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A stable phylogeny for Dactylosporaceae

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A stable phylogeny for Dactylosporaceae

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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.

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.

KEY WORDS

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

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, SSU, 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. — *Dactylospora*, 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 1– 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; Döbeler & 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 $\geq 60\%$ 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).

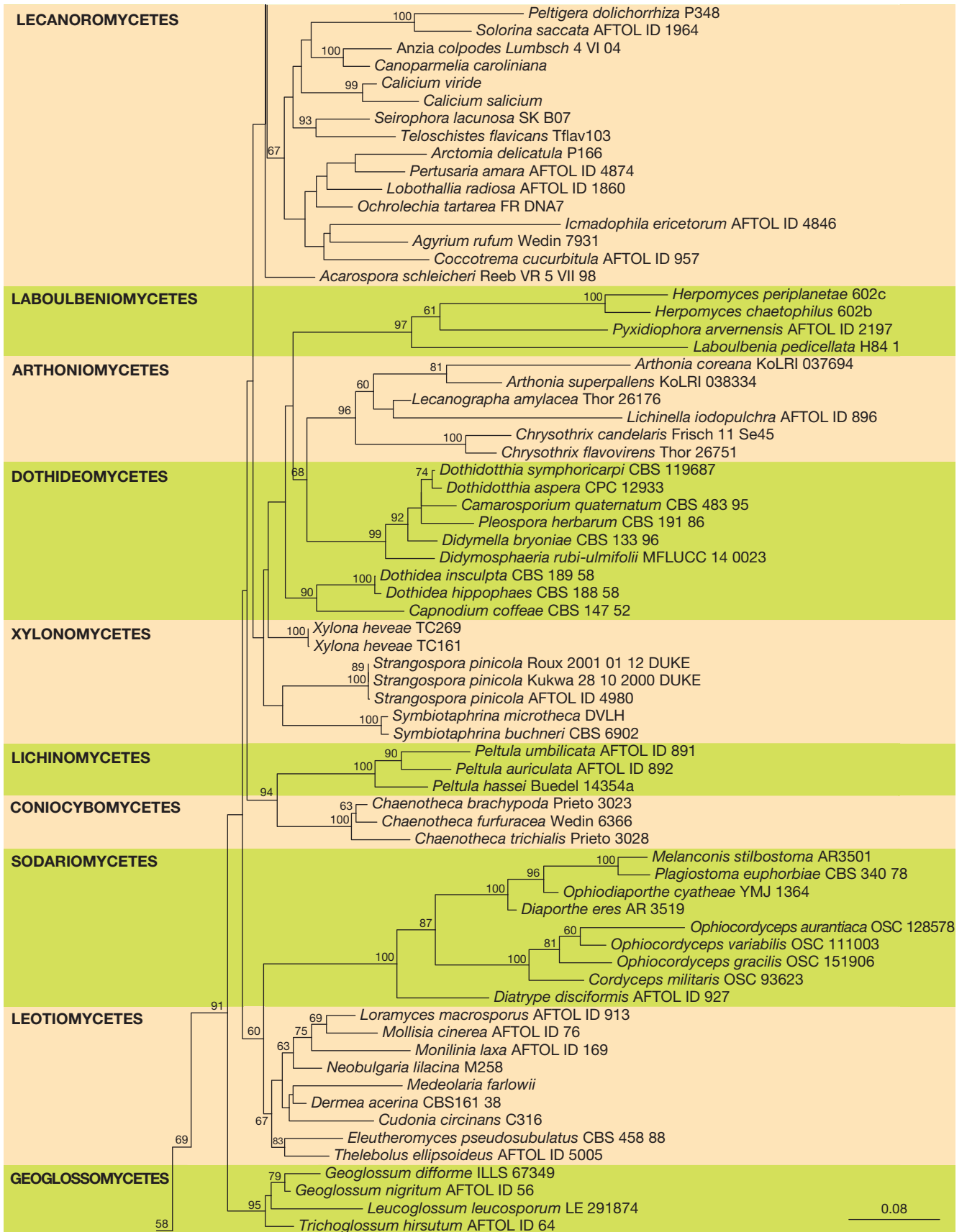


Fig. 1. — Continuation.

