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Fungal diversity notes 1387–1511: taxonomic and phylogenetic contributions on genera and species of fungal taxa

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Abstract

This article is the 13th contribution in the Fungal Diversity Notes series, wherein 125 taxa from four phyla, ten classes, 31 orders, 69 families, 92 genera and three genera *incertae sedis* are treated, demonstrating worldwide and geographic distribution. Fungal taxa described and illustrated in the present study include three new genera, 69 new species, one new combination, one reference specimen and 51 new records on new hosts and new geographical distributions. Three new genera, *Cylindrotorula* (*Torulaceae*), *Scolecoleotia* (*Leotiales* genus *incertae sedis*) and *Xenovaginatispora* (*Lindomycetaceae*) are introduced based on distinct phylogenetic lineages and unique morphologies. Newly described species are *Aspergillus lannaensis*, *Cercophora dulciaquae*, *Cladophialophora aquatica*, *Coprinellus punjabensis*, *Cortinarius alutarius*, *C. mammillatus*, *C. quercoflocculosus*, *Coryneum fagi*, *Cruentomycena uttarakhandina*, *Cryptocoryneum rosae*, *Cyathus uniperidiolus*, *Cylindrotorula indica*, *Diaporthe chamaeropicola*, *Didymella azollae*, *Diplodia alanphillipsii*, *Dothiora coronicola*, *Efibula rodriguezarmasiae*, *Erysiphe salicicola*, *Fusarium queenslandicum*, *Geastrum gorgonicum*, *G. hansagiense*, *Helicosporium sexualis*, *Helminthosporium chiangraiensis*, *Hongkongmyces kokensis*, *Hydrophilomyces hydraenae*, *Hygrocybe boertmannii*, *Hyphoderma australosetigerum*, *Hyphodontia yunnanensis*, *Khaleijomyces umikazeana*, *Laboulbenia divisa*, *Laboulbenia triarthronis*, *Laccaria populina*, *Lactarius pallidozonarius*, *Lepidosphaeria strobelii*, *Longipedicellata megafusiformis*,

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Extended author information available on the last page of the article

Lophiotrema lincangensis, *Marasmius benghalensis*, *M. jinfoshanensis*, *M. subtropicus*, *Mariannaea camelliae*, *Melanographium smilaxii*, *Microbotryum polycnemoides*, *Mimeomyces digitatus*, *Minutisphaera thailandensis*, *Mortierella solitaria*, *Mucor harpali*, *Nigrograna jinghongensis*, *Odontia huanrenensis*, *O. parvispina*, *Paraconiothyrium ajrekarii*, *Parafuscosporella niloticus*, *Phaeocytostroma yomensis*, *Phaeoisaria synnematicus*, *Phanerochaete hainanensis*, *Pleopunctum thailandicum*, *Pleurotheciella dimorphospora*, *Pseudochaetosphaeronema chiangraiense*, *Pseudodactylaria albicolonia*, *Rhexoacrodictys nigrospora*, *Russula paravioleipes*, *Scolecoleotia eriocamporesi*, *Seriascoma honghense*, *Synandromyces makranczyi*, *Thyridaria aureobrunnea*, *Torula lancangjiangensis*, *Tubeufia longihelicospora*, *Wicklowia fusiformispora*, *Xenovaginatispora phichaiensis* and *Xylaria apiospora*. One new combination, *Pseudobactrodesmium stilboideus* is proposed. A reference specimen of *Comoclathris permunda* is designated. New host or distribution records are provided for *Acrocalymma fici*, *Aliquandostipite khaoyaiensis*, *Camarosporidiella laburni*, *Canalisporium caribense*, *Chaetoscutula juniperi*, *Chlorophyllum demangei*, *C. globosum*, *C. hortense*, *Cladophialophora abundans*, *Dendryphion hydei*, *Diaporthe foeniculina*, *D. pseudophoenicicola*, *D. pyracanthae*, *Dictyosporium pandanicola*, *Dyfrolomyces distoseptatus*, *Ernakulamia tanakae*, *Eutypa flavovirens*, *E. lata*, *Favolus septatus*, *Fusarium atrovinosum*, *F. clavum*, *Helicosporium luteosporum*, *Hermatomyces nabanheensis*, *Hermatomyces sphaericoides*, *Longipedicellata aquatica*, *Lophiostoma caudata*, *L. clematidis-vitalbae*, *Lophiotrema hydei*, *L. neoarundinaria*, *Marasmiellus palmivorus*, *Megacapitula villosa*, *Micropsalliota globocystis*, *M. gracilis*, *Montagnula thailandica*, *Neohelicosporium irregulare*, *N. parisporum*, *Paradictyoarthrinium diffractum*, *Phaeoisaria aquatica*, *Poaceascoma taiwanense*, *Saproamanita manicata*, *Spegazzinia camelliae*, *Submersispora variabilis*, *Thyronectria caudata*, *T. mackenziei*, *Tubeufia chiangmaiensis*, *T. roseohelicospora*, *Vaginatispora nypae*, *Wicklowia submersa*, *Xanthagaricus necopinatus* and *Xylaria haemorrhoidalis*. The data presented herein are based on morphological examination of fresh specimens, coupled with analysis of phylogenetic sequence data to better integrate taxa into appropriate taxonomic ranks and infer their evolutionary relationships.

Keywords 72 new taxa · One new combination · One reference specimen · 51 new records · Agaricomycetes · Ascomycota · Bartheletiomycetes · Basidiomycota · Dothideomycetes · Eurotiomycetes · Exobasidiomycetes · Laboulbeniomycetes · Leotiomycetes · Mortierellomycetes · Mortierellomycota · Mucoromycetes · Mucoromycota · Phylogeny · Sordariomycetes · Taxonomy

Table of contents

1393. ***Acrocalymma fici*** Crous & Trakun., ***new habitat and geographical record*** (Contributed by Mark S. Calabon)

Dictyosporiaceae Boonmee & K.D. Hyde
1394. ***Dictyosporium pandanicola*** Tibpromma & K.D. Hyde, ***new record*** (Contributed by Dan-Feng Bao)

Camarosporidiellaceae Wanas., Wijayaw., Crous & K.D. Hyde
1395. ***Camarosporidiella laburni*** (Pers.) Wanas., Bulgakov, Camporesi & K.D. Hyde, ***new record*** (Contributed by Dhanushka Wanasinghe, Yusufjon Gafforov and Aziz Abdurazakov)

Cryptocoryneaceae A. Hashim. & Kaz. Tanaka
1396. ***Cryptocoryneum rosae*** Wanas. & K.D. Hyde, ***sp. nov.*** (Contributed by Dhanushka Wanasinghe)

Didymellaceae Gruyter, Aveskamp & Verkley (=*Microsphaeropsidaceae* Qian Chen et al.)
1397. ***Didymella azollae*** Shams E., Dehghanizadeh F. & Pordel A., ***sp. nov.*** (Contributed by Esmaeil Shams, Farzaneh Dehghanizadeh, Adel Pordel and Mohammad Javan-Nikkhah)

Didymosphaeriaceae Munk
1398. ***Montagnula thailandica*** Mapook & K.D. Hyde, ***new record*** (Contributed by Saranyaphat Boonmee and Naruemon Huanraluek)
1399. ***Paraconiothyrium ajrekarii*** S. Rana & S.K. Singh, ***sp. nov.*** (Contributed by Sanjay K. Singh and Shiwali Rana)
1400. ***Spegazzinia camelliae*** N. Suwannarach, J. Kumla & S. Lumyong, ***new record*** (Contributed by Saranyaphat Boonmee)

Hermatomycetaceae Locq.
1401. ***Hermatomyces nabanheensis*** Tibpromma, Bhat & K.D. Hyde, ***new record*** (Contributed by Jing-Yi Zhang)
1402. ***Hermatomyces sphaericoides*** Koukol & G. Delgado, ***new record*** (Contributed by Saranyaphat Boonmee and Naruemon Huanraluek)

Lentitheciaceae Y. Zhang ter, C.L. Schoch, J. Fourn., Crous & K.D. Hyde
1403. ***Poaceascoma taiwanense*** Tennakoon, C.H. Kuo & K.D. Hyde, ***new geographical record*** (Contributed by Saranyaphat Boonmee)

Lindgomycetaceae K. Hiray. et al.
1404. ***Hongkongmyces kokensis*** Boonmee, Huanraluek, Chandrasirie & K.D. Hyde, ***sp. nov.*** (Contributed by Saranyaphat Boonmee, Naruemon Huanraluek and Sajini K.U. Chandrasiri)
1405. ***Xenovaginatispora*** Boonmee, Huanraluek & K.D. Hyde, ***gen. nov.*** (Contributed by Saranyaphat Boonmee)
1406. ***Xenovaginatispora phichaiensis*** Boonmee, Huanraluek & K.D. Hyde, ***sp. nov.*** (Contributed by Saranyaphat Boonmee)

Longipedicellataceae Phukhams., Bhat & K.D. Hyde
1407. ***Longipedicellata aquatica*** W. Dong, H. Zhang & K.D. Hyde, ***new record*** (Contributed by Saranyaphat Boonmee and Sajini K.U. Chandrasiri)
1408. ***Longipedicellata megafusiformis*** Chandrasiri, Boonmee & K.D. Hyde, ***sp. nov.*** (Contributed by Saranyaphat Boonmee and Sajini K.U. Chandrasiri)
1409. ***Submersispora variabilis*** W. Dong, H. Zhang & K.D. Hyde, ***new record*** (Contributed by Saranyaphat Boonmee and Naruemon Huanraluek)

Lophiostomataceae Sacc.
1410. ***Lophiostoma caudatum*** Fabre, ***new host and geographical record*** (Contributed by Janith Vishvakeerthi and Yusufjon Gafforov)
1411. ***Lophiostoma clematidis-vitalbae*** Andreasen, Jaklitsch & Voglmayr, ***new host and geographical record*** (Contributed by Janith Vishvakeerthi and Yusufjon Gafforov)
1412. ***Vaginatispora nypae*** Jayasiri, E.B.G. Jones & K.D. Hyde, ***new record*** (Contributed by Dan-Feng Bao)

Lophiotremataceae K. Hiray. & Kaz.
1413. ***Lophiotrema hydei*** J.F. Zhang, J.K. Liu & Z.Y. Liu, ***new host record*** (Contributed by Dhanushka Wanasinghe)
1414. ***Lophiotrema lincangensis*** Wanas. & K.D. Hyde, ***sp. nov.*** (Contributed by Dhanushka Wanasinghe)
1415. ***Lophiotrema neoarundinariae*** Y. Zhang ter, Kaz. Tanaka & K.D. Hyde, ***new host record*** (Contributed by Dhanushka Wanasinghe)

Macrodiplodiopsidaceae Voglmayr, Jaklitsch & Crous
1416. ***Pseudochaetosphaeronema chiangraiense*** Wijesinghe, Boonmee & K.D. Hyde, ***sp. nov.*** (Contributed by Subodini N. Wijesinghe)

Massarinaceae Munk
1417. ***Helminthosporium chiangraiense*** Boonmee, Huanraluek & K.D. Hyde, ***sp. nov.*** (Contributed by Saranyaphat Boonmee and Naruemon Huanraluek)

Nigrogranaceae Jaklitsch & Voglmayr
1418. ***Nigrograna jinghongensis*** Wanas. & K.D. Hyde, ***sp. nov.*** (Contributed by Dhanushka Wanasinghe)

Occultibambusaceae D.Q. Dai & K.D. Hyde

1419. ***Seriascoma honghense*** H.B. Jiang, Phookamsak & K.D. Hyde, ***sp. nov.*** (Contributed by Rungtiwa Phookamsak and Hong-Bo Jiang)

Paradictyoarthriniaceae Doilom, Ariyaw., Bhat & K.D. Hyde
1420. ***Paradictyoarthrinium diffractum*** Matsush., ***new record*** (Contributed by Saranyaphat Boonmee and Naruemon Huanraluek)

Phaeoseptaceae S. Boonmee, Thambug. & K.D. Hyde
1421. ***Pleopunctum thailandicum*** J.Y. Zhang, Y.Z. Lu & K.D. Hyde, ***sp. nov*****.** (Contributed by Jing-Yi Zhang)

Phaeosphaeriaceae M.E. Barr
1422. ***Phaeosphaeriopsis aloes*** Crous & Y. Marín, ***new host and new geographical record*** (Contributed by Dhanushka Wanasinghe)

Pleosporaceae Nitschke
1423. ***Comoclathris permunda*** Thambug., Camporesi & K.D. Hyde, ***reference specimen*** (Contributed by Dhanushka Wanasinghe, Yusufjon Gafforov and Aziz Abdurazakov)

Testudinaceae Arx
1424. ***Lepidosphaeria strobelii*** A.C. Lagashetti, D. Choudhary & S.K. Singh, ***sp. nov.*** (Contributed by A.C. Lagashetti and S.K. Singh)

Tetraplosphaeriaceae Kaz. Tanaka & K. Hiray
1425. ***Ernakulamia tanakae*** Rajeshkumar & K.D. Hyde, ***new record*** (Contributed by Saranyaphat Boonmee and Naruemon Huanraluek)

Thyridariaceae Q. Tian & K.D. Hyde
1426. ***Thyridaria aureobrunnea*** Boonmee, Huanraluek & K.D. Hyde, ***sp. nov.*** (Contributed by Saranyaphat Boonmee)

Torulaceae Corda
1427. ***Cylindrotorula*** Rajeshkumar, Wijayaw. & Bhat, ***gen. nov.*** (Contributed by Kunhiraman C. Rajeshkumar, Nikhil Ashtekar, Sneha Lad, Nalin N. Wijayawardene and Darbe J. Bhat)
1428. ***Cylindrotorula indica*** Rajeshkumar, Wijayaw., Bhat, N. Ashtekar & S. Lad, ***sp. nov.*** (Contributed by Kunhiraman C. Rajeshkumar, Nikhil Ashtekar, Sneha Lad, Nalin N. Wijayawardene and Darbe J. Bhat)
1429. ***Dendryphion hydei*** J.F. Li, Phookamsak & Jeewon, ***new record*** (Contributed by Hong-Wei Shen)
1430. ***Torula lancangjiangensis*** H.W. Shen, S. Boonmee, Z.L. Luo & K.D. Hyde, ***sp. nov.*** (Contributed by Hong-Wei Shen)
1431. ***Torula mackenziei*** Jun F. Li, Phook. & K.D. Hyde, ***new record*** (Contributed by Hong-Wei Shen)

Wicklowiaceae Ariyaw. & K.D. Hyde
1432. ***Wicklowia fusiformispora*** Boonmee, Huanraluek & K.D. Hyde, ***sp. nov.*** (Contributed by Saranyaphat Boonmee and Naruemon Huanraluek)
1433. ***Wicklowia submersa*** Boonmee, Sorvongxay & K.D. Hyde, ***new geographical record*** (Contributed by Saranyaphat Boonmee and Naruemon Huanraluek)

Tubeufiales Boonmee & K.D. Hyde

Tubeufiaceae M.E. Barr
1434. ***Helicosporium luteosporum*** Y.Z. Lu, Boonmee & K.D. Hyde, ***new record*** (Contributed by Saranyaphat Boonmee)
1435. ***Helicosporium sexuale*** Boonmee, ***sp. nov.*** (Contributed by Saranyaphat Boonmee)
1436. ***Neohelicosporium irregulare*** Y.Z. Lu, J.C. Kang & K.D. Hyde, ***new record*** (Contributed by Saranyaphat Boonmee)
1437. ***Neohelicosporium parvisporum*** Y.Z. Lu, J.C. Kang & K.D. Hyde, ***new record*** (Contributed by Mark S. Calabon)
1438. ***Tubeufia chiangmaiensis*** Boonmee & K.D. Hyde, ***new record*** (Contributed by Saranyaphat Boonmee)
1439. ***Tubeufia longihelicospora*** Boonmee & K.D. Hyde, ***sp. nov.*** (Contributed by Saranyaphat Boonmee)
1440. ***Tubeufia roseohelicospora*** Y.Z. Lu, Boonmee & K.D. Hyde, ***new record*** (Contributed by Saranyaphat Boonmee)

Pleosporales*, genus *incertae sedis
1441. ***Megacapitula villosa*** J.L. Chen & Tzean, ***new geographical record*** (Contributed by Saranyaphat Boonmee)

Eurotiomycetes O.E. Erikss. & Winka

Chaetothyriales M.E. Barr

Herpotrichiellaceae Munk
1442. ***Cladophialophora abundans*** P. Feng, V.A. Vicente, Najafz., van den Ende, Stielow, Badali, Boeger & de Hoog, ***new geographical record*** (Contributed by Mark S. Calabon)
1443. ***Cladophialophora aquatica*** M.S. Calabon, Boonmee, E.B.G. Jones & K.D. Hyde, ***sp. nov.*** (Contributed by Mark S. Calabon)

Eurotiales G.W. Martin ex Benny & Kimbr.

Aspergillaceae Link (=*Monascaceae* J. Schröt.)
1444. ***Aspergillus lannaensis*** N. Suwannarach, S. Khuna & S. Lumyong, ***sp. nov.*** (Contributed by Nakarin Suwannarach, Surapong Khuna and Saisamorn Lumyong)

Sclerococcales Réblová, Unter. & W. Gams

Dactylosporaceae Bellem. & Hafellner (= *Sclerococcaceae* Réblová et al.)
1445. ***Pseudobactrodesmium stilboideum*** (R.F. Castañeda & G.R.W. Arnold) M.S. Calabon, Boonmee, E.B.G. Jones, K.D. Hyde, ***comb. nov.*** (Contributed by Mark S. Calabon)

Laboulbeniomycetes Engl.

Laboulbeniales Lindau

Laboulbeniaceae G. Winter
1446. ***Hydrophilomyces hydraenae*** W. Rossi & M. Leonardi, ***sp. nov.*** (Contributed by Walter Rossi and Marco Leonardi)
1447. ***Laboulbenia divisa*** W. Rossi & M. Leonardi, ***sp. nov.*** (Contributed by Walter Rossi and Marco Leonardi)
1448. ***Laboulbenia triarthronis*** W. Rossi & M. Leonardi, ***sp. nov.*** (Contributed by Walter Rossi and Marco Leonardi)
1449. ***Mimeomyces digitatus*** W. Rossi & M. Leonardi, ***sp. nov.*** (Contributed by Walter Rossi and Marco Leonardi)
1450. ***Synandromyces makranczyi*** W. Rossi & M. Leonardi, ***sp. nov.*** (Contributed by Walter Rossi and Marco Leonardi)

Leotiomycetes O.E. Erikss. & Winka

Erysiphales Warm.

Erysiphaceae Tul. & C. Tul.
1451. ***Erysiphe salicicola*** Hyang B. Lee, P.M. Kirk & T.T.T. Nguyen, ***sp. nov.*** (Contributed by Hyang Burm Lee, Thuong T.T. Nguyen and Paul M. Kirk)

Leotiomycetes O.E. Erikss. & Winka

Leotiales Korf & Lizoň
Leotiales, **genus *incertae sedis***
1452. ***Scolecoleotia*** H.B. Jiang, Phookamsak & K.D. Hyde, ***gen. nov.*** (Contributed by Rungtiwa Phookamsak and Hong-Bo Jiang)
1453. ***Scolecoleotia eriocamporesi*** H.B. Jiang, Phookamsak & K.D. Hyde, ***sp. nov.*** (Contributed by Rungtiwa Phookamsak and Hong-Bo Jiang)

Sordariomycetes O.E. Erikss. & Winka

Diaporthales Nannf.

Coryneaceae Corda (= *Pseudovalsaceae* M.E. Barr)
1454. ***Coryneum fagi*** C.M. Tian & N. Jiang, ***sp. nov***. (Contributed by Ning Jiang and Cheng-Ming Tian)

Diaporthaceae Höhn. ex Wehm.
1455. ***Diaporthe chamaeropicola*** D.R.S. Pereira & A.J.L. Phillips, ***sp. nov.*** (Contributed by Diana S. Pereira and Alan J.L. Phillips)
1456. ***Diaporthe foeniculina*** (Sacc.) Udayanga & Castl., ***new record*** (Contributed by Diana S. Pereira and Alan J.L. Phillips)
1457. ***Diaporthe pseudophoenicicola*** R.R. Gomes, C. Glienke & Crous, ***new record*** (Contributed by Diana S. Pereira and Alan J.L. Phillips)
1458. ***Diaporthe pyracanthae*** L. Santos & A. Alves, ***new record*** (Contributed by Diana S. Pereira and Alan J.L. Phillips)
1459. ***Phaeocytostroma yomensis*** Boonmee, Chandrasiri & K.D. Hyde, ***sp. nov.*** (Contributed by Saranyaphat Boonmee and Sajini K.U. Chandrasiri)

Fuscosporellales Jing Yang, Bhat & K.D. Hyde

Fuscosporellaceae Jing Yang, Bhat & K.D. Hyde
1460. ***Parafuscosporella nilotica*** Abdel-Aziz, ***sp. nov.*** (Contributed by Mohamed A. Abdel-Wahab and Faten A. Abdel-Aziz)

Hypocreales Lindau

Nectriaceae Tul. & C. Tul.
1461. ***Fusarium atrovinosum*** L. Lombard & Crous, ***new record*** (Contributed by Tarynn B. Potter, Roger G. Shivas, Adam H. Sparks and Niloofar Vaghefi)
1462. ***Fusarium clavum*** J.W. Xia, L. Lombard, Sand.-Den., X.G. Zhang & Crous, ***new record*** (Contributed by Tarynn B. Potter, Roger G. Shivas, Adam H. Sparks and Niloofar Vaghefi)
1463. ***Fusarium queenslandicum*** T.B. Potter, A.H. Sparks, Vaghefi & R.G. Shivas, ***sp. nov.*** (Contributed by Tarynn B. Potter, Roger G. Shivas, Adam H. Sparks and Niloofar Vaghefi)
1464. ***Mariannaea camelliae*** N. Suwannarach & J. Kumla, ***sp. nov.*** (Contributed by Nakarin Suwannarach and Jaturong Kumla)
1465. ***Thyronectria caudata*** (Desm.) Seeler, ***new record*** (Contributed by Dhanushka Wanasinghe, Yusufjon Gafforov and Aziz Abdurazakov)

Pleurotheciales Réblová & Seifert

Pleurotheciaceae Réblová & Seifert
1466. ***Phaeoisaria aquatica*** Z.L. Luo, X.J. Su & K.D. Hyde, ***new record*** (Contributed by Saranyaphat Boonmee)
1467. ***Phaeoisaria synnematicus*** P.N. Singh & S.K. Singh, ***sp. nov.*** (Contributed by P.N. Singh and S.K. Singh)

1468. ***Pleurotheciella dimorphospora*** H.B. Jiang, Phookamsak & K.D. Hyde, ***sp. nov.*** (Contributed by Rungtiwa Phookamsak)

Pseudodactylariales Crous

Pseudodactylariaceae Crous
1469. ***Pseudodactylaria albicolonia*** R.J. Xu, Boonmee & K.D. Hyde, ***sp. nov.*** (Contributed by Rong-Ju Xu)

Savoryellales Boonyuen, Suetrong, Sivichai, K.L. Pang & E.B.G. Jones

Savoryellaceae Jaklitsch & Réblová
1470. ***Canalisporium caribense*** (Hol.-Jech. & Mercado) Nawawi & Kuthub., ***new record*** (Contributed by Saranyaphat Boonmee and Sajini K.U. Chandrasiri)
1471. ***Rhexoacrodictys nigrospora*** Boonmee, D.F. Bao & K.D. Hyde, ***sp. nov.*** (Contributed by Saranyaphat Boonmee)

Lasiosphaeriaceae Nannf.
1472. ***Cercophora dulciaquae*** M.S. Calabon, E.B.G. Jones & K.D. Hyde, ***sp. nov.*** (Contributed by Mark S. Calabon)

Torpedosporales E.B.G. Jones, Abdel-Wahab & K.L. Pang

Juncigenaceae E.B.G. Jones, Abdel-Wahab & K.L. Pang
1473. ***Khaleijomyces umikazeanus*** Abdel-Wahab, ***sp. nov.*** (Contributed by Mohamed A. Abdel-Wahab and Faten A. Abdel-Aziz)

Xylariales Nannf.

Diatrypaceae Nitschke
1474. ***Eutypa flavovirens*** Nitschke, ***new record*** (Contributed by Subodini N. Wijesinghe)
1475. ***Eutypa lata*** (Pers.) Tul. & C. Tul., ***new record*** (Contributed by Subodini N. Wijesinghe)

Xylariaceae Tul. & C. Tul.
1476. ***Xylaria apiospora*** M. Niranjan & V.V. Sarma, ***sp. nov.*** (contribution by M. Niranjan and V. Venkateswara Sarma)
1477. ***Xylaria haemorrhoidalis*** Berk. & Broome, ***new record*** (contribution by M. Niranjan and V. Venkateswara Sarma)

Xylariales* genus *incertae sedis
1478. ***Melanographium smilacis*** Boonmee, Huanraluek & K.D. Hyde, ***sp. nov.*** (contribution by Saranyaphat Boonmee and Naruemon Huanraluek)

Basidiomycota R.T. Moore
Agaricomycetes Doweld

Agaricales Underw.

Agaricaceae Chevall.
1479. ***Chlorophyllum demangei*** (Pat.) Z.W. Ge & Zhu L. Yang, ***new record*** (contribution by Phongeun Sysouphanthong and Naritsada Thongklang)
1480. ***Chlorophyllum globosum*** (Mossebo) Vellinga, ***new record*** (contribution by Phongeun Sysouphanthong and Naritsada Thongklang)
1481. ***Chlorophyllum hortense*** (Murrill) Vellinga, ***new record*** (contribution by Phongeun Sysouphanthong and Naritsada Thongklang)
1482. **M*icropsalliota globocystis*** Heinem., ***new record*** (contribution by Phongeun Sysouphanthong and Naritsada Thongklang)
1483. ***Micropsalliota gracilis*** Heinem., ***new record*** (contribution by Phongeun Sysouphanthong and Naritsada Thongklang)
1484. ***Xanthagaricus necopinatus*** Iqbal Hosen, T.H. Li, & G.M. Gates, ***new record*** (contribution by Phongeun Sysouphanthong and Naritsada Thongklang)

Amanitaceae E.-J. Gilbert
1485. ***Saproamanita manicata*** (Berk. & Broome) Redhead, Vizzini, Drehmel & Contu, ***new record*** (contribution by Nakarin Suwannarach and Surapong Khuna)

Cortinariaceae R. Heim ex Pouzar
1486. ***Cortinarius alutarius*** Kałucka & Liimat., ***sp. nov.*** (Contributed by Izabela L. Kałucka, Andrzej M. Jagodziński and Kare Liimatainen)
1487. ***Cortinarius mammillatus*** Kałucka, Kytöv., Niskanen & Liimat., ***sp. nov.*** (Contributed by Izabela L. Kałucka, Andrzej M. Jagodziński and Kare Liimatainen)
1488. ***Cortinarius quercoflocculosus*** Kałucka & Liimat., ***sp. nov.*** (Contributed by Izabela L. Kałucka, Andrzej M. Jagodziński and Kare Liimatainen)

Hydnangiaceae Gäum. & C.W. Dodge
1489. ***Laccaria populina*** Dovana, ***sp. nov.*** (Contributed by Francesco Dovana)

Hygrophoraceae Lotsy
1490. ***Hygrocybe boertmannii*** U. Singh & R.P. Bhatt, ***sp. nov.*** (Contributed by Upendra Singh)

Marasmiaceae Roze ex Kühner
1491. ***Marasmius benghalensis*** A.K. Dutta & K. Acharya, ***sp. nov.*** (Contributed by Arun Kumar Dutta and Krishnendu Acharya)
1492. ***Marasmius jinfoshanensis*** Chun Y. Deng & Gafforov, ***sp. nov.*** (Contributed by Chun Y. Deng, Emma Harrower,

Tohir Bozorov, Tutigul Kholmuradova and Yusufjon Gafforov)
1493. ***Marasmius subtropicus*** A.K. Dutta & K. Acharya, ***sp. nov.*** (Contributed by Arun Kumar Dutta and Krishnendu Acharya)

Mycenaceae Overeem
1494. ***Cruentomycena uttarakhandina*** U. Singh & R.P. Bhatt, ***sp. nov.*** (Contributed by Upendra Singh)

Nidulariaceae Dumort.
1495. ***Cyathus uniperidiolus*** P.N. Singh & S.K. Singh, ***sp. nov.*** (Contributed by P.N. Singh and Sanjay K. Singh)

Omphalotaceae Bresinsky
1496. ***Marasmiellus palmivorus*** (Sharples) Desjardin, ***new record*** (Contributed by Nakarin Suwannarach and Saisamorn Lumyong)

Psathyrellaceae Vilgalys, Moncalvo & Redhead
1497. ***Coprinellus punjabensis*** Usman & Khalid, ***sp. nov.*** (Contributed by Muhammad Usman and Abdul Nasir Khalid)

Geastrales K. Hosaka & Castellano

Geastraceae Corda
1498. ***Geastrum gorgonicum*** M.P. Martín, M. Dueñas & Telleria, ***sp. nov.*** (Contributed by María P. Martín, Margarita Dueñas and M. Teresa Telleria)
1499. ***Geastrum hansagiense*** Bóna, Merényi, Boros, Stielow & Bratek, ***sp. nov.*** (Contributed by Lilla Bóna, Zsolt Merényi, Lajos Boros, J. Benjamin Stielow and Bratek Zoltán)

Schizoporaceae Jülich
1500. ***Hyphodontia yunnanensis*** C.L. Zhao & Y.C. Dai, ***sp. nov.*** (Contributed by Chang-Lin Zhao and Yu-Cheng Dai)

Thelephoraceae Chevall.
1501. ***Odontia huanrenensis*** Y.H. Mu, H.S. Yuan & Y.C. Dai, ***sp. nov.*** (Contributed by Yan-Hong Mu, Hai-Sheng Yuan and Yu-Cheng Dai)
1502. ***Odontia parvispina*** Y.H. Mu, H.S. Yuan & Y.C. Dai, ***sp. nov.*** (Contributed by Yan-Hong Mu, Hai-Sheng Yuan and Yu-Cheng Dai)

Bartheletiomycetes Thines
Polyporales Gäum.

Hyphodermataceae Jülich
1503. ***Hyphoderma australosetigerum*** M. Dueñas, Telleria & M.P. Martín, ***sp. nov.*** (Contributed by Margarita Dueñas, M. Teresa Telleria and María P. Martín)

Irpicaceae Spirin & Zmitr.
1504. ***Efibula rodriguezarmasiae*** Telleria, M. Dueñas, Beltrán-Tej., Melo, Salcedo & M.P. Martín, ***sp. nov.*** (Contributed by M. Teresa Telleria, Margarita Dueñas and María P. Martín)

Phanerochaetaceae Jülich
1505. ***Phanerochaete hainanensis*** S.H. He & Y.C. Dai, ***sp. nov.*** (Contributed by Shuang-Hui He and Yu-Cheng Dai)

Polyporaceae Fr. ex Corda
1506. ***Favolus septatus*** J.L. Zhou & B.K. Cui, ***new record*** (Contributed by Deepak K. Maurya and Sanjay K. Singh)

Russulales Kreisel ex P.M. Kirk, P.F. Cannon & J.C. David

Russulaceae Losty
1507. ***Lactarius pallidozonarius*** G.J. Li & W.F. Lin, ***sp. nov.*** (Contributed by Guo-Jie Li and Wen-Fei Lin)
1508. ***Russula paravioleipes*** G.J. Li & W.F. Lin, ***sp. nov.*** (Contributed by Guo-Jie Li and Wen-Fei Lin)

Microbotryomycetes R. Bauer et al.
Microbotryales R. Bauer & Oberw.

Microbotryaceae R.T. Moore
1509. ***Microbotryum polycnemoides*** T. Denchev, Denchev, Kemler & Begerow, ***sp. nov.*** (Contributed by Teodor T. Denchev, Cvetomir M. Denchev, Martin Kemler and Dominik Begerow)

Mortierellomycota Tedersoo et al.

Mortierellomycetes Doweld
Mortierellales Caval.-Sm.

Mortierellaceae A. Fisch.
1510. ***Mortierella solitaria*** Telagathoti, M. Probst & Peintner, ***sp. nov.*** (Contributed by Anusha Telagathoti, Maraike Probst and Ursula Peintner)

Mucoromycota Doweld
Mucoromycetes Doweld

Mucorales Dumort.

Mucoraceae Fr.

1511. ***Mucor harpali*** Hyang B. Lee, P.M. Kirk & T.T.T. Nguyen, ***sp. nov.*** (Contributed by Hyang Burm Lee, Thuong T.T. Nguyen and Paul M. Kirk)

Introduction

The Fungal Diversity Notes series provides evidence of a largescale wave of species discovery, the rapid description of these novel species, and the implication of many yet undescribed taxa (Hyde et al. 2020c). These notes show that in countries where mycological studies are taking place, there is a high diversity of undiscovered fungi that was previously not apparent (Hyde et al. 2018b). The series provides an outlet for publishing new species, new records and new combinations.

From the first to 13th series of the Fungal Diversity Notes 1–1511, a total of 1511 taxa were included with 11 new families, 115 new genera and 1068 new species (Ariyawansa et al. 2015a; Liu et al. 2015a; Li et al. 2016a; Hyde et al. 2016, 2017, 2019, 2020a; Tibpromma et al. 2017b, 2018; Wanasinghe et al. 2018; Phookamsak et al. 2017a, 2019; Yuan et al. 2020; this study). Nineteen phyla have been accepted in the kingdom of Fungi following an updated outline of fungi and fungus-like taxa in Wijayawardene et al. (2020). The *Fungal Diversity Notes Series* largest contribution to diversity can be found in the phyla of Ascomycota and Basidiomycota.

The newly published records are also important for species documentation in order to provide comprehensive understanding of their taxonomic and phylogenetic relationships with up to date sequence data (Hyde et al. 2020a; Chethana et al. 2021). The new records will also benefit future studies which cover critical fields including fungal diagnostics and identification, economics and environmental management (Chethana et al. 2021). Several contemporary webpages provide data on fungal taxa from different habitats and regions, including descriptions, illustrations, phylogenetic trees, notes and the current number of accepted species (Pem et al. 2019a; Bundhun et al. 2020; Calabon et al. 2020b; Wijesinghe et al. 2021).

As mycologists strive to accurately define species with an ever-increasing amount of supporting evidence, new records will help determine the boundaries of a species (Hyde et al. 2020a; Chethana et al. 2021; Lucking et al. 2021). When an abundance of evidence including: full descriptions, illustrations and plates, molecular data and material examined are provided, the taxa can be described and accepted as a novel species. In cases where new species become less distinct with further data, those species can then be synonymized. The data also provides new distribution and host records.

The aim of this paper is to provide thorough descriptions of 72 new taxa, one new combination, one reference specimen and 51 new records with supporting taxonomic and phylogenetic evidence. A compilation of notes on new taxonomic contributions, distribution and host records are provided under each fungal taxon.

Materials and methods

Materials and methods follow the recent Fungal Diversity Notes (Hyde et al. 2020b). Fresh specimens were collected from Africa, America, Asia and Europe (i.e., Austria, Cape Verde, Chile, China, Ecuador, Egypt, Hungary, India, Iran, Italy, Japan, Pakistan, Peru, Poland, Portugal, Republic of Costa Rica, Republic of Korea, Russia, Spain, Thailand and USA). Microscopic characters, illustration photo-plates and molecular phylogenetic analyses were performed as previously described in recent publications (Phookamsak et al. 2019; Senanayake et al. 2020; Yuan et al. 2020).

Taxonomy

Ascomycota Caval.-Sm.

Notes: The latest updated account of Ascomycota see Wijayawardene et al. (2020).

Dothideomycetes O.E. Erikss & Winka.

Notes: We follow the latest treatments and updated accounts of Dothideomycetes as available in Hongsanan et al. (2020a, b).

Botryosphaeriales C.L. Schoch et al.

Notes: *Botryosphaeriales* was introduced with a single family *Botryosphaeriaceae* (Schoch et al. 2006). In the last decade, several researchers have extensively contributed to the taxonomy and phylogeny of species within the *Botryosphaeriales* (Liu et al. 2012; Slippers et al. 2013; Yang et al. 2017b; Phillips et al. 2019; Zhang et al. 2021). The most recent phylogenetic analyses on *Botryosphaeriales*, recognized six families: *Aplosporellaceae*, *Botryosphaeriaceae*, *Melanopsaceae*, *Phyllostictaceae*, *Planistromellaceae* and *Saccharataceae* (Phillips et al. 2019; Hongsanan et al. 2020b).

Botryosphaeriaceae Theiss. & P. Syd.

Notes: So far 22 genera have been characterized within *Botryosphaeriaceae* (Hongsanan et al. 2020b). To identify *Botryosphaeriaceae* genera and species, along with morphology, it is necessary to use sequence data of SSU, ITS, LSU, TEF1-α and *β-tubulin* loci (Phillips et al. 2013; Dissanayake et al. 2016; Wu et al. 2021). Herein a new species of *Diplodia* is introduced based on morphology and DNA fingerprinting patterns along with ITS and TEF1-α sequence data.

Diplodia Fr.

Diplodia was introduced by Montagne (1834) based on the type species *D. mutila*. *Diplodia* species are pathogens, endophytes or saprobes on a wide range of woody hosts (Phillips et al. 2012; Zhang et al. 2021). Pathogenic species are associated with different disease symptoms such as twig blight, canker, die-back, gummosis and fruit rot (Abdollahzadeh 2015). More than 1000 species have been listed in Index Fungorum, MycoBank and Species Fungorum databases. Sequences data are available for a limited number of species. In this study, *Diplodia alanphillipsii* is introduced as a new species (Figs. 1 and 2).

Diplodia alanphillipsii Abdollahz. & A. Javadi, ***sp. nov.***

Index Fungorum number: IF557831; *Facesoffungi number*: FoF 09953; Fig. 1

Etymology: Named after Dr. Alan J.L. Phillips for his extensive, qualitative and valuable research on the systematics of the *Botryosphaeriaceae*.

Holotype: IRAN 14273F

On twigs of *Citrus* sp. **Sexual morph** Undetermined. **Asexual morph** *Conidiomata* pycnidial, solitary or clustered, immersed in the host or partially erumpent, globose, dark brown to black, ostiolate, apapillate, unilocular, thick-walled with outer dark brown layers and inner thin-walled hyaline *textura angularis*. *Paraphyses* not observed. *Conidiophores* reduced to conidiogenous cells or with a supporting cell. *Conidiogenous cells* hyaline, thin-walled, smooth, cylindrical, swollen at the base, discrete, enteroblastic, annellidic, indeterminate, often proliferating internally giving rise to periclinal thickenings or proliferating percurrently forming 2–3 annellations. *Conidia* (17–)20–22(–26) × (8–)10–11(–13.5) µm (av. ± SD = 21.5 ± 1.5 × 10.5 ± 0.8 µm, l/w ratio = 2.2 ± 0.2), aseptate, ovoid, widest in the middle, obtuse at the apex, truncate or rounded at the base, initially hyaline, becoming dark brown before release from the pycnidium, moderately thick-walled, externally smooth, roughened on the inner surface.

Material examined: IRAN, Hormozgan Province, Minab, Hajikhademi, on twigs of *Citrus* sp., 3 March 2007, J. Abdollahzadeh and A. Javadi (IRAN 14273F, **holotype**), ex-type living culture, IRAN 1508C = CBS 124713; Rodan, on twigs of *Mangifera indica*, 3 March 2007, J. Abdollahzadeh and A. Javadi, IRAN 1509C; on twigs of *Citrus* sp., 3 March 2007, J. Abdollahzadeh and A. Javadi, IRAN 1574C = CBS 124712.

GenBank numbers: IRAN 1508C: ITS = KF890208, TEF1-α = KF890190; IRAN 1509C: ITS = KF890209, TEF1-α = KF890191; IRAN 1574C: ITS = MT258875; TEF1-α = MT270153.

Notes: *Diplodia alanphillipsii* is close to *D. citricarpa* with 4 base pairs differences in ITS (3 substitutions, 1 deletion/insertion) and one in TEF1-α (substitution), but can be distinguished due to the relatively smaller conidia when compared to *D. citricarpa* (22–25 × 9–10 µm) (Yang et al. 2017b). These two species are also differentiated based on the ISSR (data not shown) and rep-PCR fingerprinting patterns (Abdollahzadeh and Zolfaghari 2014). Sequences generated for *D. citricarpa* were deposited in GenBank: IRAN 1578C = CBS 124715 (ITS: KF890207; TEF1-α: KF890189); IRAN 1511C (ITS: KF890206; TEF1-α: KF890188); IRAN 1510C (ITS: MT258874; TEF1-α: MT270152).

Capnodiales Woron.

Notes: The latest updated account of *Capnodiales* includes 19 families and 243 genera (Wijayawardene et al. 2020).

Dissoconiaceae Crous & de Hoog

Notes: *Dissoconiaceae* is a family within *Capnodiales* (Dothideomycetes) that was introduced by Crous et al. (2009) to accommodate the genera *Dissoconium* and *Ramichloridium*. The number of genera within the *Dissoconiaceae* has increased to four after *Pseudoveronaea* was introduced, and *Uwebraunia*, a former synonym of *Dissoconium* was reinstated, to accommodate taxa of a distinct clade within the latter genus (Li et al. 2012). The new genus *Globoramichloridium* has also been incorporated (Marín-Félix et al. 2019a). In general, species in this family produce pseudothecial ascomata, which are immersed, globose, unilocular, papillate, and ostiolate with a periphysate canal (Crous et al. 2009). Pseudoparaphyses are absent and bitunicate asci are of a fasciculate manner. Asci contain eight spores, which are usually ellipsoid to fusoid with 1 septum, hyaline, and with or without a gelatinous sheath. In the asexual cycle, these fungi produce subcylindrical, subulate or lageniform to cylindrical conidiophores and solitary conidia, which are often pale olivaceous-brown, smooth or coarsely verrucose, ellipsoid to obclavate or globose, and 0–1-septate. Species in this family are mainly saprobic and pathogens of plants; some cause sooty blotch and flyspeck on their hosts and are widespread across different landmasses (Diaz Arias et al. 2010; Chen et al. 2014). From a phylogenetic perspective, we followed the two most comprehensive assessments of *Dissoconiaceae* based on multi-locus sequence data (Crous et al. 2009; Marín-Félix et al. 2019a) to demonstrate that the monotypic *Chaetoscutula* (Müller 1958) belongs to this family.

Chaetoscutula E. Müll.

