protocol. Five genes were selected in this study: the 28S subunit rDNA (LSU), the 18S subunit rDNA (SSU), the internal transcribed spacers (ITS), the translation elongation factor 1 (tef1-α), and the RNA polymerase II subunit 2 (rpb2). Polymerase chain reaction (PCR) was carried out in 20 μL reaction volume which contained 10 μL 2 × PCR Master Mix, 7 μL ddH₂O, 1 μL of each primer, and 1 μL template DNA. The PCR thermal cycle program and primers are given (Table 1). Purification and sequencing of PCR products were carried out at SinoGenoMax (Beijing) Co., China.
**Phylogenetic analyses**

BLASTn (https://blast.ncbi.nlm.nih.gov//Blast.cgi) was used to evaluate closely related strains to our new taxa. Other sequences used in this study were obtained from GenBank referring to Zhang et al. (2012, 2018) and Hongsanan et al. (2020a, 2021) (Table 2). The single gene sequences were viewed using BioEdit v. 7.0.9.0 (Hall 1999). Alignments for each locus were generated with MAFFT v.7 (https://mafft.cbrc.jp/alignment/server/) and manually improved using AliView (Larsson 2014) for maximum alignment and minimum gaps. The final single gene alignments were combined by SequenceMatrix 1.7.8 (Vaidya et al. 2011).

The single locus and combined analyses were carried out for maximum likelihood (ML) and Bayesian posterior probability (BYPP). The ML analyses were carried out using IQ-TREE (Nguyen et al. 2015; Trifinopoulos et al. 2016) on the IQ-TREE web server (http://iqtree.cibiv.univie.ac.at, 30 September 2021) under partitioned models. The best-fit substitution models were determined by WIQ-TREE (Chernomor et al. 2016): SYM+I+G4 for LSU and SSU; TIM+F+I+G4 for tef1-α; GTR+F+I+G4 for rpb2; TIM2+F+I+G4 for ITS. Ultrafast bootstrap analysis was implemented with 1,000 replicates (Minh et al. 2013; Hoang et al. 2018).

The BYPP analyses were performed in CIPRES (Miller et al. 2010) with MrBayes on XSEDE 3.2.7a (Ronquist et al. 2012). The best nucleotide substitution model for each data partition was evaluated by MrModeltest 2.2 (Nylander 2004). The substitution model GTR+I+G was decided for LSU, SSU, ITS, tef1-α and rpb2 sequences. The Markov chain Monte Carlo (MCMC) sampling approach was used to calculate posterior probabilities (PP) (Rannala and Yang 1996). Six simultaneous Markov chains were run for 10 million generations and trees were sampled every 1,000th generation. The first 20% of trees, representing the burn-in phase of the analyses, were discarded and the remaining trees were used for calculating posterior probabilities (PP) in the majority rule consensus tree.

---

**Table 1. Primers and PCR procedures used in this study.**

| Locus                  | Name  | Sequence (5’–3’) | PCR procedures | References                                      |
|------------------------|-------|------------------|----------------|-------------------------------------------------|
| Large subunit (LSU)    | LR0R  | ACCCGCTGAACCTTAAGC | 94 °C 3 min; 35 cycles of 94 °C | Vilgalys and Hester (1990)                       |
|                        | LR5   | TCCTGAGGGAACCTCG  | 30 s, 52 °C 30 s, 72 °C 1 min; 72 °C 8 min; 4 °C on hold | Rehner and Samuels (1994)                        |
| Small subunit (SSU)    | NS1   | GTAGCTCATAGCCTGCTGTC  | 94 °C 2 min; 36 cycles of 66 °C – 56 °C (touchdown 9 cycles), 94 °C 30 sec, 56 °C 1 min, 72 °C 1 min; 72 °C 10 min; 4 °C on hold | White et al. (1990)                               |
| Internal transcribed   | ITS5  | GGAAGTAAAAGCTGTAACAGG | 94 °C 3 min; 40 cycles of 94 °C | Rehner and Buckley (2005)                        |
| space (ITS)            | ITS4  | TCCCTCAGTATTGATGATG | 94 °C 3 min; 40 cycles of 94 °C | Liu et al. 1999                                  |
| Elongation factor-1    | EF1-983F | GCCYCCYGHCAYGCTGAYTTYAT | 94 °C 2 min; 36 cycles of 66 °C – 56 °C (touchdown 9 cycles), 94 °C 30 sec, 56 °C 1 min, 72 °C 1 min; 72 °C 10 min; 4 °C on hold | Li et al. 1999                                   |
| alpha (tef1-α)         | EF1-2218R | ATGACACCRACRGCRACRGCTTGYTG | 94 °C 2 min; 36 cycles of 66 °C – 56 °C (touchdown 9 cycles), 94 °C 30 sec, 56 °C 1 min, 72 °C 1 min; 72 °C 10 min; 4 °C on hold | Li et al. 1999                                   |
| RNA polymerase II      | RPB2-5F | GAYGAYMGWGATCAYTTYGG | 94 °C 3 min; 40 cycles of 94 °C | Liu et al. 1999                                  |
| subunit (rpb2)         | RPB2-7cR | CCCATRGGCTTGYTTCCCAT | 94 °C 3 min; 40 cycles of 94 °C | Liu et al. 1999                                  |
Table 2. Taxa of Pleosporales used in the phylogenetic analysis with the corresponding GenBank accession numbers. The newly generated strains are indicated in bold. N/A: Not available.