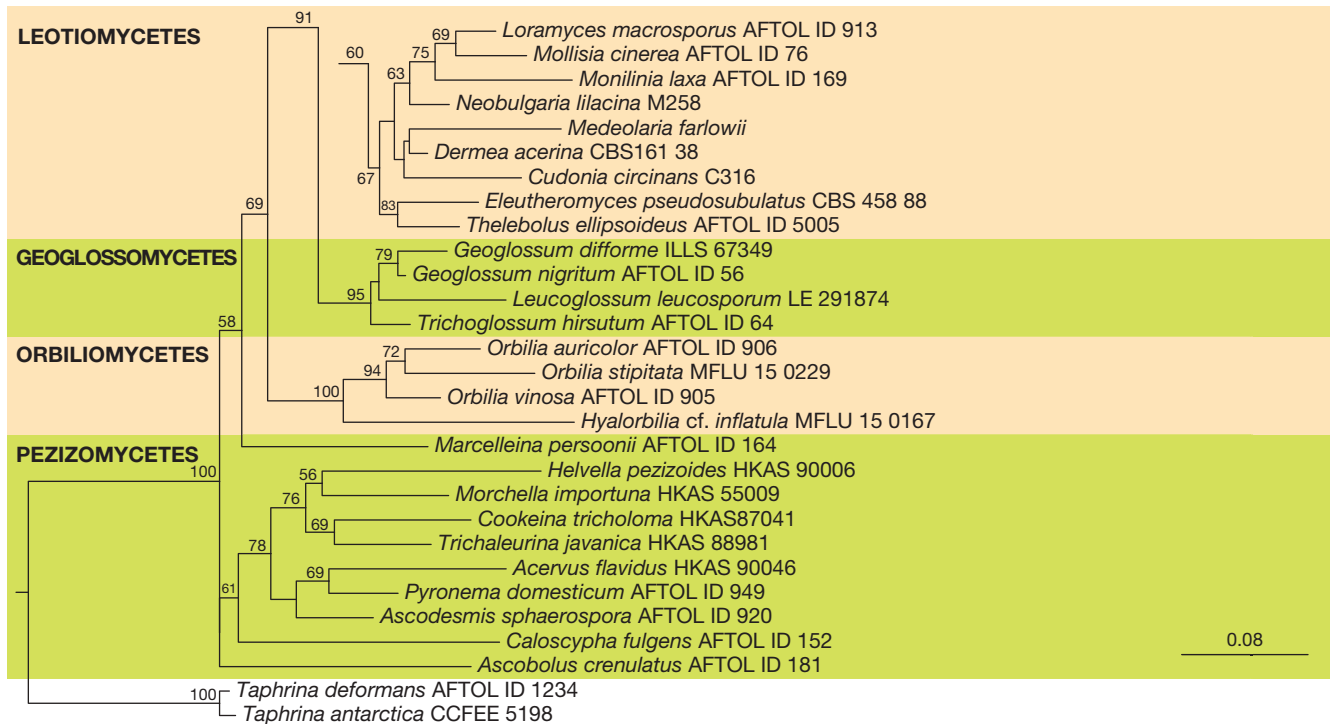


Fig. 1. — Continuation.

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.