Notes: *Chaetoscutula* is a monotypic genus based on *Chaetoscutula juniperi* E. Müll (Müller 1958). It grows on

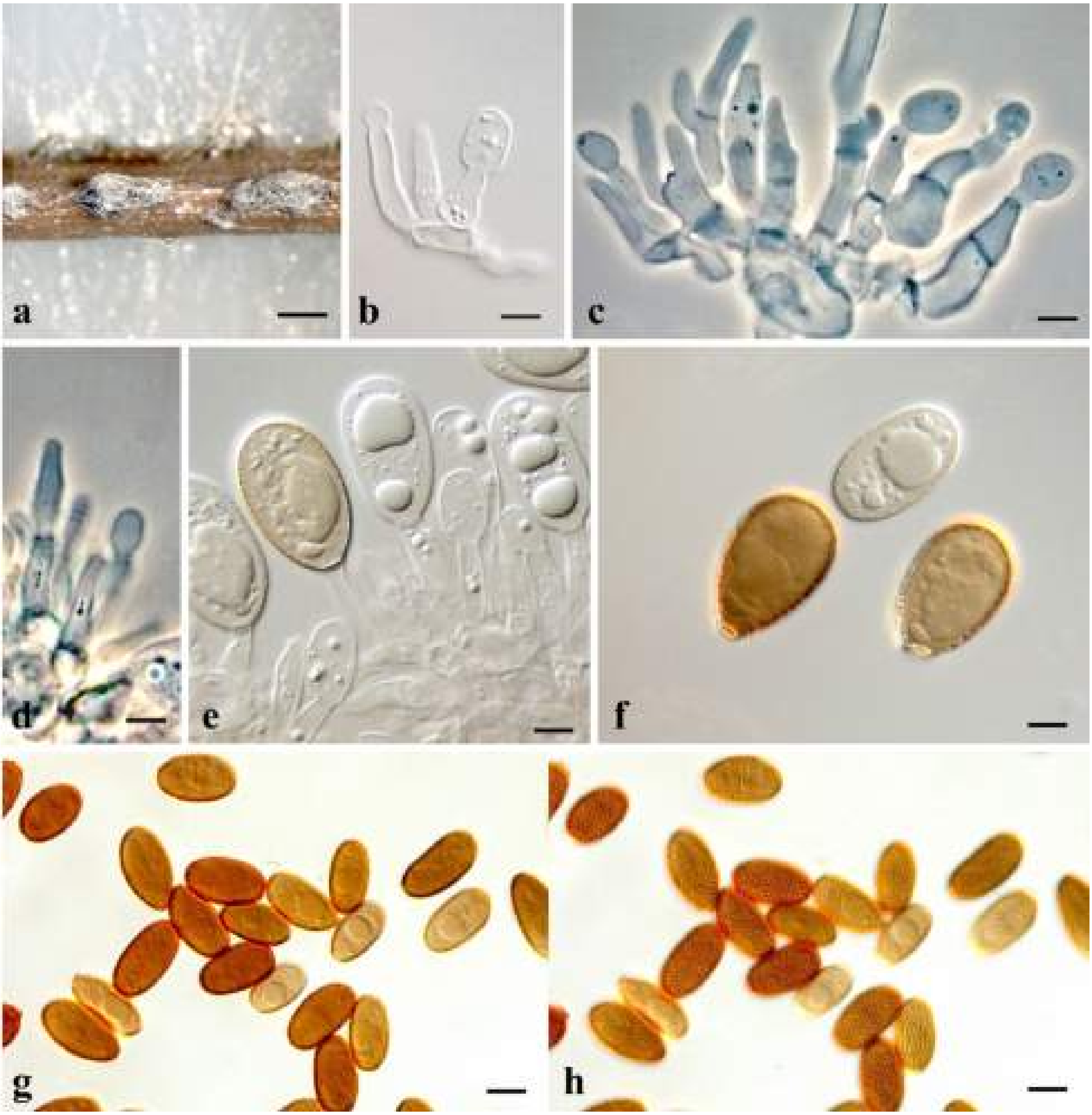


Fig. 1 ***Diplodia alanphillipsii*** (IRAN 14273F, **holotype**). **a** Conidiomata on pine needles in culture. **b** Hyaline immature conidia developing on conidiogenous cells. **c**, **d** Conidiogenous cells with periclinal thickenings or annellations. **e** Brown aseptate conidia on conidiogenous cells. **f** Mature brown conidia. **g, h** Mature conidia in two different focal planes. Scale bars: **a** = 500 µm, **b**–**f** = 5 µm, **g**, **h** = 10 µm

Juniperus spp. (*Cupressaceae*) and, although the mycelium is usually inconspicuous, this fungus produces tiny black hemispherical ascomata, solitary or gregarious, between adjacent leaves of the plant. The absence of signs of damage to the host suggests that the species is saprobic. The ascomata surface is characterized by displaying more or less dense, long and gnarled setae. Asci are bitunicate, 8-spored, and spores are cylindrical to clavate, two-celled, at first hyaline and then slightly brownish when mature. The genus was formerly placed within *Schizothyriaceae*, and later in *Saccardiaceae* (Müller and von Arx 1962; von Arx and Müller 1975) based on morphological comparisons. Recently, Tian et al. (2014) transferred *Chaetoscutula* to *Pseudoperisporiaceae* on the basis of the anatomical similarities to species in *Pododimeria*, a genus included in that family that also grows on *Juniperus* leaves (Müller 1958). In this

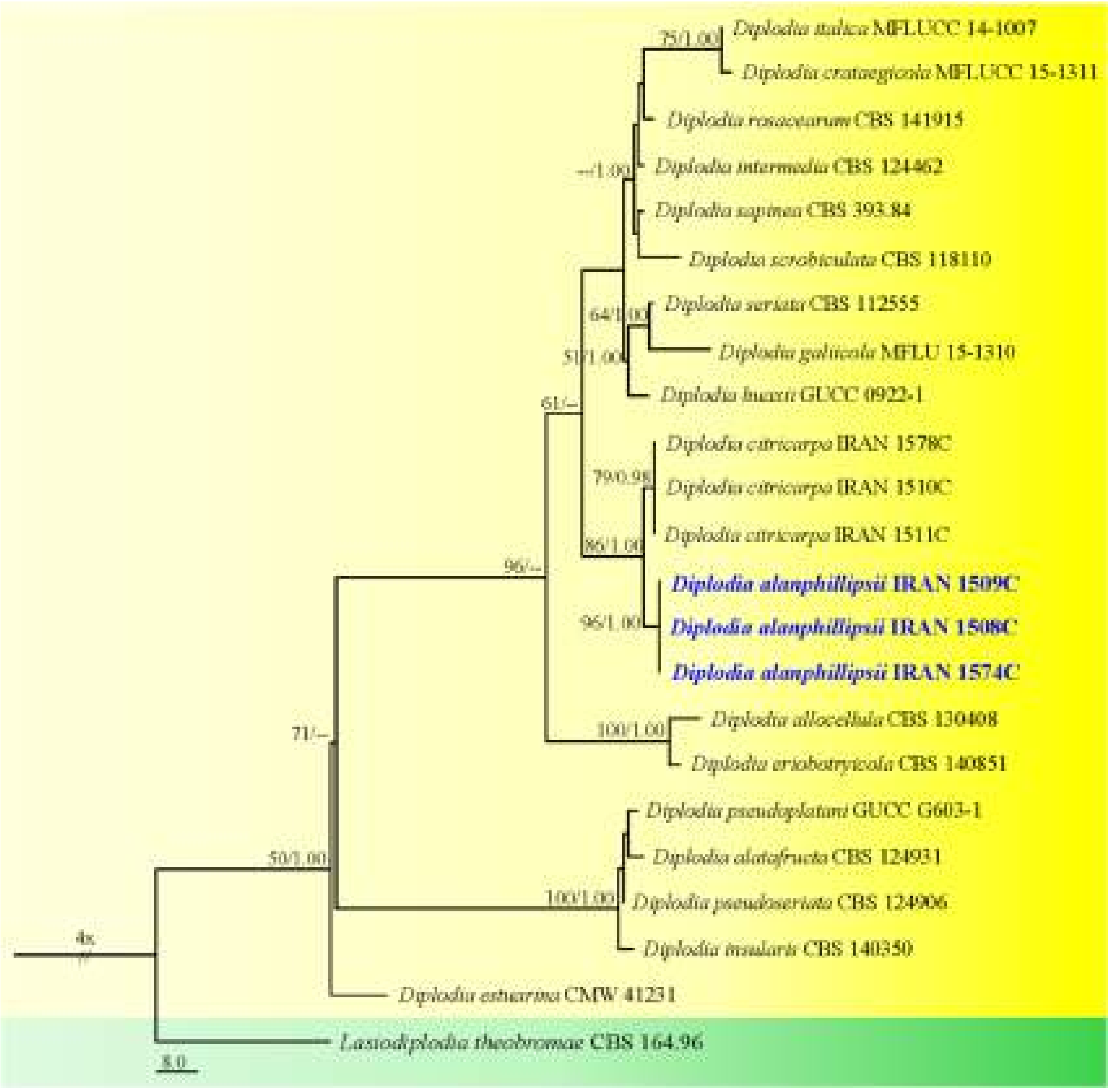


Fig. 2 Phylogram generated Maximum parsimony analysis based on combined ITS and TEF1-α sequence data of *Diplodia* species. The tree is rooted with *Lasiodiplodia theobromae* (CBS 164.96). The scale bar represents the expected number of changes per site. The MP analysis resulted one of the 36 equally most parsimonious trees (TL = 246, CI = 0.87, HI = 0.13, RI = 0.83). Bootstrap values for maximum parsimony (MPBS, left) based on 1000 pseudoreplicates equal to or greater than 50% are indicated at the nodes and posterior probabilities from Bayesian analysis (BYPP, right) equal to or greater than 0.95 are indicated at the nodes. The isolates of new species characterized in this study are in blue bold

study, we transfer *Chaetoscutula* to *Dissoconiaceae* based on phylogenetic results (Fig. 4) of novel sequence data from three regions of the nuclear ribosomal DNA: the ITS, LSU and SSU.

Chaetoscutula juniperi E. Müll., Sydowia 12(1–6): 191 (1959) [1958]

Index Fungorum number: IF294737; *Facesoffungi number*: FoF 03694; Fig. 3

Saprobic on leaves of *Juniperus* spp. **Sexual morph** *Ascomata* growing in the contact zone between two adjacent leaves, solitary or gregarious, superficial, hemispherical, 146–200 µm diam. ($\bar{x}$ = 179 µm, n = 5), dark brown to black, and always ornamented with more or less dense, long and gnarled setae, 80–128 × 3.5–4.4 µm ($\bar{x}$ = 99 × 3.9 µm, n = 8) and with a thickened wall up to 2 µm. Shorter, lighter and blunt developing setae interspersed among the former. *Peridium* thin of dark brown, 4–9 µm wide, thick-walled cells of *textura angularis*. *Ostiole* inconspicuous. *Hamathecium* not distinguishable, but hyaline gelatinous matrix is discernible among asci. *Asci* 50–84 × 20–30 µm ($\bar{x}$ = 66 × 25 µm, n = 7), 8-spored, bitunicate, arranged in parallel and originating

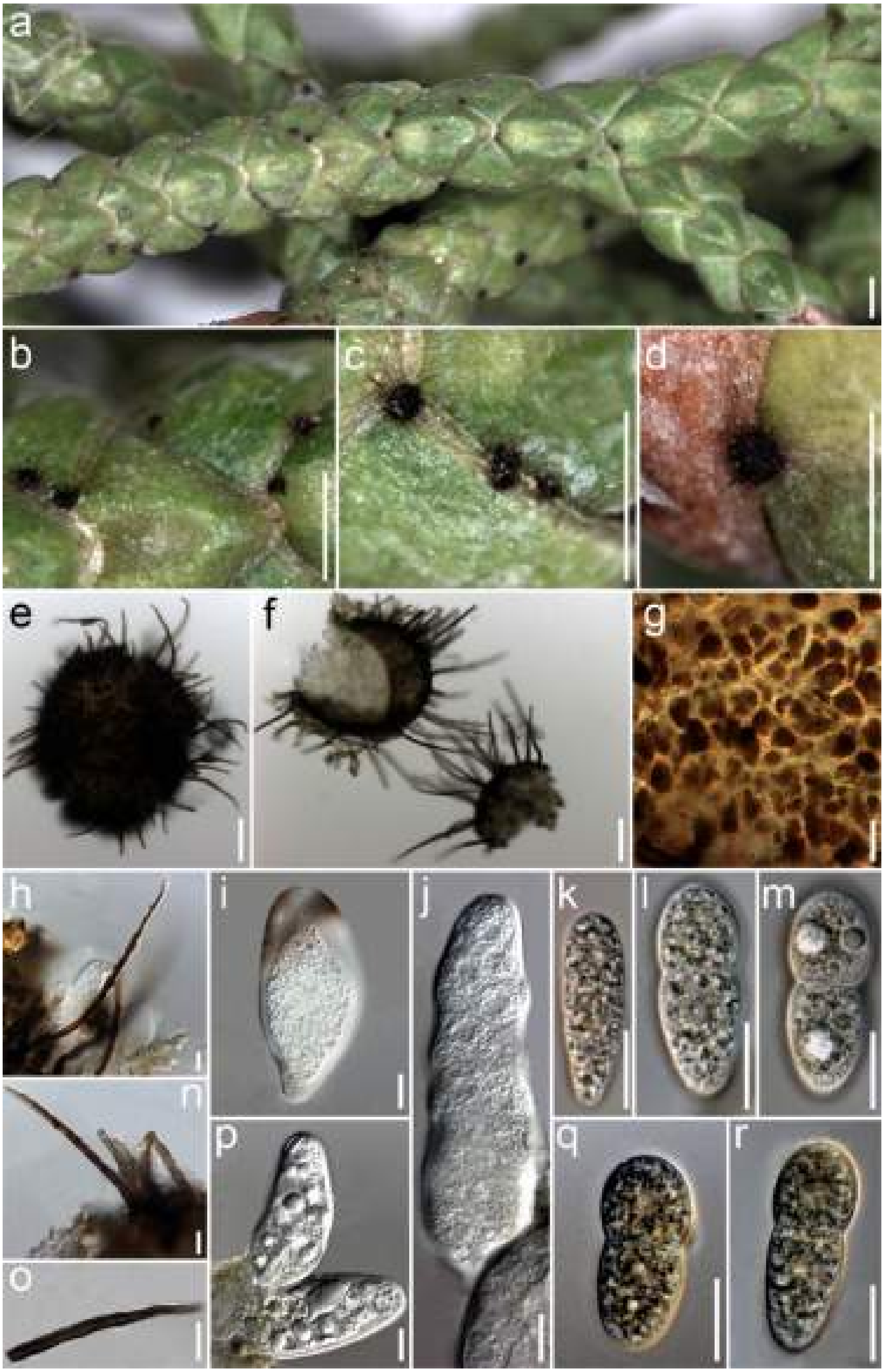


Fig. 3 ***Chaetoscutula juniperi*** (MA-90552, **new record**). **a**–**d** Ascomata on leaves of *Juniperus phoenicea*. **e**, **f** Ascomata immersed in water showing their hemispherical shape and their surface with dense, long and gnarled setae. **g** Peridium cells in surface view. **h**, **n, o** Setae. **i**, **j**, **p** Asci in several developmental stages. **k**–**m, q**, **r** Ascospores in several developmental stages. Scale bars: **a**–**d** = 0.5 mm, **e**, **f** = 50 µm, **g**–**r** = 10 µm

from a basal layer of hyaline, subcylindrical, broadly ellipsoid to obpyriform, loosely interwoven hyphae. *Ascospores* 23–28 µm long ($\bar{x}$ = 25.5 µm, n = 10), cylindrical to clavate, 1-septate, constricted at the septum, heteropolar, smaller cell width of 8.3–10.8 µm ($\bar{x}$ = 9.6 µm, n = 10), larger cell width of 9.7–11.5 µm ($\bar{x}$ = 10.5 µm, n = 10), rounded at both extremes, first hyaline and then slightly brownish when mature, not surrounded by a distinct gelatinous sheath. **Asexual morph** Undetermined.

Material examined: SPAIN, Comunitat Valenciana, Valencia Province, Racó d'Ademús, Vallanca, on leaves of *Juniperus phoenicea* growing along the Bohílgues River margin, 40°3′50.08″ N 1°20′50.88″ W, 958 msl, 19 August 2019, I. Garrido-Benavent, IGB756 (Real Jardín Botánico herbarium, MA-90552); Alacant Province, Vall d'Ebo, Corrals de Pego, entrance to the Barranc de l'Infern, on leaves of *J. phoenicea*, 38°48′23.59″ N 0°08′23.41″ W, 377 msl, 29 December 2019, I. Garrido-Benavent, IGB857 (MA-92235); Castelló Province, Vistabella del Maestrat, between Alt de l'Asevar and El Chaparral, on leaves of *J. sabina* in a forest of *Pinus sylvestris*, 40°15′55.94″ N 0°22′57.52″ W, 1624 msl, 21 August 2014, I. Garrido-Benavent, IGB793 (MA-90553); Pina de Montalgrao, on leaves of *J. phoenicea*, 40°01′16.47″ N 0°39′24.86″ W, 1034 msl, 21 August 2014, I. Garrido-Benavent, IGB794 (MA-90554); Castilla y León, Soria Province, Abejar, Sierra de Cabrejas, road to Calatañazor, on leaves of *J. thurifera*, 41°46′37.50″ N 2°46′41.20″ W, 1161 msl, 17 March 2014, I. Garrido-Benavent, IGB795 (MA-90641); Aragón, Teruel Province, La Puebla de Valverde, Corral de la Ceja, on leaves of *J. sabina*, 40°12′41.65″ N 0°57′36.61″ W, 1276 msl, 17 March 2014, I. Garrido-Benavent, IGB796 (MA-90556); Castilla-La Mancha, Albacete Province, Férez, Montes de Aguas Calientes, on leaves of *J. phoenicea*, 38°25′24.82″ N 1°52′40.46″ W, 501 msl, 27 December 2019, I. Garrido-Benavent, IGB835 (MA-92233); Murcia, Moratalla, between Benízar and Casicas del Portal, on leaves of *J. phoenicea*, 38°14′49.05″ N 1°59′59.85″ W, 1170 msl, 27 December 2019, I. Garrido-Benavent, IGB845 (MA-92234); *Ibidem*, El Sabinar, close to Cortijo de la Leona, road to Letur, on leaves of *J. thurifera*, 38°13′01.38″ N 2°08′07.61″ W, 1194 msl, I. Garrido-Benavent, IGB842.

GenBank numbers: ITS = MN756704, LSU = MN756705, SSU = MN756706 (all sequences obtained from the voucher MA-90552).

Notes: The morphological description of Iberian *Chaetoscutula juniperi* (Fig. 3) specimens that we provide here is in the agreement with the original species description (Müller 1958). There are, however, subtle differences in the size of setae and spores, which in our specimens tend to be slightly larger than previously described. Tian et al. (2014) provided the second and most recent description of the species based on material collected by E. Müller in France (collection S-F225899). Although the authors claimed that the studied ascomata "sometimes" displayed setae, the ascomata represented in the photographic plate (Tian et al. 2014; Fig. 1d) and the associated text description do not seem to match well with the concept of *C. juniperi*. Either in the present description or the one provided in the original publication (Müller 1958), *C. juniperi* has always been characterized as forming setae on the surface of ascomata; besides, ascomata were described as hemispherical, whereas Tian et al. (2014) described it as globose to subglobose and with much smaller ascomata (see Tian et al. 2014; Fig. 1e, f). A reevaluation of the collection S-F225899 must be conducted to ascertain whether it corresponds to the true C. *juniperi* or to other species growing on the same substrate (*Juniperus* leaves) such as *Pododimeria gallica* and *Seynesiella juniperi*, which share some microscopic characters with *C. juniperi* and co-occurred in the type collection (ZT Myc 60709).

Data provided in the present work increase the range of known *Juniperus* species to which *Chaetoscutula juniperi* is associated, as we found it on *J. sabina* and *J. phoenica* (Müller 1958), but also on *J. thurifera*, a tree species up to 20 m tall that is mainly distributed at high altitude regions in the inner Iberian Peninsula. Müller (1958) found this fungus growing on leaves of *J. chinensis* in the botanical garden of Munich. From a geographic perspective, the species appears to be present in France, Italy, Germany and Switzerland according to Müller (1958), Spain (present study) and possibly also in Canada (Annotated checklist for larger fungi on vancouver island 2020; http://azkurs.org/annotated-checklist-for-larger-fungi-on-vancouver-island.html?page=3), despite the fact that there are no associated metadata to the Canadian reference. In the Global Biodiversity Information Facility (GBIF) database, there is an additional Canadian specimen collected in 1963 occurring on *J. communis*, as well as eight observation records of this fungus in Scotland. Finally, our three-loci phylogeny (Fig. 4) revealed *Chaetoscutula* as a new member of *Dissoconiaceae*, thus widening the spectrum of morphological variation of ascomata that characterizes this family. The phylogenetically closest genus is *Pseudoveronaea*. Only the asexual state of the two species included in the latter genus, *P. ellipsoidea* and *P. obclavata* is known (Li et al. 2012), so that it is currently not possible to conduct a comprehensive morphological comparison between *Chaetoscutula* and *Pseudoveronaea*.

Dothideales Lindau (= *Neocelosporiales* Crous)

Notes: Latest updated accounts of *Dothideales* includes four families and 24 genera (Hongsanan et al. 2020a).

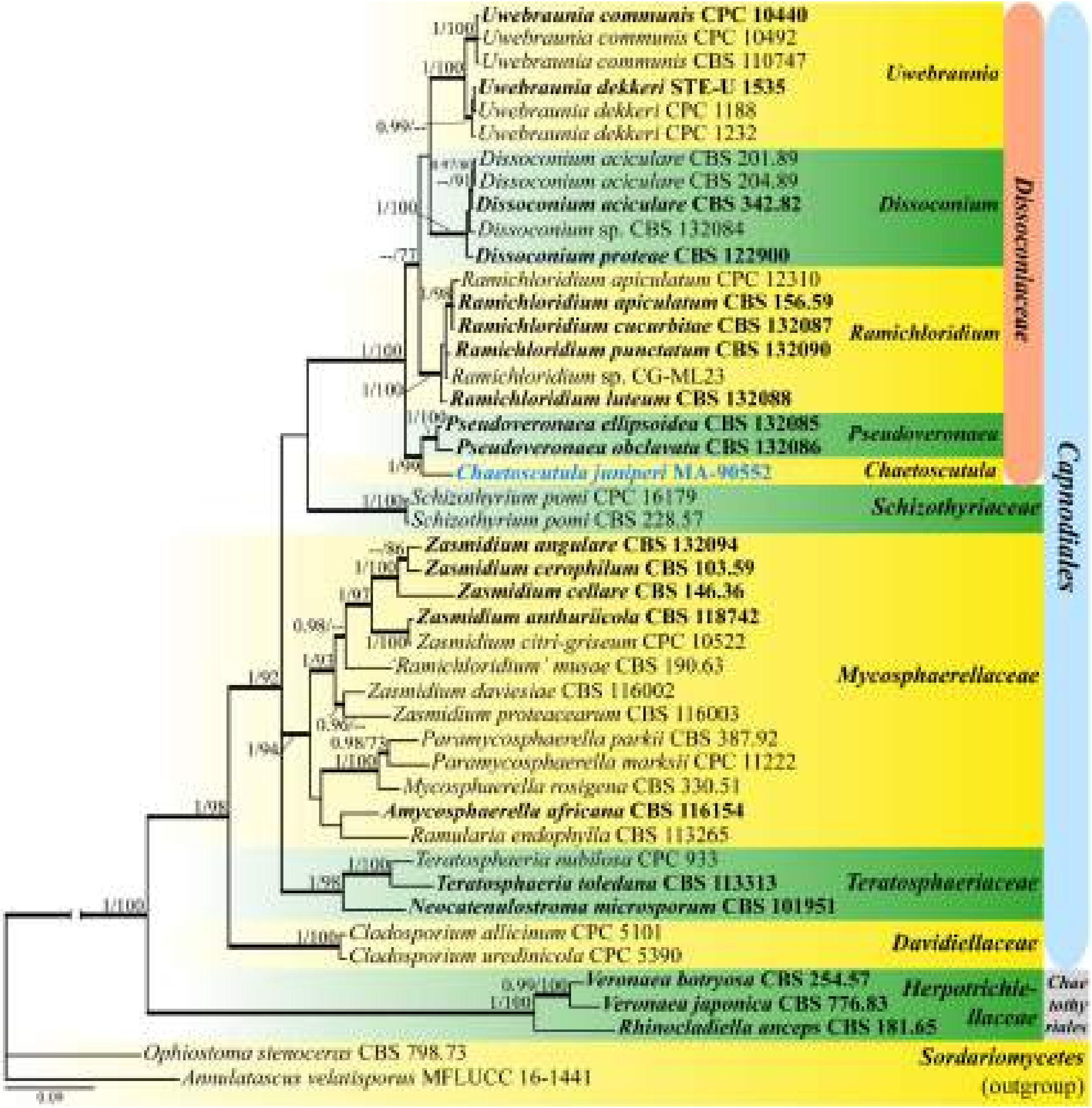


Fig. 4 Phylogram depicting the evolutionary relationships of *Chaetoscutula* and related clades in *Dissoconiaceae* (*Capnodiales*) based on a three-locus dataset (ITS, LSU and SSU). Species sampling was based on Li et al. (2012). The alignment matrix consisted of 2220 bp and inferred substitution models were GTR + Γ (ITS1 + ITS2), K80 + I + Γ (5.8S, SSU), and GTR + I + Γ (LSU). The represented topology is obtained under a Bayesian framework with MrBayes v.3.2.6. Posterior Probabilities (PP) are represented on branches leading to nodes. Bootstrap support values obtained in a complementary Maximum Likelihood analysis (MLBS, right) with RAxML using 1000 pseudoreplicates are provided after the BYPP values (left). Branches in bold had MLBS equal or greater than 70% and BYPP equal or greater than 0.95. For each terminal, the species name and the voucher/herbarium code are indicated, and type strains are in bold and new isolate is in blue

Dothideaceae Chevall.

Notes: Chevallier (1826) introduced *Dothideaceae* as 'Dothideae', and later Fuckel (1869) designated *Dothidea* as the type genus with *D. gibberulosa* (Ach.) Fr. as the type species. Recently, *Dothideaceae* was treated with 15 genera by Thambugala et al. (2014a). *Dothideaceae* is characterized by immersed to erumpent or superficial, uni or multiloculate ascostromata, 8- or polyspored, bitunicate asci and hyaline or brown, transversely septate and sometimes muriform ascospores (Thambugala et al. 2014a).

Dothiora Fr.

Notes: *Dothiora* was introduced by Fries (1849) with *D. pyrenophora* as the type species. *Dothiora* (based on *D. pyrenophora*) produces a *Dothichiza* asexual morph in culture (Crous and Groenewald 2017). Species of *Dothiora* are commonly isolated from dead branches of woody hosts (Sivanesan 1984), while Crous and Groenewald (2016) also reported some species from dead leaves and fruits of diverse hosts, indicating that it is a saprobe, possibly acting as a weak pathogen on stressed plant tissues.

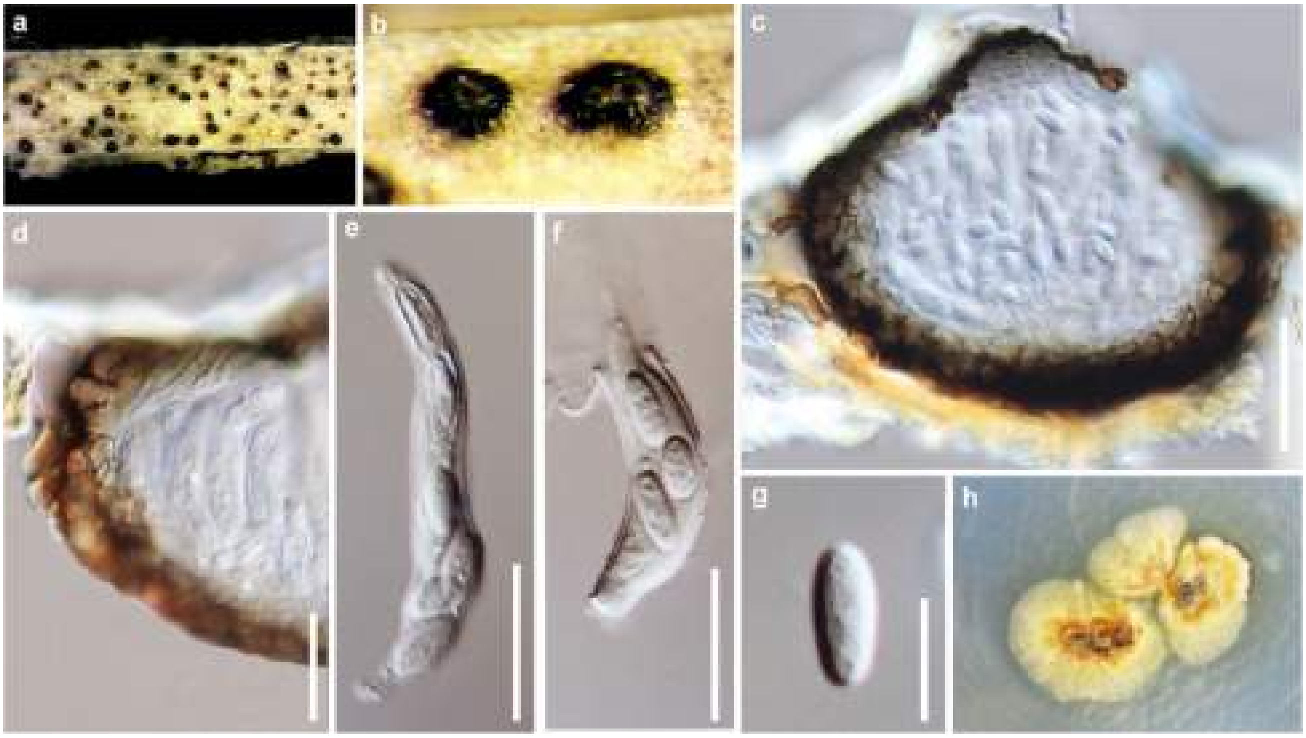


Fig. 5 *Dothiora coronicola* (MFLU 16-1110, **holotype**). **a**, **b** Ascomata on host surface. **c** Section through the ascoma. **d** Peridium. **e**, **f** Asci. **g** Ascospore. **h** Culture on PDA. Scale bars: **c**, **d** = 100 µm, **e**, **f** = 50 µm, **g** = 20 µm

Dothiora coronicola Dissanayake, Camporesi & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF556815; *Facesoffungi number*: FoF 06509; Fig. 5

Etymology: In reference to the host *Coronilla*, and cola meaning loving.

Holotype: MFLU 16-1110

Saprobic on dead aerial branch of *Coronilla emerus* L. **Sexual morph** *Ascomata* 215–430 × 240–285 µm, immersed or erumpent through the epidermis, solitary or clustered, globose, brown to black, with single locules. *Peridium* 39–76 µm wide, two-layered, outer layer composed of dark brown or brown, thick-walled cells of *textura angularis*, inner layer composed of hyaline, thin-walled cells of *textura angularis*. *Asci* 80–145 × 15–30 µm ($\bar{x}$ = 120 × 24 µm, n = 20), 8-spored, bitunicate, fissitunicate, cylindro-clavate, pedicellate, apically rounded, with a small ocular chamber. *Ascospores* 21–25 × 8–11 µm ($\bar{x}$ = 23 × 10 µm, n = 30), bi-seriate to multi-seriate, hyaline, aseptate, fusoid to ovoid, one end narrower than the other, smooth-walled with granular contents, lacking a mucilaginous sheath. **Asexual morph** Undetermined.

Culture characteristics: Colonies on PDA reaching 2 cm after 14 days at 25 °C, mycelium velvety and moderately fluffy with an irregular margin, surface initially white and later turning dark yellow from the middle of the colony and dark grey in reverse.

Material examined: ITALY, Province of Forlì-Cesena, near Passo delle Forche- Galeata, on dead aerial branch of *Coronilla emerus* (*Fabaceae*), 30 March 2016, E. Camporesi, IT 2894 (MFLU 16-1110, **holotype**), ex-type living culture, MFLUCC 17-1007.

GenBank numbers: ITS = MZ571206, LSU = MZ571207.

Notes: We were able to obtain a culture from a single conidium. In the phylogenetic analysis, *Dothiora coronicola* forms a distinct lineage basal to *D. buxi*, *D. cactacearum*, *D. coronillae* and *D. spartii* with 96% MLBS support (Fig. 6). However, this taxon can be differentiated from above mentioned species as follows. *Dothiora buxi* has polysporous asci with 32 ascospores in an ascus, while *D. coronicola* has asci with only eight ascospores. *Dothiora buxi* also has pale brown ascospores, whereas *D. coronicola* has hyaline ascospores (Fig. 5). The placement of *D. buxi* within the *Dothiora* was proven by molecular data (Hyde et al. 2016). Morphological variations of *D. coronicola* and *D. cactacearum* cannot be compared as the latter composed only an asexual morph. *Dothiora coronicola* can be easily distinguished from *D. coronillae* as the latter comprised with cylindro-clavate asci (Hyde et al. 2017). Both *D. coronicola* and *D. spartii* are morphologically comparable but phylogenetically they cluster in two different places (Fig. 6).

Dyfrolomycetales K.L. Pang, K.D. Hyde & E.B.G. Jones

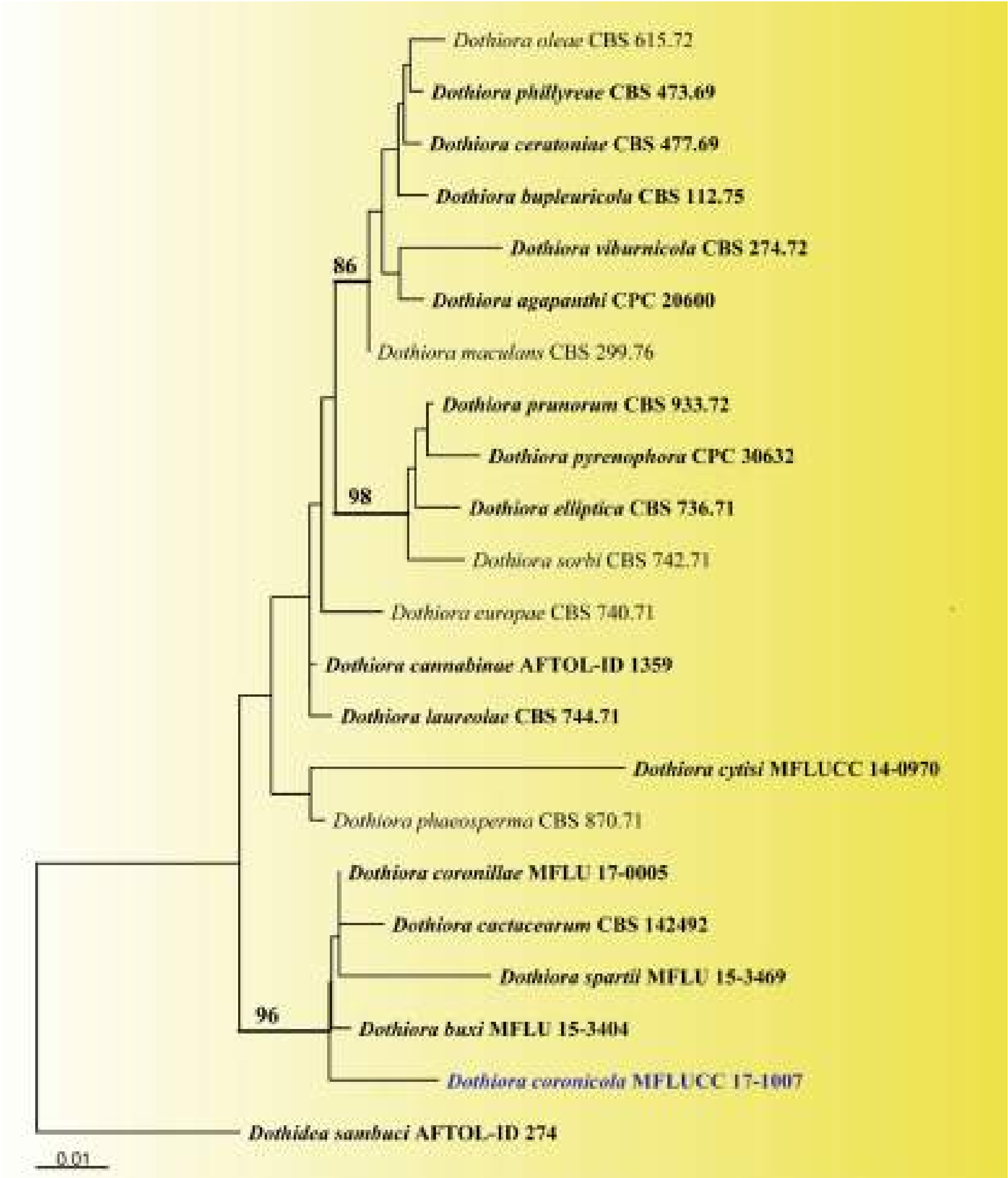


Fig. 6 Phylogram generated from maximum likelihood analysis based on combined LSU and ITS sequence data representing *Dothiora coronicola* (MFLUCC 17-1007) and related species. The scale bar indicates 0.01 changes. The tree is rooted to *Dothidea sambuci* (AFTOL-ID 274). Related sequences were taken from Hongsanan et al. (2020a). Twenty-two sequences are included in the analysis which comprise 1396 characters after alignment. The best RAxML tree with a final likelihood value of − 3690.034105 is presented. The matrix had 195 distinct alignment patterns, with 5.69% undetermined characters or gaps. Estimated base frequencies are as follows: A = 0.251756, C = 0.223630, G = 0.280088, T = 0.244526; substitution rates AC = 1.042605, AG = 2.446647, AT = 1.739048, CG = 0.584297, CT = 5.850014, GT = 1.000000; gamma distribution shape parameter α = 0.020014. Bootstrap values for maximum likelihood (MLBS) equal to or greater than 70% are indicated at the nodes. Type and ex-type strains are in bold and the newly generated sequence is in blue

Notes: *Dyfrolomycetales* was introduced by Pang et al. (2013) based on the collection of marine fungi *Dyfrolomyces tiomanensis* from Tioman Island, Malaysia. Only the single family *Pleurotremataceae* was accepted in this order with three associated genera *Dyfrolomyces, Melomastia* and *Pleurotrema*. The latest treatment of the order follows Hongsanan et al. (2020b).

Pleurotremataceae Walt. Watson (= *Dyfrolomycetaceae* K.D. Hyde et al.)

Notes: *Pleurotremataceae*, typified by *Pleurotrema* with *Pleurotrema polysemum*, was introduced by Watson (1929) and accepted as a monotypic genus *Pleurotrema* within the order *Chaetosphaeriales*. *Pleurotremataceae* was assigned to *Xylariales* based on the non fissitunicate ascus character by Barr (1994) with five genera included: *Daruvedia*, *Melomastia*, *Phomatospora*, *Pleurotrema* and *Saccardoella*. The taxonomic placement of *Pleurotremataceae* was revised by various authors (Hyde 1992; Hawksworth et al. 1995; Tsui et al. 1998; Kirk et al. 2008; Suetrong et al. 2009; Lumbsch and Huhndorf 2010; Hu et al. 2010b; Hyde et al. 2013; Pang et al. 2013; Senanayake et al. 2016). Maharachchikumbura et al. (2015) resulting in it being accepted as *Pleurotrema* in *Pleurotremataceae* and placing it under *Chaetosphaeriales*, Sordariomycetes. Maharachchikumbura et al. (2016) synonymized *Dyfrolomycetaceae* under *Pleurotremataceae* and excluded it from Sordariomycetes based on morphology of the *Pleurotrema polysemum* isotype. This family comprises three genera characterized by perithecial, ostiolate, glabrous, ovoid to subglobose ascomata, clavate to cylindrical, bitunicate, short pedicellate asci, with a J-apical ring, and hyaline, ellipsoidal to cylindrical, multi-distoseptate, guttulate ascospores that are uni-seriate arranged in the asci (Hongsanan et al. 2020b).

Dyfrolomyces K.D. Hyde, K.L. Pang, Alias, Suetrong & E.B.G. Jones

Notes: *Dyfrolomyces* was introduced by Pang et al. (2013) to accommodate taxa observed on unidentified mangrove wood in Malaysia. Pang et al. (2013) transferred the three marine *Saccardoella* species to *Dyfrolomyces* viz. *D. mangrovei, D. marinosporus* and *D. rhizophorae* based on ascomatal structure and three-loci phylogenetic analysis. Ten species are included in the genus which are characterized by the presence of relatively large, immersed, globose or subglobose, clypeate, ostiolate, papillate ascomata, bitunicate, fissitunicate, cylindrical asci and broadly fusiform, symmetrical, hyaline, septate ascospores, with or without a mucilaginous sheath (Pang et al. 2013; Dayarathne et al. 2020; Hongsanan et al. 2020b).

Dyfrolomyces distoseptatus M. Niranjan & V.V. Sarma, in Hongsanan et al., Fungal Diversity 105:73 (2020)

Index Fungorum number: IF556726; *Facesoffungi number*: FoF 06625; Fig. 7

Saprobic on submerged decaying wood in a freshwater habitat. **Sexual morph** *Ascomata* 600–800 × 350–530 µm ($\overline{x}$ = 682 × 433 µm, n = 10), perithecial, immersed in periderm, erumpent neck with pseudoparaphyses, clypeate, ostiolate, papillate. *Peridium* 30–40 µm, with two strata, outer thick, carbonaceous and inner brown and hyaline cells of *textura angularis*. *Peridium* comprising of dark pigmented cells of *textura angularis*. *Hamathecium* pseudoparaphyses, filamentous, septate, unbranched, 2–4 µm wide, long, dense, longer than asci. *Asci* thin walled and quickly evanescent, unable to observed. *Ascospores* 17–26 × 3.5–6 µm ($\overline{x}$ = 23 × 5 µm, n = 30), uniseriate, hyaline, 1–2-distoseptate in early stages, usually 3-distoseptate, with a large guttules at each cell, fusoid, acute ends, apical ends slightly bent. **Asexual morph** Undetermined.

Culture characteristics: Conidia germinating on malt extract agar (MEA) within 24 h. Germ tubes produced from the basal and apical cell of conidia. Colonies growing on MEA, reaching 25–30 mm in 2 weeks at 25 °C, colony circular, entire to filiform edge, dry, surface rough, with dense mycelium, grayish brown in top view, reverse dark brown.

Material examined: THAILAND, Tak Province, Tha Sing Yang, Ban Mae Ja Wang on submerged decaying wood in a freshwater river, 17 October 2019, N. Padaruth, CC51 (MFLU 21-0121, **new geographical record**), living culture, MFLUCC 21-0102.

GenBank numbers: ITS = MT864349, LSU = MT860427.