| Species names                     | Strain number | LSU        | SSU        | ITS         | tef1-α       | rpb2       |
|-----------------------------------|---------------|------------|------------|-------------|--------------|------------|
| Acrocalymma aquatica              | MFLUCC 11-0208| JX276952   | JX276953   | JX276951    | N/A          | N/A        |
| Acrocalymma pterocarpi            | MFLUCC 17-0926| MK347949   | MK347840   | MK347732    | MK360040     | N/A        |
| Acuminatispora palmarum           | MFLUCC 18-0564| MH390437   | MH390401   | MN749106    | MH399249     | N/A        |
| Agitalis grandis                  | BCC 20000     | GU479775   | GU479739   | N/A         | GU479839     | N/A        |
| Alternaria alternata              | AFTOL ID-1610 | DQ678082   | KC584507   | KF65761     | KC584634     | KC584375   |
| Aminiculicola aquatica            | MFLUCC 16-1123| MK106096   | MK106108   | N/A         | MK109800     | N/A        |
| Anomoeclophoma cassia             | MFLUCC 17-2283| MK347796   | NG_065775  | MK347739    | MK360041     | MK348949   |
| Angustinaurata lonicerae           | MFLUCC 15-0087| KY496724   | N/A        | KY496759    | N/A          | N/A        |
| Antagonialonium parvulum           | SMHS223       | GQ221909   | N/A        | GQ221918    | N/A          | N/A        |
| Aquasubmersa japonica             | HHUF 30469    | NG_057138  | NG_062426  | N/A         | LC194384     | LC194421   |
| Aquasubmersa micrensis            | MFLUCC 11-0401| NG_042699  | NG_061141  | JX276954    | N/A          | N/A        |
| Aigialus grandis                  | BCC 20000     | GU479775   | GU479739   | N/A         | GU479839     | N/A        |
| Alternaria alternata              | AFTOL ID-1610 | DQ678082   | KC584507   | KF65761     | KC584634     | KC584375   |
| Aminiculicola aquatica            | MFLUCC 16-1123| MK106096   | MK106108   | N/A         | MK109800     | N/A        |
| Anomoeclophoma cassia             | MFLUCC 17-2283| MK347796   | NG_065775  | MK347739    | MK360041     | MK348949   |
| Angustinaurata lonicerae           | MFLUCC 15-0087| KY496724   | N/A        | KY496759    | N/A          | N/A        |
| Antagonialonium parvulum           | SMHS223       | GQ221909   | N/A        | GQ221918    | N/A          | N/A        |
| Aquasubmersa japonica             | HHUF 30469    | NG_057138  | NG_062426  | N/A         | LC194384     | LC194421   |
| Aquasubmersa micrensis            | MFLUCC 11-0401| NG_042699  | NG_061141  | JX276954    | N/A          | N/A        |
| Aigialus grandis                  | BCC 20000     | GU479775   | GU479739   | N/A         | GU479839     | N/A        |
| Alternaria alternata              | AFTOL ID-1610 | DQ678082   | KC584507   | KF65761     | KC584634     | KC584375   |
| Aminiculicola aquatica            | MFLUCC 16-1123| MK106096   | MK106108   | N/A         | MK109800     | N/A        |
| Anomoeclophoma cassia             | MFLUCC 17-2283| MK347796   | NG_065775  | MK347739    | MK360041     | MK348949   |
| Angustinaurata lonicerae           | MFLUCC 15-0087| KY496724   | N/A        | KY496759    | N/A          | N/A        |
| Antagonialonium parvulum           | SMHS223       | GQ221909   | N/A        | GQ221918    | N/A          | N/A        |
| Species names                          | Strain number | LSU     | SSU     | ITS      | tef1-α | rpb2 |
|----------------------------------------|---------------|---------|---------|----------|--------|------|
| Fuscostagonospora sasae                | HHUF 29106    | AB80754 | AB979258| AB809636 | AB808524| N/A  |
| Fusculina eucalypti                    | CBS 120083    | DQ923531| N/A     | DQ923531| N/A    | N/A  |
| Fusculina eucalyptorum                 | CBS 145083    | MK047499| N/A     | NR161140 | N/A    | N/A  |
| Halodiplodiopsis avicenniae            | BCC 20173     | GU371822| GU371830| N/A     | GU371815|GU371786|
| Halothia pentoniae                     | BBH 22481     | GU479786| GU479752| N/A     | N/A    | N/A  |
| Hausera fuscata                        | CBS 136437    | KF777198| N/A     | KF777142| N/A    | N/A  |
| Heliophthora velutinum                 | L131          | KY984352| KY984342| KY984352| KY984463|KY984413|
| Hermatomyces iriomotensis             | HHUF 30518    | LC194367| LC194325| LC194483| LC194394|LC194449|
| Hermatomyces tectonae                 | MFLUCC 11-1400| KU766495| KU712465| KU149417| KU827576|KU732686|
| Hypnopomma caimitidelense              | GKM1165       | GU358100| N/A     | N/A     | N/A    | N/A  |
| Hypnopomma caxiolaris                  | SMH5005       | GU358181| N/A     | N/A     | N/A    | N/A  |
| Hypsostroma caimitalense               | CBS 123334    | FJ161207| N/A     | N/A     | N/A    | N/A  |
| Hypsostroma saxicola                   | CBS 114601    | FJ161174| FJ161135| N/A     | FJ161091|FJ161114|
| Latorua caligans                       | CBS 576.65    | NG058180| N/A     | N/A     | N/A    | N/A  |
| Latorua grootfonteinensis              | CBS 369.72    | NG058181| N/A     | N/A     | N/A    | N/A  |
| Lentimurispora urifornis               | MFLUCC 18-0497| MH179144| MH179160| MH179160|MH188055|N/A   |
| Lentithecium clioninum                 | HHUF 28199    | NG059391| NG064845| NR154137| AB808515|N/A   |
| Lentithecium pseudoclioninum           | HHUF 29055    | NG059392| NG064847| AB809633| AB808521|N/A   |
| Lepidophaeria nicotiae                 | AFTOL 1576    | DQ678067| N/A     | DQ677910|DQ677963|N/A   |
| Lepidophaeria cichorium                | MFLUCC 14-1063|KT454712|KT454728|KT454720|N/A     |N/A   |
| Leucosporidium phaeum                  | MFLUCC 18-0472|MK348003| NG056784| MK347785|MK360060|MK34867|
| Libertsea mycopori                     | CPC 27354     | NG058241| N/A     | N/A     | N/A    | N/A  |
| Ligninophthora gongospora              | MFLUCC 15-0641|NG059642|N/A     | N/A     | N/A    | N/A  |
| Lindalinae spicata                     | MFLUCC 12-0562|GU366470| N/A     | GU371247|N/A     |N/A   |
| Longipediculata aptrootsi             | MFLUCC 10-0297|KU238894| KU238893|KU238892|KU238892|N/A   |
| Lophioatra macrostoma                  | KT082         | AB619010| AB618691| N/A     | LC001751|N/A   |
| Lophiotremata eburnoides               | KT4241        | LC001707| LC001706| LC194403|LC194458|N/A   |
| Macrodictaphisus derzhavinii           | CBS 140062    | NG058182| N/A     | NR132924| N/A    |N/A   |
| Masaria anomia                         | CBS 59178     | GU301839| GU296169| N/A     | N/A    |N/A   |
| Masaria inquinae                       | M19           | N/A     | HQ599444| HQ599402|HQ599460|N/A   |
| Melanoconiothyrium persooniae          | MFLUCC 11-0180|KJ474839| N/A     | KJ474827| KJ474836|N/A   |
| Melanomma japonicum                    | MAFF 239634   | NG060360| NG065120| NR154215| LC203367|LC203395|
| Melanomma pulvis pyrius                | CBS 124080    | MHH47873| GU456302| MH863349|GU456265|GU456350|
| Mieletaspora aurantonontata            | GKM 1238      | NG059927| N/A     | GU327761|N/A     |N/A   |
| Morosphaeria muthupetensis             | NFFCH4219     | MF614796| MF614795| MF614795|MF614798|N/A   |
| Morosphaeria undulata                  | KH221         | AB807556| AB797266| LC014572|AB808532|N/A   |
| Multicoccidium laevisiae               | MFLUCC 11-0180|GU363438| GU363442| GU363446|N/A     |N/A   |
| Musriina galii                         | MFLUCC 13-0819|KT091175| KT091182| KT091189|KT091189|N/A   |