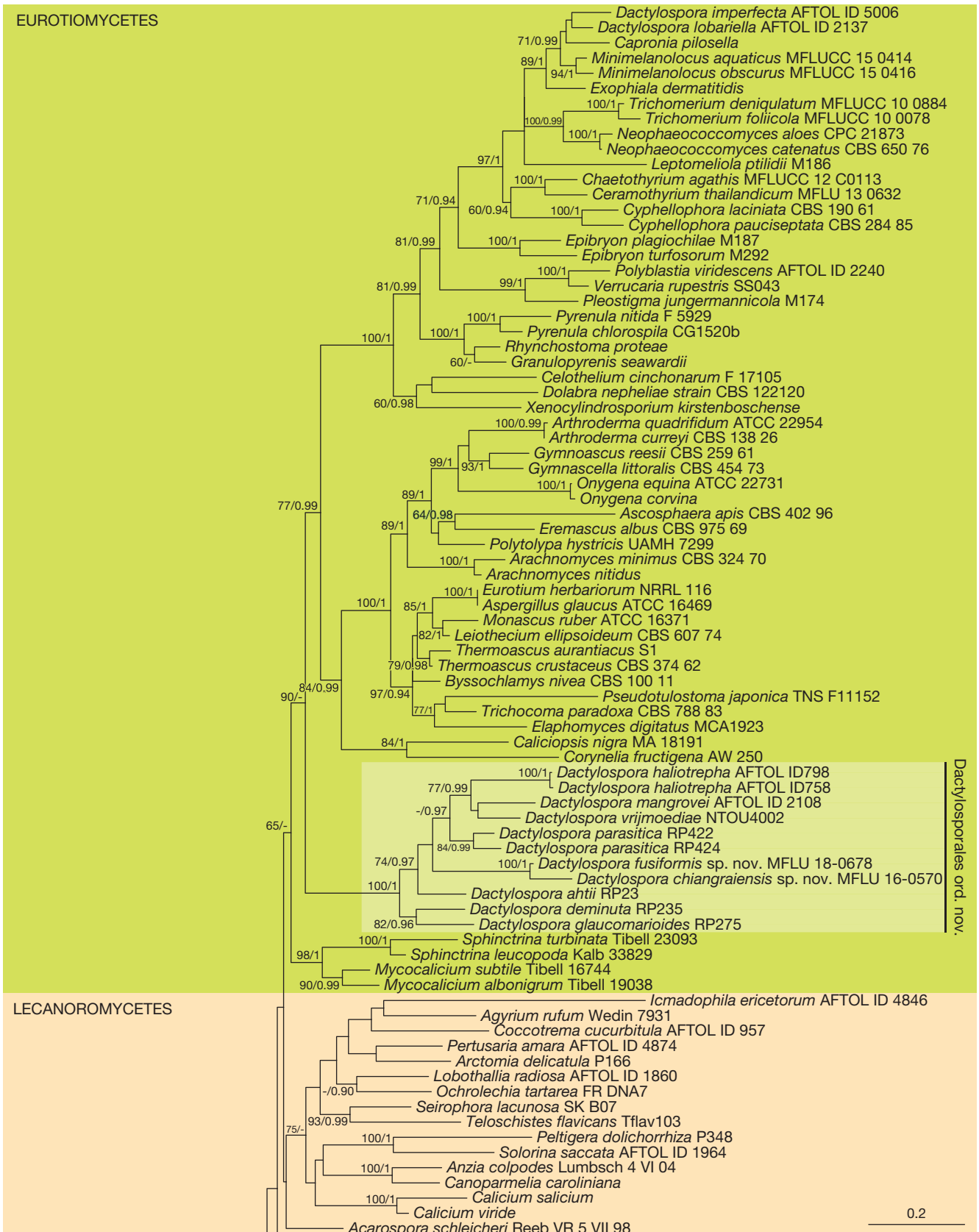


FIG. 2. — Phylogram generated from maximum likelihood analysis of sequences of Pezizomycotina including *Dactylospora* based on ITS, LSU, SSU, TEF, RPB1 and RPB2 sequence data. Maximum likelihood bootstrap values $\geq 60\%$ and Bayesian Posterior Probabilities ≥ 0.90 are given above the nodes. Strain/culture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

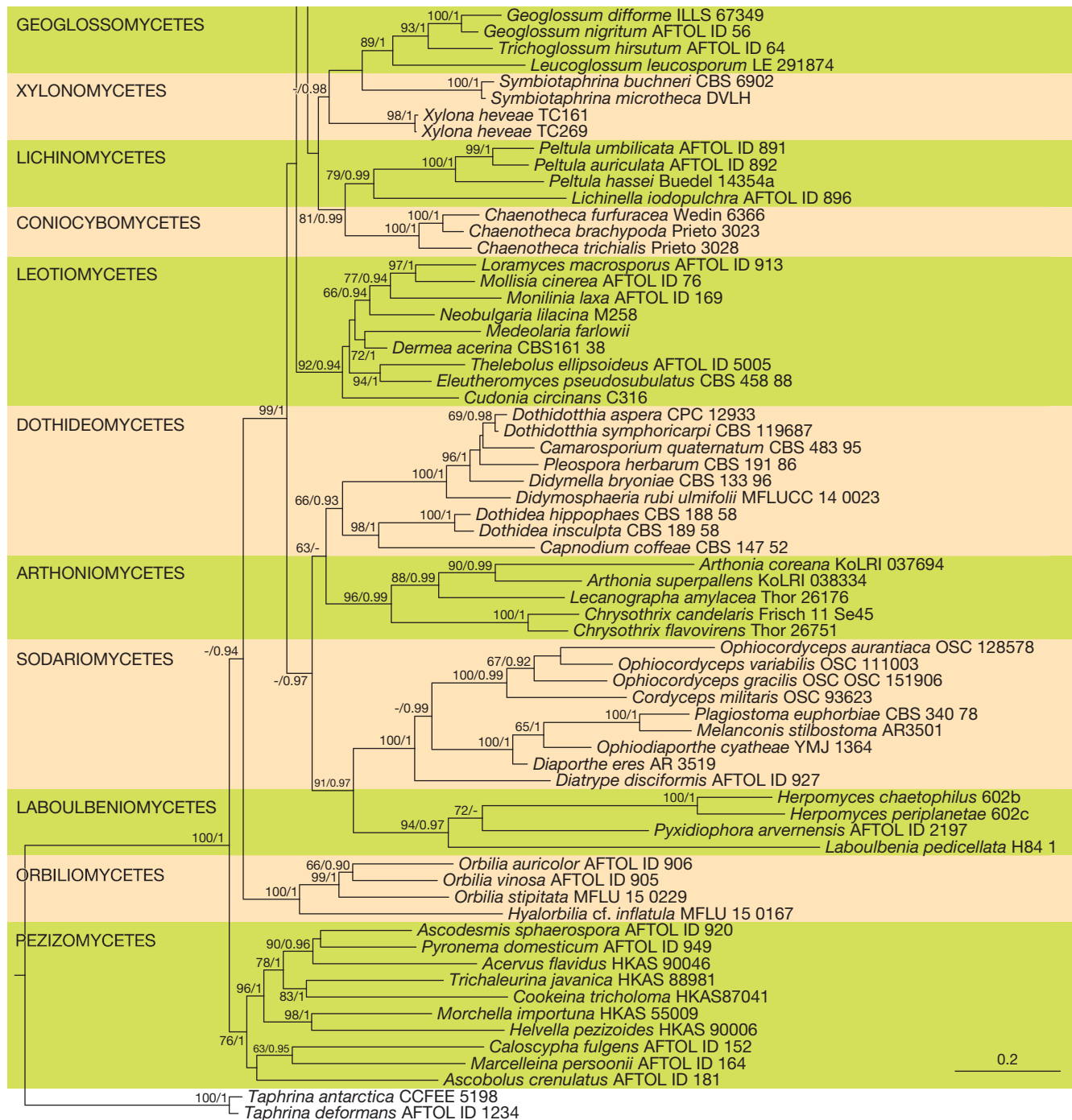


FIG. 2. — Continuation.