Notes: *Dyfrolomyces distoseptatus* was introduced by Hongsanan et al. (2020b) isolated from an unidentified decaying twig in India. Our new isolate, *Dyfrolomyces distoseptatus* MFLUCC 21-0102 clustered with *D. distoseptatus* strain NFCCI: 4377 with 95% MPBS, 96% MLBS, 1.00 BYPP (Fig. 8). *Dyfrolomyces distoseptatus* clustered with *D. sinensis* and *D. phetchaburiensis*, however, *D. distoseptatus* differs having 2–3 septate ascospores with acute ends, while *D. sinensis* and *D. phetchaburiensis* have 6–7 septate and 1–10 septate ascospores, respectively (Hyde et al. 2017, 2018a). Unlike other species (viz. *D. aquatica*, *D. mangrovei*, *D. marinosporus*, *D. rhizophorae* and *D. thailandicus*), *D. distoseptatus* lacks a gelatinous sheath around the ascospores (Hyde 1992; Tsui et al. 1998; Pang et al. 2013; Hongsanan et al. 2020b). In addition, *Dyfrolomyces distoseptatusis* strains (MFLUCC 21-0102 and NFCCI: 4377) clustered with *D. thamplaensis*, however, *D. distoseptatusis* differs in having longer ascospores (17–26.5 × 3.5–6.5 µm) whereas *D. thamplaensis* has shorter ascospores (9.5–23.5 × 5–6.5 µm) (Fig. 7). A comparison of the ITS nucleotides indicates that our strain of *D. distoseptatus* is largely similar to strain NFCCI: 4377 based on DNA sequence (Jeewon and Hyde 2016). Therefore, we identify our new collection as *D. distoseptatus* which is the new record from a freshwater habitat in Thailand. Since the ascal morphology was not included in the observed substrates, recollection of the specimen is recommended.

Jahnulales K.L. Pang, Abdel-Wahab, El-Shar., E.B.G. Jones & Sivichai

Notes: *Jahnulales* was introduced by Pang et al. (2002) to accommodate three genera *Aliquandostipite*, *Jahnula* and *Patescospora*. We follow the latest treatment and updated accounts of *Jahnulales* in Hongsanan et al. (2020b). The order includes *Aliquandostipitaceae* (seven genera) and *Manglicolaceae* (one genus) which are commonly isolated from submerged decaying wood.

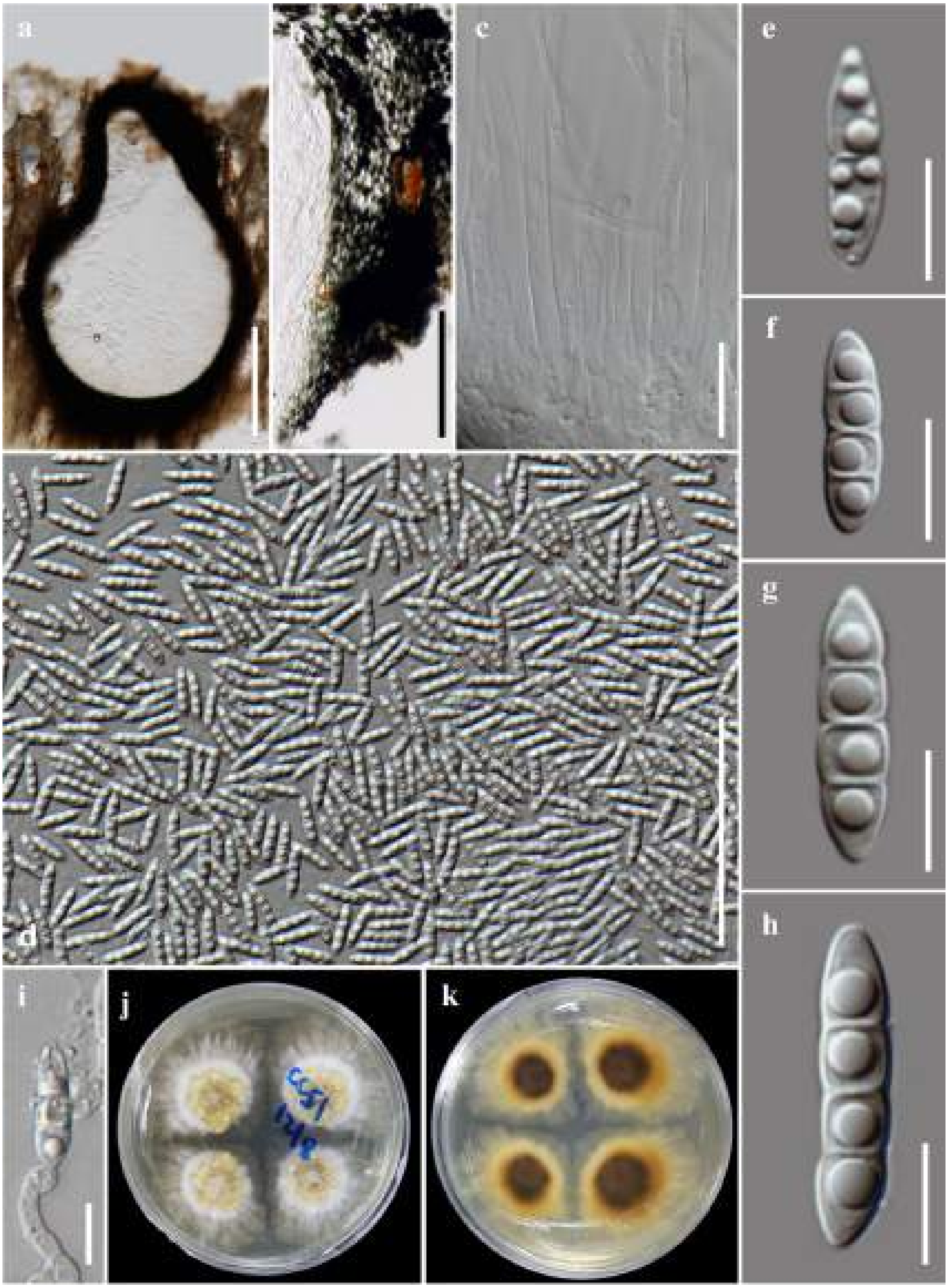


Fig. 7 ***Dyfrolomyces distoseptatus*** (MFLU 21-0121, **new geographical record**). **a** Vertical section of ascoma. **b** Peridium. **c** Pseudoparaphyses. **d**–**h** Ascospores (Note: Asci thin walled and quickly evanescent, unable to observe). **i** Germinated ascospore. **j**, **k** Culture on MEA from surface and reverse. Scale bars: **a** = 200 µm, **b** = 100 µm, **c** = 20 µm, **d**–**i** = 10 µm

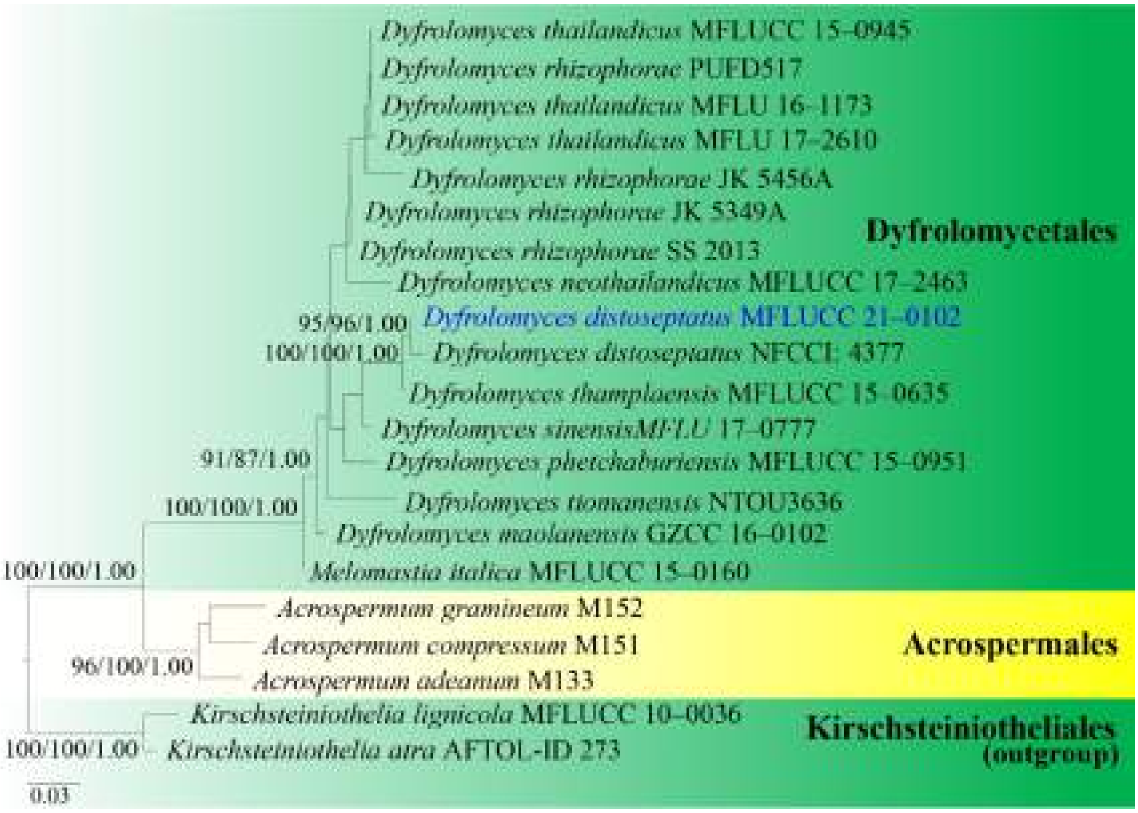


Fig. 8 Phylogram generated from maximum likelihood analysis based on combined LSU, SSU and ITS sequence data representing the species of *Dyfrolomycetales* and *Acrospermales*. Related sequences are taken from Hongsanan et al. (2020b). *Kirschsteiniothelia lignicola* (MFLUCC 10-0036) and *K. atra* (AFTOL-ID 273) are used as the outgroup taxa. Twenty-one taxa are included in the combined analyses which comprised 3532 characters (1359 characters for LSU, 1669 characters for SSU, 504 characters for ITS) after alignment. The best scoring RAxML tree with a final likelihood value of − 10567.325091 is presented. The matrix had 700 distinct alignment patterns, with 44.47% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.242587, C = 0.243215, G = 0.300854, T = 0.213344; substitution rates: AC = 1.335920, AG = 2.320033, AT = 0.575696, CG = 1.101975, CT = 5.314102, GT = 1.000000; gamma distribution shape parameter α = 0.248862. The MP analysis resulted a single most parsimonious tree (TL = 1145, CI = 0.851, RI = 0.803, RC = 0.683, HI = 0.149). Bootstrap support values for ML and MP equal to or greater than 70% and BYPP equal to or greater than 0.95 are given above the nodes. The newly generated sequence is in blue

Aliquandostipitaceae Inderbitzin

Notes: Inderbitzin et al. (2001) introduced *Aliquandostipitaceae* that are characterized by the widest hyphae reported in the ascomycetes, and the formation of both sessile and stalked ascomata side by side on the substrate. Seven genera, *Aliquandostipite*, *Brachiosphaera*, *Jahnula*, *Megalohypha*, *Neojahnula*, *Pseudojahnula* and *Xylomyces* are accepted in *Aliquandostipitaceae* (Hongsanan et al. 2020b).

Aliquandostipite Inderbitzin

Notes: *Aliquandostipite* was introduced to accommodate two species, *Aliquandostipite khaoyaiensis* and *A. sunyatsenii* based on SSU sequence data (Inderbitzin et al. 2001). *Aliquandostipite* includes six accepted species which are supported by both morphology and phylogenetic analysis (Suetrong et al. 2011; Liu et al. 2015a, Species Fungorum 2021).

Aliquandostipite khaoyaiensis Inderbitzin, Am. J. Bot. 88: 54 (2001)

Index Fungorum number: IF483979; *Facesoffungi number*: FoF 09158; Fig. 9

Saprobic on submerged wood. **Sexual morph** *Ascomata* 340–415 µm high, 250–290 µm diam., hyaline to pale brown, becoming dark brown with age, scattered, superficial, sometimes seated in a pseudostroma, globose or subglobose, sessile, membranous, papillate, ostiolate. *Ostioles* 100–135 µm apically lined by elongated cells. *Peridium* 30–40 µm thick, membranous, composed of thin-walled, pale brown, compressed cells of *textura angularis*. *Pseudoparaphyses* 2–5 µm diam., numerous, sparsely branched, hyaline, septate. *Asci* 155–200 × 35–65 µm ($\bar{x}$ = 175 × 50 µm, n = 20), 8-spored, bitunicate, fissitunicate, clavate, thickened at apex, sessile or short pedicellate, with a well-developed ocular chamber. *Ascospores* 55–70 × 15–25 µm ($\bar{x}$ = 65 × 19 µm, n = 30), variably arranged in asci, oval, hyaline to pale brown, 1-septate, deeply constricted at the septum, asymmetric, upper cell shorter and wider than lower cell, guttulate, straight or curved, thin-walled, smooth, sheathed.

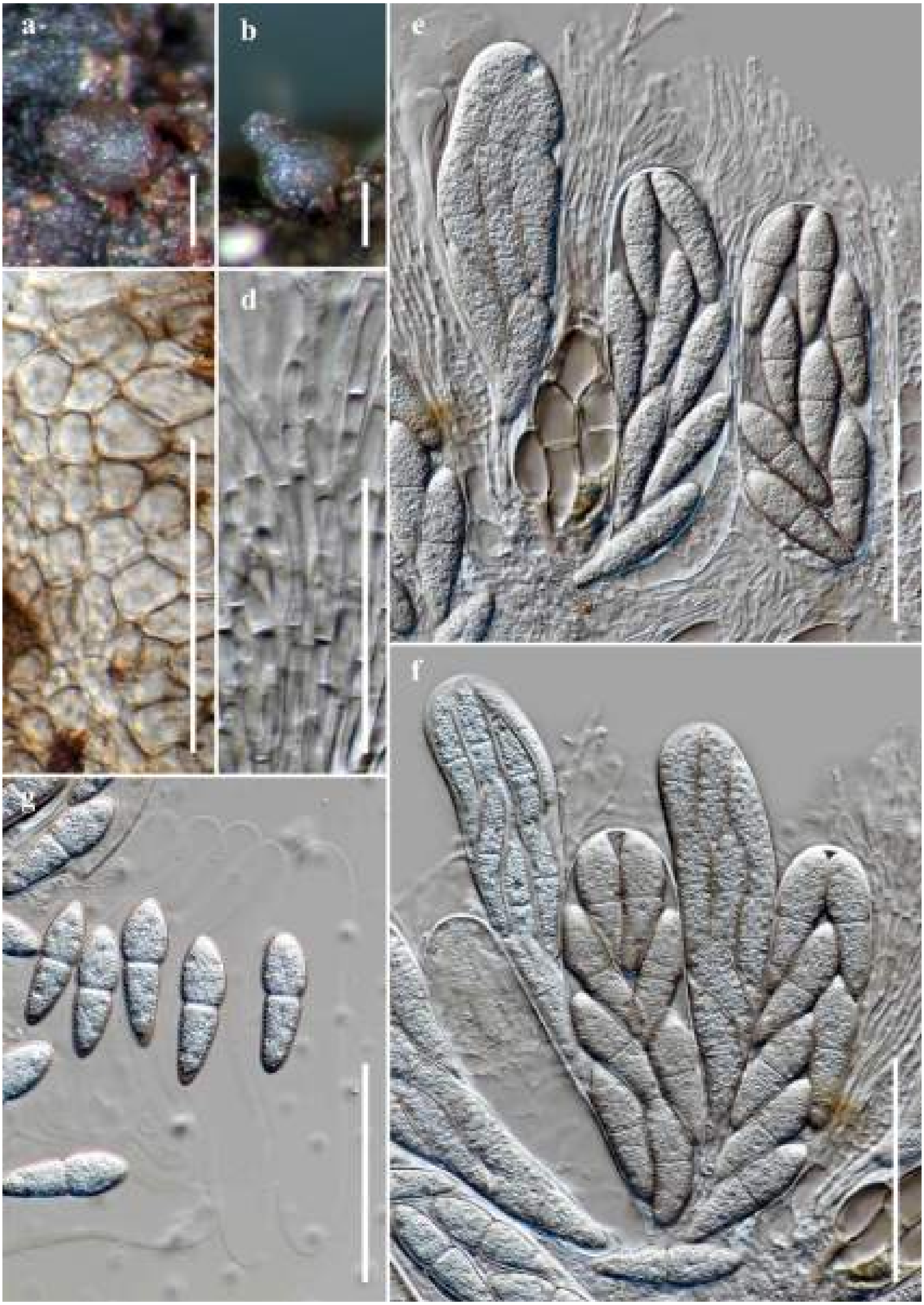


Fig. 9 ***Aliquandostipite khaoyaiensis*** (MFLU 21-0125, **new record**). **a**, **b** Ascomata superficial on host surface. **c** Peridium cells. **d** Pseudoparaphyses. **e**, **f** Asci. **g** Ascospores. Scale bars: **a**, **b**, **e**, **f** = 200 µm, **c**, **g** = 100 µm, **d** = 20 µm

Sheath first appressed to the ascospore wall, expanding and detaching from the polar regions when mounted in water, becoming balloon-like at the two poles, finally surrounding the entire ascospore. **Asexual morph** Undetermined.

Culture characteristics: Conidia germinating on malt extract agar (MEA) within 24 h. Germ tubes produced from the basal and apical cells of conidia. Colonies growing on MEA, reaching 20–25 mm in 2 weeks at 25 °C, colony circular, entire edge, dry, surface rough, with dense mycelium, pale yellow from above, dark brown from below

Material examined: THAILAND, Phitsanulok Province, Wang Thong, Kaeng Sopha stream, on submerged wood, 25 July 2019, S. Boonmee, ISAN100 (MFLU 21-0125, **new record**), living culture, MFLUCC 21-0106.

GenBank numbers: ITS = MT864350, LSU = MT860428, SSU = MT860445, TEF1-α = MT873577, RPB2 = MT873578.

Notes: *Aliquandostipite khaoyaiensis* has been recorded from Costa Rica (Raja et al. 2005), Thailand (Campbell et al. 2007) and U.S.A. (Raja et al. 2009). Our isolate MFLUCC 21-0106 resembles the generic description of the species except it lacks stalked ascomata. Furthermore, *A. khaoyaiensis* (MFLUCC 21-0106) has shorter ascospores compared to *A. khaoyaiensis* UBC F13875, the holotype isolated from Khao Yai National Park, Thailand (55–70 × 15–25 µm vs. 39–52 × 16–23 µm). In the phylogenetic tree, our new isolate clustered with other strains of *A. khaoyaiensis* and *A. siamensis* with 99% MPBS, 0.99 BYPP support (Fig. 10), which appears to be conspecific. *Aliquandostipite siamensis* is distinct from *A. khaoyaiensis* in having dimorphic, hyaline or brown ascospores without a sheath while the latter produces monomorphic, pale brown ascospores with well-developed sheaths (Inderbitzin et al. 2001; Pang et al. 2002; Campbell et al. 2007). We therefore report our collection as

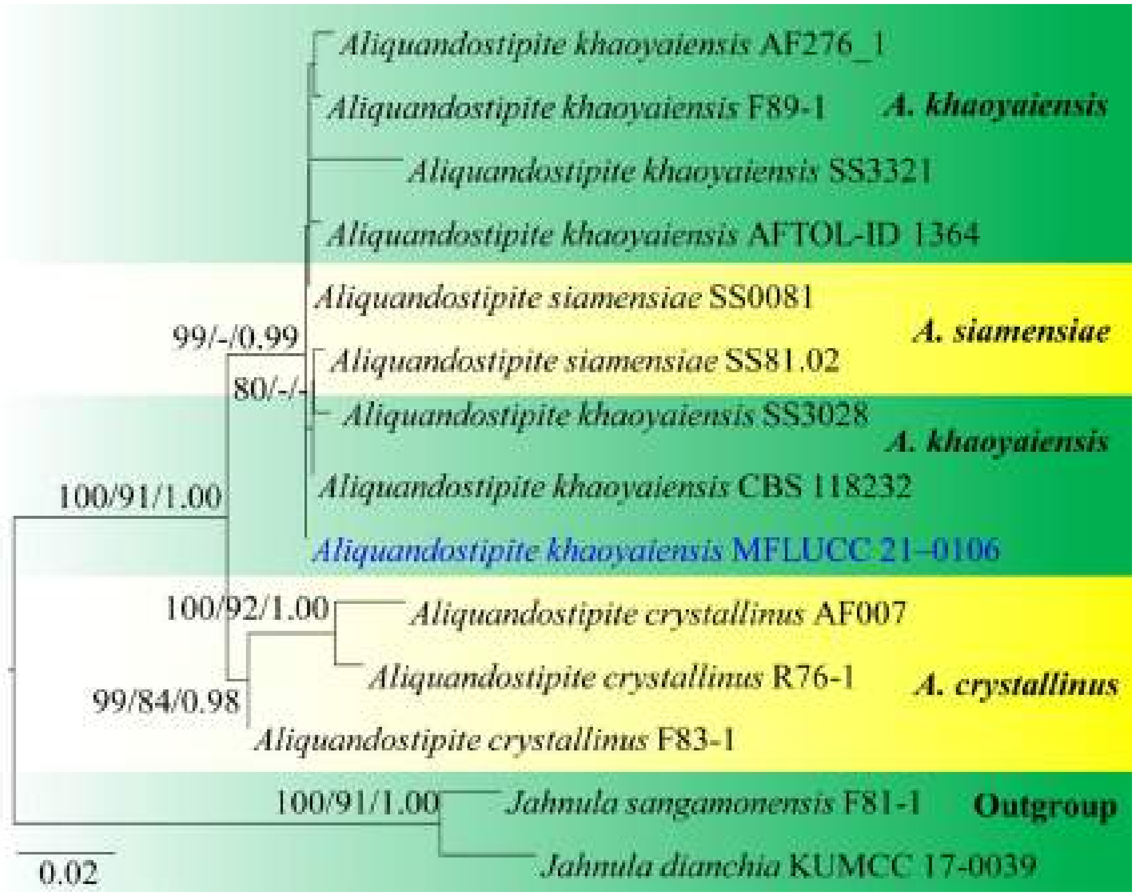


Fig. 10 Phylogram generated from maximum likelihood analysis based on combined LSU, SSU, ITS, TEF1-α and RPB2 sequence data representing the species of *Aliquandostipite*. Related sequences are taken from Suetrong et al. (2011). *Jahnula sangamonensis* (F81-1) and *J. dianchia* (KUMCC 17-0039) in *Aliquandostipitaceae* (*Jahnulales*) were used as the outgroup taxa. Fourteen taxa are included in the combined analyses which comprised 4306 characters (1006 characters for LSU, 1005 characters for SSU, 587 characters for ITS, 726 characters for TEF1-α, 982 characters for RPB2) after alignment. The best scoring RAxML tree with a final likelihood value of − 8403.913612 is presented. The matrix had 301 distinct alignment patterns, with 51.74% of undetermined characters or gaps. The MP analysis resulted a single most parsimonious tree (TL = 442, CI = 0.986, RI = 0.977, RC = 0.964, HI = 0.014). Bootstrap support values for ML and MP equal to or greater than 75% and BYPP equal to or greater than 0.95 are given above the nodes. The newly generated sequence is in blue

a fourth record of *A. khaoyaiensis* from submerged wood in Thailand (Fig. 9).

Minutisphaerales Raja, Oberlies, Shearer & A.N. Mill.

Notes: *Minutisphaerales* comprises a single family *Minutisphaeraceae* to accommodate the monotypic genus *Minutisphaera* (Raja et al. 2015). We follow the latest treatment and update accounts of *Minutisphaerales* in Bao et al. (2019a).

Minutisphaeraceae Raja, Oberlies, Shearer & A.N. Mill.

Notes: *Minutisphaeraceae* comprises single genus *Minutisphaera* and its members commonly found as saprobic on submerged wood in freshwater habitat (Ferrer et al. 2011; Raja et al. 2015; Bao et al. 2019a). The family is characterized by globose to subglobose, erumpent to superficial, dark pigmented ascomata, obpyriform to obclavate asci, oblong, clavate to broadly fusiform, septate, hyaline to pale brown ascospores, with or without a gelatinous sheath and filamentous appendages (Raja et al. 2015).

Minutisphaera Shearer, A.N. Mill. & A. Ferrer

Notes: A monotypic genus *Minutisphaera* was introduced by Ferrer et al. (2011) and is typified by *Minutisphaera fimbriatispora*. Only five species are presently listed in this genus (Bao et al. 2019a; Index Fungorum 2021). *Minutisphaera thailandensis* is introduced as the sixth species in this genus.

Minutisphaera thailandensis R.J. Xu, Boonmee & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF558547; *Facesoffungi number*: FoF 09943; Fig. 11

Etymology: The specific epithet "*thailandensis*" referring to the country from which the species was collected.

Holotype: MFLU 21-0094

Saprobic on submerged wood, submerged in freshwater habitats. **Sexual morph** *Ascomata* 80–108 μm high, 95–101 μm diam., immersed to erumpent, solitary, scattered, globose to subglobose, dark brown to black, ostiolate. *Peridium* thin, soft, composed of brown to dark brown cells of *textura angularis*. *Hamathecium* pseudoparaphyses not seen. *Asci* 40–56 × 15–27 μm ($\overline{x}$ = 47 × 21 μm, n = 10), 8-spored, bitunicate, obpyriform to broadly clavate, slightly curved, rounded at the apex, sessile to obtuse at the base. *Ascospores* 21–27 × 5–8 μm ($\overline{x}$ = 24 × 7 μm, n = 20), 2–3-seriate overlapping, ovoid to obovoid, apex wider, narrower towards the lower and rounded end, 1-septate, slightly above the middle, constricted at the septum, hyaline, surrounded by prominent mucilaginous sheath, sheath constricted the septum, with long filamentous appendages separating out of the sheath, numerous granular contents, smooth-walled. **Asexual morph** Undetermined.

Culture characteristics: Ascospores germinating on MEA within 12 h. Colonies on MEA, reaching 5 cm diam. after 4 weeks at room temperature, mycelium dense, brown to dark brown on surface, dark brown to black in reverse with entire edge.

Material examined: THAILAND, Chiang Rai Province, Mueang, Ban Nang Lae (99°52′52.93″ E 20°3′2.52″ N), on submerged wood in freshwater stream, 27 May 2020, R.J. Xu, MD-39 (MFLU 21-0094, **holotype**), ex-type living culture, MFLUCC 21-0072.

GenBank numbers: ITS = MZ493355, LSU = MZ493343, SSU = MZ493342.

Notes: Multigene phylogenetic analysis indicates our new taxon consistently clustered with *Minutisphaera aquaticum* with 100% MLBS, 1.00 BYPP support (Fig. 12). However, *M. thailandensis* (MFLUCC 21-0072) significantly differs from *M. aquaticum* in term of the ascospore features including having a septum located in the upper cell and possessing long filament appendages (Fig. 11). In addition, *M. thailandensis* shares similarly characterized ascomata and ascospores with some species, namely *M. fimbriatispora* and *M. parafimbriatispora* but they differ in shape and size (Ferrer et al. 2011; Raja et al. 2015). Furthermore, *M. thailandensis* differs from *M. aspera* and *M. japonica* in both shape and pigmentation of the ascospores (Raja et al. 2013, 2015). Therefore, *Minutisphaera thailandensis* is introduced as a new species based on its distinct morphology and phylogenetic evidence.

Pleosporales Luttr. ex M.E. Barr

Notes: We follow the latest updated account of *Pleosporales* included in Hongsanan et al. (2020a).

Acrocalymmaceae Crous & Trakun

Notes: *Acrocalymmaceae* was introduced by Trakunyingcharoen et al. (2014) to accommodate the monotypic genus *Acrocalymma* (Wijayawardene et al. 2017, 2020; Hongsanan et al. 2020a), and establishment was supported by additional evidence using divergence estimates (Liu et al. 2017; Hongsanan et al. 2020a). We follow the latest updated account of *Acrocalymmaceae* included in Mortimer et al. (2021).

Acrocalymma Alcorn & J.A.G. Irwin

Notes: Alcorn and Irwin (1987) introduced *Acrocalymma* with *A. medicaginis* as the type species. *Acrocalymma medicaginis*, a root pathogen, was linked by Shoemaker et al. (1991) as the asexual morph of *Massarina walkeri*, but based on the study of Trakunyingcharoen et al. (2014), the two species are phylogenetically distinct, resulting in the new combination, *A. walkeri*. In addition, *Rhizopycnis vaga*, the type species of *Rhizopycnis,* clustered in *Acrocalymma* sensu stricto and hence, *Rhizopycnis* has been treated as a

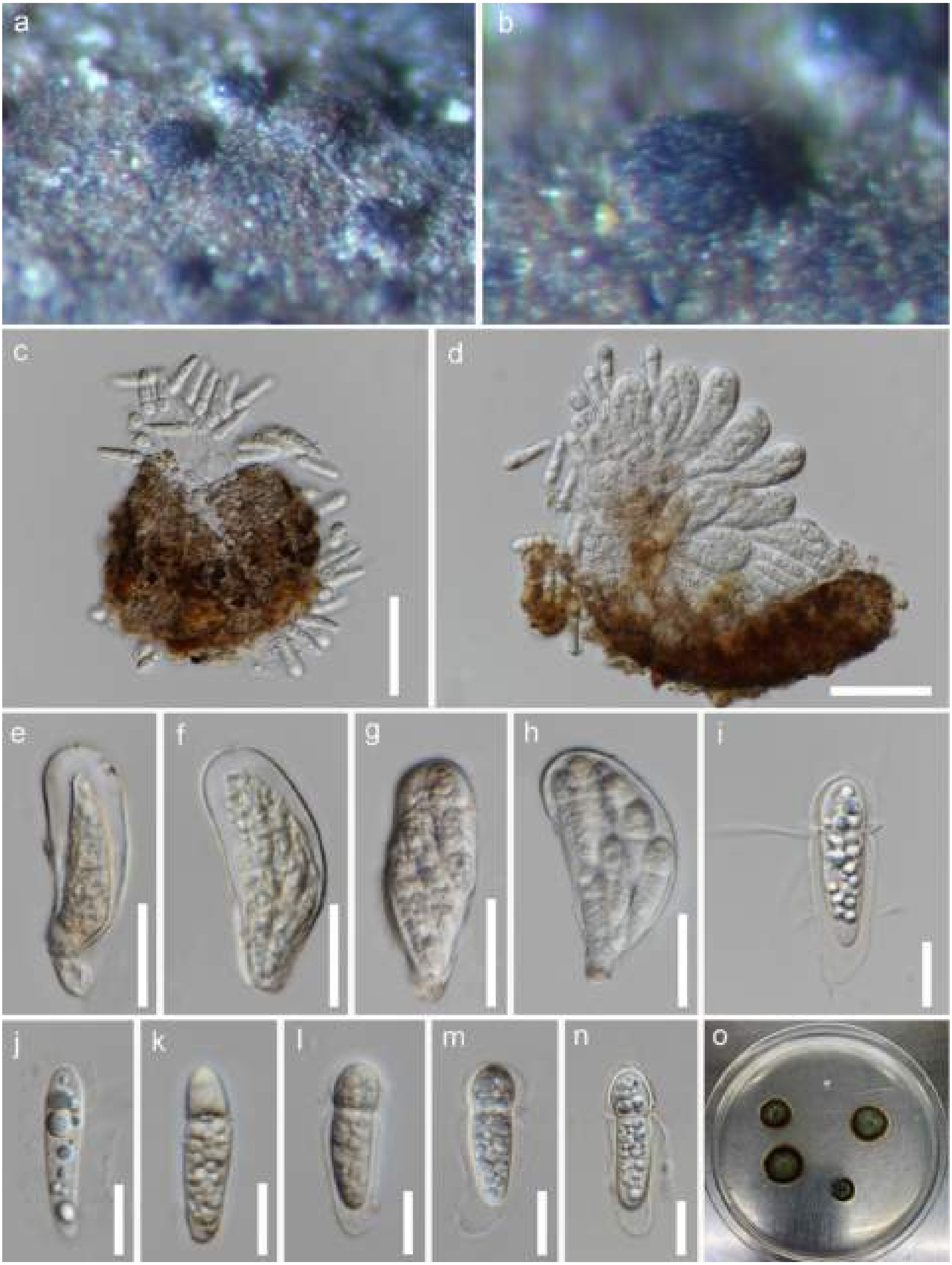


Fig. 11 ***Minutisphaera thailandensis*** (MFLU 21-0094, **holotype**). **a**, **b** Ascomata on submerged wood. **c, d** Squash of ascoma. **e**–**h** Asci. **i**–**n** Ascospores. **o** Culture on PDA. Scale bars: **c**, **d** = 50 µm, **e**–**h** = 20 µm, **i**–**n** = 10 µm

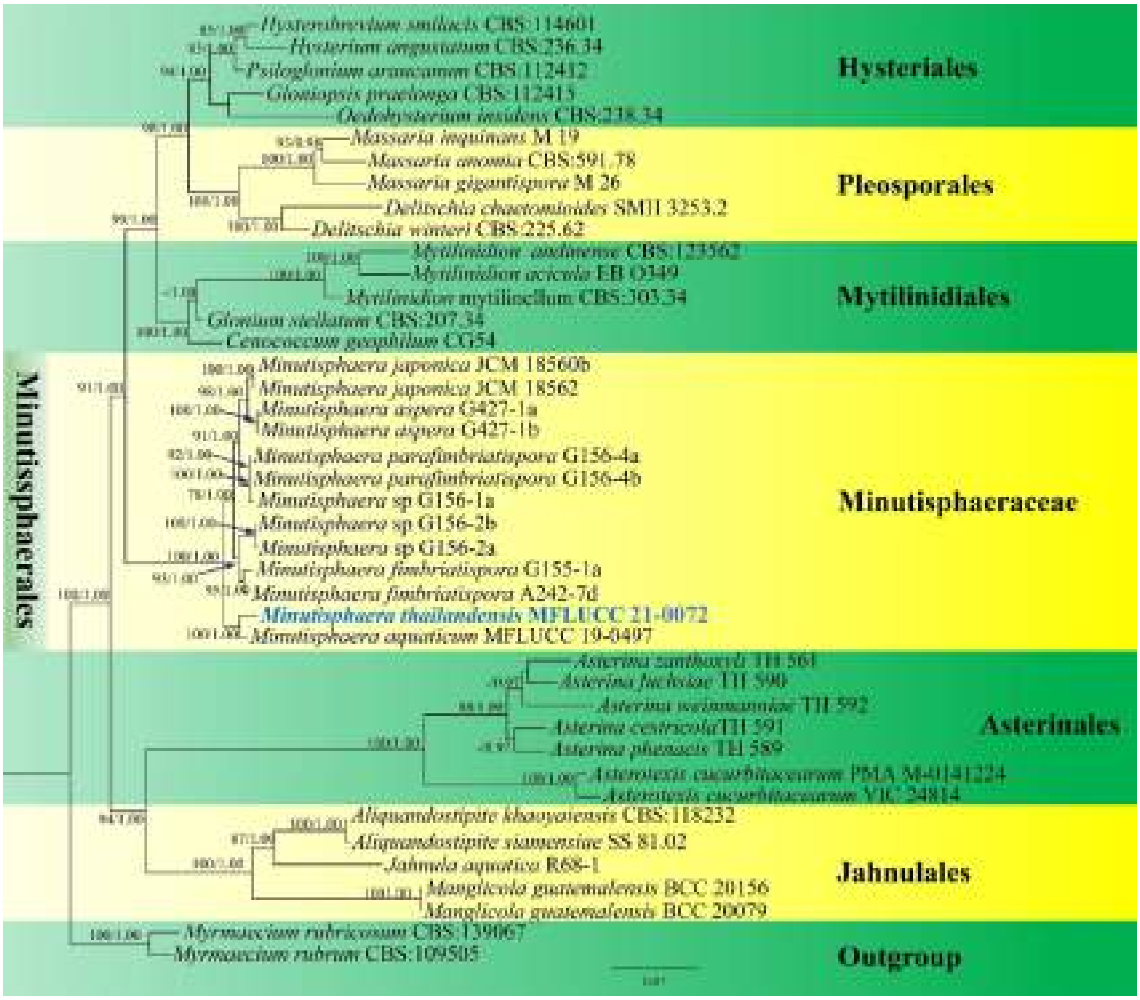


Fig. 12 Phylogram generated from maximum likelihood analysis based on combined LSU, SSU and ITS sequence data representing the species of *Minutisphaera* in *Minutisphaeraceae*. *Myrmaecium rubricosum* CBS139067 and *M. rubrum* CBS109505 are selected as the outgroup taxa. The best RAxML tree with a final likelihood value of − 17637.597976 is presented. RAxML analysis yielded 1292 distinct alignment patterns and 38.19% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.254974, C = 0.223826, G = 0.282377, T = 0.238823, with substitution rates AC = 1.255015, AG = 2.734543, AT = 1.149276, CG = 1.117855, CT = 6.544858, GT = 1.000000; gamma distribution shape parameter alpha = 0.206169. Bootstrap support values for maximum likelihood (MLBS, left) equal to or greater than 70% is given above the nodes. Bayesian posterior probabilities (BYPP, right) equal to or greater than 0.95 are given above the nodes. Ex-type strains are in bold and newly generated sequence is in blue

synonym of *Acrocalymma* (Trakunyingcharoen et al. 2014). Eleven species are currently known in this genus (Index Fungorum 2021). The most recent treatment for *Acrocalymma* is in Mortimer et al. (2021). In this study, *Acrocalymma fici* is reported as a new habitat and geographical record from Thailand.

Acrocalymma fici Crous & Trakun., IMA Fungus 5(2): 405 (2014)

Index Fungorum number: IF810838; *Facesoffungi number*: FoF 09155; Fig. 13

Saprobic on submerged decaying wood. **Sexual morph** Undetermined. **Asexual morph** *Conidiomata* 80–200 × 40–120 µm ($\bar{x}$ = 110 × 85 µm, n = 10), pycnidial, globose to subglobose, erumpent, separate but aggregated in clusters, sub-hyaline with dark brown to black region around ostiole. *Pycnidial wall* 41–55 µm diam., 3–6 layers of hyaline to subhyaline cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 4–15 × 2–5 µm ($\bar{x}$ = 7 × 3 µm, n = 20), ampulliform to doliiform, hyaline, smooth, 5–12 × 3–5 µm, with inconspicuous percurrent proliferation visible at apex. *Conidia* 12–15 × 2–3 µm ($\bar{x}$ = 13 × 3 µm), hyaline, smooth, guttulate, cylindrical, with subobtuse at the apex, acutely tapered at base to a small flattened central scar, 0–1-septate, not constricted at septum, with flaring mucoid apical appendage, 2–5 µm wide, visible in water mounts.

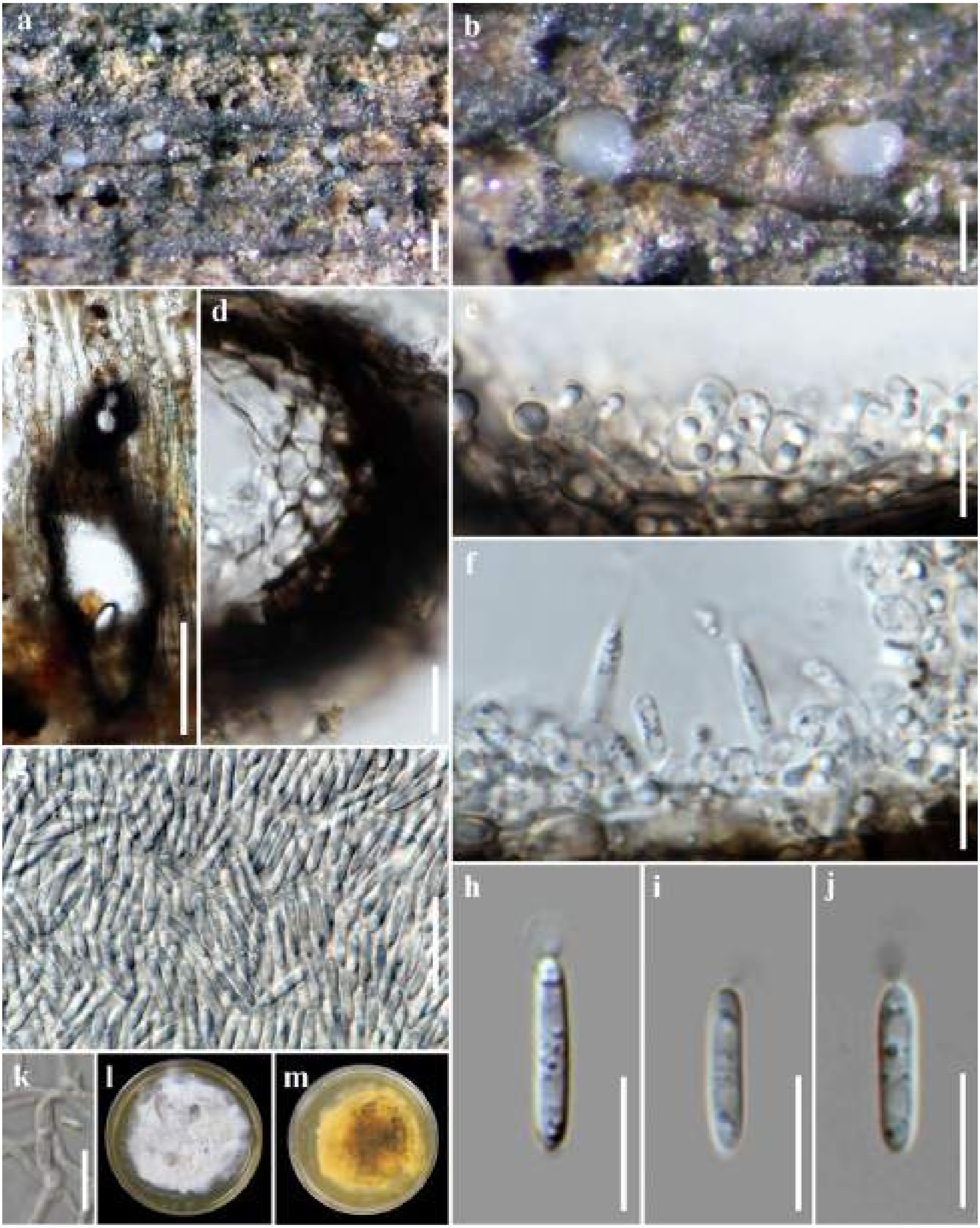


Fig. 13 ***Acrocalymma fici*** (MFLU 21-0124, **new habitat and geographical record**). **a**, **b** Appearance of erumpent fruiting bodies on host substrate. **c** Section through conidioma. **d** Section through pycnidial wall. **e**, **f** Immature and mature conidia attached to conidiogenous cells. **g–j** Conidium. **k** Germinated conidium **l**, **m** Culture on MEA (upper and lower view). Scale bars: **a** = 500 μm, **b** = 200 μm, **c** = 100 μm, **d**, **f**, **h–k** = 10 μm, **e** = 5 μm, **g** = 20 μm

Culture characters: Conidia germinated on MEA within 24 h. Colonies on MEA reaching 4–5 cm after 4 weeks at room temperature, colonies irregular, medium dense, flat with smooth and filiform margins; white to smoke-grey in top view, reverse yellowish orange in center and yellowish in the outer region.