| Neocamariospora goegapense             | CPC 23676     | KJ869220| N/A     | KJ869163| N/A    |N/A   |
| Neocomiobolus peroniforme             | CBS 143175    | MG386099| N/A     | MG386041|N/A     |N/A   |
| Neocasariopsis formana                 | MFLUCC 16-1875|KX524145| NG061245| N/A     | KX524149|N/A   |
| Neocasaria fuscidula                   | MFLUCC 17-007 | MH174576| MH174579| MH174762|MH174765|N/A   |
| Neocasaria thailandica                 | MFLUCC 17-1432|MFLUCC 17-0809|MG829033| MG828924|MG829217|N/A   |
| Neopyrenochaeta roea                    | CPC 21264     | NG059718| N/A     | NR154244| N/A    |N/A   |
| Neopyrenochaeta filamentosa            | CBS 102202    | QC837577| QC837516| JF740259|GU349084|GU371773|
| Neopyrenochaeta phragmitisola          | KUMCC 16-0210 | MG837009| NG057357| N/A     | MG838020|N/A   |
| Neotestudina bambusae                  | MFLUCC 11-0180|KX693438| KX693442| KX693446|N/A     |N/A   |
| Nigrograna fuscidula                   | CPC 36068     | MN567619| N/A     | NR166316| N/A    |N/A   |
| Neotestudina bambusae                  | MFLUCC 12-0890|MC437932| MC437823| MC437718|MC439408|N/A   |
| Neotestudina hominis                   | MFLUCC 11-0124|KJ474839| N/A     | KJ474827|KJ474848|KJ474856|
| Neotestudina smutista                  | CBS 690.82    | DQ384017| DQ384006| N/A     | N/A    |N/A   |
| Neopyrenochaeta acicola                | CBS 812.95    | QC837502| QC837541| NR160055| N/A    |N/A   |
| Neopyrenochaeta fuscida                | CBS 14555     | KC650550| N/A     | NR147653| KC65025 |N/A   |
| Species names | Strain number | LSU | SSU | ITS | tef1-α | rpb2 |
|---------------|--------------|-----|-----|-----|--------|------|
| Nigrograna mackinnonii | CBS 674.75 | GQ387613 | NG_061081 | NR_132037 | KF407986 | KF015703 |
| Ocultibambusa bambusae | MFLUCC 13-0855 | KU683112 | N/A | KU940123 | KU940193 | KU940170 |
| Ocultibambusa jonissi | GZCC 16-0117 | KY628322 | KY628324 | N/A | KY814756 | KY814758 |
| Parabambusicola bambusana | KH 139 | AB807537 | AB799247 | LC014579 | AB808512 | N/A |
| Paradictyoarthrinium aquatica | MFLUCC 16-1116 | NG_064501 | N/A | NR_158861 | N/A | N/A |
| Paradictyoarthrinium diffusum | MFLUCC 13-0466 | KP744498 | KP753960 | KP744455 | N/A | KX437764 |
| Paralophiostoma hysterioides | PUENI 17617 | MT912850 | MN582762 | MN582875 | N/A | MT926117 |
| Parapyrenochaeta protonema | CBS 131315 | JQ044453 | N/A | JQ044434 | N/A | LT717683 |
| Pariconia delonicis | MFLUCC 17-2584 | NG_068611 | NG_065770 | N/A | N/A | MK439001 |
| Pariconia pseudodigitata | MFLUCC 13-0219 | KT454717 | KT454732 | KT454725 | N/A | N/A |
| Phaeoseptum mali | MFLUCC 17-2108 | MK625197 | N/A | MK659580 | MK647990 | MK647991 |
| Phaeoseptum terricola | MFLUCC 10-0102 | MH105770 | MH105778 | MH105781 | MH105782 |
| Phaeosphaeria oryzae | CBS 110110 | KF251689 | GQ387530 | KF251186 | N/A | KF252193 |
| Phaeosphaeriopsis triseptata | MFLUCC 13-0271 | KJ522479 | KJ522484 | KJ522475 | MG520919 | KJ522485 |
| Plenodomus salvia | MFLUCC 13-0219 | KT454717 | KT454732 | KT454725 | N/A | N/A |
| Pleohelicoon richonis | CBS 282.54 | AY856952 | MH857332 | N/A | N/A | |
| Pleomonodictys descalsii | FMR 12716 | KY853522 | KY853461 | N/A | N/A | |
| Preussia funiculate | CBS 659.74 | GU301864 | GU296187 | GU349032 | GU371799 | |
| Pseudoastrosphaeriella longicolla | MFLUCC 11-0171 | KT955478 | N/A | KT955438 | KT955420 | |
| Pseudoastrosphaeriella thailandensis | MFLUCC 11-0144 | MK131260 | MK131259 | MK131261 | N/A | |
| Pseudodidymosphaeria spartii | MFLUCC 13-0273 | KP325436 | KP325438 | KP325434 | N/A | |
| Pseudopyrenochaeta lycopersici | FMR 15746 | EU754205 | NG_062728 | NR_103580 | LT623287 | |
| Pseudopyrenochaeta terretris | FMR 15327 | LT623216 | LT623225 | LT623228 | N/A | LT623287 |
| Pseudotetraploa longissima | HC 4933 | AB524612 | AB524471 | AB524794 | AB524827 | N/A |
| Pseudoxylomyces elegans | KT 2887 | AB524612 | AB524471 | AB524794 | AB524827 | N/A |
| Pyrenochaetopsis leptospora | CBS 101635 | MK035992 | MK035977 | MK035980 | MK035990 | MK035988 |
| Pyrenochaetopsis tabarestanensis | IBRC M 30051 | MK035993 | MK035978 | MK035980 | MK035991 | MK035992 |
| Quadricrura bicornis | CBS 166.73 | MH872355 | N/A | MH857332 | N/A | |
| Quercicola fusiformis | MFLUCC 18-0479 | MK348009 | MK347898 | MK347790 | MK360085 | MK343864 |
| Quercicola gutulosa | MFLUCC 18-0481 | MK348010 | MK347898 | MK347790 | MK360085 | MK343864 |
| Quixadomyces cearensis | HU134 | MG970695 | N/A | MG970695 | N/A | |
| Roussoella nitidula | MFLUCC 11-0185 | KX534216 | KX534222 | KX534227 | N/A | |
| Salsuginea phoenicis | MFLUCC 12-0385 | KU764709 | N/A | KU764709 | N/A | |
| Salsuginea ramicola | MFLUCC 12-0565 | KU764701 | N/A | KU764701 | N/A | |
| Seltsamia ulmi | MFLUCC 12-0004 | KT454717 | KT454717 | KT454717 | N/A | |
| Shiraia bambusicola | GZAAS2.629 | KC460980 | N/A | KC460980 | N/A | |
| Splanchnonema platani | CBS 222.37 | KJ474827 | MG970695 | N/A | MG970695 | MG970695 |
| Sporormia fimetaria | UPS Dissing Gr.81.194 | MQ387613 | MQ387613 | MQ387613 | MQ387613 | MQ387613 |
| Sporormia isomerobia | CBS 166.73 | MH872355 | N/A | MH857332 | N/A | |
| Stemphylium herbarum | CBS 191.86 | GU38160 | GU38160 | GU38160 | GU38160 | GU38160 |
| Streptomyces hericus | MFLUCC 16-0286 | MK035995 | MK035977 | MK035977 | MK035977 | MK035977 |
| Subaphloia thailandica | MFLUCC 11-0185 | KX534216 | KX534222 | KX534227 | N/A | |
| Subplenodomus violicola | CBS 306.68 | MBH0849 | GU238231 | MBH0849 | N/A | |
| Sukatipsa acerina | KT 2982 | LC014605 | LC014605 | LC014605 | LC014605 | LC014605 |
| Sukatipsa bacchartica | KT 1607 | AB807534 | AB979244 | AB809635 | AB808509 | N/A |
| Sulcoporum thailandica | MFLUCC 12-0004 | KT426563 | KT426564 | MG520958 | N/A | |
| Tetraploa sp. | C24 | KE015191 | N/A | KE015191 | N/A | |
| Tetraploa sp. | CBS 131315 | AB524631 | AB524490 | AB524807 | AB524838 | N/A |
| Species names            | Strain number | LSU          | SSU          | ITS           | tef1-α        | rpb2         |
|-------------------------|---------------|--------------|--------------|--------------|---------------|--------------|
| Thyridaria acaciae      | CBS 138873    | NG_058127    | N/A          | KP004469     | N/A           | N/A          |
| Thyridaria bronsonetiae | TB1           | KX650568     | KX650515     | KX650568     | KX650539      | KX650586     |
| Torula aquatica         | MFLUCC 16-1115| MG208146     | N/A          | MG208167     | N/A           | MG207977     |
| Torula multispicata     | MFLUCC 14-0437| KY197855     | KY197862     | MN061338     | KY197875      | KY197869     |
| Trematocapsa arundinacea| MFLU 16-1275  | KX274248     | KX274254     | KX274241     | KX284706      | N/A          |
| Trematospora gracilis   | CBS 332.50    | NG_057979    | NG_062930    | NR_132039    | KF015698      | KF015720     |
| Trematospora pertusa    | CBS 122368    | NG_057809    | FJ201991     | NR_132040    | KF015701      | FJ795476     |
| Tzeanania taiwanensis   | NTUCC 17-006  | MH461121     | MH461127     | MH461124     | MH461131      | N/A          |
| Wicklowia aquatica      | CBS 125634    | MH875044     | NG_061099    | N/A          | N/A           | N/A          |
| Wicklowia submera       | MFLUCC 18-0373| MK637644     | MK637643     | N/A          | N/A           | N/A          |
| Xenopyrenochaetopsis pratorum | CBS 445.81  | GU238136     | NG_062792    | MH861363     | N/A           | KT389671     |

