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Anusha H. EKANAYAKA, E. B. Gareth JONES,
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A stable phylogeny for Dactylosporaceae

Anusha H. EKANAYAKA
Key Laboratory for Plant Diversity and Biogeography of East Asia, Kunming Institute of Botany, Chinese Academy of Sciences, Kunming 650201, Yunnan (China)
and Center of Excellence in Fungal Research, Mae Fah Luang University, Chiang Rai, 57100 (Thailand)
hasinie88@gmail.com

E. B. Gareth JONES
Department of Entomology and Plant Pathology, Faculty of Agriculture, Chiang Mai University, 50200 (Thailand)
torperadgj@gmail.com

Kevin D. HYDE
Key Laboratory for Plant Diversity and Biogeography of East Asia, Kunming Institute of Botany, Chinese Academy of Sciences, Kunming 650201, Yunnan (China)
and Center of Excellence in Fungal Research, Mae Fah Luang University, Chiang Rai, 57100 (Thailand)
kdhyde3@gmail.com

Qi ZHAO
Key Laboratory for Plant Diversity and Biogeography of East Asia, Kunming Institute of Botany, Chinese Academy of Sciences, Kunming 650201, Yunnan (China)
zhaoqi@mail.kib.ac.cn (corresponding author)

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ABSTRACT
The apothecial ascomycete family Dactylosporaceae includes saprobes and lichenicolous fungi. In recent studies, the phylogenetic position of this family was unstable within the subphylum Pezizomycotina. The present study provides a stable phylogenetic placement for Dactylosporaceae within the class Eurotiomycetes and we introduce the new order: Dactylosporales Ekanayaka, E.B.G. Jones, Q. Zhao & K.D. Hyde, ord. nov. to accommodate this family. We also introduce two new species: *Dactylospora chiangraiensis* Ekanayaka, E.B.G. Jones, Q. Zhao & K.D. Hyde, sp. nov. and *Dactylospora fusiformis* Ekanayaka, E.B.G. Jones, Q. Zhao & K.D. Hyde, sp. nov. to this family and their relationships with other taxa are represented in a multigene phylogeny.

KEY WORDS
Apothecial ascomycetes, Eurotiomycetes, Pezizomycotina *incertae sedis*, polyphyletic, new order, new species.

RÉSUMÉ
Une phylogénie stable pour les Dactylosporaceae.
La famille des ascomycètes apothéciales, les Dactylosporaceae, comprend des saprobes et des champignons lichénicoles. Dans des études récentes, la position phylogénétique de cette famille était instable dans le sous-phylum Pezizomycotina. La présente étude fournit un placement phylogénétique stable pour les Dactylosporaceae dans la classe des Eurotiomycètes. Nous décrivons un nouvel ordre : les Dactylosporales Ekanayaka, E.B.G. Jones, Q. Zhao & K.D. Hyde, ord. nov. pour accueillir cette famille. Nous introduisons également deux nouvelles espèces: *Dactylospora chiangraiensis* Ekanayaka, E.B.G. Jones, Q. Zhao & K.D. Hyde, sp. nov. et *Dactylospora fusiformis* Ekanayaka, E.B.G. Jones, Q. Zhao & K.D. Hyde, sp. nov. dans cette famille, et leurs relations avec d'autres taxons sont représentées dans une phylogénie multigénique.

MOTS CLÉS
Ascomycètes apothéciaux, Eurotiomycètes, Pezizomycotina *incertae sedis*, polyphylétique, ordre nouveau, espèces nouvelles.

INTRODUCTION

The family Dactylosporaceae was established by Bellemère & Hafellner (1982). Species of this family are mostly saprotrophic on bark, wood and liverworts and sometimes are lichenicolous (Pang *et al.* 2014; Jaklitsch *et al.* 2016). Currently, this family includes a single genus *Dactylospora* which has around 70 species (Jaklitsch *et al.* 2016; Index fungorum 2018). However, Pang *et al.* (2014) and Diederich (2015) suggested a close phylogenetic relationship of the asexual genus *Sclerococcum* with *Dactylospora*.

Various placements have been assigned for this family based on different molecular studies. This family was originally placed within Lecanoromycetes based on its morphology. Schoch *et al.* (2009), Diederich *et al.* (2013) and Pang *et al.* (2014) suggested its position should be within Eurotiomycetes. Miadlikowska *et al.* (2014) and Pino-Bodas *et al.* (2017) provide a phylogenetic analysis, suggesting the phylogenetic position for Dactylosporaceae should be in Lecanoromycetes. However, according to Jaklitsch *et al.* (2016) this family should be referred to the Pezizomycotina *incertae sedis*, while Wijayawardene *et al.* (2018) placed this family within Eurotiomycetes *incertae sedis*. Thus, the phylogenetic status of the family is presently unresolved.

The present study provides a multi-gene phylogenetic tree (ITS, LSU, SSU, TEF, RPB1 and RPB2) for Pezizomycotina, a stable phylogenetic position for the family Dactylosporaceae and introduces a new order: Dactylosporales Ekanayaka, E.B.G. Jones, Q. Zhao & K.D. Hyde, ord. nov. within the class Eurotiomycetes. Moreover, we introduce two new species to this family from Thailand and compare their morphology with similar taxa. Phylogenetic analysis inferred from LSU and ITS gene regions for Eurotiomycetes are provided to show the phylogenetic relationship of the new taxa.

MATERIAL AND METHODS

Sample collection, specimen examination and deposition

Dactylospora specimens were collected from Chiang Rai Province, Thailand. A Motic SMZ-168 stereo microscope was used to observe the apothecial structures. Thin hand sections of apothecia were made with a razor blade and mounted in water. A Nikon ECLIPSE 80i compound microscope was used to observe the microscopic characters. Photomicrography was carried out with a Canon 450D digital camera fitted to the microscope. Measurements of paraphyses, asci and ascospores were made from material mounted in water and the mean values were used in the descriptions. Measurements were made with the Taro soft (R) Image Frame Work v. 0.9.7 program and images used for figures were processed with Adobe Photoshop CS6 software (Adobe Systems Inc.). The type specimens are deposited in the Mae Fah Luang University Herbarium (MFLU), Chiang Rai, Thailand and in the Herbarium of Cryptogams of Kunming Institute of Botany, Chinese Academy of Sciences (KUN-HKAS). Facesoffungi and Index Fungorum numbers are registered as described in Jayasiri *et al.* (2015) and Index Fungorum (2018).

DNA extraction, PCR and sequencing

Genomic DNA was extracted directly from the apothecia using a Plant DNA Rapid Extraction Kit (Bio Teke corporation, Beijing, China). Polymerase chain reactions (PCR) for this study were carried out for the internal transcribed spacer (ITS), using ITS4 and ITS5 (White *et al.* 1990) primers and for the nuclear ribosomal large subunit (LSU) using LROR and LR5 (Vilgalys & Hester 1990) primers. The PCR mixtures (25 µL) contained ddH2O (11 µL), PCR Master Mix (QinKe Co., China) (11 µL; 2×), DNA template (1 µL), each primer (1 µL; 10 µM). PCR amplification conditions were consisted an initial denaturation step of 5 min at 94°C, 35 cycles consisted of denaturation at 94°C for 1 minute, annealing at 53°C for 50 seconds and elongation at 72°C for 3 minute and final extension step of 7 minutes at 72°C for all gene regions. The PCR products were viewed on 1% agarose electrophoresis gels, stained with ethidium bromide. PCR products were sent to a commercial sequencing provider, Qinke in Kunming, China.

Sequence alignment and phylogenetic analysis

Newly generated sequences in this study were subjected to a standard BLAST search of GenBank for rough identification and are deposited in GenBank (Appendix 1).

Data set for phylogenetic analysis I includes sequences belonging to 5.8s, LSU and SSU gene regions from representative Pezizomycotina species and the out-group taxon *Taphrina deformans* (Berk.) Tul. and *Taphrina antarctica* Selbmann & Turchetti, were downloaded from GenBank (Appendix 1). Data set for phylogenetic analysis II includes sequences belonging to ITS, LSU, SS U, TEF, RPB1 and RPB2 gene regions from representative Pezizomycotina species and the out-group taxon *Taphrina deformans* (Berk.) Tul. and *Taphrina antarctica* Selbmann & Turchetti, were downloaded from GenBank (Appendix 1). Data set for phylogenetic analysis III includes sequences belonging to ITS, LSU and SSU gene regions from representative Eurotiomycetes species and the out-group taxon *Teloschistes flavicans* (Sw.) Norman, were downloaded from GenBank (Appendix 2).

For both phylogenetic analyses, the consensus sequences for each gene were aligned using MAFFT v. 6.864b (http://mafft.cbrc.jp/alignment/server/ last consultation on 10 April 2019). The alignment was improved manually where necessary using Bioedit (Hall 2004). Ambiguously aligned regions were excluded and gaps were treated as missing data. The individual datasets were concatenated into a combined dataset using FaBox (1.41) (Villesen 2007). The model of evolution was estimated by using MrModeltest 2.2 (Nylander 2004). Maximum likelihood phylogenetic analyses were performed in the CIPRES web portal (Miller *et al.* 2010) using RAxML-HPC2 Workflow on XSEDE (8.2.9) tool. The bootstrap analysis for each ML tree was performed with 1000 thorough bootstrap replicates with the same parameter settings using the GTR+I+G substitution model. The resultant trees were viewed

with FigTree v.1.4.0 (http://tree.bio.ed.ac.uk/software/figtree/ last consultation on 10 April 2019). Posterior probabilities (PP) (Rannala & Yang 1996; Zhaxybayeva & Gogarten 2002) were determined by Markov Chain Monte Carlo sampling (MCMC) in MrBayes v. 3.0b4 (Huelsenbeck & Ronquist 2001). Ambiguously aligned regions were excluded from the analysis; gaps were treated as missing data. Four simultaneous Markov chains were run for 5,000,000 generations for Phylogenetic analysis II and III and trees were sampled every 100th generation. MCMC heated chain was set with a "temperature" value of 0.15. The distribution of loglikelihood scores was examined to determine stationary phase for each search and to decide if extra runs were required to achieve convergence, using the program Tracer 1.5 (Rambaut & Drummond 2009). All sampled topologies beneath the asymptote (20%) were discarded as part of a burn-in procedure, while the remaining trees were used for calculating posterior probabilities in the majority rule consensus tree. The resultant trees were viewed with FigTree v.1.4.0 (http://tree.bio.ed.ac.uk/software/figtree/). Maximum Likelihood (ML) bootstrap values equal or greater than 60% are given as the first set of numbers above the nodes and Bayesian Posterior Probabilities (BYPP) equal or greater than 0.90 are given as the second set of numbers above the nodes (Figs 1-3).