Material examined: THAILAND, Kanchanaburi Province, Sangkhla Buri, Liwo, on submerged decaying wood in a stream, 27 June 2019, N. Chaiwan, TFW5 (MFLU 21-0124, **new habitat and geographical record**), living culture, MFLUCC 21-0103.

GenBank numbers: ITS = MT864351, LSU = MT860429.

Notes: *Acrocalymma fici*, introduced by Trakunyingcharoen et al. (2014), was collected from *Ficus* sp. in a terrestrial habitat. Based on phylogenetic analysis of combined LSU and ITS sequence data, our isolate MFLUCC 21-0103 clustered with the ex-type strain of *Acrocalymma fici* (CBS 317.76) with 96% MLBS and 97% MPBS bootstrap support (Fig. 14). Our isolate resembles *A. fici* in shape and size of the conidiomata, conidiogenous cells and conidia (Fig. 13). Moreover, there are no base pair differences of the ITS nucleotides. However, *Acrocalymma fici* strain CBS 317.76 was isolated from a terrestrial host, *Ficus* sp., while our isolate was collected from a freshwater habitat. Therefore, we report this isolate as a new record of *A. fici* from a freshwater habitat.

Dictyosporiaceae Boonmee & K.D. Hyde

Notes: *Dictyosporiaceae* was established by Boonmee et al. (2016) with *Dictyosporium* as the type genus. Species in this family are cosmopolitan with a worldwide distribution. They are mainly found from decaying wood and plant litter in both terrestrial and aquatic habitats. Fifteen genera are currently listed in *Dictyosporiaceae* (Hongsanan et al. 2020a).

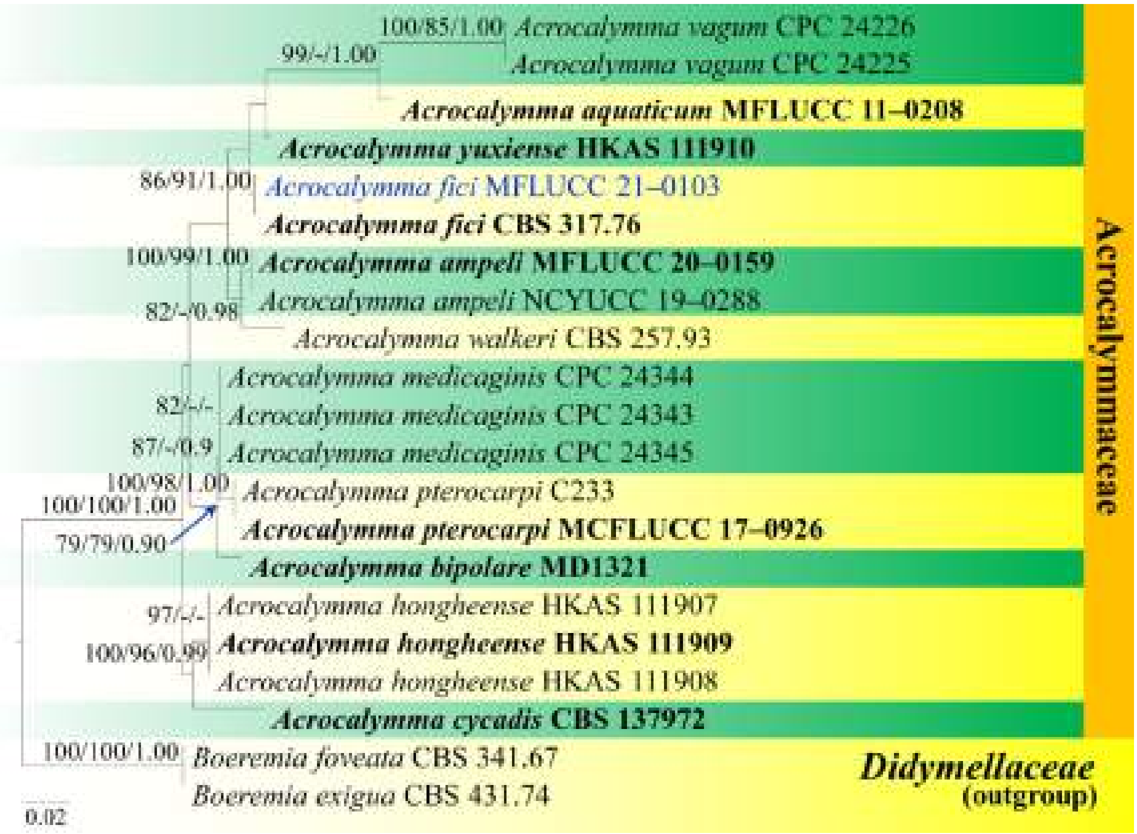


Fig. 14 Phylogenetic tree generated from maximum likelihood (ML) analysis based on combined LSU and ITS sequence data for the species from *Acrocalymmaceae*. *Boeremia exigua* (CBS 431.74) and *Boeremia foveata* (CBS 341.67) are used as the outgroup taxa. The dataset comprised 1997 characters after alignment including gaps (LSU = 1308 bp and ITS = 689 bp). The RAxML analysis of the combined dataset yielded a best scoring tree with a final ML optimization likelihood value of − 4737.006546. The matrix had 316 distinct alignment patterns, with 31.82% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.245559, C = 0.218996, G = 0.276710, T = 0.258736; substitution rates: AC = 1.502433, AG = 1.688434, AT = 1.833814, CG = 0.473416, CT = 4.863789, GT = 1.000000; gamma distribution shape parameter α = 0.020000. The MP analysis resulted a single most parsimonious tree (TL = 391, CI = 0.831, RI = 0.875, RC = 0.727, HI = 0.169). Bootstrap support values for MLBS and MPBS equal to or greater than 75% BYPP equal to or greater than 0.95 are given above the nodes. Ex-type strains are in bold and newly generated sequence is in blue

Dictyosporium Corda

Notes: *Dictyosporium* was established by Corda (1836) with a single species, *Di. elegans* Corda. Since then, many new species have been introduced to this genus (Boonmee et al. 2016; Tibpromma et al. 2018; Yang et al. 2018a; Hyde et al. 2020a). Currently, 83 species epithets are listed in Index Fungorum (2021) and only 60 species are accepted in Species Fungorum (2021). The genus is characterized by superficial, subglobose ascomata, bitunicate, cylindrical asci and hyaline, fusiform uniseptate ascospores with or without a sheath; sporodochial colonies, micronematous to macronematous conidiophores and cheiroid, digitate complanate conidia with several parallel rows of cells (Boonmee et al. 2016; Yang et al. 2018a). Species in *Dictyosporium* have been recorded worldwide from dead wood, decaying leaves and plant litter in terrestrial and aquatic habitats (Goh et al.1999; Ho et al. 2002; Pinnoi et al. 2006; Pinruan et al. 2007; Boonmee et al. 2016; Yang et al. 2018a; Hyde et al. 2020a).

Dictyosporium pandanicola Tibpromma & K.D. Hyde, in Tibpromma et al., Fungal Diversity: 93: 20 (2018)

Index Fungorum number: IF554481; *Facesoffungi number*: FoF 04491; Fig. 15

Saprobic on submerged decaying wood. **Sexual morph** Undetermined. **Asexual morph** *Colonies*, punctiform, sporodochial, scattered, dark brown to black, glistening. *Mycelium* mostly immersed, composed of smooth, septate, branched, hyaline to pale brown hyphae. *Conidiomata* sporodochia on the natural substrate in small groups, dark brown. *Conidiophores* 10–20 × 2.5–3 µm, micronematous, mononematous, cylindrical, subhyaline to pale brown, septate, smooth, sometimes reduced to conidiogenous cell. *Conidiogenous cells* holoblastic, integrated, indeterminate, subhyaline to pale brown. *Conidia* 40–48 × 20–25 µm ($\overline{x}$ = 44 × 23 µm, n = 35), solitary, oval to ellipsoid, cheiroid, smooth-walled, consisting of 5–6 arms, 9–13-euseptate in each arm, with a basal connecting cell, yellow–brown to brown with age, sometimes with a hyaline, globose, apical appendage.

Culture characters: Conidia germinated on PDA within 24 h. Colonies on PDA reaching 2.5–3.5 cm diam., after 4 weeks at room temperature, colonies irregular, medium dense, white to yellow in top view. In reverse, yellow in the middle and white at the margin.

Material examined: THAILAND, Surat Thani Province, Sai Daeng, on decaying wood submerged in a small river, 2 October 2017, Z.L. Luo, B77 (MFLU 20-0425, **new record**), living culture, MFLUCC 18-0331.

GenBank numbers: ITS = MZ490792, LSU = MZ490775, TEF1-α = MZ501208.

Notes: In the phylogenetic analysis (Fig. 16), the new isolate of *Dictyosporium pandanicola* (MFLUCC 18-0331) clusters with *Di. pandanicola* (MFLU 16-1886) with high bootstrap support (100% MLBS, 0.97 BYPP). In addition, there is only 1 base pair difference observed in the ITS region between these two strains. These two strains share some similar characters such as micronematous conidiophores, holoblastic conidiogenous cells and oval to ellipsoid, cheiroid, yellow–brown to brown conidia with 5–6 arms and overlapping conidia size (40–48 × 20–25 µm vs. 30–50 × 15–33 µm). However, conidia of MFLUCC 18-0331 sometimes have a hyaline, globose, apical appendage. While conidia of MFLU 16-1886 lack apical appendages. This difference in appendages may be because of the different habitats. MFLU 16-1886 was collected form a terrestrial habitat on *Pandanus*, while MFLUCC 18-0331 was collected from a freshwater habitat on submerged wood. Based on both morphology and molecular data, we consider the isolate MFLUCC 18-0331 and *Di. pandanicola* to be conspecific.

Tibpromma et al. (2018) discussed *Dictyosporium pandanicola* as being phylogenetically close to *Di. strelitziae*. The ITS blast result in NCBI GenBank showed that *Di. pandanicola* (MFLU 16-1886) is 99% similar to *Di. strelitziae* (CBS 123359). We also obtained the same result and found that there are only 3 bp of difference in the ITS region between *Di. pandanicola* and *Di. strelitziae*. Tibpromma et al. (2018) distinguished *Di. pandanicola* and *Di. strelitziae* by the apical appendage and number of arms and cells. However, in this study, we found that the conidia of the new isolate of *Di. pandanicola* (MFLUCC 18-0331) also has apical appendages (Fig. 15). Thus, future morpho-molecular studies are needed to confirm the relationship between *Di. pandanicola* and *Di. strelitziae*.

Camarosporidiellaceae Wanas., Wijayaw., Crous & K.D. Hyde

Notes: Wanasinghe et al. (2017) introduced *Camarosporidiellaceae* to accommodate *Camarosporidiella* which are saprobic and sometimes can be endophytic or pathogenic and potentially opportunistic pathogens on leaves and woody materials. We follow the latest treatment of this family in Hongsanan et al. (2020a). In this study, we introduce a geographical record of *Camarosporidiella laburni* from Uzbekistan.

Camarosporidiella Wanas., Wijayaw., K.D. Hyde

Notes: *Camarosporidiella* is similar to other camarosporium-like genera in that distinguishing species and species identification based solely on morphology and plant host association can be problematic (Wanasinghe et al. 2017). Wanasinghe et al. (2017) recommended to use a combination of LSU, SSU, ITS and TEF1-α loci for investigating phylogenetic relationships of taxa in this genus. Currently there are 23 *Camarosporidiella* species accepted in Species Fungorum (2021).

Fig. 15 ***Dictyosporium pandanicola*** (MFLU 20-0425, **new record**). **a**–**c** Colonies on wood. **d**–**h** Conidiophores, conidiogenous cells and conidia. **i**–**j**, **l**–**n** Conidia. **k** Conidiophores. **o** Germinated conidia. **p** Mycelium. **q**, **r** Culture on MEA (upper and lower view). Scale bars: **d**–**i**, **k**–**p** = 20 μm, **k** = 10 μm

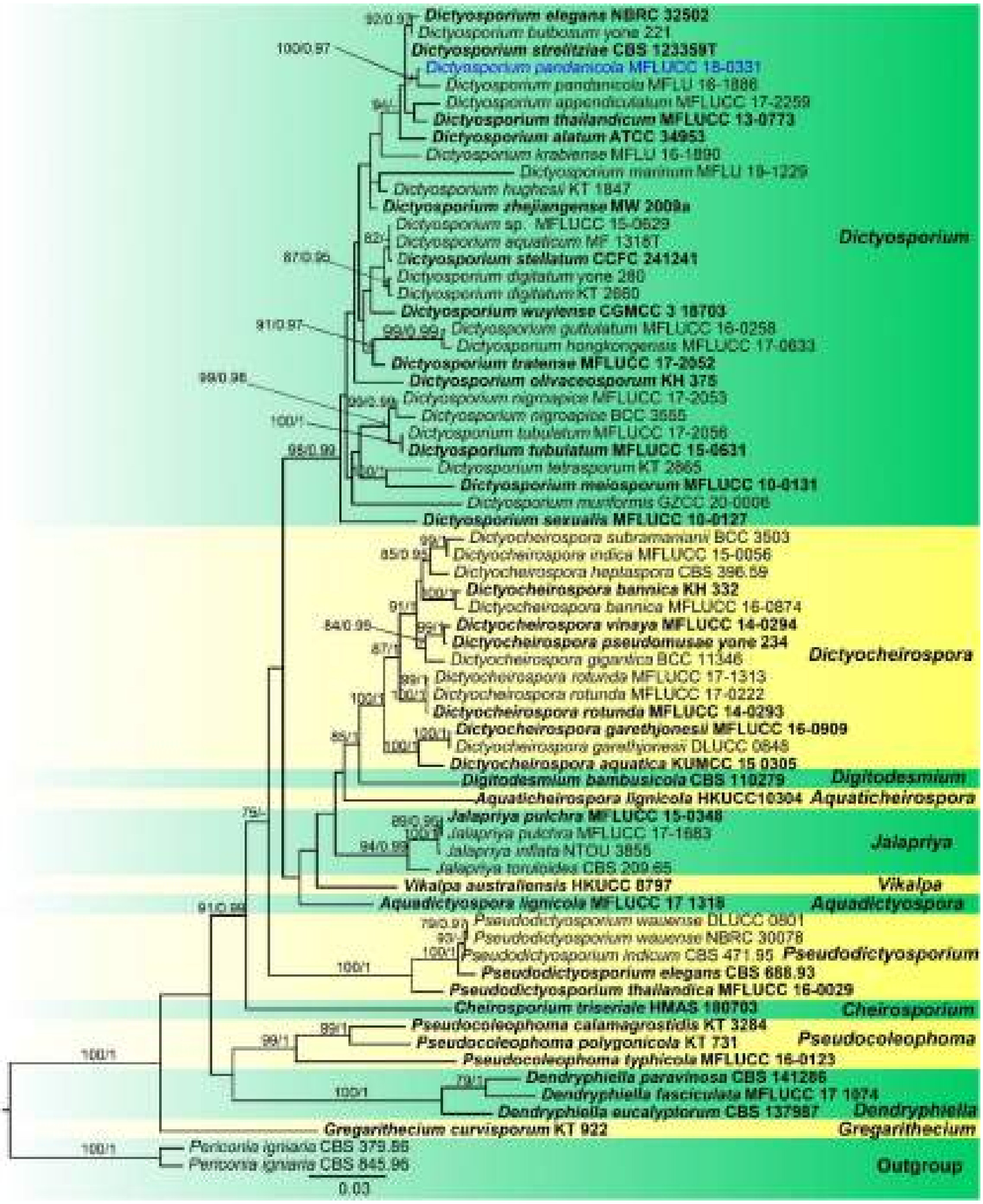


Fig. 16 Phylogenetic tree generated from maximum likelihood (ML) analysis based on combined LSU, ITS and TEF1-α sequence data for the species from *Melanommataceae*. *Periconia igniaria* (CBS 379.86 and CBS 845.96) are used as the outgroup taxa. The dataset comprised 2694 characters after alignment including gaps (LSU = 1245 bp; ITS = 537 bp, TEF1-α = 912 bp and RPB2 = 1006 bp). The RAxML analysis of the combined dataset yielded a best scoring tree with a final ML optimization likelihood value of − 14912.416315. The matrix had 871 distinct alignment patterns, with 36.52% undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.239281, C = 0.249660, G = 0.270492, T = 0.240568; substitution rates AC = 1.684833, AG = 3.636355, AT = 2.551537, CG = 0.785971, CT = 9.189334, GT = 1.000000; gamma distribution shape parameter α = 0.180969. Support values for maximum likelihood (MLBS) above than 75% and Bayesian posterior probabilities (BYPP) greater than 0.95 are given at the nodes. Ex-type strains are in bold and newly generated sequence is in blue

Camarosporidiella laburni (Pers.) Wanas., Bulgakov, Camporesi & K.D. Hyde, Stud. Mycol. 87: 233 (2017)

Index Fungorum number: IF821952; *Facesoffungi number*: FoF 03540; Fig. 17

≡ *Sphaeria laburni* Pers., Observ. mycol. (Lipsiae) 1: 68 (1796)

Saprobic on woody branches. **Sexual morph** *Ascomata* 400–550 µm high, 450–550 µm diam. ($\overline{x}$ = 485.5 × 488 µm, n = 10), black, superficial to semi-immersed, confluent, gregarious, sometimes scattered beneath the host periderm or on decorticated wood, fully or partly erumpent, globose, uniloculate, ostiolate. *Ostiole* central, short, slightly sunken, minute and inconspicuous at the surface, smooth, ostiolar canal filled with hyaline cells. *Peridium* 30–50 µm wide at the base, 60–90 µm wide in sides, thick, comprising two layers, outermost layer heavily pigmented, thin-walled, comprising blackish to dark brown loosely packed cells of *textura angularis*, inner layer composed of pale brown to hyaline, cells towards the inside lighter, flattened, thick-walled cells of *textura angularis*. *Hamathecium* comprising numerous, 2–3 µm (n = 30) wide, filamentous, branched septate, cellular pseudoparaphyses. *Asci* 150–220 × 12–16 µm ($\overline{x}$ = 178 × 13 µm, n = 30), 8-spored, bitunicate, fissitunicate, cylindrical, short-pedicellate, apex rounded with a minute ocular chamber. *Ascospores* 24–30 × 10–13 µm ($\overline{x}$ = 29 × 11 µm, n = 30), overlapping uni-seriate, muriform, mostly ellipsoidal, 6–7-transversely septate, with 1–2 longitudinal septa, deeply constricted at the middle septum, slightly constricted at remaining septa, initially hyaline, becoming pale brown at maturity, asymmetrical, slightly paler, conical and narrowly rounded at the end cells, lacking a mucilaginous sheath.

Material examined: UZBEKISTAN, Jizzakh Province, Zaamin District, Zaamin National Nature Park, river of Uriklisoy, Turkestan range of Pamir-Alay Mountains, on dead stem of *Astragalus* sp. (*Fabaceae*), 12 July 2019, Y. Gafforov YG-Z48-2 (TASM 6162, **new record**); *ibid*., on dead stems of unidentified plant, 14 July 2019, Y. Gafforov and A. Abdurazakov, YG-Z59-2 (TASM 6163).

GenBank numbers: ITS = MZ493295, MZ493296, LSU = MZ493309, MZ493310, SSU: MZ493281, MZ493282, TEF1-α = MZ508404, MZ508405.

Notes: Wanasinghe et al. (2017) introduced a combination species *Camarosporidiella laburni* from Italy based on the morphological features of its holomorph and multi-locus phylogeny. The species was previously established as *Cucurbitaria laburni* by De Notaris (1862) and detailed morphological studies were carried out by Green (1931) and Mirza (1968). This species was noted as clearly distinct from the remaining described species in *Cucurbitaria* (Wanasinghe et al. 2017). Multi-locus phylogeny demonstrated the species within *Camarosporidiellaceae*, distant from *Cucurbitaria* in *Cucurbitariaceae* (Wanasinghe et al. 2017). *Camarosporidiella laburni* is widely distributed in Europe and North America and host preferences are currently restricted to the family *Fabaceae*. Table 1 shows the updates on host species and geographic distribution of *Camarosporidiella laburni* and it indicates that this fungus is specific to *Fabaceae* hosts.

In this study, our new strains (TASM 6162 and TASM 6163) clustered with *Camarosporidiella laburni* strains MFLUCC 14-0885 and MFLUCC 14-0919 with 60% MLBS support (Fig. 18). However, a nucleotide base comparison of ITS and TEF1-α demonstrated that our new strains are identical to *Camarosporidiella laburni* strains MFLUCC 14-0885 and MFLUCC 14-0919 (0/542 bp) of ITS, and 1/926 bp (0.1%) and 2/926 bp (0.1%) of TEF1-α), respectively. Therefore, we identified our new collections as *C. laburni* and the species is reported from *Astragalus* sp. in Uzbekistan for the first time (Fig. 17).

Cryptocoryneaceae A. Hashim. & Kaz. Tanaka

Notes: Hashimoto et al. (2017) introduced *Cryptocoryneaceae* to accommodate the single genus *Cryptocoryneum* Fuckel. *Cryptocoryneaceae* is phylogenetically closely affiliated with *Lophiotremataceae*. We follow the latest treatment of this family in Hashimoto et al. (2017) and Hongsanan et al. (2020a). An updated phylogenetic tree for *Cryptocoryneaceae* is presented in Fig. 20. In this study, we introduce a new saprobic species *Cryptocoryneum rosae*, which collected on *Rosa* sp. in Yunnan Province, China.

Cryptocoryneum Fuckel

Notes: *Cryptocoryneum* was introduced based on *C. fasciculatum* (Fuckel 1865), however, its taxonomic status was contested by later studies (Hashimoto et al. 2016). Hashimoto et al. (2016) examined holotype specimens of *C. fasciculatum*, *C. hysterioides*, and *Torula uniformis*, and concluded that these species are conspecific. Thus, Hashimoto et al. (2016) designated *Cryptocoryneum hysterioides* as the type species. Most species of *Cryptocoryneum* have been reported on dead wood (Hashimoto et al. 2016), with some species rarely reported from leaf litter (Kirk 1983) or arthropod dung (Talbot 1952). This genus is only known from its asexual morph, and is characterized by stromatic sporodochia, monoblastic conidiogenous cells, cheiroid conidia and conidial arms developing downward from the cap cells (Schoknecht and Crane 1977; Hashimoto et al. 2016; Hongsanan et al. 2020a). Sixteen species are currently listed under *Cryptocoryneum* in Species Fungorum (2021) and only eight of these have been confirmed by DNA base evidence.

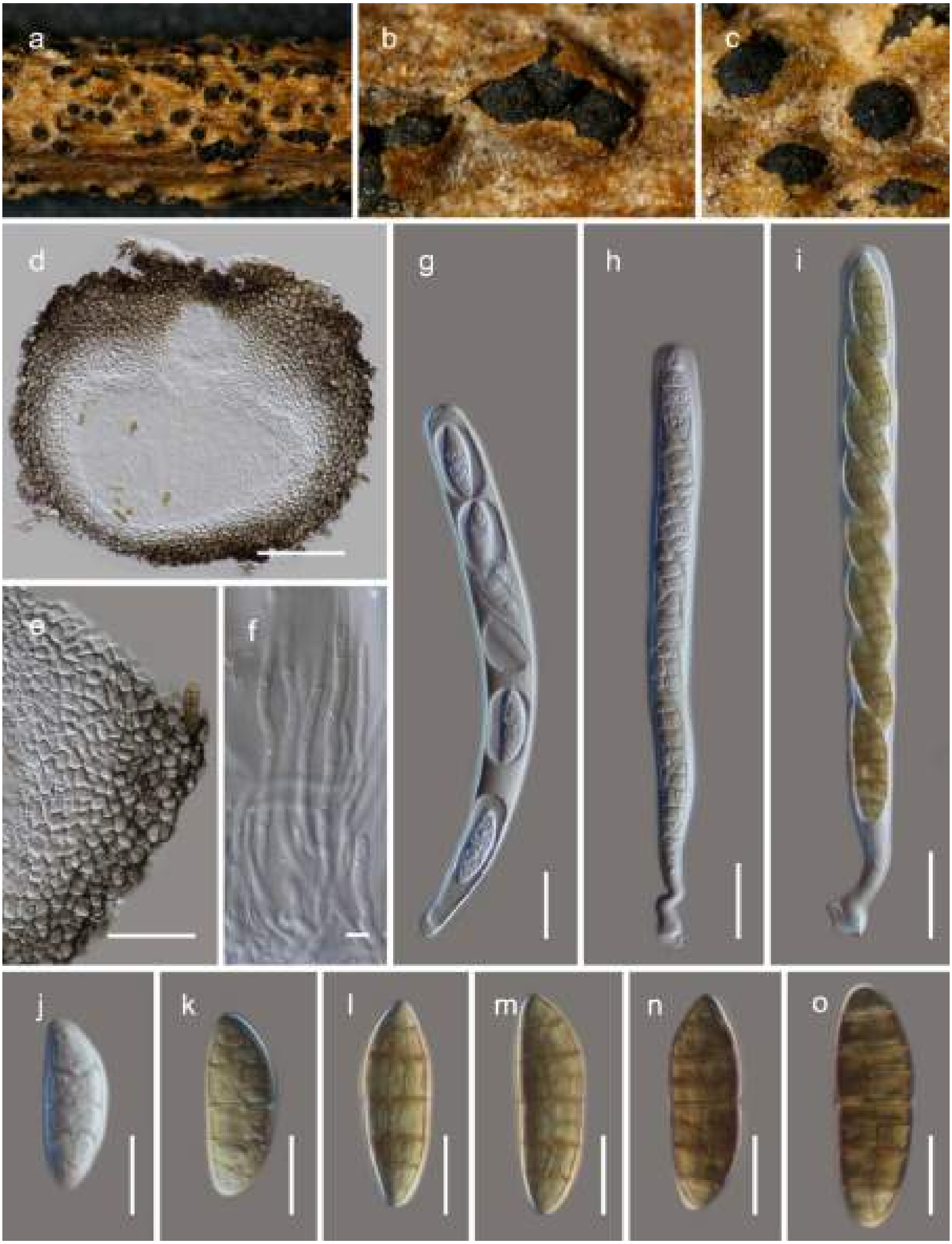


Fig. 17 ***Camarosporidiella laburni*** (TASM 6162, **new record**). **a–c** Appearance of ascomata on host surface. **d** Longitudinal section of an ascoma. **e** Section of the peridium. **f** Pseudoparaphyses. **g–i** Asci. **j–o** Ascospores. Scale bars: **d** = 100 µm, **e** = 50 µm, **f** = 5 µm, **g–i** = 20 µm, **j–o** = 10 µm

Table 1 Known hosts found for *Camarosporidiella laburni*

Host species	Host Family	Country	References
Astragalus sp.	*Fabaceae*	Uzbekistan	This study
Chamaecytisus sp.	*Fabaceae*	Ukraine	Dudka et al. (2004)
Cytisus alpinus	*Fabaceae*	Germany	Mirza (1968)
Cytisus laburnum	*Fabaceae*	England	Dennis (1978)
Cytisus radiatus	*Fabaceae*	Italy	Mirza (1968)
		Switzerland	Mirza (1968)
Laburnum alpinum	*Fabaceae*	Denmark	Munk (1957)
		Sweden	Eriksson (1992)
Laburnum anagyroides	*Fabaceae*	Denmark	Munk (1957)
		Germany	Spaulding (1961)
		Italy	Wanasinghe et al. (2017)
		Poland	Mulenko et al. (2008)
		Russia	Wanasinghe et al. (2017)
		Scotland	Foister (1961)
		Sweden	Eriksson (1992)
		Switzerland	Mirza (1968)
		Ukraine	Dudka et al. (2004)
		USA	Farr and Rossman (2021)
Laburnum sp.	*Fabaceae*	United Kingdom	Cannon et al. (1985)
		Russia	Wanasinghe et al. (2017)
Ononis tridentata	*Fabaceae*	Spain	Larios et al. (1988), Checa (2004)
Ononis tridentata var. *intermedia*	*Fabaceae*	Spain	Unamuno (1941)
Retama sphaerocarpa	*Fabaceae*	Spain	Checa (2004)

Cryptocoryneum rosae Wanas. & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF558583; *Facesoffungi number*: FoF 09944; Fig. 19

Etymology: The specific epithet "*rosae*" refers to the *Rosa*.

Holotype: KUN-HKAS 115780

Saprobic on dead wood of *Rosa* sp. **Sexual morph** Undetermined. **Asexual morph** *Sporodochia* 100–300(–450) µm diam., 20–55 µm high, pulvinate, often confluent, dark brown to black. *Conidiophores* arising from the stromatic cells, straight, simple, septate, hyaline to pale brown, smooth. *Conidiogenous cells* 5–7 × 4–6 µm ($\overline{x}$ = 5.8 × 4.8 µm, n = 20), monoblastic, cylindrical, terminal, determinate, hyaline to pale brown. *Conidia* 30–50 × 20–30 µm ($\overline{x}$ = 36 × 27.5 µm, n = 30), l/w 1.2–1.6 ($\overline{x}$ = 1.3, n = 30), solitary, acrogenous, branched, cheiroid, with dark brown cap cells firmly united together, basal cells brown, cuneiform, smooth, thin-walled, with 4–12 arms ($\overline{x}$ = 9 arms, n = 40). *Arms* 20–30(–37) × 3.5–6 µm ($\overline{x}$ = 26 × 4.5 µm, n = 40), cylindrical, brown, branched at the base, smooth, (5)8–12-septate ($\overline{x}$ = 9 µm, n = 40).

Culture characteristics: *Conidia* germinating on PDA within 24 h and germ tubes arising from both end cells. Colonies on PDA, slow growing, reaching 2 cm diam. after 4 weeks of at room temperature, initially white becoming dark brown at maturity, slightly effuse, radially with an undulate edge, reverse blackish brown.

Material examined: CHINA, Yunnan, Diqing Autonomous Prefecture, Shangri-La, Xiaozhongdianzhen, 27.425825° N, 99.845329° E, 3195 msl, on dead wood of *Rosa* sp. (*Rosaceae*), 30 August 2020, GC Ren, NX25-1 (KUN-HKAS 115780, **holotype**), living culture (KUMUCC 21-0033), *ibid*., NX25-2 (KUN-HKAS 115781), living culture (KUMUCC 21-0034).

GenBank numbers: ITS = MZ493300, MZ493301, LSU = MZ493314, MZ493315; SSU = MZ493286, MZ493287, RPB2 = MZ508418, MZ508419, TEF1-α = MZ508409, MZ508410.

Notes: *Cryptocoryneum rosae* was collected from Uzbekistan on *Rosa* and representing the first report of a *Cryptocoryneum* species from Central Asia and *Rosa* sp. (Farr and Rossman 2021). The new fungus resembling *Cryptocoryneum* species well in its pulvinate sporodochia, monoblastic conidiogenous cells and acrogenous, branched, cheiroid, brown conidia with multiple arms (Fig. 19). In the phylogenetic analyses of concatenated SSU, LSU, ITS, TEF1-α and RPB2, *C. rosae* is related to *C. akitaense* and *C. brevicondensatum* with 99% MLBS support (Fig. 20). Comparatively, *C. rosae* has shorter and narrower conidia ($\overline{x}$ = 36.3 × 27.5 µm) than *C. akitaense* ($\overline{x}$ = 49.1 × 38.6 µm) and *C. brevicondensatum* ($\overline{x}$ = 57.5 × 34.2 µm). In

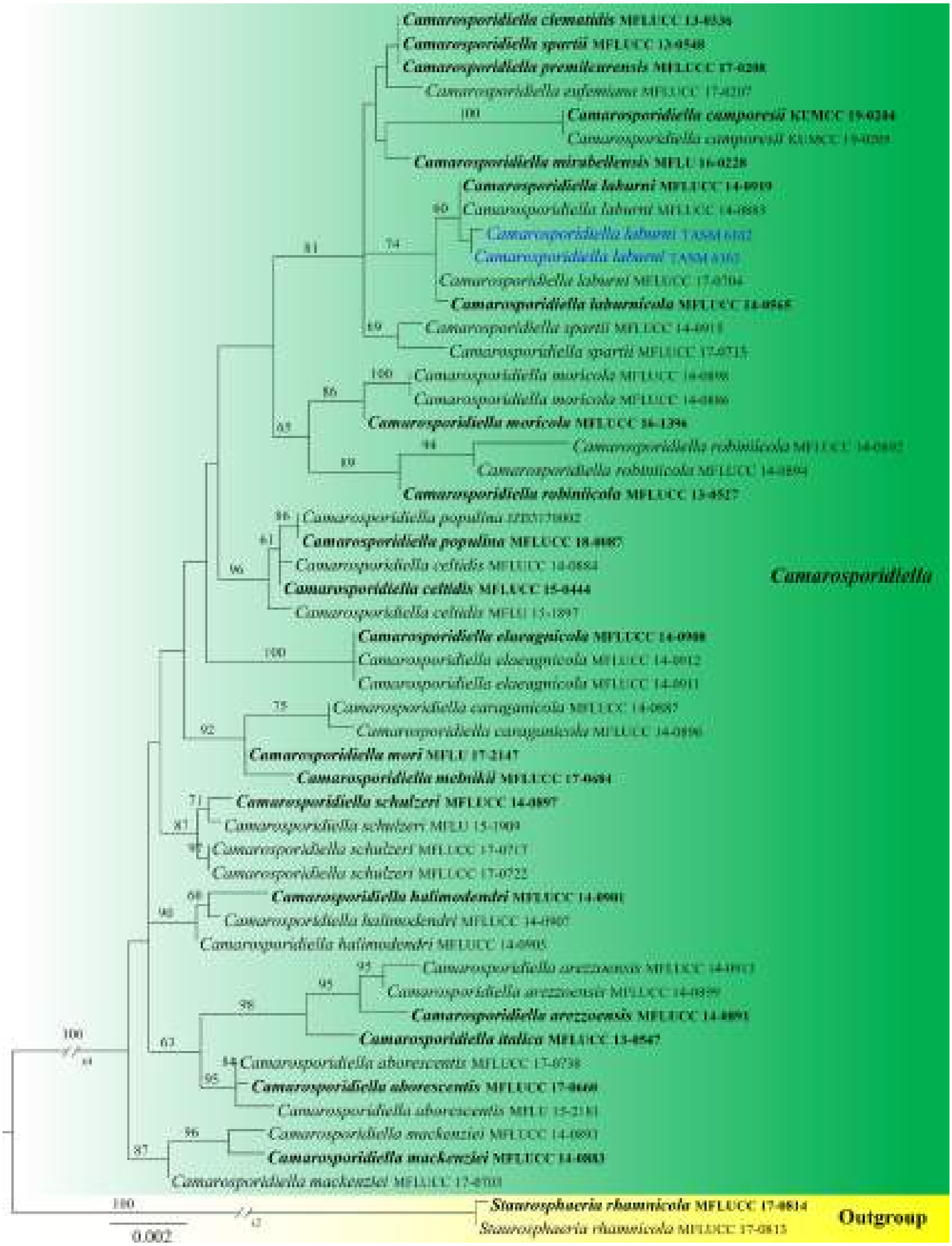


Fig. 18 Phylogram generated from the best scoring of the RAxML tree based on combined SSU, LSU, ITS, and TEF1-α sequence dataset to indicate *Camarosporidiella* and related species. Fifty-two strains are included in the combined analyses which comprise a total of 3309 characters. *Staurosphaeria rhamnicola* (MFLUCC 17-0813 and MFLUCC 17-0814) is selected as the outgroup taxon. The best RAxML tree with a final likelihood value of − 6629.415262 is presented. RAxML analysis yielded 226 distinct alignment patterns and 5.73% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.240666, C = 0.244239, G = 0.266553, T = 0.248542, with substitution rates AC = 1.544599, AG = 4.613774, AT = 3.7595, CG = 0.783994, CT = 9.045003, GT = 1.000000; gamma distribution shape parameter alpha = 0.997372. Bootstrap support values for maximum likelihood (MLBS, left) equal to or greater than 70% is given above the nodes. Ex-type strains are in bold and newly generated sequences are in blue

Fig. 19 ***Cryptocoryneum rosae*** (KUN-HKAS 115780, **holotype**). **a**–**c** Appearance of sporodochia on host surface. **d**–**g** Conidia. **h** Germinated conidium. **i**, **j** Culture on PDA from surface and reverse. Scale bars: **d** = 30 μm, **e**, **f**, **h** = 20 μm, **g** = 15 μm, **i**, **j** = 3 cm

Cryptocoryneum, there were not many base pair differences between species in the ITS region (except *C. condensatum*). We observed, on the other hand, that there were greater differences in the TEF1-α and RPB2 gene regions. Between *Cryptocoryneum rosae* and *C. akitaense*, TEF1-α had a base pair variation of 3.2% (29/898) and RPB2 had a variation of 4% (40/988). Between *Cryptocoryneum rosae* and *C. brevicondensatum* there were 2.9% (26/898) and 3.5% (34/988) base pair differences respectively in TEF1-α and RPB2 gene regions.

Didymellaceae Gruyter, Aveskamp & Verkley (= *Microsphaeropsidaceae* Qian Chen, L. Cai & Crous)

Notes: *Didymellaceae* has a wide host range and represents an important pathogenic, endophytic and saprobic species (Hyde et al. 2020b). Thirty-five genera are listed in this family (Hongsanan et al. 2020a).

Didymella Sacc. ex D. Sacc.

Notes: We follow the latest treatment and updated accounts of *Didymella* in Hongsanan et al. (2020a).

Didymella azollae E. Shams, F. Dehghanizadeh, A. Pordel & M. Javan-Nikkhah, ***sp. nov.***

Index Fungorum number: IF558550; *Facesoffungi number*: FoF 09945; Figs. 21, 22

Etymology: Name refers to the host plant species, *Azolla filiculoides*.

Holotype: IRAN 18020 F

Endophytic from leave of *Azolla filiculoides*. **Sexual morph** Undetermined. **Asexual morph** Coelomycetous. *Conidiomata* 118–275 μm high, 80–200 μm diam., pycnidial, brown, solitary or confluent, globose, subglobose to pyriform, often with a short neck, glabrous or with some hyphal outgrows. *Pycnidial wall* pseudoparechymatous,

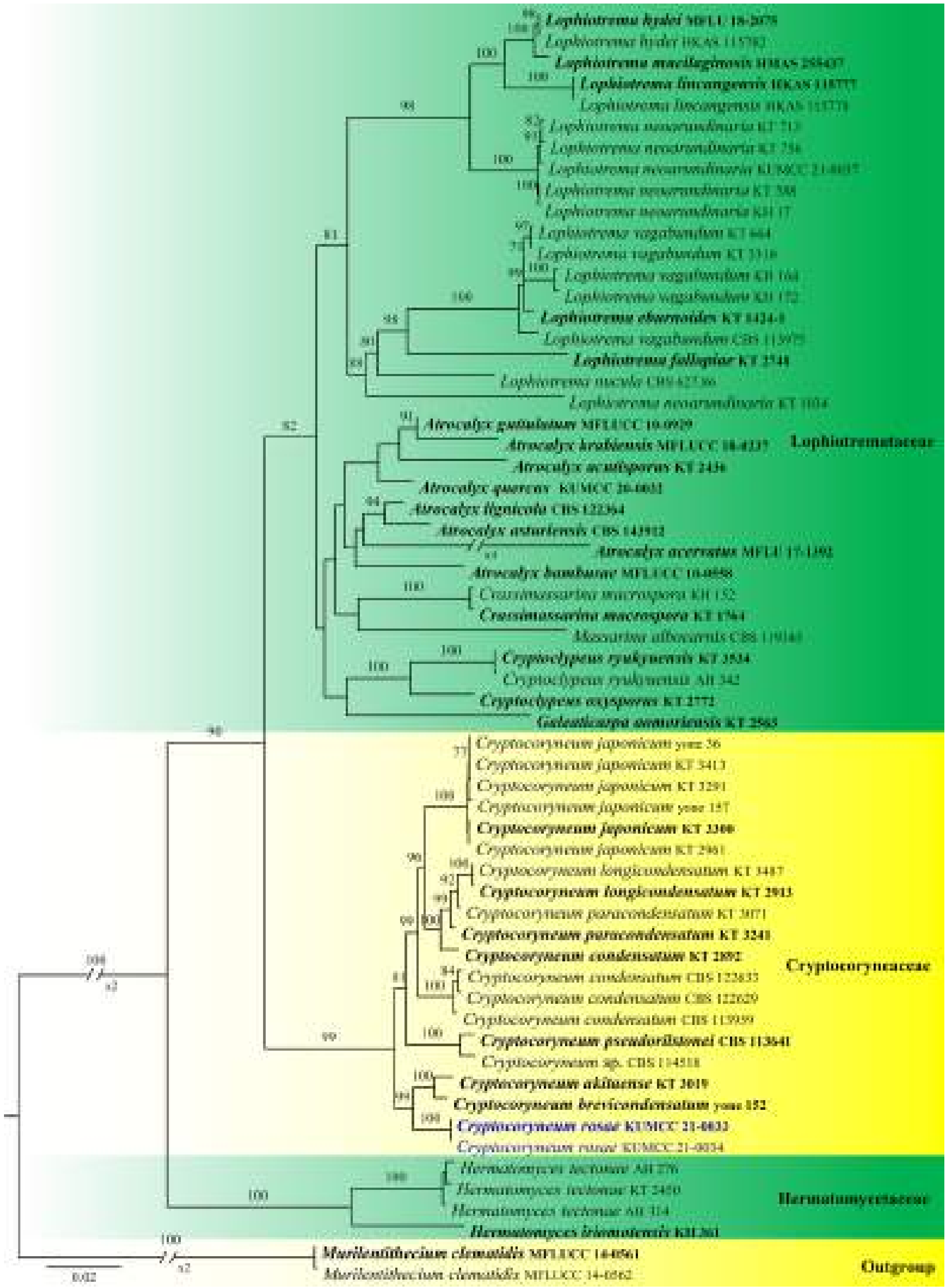


Fig. 20 Phylogram generated from the best scoring of the RAxML tree based on combined SSU, LSU, ITS, TEF1-α and RPB2 sequence dataset to indicate the new species in *Cryptocoryneaceae*. Sixty strains are included in the combined analyses which comprise a total of 4357 characters. *Murilentithecium clematidis* (MFLUCC 14-0561 and MFLUCC 14-0562) is selected as the outgroup taxon. The best RAxML tree with a final likelihood value of − 24211.323363 is presented. RAxML analysis yielded 1272 distinct alignment patterns and 6.17% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.246394, C = 0.256619, G = 0.267068, T = 0.229919, with substitution rates AC = 1.576531, AG = 4.38051, AT = 1.49611, CG = 1.339907, CT = 10.502267, GT = 1.000000; gamma distribution shape parameter alpha = 0.450773. Bootstrap support values for maximum likelihood (MLBS, left) equal to or greater than 70% is given above the nodes. Ex-type strains are in bold and newly generated sequences are in blue

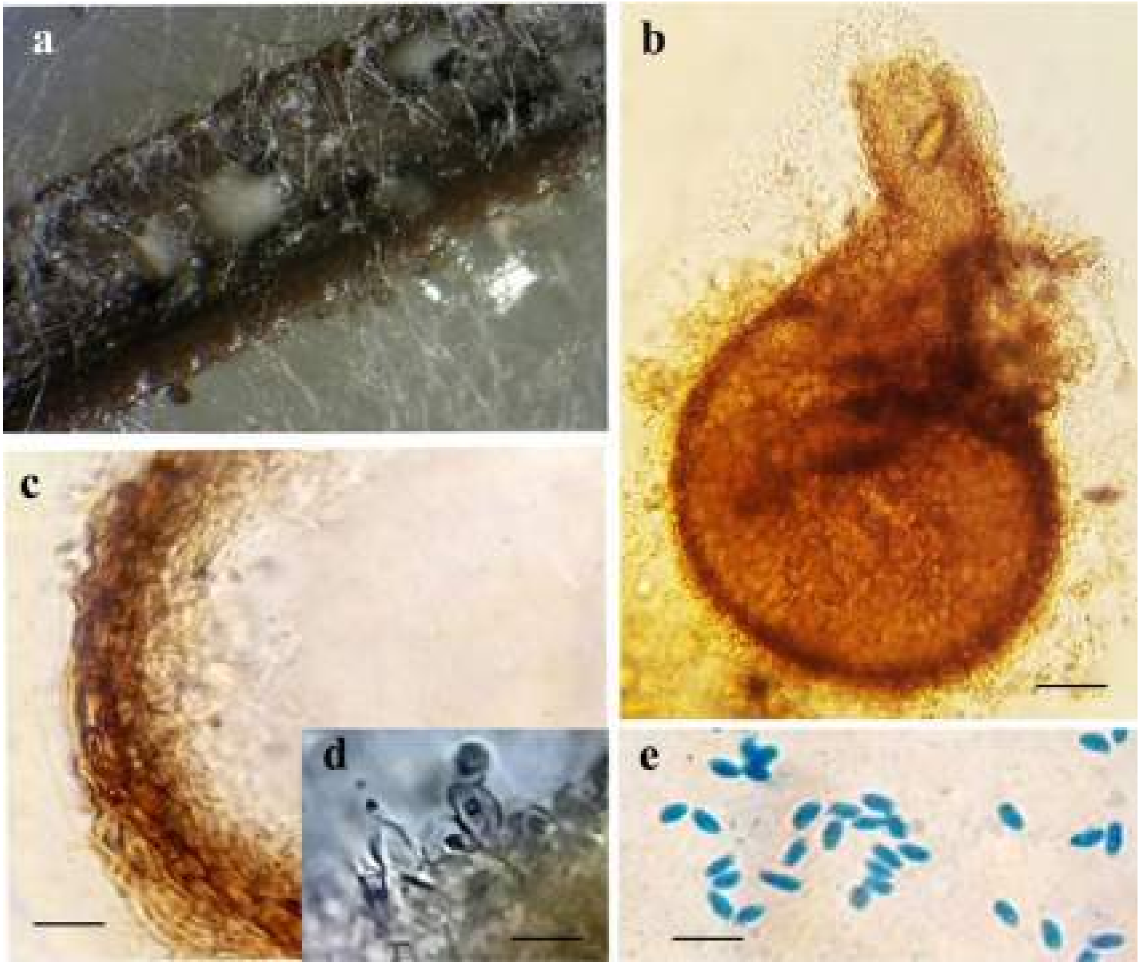


Fig. 21 ***Didymella azollae*** (IRAN 18020F, **holotype**). **a** Pycnidia on host. **b** Pycnidia. **c** Pycnidial wall. **d** Conidiogenous cells. **e** Conidia. Scale bars: **b**–**e** = 10 µm

comprising several layers of dark brown to lightly pigmented cells of *textura angularis*, outer layers 3–5 layers, 3–30 µm thick, pigmented, inner layers lightly pigmented. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* phialidic, hyaline, smooth, ampulliform to doliiform. *Conidia* 3–5 × 1.5–2 µm ($\bar{x}$ = 4.2 × 2 µm, n = 30), subglobose or ellipsoidal, hyaline, aseptate, smooth-walled.