Phylogenetic trees were viewed using FigTree v1.4.0 (Rambaut and Drummond 2008) and modified in Microsoft Office PowerPoint 2010 and converted to jpg file using Adobe Photoshop CS6 Extended 10.0 (Adobe Systems, San Jose, CA, USA). The new sequences derived from this study were deposited in GenBank. The final alignment and tree were deposited in TreeBase (http://purl.org/phylo/treebase/phylows/study/TB2:S291999).

Results

Phylogenetic analyses

Blast searches of LSU, tef1-α, rpb2 and ITS sequences data in NCBI showed that our sequences were related to Acrocalymmaceae, Amorosiaceae, Sporormiaceae and Sublophiostomataceae. One hundred and seventy-six taxa, representing all families in Pleosporales, with *Hysterium angustatum* Alb. & Schwein (CBS 123334) and *Hysterobrevium smilacis* (Schwein.) E. Boehm & C.L. Schoch (CBS 114601) as the outgroups, were selected for the analyses. The final combined dataset consisted of 4,953 characters (LSU: 1–850 bp, SSU: 851–1,851 bp, tef1-α: 1,852–2,720 bp, rpb2: 2,721–3,701 bp, ITS: 3,702–4,953 bp), including alignment gaps. Among them, 2,336 characters were constant, 608 variable characters were parsimony-uninformative, and 2,009 characters were parsimony informative. The most likely tree (-ln = 98,965.704) is presented (Figure. 1) to show the phylogenetic placement of the newly introduced genus and its relationship with other members in Pleosporales.

Analyses of both ML and BYPP (not shown) yielded almost identical results, and the topology of the trees were similar to previous studies (Zhang et al. 2018; Hong-sanan et al. 2020a, 2021). The combined analyses showed that two suborders Massarineae and Pleosporineae were well-supported and formed an upper clade in Pleosporales. Our two newly obtained fungal isolates (MFLUCC 21-0222 and MFLUCC 21-0223) clustered together and formed a distinct clade with maximum support (ML-BS = 100%, BYPP = 1.00) and they grouped with Amorosiaceae, Sporormiaceae and Sublophiostomataceae with weak support.
A new genus from medicinal plants in northern Thailand

Figure 1. Maximum likelihood tree generated by IQ-Tre, based on analysis of a combined dataset of LSU, SSU, tef1-α, rpb2 and ITS sequence data. Bootstrap support values for ML greater than 75% and Bayesian posterior probabilities greater than 0.95 are given near nodes, respectively. Ex-type strains are in bold, the new isolates are in red.
Taxonomy

**Pleocatenata** Y.R. Sun, Yong Wang bis & K.D. Hyde, gen. nov.
Index Fungorum number: IF559457
Facesoffungi number: FoF 10630

**Etymology.** “Pleo-” an abbreviation of Pleosporales, the order in which this fungus is classified; “-catenata” refers to the catenate conidia of this fungus.

**Description.** Saprobic on decaying twigs in terrestrial habitats. **Asexual morph:** Hyphomycetous. Colonies on natural substrate effuse, dark, velvety. Conidiophores macronematous, mononematous, straight or slightly curved, cylindrical, unbranched, septate, brown or dark brown. Conidiogenous cells monotretic, integrated, terminal, cylindrical, brown to dark brown. Conidia catenate, formed in acropetal chains, straight or bent, obclavate, olivaceous to dark brown, multi-euseptate, slightly constricted at septa, distal conidia rounded at apex, truncate at base, intercalary conidia truncate at both ends, with thickened and darkened scars at base or both ends. **Sexual morph:** Undetermined.

**Type species.** *Pleocatenata chiangraiensis* Y.R. Sun, Yong Wang bis & K.D. Hyde

**Notes.** The morphology of *Pleocatenata* is distinguished from members in other families in Pleosporales by its tretic conidiogenous cells and catenate, euseptate conidia, and phylogenetic analyses indicated it does not belong to any existing families. To avoid establishing a new family with only one species, *Pleocatenata* is introduced as a new genus and assigned to Pleosporales, genera incertae sedis. *Pleocatenata* is a monotypic genus reported from terrestrial habitats but without a known sexual morph. Further discovery of other species in *Pleocatenata* or phylogenetic related genera with supported monophyly will determine the familial level of *Pleocatenata.*

---

**Pleocatenata chiangraiensis** Y.R. Sun, Yong Wang bis & K.D. Hyde, sp. nov.
Index Fungorum number: IF559458
Facesoffungi number: FoF 10631

**Etymology.** The epithet referring to the location in which the fungus was collected.

**Holotype.** MFLU: 22-0002

**Description.** Saprobic on twigs of *Clerodendrum quadriloculare* and *Tarenna stellulata.* **Asexual morph:** Hyphomycetous. Colonies on natural substrate effuse, dark, velvety. Mycelium immersed, composed of septate, branched, hyaline to subhyaline hyphae. Conidiophores macronematous, mononematous, erect, straight or slightly curved, cylindrical, unbranched, robust, 4–6-septate, brown or dark brown, rough, 35–100 μm long, 5.5–8.5 μm wide. Conidiogenous cells monotretic, integrated, terminal, determinate, cylindrical, dark brown. Conidia catenate, formed in acropetal chains of 2–3, straight or curved, obclavate, olivaceous to brown when young, blackish brown.
Figure 2. Pleocatenata chiangraiensis (MFLU 22-0002, holotype) a host (Tarenna stellulata) b, c colonies on natural substrate d, e conidiophores with conidia f conidiogenous cells g–k conidia l germinated conidium m, n colonies on PDA (upper view and lower view). Scale bars: 1 mm (b); 100 μm (c); 20 μm (d–l).
when mature, 5–8-euseptate, slightly constricted at septa, distal conidia rounded at apex, truncate at base, intercalary conidia truncate at both ends, with thickened and darkened scars at base or both ends, 34–70 μm long, 6.5–12 μm at the widest. **Sexual morph:** Unknown.

**Culture characteristics.** Conidia germinated on PDA within 12 hours at 26 °C. Germ tubes were produced from both ends. Colony reached 20–25 mm diameter after 4 weeks at room temperature on PDA media. Mycelia superficial, irregularly circular, entire edge, dark brown from above, black from below, pigment produced which turns the media reddish brown.

**Material examined.** Thailand, Chiang Rai Province, Mae Fah Luang University, on twigs of *Tarenna stellulata*, 3 July 2020, Y.R. Sun, MFU5 (MFLU 22-0002, holotype, ex-type living culture MFLUCC 21-0222). Thailand, Chiang Rai Province, Medicinal Plants Garden, on twigs of *Clerodendrum quadriloculare*, 7 June 2020, Y.R. Sun, B45 (MFLU 22-0001, living culture MFLUCC 21-0223).

**Notes.** Two isolates collected from different hosts share similar morphology and clustered together in the phylogenetic tree. There are no base pair differences in LSU and *tef1*-α genes between these two isolates. One base pair and two base pair differences (without gaps) are observed in ITS and *rpb2*, respectively. Therefore, the two isolates MFLUCC 21-0222 and MFLUCC 21-0223 are identified as conspecific.

**Discussion**

*Pleocatenata* is phylogenetically related to Amorosiaceae, Sporormiaceae, and Sublophiostomataceae in our multi-gene analyses, but their monophyly was not well-supported, indicating their uncertain phylogenetic affinities. No hyphomycetous asexual morph has been reported in Sporormiaceae or Sublophiostomataceae (Hongsanan et al. 2020a, 2021). However, in Amorosiaceae, only two known hyphomycetous genera, *Amorosia* and *Angustimassarina*, are characterized by micronematous to semimacronematous, pale brown conidiophores, monoblastic conidiogenous cells, and single, obclavate conidia (Mantle et al. 2006; Thambugala et al. 2015; Hongsanan et al. 2020a). *Pleocatenata* can be distinguished from these two genera by having monotretic conidiogenous cells and catenate, obclavate conidia.

A recently introduced species, *Corynespora sinensis* Jian Ma, X.G. Zhang & R.F. Castañeda, resembles *Pleocatenata* in its unbranched, cylindrical conidiophores and monotretic, terminal conidiogenous cells that produce catenate, obclavate conidia (Xu et al. 2020). Morphologically, *Corynespora sinensis* is more similar to *P. chiangratiensis* than to the type species of *Corynespora*, *C. cassiicola* (Berk. & M.A. Curtis) C.T. Wei (Wei 1950). Since *Corynespora* (Corynesporasaceae, Pleosporales) is a polyphyletic genus (Schoch et al. 2009; Voglmayr and Jaklitsch 2017), and there is no available sequence data for *C. sinensis*, we presume that *C. sinensis* may belong to *Pleocatenata*. However, due to lack of molecular data, and since morphology-based classification is not reliable for many hyphomycetous genera (Shenoy et al. 2006; Su et al. 2016; Yang...
et al. 2018), we retain the current classification. Sequences of *C. sinensis* are needed to resolve its phylogenetic placement. Detailed morphological comparison among *C. cassiicola*, *C. sinensis* and *P. chiangraiensis* is provided (Table 3).