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. stygia* (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. diminuta* (Th. Fr.) Triebel, 1989, *D. urceolata* (Th. Fr.) Arnold, 1874, *D. frigida* Hafellner,

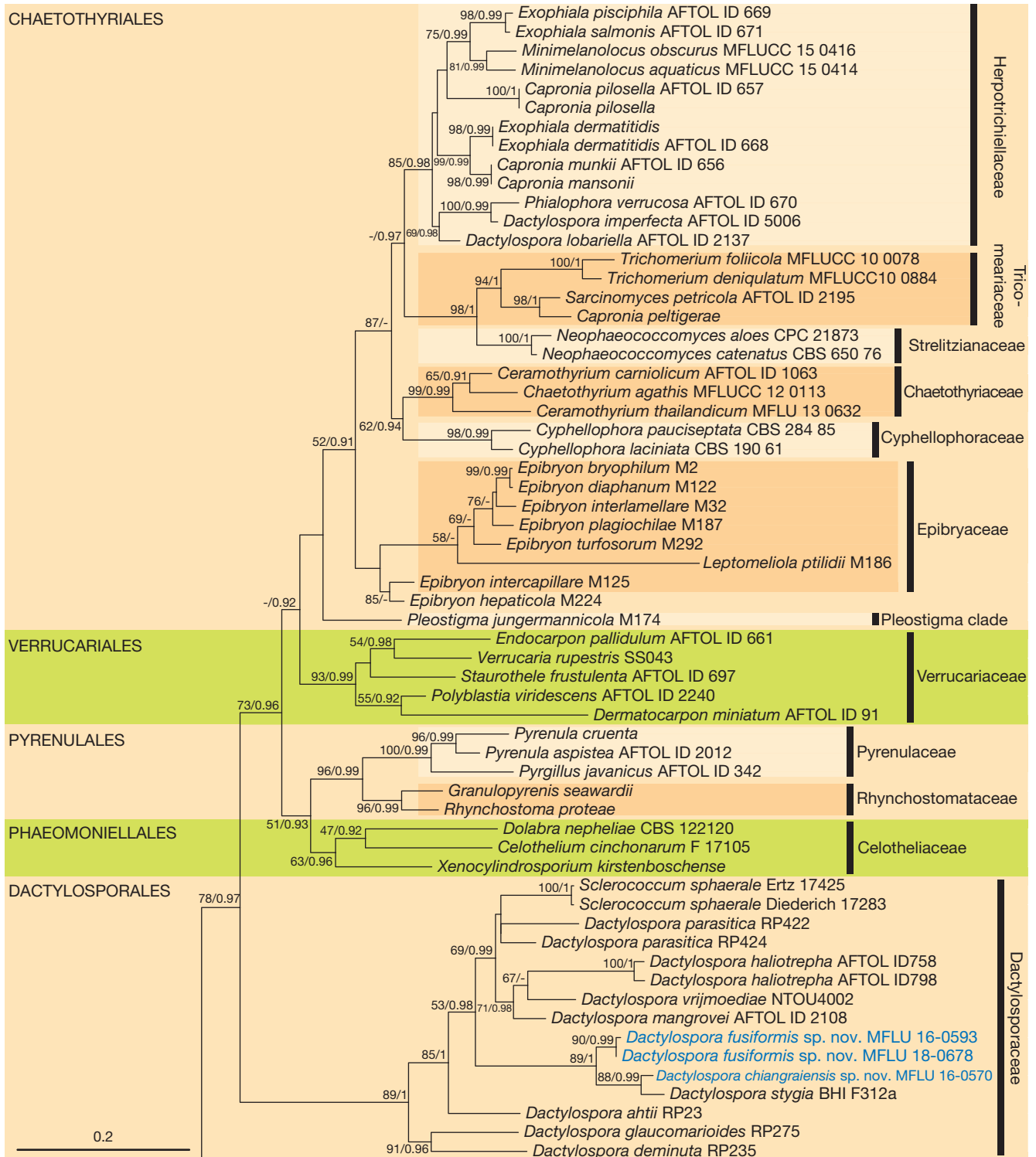


FIG. 3. — Phylogram generated from maximum likelihood analysis of sequences of Eurotiomycetes including *Dactylospora* based on ITS and LSU sequence data. Maximum likelihood bootstrap values $\geq 60\%$ and Bayesian Posterior Probabilities ≥ 0.90 are given above the nodes. Strain/culture numbers are 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