Culture characteristics: Colonies on PDA, 40–48 mm diam. after 7 days, margin regular, densely covered by floccose aerial mycelia, greenish brown, reverse black (Fig. 22A). Colonies on OA, margin regular, floccose, aerial mycelia sparse, grayish brown, reverse black (Fig. 22B). Colonies on MEA, margin regular, floccose, buff, dense, reverse dark brown (Fig. 22C).

Material examined: IRAN, Guilan Province, endophytic from leave of *Azolla filiculoides* (*Salviniaceae*), 15 December 2016, E. Shams, (IRAN 18020F, **holotype**), ex-type living culture, IRAN 3058C.

GenBank numbers: ITS = MT514913, MT514914, MT514915, LSU = MT514910, MT514911, MT514912, TUB2 = MT512516, MT512517, MT512518.

Notes: Didymella azollae was isolated from *Azolla filiculoides* in Guilan, Iran. The characters of the conidia and colony (Figs. 21 and 22) fit the generic concept of *Didymella* (Chen et al. 2015). The species identified in the present study is closely related to *Didymella dactylidis* (CBS 124513) and *D. rhei* (CBS 109177) (Fig. 23). *Didymella azollae* differs from *D. dactylidis* in type of conidia (Chen et al. 2017). In pairwise nucleotide comparisons of *Didymella azollae* with the type strain of *D. dactylidis* (CBS 124513), there is a nucleotide difference of 0.75% (6 bp) in LSU (of 799 nucleotides altogether) and 1.37% (5 bp) nucleotide difference in ITS (of 435 nucleotides altogether). However, in the protein-coding region of TUB2, the nucleotide difference was 6.7% (20 bp) across 286 nucleotides. *Didymella rhei* differs from *D. azollae* by conidia size (3.5–) 5–8 (–10.5) × 1.5–3 µm). In pairwise nucleotide comparisons of *Didymella azollae* with

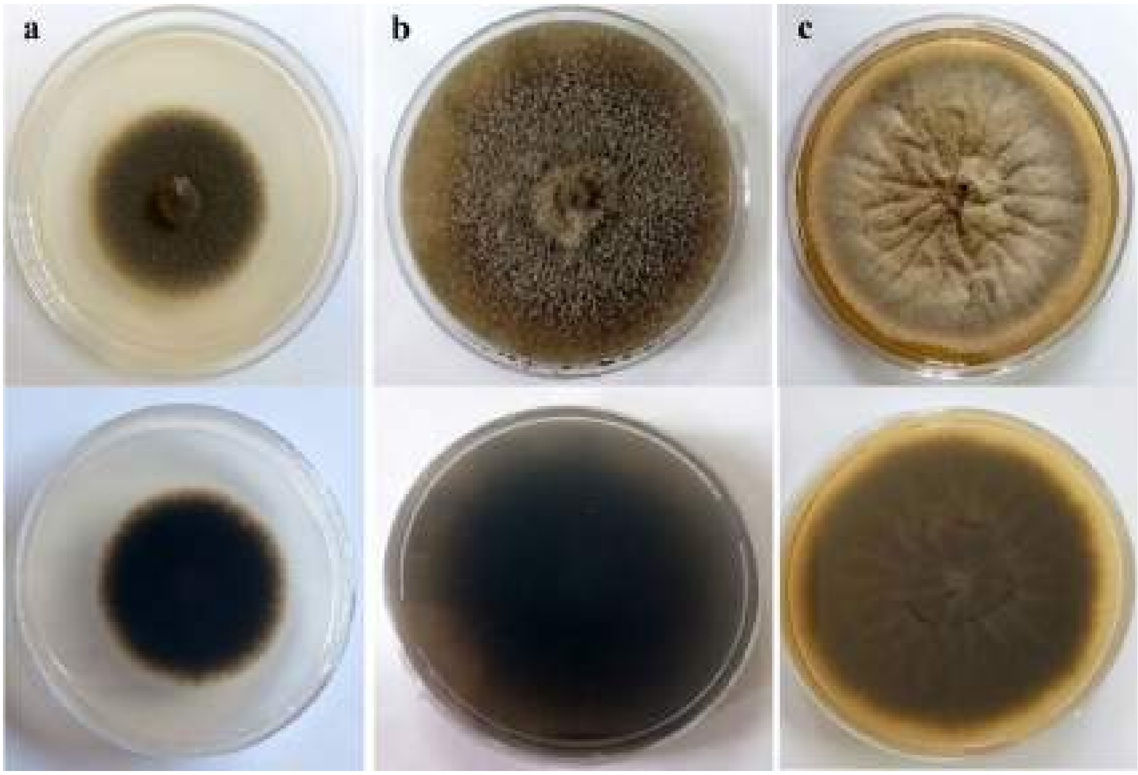


Fig. 22 ***Didymella azollae*** (IRAN 3058C, **ex-type culture**) cultures after 7 days at 25 °C on different media. **a** PDA. **b** OA. **c** MEA

the type strain of *D. rhei* (CBS 109177), there is a nucleotide difference of 0.85% (7 bp) in LSU (of 817 nucleotides altogether), 1.33% (6 bp) nucleotide difference in ITS (of 450 nucleotides altogether) and in the protein-coding region of TUB2, there is a large nucleotide difference of 6.7% (20 bp out of 286 nucleotides).

Didymosphaeriaceae Munk

Notes: *Didymosphaeriaceae* was established by Munk (1953) with *Didymosphaeria* Fuckel as the type genus. This family consists of 32 genera, which includes isolates from different habitats including terrestrial, aquatic, saprotrophic, parasitic, and hemibiotrophic (Hongsanan et al. 2020a). *Didymosphaeriaceae* is characterized by immersed, gregarious or scattered ascomata with two to three layered peridium composed of cells of *textura angularis* or *textura intricate*, septate hamathecium with or without trabeculate pseudoparaphyses. Asci bitunicate, fissitunicate, cylindrical or oblong, septate or muriform and pedicellate. Ascospores uni-seriate or biseriate, oblong, verruculose, with or without a gelatinous sheath. The asexual morphs were known as coelomycetous and hyphomycetous taxa (Ariyawansa et al. 2014a, 2015b). Based on phylogenetic analysis of ITS, LSU and *β-tubulin* sequence data, a novel species *Paraconiothyrium ajrekarii* is introduced. In addition, two new records, *Montagnula thailandica* and *Spegazzinia camelliae* are described as new record based on morphological and phylogenetic analyses.

Montagnula Berl.

Notes: We follow the latest treatment and updated accounts of *Montagnula* in Mapook et al. (2020). Although 44 epithets of *Montagnula* are listed in Species Fungorum (Index Fungorum 2021), only 17 species have been confirmed in *Montagnula* based on molecular data (Fig. 7).

Montagnula thailandica Mapook & K.D. Hyde, in Mapook et al., Fungal Diversity 101: 35 (2020)

Index Fungorum number: IF557299; *Facesofungi number*: FoF 07792; Fig. 24

Saprobic on dead stems. **Sexual morph** *Ascomata* (333–)463–514 × 264–505 µm, immersed to erumpent, scattered, gregarious to grouped, uni-loculate, globose to obpyriform, coriaceous, brown to dark brown, with papillate ostiole in the centre. *Peridium* (44–)60–81 µm wide, comprising several layers of thick-walled, brown to dark brown cells of *textura angularis*. *Hamathecium* comprising 1–2 µm wide, cylindrical to filiform, septate, branched, hyaline pseudoparaphyses. *Asci* 66–121 × 6–11 µm ($\overline{x}$ = 82 × 10 µm, n = 20), 8-spored, bitunicate, fissitunicate, elongate-clavate, slightly curved, long pedicel. *Ascospores* 14–17 × 4–6 µm ($\overline{x}$ = 15 × 5 µm, n = 20), overlapping 1-2-seriate, broadly

Fig. 23 Maximum Likelihood tree inferred by MEGA v.7 from the combined ITS, LSU, and *TUB* gene regions of 92 isolates. Bootstrap support values from ML equal to or greater than 90% are provided above or below the branches. Ex-type strains are in bold and novel species is shown in blue

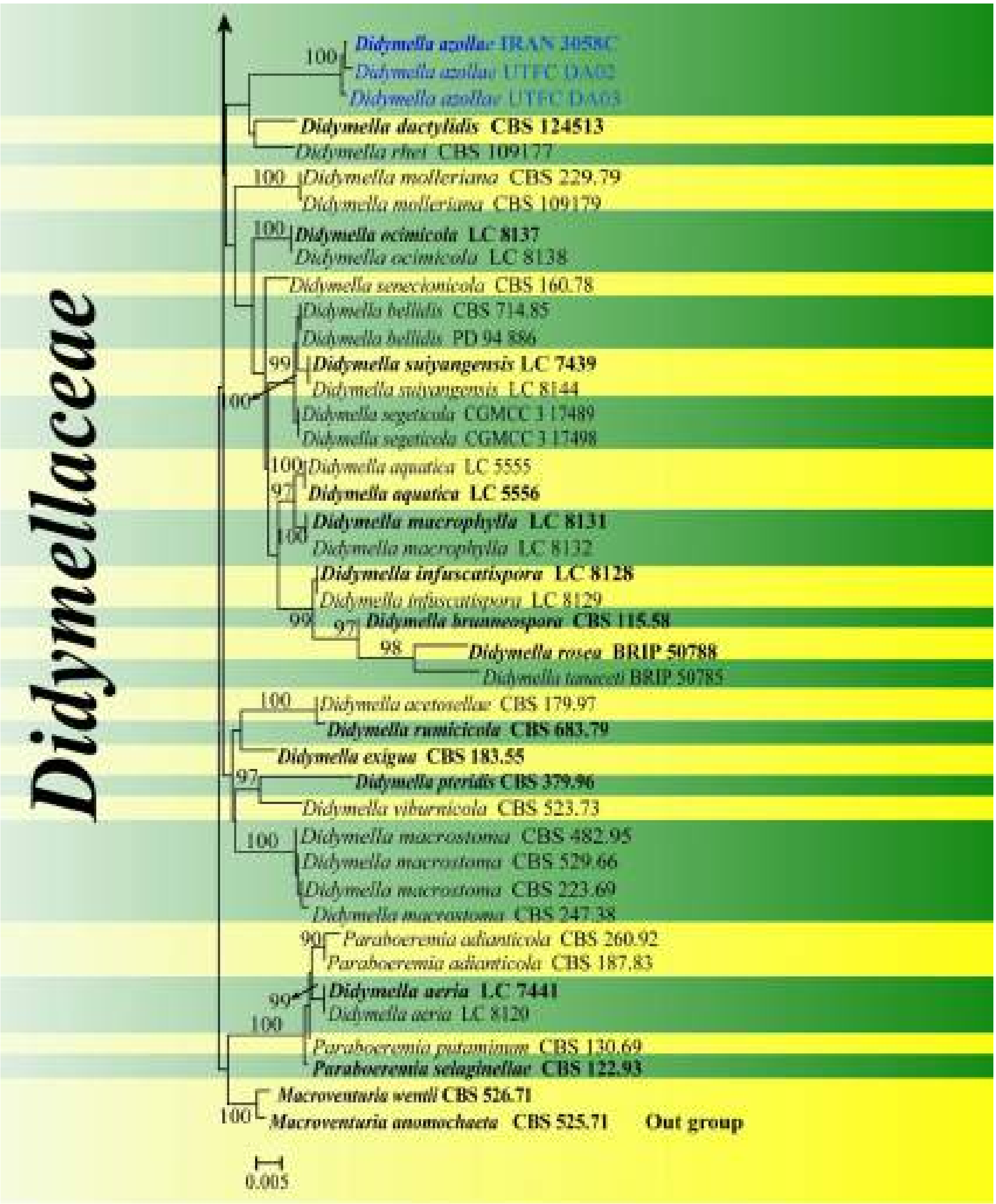


Fig. 23 (continued)

fusiform to ellipsoid, hyaline to pale brown when immature, becoming brown to dark brown when mature, 1-septate, constricted at the septum, slightly wider upper cell and tapering towards ends, slightly curved, with 2–4-guttulate, smooth-walled. **Asexual morph** Undetermined.

Culture characteristics: Ascospores germinating on PDA within 24 h at room temperature and germ tubes produced from both cells. Colonies on PDA circular, mycelium velvety with moderately fluffy, filamentous at margin, cultures grey with white from the centre of the colony on surface, darkened from reverse.

Fig. 24 ***Montagnula thailandica*** (MFLU 21-0052, **new record**). **a**, **b** Appearance of ascomata on woody substrate. **c** Section of ascoma through ostiole. **d** Section of ostiole. **e** Peridium. **f** Pseudoparaphyses. **g**–**k** Immature and mature asci. **l**–**n** Ascospores. **o** Germinated ascospore. **p**, **q** Culture on PDA from surface and reverse. Scale bars: **c** = 200 μm, **d**, **e** = 100 μm, **f**–**k** = 50 μm, **l**–**n** = 10 μm, **o** = 20 μm

Material examined: THAILAND, Chiang Rai Province, Muang, Mae Yao, on dead stems of unidentified host, 23 September 2019, N. Huanraluek, MY04 (MFLU 21-0052, **new record**), living culture, MFLUCC 21-0075.

GenBank numbers: ITS = MZ538515, LSU = MZ538549, TEF1-α = MZ567092.

Notes: The new collection shares cluster and a phylogenetic affinity to the ex-type strain *Montagnula thailandica* (MFLUCC 17-1508) based on a combined LSU, ITS, SSU and TEF1-α sequence analysis but with low statistical support (Fig. 25). Comparisons of ITS, TEF1-α and LSU sequences show that our isolate MFLUCC 21-0075 differs from the ex-type strain *M. thailandica* (MFLUCC 17-1508) in 1/550 bp (0.18%) of ITS and 7/907 bp (0.77%) of TEF1-α, while LSU has no base pair difference. In addition, our collection MFLUCC 21-0075 shares identical characters with *M. thailandica* (MFLUCC 17-1508) isolated by Mapook et al. (2020) from dead stems of *Chromolaena odorata* from Chiang Mai, Thailand. This is a second report of this species on dead stems as a new record from Thailand (Fig. 24).

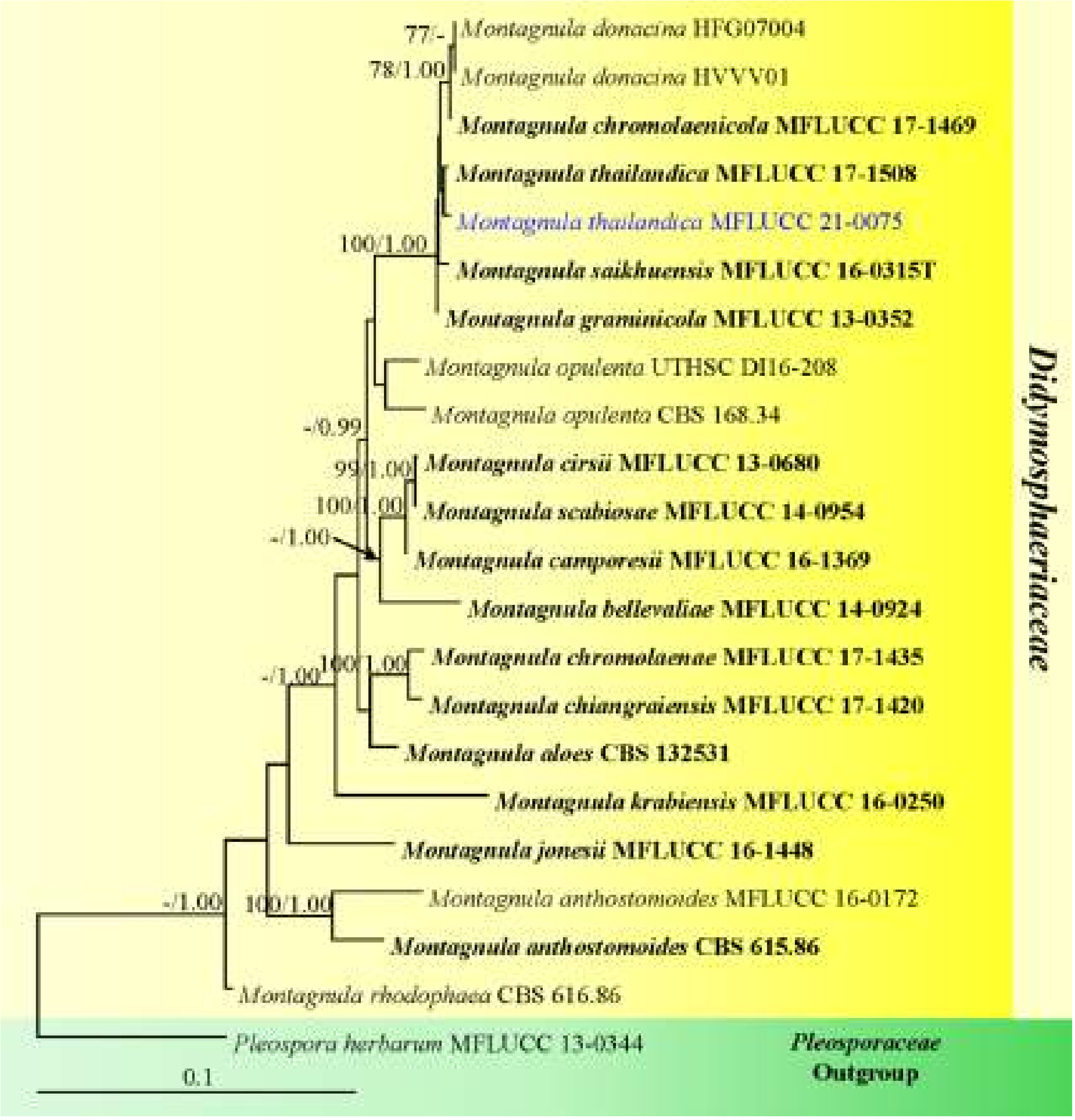


Fig. 25 Phylogram generated from maximum likelihood analysis based on combined LSU, ITS, SSU and TEF1-α sequence data of *Montagnula* taxa. The tree is rooted with *Pleospora herbarum* (MFLUCC 13-0344). Bootstrap support values for maximum likelihood (MLBS, left) equal to or greater than 70% is given above the nodes. Bayesian posterior probabilities (BYPP, right) equal to or greater than 0.95 are given above the nodes. Ex-type strains are in bold and newly generated sequence is in blue

Paraconiothyrium G.J.M. Verkley

Notes: *Paraconiothyrium*, a close relative genus of *Paraphaeosphaeria* was introduced by Verkley et al. (2004) to accommodate four species viz. *P. estuarinum*, *P. brasiliense*, *P. cyclothyrioides* and *P. fungicola*. Whereas, the two mycoparasites *Coniothyrium minitans* and *C. sporulosum* were therefore transferred to *Paraconiothyrium* (as *P. minitans*) based on phylogeny. Verkley et al. (2014) transferred *Paraconiothyrium minitans* and *P. sporulosum* to *Paraphaeosphaeria* based on multigene phylogenetic analysis. Ariyawansa et al. (2020) demonstrated that *Paraconiothyrium* species are polyphyletic within *Didymosphaeriaceae*. Members of *Paraconiothyrium* are used as biocontrol agents, antibiotic producers and potential bioremediators. In this study, a new species *Paraconiothyrium ajrekarii* is introduced based on evidence of morphology and phylogenetic placement (Figs. 26 and 27).

Paraconiothyrium ajrekarii S. Rana & S.K. Singh, ***sp. nov.***

Index Fungorum number: IF557844; *Facesoffungi number*: FoF 08020; Fig. 26

Etymology: Named after Late Professor S.L. Ajrekar, who was a distinguished mycologist and plant pathologist of India.

Holotype: AMH 10218

Color Codes Follow: Methuen Handbook of Colour (Kornerup and Wanscher 1978).

From leaf phylloplane of *Mangifera indica* L. (*Anacardiaceae*). **Sexual morph** Undetermined. **Asexual morph** *Hyphae* 1–4 µm ($\overline{x}$ = 3 µm, n = 15), hyaline to light olivaceous, smooth-walled. *Chlamydospores* 6–23.5 × 6–10.5 µm ($\overline{x}$ = 10.5 × 8 µm, n = 15), solitary or in chains, globose to sub globose, wall thickened and darkened, sub hyaline to light olivaceous to dark brown. *Conidiomata* up to 500 × 300 µm diam., pycnidial, deeply seated, produced in groups, globose to sub globose to oval, dark brown, sometimes with elongated ostiolar neck (up to 245 × 84 µm). *Peridium* up to 33 µm, multi-layered, *textura angularis*, delicate, pale brown. *Conidiophores* reduced to conidiogenous cells, variable in shape and size. *Conidiogenous cells* 7.5–21 × 3–8.5 µm ($\overline{x}$ = 12 × 5 µm, n = 15), short, phialidic, with a collarette, flask-shaped, elongated, ampuliform with swollen basal cell, smooth walled, hyaline. *Conidia* 3–6 × 1–4 µm ($\overline{x}$ = 5 × 3 µm, n = 30), subhyaline, light olivaceous to olivaceous brown, oval to broadly fusoid, rarely angular, aseptate, wall smooth, thickened and darkened.

Culture characteristics: Colonies on PDA reaching 34 mm diam. after 2 weeks, at 25 °C; floccose, circular, umbonate with smooth margins; sulcate on both sides; front colour pinkish white (7A2) to chalky white (7A1), reverse grayish brown at center, light yellow (4A4) towards margin. Colonies on V8 juice agar reaching 46 mm after 2 weeks, at 25 °C; circular, flat, slightly floccose, margin smooth and regular; front colour yellowish white (4A2), reverse grayish yellow (golden wheat) (4B5) and sulcate. Colonies on oat meal agar reaching 61 mm after 2 weeks, at 25 °C; circular, floccose, umbonate, sulcate, margins smooth; front colour orange white (6A2) to white (1A1), reverse light yellow (4A4) and sulcate. Colonies on PCA reaching 57 mm after 2 weeks, at 25 °C; circular, floccose, slightly raised, margins smooth, regular; front colour pale orange (5A3) to dull green (25E3), periphery beige (4C3), reverse dark green (28F6) to light yellow (4A4). Colonies on Czapek Dox agar (CDA) reaching 61 mm after 2 weeks at 25 °C; circular, slightly floccose, velvety, sulcate, margins smooth and regular; colour from front orange grey (5B2) in centre and reddish blond (5C3) towards periphery, reverse brownish orange (5C3) in centre and periphery, beaver (5F4) in middle, sulcate. Colonies on MEA reaching 53 mm after 2 weeks at 25 °C; circular, slightly floccose, margins smooth, regular; front colour white (1A1) in centre and dark blonde (5D4) towards periphery, reverse chocolate brown (6F3) in centre and clay (5D5) towards margins.

Material examined: INDIA, Himachal Pradesh, Kangra, Baijnath, Simbal, from leaf phylloplane of *Magnifera indica* L. (*Anacardiaceae*), 10 May 2019, S. Rana (AMH 10218, **holotype**), ex-type living culture, NFCCI 4810.

GenBank numbers: *β-tubulin* = MT394161, ITS = MT372906, LSU = MT372905.

Notes: This current taxon is placed in *Paraconiothyrium* based on pycnidial conidiomata, phialidic conidiogenous cells producing aseptate, thick and smooth-walled, light olivaceous to olivaceous brown conidia (Verkley et al. 2004). *Paraconiothyrium ajrekarii* differs from other known species based on its phylogenetic as well as morphological analyses (Fig. 26). The combined *β-tubulin*, ITS and LSU phylogeny indicates that *Paraconiothyrium ajrekarii* forms a sister taxon with *P. archidendri* and *P. magnoliae*. *Paraconiothyrium ajrekarii* differs from *P. archidendri* based on its combination of characters such as dimensions of conidiomata and conidiogenous cells (Verkley et al. 2014). *Paraconiothyrium ajrekarii* has somewhat slender conidia in comparison to *P. archidendri* (Table 2). Conidiogenous cells in *P. ajrekarii* has collarette, flask shaped

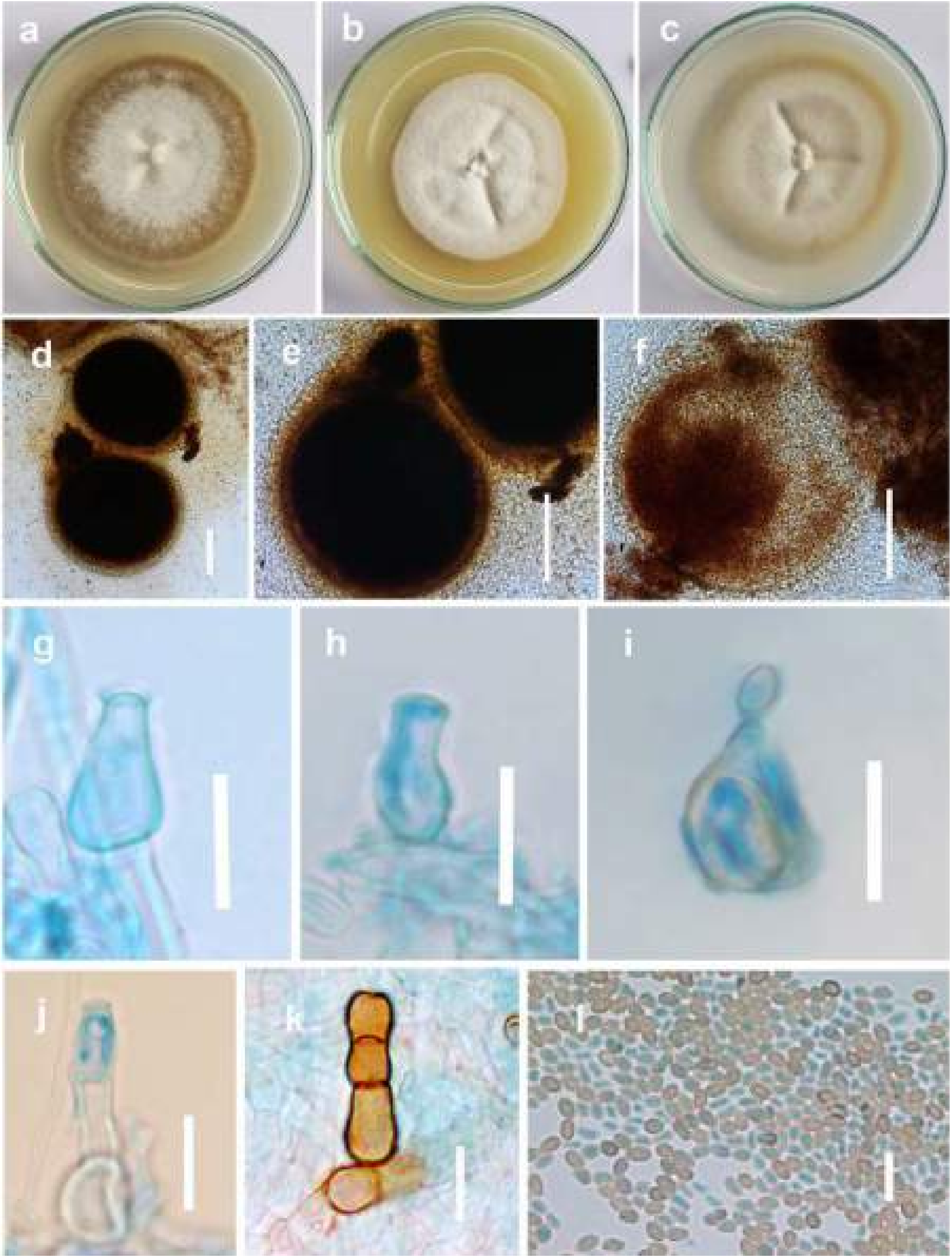


Fig. 26 ***Paraconiothyrium ajrekarii*** (AMH 10218, **holotype**). **a**–**c** Colonies from surface on various media after 2 weeks; **a** MEA, **b** V8 juice agar, **c** Czapek Dox agar. **d** Conidiomata. **e**, **f** Enlarged view of conidiomata. **g**, **h** Conidiogenous cells showing distinct collarette rings. **i**, **j** Condiogenous cells bearing developing conidia. **k** Chlamydospores. **l** Conidia. Scale bars: **d**–**f** = 100 μm, **g**–**l** = 10 μm

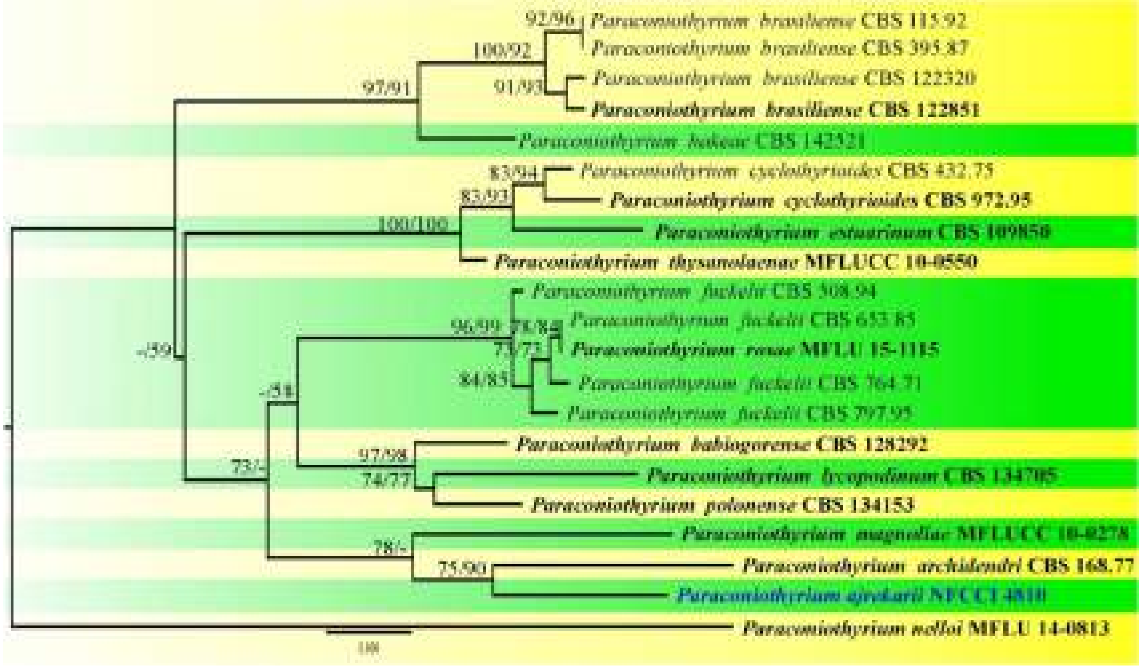


Fig. 27 Molecular phylogenetic analysis by maximum-likelihood (ML) method based on combined *β-tubulin*, LSU and ITS sequence data. Statistical supports are indicated next to each node, non-parametric maximum likelihood ultrafast-bootstrap (UFBS) values and SH-aLRT obtained from 1000 replicates using IQ-TREE and the TIM3 + F + I + G4 model. Bootstrap values for maximum likelihood (MLBS) equal to or greater than 50% are labeled on the nodes. Twenty-one strains are included in the combined analyses which comprise 2393 sites of which 2089 were found to be conserved, 286 were the variable sites and included nearly 178 parsimony-informative sites. The optimized log-likelihood values of − 5846.542 is presented. Estimated base frequencies are as follows: A = 0.300, C = 0.183, G = 0.205, T = 0.312; substitution rates AC = 2.10979, AG = 3.70012, AT = 1.00000, CG = 2.10979, CT = 8.84516, GT = 1.00000; gamma distribution shape parameter α = 0.559. New sequence data of *Paraconiothyrium ajrekarii* (AMH 10,218; NFCCI 4810) is highlighted in blue bold and all sequences from type specimen is in bold

Table 2 Morpho-taxonomic comparison of *Paraconiothyrium ajrekarii* sp. nov. with closest taxa

Species	Host	Locality	Conidiogenous cells	Conidial septa and sizes	References
Paraconiothyrium ajrekarii sp. nov	*Mangifera indica* (Phylloplane)	India	Phialidic, with collarette, flask shaped,	Aseptate, 3–6 × 1–4 μm	This study
P. archidendri	*Pithecellobium bigeminum* (Leaf spots)	Myanmar	Holoblastic, occasionally annellidic, discrete	Aseptate, 3.5–6 × 2.5–3.5(–4) μm	Verkley et al. (2014)
P. magnoliae	*Magnolia liliifera* (Dead leaves)	Thailand	N/A	N/A	Ariyawansa et al. (2014b)

N/A Data not available

with swollen basal cells as against blastic to annellidic in *P. archidendri.* However, *Paraconiothyrium ajrekarii* is an asexual morph and hence cannot be compared with morphological characters of *P. magnoliae* as it is reported to have only a sexual morph (Ariyawansa et al. 2014b). However, *Paraconiothyrium ajrekarii* is an asexual morph and cannot be compared with *P. magnoliae* reported to have only a sexual morph (Ariyawansa et al. 2014b). A megablast search using the ITS sequence data of *P. ajrekarii* revealed closest affinities with members of *Paraconiothyrium*, i.e. *Paraconiothyrium archidendri* CBS 168.77 (similarity = 552/571 bp, 96.67%) and *P. magnoliae* MFLUCC 10-0278 (similarity = 496/517 bp, 95.94%). In the phylogenetic analysis based on combined *β-tubulin*, LSU and ITS sequence data, *Paraconiothyrium ajrekarii* forms a distinct linage from *P. archidendri* with 75% MLBS, 0.90 BYPP support (Fig. 27). Thus, we illustrated and described as a novel species.

Spegazzinia Sacc.

Notes: *Spegazzinia* was introduced by Saccardo (1880) with the type species *S. ornata* and is characterized as having two conidial types (a-conidia with the long spines and b-conidia with the shorter spines to smooth-walled). The genus was included in *Didymosphaeriaceae* based on molecular phylogenetic placement (Tanaka et al. 2015; Hongsanan et al. 2020a). We follow the latest treatment and updated members of *Spegazzinia* in Samarakoon et al. (2020). A new record, *S. camelliae* is described based on its morphological characteristics and phylogenetic evidence.

Spegazzinia camelliae N. Suwannarach, J. Kumla & S. Lumyong, Phytotaxa 483(2): 120 (2021)

MycoBank number: MB837969; *Facesoffungi number*: FoF 09467; Fig. 28

Saprobic on decaying wood. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Colonie*s punctiform, effuse, scattered, dark brown to black on natural wood substrate. *Mycelium* slight raised on host surface, branched, septate, hyaline to pale brown. *Conidiophores* micronematous, mononematous, basauxic, slight erect, flexuous, simple, unbranched, intercalarily, pale brown. *Conidiogenous cells* indiscrete, indeterminate, terminal. *Conidia* 14–17 diam. µm, holoblastic, globose to subglobose, 4-celled, cruciately septate and constricted at the septa, dentate at the margin, brown to dark brown, darker at the septa, faint septa at maturity, guttulate when immature, smooth-walled.

Culture characteristics: Conidium germinating on PDA within 24 h and germ tubes arising from terminal end. Colonies on PDA, slow growing, reaching 5 cm diam. after 1 month at room temperature, flat to slightly effuse, surface smooth, circular, radial striations and entire edges, olivaceous brown to dark brown, and sporulated conidia in cultures after 14 days. Mycelium superficial, partly immersed, composed of branched, septate, hyaline to pale brown, smooth-walled. *Conidia* 11–17 µm diam., globose to subglobose, 4-celled cruciate septate and constricted at the septa, dentate at the margin, brown to dark brown, darker at the septa, guttulate, smooth-walled.

Material examined: THAILAND, Phitsanulok Province, Wang Thong, Wang Nok Aen, on decaying wood, 25 July 2019, S. Boonmee, WNA03 (MFLU 21-0053, **new record**), living culture, MFLUCC 21-0076.

GenBank numbers: ITS = MZ538526, LSU = MZ538560, TEF1-α = MZ567102.

Notes: *Spegazzinia camelliae* was described as an endophytic isolate from living leaves of the *Camellia sinensis* plant in northern Thailand (Suwannarach et al. 2021). Based on phylogenetic analysis of a combined LSU, ITS and TEF1-α sequence dataset of *Spegazzinia* species, our strain MFLUCC 21-0076 clusters with the ex-type strain SDBR-CMU328 with 88% MLBS, 1.00 BYPP support (Fig. 29). When compared our strain was similar with the type specimen of *S. camelliae* (SDBR-CMU328), they are morphologically similar (Fig. 28). This is the first record of *S. camelliae* (MFLU 21-0053) as a saprobic strain on decaying wood.

Hermatomycetaceae Locq.

Notes: *Hermatomycetaceae* was introduced to accommodate a single genus *Hermatomyces* that is characterized by sporodochial conidiomata with one to two types of muriform and dark brown to black conidia (Locquin 1984; Hashimoto et al. 2017). We follow the latest treatments and updated accounts of *Hermatomycetaceae* in Hongsanan et al. (2020a).

Hermatomyces Speg.

Notes: Members of *Hermatomyces* are commonly recognized as saprobes on dead decaying or rotten plant substrates in terrestrial habitats (Koukol et al. 2018; Hyde et al. 2019; Jayasiri et al. 2019; Koukol and Delgado 2019; Nuankaew et al. 2019). *Hermatomyces* currently includes 28 epithets that are listed in Index Fungorum (2021). In this study, we provided on new host record for *Hermatomyces nabanheensis* from China and a new geographical record for *H. sphaericoides* from Thailand. The phylogenetic tree is presented in Fig. 32.

Hermatomyces nabanheensis Tibpromma, Bhat & K.D. Hyde, Fungal Diversity 87: 39 (2017)

Index Fungorum number: IF552901; *Facesoffungi number*: FoF 03135; Fig. 30

Saprobic on dead rachis of *Cyathea spinulosa*. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetes. *Colonies* on natural substrate dry, blackish brown, superficial, circular or oval, bird nest-like, doughnut-shaped, scattered, blackish brown, glistening, conidia readily liberated when disturbed. *Mycelium* 1.7–3.3 µm wide, superficial, composed of a network of branched, septate, hyaline to pale brown. *Conidiophores* are reduced to Conidiogenous cells, micronematous, short, hyaline to pale brown, arising from prostrate hyphae at the centre of circular colony. *Conidiogenous cells* 4–5.5 (–8.5) × 2.4–3.7, holoblastic, monoblastic, integrated, terminal, cylindrical, hyaline to subhyaline. *Conidia* dimorphic, lenticular and cylindrical, thick-walled. *Lenticular conidia* 30–39 × 20–28 µm ($\bar{x}$ = 34 × 23.5 µm, n = 20), numerous, thick-walled, central cells dark brown, hyaline to pale brown peripheral cells with septa, forming a distinct ring on the outside. *Cylindrical conidia* 32–39 × 19.5–27 µm ($\bar{x}$ = 36 × 24 µm, n = 15) µm in broadest part of lower cells, with 2 forked columns of 2–4 cells, cylindrical, swollen, constricted at septa, subhyaline, upper part of terminal cells dark brown, granulate, rough.