**Pleocatenata** is similar to *Sporidesmium sensu stricto*, which is characterized by distinct, unbranched conidiophores, monoblastic, determinate or proliferating conidiogenous cells, and acrogenous, solitary, transversely septate conidia (Ellis 1958, 1971; Shenoy et al. 2006; Boonmee et al. 2012; Su et al. 2016; Yang et al. 2018). However, *Pleocatenata* is different from *Sporidesmium* by having catenate conidia. Additionally, *Pleocatenata* is phylogenetically distinct from *Sporidesmium*, supporting the introduction of the new genus.

The catenate, obclavate phragmoconidia of *P. chiangraiensis* are similar to capnodendron asexual morph of *Antennulariella* Woron (Antennulariellaceae, Capnodiales) (Hughes 1976, 2000; Seifert et al. 2011). Although sequence data of *Antennulariella* is not available, morphological characters, such as holoblastic conidiogenous cells and branched conidiophores of *Antennulariella*, support its separation from *P. chiangraiensis* (Hughes 1976, 2000; Seifert et al. 2011). *Pleocatenata* is also similar to *Corynesporina* Subram (Pezizomycotina, *incertae sedis*) in having unbranched, robust conidiophores and catenate conidia (Seifert et al. 2011). However, they differ in that the distoseptate conidia form in basipetal chains in *Corynesporina* and euseptate conidia form in acro-petal chains in *Pleocatenata*.

### Acknowledgements

We would like to thank Dr. Shaun Pennycook for checking the nomenclature. Ya-Ru Sun thanks Mae Fah Luang University for the award of a fee-less scholarship. Ya-Ru Sun also thanks the director of the Mae Fah Luang University Botanical Garden, the botanist Dr. Jantrararuk Tovaranonte for her support. The study was funded by Guizhou Science Technology Department International Cooperation Basic project ([2018]5806), National Natural Science Foundation of China (No.31972222,
31560489), Program of Introducing Talents of Discipline to Universities of China (111 Program, D20023), and Talent project of Guizhou Science and Technology Co-operation Platform ([2017]57885, [2019]5641 and [2020]5001).

References

Abtahi F, Nourani SL (2017) The most important fungal diseases associated with some useful medicinal plants. In: Ghorbanpour M, Varma A (Eds) Medicinal plants and environmental challenges. Springer International Publishing, Cham, 279–293. https://doi.org/10.1007/978-3-319-68717-9_16

Abutaha N, Mashaly AM, Al-Mekhlafi FA, Farooq M, Al-shami M, Wadaan MA (2015) Larvicidal activity of endophytic fungal extract of Cochliobolus spicifer (Pleosporales: Pleosporaceae) on Aedes caspius and Culex pipiens (Diptera: Culicidae). Applied Entomology and Zoology 50: 405–414. https://doi.org/10.1007/s13355-015-0347-6

Barghoorn ES (1944) Marine fungi: their taxonomy and biology. Farlowia 1: 395–467. https://doi.org/10.5962/p.315987

Barr ME (1987) Prodromus to class Loculoascomycetes. Amherst. University of Massachusetts, Massachusetts.

Bhagat J, Kaur A, Sharma M, Saxena AK, Chadha BS (2012) Molecular and functional characterization of endophytic fungi from traditional medicinal plants. World Journal of Microbiology and Biotechnology 28: 963–971. https://doi.org/10.1007/s11274-011-0894-0

Bonnardeaux Y, Brundrett M, Batty A, Dixon K, Koch J, Sivasithamparam K (2007) Diversity of mycorrhizal fungi of terrestrial orchids: compatibility webs, brief encounters, lasting relationships and alien invasions. Mycological Research 111: 51–61. https://doi.org/10.1016/j.mycres.2006.11.006

Boonmee S, Ko TWK, Chukeatirote E, Hyde KD, Chen H, Cai L, McKenzie EHC, Jones EBG, Kodsueb R, Hassan BA (2012) Two new Kirschsteiniothelia species with Dendryphiopsis anamorphs cluster in Kirschsteiniotheliaceae fam. nov. Mycologia 104: 698–714. https://doi.org/10.3852/11-089

Castañeda-Ruiz RF, Heredia GP, Arias RM, Saikawa M, Minter DW, Stadler M, Guarro J, Decock C (2004) Two new hyphomycetes from rainforests of México, and Briansuttonia, a new genus to accommodate Corynespora alternarioides. Mycotaxon 89: 297–305.

Chernomor O, Von Haeseler A, Minh BQ (2016) Terrace aware data structure for phylogenomic inference from supermatrices. Systematic Biology 65: 997–1008. https://doi.org/10.1093/sysbio/syw037

Chomnunti P, Hongsanan S, Aguirre-Hudson B, Tian Q, Peršoh D, Dhami MK, Alias AS, Xu JC, Liu XZ, Stadler M, Hyde KD (2014) The sooty moulds. Fungal Diversity 66: 1–36. https://doi.org/10.3825/11-089

Crous PW, Wingfield MJ, Burgess TI, Hardy GESJ, Barber PA, Alvarado P, Barnes CW, Buchanan PK, Heykoop M, Moreno G, Thangavel R, van der Spuy S, Barili A, Barrett S, Cacciola SO, Cano-Lira JF, Crane C, Decock C, Gibertoni TB, Guarro J, Guevara-Suarez
M, Hubka V, Kolářík M, Lira CRS, Ordoñez ME, Padamsee M, Ryvarden L, Soares AM, Stschigel AM, Sutton DA, Vizzini A, Weir BS, Acharya K, Aloï F, Baseia IG, Blanchette RA, Bordallo JJ, Bratek Z, Butler T, Cano-Canals J, Carlavilla JR, Chander J, Cheewangkoon R, Cruz RHSSF, da Silva M, Dutta AK, Ercole E, Escobio V, Esteve-Raventós F, Flores JA, Gené J, Góis JS, Haines L, Held BW, Jung MH, Hosaka K, Jung T, Jurjević Ž, Kautman V, Kautmanova I, Kiyashko AA, Kozanek M, Kubátová A, Lafourcade M, La Spada F, Latha KPD, Madrid H, Malyshева EF, Manimohan P, Manjón JL, Martín MP, Mata M, Merényi Z, Morte A, Nagy I, Normand AC, Paloi S, Pattison N, Pawlowska J, Pereira OL, Petterson ME, Picillo B, Raj KNA, Roberts A, Rodríguez A, Rodríguez-Campo FJ, Romański M, Ruszkiewicz-Michalska M, Scanu B, Schena L, Semelbauer M, Sharma R, Shouche YS, Silva V, Staniszek-Kik M, Stiewol JB, Tapia C, Taylor PWJ, Toome-Heller M, Vabeikhokhei JMC, van Diepeningen AD, Van Hoa N, M VT, Wiedenhold NP, Wrzosek M, Zoňhanszája J, Groenewald JZ (2017) Fungal Planet description sheets: 558–624. Persoonia 38: 240–384. https://doi.org/10.3767/003158517X698941

Ellis MB (1958) *Clasterosporium* and some allied Dematiaceae Phragmosporae: I. Mycological Papers 7: 1–89.

Ellis MB (1971) Dematiaceous hyphomycetes. Commonwealth Mycological Institute, Kew.

Ferdinandz HS, Manamgoda DS, Udayanga D, Deshappriya N, Munasinghe MS, Castlebury LA (2021) Molecular phylogeny and morphology reveal three novel species of *Curvularia* (Pleosporales, Pleosporaceae) associated with cereal crops and weedy grass hosts. Mycological Progress 20: 431–451. https://doi.org/10.1007/s11557-021-01681-0

Hall TA (1999) BioEdit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. In, 95–98.