RESULTS

Phylogenetic analyses

In this study, the phylogenetic relationships of the family Dactylosporaceae within Pezizomycotina was investigated in the phylogenetic analysis I and II (Figs 1; 2). Phylogenetic analysis I based on 5.8s, LSU and SSU and the alignment of combined genes included 6656bp (LSU-1-1003, 5.8s-1004-1174, SSU-1175-2381). The analysis II based on LSU, ITS, SSU, TEF, RPB1 and RPB2 sequence data and the alignment of combined genes included 6656bp (LSU-1-1003, ITS-1004-1962, SSU-1963-2618, TEF-2619-3518, RPB1-3519-4565, RPB2-4566-6656). According to the results of the phylogenetic analysis I and II, the family Dactylosporaceae grouped within Eurotiomycetes (Figs 1; 2). Phylogenetic analysis III shows the phylogenetic relationships of the family Dactylosporaceae within Eurotiomycetes based on analysis of LSU and ITS sequence data (Fig. 3). The alignment of combined genes included 1740bp (LSU-1-944, ITS-945-1740). The topology of the trees from maximum likelihood analysis was similar to the tree from Bayesian analysis.

Taxonomy

Dactylosporales Ekanayaka, E.B.G. Jones, Q. Zhao & K.D. Hyde, ord. nov.

Index Fungorum number. — IF555303.

Facesoffungi number. — FoF 04851.

Type genus. — *Dactylospora* Körb.

Description

Saprobic or lichenicolous.

Sexual morph

Apothecial, superficial, sessile to stipitate.

Hamathecium. Cupulate.

Hymenium. Embedded in a thick gelatinous matrix.

Paraphyses. Sparingly branched, septate, apices slightly swollen.

Asci. Cylindrical to clavate, with an outer gelatinized layer, mostly amyloid.

Ascospores. Mostly 8 per ascus, septate, subglobose to broadly fusiform or ellipsoid, brown to greenish, non-amyloid.

Asexual morph

Sporodochial in the host thallus, conidia dark, consisting of two to several fused, subglobose cells.

Remark

Our phylogenetic study suggested the phylogenetic position for Dactylosporaceae within Eurotiomycetes and here we introduce the new order Dactylosporales Ekanayaka, E.B.G. Jones, Q. Zhao & K.D. Hyde, ord. nov. to accommodate it.

Family Dactylosporaceae Bellem. & Hafellner

In Cryptog. Mycol. 3: 79 (1982).

Facesoffungi number. — FoF 04852

Genera included. — *Dactylospor*a, possibly also *Sclerococcum*

Description

Dactylosporaceae taxa are saprotrophic on bark and wood, liverworts or lichenicolous. This family includes two genera: *Dactylospora* and *Sclerococcum*. *Dactylospora* is a sexual genus and characterized by superficial to stalked blackish apothecia, excipulum composed of *textura angularis* to *globulosa* cells, hymenium consists of a thick gelatinous matrix, sparingly branched paraphyses apices slightly swollen and pigmented, cylindrical to clavate amyloid asci with I– tholus covered by an I+ blue external gelatinous cap, subglobose to ellipsoid and one to several transverse septate ascospores, mostly 8 per ascus (Hafellner 1979, Bellemère & Hafellner 1982; Döbbeler & Buck 2017). *Sclerococcum* is an asexual genus and characterized by sporodochial conidiomata (Diederich *et al.* 2013, Miadlikowska *et al.* 2014). In this paper, we introduce two new species of *Dactylospora*.

FIG. 1. — Phylogram generated from maximum likelihood analysis of sequences of Pezizomycotina including *Dactylospora* based on 5.8s, LSU and SSU sequence data. Maximum likelihood bootstrap values ≥ 60% are given above the nodes. Strain/culture numbers are given after the taxon names. The tree was rooted with *Taphrina antarctica* Selbmann & Turchetti (CCFEE 5198) and *Taphrina deformans* (Berk.) Tul. (AFTOL ID 1234).

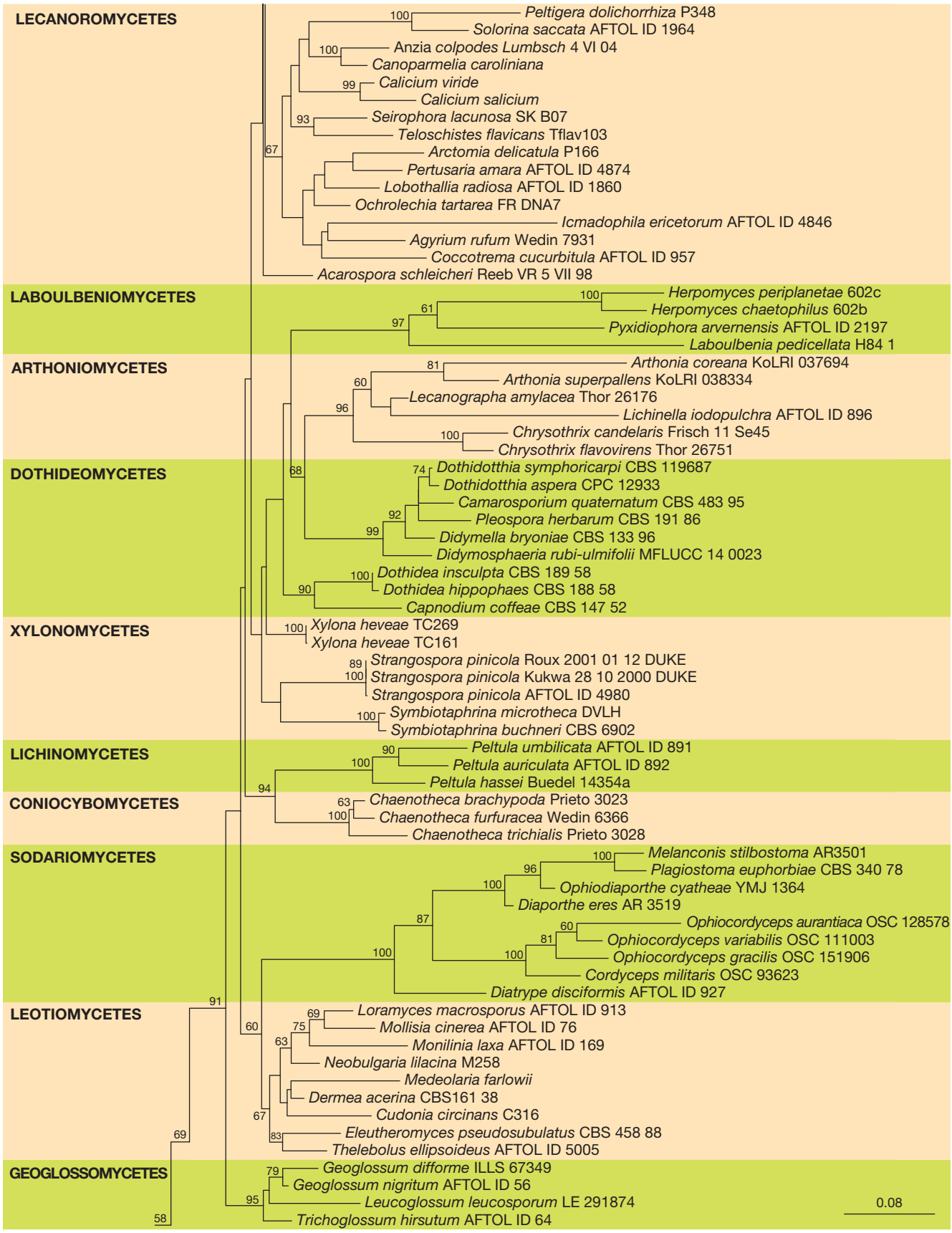

FIG. 1. — Continuation.

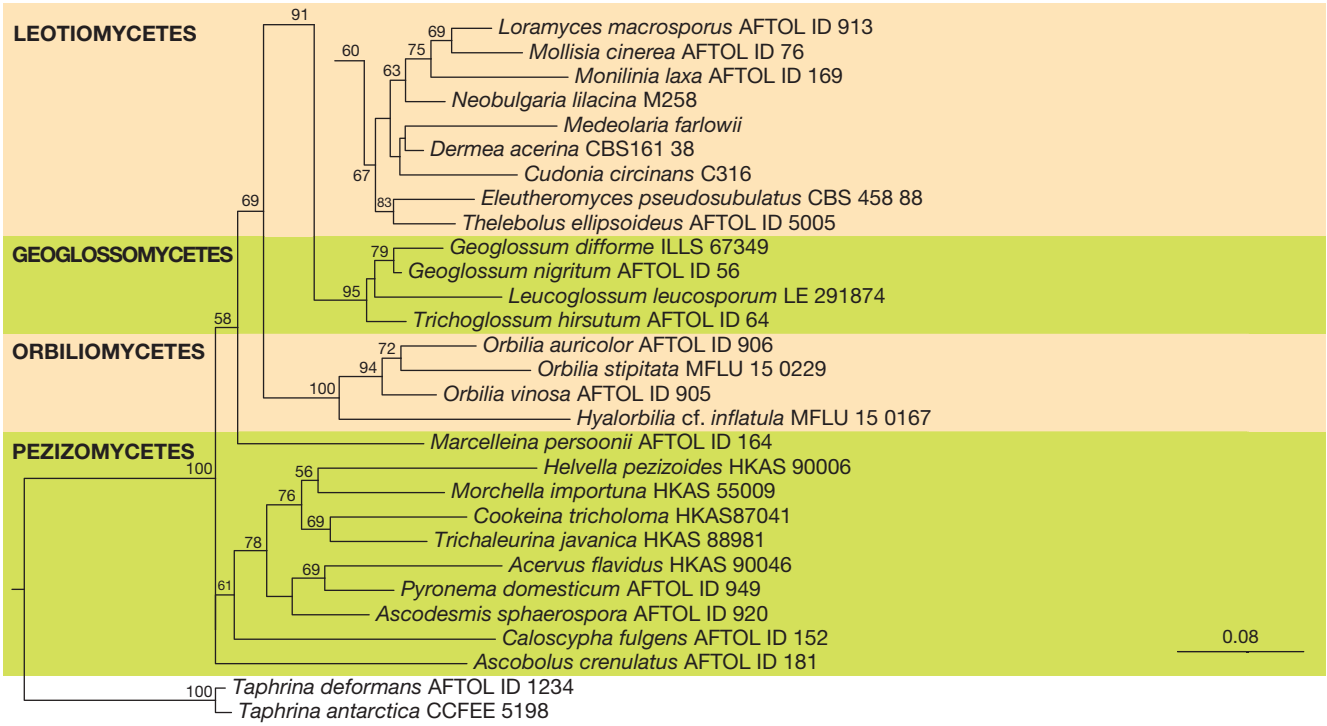

FIG. 1. — Continuation.

Genus *Dactylospora* Körb.