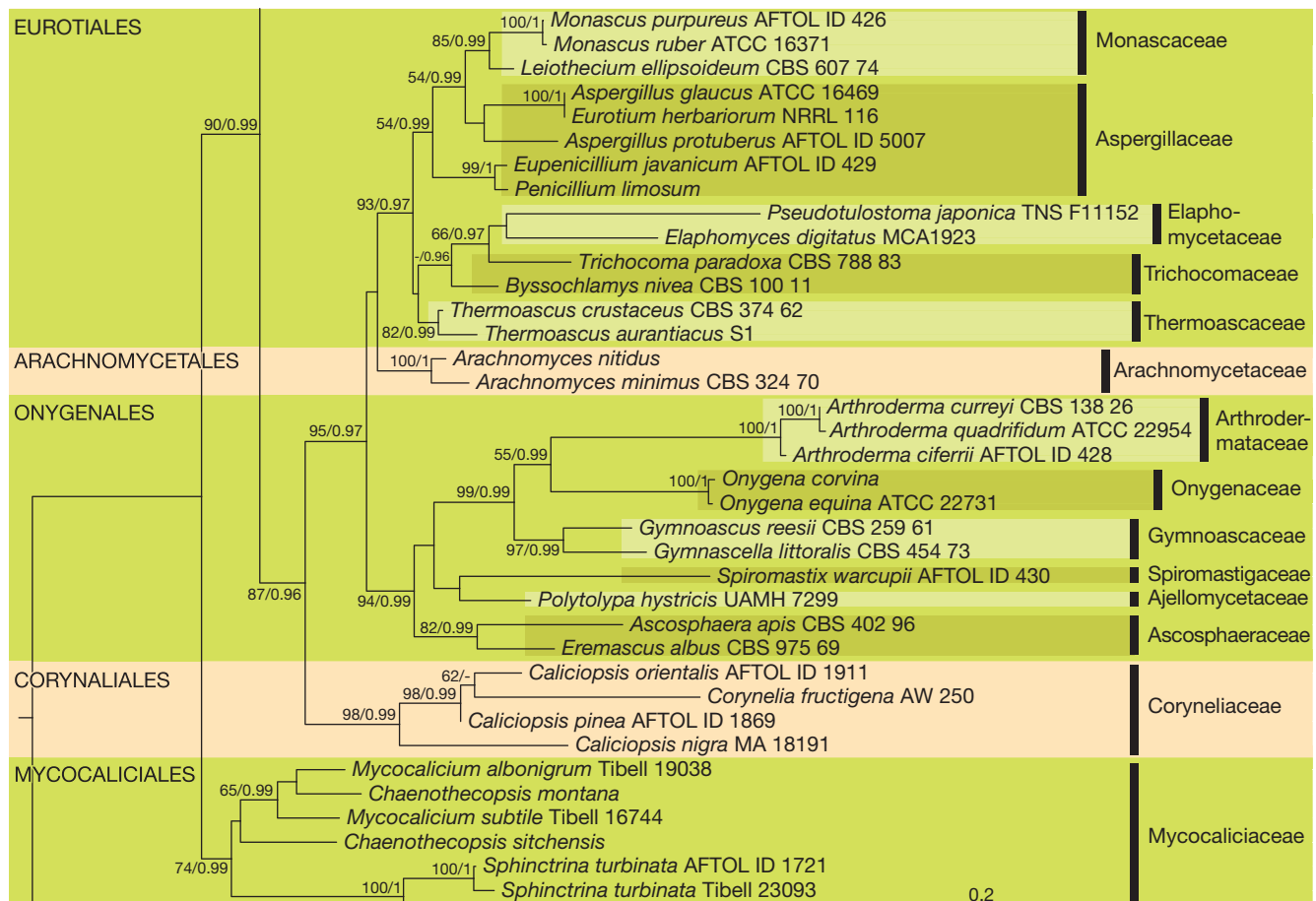


FIG. 3. — Continuation.

(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. protohallina* (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, cylindrical-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.