Hashimoto A, Matsumura M, Hirayama K, Tanaka K (2017) Revision of *Lophiotremataceae* (Pleosporales, Dothideomycetes): *Aquasubmersaceae, Cryptocoryneaceae, and Hermatomycetaceae* fam. nov. Persoonia 39: 51–73. https://doi.org/10.3767/persoonia.2017.39.03

Hoang DT, Chernomor O, Von Haeseler A, Minh BQ, Vinh LS (2018) UFBoot2: improving the ultrafast bootstrap approximation. Molecular Biology and Evolution 35: 518–522. https://doi.org/10.1093/molbev/msx281

Hongsanan S, Hyde KD, Phookamsak R, Wanasinghe DN, McKenzie EHC, Sarma VV, Boonmee S, Lücking R, Bhat DJ, Liu NG, Tennakoon DS, Pem D, Karunarathna A, Jiang SH, Jones EBG, Phillips AJL, Manawasinghe IS, Tibpromma S, Jayasiri SC, Sandamali DS, Jayawardena RS, Wijayawardene NN, Ekanayaka AH, Jeewon R, Lu YZ, Dissanayake AJ, Zeng XY, Luo ZL, Tian Q, Phukhamsakda C, Thambugala KM, Dai DQ, Chethana KWT, Samarakoon MC, Ertz D, Bao DF, Doilom M, Liu JK, Pérez-Ortega S, Suija A, Senwanna C, Wijesinghe SN, Konta S, Niranjan M, Zhang SN, Ariyawansa HA, Jiang HB, Zhang JF, Norphanphoum C, de Silva NI, Thiagaraja V, Zhang H, Bezerra JDP, Miranda-González R, Áptroot A, Kashiwadani H, Harishchandra D, Sérusiaux E, Aluthmuhandiram JVS, Abeywickrama PD, Devadatha B, Wu HX, Moon KH, Gueidan C, Schumm F, Bundhun D, Mapook A, Monkai J, Chomnunti P, Suetrong S, Chaiwan N, Dayaratne MC, Yang J, Rathnayaka AR, Bhunjun CS, Xu JC, Zheng JS, Liu G, Feng Y, Xie N (2020a) Refined families of Dothideomycetes: Dothideomycetidae and Pleosporomycetidae. Mycosphere 11: 1553–2107. https://doi.org/10.5943/mycosphere/11/1/13
Kuo CH, McKenzie EHC, Wen TC, Yan JY, Zhao Q (2018) Mycosphere notes 169–224. Mycosphere 9: 271–430. https://doi.org/10.5943/mycosphere/9/2/8

Hyde KD, Xu JC, Rapior S, Jeewon R, Lumyong S, Niego AGT, Abeywickrama PD, Aluthmuhandiram JVS, Brahamanage RS, Brooks S, Chaiyasen A, Chethana KWT, Chomnunti P, Chepkirui C, Chuankid B, de Silva NI, Doilom M, Faulds C, Gentekaki E, Gopalan V, Kakumyan P, Harishchandra D, Hemachandran H, Hongsanan S, Karunarathna A, Karunarathna SC, Khan S, Kumla J, Jayawardena RS, Liu JK, Liu NG, Luangharn T, Macabeo APG, Marasinghe DS, Meeks D, Mortimer PE, Mueller P, Nadir S, Nataraja KN, Nontachaiyapoom S, O’Brien M, Penkhrue W, Phukhamsakda C, Ramanan US, Rathnayaka AR, Sadaba RB, Sandargo B, Samarakooc BC, Tennakoon DS, Siva R, Sriprom W, Suryanarayanan TS, Sujaer K, Suwannarach N, Suwunwong T, Thongbai B, Thongklang N, Wei D, Wijesinghe SN, Winiski J, Yan J, Yasanthika E, Stadler M (2019) The amazing potential of fungi: 50 ways we can exploit fungi industrially. Fungal Diversity 97: 1–136. https://doi.org/10.1007/s13225-019-00430-9

Hyde KD, Dong Y, Phookamsak R, Jeewon R, Bhat DJ, Jones EBG, Liu NG, Abeywickrama PD, Mapook A, Wei DP, Perera RH, Manawasinghe IS, Pem D, Bundhun D, Karunarathna A, Ekanayake AH, Bao DF, Li JF, Samarakooc MC, Chaiwan N, Lin CG, Phuthcharoen K, Zhang SN, Senanayake IC, Goonasekara ID, Thambugala KM, Phukhamsakda C, Tennakoon DS, Jiang HB, Yang J, Zeng M, Huanraluek N, Liu JK, Wijesinghe SN, Tian Q, Tibpromma S, Brahamanage RS, Boonmee S, Huang SK, Thiagaraja V, Lu YZ, Jayawardena RS, Dong W, Yang EF, Singh SK, Singh SM, Rana S, Lad SS, Anand G, Devadatha B, Niranjan M, Sarma VV, Liimatainen K, Aguirre-Hudson B, Niskanen T, Overall A, Alvarenga RLM, Gibertoni TB, Pfieglger WP, Horváth E, Imre A, Alves AL, da Silva Santos AC, Tiago PV, Bulgakov TS, Wanasinghe DN, Bahkali AH, Doilom M, Elgornan AM, Maharachchikumbura SSN, Rajeshkumar KC, Haelewaters D, Mortimer PE, Zhao Q, Lumyong S, Xu J, Sheng J (2020) Fungal diversity notes 1151–1276: taxonomic and phylogenetic contributions on genera and species of fungal taxa. Fungal Diversity 100: 5–277. https://doi.org/10.1007/s13225-020-00439-5

Iturrieta-González I, Pujol I, Iftimie S, García D, Morente V, Queralt R, Guevara-Suarez M, Alastruey-Izquierdo A, Ballester F, Hernández-Restrepo M (2020) Polyphasic identification of three new species in Alternaria section Infectoriae causing human cutaneous infection. Mycoses 63: 212–224. https://doi.org/10.1111/myc.13026

Jayasiri SC, Hyde KD, Ariyawansa HA, Bhat J, Buyck B, Cai L, Dai YC, Abd-Elsalam KA, Ertz D, Hidayat I, Jeewon R, Jones EBG, Bahkali AH, Karunarathna SC, Liu JK, Luangs-aard JJ, Lumbsch HT, Maharachchikumbura SSN, McKenzie EHC, Moncalvo JM, Gbadon-Nejhad M, Nilsson H, Pang KL, Pereira OL, Phillips AJL, Rapšė O, Rollins AW, Romero AI, Etayo J, Selçuk F, Stephenson SL, Suetrong S, Taylor JE, Tsui CKM, Vizzini A, Abdel-Wahab MA, Wen TC, Boonmee S, Dai DQ, Dananagama DA, Dissayake AJ, Ekanayaka AH, Fryar SC, Hongsanan S, Jayawardena RS, Li WJ, Perera RH, Phookamsak R, de Silva NI, Thambugala KM, Tian Q, Wijayawardene NN, Zhao RL, Zhao Q, Kang JC, Promptutta I (2015) The Faces of Fungi database: fungal names linked with morphology, phylogeny and human impacts. Fungal Diversity 74: 3–18. https://doi.org/10.1007/s13225-015-0351-8
Kirk PM, Cannon PF, Minter DW, Staplers JA (2008) Dictionary of the Fungi 10th edn. CABI Bioscience, UK.