Dactylospora chiangraiensis Ekanayaka, E.B.G. Jones, Q. Zhao & K.D. Hyde, sp. nov. (Fig. 4)

Black apothecia with maroon to brown margins, ectal excipulum of *textura angularis*, paraphyses with slightly swollen apices, unitunicate, cylindrical, short pedicellate, inoperculate asci with an amyloid gelatinous cap and smooth one-septate ascospores.

INDEX FUNGORUM NUMBER. — IF555304.

FACESOFFUNGI NUMBER. — FoF 04853.

HOLOTYPE. — MFLU 16-0570.

TYPE LOCALITY. — Thailand

ETYMOLOGY. — With reference to the province where the holotype was collected.

MATERIAL EXAMINED. — **Thailand**. Tham Pla Temple M.14 (Bann Tham Pla Temple), Pongpha, Mae Sai District, Chiang Rai Province, 25th November 2014, A. H. Ekanayaka (HD 003) (holo-, MFLU [MFLU 16-0570]; iso-, HKAS). Sequence data: ITS-MH718440, LSU-MH718433

DESCRIPTION

Saprobic on unidentified wood, stems and twigs.

Sexual morph

Apothecia. 450-500 × 1000-1500 µm ($\bar{x}$ = 469.7 × 1242.5 µm, n = 10) superficial, sessile, arising singly or in small groups.

Hamathecium. Cupulate, outer surface black.

Margins. Raised, maroon to brown, rough surface.

Disc. Flat to slightly concave, black, rough granulated surface.

Ectal excipulum. 55-65 µm wide at margins, comprising cells of *textura angularis*, outer cell layer is dark brown to light brown, inner cells are hyaline to brownish.

Medullary excipulum. 15-25 µm wide at margins, composed of brown intertwined hyphae, embedded in a gelatinous matrix.

Pseudo epithecium. Composed of hyaline to brown amorphous matter surrounding the paraphysis tips.

Paraphyses. 1.8-2.3 µm ($\bar{x}$ = 2.1 µm, n = 10) wide at the middle, 3.5-5 µm ($\bar{x}$ = 4.3 µm, n = 10) wide at the tips, numerous, filamentous, septate, branched, slightly swollen and branched at the apices extending beyond the asci and apices are glued together to form the epithecium.

Asci. 65-75 × 12-15 µm ($\bar{x}$ = 69.7 × 13.6 µm, n = 30), 8-spored, unitunicate, cylindrical, short pedicellate, inoperculate with an amyloid gelatinous cap.

Ascospore. 12-15 × 4-4.5 µm ($\bar{x}$ = 14.2 × 4.3 µm, n = 40), ellipsoid to fusoid, hyaline at immature stage and brown at maturity, one-septate, smooth walled, guttulate.

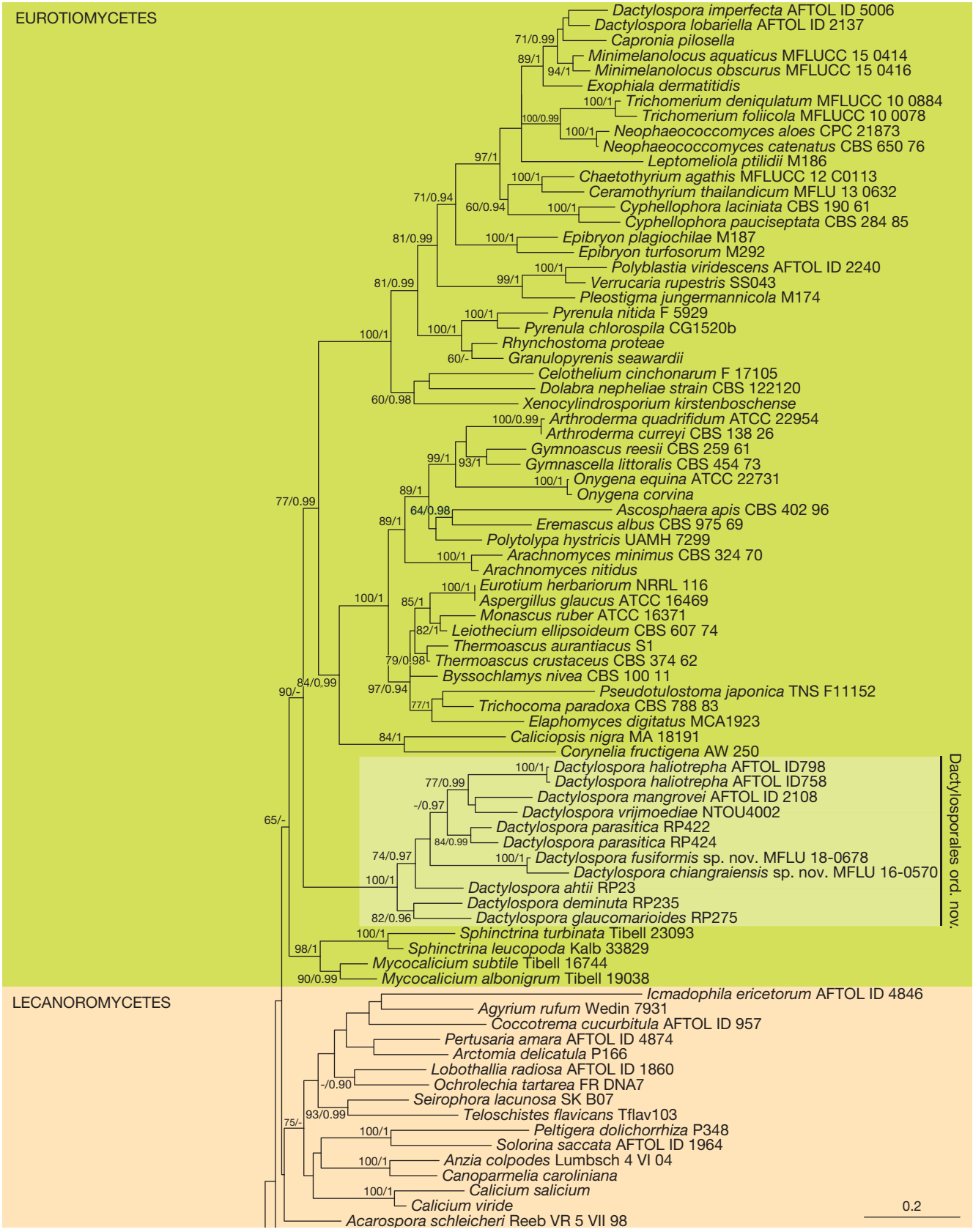

Fig. 2. — Phylogram generated from maximum likelihood analysis of sequences of Pezizomycotina including *Dactylospora* based on ITS, LSU, SSU, TEF, RPB1 and RPB2 sequence data. Maximum likelihood bootstrap values ≥ 60% and Bayesian Posterior Probabilities ≥ 0.90 are given above the nodes. Strain/culture numbers are given after the taxon names. The tree was rooted with *Taphrina antarctica* (CCFEE 5198) and *Taphrina deformans* (AFTOL ID 1234).

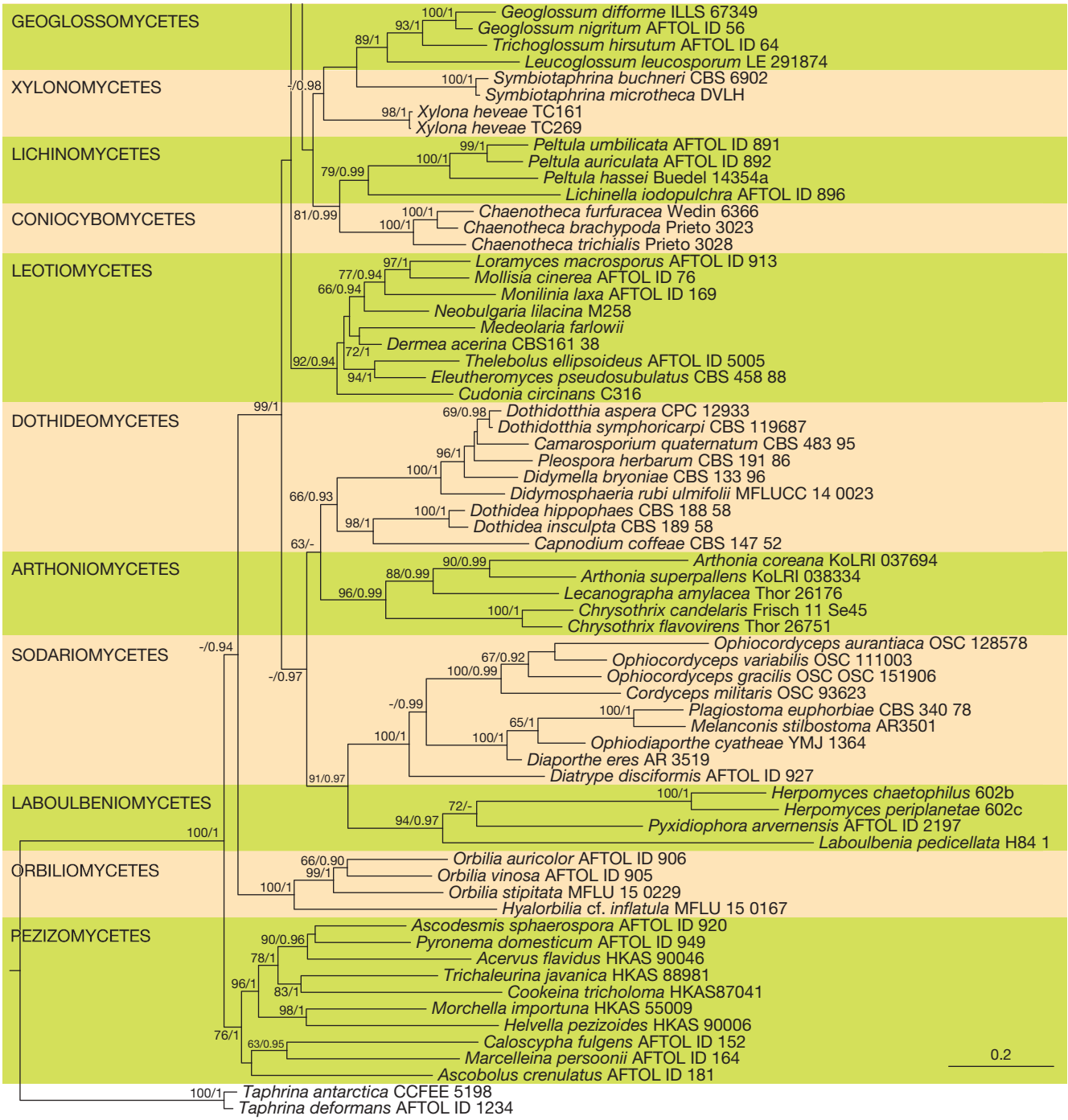

Fig. 2. — Continuation.