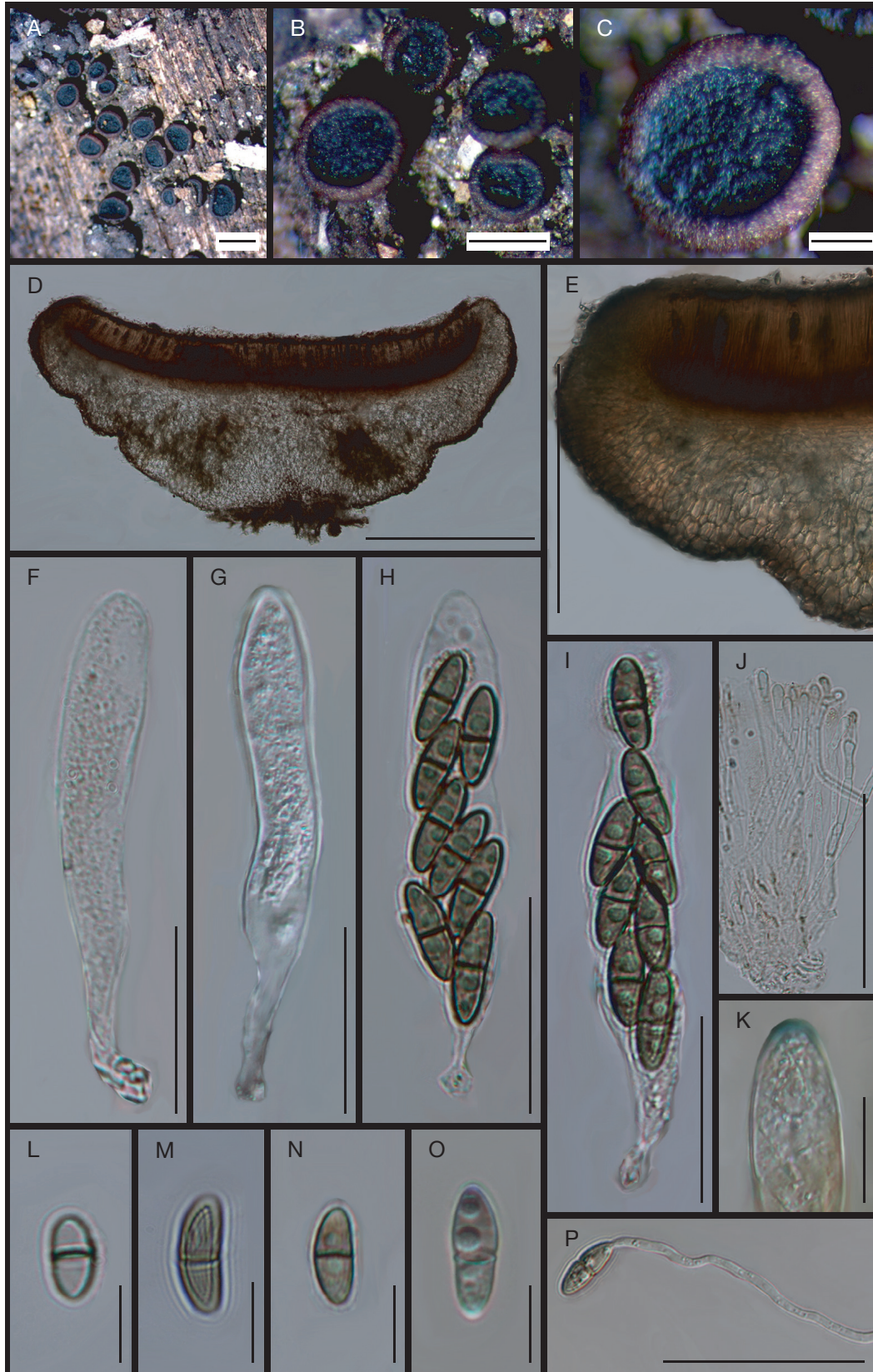


FIG. 4. — Morphology of *Dactylospora chiangraiensis* Ekanayaka, E.B.G. Jones, Q. Zhao & K.D. Hyde, sp. nov. (Holotype MFLU 16-0570): **A, B**, ascomata in wood; **C**, ascoma in wood; **D**, cross section of a ascoma; **E**, peridium of ascoma; **F-I**, asci in water; **J**, paraphyses in water; **K**,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

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, cylindrical-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. amygdalariæ* 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. rhy-*

parizae, *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 Dactylosporaales (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