Culture characteristics: Conidia germinated on PDA within 15 h at incubator at 25℃. Germ tubes produced around conidia and were transferred to fresh PDA media. Pure cultures were incubated at 25°C and reaching 2.2 cm diam. in 10 days, circular, smooth surface, velvety and raised, gray to brown to gray from center to margin from

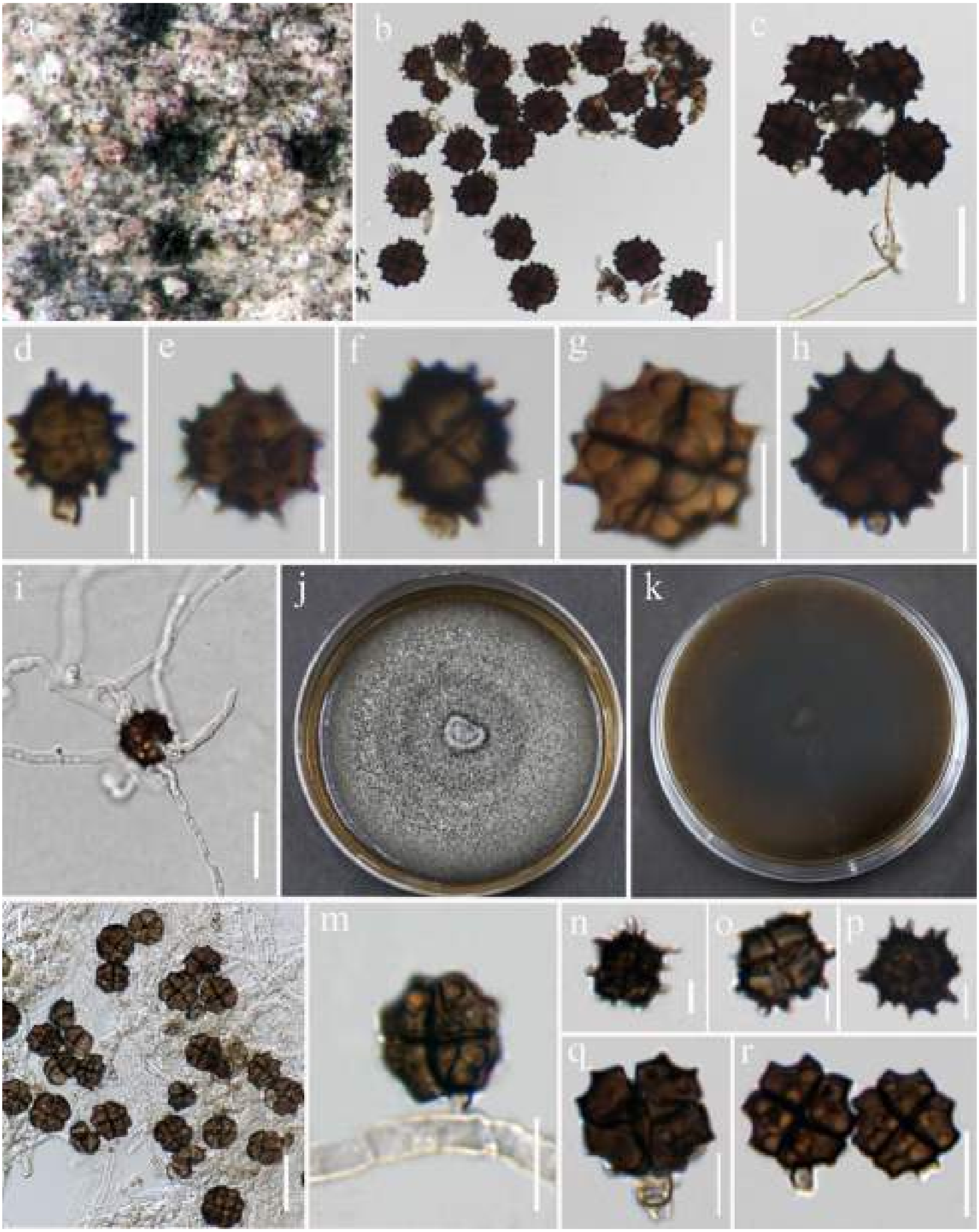


Fig. 28 ***Spegazzinia camelliae*** (MFLU 21-0053, **new record**). **a** Colonies on wood substrate. **b**, **c** Conidiophores and conidiogenous cells. **d**–**h** Conidia. **i** Germinated conidium. **j**, **k** Culture on PDA from surface and reverse at 1 month. **l**–**r** Conidia developing in culture. Scale bars: **b**–**c**, **i**, **l** = 20 μm, **d**–**f**, **n**–**p** = 5 μm, **g**–**h**, **m**, **q**–**r** = 10 μm

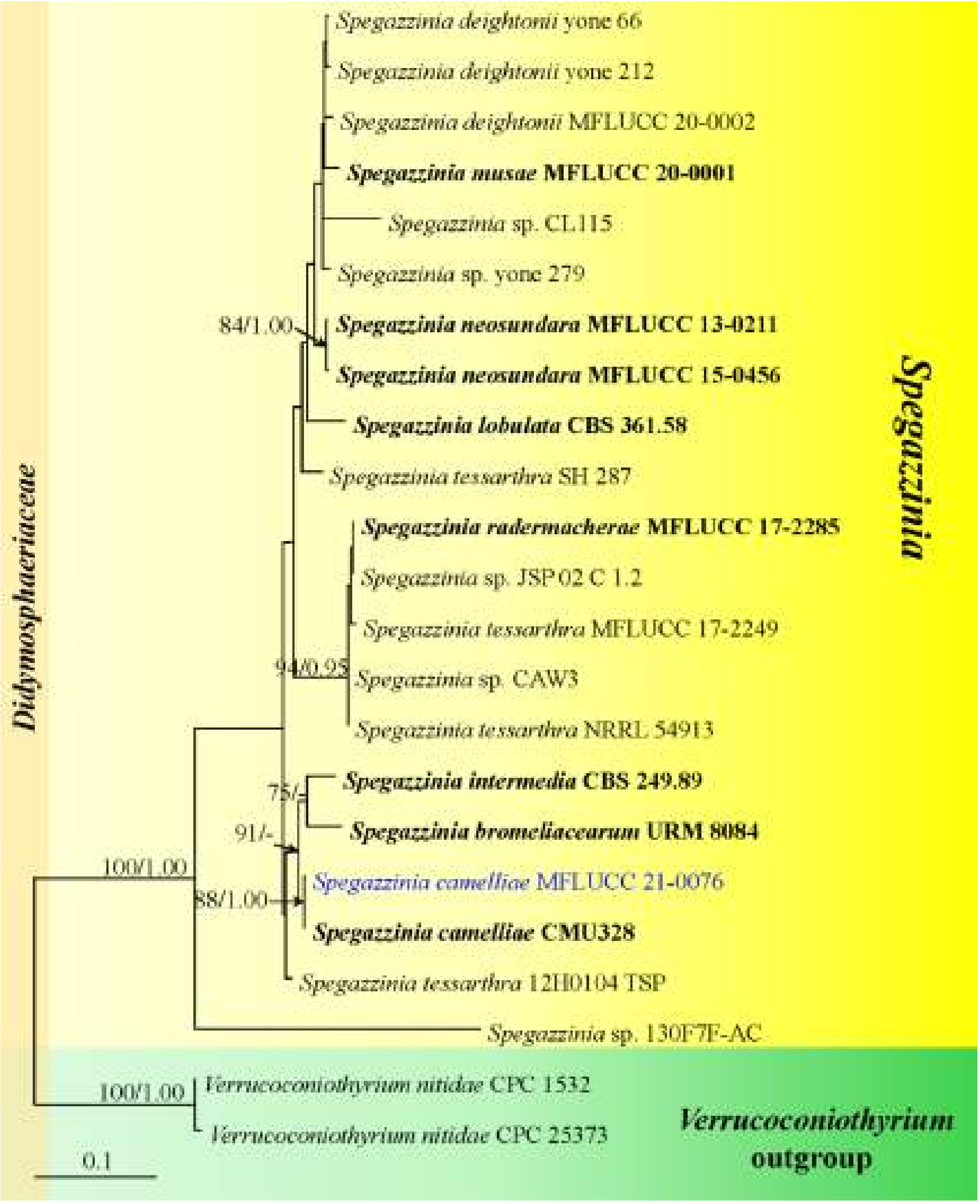


Fig. 29 Phylogram generated from maximum likelihood analysis based on combined LSU, ITS and TEF1-α sequence data of *Spegazzinia* taxa. *Verrucoconiothyrium nitidae* (CPC1532 and CPC25373) are selected as the outgroup taxa. Bootstrap support values for maximum likelihood (MLBS, left) equal to or greater than 70% is given above the nodes. Bayesian posterior probabilities (BYPP, right) equal to or greater than 0.95 are given above the nodes. Ex-type strains are in bold and newly generated sequence is in blue

the forward of culture, yellow–brown in the centre while white at the edge from the reverse of culture.

Material examined: CHINA, Guizhou Province, Zunyi, Chishui, Hushi, Chishui Alsophila Natural Reserve (28°29′43″ N 106°0′24″ E), on dead rachis of *Cyathea spinulosa*, 22 September 2019, J.Y. Zhang, C30 (MFLU 21-0025, **new record**), living culture, MFLUCC 21-0024.

GenBank numbers: ITS = MZ198895, LSU = MZ198897.

Notes: The phylogenetic analysis based on multi-gene phylogenetic analysis indicates that our new isolate

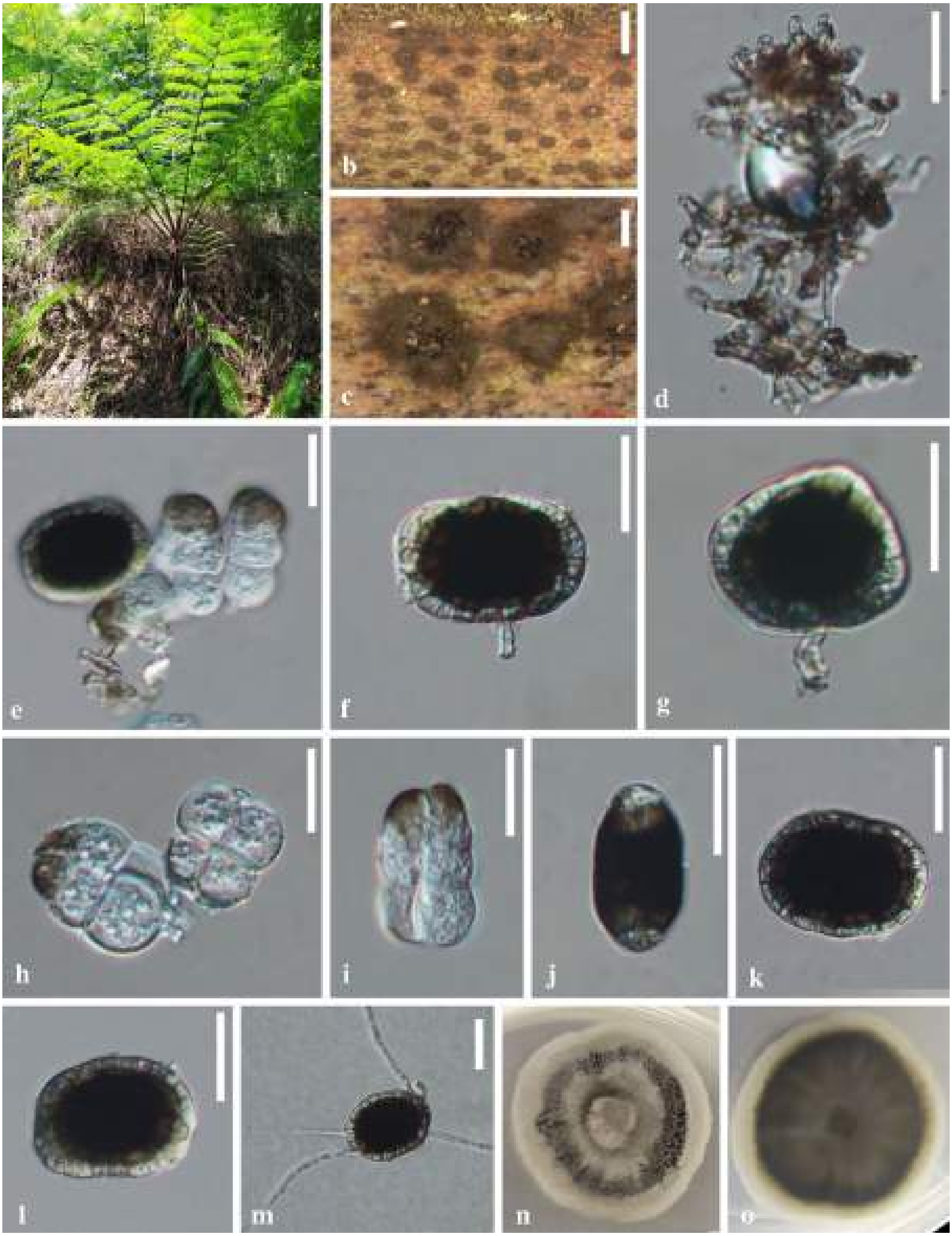


Fig. 30 ***Hermatomyces nabanheensis*** (MFLU 21-0025, **new record**). **a** Host. **b**, **c** Colonies on substrate. **d** Mycelium. **e**–**g** Conidia with conidiogenous cells. **h**, **i** Cylindrical conidia. **j**–**l** Lenticular conidia. **m** Germinated conidium. **n**, **o** Culture on PDA from above and below. Scale bars: **b** = 1000 μm, **c** = 200 μm, **d**–**m** = 20 μm

clustered together with the ex-type strain *Hermatomyces nabanheensis* (KMUCC 16-0149) with 100% MLBP, 1.00 BYPP support (Fig. 32). A comparison of base pair sequences between *H. nabanheensis* (KMUCC 16-0149; Hyde et al. 2017) and our isolate (MFLUCC 21-0024) showed that they differ by 3 bases in LSU and 5 bases in ITS. The new isolate is similar to *H. nabanheensis* (KMUCC 16-0149) in shape of colony, conidiophores, conidiogenous cells and conidia (Hyde et al. 2017; see Fig. 28). However, the new isolate differs from *H. nabanheensis* (HKAS96214) in having larger conidia (lenticular conidia 30–39 × 20–28 µm vs. 20.2–25 × 16.6–20.7; cylindrical conidia 30–37 × 19.5–25 µm vs. 15–26.8 × 12.1–18.2) (Fig. 30). Based on the evidence of phylogeny and morphological characteristics, we consider the new isolates conspecific to *H. nabanheensis* and this is the first record of *H. nabanheensis* from a fern (*Cyathea spinulosa*).

Hermatomyces sphaericoides Koukol & G. Delgado, IMA Fungus 9(1): 122 (2018)

Index Fungorum number: IF824248; *Facesoffungi number*: FoF 09190; Fig. 31

Saprobic on decaying wood. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Colonies* on the natural substrate superficial, dry, scattered to partly grouped, black. *Mycelium* 2–3 µm wide, superficial and partly immersed, composed of branched, septate, pale brown or brown, sparsely network hyphae. *Conidiophores* micronematous, mononematous, flexuous, inconspicuous, septate, hyaline to pale brown. *Conidiogenous cells* 4–6 × 2–3 µm, holoblastic, monoblastic, integrated, terminal, determinate, cylindrical, pale brown. *Conidia* 25.5–32 × 21–27.5 µm ($\bar{x}$ = 28.5 × 25 µm, n = 20), solitary, acrogenous, cheiroid, globose to subglobose, inwardly curved at the apex, arising from a basal cell, consisting 4–5 rows, row digitate, each row composed of 4–5(–6) cells, multi-septate, constricted at the septa, dark brown to black, smooth-walled.

Culture characteristics: Conidium germinating on PDA within 24 h and germ tubes arising from terminal end of conidium. Colonies on PDA, fast growing, reaching 30 mm diam. after 2 weeks at room temperature, flat, with slightly crenated to radially striated with lobate margin, with white–grey mycelium, pastel grey in middle towards dark brown, greenish brown at margin, dark green to brown in reverse view, not sporulating in cultures after 2 months.

Material examined: THAILAND, Phetchabun Province, Lom Sak, on decaying wood, 25 July 2019, S. Boonmee, LSP01 (MFLU 21-0054, **new record**), living culture, MFLUCC 21-0077.

GenBank numbers: ITS = MZ538505, LSU = MZ538539, TEF1-α = MZ567083.

Notes: *Hermatomyces sphaericoides* was described on dry rotten twig of an unidentified tree in Panama and shares similar conidial features with *H. sphaericus*, but it differs in conidial characteristic details in having dark brown to blackish brown and finely verruculose with an outer ring of peripheral cells (Koukol et al. 2018). Furthermore, phylogenetic analyses indicate that *H. sphaericoides* and *H. sphaericus* are distinct species. Our strain MFLUCC 21-0077 shows some similarities with *H. sphaericoides* in terms of conidial characteristics (Koukol et al. 2018). Multi-gene phylogenetic analysis of a combined ITS, LSU and TEF1-α dataset indicated that our isolate MFLUCC 21-0077 clustered together with *H. sphaericoides* isolates (CCF 5896, CCF 5907, CCF 5908 (ex-type) and KZP 470) with 100% MLBS, 1.00 BYPP support (Fig. 32), whereas CCF 5895 forms a basal lineage. Therefore, we identify our collection as *H. sphaericoides* (Fig. 31) and it is reported here as a new geographical record from Thailand.

Lentitheciaceae Y. Zhang ter, C.L. Schoch, J. Fourn., Crous & K.D. Hyde

Notes: We follow the latest treatments and the updated accounts of *Lentitheciaceae* in Hongsanan et al. (2020a). Based on phylogenetic analysis of a combined LSU, TEF1-α, SSU and ITS sequences, the isolate is identified as *Poaceascoma taiwanense* and is a new geographical record from Thailand.

Poaceascoma Phookamsak & K.D. Hyde

Notes: *Poaceascoma* was introduced by Phookamsak et al. (2015) to accommodate a taxon occurring on dead stems and roots of *Digitaria sanguinalis* (*Poaceae*) host in a terrestrial habitat. *Poaceascoma* is typified by *P. helicoides* Phookamsak & K.D. Hyde and is characterized by semi-immersed to erumpent, sphaerical, short to long papilla, turf-like surrounded ascomata; bitunicate, fissitunicate, cylindrical asci and fasiculate, sometime spiral, filiform, multi-septate, hyaline ascospores (Phookamsak et al. 2015). Five species have been accepted and confirmed for *Poaceascoma* by phylogenetic evidence (Crous et al. 2020b; Hongsanan et al. 2020a; Index Fungorum 2021).

Poaceascoma taiwanense C.H. Kuo & K.D. Hyde, Mycosphere 9(2): 297 (2018)

Index Fungorum number: IF554200; *Facesoffungi number*: FoF 04084; Fig. 33

Saprobic on submerged wood. **Sexual morph** *Ascomata* 117–200 µm high, 198–209 µm diam., immersed to erumpent when mature, solitary, scattered or sometimes grouped beneath the host tissues, globose, dark brown to black, coriaceous, ostiolate, papillate. *Peridium* 22–31 µm wide, with thick walls, composed of several layers of pseudoparenchymatous cells, outer layer comprising several layers of dark brown cells, arranged in a *textura angularis*, inner layer comprising several layers of

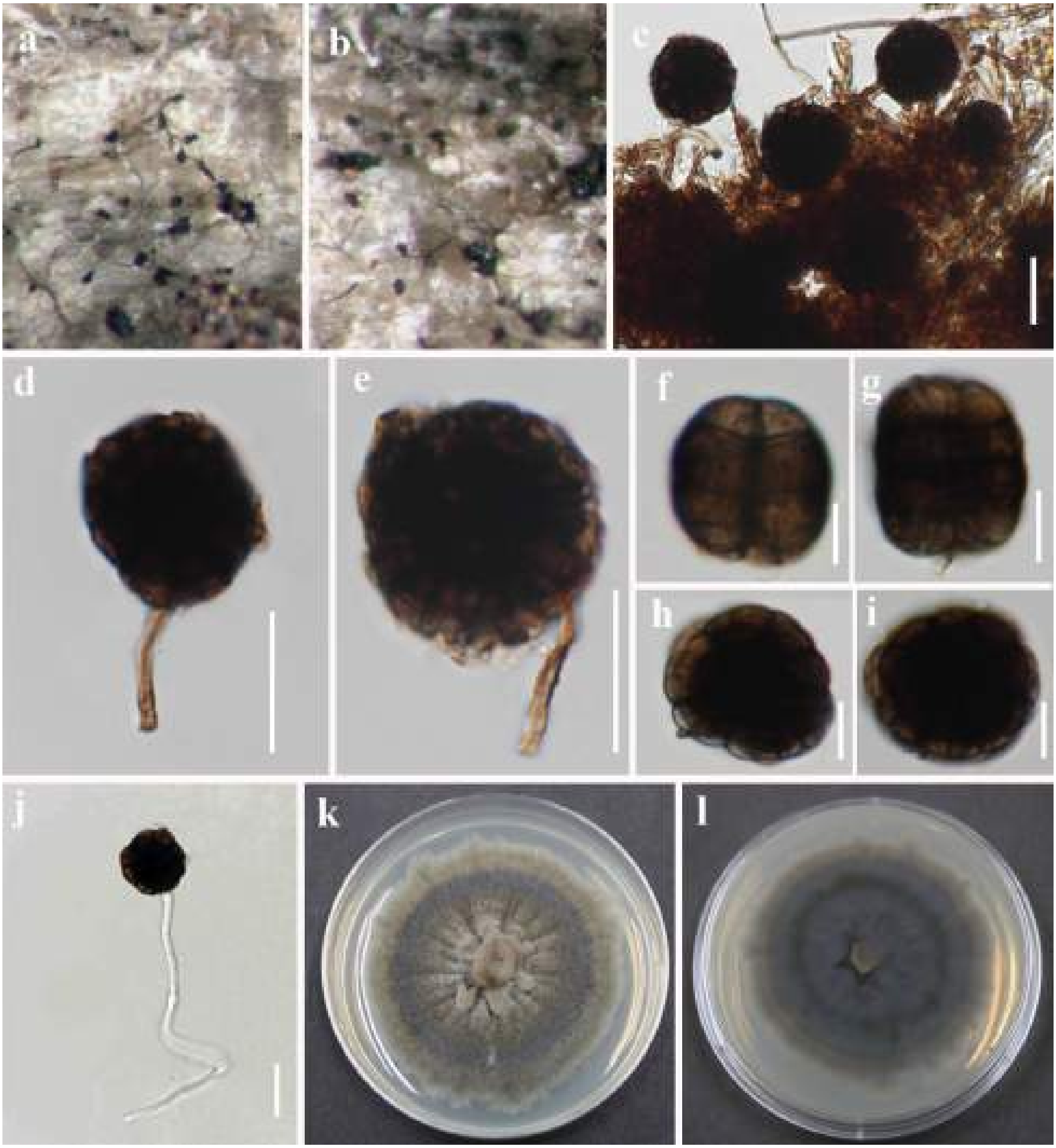


Fig. 31 ***Hermatomyces sphaericoides*** (MFLU 21-0054, **new record**). **a**, **b** Colonies on the natural substrate. **c**–**e** Conidiogenous cells. **f**–**i** Conidia. **j** Germinated conidium. **k**, **l** Culture on PDA from surface and reverse at 1 month. Scale bars: **c**–**e**, **j** = 20 μm, **f**–**i** = 10 μm

hyaline, flattened cells, arranged in a *textura angularis* to *textura prismatica. Hamathecium* composed of numerous, 1.5–2 μm wide, filamentous, broad, cellular pseudoparaphyses, with distinct septa, embedded in a mucilaginous matrix. *Asci* 63–77 × 8.5–10 μm ($\bar{x}$ = 70 × 9.5 μm, n = 10), 8-spored, bitunicate, cylindrical clavate, short pedicellate, apically rounded with minute ocular chamber. *Ascospores* 42–54 × 2.5–3 μm ($\bar{x}$ = 49 × 3 μm, n = 10), fasciculate, scolecosporous, hyaline, elongate, cylindrical filiform, tapering towards the rounded ends, slightly curved, 6–7-septate, slightly constricted at the septa, smooth-walled. **Asexual morph** Undetermined.

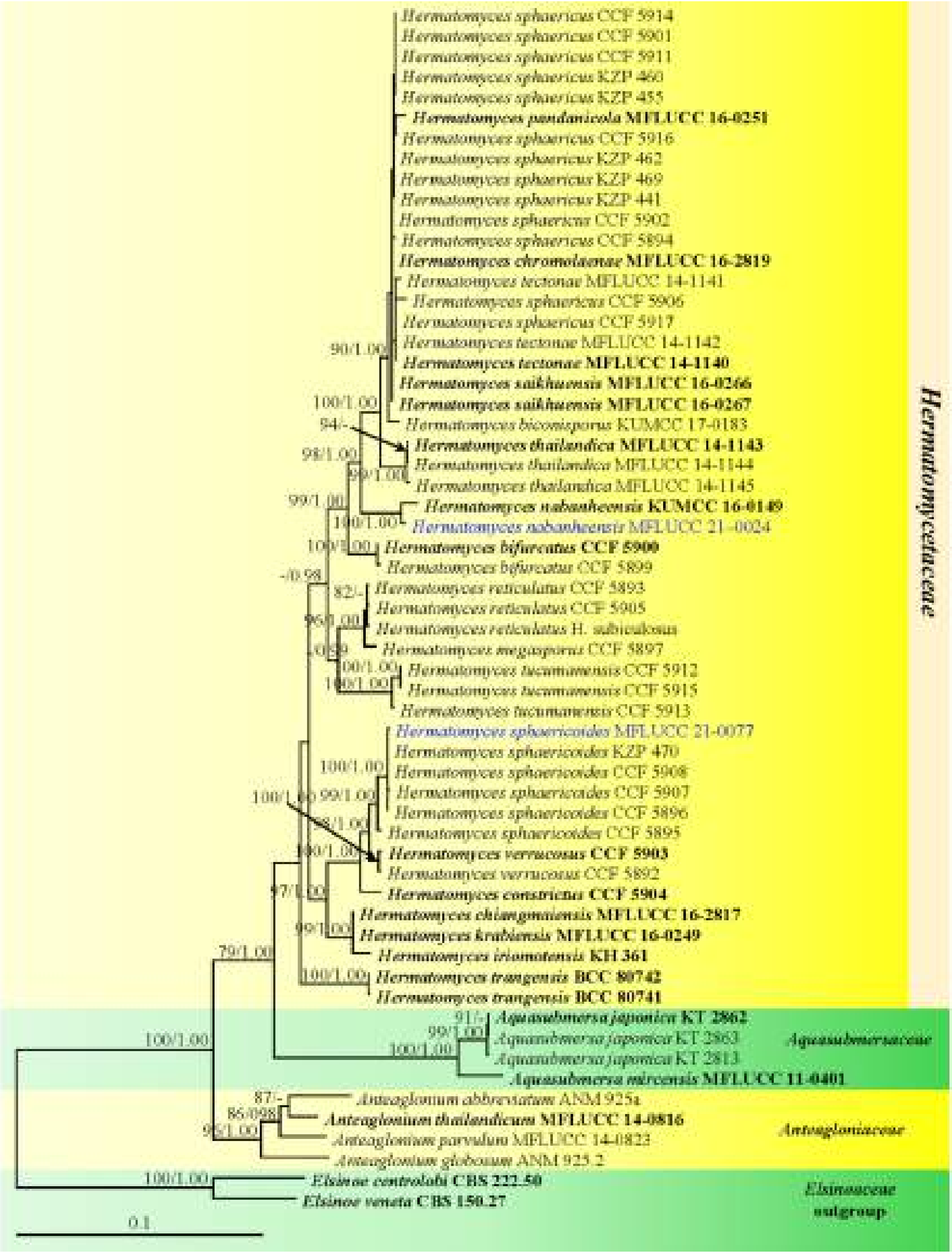


Fig. 32 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU and TEF1-α sequence data of *Hermatomyces* taxa (*Hermatomycetaceae*) and closely related families *Aquasubmersaceae* and *Anteagloniaceae*. *Elsinoe centrolobi* CBS 222.50 and *E. veneta* CBS 150.27 are selected as the outgroup taxa. Bootstrap support values for maximum likelihood (MLBS, left) equal to or greater than 70% is given above or below the nodes. Bayesian posterior probabilities (BYPP, right) equal to or greater than 0.95 are given above the nodes. Ex-type strains are in bold and newly generated sequences are in blue

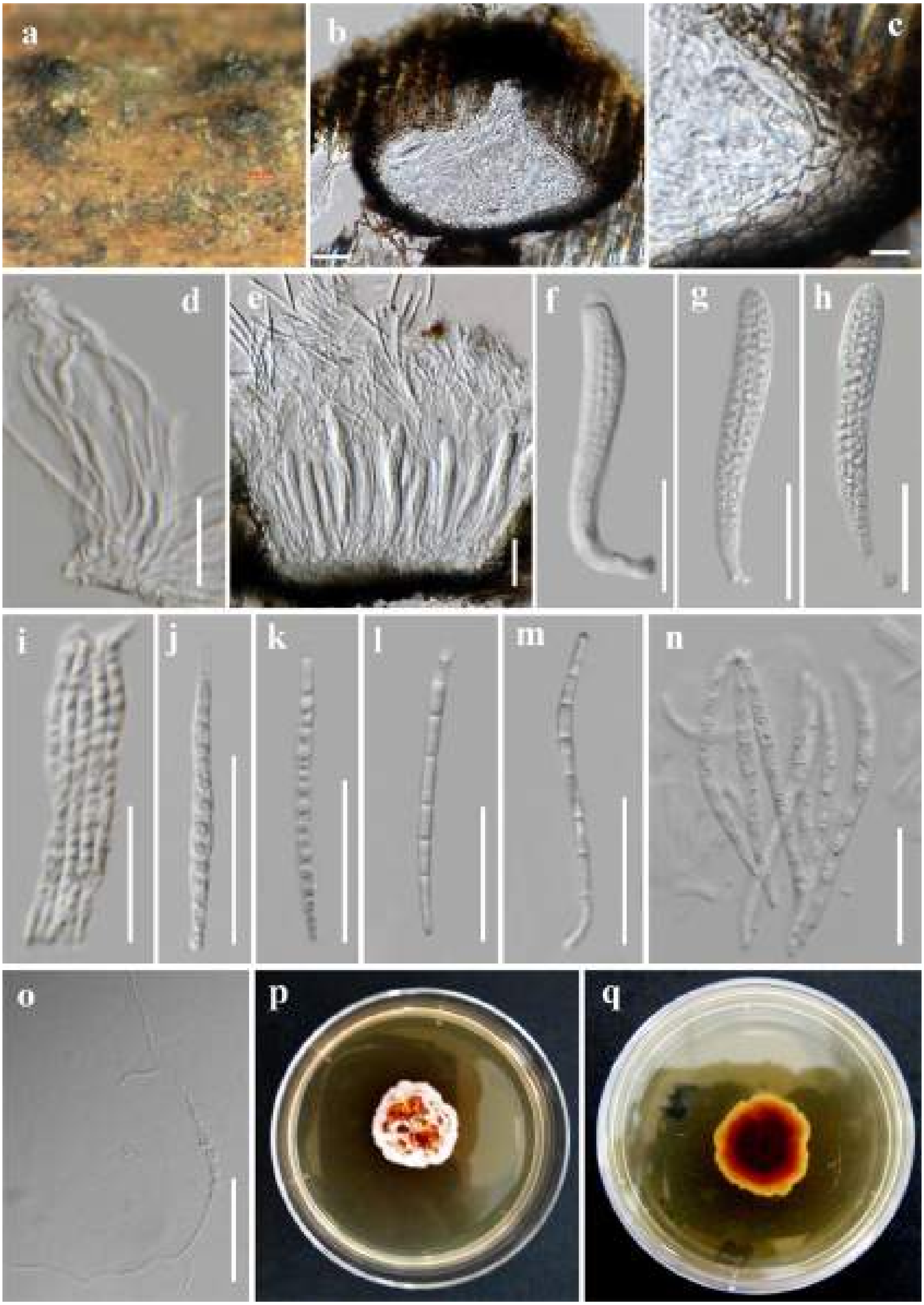


Fig. 33 ***Poaceascoma taiwanense*** (MFLU 21-0055, **new record**). **a** Ascomata immersed, aggregated, erumpent on the dead wood. **b** Longitudinal sections of ascomata. **c** Peridium. **d** Pseudoparaphyses. **e**–**h** Asci. **i**–**n** Ascospores. **o** Germinated ascospore. **p**, **q** Culture on MEA from surface and reverse at 1 month. Scale bars: **b** = 50 μm, **c**–**n** = 20 μm, **o** = 30 μm

Culture characteristics: Ascospores germinating on PDA within 24 h and germ tubes arising from both ends. Colonies on MEA reaching 20 mm after 1 month at room temperature, slightly effuse, dense, radially with undulate edge, surface white with forming the water drops on the mycelium, with orangish pigmented at the surface, reverse dark purple at the middle, radiating dark pink to yellowish orange towards the edge.

Material examined: THAILAND, Phayao Province, Pong, on submerged wood in a small freshwater stream, 26 March 2019, S. Boonmee, PY1 (MFLU 21-0055, **new record**), living culture, MFLUCC 21-0078.

GenBank numbers: ITS = MZ538523, LSU = MZ538557, TEF1-α = MZ567099.

Notes: Multigene phylogenetic analysis indicates that our strain MFLUCC 21-0078 is sister to the type strain *P. taiwanense* (MFLU 18-0083) with high levels of support (100% MLBS, 1.00 BYPP (Fig. 34). A comparison of LSU and ITS nucleotide base pairs indicates that our strain is highly to *P. taiwanense* (3/842 bp differences (0.35%) in LSU and 5/564 bp differences (0.89%) in ITS). Therefore, we identify our strain MFLUCC 21-0078 as *P. taiwanense* (Fig. 33). Our strain shares similar characteristics of the ascomata, asci and ascospores to *P. taiwanense* (MFLU 18-0083). Although, our strain differs in having 8-spored in ascus and 6–7-septate ascospores, while *P. taiwanense* (MFLU 18-0083) having 4-spored in ascus and 15–17-septate. However, LSU and ITS sequences indicated that they are conspecific (Hyde et al. 2018a; see Fig. 14). Therefore, *P. taiwanense* is reported from submerged wood in a freshwater habitat for the first time in Thailand. If we used protein coding genes, they may however prove to be distinctive species, as showed by the morphological evidence.

Lindgomycetaceae K. Hiray., Kaz. Tanaka & Shearer

Notes: *Lindgomycetaceae* includes seven genera, *Arundellina*, *Clohesyomyces*, *Hongkongmyces*, *Lindgomassariosphaeria*, *Lindgomyces* (generic type), *Lolia, Massariosphaeria* and *Neolindgomyces* (Dong et al. 2020b; Wijayawardene et al. 2020). Most taxa are saprobes on submerged decaying wood in a freshwater habitat and some species (e.g. *Hongkongmyces pedis* have been found to cause human diseases (Tsang et al. 2014). We follow the latest treatment of this family in Dong et al. (2020b). An updated phylogenetic tree for *Lindgomycetaceae* is presented in Fig. 37. In this study, a new genus *Xenovaginatispora* with *X. phichaiensis* as a type species and a new species in *Hongkongmyces* are introduced.

Hongkongmyces C.C.C. Tsang et al.

Notes: Tsang et al. (2014) introduced *Hongkongmyces* which was isolated from biopsy tissues of an infected foot, resulting in the establishment of *Lindgomycetaceae*. Currently, *Hongkongmyces* comprises sexual and asexual morphs of four species which are namely *Hongkongmyces aquaticus*, *H. pedis*, *H. snookiorum* and *H. thailandica* (Tsang et al. 2014; Hyde et al. 2017; Crous et al. 2018; Dong et al. 2020b). The new species of *Hongkongmyces*, *H. kokensis* is introduced here with morphology and phylogeny evidences.

Hongkongmyces kokensis Boonmee, Chandrasiri, Huanraluek & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF558535; *Facesoffungi number*: FoF 09946; Fig. 35

Etymology: The specific epithet "*kokensis*" refers to the Kok river.

Holotype: MFLU 21-0056

Saprobic on submerged decaying wood in the river. **Sexual morph** Undetermined. **Asexual morph** Coelomycetous. *Conidiomata* 261–347 µm high, 264–417 µm diam., pycnidial, scattered, semi-immersed or erumpent, subglobose or ellipsoidal, dark brown to black, coriaceous, ostiolate. *Conidiomata wall* 13–38 µm thick, composed of several layers of dark brown cells of *textura angularis*, difficult to distinguish from conidiogenous cells. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 7–21 × 3–12 µm ($\bar{x}$ = 12 × 6 µm, n = 10), phialidic, determinate, cylindrical to subcylindrical, hyaline, thin-walled. *Conidia* 10–15 × 8–14 µm ($\bar{x}$ = 12 × 10 µm, n = 20), subglobose to obovoid, hyaline, aseptate, large guttule present when immature, lacking a mucilaginous sheath, smooth-walled.

Culture characteristics: Conidia germinated on PDA within 24 h. Colonies on PDA reaching 3.5 cm diam. after 3 weeks at room temperature, circular, entire to slightly undulate edge, raised effuse, olivaceous brown to brown from the center towards margin, surrounded by light brown at the margin, dark brown at the reverse with surrounded by light brown at the margin, superficial and velvety mycelia.

Material examined: THAILAND, Chiang Rai Province, Muang, Mae Yao, Kok river, on submerged decaying wood in the river shore, 4 December 2019, S. Boonmee and K.S.U. Chandrasiri, N-KR4 (MFLU 21-0056, **holotype**), ex-type living culture, MFLUCC 21-0079; Chiang Rai Province, Wiang Pa Pao, Lao River, on submerged decaying wood in the river shore, 11 December 2019, S. Boonmee and K.S.U. Chandrasiri, LR4 (MFLU 21-0057), living culture, MFLUCC 21-0080; Phrae, Pong, Yom River, on submerged decaying wood in the river shore, 18 December 2019, S. Boonmee and K.S.U. Chandrasiri, YR21 (MFLU 21-0058), living culture, MFLUCC 21-0081.

GenBank number: LR4: ITS = MZ538507, LSU = MZ538541, TEF1-α = MZ567085; N-KR4: ITS = MZ538506, LSU = MZ538540, TEF1-α = MZ567084; YR21: ITS = MZ538508, LSU = MZ538542, TEF1-α = MZ567086.