Asexual morph
Undetermined.

Remarks

Dactylospora chiangraiensis sp. nov. is characterized by black apothecia with maroon to brown margins, paraphyses with slightly swollen apices and smooth one-septate ascospores. Our species is phylogenetically close to *D. stygi*a (Berk. & M.A. Curtis) Hafellner. However, *D. chiangraiensis* sp. nov. differs from *D. stygia* by having maroon to brown raised margins with rough granulated surface in disc, margins and outer surface of apothecia (Berkeley 1875; Baral & Marson 2005).

Dactylospora parellaria (Nyl.) Arnold, 1877, *D. borealis* Holien & Ihlen, 2004, *D. rhyparizae* Arnold, 1874, *D. parasitica* (Flörke) Arnold, 1887, *D. attendenda* (Nyl.) Arnold, 1895, *D. deminuta* (Th. Fr.) Triebel, 1989, *D. urceolata* (Th. Fr.) Arnold, 1874, *D. frigida* Hafellner,

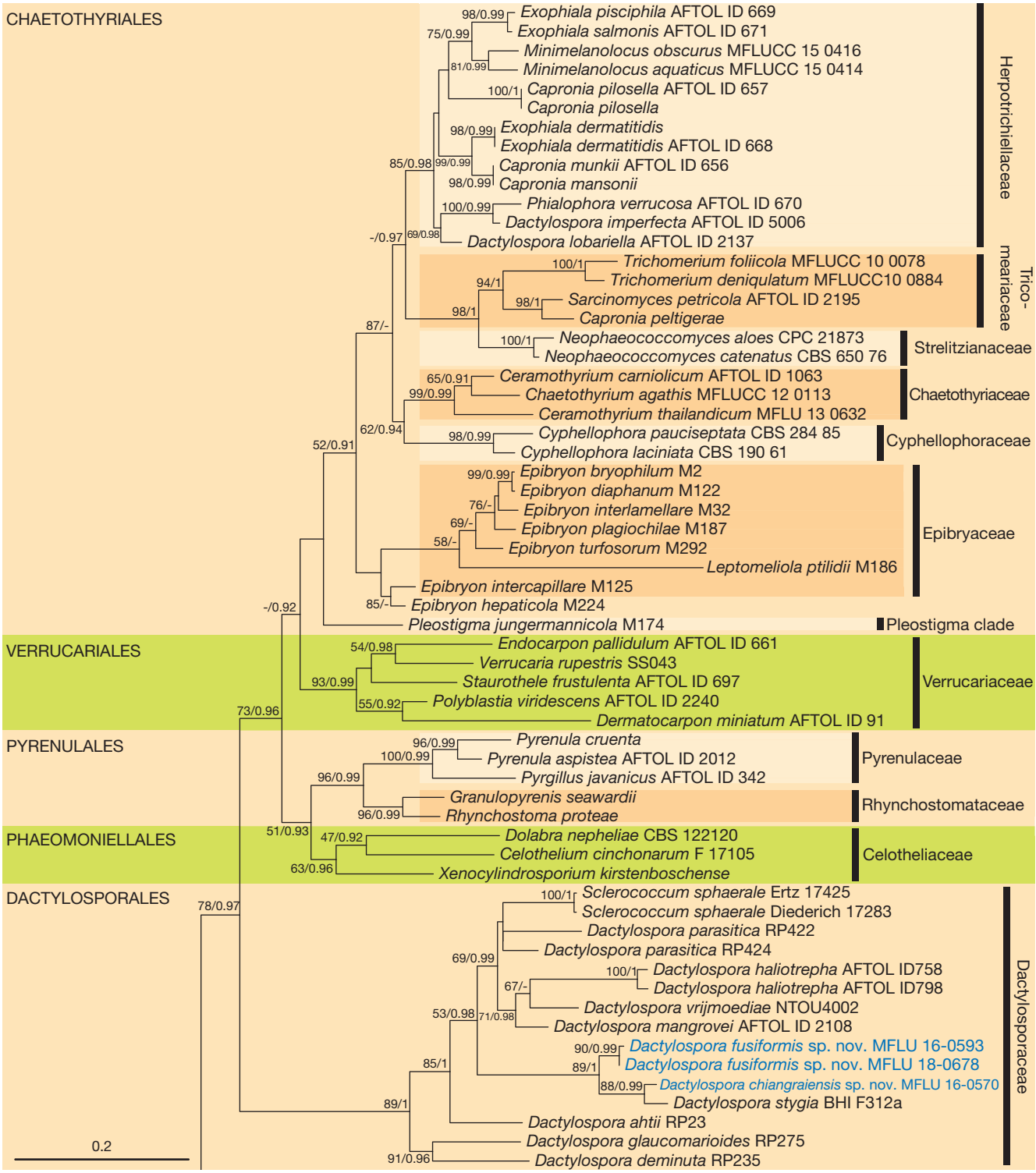

FIG. 3. — Phylogram generated from maximum likelihood analysis of sequences of Eurotiomycetes including *Dactylospora* based on ITS and LSU sequence data. Maximum likelihood bootstrap values ≥ 60% and Bayesian Posterior Probabilities ≥ 0.90 are given above the nodes. Strain/culture numbers are given after the taxon names. The newly generated sequences are in blue bold. The tree was rooted with *Teloschistes flavicans* (Sw.) Norman Tflav103.

1985, *D. suburceolata* Coppins & Fryday, 2012, *D. imperfecta* (Ellis) Hafellner, 1979 and *D. pertusariicola* (Willey ex Tuck.) Hafellner, 1979 differ from *D. chiangraiensis* sp. nov. by having ascospores with more than 1 septa (Ihlen *et al.* 2004). *Dactylospora rimulicola* (Müll. Arg.) Hafellner, 1979, *D. ahtii* Zhurb. & Pino-Bodas, 2017, *D. saxatilis* (Schaer.) Hafellner, 1979, *D. homoclinella* (Nyl.) Hafellner, 1979, *D. australis* Triebel & Hertel, 1989 and *D. amygdalariae* Triebel, 1989 differ from *D. chiangraiensis* sp. nov. by having stipitate apothecia

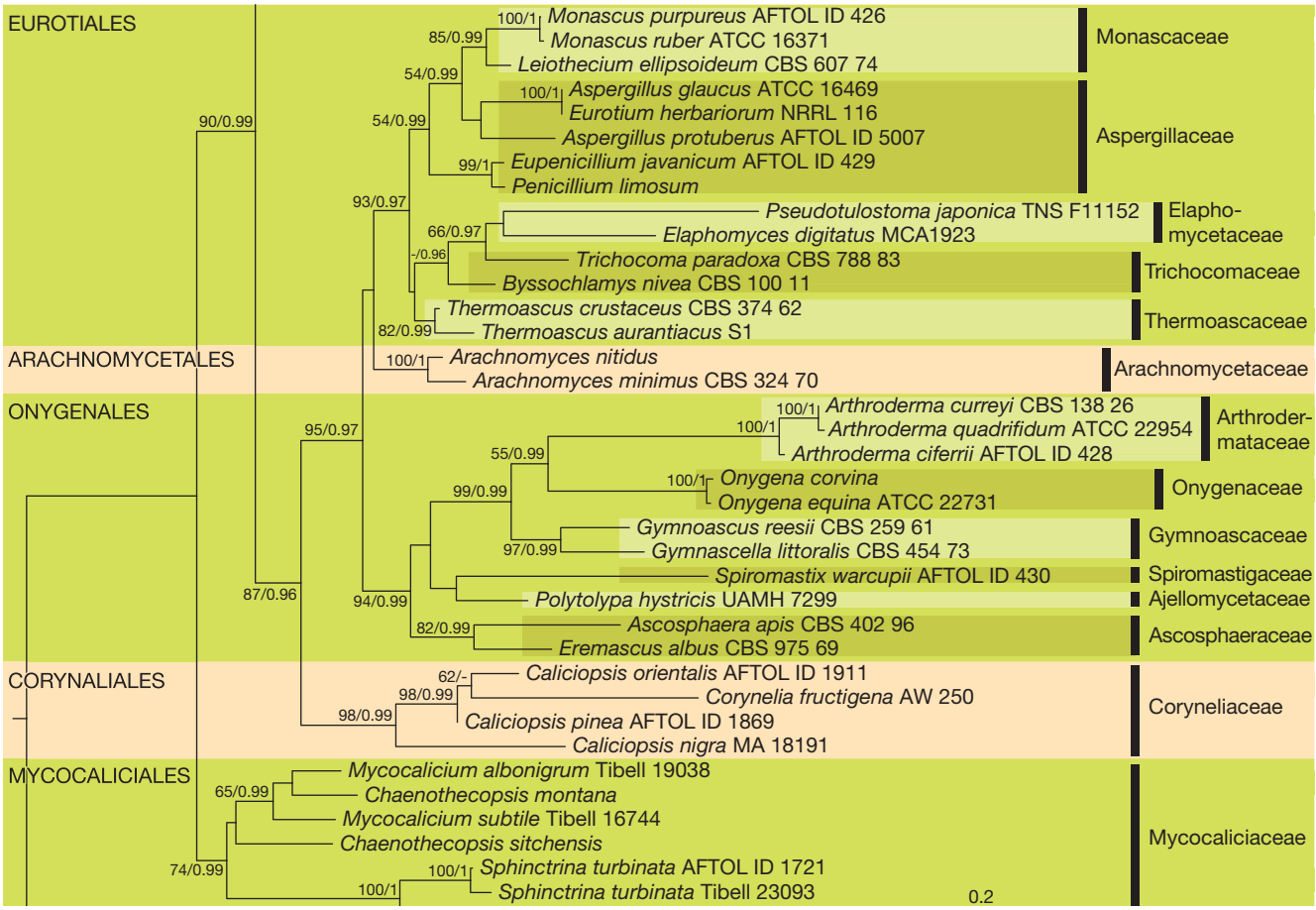

FIG. 3. — Continuation.