Larsson A (2014) AliView: a fast and lightweight alignment viewer and editor for large datasets. Bioinformatics 30: 3276–3278. https://doi.org/10.1093/bioinformatics/btu531

Li GJ, Hyde KD, Zhao RL, Hongsanan S, Abdel-Aziz FA, Abdel-Wahab MA, Alvarado P, Alves-Silva G, Ammirati JF, Ariyawansa HA, Baghela A, Bahkali AH, Beug M, Bhat DJ, Bojantchev D, Boonpratuang T, Bulgakov TS, Camporesi E, Boro MC, Ceska O, Chakraborty D, Chen JJ, Chethana KWT, Chomnunti P, Consiglio G, Cui BK, Dai DQ, Dai YC, Daranagama DA, Das K, Dayarathe MC, De Crop E, De Oliveira RJV, de Souza CAF, de Souza JI, Dentinger BTM, Dissanayake AJ, Doilom M, Drechsler-Santos ER, Ghabad-Nejhad M, Gilmore SP, Góes-Neto A (2016) Fungal diversity notes 253–366: taxonomic and phylogenetic contributions to fungal taxa. Fungal Diversity 78: 1–237. https://doi.org/10.1007/s13225-016-0366-9

Liu YJ, Whelen S, Hall BD (1999) Phylogenetic relationships among Ascomycetes: evidence from an RNA polymerse II subunit. Molecular Biology and Evolution 16: 1799–1808. https://doi.org/10.1093/oxfordjournals.molbev.a026092

Long H, Zhang Q, Hao YY, Shao XQ, Wei XX, Hyde KD, Wang Y, Zhao DG (2019) Diaporthe species in south-western China. MycoKeys 57: 113–127. https://doi.org/10.3897/mycokeys.57.35448

Luttrell ES (1955) The ascostromatci Ascomycetes. Mycologia 47: 511–532. https://doi.org/10.2307/3755666

Ma XY, Maharachchikumbura SSN, Chen BW, Hyde KD, McKenzie EHC, Chomnunti P, Kang JC (2019) Endophytic pestalotiod taxa in Dendrobium orchids. Phytotaxa 419: 268–286. https://doi.org/10.11646/phytotaxa.419.3.2

Mantle PG, Hawksworth DL, Pazoutova S, Collinson LM, Rassing BR (2006) Amorosia littoralis gen. sp. nov., a new genus and species name for the scorpinone and caffeine-producing hyphomycete from the littoral zone in The Bahamas. Mycological Research 110: 1371–1378. https://doi.org/10.1016/j.mycres.2006.09.013

Mathiyazhagan S, Kavitha K, Nakkeeran S, Chandrasekar G, Manian K, Renukadevi P, Krishnamoorthy AS, Fernando WGD (2004) PGPR mediated management of stem blight of Phyllanthus amarus (Schum and Thonn) caused by Corynespora cassiicola (Berk and Curt) Wei. Archives of Phytopathology and Plant Protection 37: 183–199. https://doi.org/10.1080/03235400410001730658

Miller MA, Pfeiffer W, Schwartz T (2010) “Creating the CIPRES Science Gateway for inference of large phylogenetic trees” in Proceedings of the Gateway Computing Environments Workshop (GCE), 14 Nov. 2010, New Orleans, LA, 1–8. https://doi.org/10.1109/GCE.2010.5676129

Minh BQ, Nguyen MAT, von Haeseler A (2013) Ultrafast approximation for phylogenetic bootstrap. Molecular Biology and Evolution 30: 1188–1195. https://doi.org/10.1093/molbev/mst024
Nguyen LT, Schmidt HA, Von Haeseler A, Minh BQ (2015) IQ-TREE: a fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. Molecular Biology and Evolution 32: 268–274. https://doi.org/10.1093/molbev/msu300

Nylander JAA (2004) MrModeltest v2.2. Program distributed by the author: 2. Evolutionary Biology Centre, Uppsala University, 1–2.

Obrist W (1959) Untersuchungen über einige” dothideale” Gattungen. Phytopathologische Zeitschrift 35: 357–388. https://doi.org/10.1111/j.1439-0434.1959.tb01833.x

Ramesh C (2003) Loculoascomycetes from India. Rao GP, Manoharachari C, Bhat DJ (Eds) Frontiers of Fungal Diversity in India, International Book Distributing Company, Lucknow, India, 457–479.

Rambaut A, Drummond A (2008) FigTree: Tree figure drawing tool, version 1.2. 2. Institute of Evolutionary Biology, University of Edinburgh.

Rannala B, Yang ZH (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

Rasool-Hassan BA (2012) Medicinal plants (importance and uses). Pharmaceut Anal Acta 3: 2153–2435. https://doi.org/10.4172/2153-2435.1000e139

Rehner SA, Samuels GJ (1994) Taxonomy and phylogeny of Gliocladium analysed from nuclear large subunit ribosomal DNA sequences. Mycological Research 98: 625–634. https://doi.org/10.1016/S0953-7562(09)80409-7

Rehner SA, Buckley E (2005) A beauveria phylogeny inferred from nuclear ITS and EF1-α sequences: evidence for cryptic diversification and links to Cordyceps teleomorphs. Mycologia 97(1): 84–98. https://doi.org/10.1080/15572536.2006.11832842

Ronquist F, Teslenko M, Van Der Mark P, Ayres DL, Darling A, Höhna S, Larget B, Liu L, Suchard MA, Huelsenbeck JP (2012) MrBayes 3.2: efficient Bayesian phylogenetic inference and model choice across a large model space. Systematic Biology 61: 539–542. https://doi.org/10.1093/sysbio/sys029

Schoch C, Crous PW, Groenewald JZ, Boehm E, Burgess TI, De Gruyter J, De Hoog GS, Dixon L, Grube M, Gueidan C (2009) A class-wide phylogenetic assessment of Dothideomycetes. Studies in Mycology 64: 1–15. https://doi.org/10.3114/sim.2008.61.08

Seifert K, Morgan-Jones G, Gams W, Kendrick B (2011) The genera of hyphomycetes. CBS-KNAW Fungal Biodiversity Centre, Utrecht.

Senanayake IC, Rathnayake AR, Marasinghe DS, Calabon MS, Gentekaki E, Lee HB, Hurdeal VG, Pem D, Dissanayake LS, Wijesinghe SN, Bundhun D, Nguyen TT, Goonasekara ID, Abeywickrama PD, Bhunjun CS, Jayawardena RS, Wanasighe DN, Jeewon R, Bhat DJ, Xiang MM (2020) Morphological approaches in studying fungi: collection, examination, isolation, sporulation and preservation. Mycosphere 11: 2678–2754. https://doi.org/10.5943/mycosphere/11/1/20

Shenoy BD, Jeewon R, Wu WP, Bhat DJ, Hyde KD (2006) Ribosomal and RPB2 DNA sequence analyses suggest that Sporidesmium and morphologically similar genera are polyphyletic. Mycological Research 110: 916–928. https://doi.org/10.1016/j.mycres.2006.06.004

Strobel G, Stierle A, Stierle D, Hess WM (1993) Taxomyces andreanae, a proposed new taxon for a bulbiliferous hyphomycete associated with Pacific Yew (Taxus brevifolia). Mycotaxon. 47: 71–80.
Su H, Kang JC, Cao JJ, Mo L, Hyde KD (2014) Medicinal plant endophytes produce analogous bioactive compounds. Chiang Mai Journal Science 41: 1–13.

Su HY, Hyde KD, Maharachchikumbura SSN, Ariyawansa HA, Luo ZL, Promputtha I, Tian Q, Lin CG, Shang QJ, Zhao YC, Chai HM, Liu XY, Bahkali AH, Bhat JD, McKenzie EHC, Zhou DQ (2016) The families Distoseptisporaceae fam. nov., Kirschsteiniotheliaceae, Sporormiaceae and Torulaceae with new species from freshwater in Yunnan Province, China. Fungal Diversity 80: 375–409. https://doi.org/10.1007/s13225-016-0362-0

Sun JZ, Liu XZ, McKenzie EHC, Jeewon R, Liu JK, Zhang XL, Zhao Q, Hyde KD (2019) Fungiculous fungi: terminology, diversity, distribution, evolution, and species checklist. Fungal Diversity 95: 337–430. https://doi.org/10.1007/s13225-019-00422-9

Sun YR, Jayawardena RS, Hyde KD, Wang Y (2021) Kirschsteiniothelia thailandica sp. nov. (Kirschsteiniotheliaceae) from Thailand. Phytotaxa 490(2): 172–182. https://doi.org/10.11646/phytotaxa.490.2.3

Tan YP, Crous PW, Shivas RG (2016) Eight novel Bipolaris species identified from John L. Alcorn’s collections at the Queensland Plant Pathology Herbarium (BRIP). Mycological Progress 15: 1203–1214. https://doi.org/10.1007/s11557-016-1240-6

Tennakoon DS, Kuo CH, Maharachchikumbura SSN, Thambugala KM, Gentekaki E, Phillips AJL, Bhat DJ, Wanasinghe DN, de Silva NI, Promputtha I, Hyde KD (2021) Taxonomic and phylogenetic contributions to Celtis formosana, Ficus ampelas, F. septica, Macaranga tanarius and Morus australis leaf litter inhabiting microfungi. Fungal Diversity 108: 1–215. https://doi.org/10.1007/s13225-021-00474-w

Thambugala KM, Hyde KD, Tanaka K, Tian Q, Wanasinghe DN, Ariyawansa HA, Jayasiri SC, Boonmee S, Camporesi E, Hashimoto A, Hirayama K, Schumacher RK, Promputtha I, Liu ZY (2015) Towards a natural classification and backbone tree for Lophiostomataceae, Floricolaceae, and Amorosiaceae fam. nov. Fungal Diversity 74: 199–266. https://doi.org/10.1007/s13225-015-0348-3

Tóth S (1975) Some new microscopic fungi, III. Annales Historico-naturales Musel nationalis Hungarici 67: 31–35.