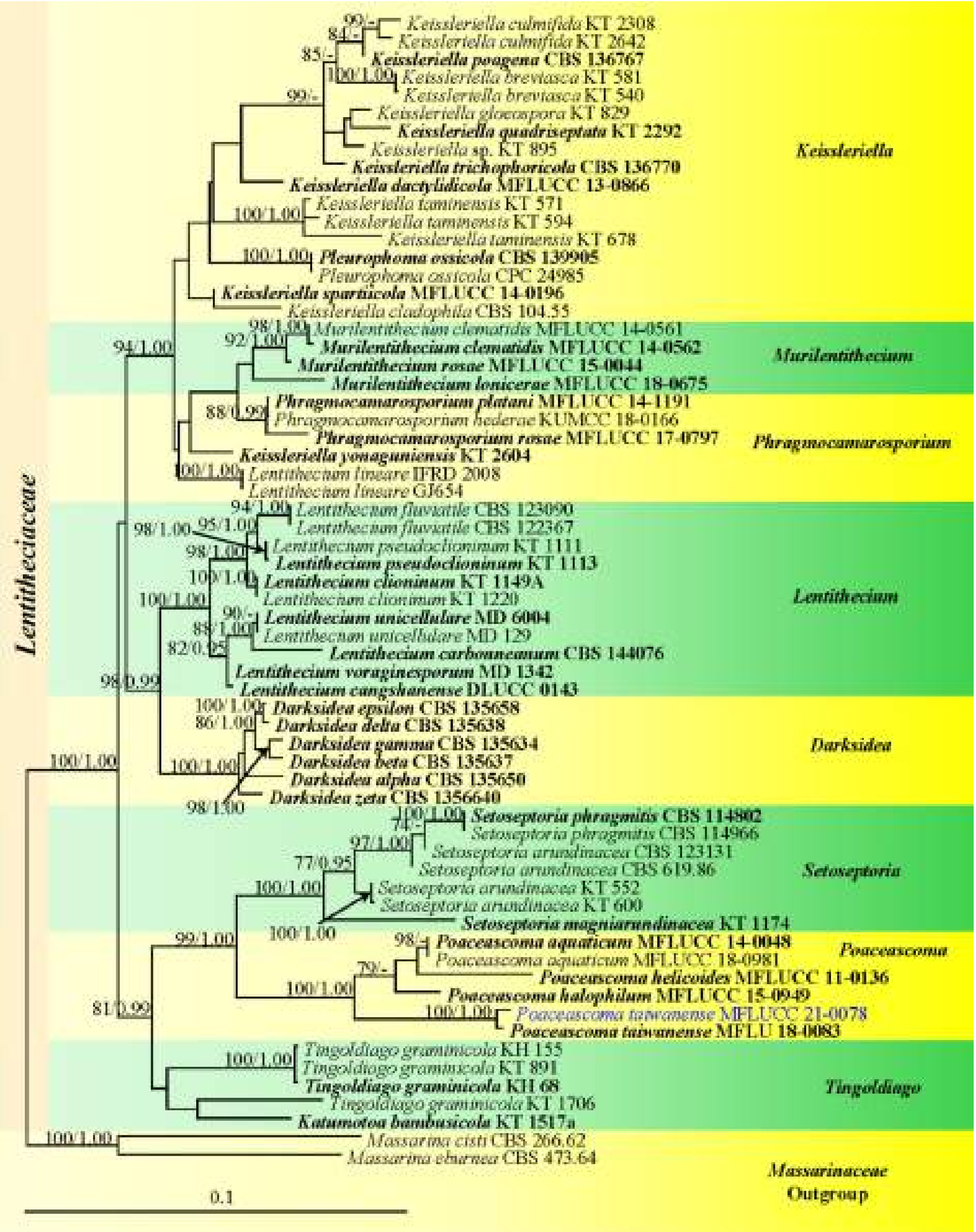


Fig. 34 Phylogram generated from maximum likelihood analysis based on combined LSU, TEF1-α, SSU and ITS sequence data of *Poaceascoma* taxa and related genera in *Lentitheciaceae*. *Massarina cisti* CBS 266.62 and *M. eburnea* CBS 473.64 are selected as the outgroup taxa. Bootstrap support values for maximum likelihood (MLBS, left) equal to or greater than 70% is given above the nodes. Bayesian posterior probabilities (BYPP, right) equal to or greater than 0.95 are given above the nodes. Ex-type strains are in bold and newly generated sequence is in blue

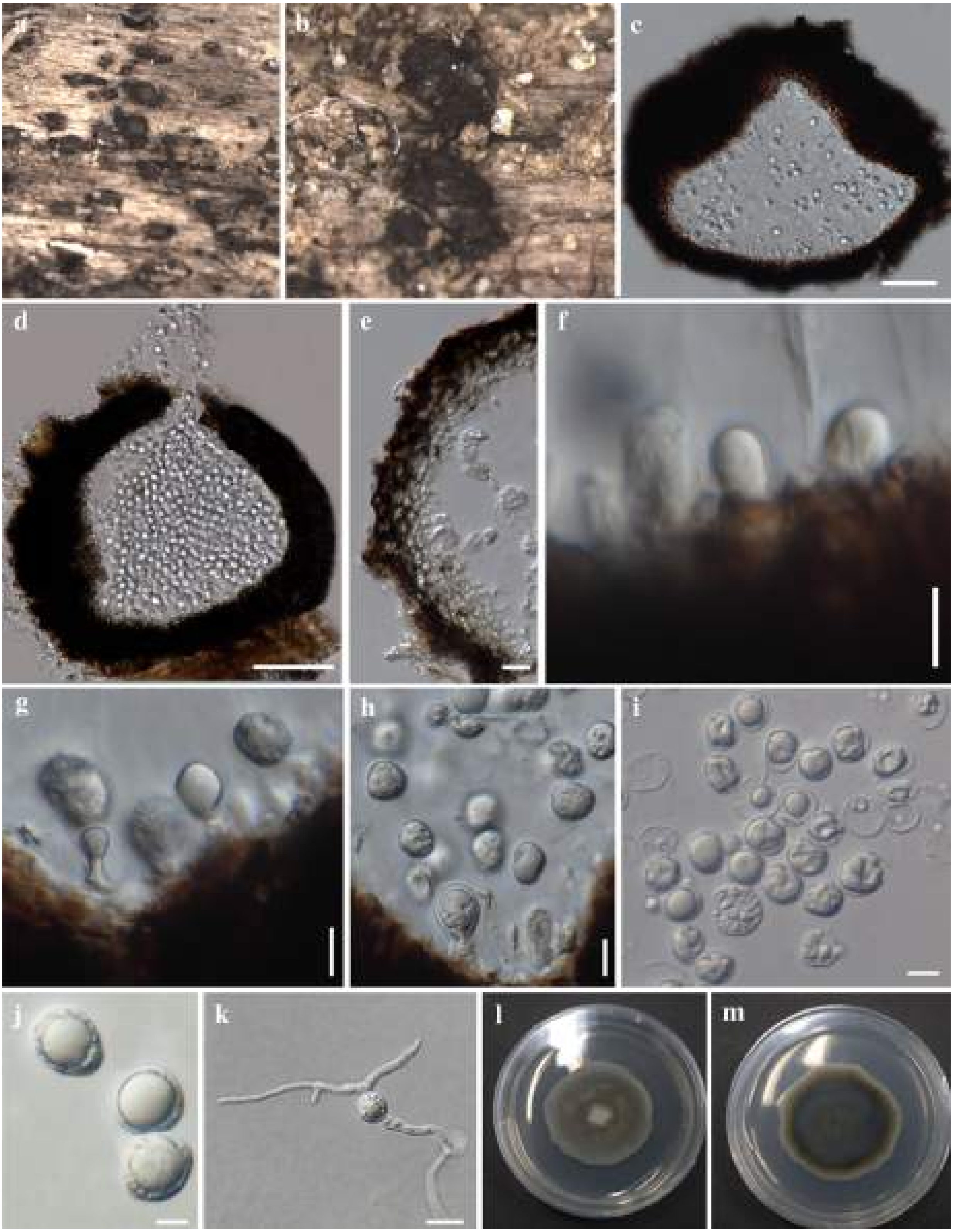


Fig. 35 ***Hongkongmyces kokensis*** (MFLU 21-0056, **holotype**). **a**, **b** Appearance of conidiomata on submerged decaying wood substrate. **c**, **d** Section through conidiomata. **e** Section of conidioma wall. **f**–**h** Conidiogenous cells and conidia. **i**, **j** Conidia. **k** Germinated conidium. **l**, **m** Culture on PDA (l = from above, m = from below). Scale bars: **c** = 50 μm, **d** = 200 μm, **e**, **g**, **h** = 20 μm, **f**, **i**, **k** = 10 μm, **j** = 5 μm

Notes: Multigene phylogenetic analysis of a combined LSU, ITS and TEF1-α sequence dataset indicated that *Hongkongmyces kokensis* forms a sister clade with the sexual species *H. thailandica* with 97% MLBS and 1.00 BYPP support (Fig. 37). A comparison of LSU and ITS base pair shows that *H. kokensis* differs from *H. thailandica* with by 14/788 bp (1.77%) of LSU and 86/994 bp (8.65%) with 21 gaps of ITS. Furthermore, the morphological characters of *H. kokensis* and *H. thailandica* could not be directly compared as they represent as different morphs (Hyde et al. 2017). *Hongkongmyces kokensis* also shares some morphological features of conidiomata and conidia with *H. aquaticus* (Dong et al. 2020b), but they differ in shape and size of conidiomata and conidia (Fig. 35). However, phylogenetic analysis indicates that *H. kokensis* is a distinct species from *H. aquaticus* and *H. thailandica*. We therefore, introduce *Hongkongmyces kokensis* as a new species following the guidelines of Jeewon and Hyde (2016). The addition of protein coding gene data would likely strengthen the distinction of the new taxa.

Xenovaginatispora Boonmee, Huanraluek & K.D. Hyde, ***gen. nov.***

Index Fungorum number: IF558536; *Facesoffungi number*: FoF 09188.

Etymology: Named after its morphological similarity to *Vaginatispora*, but phylogenetically distinct.

Saprobic on submerged decaying wood. **Sexual morph** *Ascomata* immersed to semi-immersed, erumpent, solitary, scattered, globose to subglobose, dark brown, coriaceous to carbonaceous, ostiolate. *Papilla* slit-like, variable in shape, central, crest-like at the apex, with irregular pore-like opening. *Peridium* composed of several layers of dark brown cells of *textura angularis*, merged with the host tissues. *Hamathecium* comprising numerous, filamentous, rarely branched and anastomosed, hyaline, pseudoparaphyses, embedded in a gelatinous matrix. *Asci* 8-spored, bitunicate, elongate ovoid to clavate, short pedicellate, knob-like or obtuse, slightly narrow, rounded at the apex. *Ascospores* 1–2-seriate, overlapping, broadly fusoid to fusiform, septate, slightly constricted at the septum, both cells at central septum wider, with a single large guttule towards the centre of each cell, surrounded by a prominent and thick-walled mucilaginous sheath with wavy edge, drawn out towards each end to forming tapering appendages. **Asexual morph** Undetermined.

Type species: ***Xenovaginatispora phichaiensis*** Boonmee, Huanraluek & K.D. Hyde

Notes: *Xenovaginatispora* shares similarities with *Vaginatispora* taxa in having immersed to semi-immersed, erumpent, slit-like openings in the ascomata and broadly fusoid to fusiform, 1-septate, guttulate, surrounded by a prominent mucilaginous sheath, hyaline ascospores, which are variable in shape (Thambugala et al. 2015; Wanasinghe et al. 2016; Hashimoto et al. 2018; Hyde et al. 2019; Jayasiri et al. 2019). Phylogenetically, *Xenovaginatispora* belongs to *Lindgomycetaceae*, whereas *Vaginatispora* belongs to *Lophiostomataceae* (Thambugala et al. 2015). *Xenovaginatispora* forms a basal lineage to *Neolindgomyces* with high statistical support (93% MLBS, 1.00 BYPP). Based on morphology and phylogenetic distinctions, we introduce our collection as a new genus with the monotypic species, *Xenovaginatispora phichaiensis*.

Xenovaginatispora phichaiensis Boonmee, Huanraluek & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF558537; *Facesoffungi number*: FoF 09191; Fig. 36

Etymology: The specific epithet "*phichaiensis*" refers to the Phichai District, Uttaradit Province, Thailand.

Holotype: MFLU 21-0059

Saprobic on submerged decaying wood in a freshwater stream. **Sexual morph** *Ascomata* 151–225 μm high, 187–211 μm diam., immersed to semi-immersed, erumpent, solitary, scattered, globose to subglobose, dark brown, coriaceous to carbonaceous, ostiolate. *Papilla* slit-like, variable in shape, central papilla, coriaceous, crest-like at the apex, with an irregular pore-like opening. *Peridium* 27–38 μm wide, composed of several layers of dark brown cells of *textura angularis*, merged with the host tissues. *Hamathecium* comprising numerous, 1.5–3.5 μm wide, filamentous, rarely branched and anastomosed, hyaline, pseudoparaphyses, embedded in a gelatinous matrix. *Asci* 98–115.5 × 22–28 μm ($\bar{x}$ = 107 × 24 μm, n = 15), 8-spored, bitunicate, elongate ovoid to clavate, short pedicellate, with knob-like or obtuse, slightly narrow to rounded at the apex. *Ascospores* 35–42 × 10–13 μm ($\bar{x}$ = 39 × 12 μm, n = 10), overlapping 1–2-seriate, broadly fusoid to fusiform, 1-septate, slightly constricted at the septum, both cells at central septum wider, with a single large guttule, 8–12 μm diam., towards the centre of each cell, surrounded by a prominent and thick-walled mucilaginous sheath with wavy edge, drawn out towards each end to form tapering appendages. **Asexual morph** Undetermined.

Culture characteristics: Ascospores germinating on PDA within 24 h and germ tubes arising from both ends. Colonies on MEA, slow growing, reaching 3 cm diam. after 1 month of incubation at room temperature, initially dull white to light grey becoming dark grey at maturity, slightly effuse, radially with an undulate edge, greyish, light brown with brown pigmented in media, no sporulating in culture after 60 days.

Material examined: THAILAND, Uttaradit Province, Phichai, Thasak, Chom Tok Village, on submerged decaying wood in a small freshwater stream, 29 December 2018,

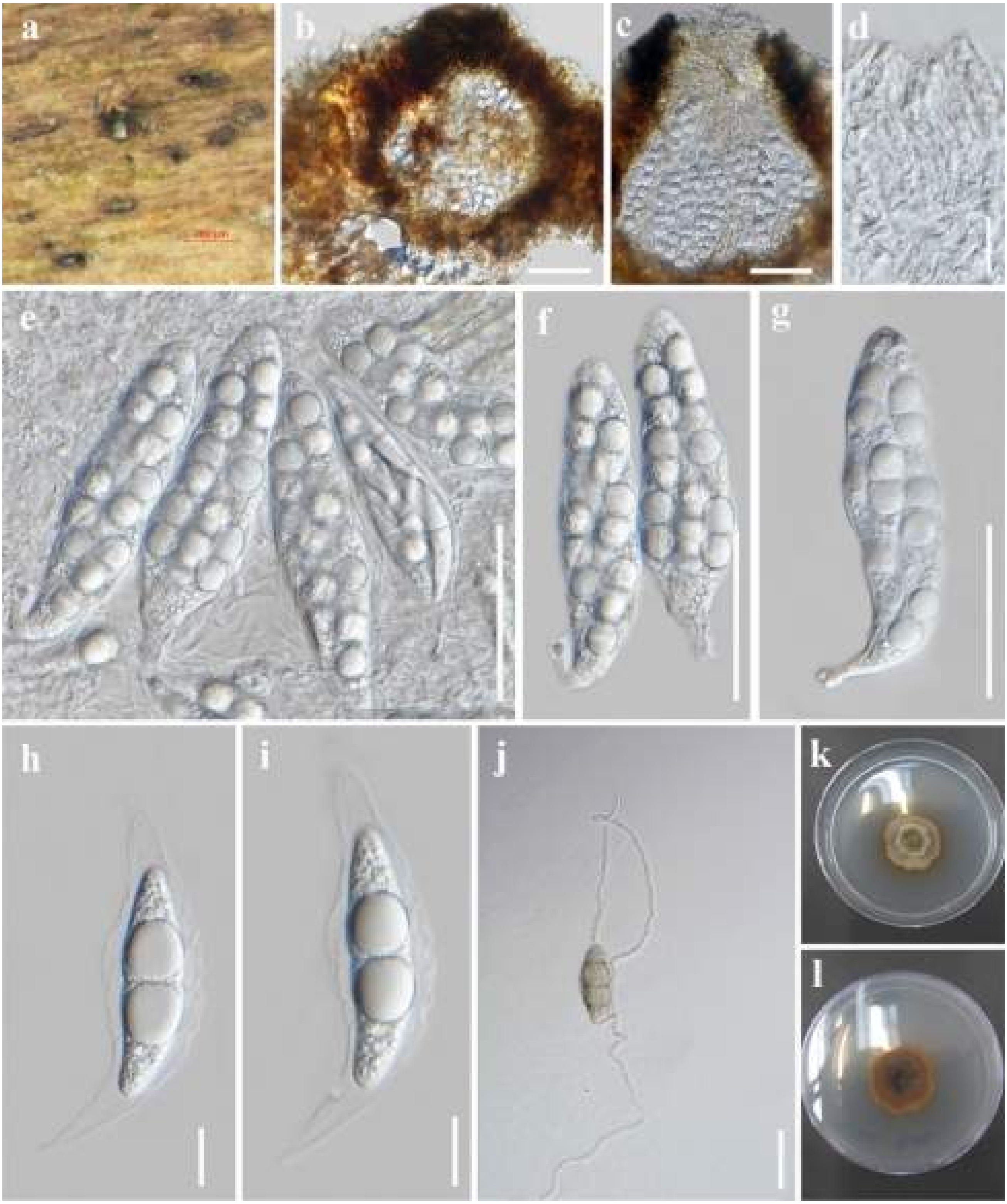


Fig. 36 ***Xenovaginatispora phichaiensis*** (MFLU 21-0059, **holotype**). **a** Appearance of ascomata. **b** Longitudinal sections of ascomata. **c** Ascomata with ostiole. **d** Pseudoparaphyses. **e**–**g** Asci. **h**, **i** Ascospores surrounded by mucilaginous sheath and distinct apical appendages. **j** Germinated ascospore. **k**, **l** Culture on MEA at 1 month (**k** = from surface and l = reverse). Scale bars: **b** = 100 µm, **c**, **d** = 50 µm, **e**–**g**, **j** = 20 µm, **h**–**i** = 10 µm

S. Boonmee, CTU8 (MFLU 21-0059, **holotype**), ex-type living culture, MFLUCC 21-0082.

GenBank numbers: ITS = MZ538534, LSU = MZ538569, SSU = MZ538577, TEF1-α = MZ567110.

Notes: In the NCBI BLASTn search of LSU and SSU sequences, *Xenovaginatispora phichaiensis* MFLUCC 21-0082 is most similar to an undescribed taxon *Pleosporales* sp. (F65-1) with 99.19% (LSU) and 99.70% (SSU) similarity. Unfortunately, we cannot compare the morphology in Shearer et al. (2009) as it lacks a description. Multigene phylogenetic analysis indicates that *Xenovaginatispora phichaiensis* clusters with the undescribed *Pleosporales* sp. (F65-1) and both of them form a subclade basal to *Neolindgomyces* species (*Lindgomycetaceae*) with 93% MLBS, 1.00 BYPP support (Fig. 37). *Xenovaginatispora phichaiensis* differs from *Neolindgomyces* species (Jayasiri et al. 2019) in having characteristics such as elongate ovoid to clavate asci and broadly fusoid to fusiform, only 1-septate ascospores, with two distinct large guttules in both cells. Therefore, we introduce *X. phichaiensis* as a new species based on morphology and phylogenetic evidences (Figs. 36 and 37).

Longipedicellataceae Phukhams., Bhat & K.D. Hyde

Notes: *Longipedicellataceae* was introduced to accommodate two genera *Longipedicellata* and *Pseudoxylomyces*, and the members of this family can be found in freshwater habitats (Phukhamsakda et al 2016). Recently, Dong et al. (2020b) included a new genus *Submersispora* in *Longipedicellataceae*, thus three genera are accepted in this family.

Longipedicellata H. Zhang, K.D. Hyde & Jian K. Liu

Notes: Since *Longipedicellata* was introduced by Zhang et al. (2016a), there are only two species included i.e., *Longipedicellata aptrootii* and *L. aquatica* (Dong et al. 2020b). We follow the latest treatment and the updated accounts of *Longipedicellata* in Dong et al. (2020b). Based on morphological uniqueness and phylogenetic evidence, a new species, *Longipedicellata fusiformispora* is introduced and three new isolates of *L. aquatica* are reported.

Longipedicellata aquatica W. Dong, H. Zhang & K.D. Hyde, in Dong et al., Fungal Diversity 105: 435 (2020)

Index Fungorum number: IF557915; *Facesoffungi number*: FoF 09257; Fig. 38

Saprobic on submerged decaying wood in the river. **Sexual morph** *Ascomata* 138–278 µm high, 148–276 µm diam., scattered, gregarious, immersed to, erumpent through the host surface, uni-loculate, sometimes bi-loculate, subglobose, dark brown to black, ostiolate. *Peridium* 15–25 µm thick, composed of several layers of brown to black cells of *textura angularis*. *Hamathecium* composed of sparse, anastomosed pseudoparaphyses, indistinctly septate. *Asci* 53–84 × 17–32 µm ($\bar{x}$ = 68 × 23 µm, n = 20), 8-spored, bitunicate, broadly clavate to spatulate, thickness and rounded at the apex, with a minute ocular chamber, short to long pedicellate. *Ascospores* 20–25 × 7–10 µm ($\bar{x}$ = 22 × 8 µm, n = 20), 2–3-seriate overlapping, broadly fusiform to ellipsoidal, rounded at both ends, asymmetrical, hyaline, 1-septate, constricted at the septum, the upper cell slightly broader and shorter than the lower cell, with large distinctive guttule in each cell when immature, surrounded by thickened mucilaginous sheath, smooth-walled. **Asexual morph**: Undetermined.

Culture characteristics: Ascospores germinating on MEA within 12 h at room temperature. Colony reaching 3 cm diam., dense, entire to slightly undulate edge, raised, dark grey, fluffy with aerial mycelium, with a lobate at the centre from above, darkened from reverse.

Material examined: THAILAND, Chiang Mai, Mae Ai, Tha Ton, Kok River, on submerged decaying wood in the river shore, 9 December 2019, S. Boonmee and N. Huanraluek, N-KR7 (MFLU 21-0060, **new record**), living culture, MFLUCC 21-0083; N-KR11 (MFLU 21-0096), living culture, MFLUCC 21-0100; Chiang Rai Province, Wiang Pa Pao, Lao River, on submerged decaying wood in the river shore, 11 December 2019, S. Boonmee and K.S.U. Chandrasiri, LR6 (MFLU 21-0061), living culture, MFLUCC 21-0084.

GenBank numbers: LR6: ITS = MZ538511, LSU = MZ538545, TEF1-α = MZ567089; N-KR7: ITS = MZ538510, LSU = MZ538544, SSU = MZ538571, TEF1-α = MZ567088; N-KR11: ITS = MZ538509, LSU = MZ538543, SSU = MZ538570, TEF1-α = MZ567087.

Notes: Multigene phylogenetic analysis of a combined LSU, ITS, TEF1-α and SSU sequence dataset indicates that our three new collections (MFLUCC 21-0083, MFLUCC 21-0084 and MFLUCC 21-0100) grouped with the ex-type strain *Longipedicellata aquatica* MFLUCC 17-2334 and other isolates with 79% MLBS, 0.97 BYPP; 79% MLBS and 96% MLBS support clade, respectively (Fig. 41). The morphological characters of the three new collections such as dark and immersed ascomata with apical erumpent ostiole, broadly clavate to spatulate, long pedicellate asci and broadly fusiform to ellipsoidal, hyaline, 1-septate, ascospores with a large distinctive guttule and surrounded by a mucilaginous sheath (Fig. 38) are similar to the ex-type strain MFLUCC 17-2334 (Dong et al. 2020a). Therefore, our three new collections as new freshwater records from Thailand.

Longipedicellata megafusiformis Chandrasiri, Boonmee & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF558538; *Facesoffungi number*: FoF 09947; Fig. 39

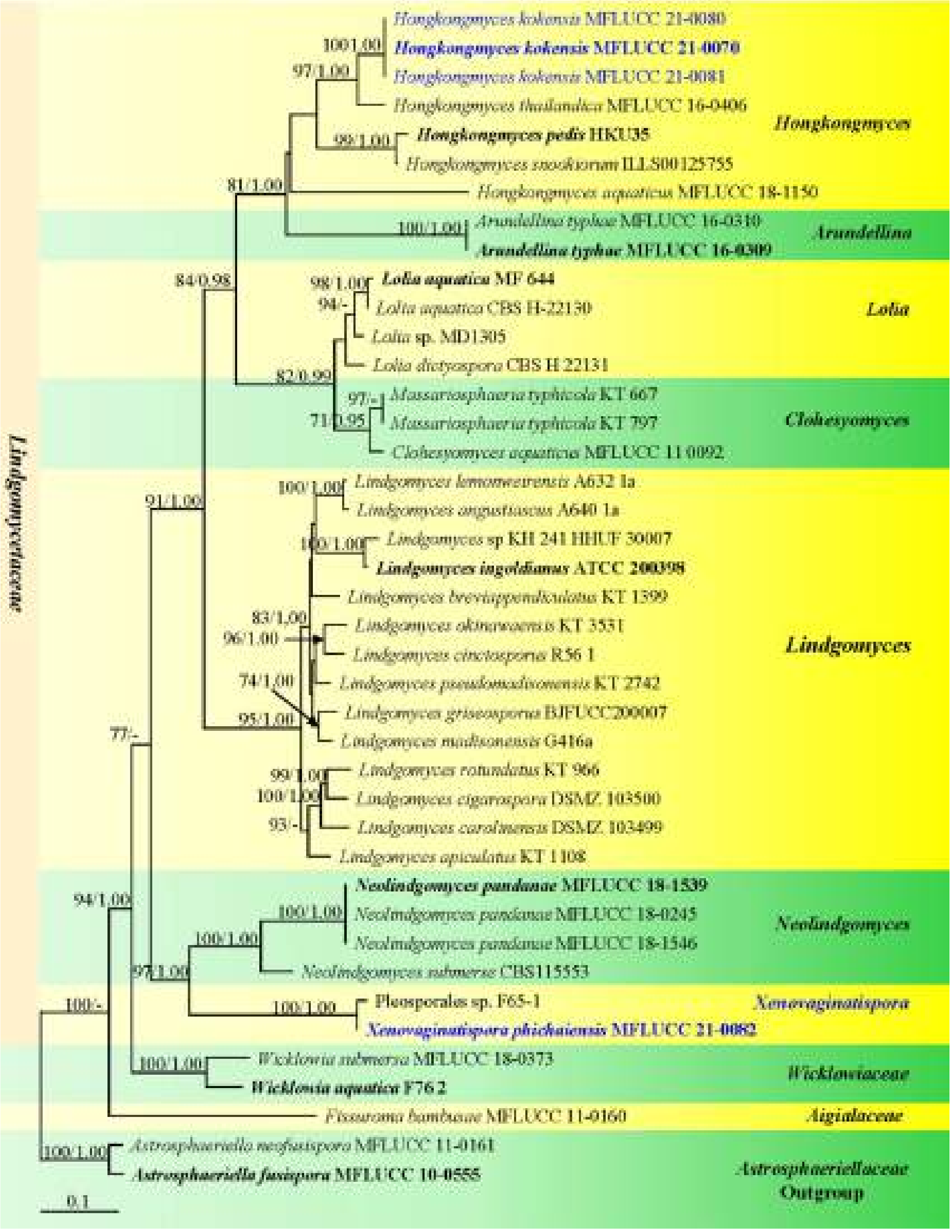


Fig. 37 Phylogram generated from maximum likelihood analysis based on combined LSU, SSU, ITS, and TEF1-α sequence data of new species and new genus in *Lindgomycetaceae*. *Astrosphaeriella neofusispora* MFLUCC 11-0161 and *A. fusispora* MFLUCC 10-0555 are selected as the outgroup taxa. Bootstrap support values for maximum likelihood (MLBS, left) equal to or greater than 70% is given above the nodes. Bayesian posterior probabilities (BYPP, right) equal to or greater than 0.95 are given above the nodes. Ex-type strains are in bold and newly generated sequences are in blue

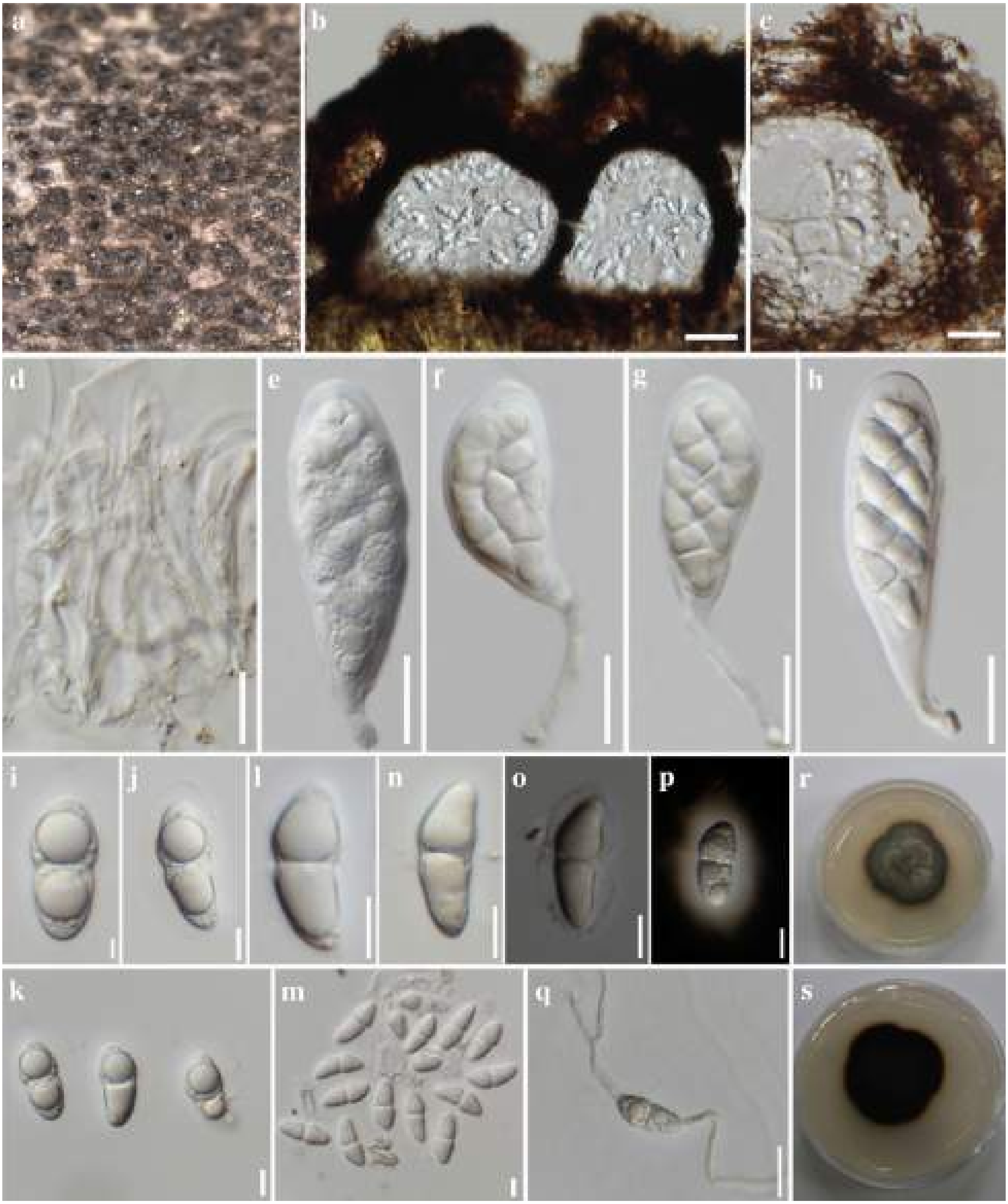


Fig. 38 ***Longipedicellata aquatica*** (MFLU 21-0060, **new record**). **a** Appearance of ascomata on submerged wood. **b** Section through ascomata. **c** Section of peridium. **d** Pseudoparaphyses. **e**–**h** Asci. **i**–**n** Ascospores. **o** Ascospore stained in Nigrosin. **p** Ascospore stained in Indian Ink. **q** Geminated ascospore. **r**, **s** Culture on MEA (r = from above, s = from below). Scale bars: **b** = 50 µm, **c**–**h**, **q** = 20 µm, **i**–**p** = 10 µm

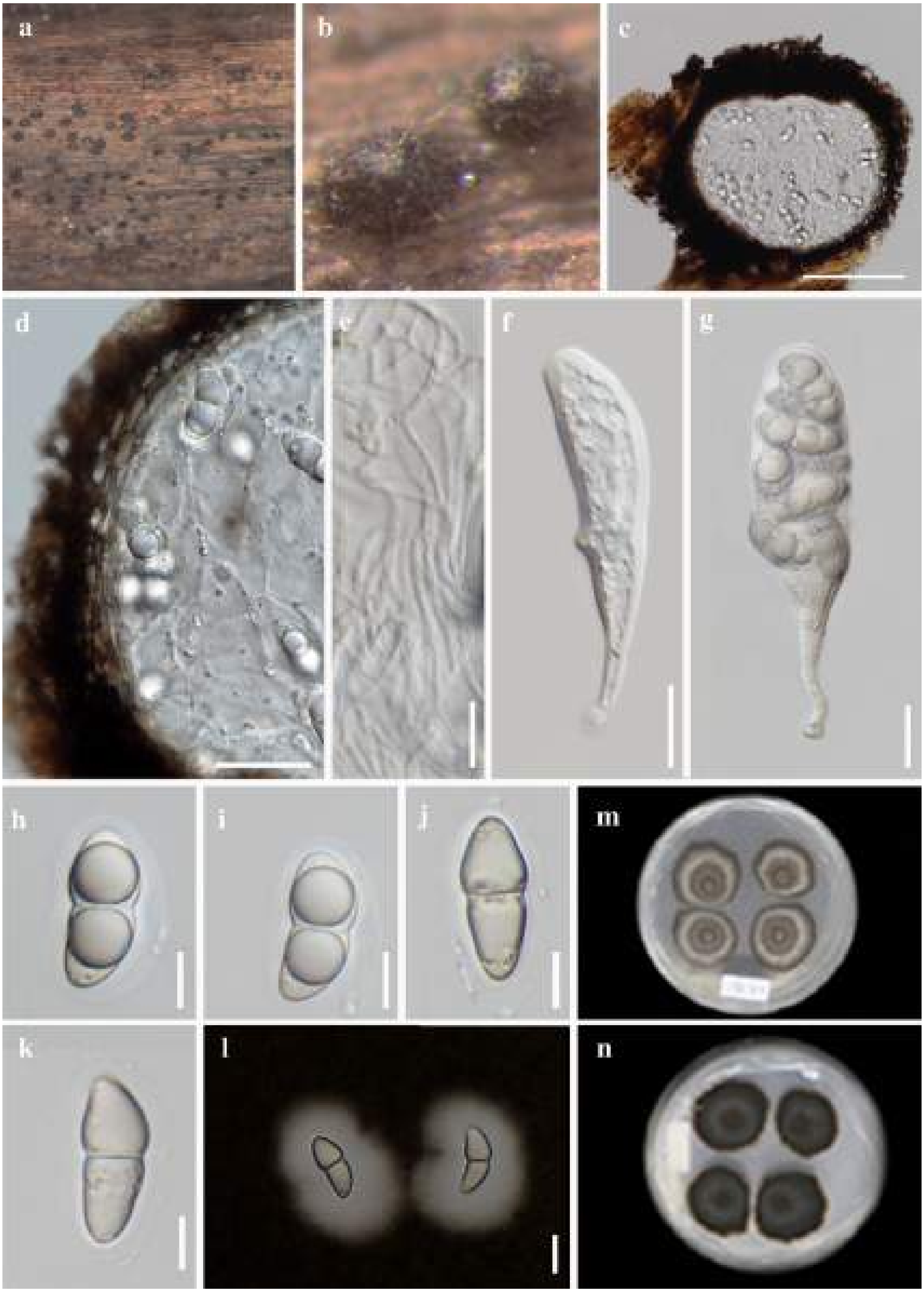


Fig. 39 ***Longipedicellata megafusiformis*** (MFLU 21-0062, **holotype**). **a**, **b** Appearance of ascomata on decaying submerged wood substrate. **c** Section through ascoma. **d** Section of peridium. **e** Pseudoparaphyses. **f**, **g** Asci. **h–k** Ascospores. **l** Ascospores stained in Indian Ink showing a mucilaginous sheath. **m**, **n** Culture on PDA (m = from above, n = from below). Scale bars: **c** = 100 μm, **b**–**g** = 20 μm, **h**–**l** = 10 μm

Etymology: The specific epithet "*megafusiformis*", in reference to the large and broad fusiform ascospores compared to other described species of *Longipedicellata*.

Holotype: MFLU 21-0062

Saprobic on decaying submerged wood in the river. **Sexual morph** *Ascomata* 153–204 µm high, 130–236 µm diam., solitary, scattered, semi-immersed to superficial, globose or subglobose, uni-loculate, black, with a bright ostiole. *Peridium* 20–30 µm thick, composed of several layers of brown to dark brown cells of *textura angularis*. *Hamathecium* comprising numerous, 1–1.5 µm wide, cylindrical filiform, sparsely branched, cellular pseudoparaphyses, embedded in gelatinous matrix. *Asci* 60–99 × 12–26 µm ($\bar{x}$ = 72 × 17 µm, n = 20), 8-spored, bitunicate, narrowly to broadly clavate. *Ascospores* 22–30 × 7–16 µm ($\bar{x}$ = 26 × 11 µm, n = 20), 2–3-seriate, ellipsoidal to fusiform, asymmetrical, upper cell wider, rounded at both ends, 1-septate, constricted at the septum, with a prominent guttule in both cells when immature, hyaline, surrounded by a large mucilaginous sheath, smooth-walled. **Asexual morph** Undetermined.

Culture characteristics: Ascospores germinating on water agar within 12 h at room temperature. Colonies growing on PDA, circular, dense, umbonate, edge entire in surface view and fimbriate in lateral view, opaque, with distinct colour zones, from periphery to middle dark grey, light grey, white and getting darker in the middle.

Material examined: THAILAND, Chiang Rai Province, Muang, Mae Yao, Kok River on decaying submerged wood in the river shore, 4 December 2019, S. Boonmee and S.K.U. Chandrasiri, SJ-KR4 (MFLU 21-0062, **holotype**), ex-type living culture, MFLUCC 21-0085.

GenBank numbers: ITS = MZ538512, LSU = MZ538546, TEF1-α = MZ567090.

Notes: The phylogenetic analysis of a combined LSU, ITS, TEF1-α and SSU sequence dataset indicates that *Longipedicellata megafusiformis* forms a distinct lineage basal to *L. aquatica* with 94% MLBS, 1.00 BYPP support (Fig. 41). *Longipedicellata megafusiformis* is different from *L. aptrootii* and *L. aquatica* in terms of the ascomata features in having single loculate with a bright ostiole on the top view and the size of ascospores (Fig. 39). However, its mucilaginous sheath and septate are not significantly different from other *Longipedicellata* species. *Longipedicellata megafusiformis* has larger ascospores (22-30 × 7–16 µm) than other species such as *L. aptrootii* (17.5–22 × 8–8.5 µm) and *L. aquatica* (19–22 × 8.5–10.5 µm) (Dong et al. 2020b). Therefore, we introduce *L. megafusiformis* as a new species in *Longipedicellata* based on morphological and phylogenetic analyses in *Longipedicellata*.

Submersispora W. Dong, H. Zhang & K.D. Hyde

Notes: *Submersispora* was introduced by Dong et al. (2020b) to accommodate a monotypic species *Submersispora variabilis* based on morphological characteristics and phylogenetic placement. The genus is characterized by freshwater inhabitants, slender semi-macronematous conidiophores and having variable in shaped chlamydospore-like conidia.

Submersispora variabilis W. Dong, H. Zhang & K.D. Hyde, in Dong et al., Fungal Diversity 105: 440 (2020)

Index Fungorum number: IF557917; *Facesofungi number*: FoF 08720; Fig. 40

Saprobic on decaying submerged wood in the river. **Sexual morph** Undetermined. **Asexual morph** *Colonies* on natural substrate superficial, solitary, scattered, gregarious black. Mycelium immersed in natural substrate. *Conidiophores* rather short, 9–26 µm long, 2–4 µm wide, semi-macronematous, mononematous, cylindrical, unbranched, septate, pale brown, thin and smooth-walled. *Conidiogenous cells* monoblastic, holoblastic, determinate, pale brown. *Conidia* 47–74 × 50–79 µm ($\bar{x}$ = 61 × 57 µm, n = 10), acrogenous, solitary, globose to subglobose, sometimes ellipsoidal to oblong, muriform, multi-septate, constricted at the septa, composed of angular cells, no septa when mature, brown to dark black, smooth-walled.

Culture characteristics: Conidia germinating on PDA within 12 h at room temperature. Colonies circular, reaching 2.5 cm in 3 weeks at room temperature, mycelium superficial, flat, slightly crenate edge, bright grey in surface, dark in reverse, with radially white grey arranges at the margin.

Material examined: THAILAND, Chiang Mai, Mae Ai District, Tha Ton, Kok River, on decaying submerged wood in the river shore, 9 December 2019, S. Boonmee and N. Huanraluek, N-KR15 (MFLU 21-0063, **new record**), living culture, MFLUCC 21-0086.

GenBank numbers: ITS = MZ538527, LSU = MZ538561, SSU = MZ538575, RPB2 = MZ567114, TEF1-α = MZ567103.

Notes: Our new collection is a typical *Submersispora* species, and it shares similar morphology with *Submersispora variabilis* in the features of conidia (Dong et al. 2020b; see Fig. 67). The multigene phylogenetic analysis showed that our isolated MFLUCC 21-0086 clustered with the type species *S. variabilis* with 100% MLBS, 1.00 BYPP support (Fig. 41). Therefore, we identify our collection (Fig. 40) as a new record for *S. variabilis* from Thailand.

Lophiostomataceae Sacc.

Notes: *Lophiostomataceae* was introduced by Saccardo (1883). The intergeneric relationships of the family have been well-studied by Thambugala et al. (2015), who provided a backbone tree for *Lophiostomataceae* and accepted 16 genera in *Lophiostomataceae* based on morphology and a multigene phylogenetic analysis. Eight additional genera have been introduced in this family (Wanasinghe et al. 2018; Hashimoto et al. 2018). Recently, Andreasen et al. (2021)

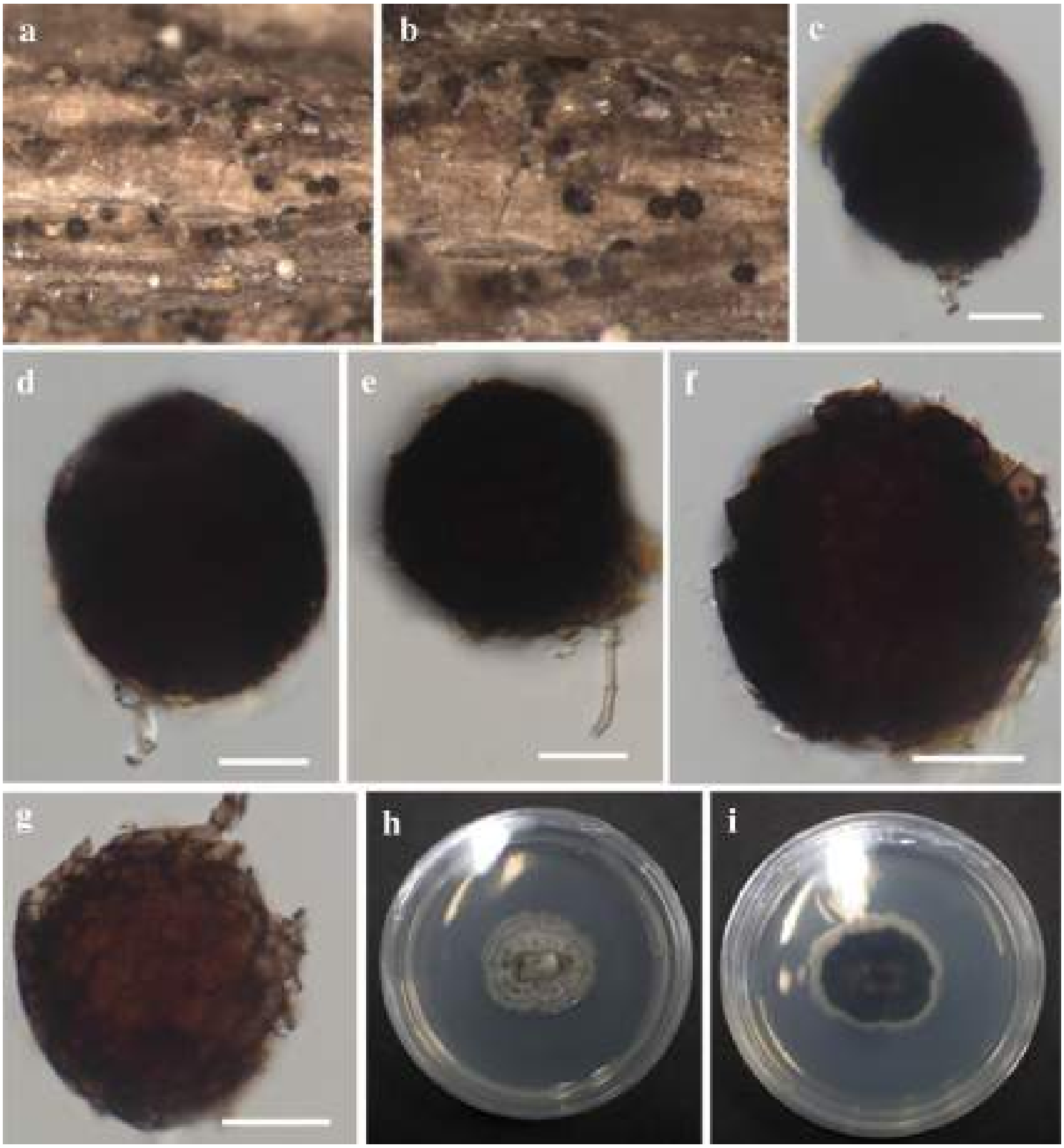


Fig. 40 ***Submersispora variabilis*** (MFLU 21-0063, **new record**). **a**, **b** Appearance of fungal colonies on woody substrate. **c–e** Conidiophores with conidia. **f**, **g** Close up of conidia. **h**, **i** Culture on PDA from surface and reverse. Scale bars: **c**–**e** = 20 µm, **f**–**g** = 10 µm

synonymized 14 genera under *Lophiostoma* and accepted 11 genera in *Lophiostomataceae*. Members of this family are characterized by immersed to erumpent, carbonaceous to coriaceous ascomata with rounded or slit-like ostioles, mostly clavate asci, one to multi-septate, hyaline to dark brown ascospores with terminal appendages or mucilaginous sheaths (Thambugala et al. 2015; Hashimoto et al. 2018; Hongsanan et al. 2020a). Most species of *Lophiostomataceae* are reported as saprobes from terrestrial, freshwater, and marine environments. (Thambugala et al. 2015; Hashimoto et al. 2018; Bao et al. 2019b; Mapook et al. 2020; Hongsanan et al. 2020a).