(Ihlen *et al.* 2004). *Dactylospora purpurascens* Triebel, 1989 and *D. athallina* (Müll. Arg.) Hafellner, 1979 differ by having an epihymenium with K+ purple reaction (Ihlen *et al.* 2004). *Dactylospora lobariella* (Nyl.) Hafellner, 1979 and *D. protothallina* (Anzi) Hafellner, 1979 differ by having a lichenized lifestyle (Ihlen *et al.* 2004). *Dactylospora inopina* Döbbeler & W.R. Buck, 2017 differs by having polyporous asci (Döbbeler & Buck 2017). *Dactylospora aeruginosa* Holien & Ihlen, 2004 differs by having an epihymenium with patches of violet-blue pigment (Ihlen *et al.* 2004). *Dactylospora microspore* Etayo, 1991 differs from *D. chiangraiensis* sp. nov. by having smaller ascospores (4-7 × 2-3 µm) (Ihlen *et al.* 2004; Joshi *et al.* 2010). *Dactylospora vrijmoediae* K.L. Pang, Sheng Y. Guo, Alias, Hafellner & E.B.G. Jones, 2014 and *D. canariensis* Kohlm. & Volkm.-Kohlm., 1998 differs from *D. chiangraiensis* sp. nov. by having ascospore appendages (Jones *et al.* 1999; Pang *et al.* 2014). *Dactylospora mangrovei* E.B.G. Jones, Alias, Abdel-Wahab & S.Y. Hsieh, 1999 and *D. haliotrepha* (Kohlm. & E. Kohlm.) Hafellner, 1979 differ from *D. chiangraiensis* sp. nov. by having ascospore wall ornamentation (Au *et al.* 1996; Jones *et al.* 1999).

Dactylospora fusiformis Ekanayaka, E.B.G. Jones, Q. Zhao & K.D. Hyde, sp. nov. (Fig. 5)

Black pulvinate apothecia, ectal excipulum of textura angularis to globulosa, paraphyses with slightly swollen apices, unitunicate, short sessile, cylindric-clavate asci and smooth one-septate ascospores.

HOLOTYPE. — MFLU 16-0593.

ETYMOLOGY. — With reference to the ascospore shape.

INDEX FUNGORUM NUMBER. — IF555305.

FACESOFFUNGI NUMBER: FoF 04854.

TYPE LOCALITY. — **Thailand**.

MATERIAL EXAMINED. —**Thailand**. Mae Fah Luang University, Chiang Rai Province, on dead stems, 20 XII 2015, A.H. Ekanayaka, (HD0047) (holo-, MFLU [MFLU 16-0593]; iso-, HKAS). Sequence data: ITS-MH718441, LSU-MH718434, Thailand, Mae Fah Luang University, Chiang Rai Province, on dead stems, 11 VII 2016, A.H. Ekanayaka, (HD0061), MFLU 18-0678. Sequence data: ITS-MH718442.

DESCRIPTION

Saprobic on dead stems.

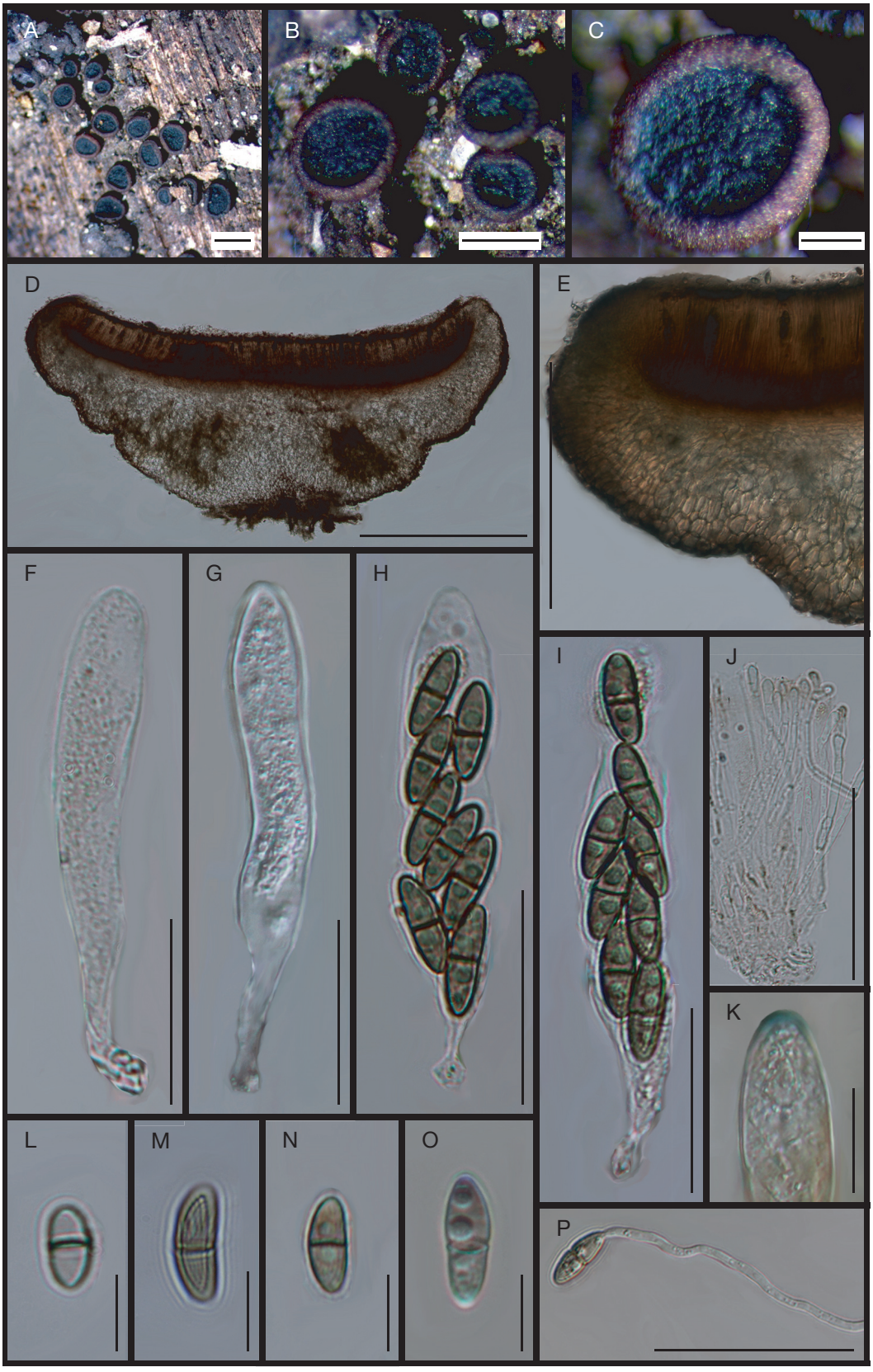

FIG. 4. — Morphology of *Dactylospora chiangraiensis* Ekanayaka, E.B.G. Jones, Q. Zhao & K.D. Hyde, sp. nov. (Holotype MFLU 16-0570): **A**, **B**, ascomata in wood; **C**, ascoma in wood; **D**, cross section of a ascoma; **E**, peridium of ascoma; **F-I**, asci in water; **J**, paraphyses in water; **K**, ascus apex with gelatinous amyloid cap (in Melzer's reagent); **L-O**, ascospores in water; P, germinated ascospore. Scale bars: A, 1000 µm; B, 500 µm; C, D, 200 µm; E, 100 µm; F-I, 25 µm; J, P, 50 µm; K-O, 10 µm.

Sexual morph

Apothecia. 400-1200 × 200-255 µm ($\bar{x}$ = 968 × 223 µm, n = 10) superficial, arising singly or in small groups, sessile.

Hamathecium. Pulvinate, outer surface black.

Margins. Not clearly differentiate from the disc, concolorous to receptacle.

Disc. Flat to slightly convex, black, smooth or finely granulated surface.

Ectal excipulum. 25-40 µm ($\bar{x}$ = 35.3 µm, n = 10) wide at lower flanks, composed of large, thin-walled, dark brown cells of *textura angularis* to *globulosa*, outer cell layer is brown, inner cells are hyaline to brownish.

Medullary excipulum. 10-15 µm ($\bar{x}$ = 13 µm, n = 10) wide at lower flanks, composed of hyaline intertwined hyphae, embedded in a gelatinous matrix.

Hymenium. Hyaline to brownish, enclosed in a thick gelatinous matrix.

Pseudo epithecium. Composed of hyaline to brown amorphous matter surrounding the paraphysis tips.

Paraphyses. 1.4-2 µm wide ($\bar{x}$ = 2.7 µm, n = 20) at the middle, 2.5-3.5 µm wide ($\bar{x}$ = 3.2 µm, n = 20) at the tips, numerous, filiform, septate, swollen and slightly branched at the apex and pigmented, extending beyond the asci and apices glued together to develop pseudo epithecium.

Asci. 70-80 × 12-18 µm ($\bar{x}$ = 73.03 × 14.5 µm, n = 30) 8-spored, unitunicate, short sessile, cylindric-clavate, rounded at the apex, inoperculate with an amyloid gelatinous cap.

Ascospore. 17-21 × 4-7 µm ($\bar{x}$ = 19.1 × 5.7 µm, n = 40), multiseriate, long ellipsoid to fusoid, immature spores are non-septate, hyaline and mature spores are one-septate, greenish brown, guttulate, smooth, thin walled.

Remarks

Dactylospora fusiformis is characterized by black pulvinate apothecia, paraphyses with slightly swollen apices and smooth one-septate ascospores. *Dactylospora fusiformis* is phylogenetically close to *D. chiangraiensis* sp. nov. and *D. stygia*. However, *D. chiangraiensis* sp. nov. and *D. stygia* differ from *D. fusiformis* by having apothecia with raised margins and shorter ascospores (Berkeley 1875, Baral & Marson 2005).

Dactylospora fusiformis differs from *D. rimulicola*, *D. ahtii*, *D. saxatilis*, *D. homoclinella*, *D. rhyparizae*, *D. australis D. amygdalariae* by having sessile apothecia (Ihlen *et al.* 2004). *Dactylospora fusiformis* differs from *D. protothallina* by having a saprobic lifestyle (Ihlen *et al.* 2004). *Dactylospora fusiformis* differs from *D. aeruginosa* in lacking epihymenial pigments (Ihlen *et al.* 2004). *Dactylospora parellaria*, *D. borealis*, *D. rhyparizae*, *D. parasitica*, *D. attendenda*, *D. deminuta*, *D. urceolate*, *D. frigida*, *D. suburceolata*, *D. imperfecta* and *D. pertusariicola* differ from *D. fusiformis* by having ascospores with more than 1 septum (Ihlen *et al.* 2004). *Dactylospora fusiformis* differs from *D. inopina* by having 8-spored asci (Döbbeler & Buck 2017). *Dactylospora purpurascens* and *D. athallina* differ by having an epihymenium with K+ purple reaction (Ihlen *et al.* 2004). *Dactylospora vrijmoediae*, *D. mangrovei, D. lobariella* and *D. canariensis* differ from *D. fusiformis* by having ornamented ascospore walls (Jones *et al.* 1999, Pang *et al.* 2014). *Dactylospora microspora* differs from *D. fusiformis* by having smaller ascospores (4-7 × 2-3 µm) (Ihlen *et al.* 2004, Joshi *et al.* 2010).