Trifinopoulos J, Nguyen LT, von Haeseler A, Minh BQ (2016) W-IQ-TREE: a fast online phylogenetic tool for maximum likelihood analysis. Nucleic Acids Research 44: W232–W235. https://doi.org/10.1093/nar/gkw256

Tzean SS, Chen JL (1990) Cheiromoniliophora elegans gen. et sp. nov. (Hyphomycetes). Mycological Research 94: 424–427. https://doi.org/10.1016/S0953-7562(09)80373-0

Vaidya G, Lohman DJ, Meier R (2011) SequenceMatrix: concatenation software for the fast assembly of multi-gene datasets with character set and codon information. Cladistics 27: 171–180. https://doi.org/10.1111/j.1096-0031.2010.00329.x

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

Voglmyr H, Jaklitsch WM (2017) Corynespora, Exosporium and Helminthosporium revisited – New species and generic reclassification. Studies in Mycology 87: 43–76. https://doi.org/10.1016/j.simyco.2017.05.001

Wei CT (1950) Notes on Corynespora. Mycological Papers 34, 10 pp.
White TJ, Bruns T, Lee SJWT, Taylor J (1990) Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In: Innis M, Gelfand D, Shinsky J, White T (Eds) PCR protocols: a guide to methods and applications. Academic Press, New York, 315–322. https://doi.org/10.1016/B978-0-12-372180-8.50042-1

Wijayawardene NN, Crous PW, Kirk PM, Hawksworth DL, Boonmee S, Braun U, Dai DQ, D’soouza MJ, Diederich P, Dissankayake A, Doilom M, Hongsanan S, Jones EBG, Grootenwald JZ, Jayawardena R, Lawrey JD, Liu JK, Lücking R, Madrid H, Manamgoda DS, Muggia L, Nelsen MP, Phookamsak R, Suetrong S, Tanaka K, Thambugala KM, Wanasinghe DN, Wikee S, Zhang Y, Aptroot A, Ariyawansa HA, Bahkali AH, Bhat DJ, Gueidan C, Chomnunti P, De Hoog GS, Knudsen K, Li WJ, McKenzie EHC, Miller AN, Phillips AJL, Piątek M, Raja HA, Shivash S, Slippers B, Taylor JE, Tian Q, Wang Y, Woudenbergh JHC, Cai L, Jaklitsch WM, Hyde KD (2014) Naming and outline of Dothideomycetes–2014 including proposals for the protection or suppression of generic names. Fungal Diversity 69: 1–55. https://doi.org/10.1007/s13225-014-0309-2

Wijayawardene NN, Hyde KD, Al-Ani LKT, Tedersoo L, Haelewaters D, Rajeshkumar KC, Zhao RL, Aptroot A, Leontyev D, Saxena RK, Tokarev YS, Dai DQ, Letcher PM, Stephenson SL, Ertz D, Lumbsch HT, Kukwa M, Issi IV, Madrid H, Phillips AJL, Selbmann L, Pfieglser WP, Horváth E, Bensch K, Kirk PM, Kolafíková K, Raja HA, Radek R, Papp V, Dima V, Ma J, Malosso E, Takamatsu S, Rambold G, Gannibal PB, Triebel D, Gautam AK, Avasthi S, Suetrong S, Timdal E, Fryar SC, Delgado G, Réblova M, Doilom M, Dola-tabadi S, Pawłowska JZ, Humber RA, Koda’sueb R, Sánchez-Castro I, Goto BT, Silva DKA, de Souza FA, Oehl F, da Silva GA, Silva IR, Błaszkowski J, Jobim K, Maia LC, Barbosa FR, Fiúza PO, Divakar PK, Shenoy BD, Castañeda-Ruiz RF, Somrithipol S, Lateef AA, Karunarathna SC, Tibpromma S, Mortimer PE, Wanasinghe DN, Phookamsak R, Xu J, Wang Y, Tian F, Alvarado P, Li DW, Kušan I, Matočec N, Mešić A, Tkalčec Z, Maharachchikumbura SSN, Papizadeh M, Heredia G, Wartchow F, Bakhshi M, Boehm E, Youssef N, Hustad VP, Lawrey JD, Santiago ALCMA, Becerra JDP, Souza-Motta CM, Firmino AL, Tian Q, Houbranken J, Hongsanan S, Tanaka K, Dissanayake AJ, Monteiro JS, Grossart HP, Suija A, Weerakoon G, Etayo J, Tsurykau A, Vázquez V, Mungai P, Damm U, Li QR, Zhang H, Boonmee S, Lu YZ, Becerra AG, Kendrick B, Brearley FQ, Motiejūnaitė J, Sharma B, Khare R, Gaikwad S, Wijesundara DSA, Tang LZ, He MQ, Flakus A, Rodríguez-Flakus P, Zhurbenko MP, McKenzie EHC, Stadler M, Bhat DJ, Liu JK, Raza M, Jeewon R, Nassonova ES, Prieto M, Jayalal RGU, Erdoğan D, Yurkov A, Schnittler M, Shchepin ON, Novozhilov YK, Silva-Filho AGS, Gentekaki E, Liu P, Cavender JC, Kang Y, Mohammad S, Zhang LF, Xu RF, Li YM, Dayaratne MC, Ekanayaka AH, Wen TC, Deng CY, Pereira OL, Navathe S, Hawksworth DL, Fan XL, Dissanayake LS, Kuhnert E, Grossart HP, Thines M (2020) Outline of Fungi and fungus-like taxa. Mycosphere 11: 1060–1456. https://doi.org/10.5943/mycosphere/11/1/8

Wijayawardene NN, Hyde KD, Anand G, Dissanayake LS, Tang LZ, Dai DQ (2021) Towards incorporating asexually reproducing fungi in the natural classification and notes for pleomorphic genera. Mycosphere 12: 238–405. https://doi.org/10.5943/mycosphere/12/1/4

Xu ZH, Kuang WG, Qiu L, Zhang XG, Castañeda-Ruiz RF, Ma J (2020) Corynespora sinensis sp. nov. from Jiangxi, China. Mycotaxon 135: 803–809. https://doi.org/10.5248/135.803
Yang J, Maharachchikumbura SSN, Liu JK, Hyde KD, Jones EBG, Al-Sadi AM, Liu ZY (2018) *Pseudostanjehughesia aquitropica* gen. et sp. nov. and *Sporidesmium sensu lato* species from freshwater habitats. Mycological Progress 17: 591–616. https://doi.org/10.1007/s11557-017-1339-4

Zhang Q, Yang ZF, Cheng W, Wijayawardene NN, Hyde KD, Chen Z, Wang Y (2020) Diseases of *Cymbopogon citratus* (Poaceae) in China: *Curvularia nanningensis* sp. nov. MycoKeys 63: 49–67. https://doi.org/10.3897/mycokeys.63.49264

Zhang SN, Hyde KD, Gareth Jones EB, Cheewangkoon R, Liu JK (2018) *Acuminatispora palmarum* gen. et sp. nov. from mangrove habitats. Mycological Progress 17: 1173–1188. https://doi.org/10.1007/s11557-018-1433-2

Zhang Y, Crous PW, Schoch CL, Hyde KD (2012) Pleosporales. Fungal Diversity 53: 1–221. https://doi.org/10.1007/s13225-011-0117-x