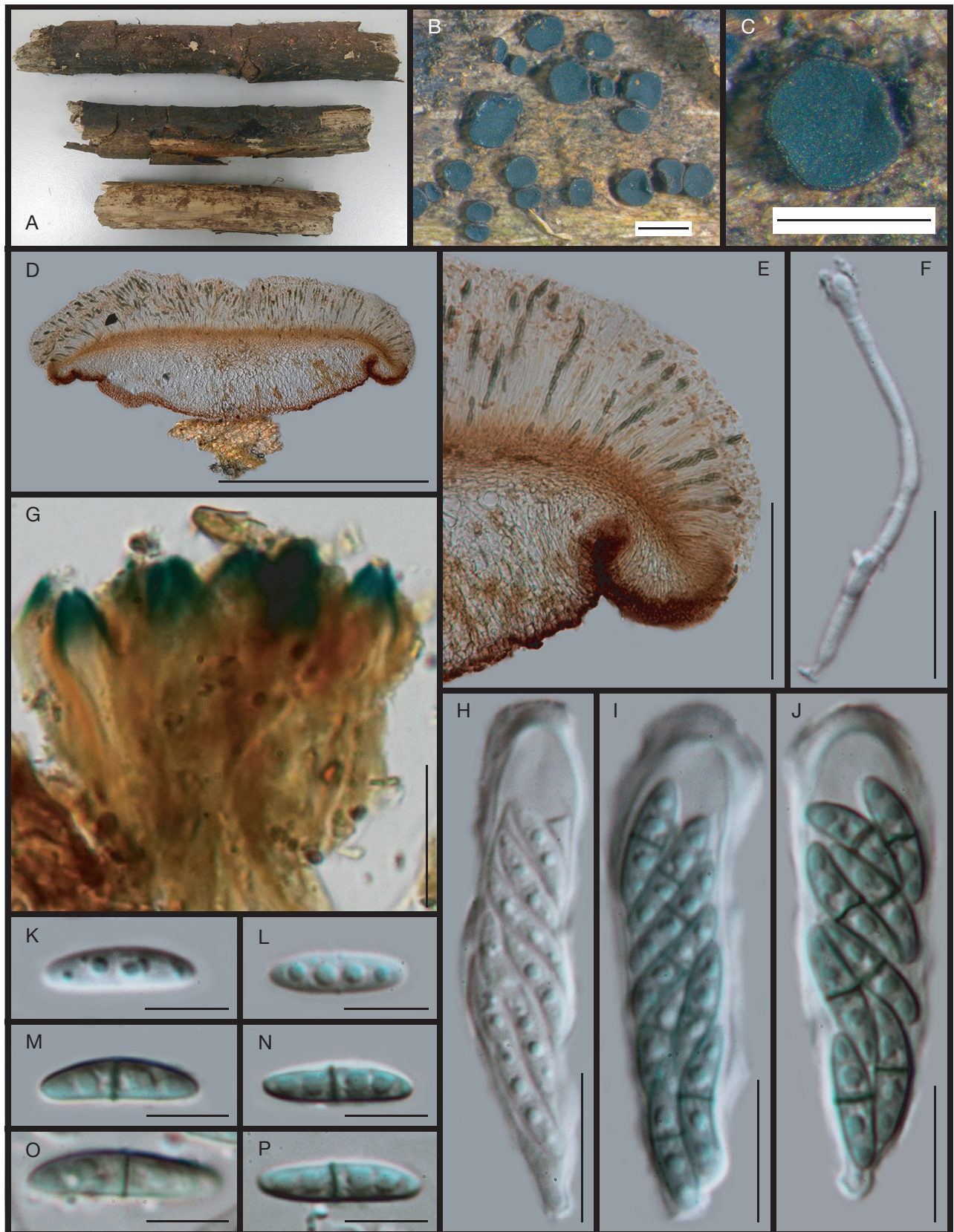


FIG. 5. — Morphology of *Dactylospora fusiformis* Ekanayaka, E.B.G. Jones, Q. Zhao & K.D. Hyde, sp. nov. (Holotype MFLU 16-0593): **A**, substrate; **B**, ascomata on wood; **C**, ascoma on wood; **D**, cross section of an ascoma; **E**, close up of a vertical section of the ascoma at margin; **F**, apically swollen 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 μ m; D, 400 μ m; E, 200 μ m; F, 30 μ m; G, J, 20 μ m; K-N, 10 μ m.

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, cylindrical 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.

Acknowledgements

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

APPENDIX 1. — Continuation.

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

APPENDIX 1. — Continuation.

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

APPENDIX 1. — Continuation.