DISCUSSION

Dactylosporaceae is a widely distributed family in both terrestrial and mangrove ecosystems (Schoch *et al.* 2009; Pang *et al.* 2014). This paper introduces new *Dactylospora* species from Thailand and a new order for the family Dactylosporaceae (Dactylosporales Ekanayaka, E.B.G. Jones, Q. Zhao & K.D. Hyde, ord. nov.). We provided 3 phylogenetic analyses here. Phylogenetic analyses I and II (Figs 1; 2) represent the subdivision Pezizomycotina from 2 different gene combinations to provide more resolved phylogeny for the family Dactylosporaceae. Phylogenetic analysis I based on LSU, 5.8s and SSU gene regions while phylogenetic analysis II obtained from ITS, LSU, SSU, TEF, RPB1 and RPB2. The phylogenetic analysis I and II shows that the family Dactylosporaceae belongs to Eurotiomycetes as suggested by Schoch *et al.* (2009) and Pang *et al.* (2014). The phylogenetic analysis II shows the stable phylogenetic position of Dactylosporaceae within a new order Dactylospoarales (Eurotiomycetes) introduced here. Moreover, it shows the phylogenetic relationships of the new species, *Dactylospora chiangraiensis* sp. nov. and *Dactylospora fusiformis* with other taxa of the family.

Moreover, Miadlikowska *et al.* (2014) showed the placement of family Dactylosporaceae within Lecanoromycetes and its close relationship with the genus *Strangospora*. However in our analysis I, we observed that the genus *Strangospora* is genetically related to Xylonomycetes.

Furthermore, Schoch *et al.* (2009) and Pang *et al.* (2014) found that the genus *Dactylospora* is polyphyletic. Similarly, in our phylogenetic analyses we found 2 clades that included *Dactylospora* species: *Dactylospora imperfecta* (Ellis) Hafellner and *Dactylospora lobariella* (Nyl.) Hafellner claded within Chaetothyriales, close to *Capronia*. However, there are no apothecial ascomycetes known within Chaetothyriales (Ekanayaka *et al.* 2017). Therefore more fresh collections and re-sequencing of samples are required to resolve the exact phylogenetic position for both *Dactylospora* species. Moreover both *Dactylospora* species may require the introduction of a new genus in the near future.

Dactylospora species are recorded from terrestrial, fresh water and marine habitats. Marine *Dactylospora* spp. include *D. vrijmoediae*, *D. haliotrepha*, *D. mangrovei* and *D. canariensis* while

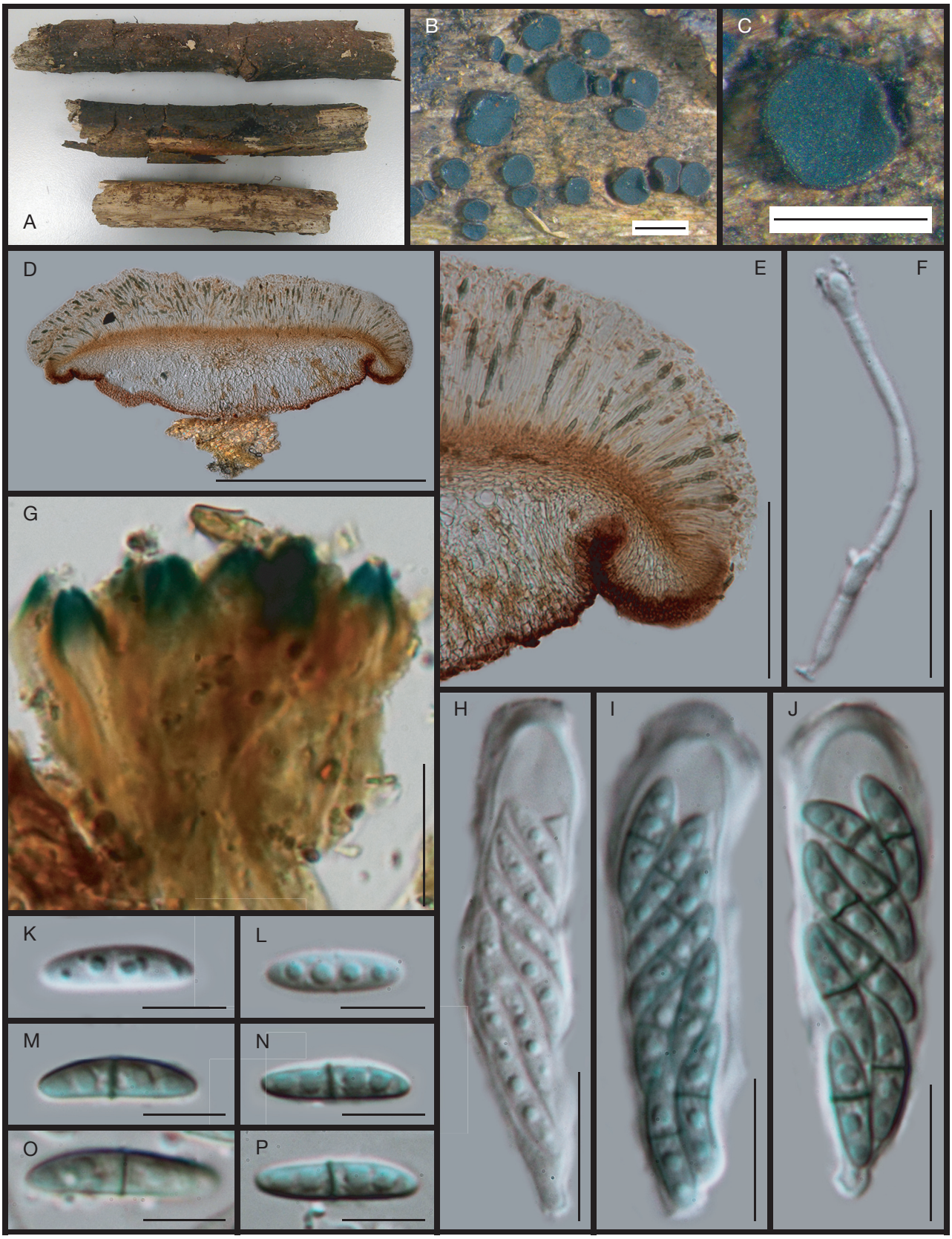

Fig. 5. — Morphology of *Dactylospora fusiformis* Ekanayaka, E.B.G. Jones, Q. Zhao & K.D. Hyde, sp. nov. (Holotype MFLU 16-0593): **A**, substrate; **B**, ascomata on wood; **C**, ascoma on wood; **D**, cross section of an ascoma; **E**, close up of a vertical section of the ascoma at margin; **F**, apically swallen paraphyses; **G**, asci with gelatinous amyloid cap (in Melzer's reagent); **H**-**J**, short sessile asci; **K**-**P**, ellipsoid to fusoid ascospores. Scale bars: B, C, 1000 µm; D, 400 µm; E, 200 µm; F, 30 µm; G, J, 20 µm; K-N, 10 µm.

D. borealis was recorded near fresh water streams and coastal lowlands. According to the literature all those non-terrestrial species are morphologically similar by having ascospore wall ornamentations and/or ascospore appendages. *Dactylospora vrijmoediae* and *D. canariensis* have appendaged ascospores, *D. haliotrepha*, *D. mangrovei* and *D. borealis* have striate, verrucose and granulated ascospore walls, while other terrestrial *Dactylospora* have smooth ascospore walls (Kohlmeyer & Volkmann-Kohlmeyer 1998; Jones *et al.* 1999; Ihlen *et al.* 2004; Fryday & Coppins 2012; Pang *et al.* 2014). Many aquatic ascomycetes have ascospore walls with ornamentations or appendages and these are thought to be an adaptation for their aquatic life (Hyde & Jones 1989; Jones 1994, Shearer & Raja 2010). Moreover, according to the phylogenetic analyses II, three marine *Dactylospora* species form a monophyletic lineage, sister to the *Sclerococcum-D. parasitica* clade. Hence, we suggest these aquatic *Dactylospora* are a phylogenetic distinct group from the terrestrial *Dactylospora* species. Furthermore, they may have evolved from terrestrial *Dactylospora* ancestors and adapted to an aquatic life style (Shearer 1993; Jones 2006).

Currently there are two discomycete families within Eurotiomycetes viz. Mycocaliciaceae and Dactylosporaceae. Taxa of these two families are similar in having sessile to stipitate apothecia, sparingly branched paraphyses, cylindric clavate asci and ellipsoid to fusiform ascospores. However, Dactylosporaceae taxa differ by having amyloid asci (Schoch *et al.* 2009; Jaklitsch *et al.* 2016; Ekanayaka *et al.* 2017).

Dactylospora is a sexual genus and there are no available records of its asexual morph. The asexual genus *Sclerococcum* claded with *Dactylospora* but its phylogenetic limitations are still unclear. Moreover, the genera *Sclerococcum* and *Dactylospora* share similar habitats and ecological affinities (Schoch *et al.* 2009; Pang *et al.* 2014; Diederich 2015). By considering the phylogenetic and ecological similarities, we suggest that *Sclerococcum* could be the asexual morph of *Dactylospora*. However, further taxon sampling, culture studies and molecular data are required to resolve the generic relationship of these two genera.

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APPENDICES

Appendix 1. — GenBank accession numbers of strains used in phylogenetic analysis I and II of this study. New sequence data in this study are in bold.

Species name	Strain number	ITS	LSU	SSU	TEF	RPB2	RPB1
Hyalorbilia inflatula	MFLU 15-0167	MG599270	MG599273	–	–	–	–
Orbilia stipitata	MFLU 15-0229	MG599272	MG599275	–	–	–	–
Orbilia auricolor	AFTOL-ID 906	DQ491512	DQ470953	DQ471001	DQ471072	DQ470903	
Orbilia vinosa	AFTOL-ID 905	DQ491511	DQ470952	DQ471000	DQ471071		DQ471145
Geoglossum nigritum	AFTOL_ID 56	DQ491490	AY544650	AY544694	DQ471044	DQ470879	DQ471115
Trichoglossum hirsutum	AFTOL_ID 64	DQ491494	AY544653	AY544697	DQ471049	DQ470881	DQ471119
Leucoglossum leucosporum	LE 291874	KP272114	KP272115	–	KX898413	–	–
Geoglossum difforme	ILLS 67349	KC222124	KC222137	–	–	–	KC222163
Ascobolus crenulatus	AFTOL ID 181	DQ491504	AY544678	AY544721	DQ471061	DQ470893	DQ471132
Ascodesmis sphaerospora	AFTOL ID 920	–	FJ176858	FJ176804	FJ238391	FJ238346	–
Caloscypha fulgens	AFTOL ID 152	DQ491483	DQ247799	DQ247807	DQ471054	DQ247787	–
Marcelleina persoonii	AFTOL ID 164	–	DQ470943	DQ470991	DQ471055	DQ470887	DQ471127
Pyronema domesticum	AFTOL ID 949	DQ491517	NG_027655	NG_013185	DQ471093	DQ247795	–
Cookeina tricholoma	HKAS87041	KY094618	MG871317	MG859239	MG980688	–	–
Trichaleurina javanica	HKAS 88981	MG871291	MG871326	MG859241	MG980693	MG980716	–
Morchella importuna	HKAS 55009	MG871294	MG871328	MG859242	MG980694	MG980719	–
Helvella pezizoides	HKAS 90006	MG871299	MG871333	–	MG980697	MG980721	–
Acervus flavidus	HKAS 90046	MG871293	KX765259	–	KX765258	MG980718	–
Chaenotheca furfuracea	Wedin 6366	JX000101	JX000087	JX000068	–	–	JX000137
Chaenotheca brachypoda	Prieto 3023	–	JX000086	–	–	–	JX000135
Chaenotheca trichialis	Prieto 3028	JX000102	JX000085	JX000069	–	–	JX000136
Lichinella iodopulchra	AFTOL_ID 896	DQ842016	DQ782916	–	DQ832327	DQ832328	DQ782857
Peltula hassei	Buedel 14354a	MF766365	MF766406	MF766283	–	–	–
Peltula umbilicata	AFTOL_ID 891	DQ832333	DQ832334	DQ782887	DQ782919	DQ832335	DQ782855
Peltula auriculata	AFTOL_ID 892	DQ832329	DQ832330	DQ832332	–	DQ832331	DQ782856
Arthonia superpallens	KoLRI 038334	–	KX913671	–	–	–	–
Arthonia coreana	KoLRI 037694	–	KX913670	–	–	KX913668	–
Chrysothrix candelaris	Frisch 11/Se45	–	KF707640	–	–	KF707663	–
Chrysothrix flavovirens	Thor 26751	–	KJ851030	–	–	–	–
Lecanographa amylacea	Thor 26176	–	KF707639	–	–	KF707659	–
Didymella bryoniae	CBS 133.96	GU237780	GU301863	–	–	GU371767	–
Didymosphaeria rubi-ulmifolii	MFLUCC 14-0023	–	KJ436586	KJ436588	–	–	–
Dothidea hippophaes	CBS 188.58	–	DQ678048	U42475	DQ677887	DQ677942	–
Dothidea insculpta	CBS 189.58	AF027764	DQ247802	DQ247810	DQ471081	AF107800	–
Dothidotthia aspera	CPC 12933	–	EU673276	EU673228	–	–	–
Dothidotthia symphoricarpi	CBS 119687	–	EU673273	EU673224	–	–	–
Pleospora herbarum	CBS 191.86	KC584239	DQ247804	DQ247812	DQ471090	DQ247794	–
Camarosporium quaternatum	CBS 483.95	KY929149	GU301806	GU296141	GU349044	–	GU357761

Appendix 1. — Continuation.

Species name	Strain number	ITS	LSU	SSU	TEF	RPB2	RPB1
Capnodium coffeae	CBS 147.52	AJ244239	DQ247800	DQ247808	DQ471089	DQ247788	–
Dermea acerina	CBS161.38	AF141164	DQ247801	DQ247809	–	–	–
Neobulgaria lilacina	M258	EU940217	EU940141	EU940066	–	EU940352	–
Medeolaria farlowii	–	GQ406809	GQ406807	GQ406808	–	–	–
Eleutheromyces pseudosubulatus	CBS:458.88	KJ710467	EU754162	EU754063	–	–	–
Cudonia circinans	C316	KC833156	KC833182	–	KC833349	KC833275	–
Thelebolus ellipsoideus	CBS 113937	AY957550	FJ176895	FJ176840	–	FJ238378	FJ238445
Mollisia cinerea	AFTOL-ID 76	DQ491498	DQ470942	DQ470990	DQ471051	DQ470883	DQ471122
Loramyces macrosporus	AFTOL-ID 913	JN033383	DQ470957	DQ471005	DQ471076	DQ470907	DQ471149
Herpomyces periplanetae	602c	KT800041	KT800010	KT800025	–	–	–
Herpomyces chaetophilus	602b	KT800039	KT800009	KT800023	–	–	–
Laboulbenia pedicellata	H84-1	–	KY350537	KY523244	–	–	–
Pyxidiophora arvernensis	AFTOL-ID 2197	–	FJ176894	FJ176839	FJ238412	FJ238377	–
Xylona heveae	TC269	JQ838225	JQ838239	JQ838236	–	JQ838246	JQ838243
Xylona heveae	TC161	JQ838232	JQ838238	JQ838237	–	JQ838244	JQ838242
Symbiotaphrina buchneri	CBS:6902	–	KY109806	–	–	–	–
Symbiotaphrina microtheca	DVLH	–	KJ004453	–	–	–	–
Cordyceps militaris	OSC 93623	JN049825	AY184966	AY184977	DQ522332	–	DQ522377
Diaporthe eres	AR 3519	–	AF362565	–	–	–	–
Diatrype disciformis	AFTOL-ID 927	–	DQ470964	DQ471012	DQ471085	–	DQ471158
Ophiocordyceps aurantiaca	OSC 128578	JN049833	DQ518770	DQ522556	DQ522345	DQ522445	DQ522391
Ophiocordyceps gracilisOSC	OSC 151906	–	KJ878890	KJ878923	KJ878969	–	–
Ophiodiaporthe cyatheae	YMJ 1364	JX570889	JX570891	JX570890	KC465406	JX570893	–
Ophiocordyceps variabilis	OSC 111003	–	EF468839	EF468985	EF468779	EF468933	–
Monilinia laxa	AFTOL-ID 169	–	AY544670	–	DQ471057	DQ470889	–
Melanconis stilbostoma	AR3501	–	AF408374	NG_013198	EU221886	EU219299	–
Plagiostoma euphorbiae	CBS 340.78	EU199198	AF408382	DQ862055	GU354016	EU219292	–
Cyphellophora laciniata	CBS 190.61	EU035416	FJ358239	FJ358307	–	–	FJ358370
Cyphellophora pauciseptata	CBS 284.85	JQ766466	JQ766515	–	–	–	JQ766415
Chaetothyrium agathis	MFLUCC 12 C0113	KP744437	KP744480	–	–	–	–
Ceramothyrium thailandicum	MFLU 13-0632	KP324928	KP324930	–	–	–	–
Trichomerium deniqulatum	MFLUCC10-0884	JX313654	JX313660	–	–	–	–
Trichomerium foliicola	MFLUCC 10-0078	NR_144963	JX313661	–	–	–	–
Neophaeococcomyces aloes	CPC 21873	KF777182	KF777234	–	–	–	–
Neophaeococcomyces catenatus	CBS 650.76	AF050277	AF050277	–	–	–	–
Minimelanolocus obscurus	MFLUCC:15-0416	KR215606	KR215611	–	–	–	–
Minimelanolocus aquaticus	MFLUCC:15-0414	KR215607	KR215612	–	–	–	–
Exophiala dermatitidis	AFTOL-ID 668	DQ826738	DQ823100	DQ823107	DQ840566	DQ840562	DQ840555

Appendix 1. — Continuation.

Species name	Strain number	ITS	LSU	SSU	TEF	RPB2	RPB1
Capronia pilosella	AFTOL-ID 657	DQ826737	DQ823099	DQ823106	DQ840565	DQ840561	DQ840554
Leptomeliola ptilidii	M186	EU940200		EU940051	–	EU940336	–
Epibryon plagiochilae	M187	EU940201	EU940124	–	–	EU940337	–
Epibryon turfosorum	M292	EU940221	EU940145	–	–	EU940355	–
Polyblastia viridescens	AFTOL-ID 2240	–	EF643771	EF689855	–	–	EF689774
Verrucaria rupestris	SS043	EU553501	EU598724	–	–	–	EU723786
Pleostigma jungermannicola	M174	EU940195	EU940119	EU940046	–	EU940331	–
Celothelium cinchonarum	F 17105	–	DQ329020	–	–	–	–
Dolabra nepheliae	CBS 122120	–	GU332517	–	GU332523	–	GU332521
Xenocylindrosporium kirstenboschense	CBS 125545	GU229890	GU229891	–	–	–	–
Pyrenula chlorospila	CG1520b	JQ927452	JQ927471	–	–	–	–
Pyrenula nitida	F 5929	JQ927458	DQ329023	–	–	–	–
Rhynchostoma proteae	–	–	AY230151	–	–	–	–
Granulopyrenis seawardii	CBS 109025	–	EF411062	–	–	–	–
Eurotium herbariorum	NRRL 116	EF652052	U29553	AB002069	–	–	–
Aspergillus glaucus	ATCC 16469	–	AY176751	–	–	–	–
Monascus ruber	ATCC 16371	AY498572	AF364996	–	–	–	–
Leiothecium ellipsoideum	CBS 607.74	–	FJ358285	FJ358350	–	–	FJ358412
Byssochlamys nivea	CBS 100.11	FJ389934	AY176750	–	–	JF417414	JN121551
Trichocoma paradoxa	CBS 788.83	–	FJ358290	FJ358354	–	–	–
Pseudotulostoma japonica	TNS-F11152	–	AB161194	–	–	–	–
Elaphomyces digitatus	MCA1923	–	JN713148	–	–	–	–
Thermoascus crustaceus	CBS 374.62	–	FJ358289	–	–	–	–
Thermoascus aurantiacus	S1	–	KJ535692	–	–	–	–
Arachnomyces minimus	CBS 324.70	–	FJ358274	AJ315167	–	–	–
Arachnomyces nitidus	IFO 32048	–	AB075351	–	–	–	–
Gymnoascus reesii	CBS 259.61	–	FJ358284	FJ358349	–	–	FJ358411
Gymnascella littoralis	CBS 454.73	–	FJ358272	FJ358340	–	–	FJ358404
Arthroderma curreyi	CBS 138.26	KT155805	AY176726	AJ315165	–	–	–
Arthroderma quadrifidum	ATCC 22954	–	AY176728	–	–	–	–
Onygena equina	ATCC 22731	–	AY176717	–	–	–	–
Onygena corvina	JCM 9546	–	AB075355	–	–	–	–
Ascosphaera apis	CBS 402.96	–	FJ358275	FJ358343	–	–	FJ358406
Eremascus albus	CBS 975.69	–	FJ358283	FJ358348	–	–	FJ358410
Polytolypa hystricis	UAMH 7299	AY527405	AY176718	–	–	–	–
Caliciopsis nigra	MA 18191	–	KP144011	–	–	–	–
Corynelia fructigena	AW 250	KP881704	KP881716	KP881720	–	–	–
Sphinctrina leucopoda	Kalb 33829	AY795875	AY796006	–	–	–	–
Sphinctrina turbinata	Tibell 23093	AY795877	DQ009001	–	–	–	–

Appendix 1. — Continuation.