Species name	Strain number	ITS	LSU	SSU	TEF	RPB2	RPB1
<i>Mycocalicium subtile</i>	Tibell 16744	–	AY796004	–	–	–	–
<i>Mycocalicium albonigrum</i>	Tibell 19038	–	AY796001	–	–	–	–
<i>Acarospora schleicheri</i>	Reeb VR 5-VII-98	–	AY640945	AY640986	–	–	–
<i>Agryrium rufum</i>	Wedin 7931	JX000097	EF581826	–	–	–	EF581822
<i>Coccotrema cucurbitula</i>	AFTOL-ID 957	–	AF274092	–	–	–	–
<i>Icmadophila ericetorum</i>	AFTOL-ID 4846	–	KJ766573	KJ766729	–	–	–
<i>Lobothallia radiosa</i>	AFTOL-ID 1860	–	KJ766596	KJ766746	–	KJ766935	KJ766870
<i>Ochrolechia tartarea</i>	FR:DNA7	JN943620	JN941358	–	–	–	JN992649
<i>Pertusaria amara isolate</i>	AFTOL-ID 4874	–	KJ766623	KJ766764	–	–	–
<i>Arctomia delicatula isolate</i>	P166	–	KR017191	KR017255	KR017563	–	KR017488
<i>Solorina saccata isolate</i>	AFTOL-ID 1964	HQ650625	KJ766661	KJ766797	–	–	–
<i>Peltigera dolichorrhiza isolate</i>	P348	KX897182	KM005745	–	KM005875	–	KM005937
<i>Teloschistes flavicans isolate</i>	Tflav103	KT291472	KT291565	–	–	KT291662	KT291604
<i>Seiophora lacunosa voucher</i>	SK B07	KT220204	KT220213	–	–	–	–
<i>Anzia colpodes</i>	Lumbsch 4.VI.04	–	DQ923651	–	–	–	–
<i>Canoparmelia caroliniana</i>	AFTOL-ID 6	–	AY584634	AY584658	–	AY584683	–
<i>Calicium salicium</i>	CBS 100898	–	KF157982	KF157970	–	KF157998	–
<i>Calicium viride</i>	Soechting 7475	–	AF356670	–	–	–	–
<i>Taphrina deformans</i>	AFTOL-ID 1234	–	DQ470973	DQ471024	DQ471097	DQ470927	DQ471170
<i>Taphrina antarctica</i>	CCFEE 5198	NR_132870	JX124717	–	–	–	–
<i>Dactylospora haliotrepha</i>	AFTOL-ID758	–	FJ176855	FJ176802	–	FJ238344	–
<i>Dactylospora haliotrepha</i>	AFTOL-ID798	–	FJ713617	–	–	FJ713614	–
<i>Dactylospora imperfecta</i>	AFTOL-ID 5006	–	FJ176896	FJ176841	–	–	–
<i>Dactylospora lobariella</i>	AFTOL-ID 2137	–	FJ176891	FJ176837	–	–	–
<i>Dactylospora mangrovei</i>	AFTOL-ID 2108	–	FJ176890	FJ176836	FJ238411	FJ238375	KJ766849
<i>Dactylospora vrijmoediae</i>	NTOU4002	NR_138396	KC692153	KC692152	–	KC692154	–
<i>Dactylospora ahtii</i>	RP23	KY661630	KY661659	–	–	–	–
<i>Dactylospora parasitica</i>	RP424	–	KY661667	–	–	–	–
<i>Dactylospora parasitica</i>	RP422	KY661646	KY661666	–	–	–	–
<i>Dactylospora glaucomarioides</i>	RP275	KY661632	KY661660	–	–	–	–
<i>Dactylospora deminuta</i>	RP235	KY661629	–	–	–	–	–
<i>Dactylospora fusiformis</i>	MFLU 16-0593	MH718441	MH718434	–	–	–	–
<i>Dactylospora chiangraiensis</i>	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
<i>Cyphellophora laciniata</i>	CBS 190.61	EU035416	FJ358239
<i>Cyphellophora pauciseptata</i>	CBS 284.85	JQ766466	JQ766515
<i>Chaetothyrium agathis</i>	MFLUCC 12 C0113	KP744437	KP744480
<i>Ceramothyrium thailandicum</i>	MFLU 13-0632	KP324928	KP324930
<i>Trichomerium deniquilatum</i>	MFLUCC10-0884	JX313654	JX313660
<i>Trichomerium foliicola</i>	MFLUCC 10-0078	NR_144963	JX313661
<i>Neophaeococcomyces aloes</i>	CPC 21873	KF777182	KF777234
<i>Neophaeococcomyces catenatus</i>	CBS 650.76	AF050277	AF050277
<i>Minimelanolocus obscurus</i>	MFLUCC:15-0416	KR215606	KR215611
<i>Minimelanolocus aquaticus</i>	MFLUCC:15-0414	KR215607	KR215612
<i>Exophiala dermatitidis</i>	AFTOL-ID 668	DQ826738	DQ823100
<i>Capronia pilosella</i>	AFTOL-ID 657	DQ826737	DQ823099
<i>Leptomeliola ptilidii</i>	M186	EU940200	–
<i>Epibryon plagiochilae</i>	M187	EU940201	EU940124
<i>Epibryon turfosorum</i>	M292	EU940221	EU940145
<i>Polyblastia viridescens</i>	AFTOL-ID 2240	–	EF643771
<i>Verrucaria rupestris</i>	SS043	EU553501	EU598724
<i>Pleostigma jungermannicola</i>	M174	EU940195	EU940119
<i>Celothelium cinchonarum</i>	F 17105	–	DQ329020
<i>Dolabra nepheliae</i>	CBS 122120	–	GU332517
<i>Xenocylindrosporium kirstenboschense</i>	CBS 125545	GU229890	GU229891
<i>Rhynchosstoma proteae</i>	–	–	AY230151
<i>Granulopyrenis seawardii</i>	CBS 109025	–	EF411062
<i>Eurotium herbariorum</i>	NRRL 116	EF652052	U29553
<i>Aspergillus glaucus</i>	ATCC 16469	–	AY176751
<i>Monascus ruber</i>	ATCC 16371	AY498572	AF364996
<i>Leiothecium ellipsoideum</i>	CBS 607.74	–	FJ358285
<i>Byssochlamys nivea</i>	CBS 100.11	FJ389934	AY176750
<i>Trichocoma paradoxa</i>	CBS 788.83	–	FJ358290
<i>Pseudotulostoma japonica</i>	TNS-F11152	–	AB161194
<i>Elaphomyces digitatus</i>	MCA1923	–	JN713148
<i>Thermoascus crustaceus</i>	CBS 374.62	–	FJ358289
<i>Thermoascus aurantiacus</i>	S1	–	KJ535692
<i>Arachnomyces minimus</i>	CBS 324.70	–	FJ358274
<i>Arachnomyces nitidus</i>	IFO 32048	–	AB075351
<i>Gymnoascus reesii</i>	CBS 259.61	–	FJ358284
<i>Gymnascella littoralis</i>	CBS 454.73	–	FJ358272
<i>Arthroderma curreyi</i>	CBS 138.26	KT155805	AY176726
<i>Arthroderma quadridum</i>	ATCC 22954	–	AY176728
<i>Onygena equina</i>	ATCC 22731	–	AY176717

APPENDIX 2. — Continuation.

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

APPENDIX 2. — Continuation.

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