Species name	Strain number	ITS	LSU	SSU	TEF	RPB2	RPB1
Mycocalicium subtile	Tibell 16744	–	AY796004	–	–	–	–
Mycocalicium albonigrum	Tibell 19038	–	AY796001	–	–	–	–
Acarospora schleicheri	Reeb VR 5-VII-98	–	AY640945	AY640986	–	–	–
Agyrium rufum	Wedin 7931	JX000097	EF581826	–	–	–	EF581822
Coccotrema cucurbitula	AFTOL-ID 957	–	AF274092	–	–	–	–
Icmadophila ericetorum	AFTOL-ID 4846	–	KJ766573	KJ766729	–	–	–
Lobothallia radiosa	AFTOL-ID 1860	–	KJ766596	KJ766746	–	KJ766935	KJ766870
Ochrolechia tartarea	FR:DNA7	JN943620	JN941358	–	–	–	JN992649
Pertusaria amara isolate	AFTOL-ID 4874	–	KJ766623	KJ766764	–	–	–
Arctomia delicatula isolate	P166	–	KR017191	KR017255	KR017563	–	KR017488
Solorina saccata isolate	AFTOL-ID 1964	HQ650625	KJ766661	KJ766797	–	–	–
Peltigera dolichorrhiza isolate	P348	KX897182	KM005745	–	KM005875	–	KM005937
Teloschistes flavicans isolate	Tflav103	KT291472	KT291565	–	–	KT291662	KT291604
Seirophora lacunosa voucher	SK B07	KT220204	KT220213	–	–	–	–
Anzia colpodes	Lumbsch 4.VI.04	–	DQ923651	–	–	–	–
Canoparmelia caroliniana	AFTOL-ID 6	–	AY584634	AY584658	–	AY584683	–
Calicium salicium	CBS 100898	–	KF157982	KF157970	–	KF157998	–
Calicium viride	Soechting 7475	–	AF356670	–	–	–	–
Taphrina deformans	AFTOL-ID 1234	–	DQ470973	DQ471024	DQ471097	DQ470927	DQ471170
Taphrina antarctica	CCFEE 5198	NR_132870	JX124717	–	–	–	–
Dactylospora haliotrepha	AFTOL-ID758	–	FJ176855	FJ176802	–	FJ238344	–
Dactylospora haliotrepha	AFTOL-ID798	–	FJ713617	–	–	FJ713614	–
Dactylospora imperfecta	AFTOL-ID 5006	–	FJ176896	FJ176841	–	–	–
Dactylospora lobariella	AFTOL-ID 2137	–	FJ176891	FJ176837	–	–	–
Dactylospora mangrovei	AFTOL-ID 2108	–	FJ176890	FJ176836	FJ238411	FJ238375	KJ766849
Dactylospora vrijmoediae	NTOU4002	NR_138396	KC692153	KC692152	–	KC692154	–
Dactylospora ahtii	RP23	KY661630	KY661659	–	–	–	–
Dactylospora parasitica	RP424	–	KY661667	–	–	–	–
Dactylospora parasitica	RP422	KY661646	KY661666	–	–	–	–
Dactylospora glaucomarioides	RP275	KY661632	KY661660	–	–	–	–
Dactylospora deminuta	RP235	KY661629	–	–	–	–	–
Dactylospora fusiformis	MFLU 16-0593	**MH718441**	**MH718434**	–	–	–	–
Dactylospora chiangraiensis	MFLU 16-0570	**MH718440**	**MH718433**	–	–	–	–

Appendix 2. — GenBank accession numbers of strains used in phylogenetic analysis II of this study. New sequence data in this study are in bold.

Species name	Strain number	ITS	LSU
Cyphellophora laciniata	CBS 190.61	EU035416	FJ358239
Cyphellophora pauciseptata	CBS 284.85	JQ766466	JQ766515
Chaetothyrium agathis	MFLUCC 12 C0113	KP744437	KP744480
Ceramothyrium thailandicum	MFLU 13-0632	KP324928	KP324930
Trichomerium deniqulatum	MFLUCC10-0884	JX313654	JX313660
Trichomerium foliicola	MFLUCC 10-0078	NR_144963	JX313661
Neophaeococcomyces aloes	CPC 21873	KF777182	KF777234
Neophaeococcomyces catenatus	CBS 650.76	AF050277	AF050277
Minimelanolocus obscurus	MFLUCC:15-0416	KR215606	KR215611
Minimelanolocus aquaticus	MFLUCC:15-0414	KR215607	KR215612
Exophiala dermatitidis	AFTOL-ID 668	DQ826738	DQ823100
Capronia pilosella	AFTOL-ID 657	DQ826737	DQ823099
Leptomeliola ptilidii	M186	EU940200	–
Epibryon plagiochilae	M187	EU940201	EU940124
Epibryon turfosorum	M292	EU940221	EU940145
Polyblastia viridescens	AFTOL-ID 2240	–	EF643771
Verrucaria rupestris	SS043	EU553501	EU598724
Pleostigma jungermannicola	M174	EU940195	EU940119
Celothelium cinchonarum	F 17105	–	DQ329020
Dolabra nepheliae	CBS 122120	–	GU332517
Xenocylindrosporium kirstenboschense	CBS 125545	GU229890	GU229891
Rhynchostoma proteae	–	–	AY230151
Granulopyrenis seawardii	CBS 109025	–	EF411062
Eurotium herbariorum	NRRL 116	EF652052	U29553
Aspergillus glaucus	ATCC 16469	–	AY176751
Monascus ruber	ATCC 16371	AY498572	AF364996
Leiothecium ellipsoideum	CBS 607.74	–	FJ358285
Byssochlamys nivea	CBS 100.11	FJ389934	AY176750
Trichocoma paradoxa	CBS 788.83	–	FJ358290
Pseudotulostoma japonica	TNS-F11152	–	AB161194
Elaphomyces digitatus	MCA1923	–	JN713148
Thermoascus crustaceus	CBS 374.62	–	FJ358289
Thermoascus aurantiacus	S1	–	KJ535692
Arachnomyces minimus	CBS 324.70	–	FJ358274
Arachnomyces nitidus	IFO 32048	–	AB075351
Gymnoascus reesii	CBS 259.61	–	FJ358284
Gymnascella littoralis	CBS 454.73	–	FJ358272
Arthroderma curreyi	CBS 138.26	KT155805	AY176726
Arthroderma quadrifidum	ATCC 22954	–	AY176728
Onygena equina	ATCC 22731	–	AY176717

Appendix 2. — Continuation.

Species name	Strain number	ITS	LSU
Onygena corvina	JCM 9546	–	AB075355
Ascosphaera apis	CBS 402.96	–	FJ358275
Eremascus albus	CBS 975.69	–	FJ358283
Polytolypa hystricis	UAMH 7299	AY527405	AY176718
Caliciopsis nigra	MA 18191	–	KP144011
Corynelia fructigena	AW 250	KP881704	KP881716
Sphinctrina leucopoda	Kalb 33829	AY795875	AY796006
Sphinctrina turbinata	Tibell 23093	AY795877	DQ009001
Mycocalicium subtile large	Tibell 16744	–	AY796004
Mycocalicium albonigrum	Tibell 19038	–	AY796001
Dactylospora haliotrepha	AFTOL-ID758	–	FJ176855
Dactylospora haliotrepha	AFTOL-ID798	–	FJ713617
Dactylospora imperfecta	AFTOL-ID 5006	–	FJ176896
Dactylospora lobariella	AFTOL-ID 2137	–	FJ176891
Dactylospora mangrovei	AFTOL-ID 2108	–	FJ176890
Dactylospora vrijmoediae	NTOU4002	NR_138396	KC692153
Dactylospora ahtii	RP23	KY661630	KY661659
Dactylospora parasitica	RP424	–	KY661667
Dactylospora parasitica	RP422	KY661646	KY661666
Dactylospora glaucomarioides	RP275	KY661632	KY661660
Dactylospora deminuta	RP235	KY661629	–
Dactylospora stygia	BHI-F312a	MF161218	–
Dactylospora fusiformis	MFLU 18-0678	**MH718442**	**–**
Dactylospora fusiformis	MFLU 16-0593	**MH718441**	**MH718434**
Dactylospora chiangraiensis	MFLU 16-0570	**MH718440**	**MH718433**
Arthroderma ciferrii	AFTOL-ID 428	–	EF413625
Aspergillus protuberus	AFTOL-ID 5007	–	FJ176897
Caliciopsis orientalis	AFTOL-ID 1911	KP881690	DQ470987
Caliciopsis pinea	AFTOL-ID 1869	–	DQ678097
Capronia mansonii	CBS 101.67	AF050247	AY004338
Capronia munkii	AFTOL-ID 656	–	EF413604
Capronia peltigerae	UAMH 11090	HQ709322	HQ613813
Ceramothyrium carniolicum	AFTOL-ID 1063	–	EF413628
Chaenothecopsis montana	Tuovila 07-086	JX119105	JX119114
Chaenothecopsis sitchensis	Tuovila 06-033	JX119102	JX119111
Dermatocarpon miniatum	AFTOL-ID 91	DQ782837	AY584644
Endocarpon pallidulum	AFTOL-ID 661	DQ826735	DQ823097
Epibryon bryophilum	M2	–	EU940090
Epibryon diaphanum	M122	EU940178	EU940101
Epibryon hepaticola	M224	EU940212	EU940136

Appendix 2. — Continuation.

Species name	Strain number	ITS	LSU
Epibryon intercapillare	M125	–	EU940102
Epibryon interlamellare	M32	EU940174	EU940097
Eupenicillium javanicum	AFTOL-ID 429	KT232212	EF413621
Eupenicillium limosum	CBS 339.97	NR_111496	EF411064
Exophiala pisciphila	AFTOL-ID 669	DQ826739	DQ823101
Exophiala salmonis	AFTOL-ID 671	–	EF413609
Monascus purpureus	AFTOL-ID 426	DQ782847	DQ782908
Phialophora verrucosa	AFTOL-ID 670	–	EF413615
Pyrenula aspistea	AFTOL-ID 2012	–	EF411063
Pyrenula cruenta	CBS 132372	KC592268	AF279407
Pyrenula pseudobufonia	VR 14-VI-02/5	–	AY640962
Pyrgillus javanicus	AFTOL-ID 342	DQ826741	DQ823103
Sarcinomyces petricola	CBS 600.93	AJ244274	FJ176893
Sclerococcum sphaerale	Diederich 17283	–	JX081673
Sclerococcum sphaerale	Diederich 17292	–	JX081672
Sclerococcum sphaerale	Ertz 17425	–	JX081674
Sphinctrina turbinata	Tibell 22478	AY795876	AY796007
Spiromastix warcupii	AFTOL-ID 430	DQ782848	DQ782909
Staurothele frustulenta	AFTOL-ID 697	DQ826736	DQ823098
Teloschistes flavicans isolate	Tflav103	KT291472	KT291565