Lophiostoma Ces. & De Not.

Notes: *Lophiostoma* is a large genus included more 100 species (Hongsanan et al. 2020a). Members of *Lophiostoma* is characterized by laterally compressed or crest-like apices ascomata and common found saprobes on dead plants in aquatic and terrestrial habitats (Hirayama and Tanaka 2011; Thambugala et al. 2015). In this study, we provided on new host and geographical records for *Lophiostoma caudatum* and *L. clematidis-vitalbae* for Uzbekistan.

Lophiostoma caudatum Fabre, Annls Sci. Nat., Bot., sér. 6 9: 103 (1879) [1878]

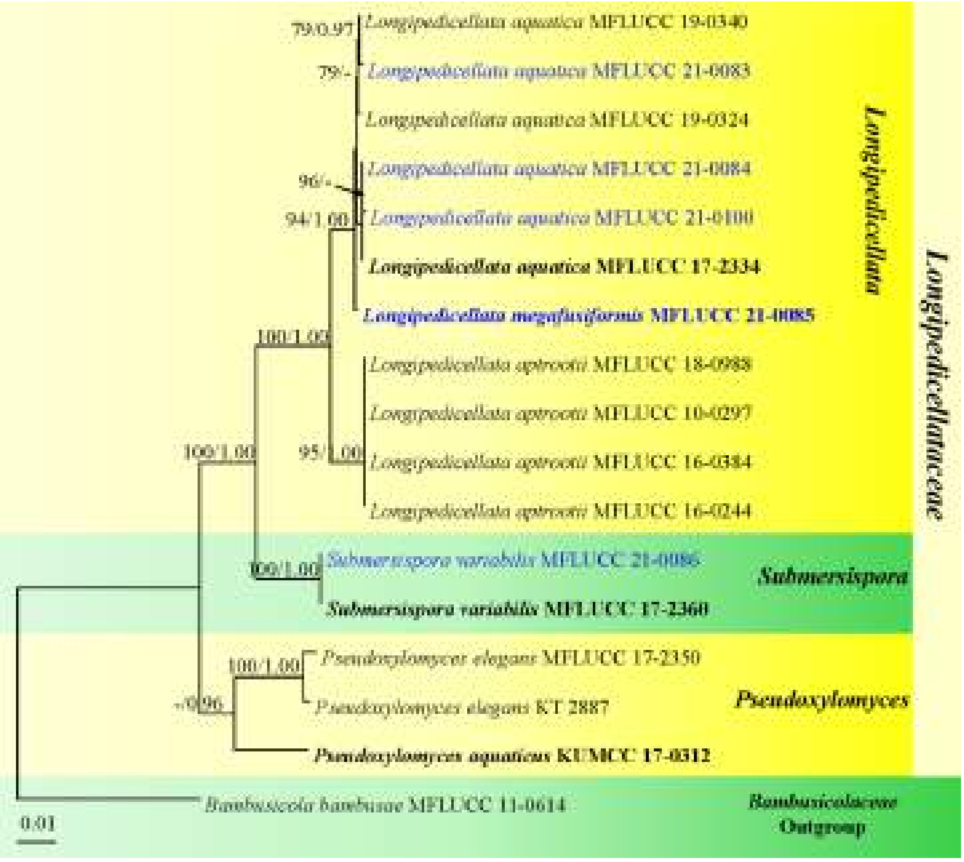


Fig. 41 Phylogram generated from maximum likelihood analysis based on combined LSU, ITS, TEF1-α and SSU sequence data of genera in *Longipedicellataceae*. The tree is rooted with *Bambusicola bambusae* (MFLUCC 11-0614). Bootstrap support values for maximum likelihood (MLBS, left) equal to or greater than 70% is given above the nodes. Bayesian posterior probabilities (BYPP, right) equal to or greater than 0.95 are given above the nodes. Ex-type strains are in bold and newly generated sequences are in blue

Index Fungorum number: IF185164; *Facesoffungi number*: FoF 00826; Fig. 42

= *Sigarispora caudata* (Fabre) Thambug., Qing Tian, Kaz. Tanaka & K.D. Hyde, in Thambugala et al., Fungal Diversity 74: 241 (2015)

Saprobic on dead stem of *Cousinia umbrosa* in a terrestrial habitat. **Sexual morph** *Ascomata* 322–349 µm high, 191–251 µm diam. ($\bar{x}$ = 336 × 211 µm, n = 10), scattered, immersed to semi-immersed, papilla erumpent through host surface, flattened at the base, coriaceous, black, ostiolate. *Ostiole* 128–175 × 35–39 µm wide ($\bar{x}$ = 146 × 37 µm, n = 5), slit-like, central, with a crest-like apex and a pore-like opening, elongated, irregular wall, filled with hyaline periphyses. *Peridium* 25–47 µm wide ($\bar{x}$ = 35 µm, n = 13), wider at the apex and thinner at the base, with dark brown to lightly pigmented, thin-walled cells of textura angularis, cells towards the inside lighter and darker towards outside, merging with the host tissues. *Hamathecium* composed of numerous, 1–2 µm wide, filamentous, septate, pseudoparaphyses. *Asci* 89–215 × 12–13.5 µm ($\bar{x}$ = 114 × 13 µm, n = 10), 8-spored, bitunicate, fissitunicate, clavate, with an apically rounded and a bulbous pedicel. *Ascospores* 23–28 × 5–7 µm ($\bar{x}$ = 25 × 6 µm, n = 18), biseriate, overlapping, brown to dark brown, fusiform with narrow, acute ends, usually 3–6 septate, not constricted at the central septum, guttulate, lacking a mucilaginous sheath, smooth-walled. **Asexual morph** Undetermined.

Material examined: UZBEKISTAN, Jizzakh Province, Zaamin District, Zaamin National Nature Park, river of Ettisuv, Turkestan range of Pamir-Alay Mountains, on dead stem of *Cousinia umbrosa* Bunge (*Compositae*), 11 July 2019, Y. Gafforov and T. Kholmuradova, YG-Z2-1 (TASM 6156, **new host and geographical record**).

GenBank Numbers: ITS = MZ576205, LSU = MZ577238, SSU = MZ577240, TEF1-α = MZ605436.

Notes: In phylogenetic analysis of *Lophiostoma*, our strain (TASM 6156) clusters with the reliable strain *Lophiostoma caudatum* (KT 530) with 83% MLBS, 0.99 BYPP (Fig. 44). However, our strain shares similar morphological characters of ascomata, asci and ascospores (Fig. 42) with *L. caudatum* (KT 530) (Thambugala et al. 2015). Pairwise comparison of the ITS, LSU, SSU and TEF1-α sequences of *L. caudatum* (TASM 6156) and *L. caudatum* (KT 530) reveals 0.61% in ITS, 0.11% in LSU and SSU, and 0.61% in TEF1-α are not significantly different. Therefore, *L. caudatum* is reported as a new host and geographical record on *Cousinia umbrosa* for Uzbekistan.

Lophiostoma clematidis-vitalbae Andreasen, Jaklitsch & Voglmayr, in Andreasen et al., Persoonia 46: 251 (2021)

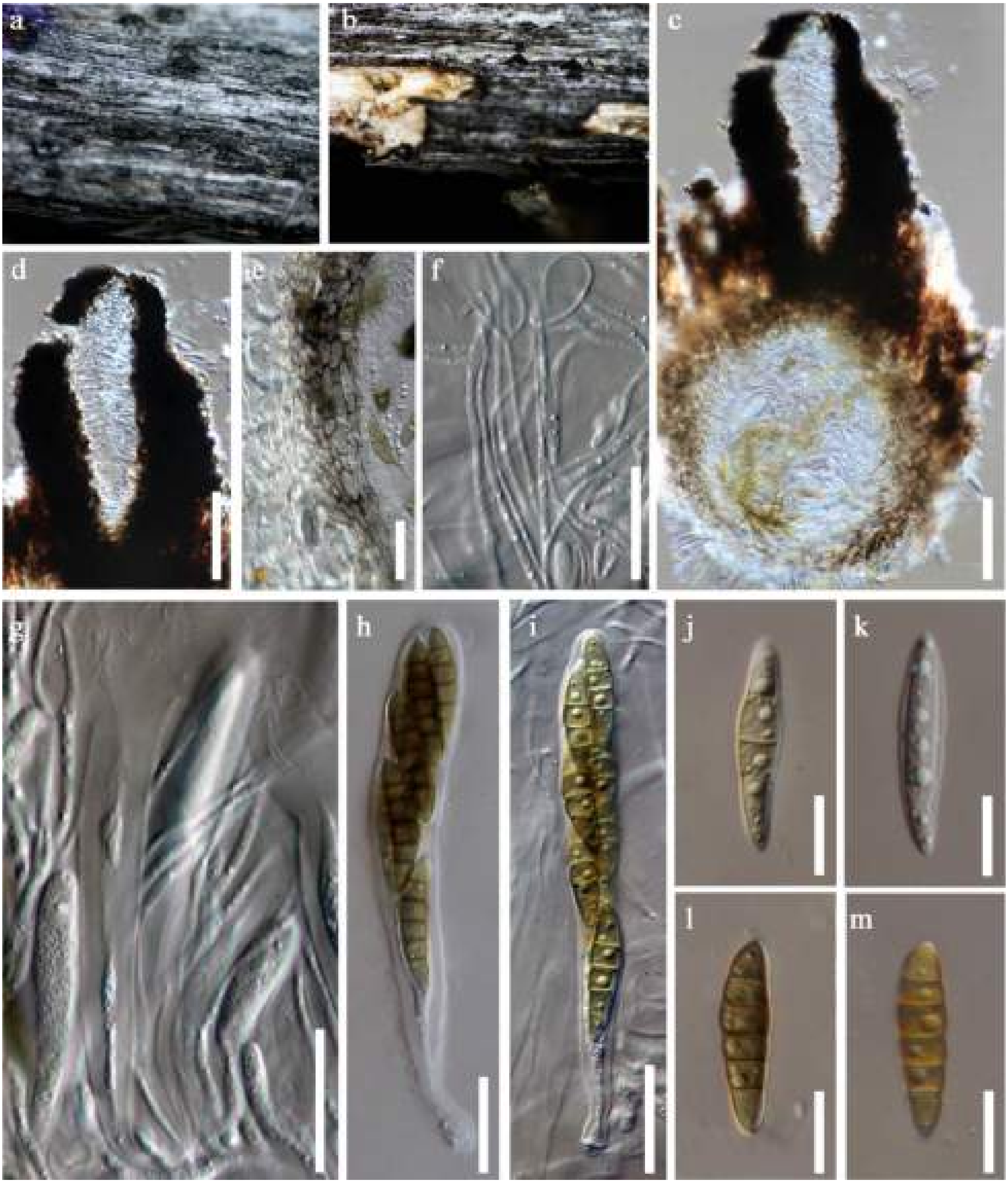


Fig. 42 ***Lophiostoma caudatum*** (TASM 6156, **new host and geographical record**). **a**, **b** Appearance of ascomata on host surface. **c** Vertical section of ascoma. **d** Ostiolar canal. **e** Peridium. **f** Pseudoparaphyses. **g**–**i** Asci. **j**–**m** Ascospores. Scale bars: **c**, **d** = 50 μm, **e**–**i** = 20 μm, **j**–**m** = 10 μm

Index Fungorum number: IF838978; *Facesoffungi number*: FoF 07294; Fig. 43

≡ *Sigarispora clematidis* Phukhams. & K.D. Hyde, in Phukhamsakda et al., Fungal Diversity 102: 53 (2020)

Saprobic on dead stem of unknown host. **Sexual morph** *Ascomata* 504–534 µm high, 372–473 µm diam. ($\overline{x}$ = 523 × 413 µm, n = 10), solitary or aggregated, semi-immersed to superficial, with only black shiny ostioles visible, globose, coriaceous, dark brown to black, rough-walled, ostiolate. *Ostioles* 165–213 × 25–98 µm ($\overline{x}$ = 193 × 52 µm, n = 5), with a crest-like apex and a pore-like opening, central, elongated and laterally compressed, irregular wall, filled with hyaline periphyses. *Peridium* 62–82 µm wide ($\overline{x}$ = 70 µm, n = 20), wider at the apex, thinner at the base, with lightly pigmented dark brown to black, thick-walled cells of textura angularis, cell towards the inside lighter, somewhat flattened. *Hamathecium* composed of numerous, dense, 1.8–2.3 µm wide, filamentous, septate, pseudoparaphyses. *Asci* 93–111 × 11–14 µm ($\overline{x}$ = 101 × 12 µm, n = 30), 8-spored, bitunicate, fissitunicate, clavate, with furcate pedicel, rounded at the apex, with an ocular chamber. *Ascospores* 19–25 × 5–7 µm ($\overline{x}$ = 23 × 6 µm, n = 50), bi-seriate or partially overlapping, broad fusiform, tapering towards the ends, initially hyaline, becoming yellowish brown at maturity, acute ends, mostly curved, 1–5 transversely eusepta, slightly constricted at the septa, cells above central septum swollen, a guttulate, with 5–9 µm long sheath drawn out to form polar appendages. **Asexual morph** Undetermined.

Material examined: UZBEKISTAN, Jizzakh Province, Zaamin District, Zaamin National Nature Park, river of Ettisuv, Turkestan range of Pamir-Alay Mountains, on dead stem of *Lonicera* sp. (*Caprifoliaceae*), 10 July 2019, Y. Gafforov and T. Kholmuradova YG-Z32-2 (TASM 6157, **new host and geographical record**).

GenBank accession numbers: ITS = MZ576206, LSU = MZ577239, SSU = MZ577241, TEF1-α = MZ605437, RPB2 = MZ605438.

Notes: In phylogenetic analysis of *Lophiostoma*, our strains (TASM 6157) clusters with the ex-type strain *Lophiostoma clematidis-vitalbae* (MFLUCC 16-1368) with 0.98 BYPP (Fig. 44). Our strain (Fig. 43) shares similar ascomata, asci and ascospores features identical to the type strain *L. clematidis-vitalbae* (MFLUCC 16-1368) (Phukhamsakda et al. 2020). Therefore, *L. clematidis-vitalbae* is reported as a new host and geographical record on *Cousinia umbrosa* for Uzbekistan.

Vaginatispora K.D. Hydes

Notes: *Vaginatispora* was introduced by Hyde (1995) to accommodate *Vaginatispora aquatica*, which was previously placed in *Massrinaceae*. Thambugala et al. (2015) treated *Vaginatispora* as a separate genus in *Lophiostomataceae* with two new combinations, *V. aquatica* and *V. fucklii*. *Vaginatispora fucklii* was later transferred to *Neovaginatispora* (Hashimoto et al. 2018). Six new species and a new combination *V. armatispora* were introduced in this genus (Wanasinghe et al. 2016; Devadatha et al. 2017; Hashimoto et al. 2018; Hyde et al. 2019; Jayasiri et al. 2019). Currently, nine species are included in this genus (Hashimoto et al. 2018; Hyde et al. 2019; Jayasiri et al. 2019). *Vaginatispora* species are characterized by depressed globose ascomata, immersed beneath a blackened neck, with a slot-like ostiole, numerous filamentous pseudoparaphyses, cylindrical to clavate asci and narrowly ellipsoidal, hyaline, 1-septate ascospores with a mucilaginous collar around its equator, having single large guttules in each cell, and a spreading papilionaceous sheath (Thambugala et al. 2015; Hashimoto et al. 2018; Hyde et al. 2020b).

Vaginatispora nypae Jayasiri, E.B.G. Jones & K.D. Hyde, Mycosphere 10(1): 84 (2019)

Index Fungorum number: IF555558; *Facesoffungi number*: FoF 05264; Fig. 45

Saprobic on submerged decaying wood. **Sexual morph** *Ascomata* 250–420 µm high, 210–270 µm diam. ($\overline{x}$ = 299 × 247 µm, n = 10), scattered to gregarious, immersed, coriaceous, dark brown to black, subglobose, ostiolate. *Ostiole* slit-like, elongated, with a pore-like opening, plugged by hyaline, filamentous hyphae, and occasionally lighter colour, periphysate. *Peridium* 30–60 µm wide, circular, symmetric, dark brown to black layers, somewhat flattened cells of *textura angularis*, inner stratum comprising hyaline cell layers of *textura angularis*. *Hamathecium* comprising numerous, filamentous, branched septate, pseudoparaphyses 1.5–2 µm wide ($\overline{x}$ = 1.8 µm, n = 30). *Asci* 80–108 × 13–15 µm ($\overline{x}$ = 94 × 14.5 µm, n = 20), 8-spored, bitunicate, fissitunicate, cylindrical-clavate, short-pedicellate, apex rounded with a minute ocular chamber. *Ascospores* 26–29 × 6–7 µm ($\overline{x}$ = 27 × 6 µm, n = 30), uni- to bi-seriate, overlapping, hyaline, fusiform with narrow, acute ends, 1-septate, slightly constricted at the septum, smooth-walled, guttulate, with a prominent mucilaginous sheath. **Asexual morph** Undetermined.

Culture characters: Conidia germinated on PDA within 24 h. Colonies on PDA reaching 3–4 cm diam., after 4 weeks at room temperature, colonies irregular, medium dense, brown to grey in top view with pale brown edge. Lower surface dark brown with radially arranges margin.

Material examined: THAILAND, Yasothon Province, Thai Charoen District, Kham Phi, on decaying wood submerged in a River, 13 November 2018, D.F. Bao, B154 (MFLU 20-0424, **new record**), living culture, MFLUCC 20-0101.

GenBank numbers: ITS = MZ490791, LSU = MZ501207, SSU = MZ490777, TEF1-α = MZ501207.

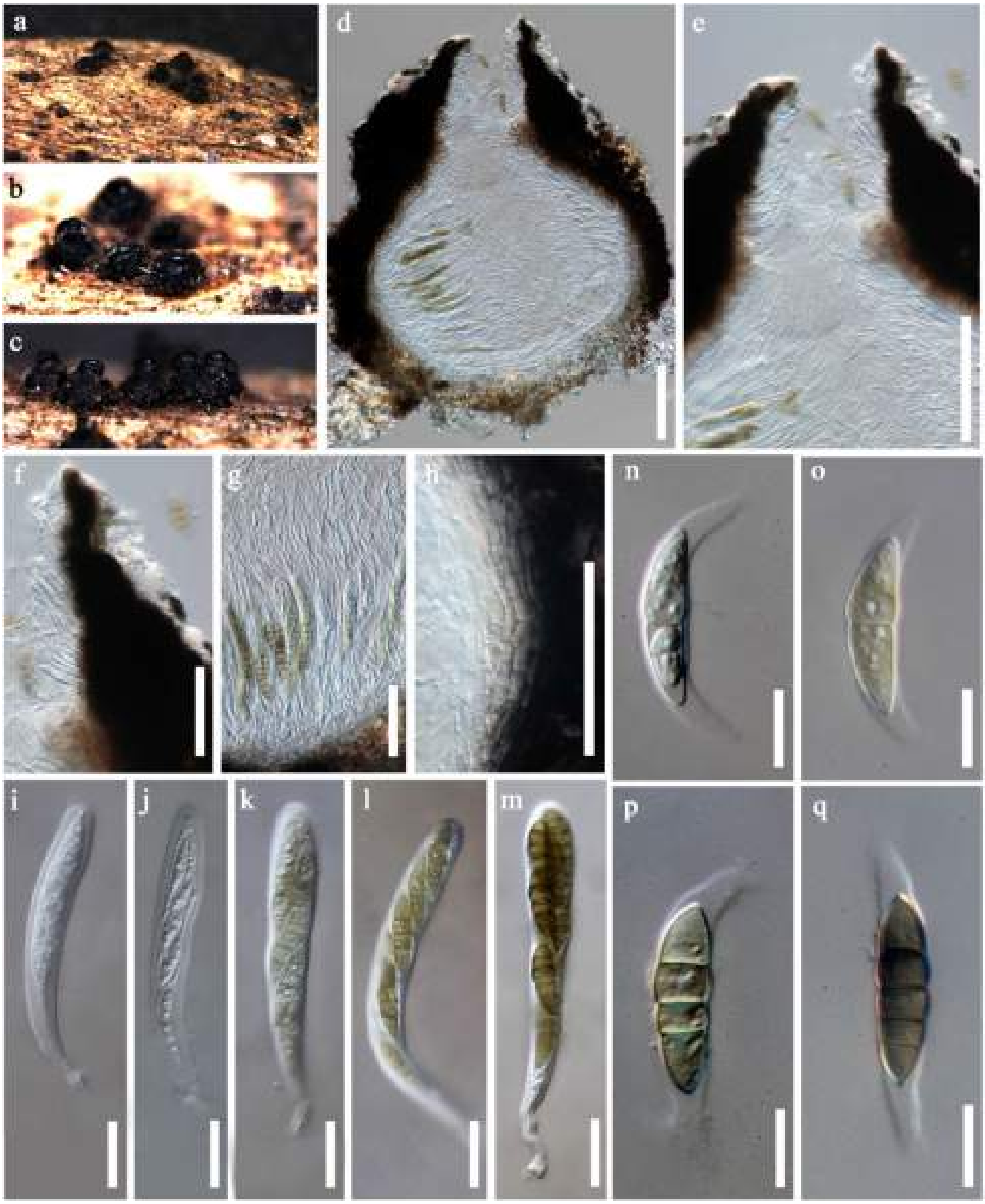


Fig. 43 ***Lophiostoma clematidis-vitalbae*** (TASM 6157, **new host and geographical record**). **a–c** Appearance of ascomata on host surface. **d** Vertical section of ascoma. **e** Ostiolar canal. **f** Periphyses at ostiole. **g** Pseudoparaphyses. **h** Peridium. **i–m** Asci. **n–q** Ascospores. Scale bars: **d**, **e** = 100 µm, **f–h** = 50 µm, **i–m** = 20 µm, **n–q** = 10 µm

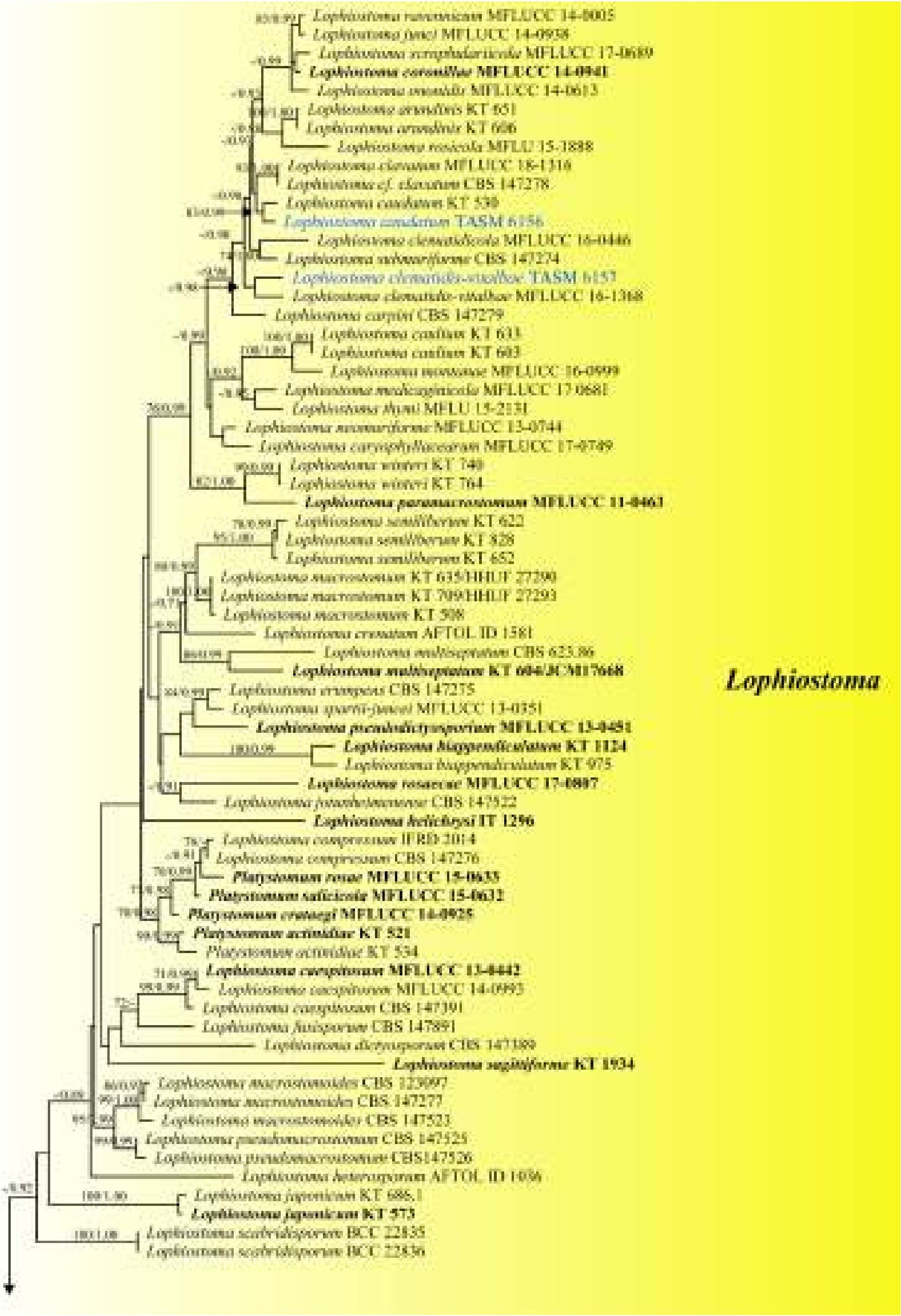


Fig. 44 Phylogram generated from maximum likelihood analysis based on combined SSU, LSU, ITS, TEF1-α and RPB2 sequence data for *Lophiostomataceae*. One hundred twelve strains are included in the combined analyses which comprise a total of 4199 characters. *Teichospora rubriostiolata* TR7 and *Teichospora trabicola* C134 are selected as the outgroup taxa. The best RAxML tree with a final likelihood value of − 30611.078207 is presented. RAxML analysis yielded 1567 distinct alignment patterns and 25.77% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.248812, C = 0.247504, G = 0.267733, T = 0.235951, with substitution rates AC = 1.717311, AG = 4.965346, AT = 1.578028, CG = 1.454739, CT = 10.722777, GT = 1.000000; gamma distribution shape parameter alpha = 0.639152. Support values for maximum likelihood (MLBS, left) greater than 70% and Bayesian posterior probabilities (BYPP, right) greater than 0.90 are given at the nodes. Ex-type strains are in bold and newly generated sequences are in blue

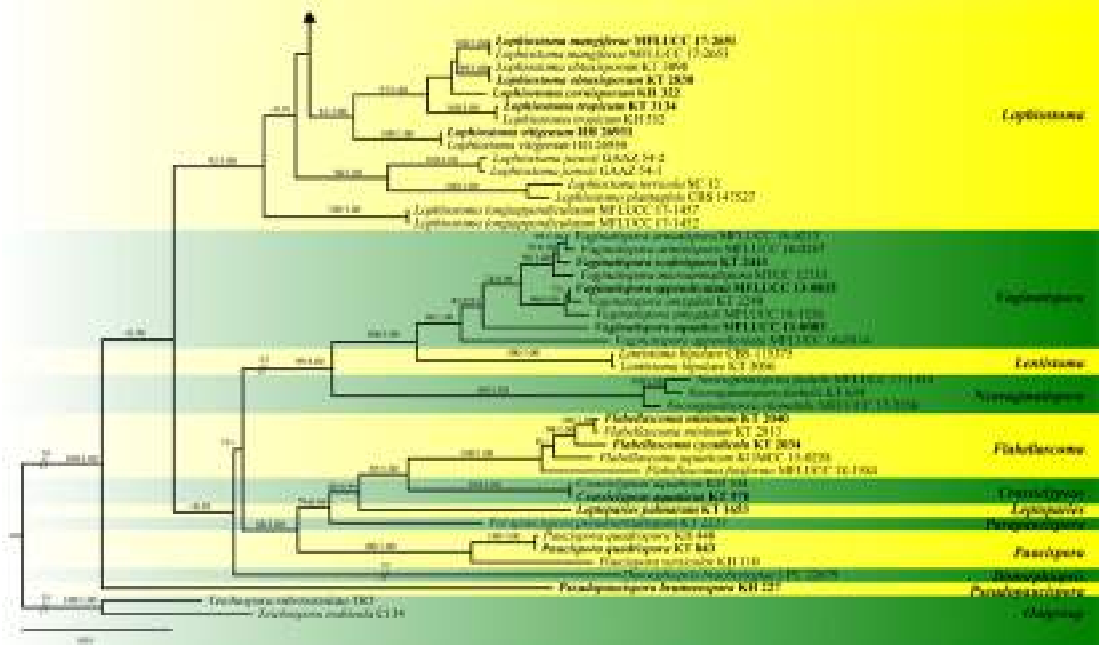


Fig. 44 (continued)

Notes: *Vaginatispora nypae* was introduced by Jayasiri et al. (2019), which was recorded from pericarp of fallen fruit of *Nypa fruticans* on terrestrial habitat in Thailand. Based on our phylogenetic analysis of combined LSU, SSU, ITS, TEF1-α and RPB2 sequence data, our isolate (MFLUCC 20-0101) clustered with the ex-type strain of *Vaginatispora nypae* (MFLUCC 18-1543) with 100% MLBS, 1.00 BYPP support (Fig. 46). Our isolate appears quite similar to *V. nypae*, in that they have similar shaped asci and ascospores. However, our isolate has larger asci (80–108 × 13–15 µm vs. 75–85 × 11–13 µm) and ascospores (26–29 × 6–7 µm vs. 22–26 × 10–13 µm), which may be explained by the different habitats (Fig. 45). Our isolate was collected from a freshwater habitat, while the strain of MFLUCC 18-1543 was collected from a terrestrial habitat. A comparison of the ITS and TEF1α nucleotides of *V. nypae* (MFLUCC 18-0245) and a new strain (MFLUCC 20-0101) revealed 2 bp (0.38%) and 6 bp (0.6%) nucleotide differences respectively. This indicates that our new strain is *V. nypae* (Jeewon and Hyde 2016). Therefore, we introduce this isolate as a new record of *V. nypae* from a freshwater habitat.

Lophiotremataceae K. Hiray. & Kaz.

Notes: Hirayama and Tanaka (2011) introduced *Lophiotremataceae* to accommodate *Lophiotrema* based on morphological characters and molecular phylogenetic analyses of LSU and SSU sequence data. Hashimoto et al. (2017) revised the family using morphological data and multigene phylogenetic analyses of ITS, LSU, RPB2, SSU and TEF1-α. In the most recent outline of Dothideomycetes, Hongsanan et al. (2020a) accepted seven genera in this family viz. *Atrocalyx*, *Crassimassarina*, *Cryptoclypeus*, *Galeaticarpa*, *Koordersiella*, *Lophiotrema* and *Pseudocryptoclypeus*. An updated phylogenetic tree for *Lophiotremataceae* is presented in Fig. 50.

Lophiotrema Sacc.

Notes: *Lophiotrema* is one of the oldest genera in *Pleosporales* of which the species are characterized by immersed ascomata with a crest-like ostiolar neck and cylindrical asci (Hashimoto et al. 2017). Species in this genus are commonly found as saprobic on various plant species and plant-based substrates in terrestrial (Holm and Holm 1988), freshwater (Hyde and Aptroot 1998), and marine environments (Hongsanan et al. 2020a). Currently there are 38 species that are included in this genus but only eight species have been confirmed by molecular data (Hongsanan et al. 2020a). In this study, we introduce a new species and two new host records from Yunnan, China.

Lophiotrema hydei J.F. Zhang, J.K. Liu & Z.Y. Liu, Phytotaxa 379(2): 172 (2018)

Index Fungorum number: IF555509; *Facesoffungi number*: FoF 05216; Fig. 47

Saprobic on wood of *Rosa* sp. **Sexual morph**: *Ascomata* 220–300 × 200–250 µm ($\bar{x}$ = 261 × 229 µm, n = 10), solitary or gregarious, immersed to erumpent through host tissue, globose to subglobose, brown to dark brown, uni-loculate, glabrous, ostiolate. *Ostiole* mostly central. *Peridium* 20–40 µm wide, composed of angular cells, outer

Fig. 45 ***Vaginatispora nypae*** (MFLU 20-0424, **new record**). **a–c** Ascomata on submerged wood. **d** Section of ascoma. **e** Ostiolar canal. **f** Peridium. **g** Pseudoparaphyses. **h–l** Asci. **m–p** Ascospore. **q**, **r** Culture on MEA from upper and lower views. Scale bars: **a** = 1000 µm, **b**, **c** = 200 µm, **d** = 100 µm, **e**, **f** = 50 µm, **g–l** = 20 µm, **m–p** = 15 µm

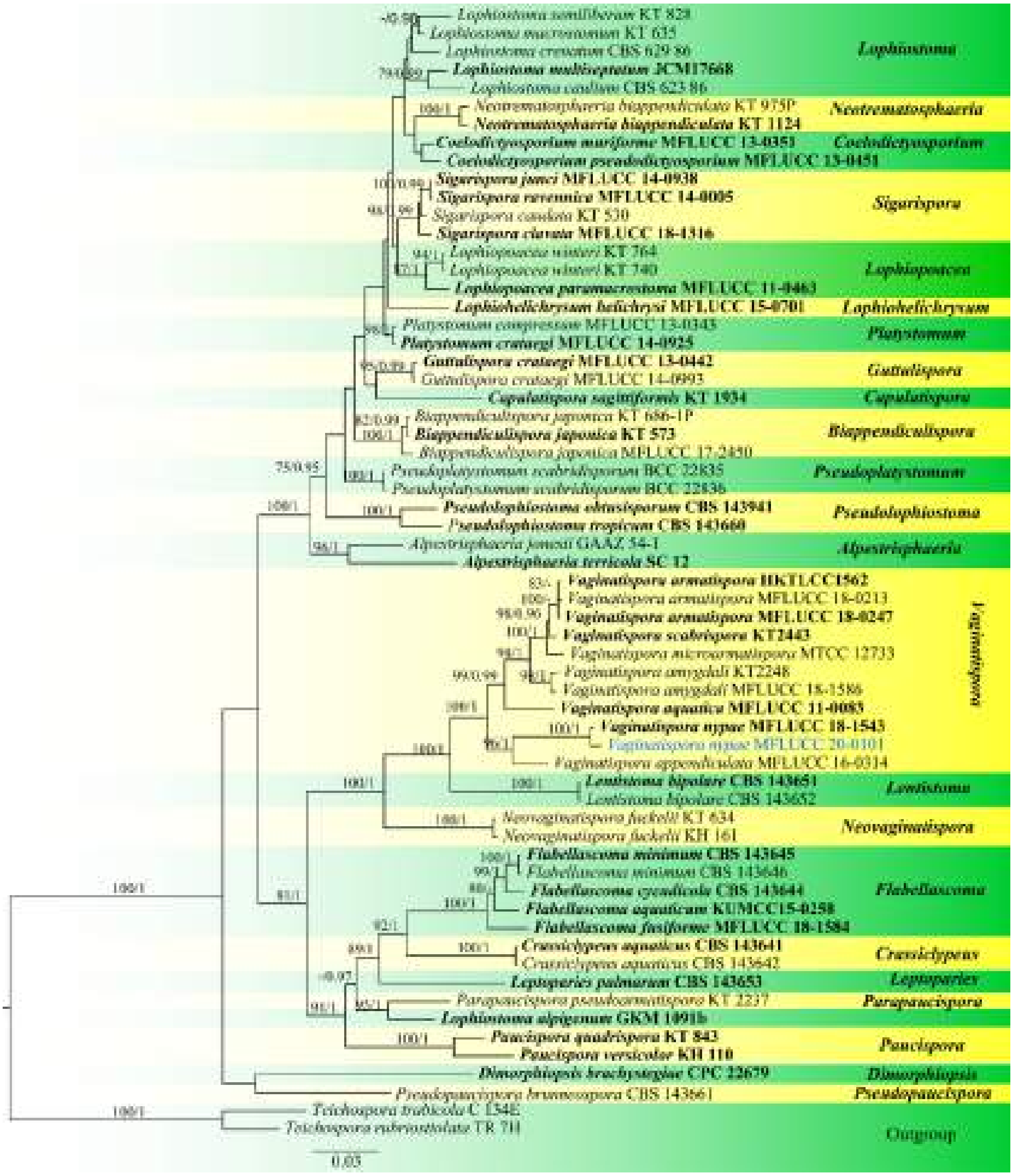


Fig. 46 Phylogenetic tree generated from maximum likelihood (ML) analysis based on combined LSU, SSU, ITS, TEF1-α and RPB2 sequence data for the species from *Melanommataceae*. *Teichospora trabicola* (C 134E) and *T. rubriostiolata* (TR 7) are used as the outgroup taxa. The dataset comprised 4379 characters after alignment including gaps (LSU = 883 bp, SSU = 966 bp, ITS = 523 bp, TEF1-α = 1001 bp and RPB2 = 1006 bp). The RAxML analysis of the combined dataset yielded a best scoring tree with a final ML optimization likelihood value of − 26352.113239. The matrix had 1530 distinct alignment patterns, with 26.20% undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.248486, C = 0.247993, G = 0.267004, T = 0.236517; substitution rates AC = 1.626883, AG = 4.007531, AT = 1.289884, CG = 1.323552, CT = 8.595651, GT = 1.000000; gamma distribution shape parameter α = 0.180969. Support values for maximum likelihood (MLBS, left) above than 75% and Bayesian posterior probabilities (BYPP, right) greater than 0.95 are given at the nodes. Ex-type strains are in bold and newly generated sequence is in blue

layer, dark brown, thick-walled cells, inner layer, hyaline with thin-walled cells. *Hamathecium* composed of numerous, 1.5–2.5 µm wide, filamentous, septate, branched, cellular pseudoparaphyses. *Asci* 80–120 × 10–13 µm ($\bar{x}$ = 105 × 11 µm, n = 20), 8-spored, bitunicate, fissitunicate, cylindrical to cylindric-clavate, short pedicellate,

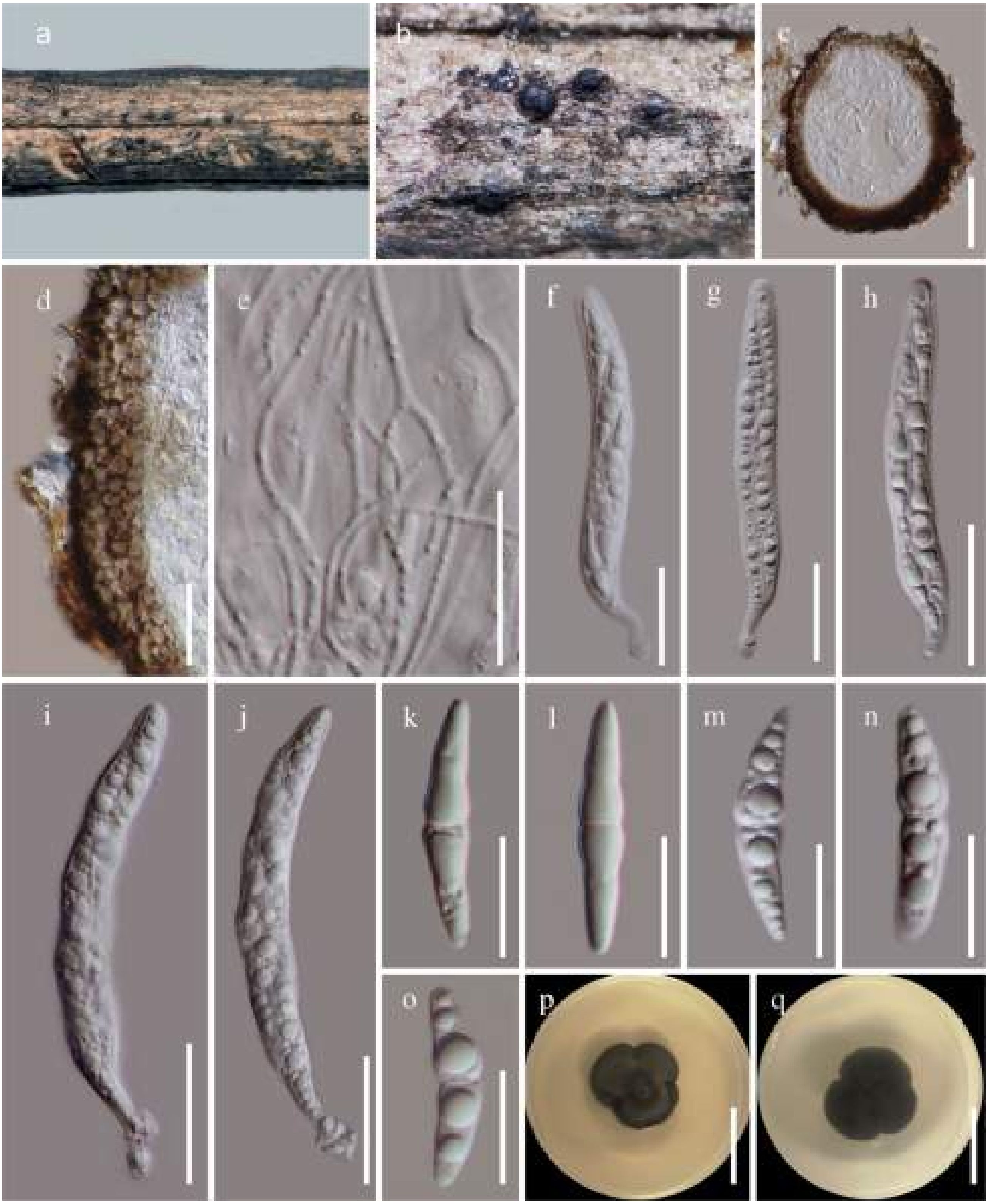


Fig. 47 ***Lophiotrema hydei*** (HKAS 115782, **new host record**). **a**, **b** Appearance of ascomata on host surface. **c** Longitudinal section of an ascoma. **d** Section of the peridium cells. **e** Pseudoparaphyses. **f**–**j** Asci. **k**–**o** Ascospores. **p**, **q** Culture characteristic on PDA (**p** = from above, **q** = from below). Scale bars: **c** = 100 μm, **d**, **f**–**j** = 20 μm, **e** = 5 μm, **k**–**o** = 10 μm, **p**, **q** = 10 mm

apically rounded, with a minute ocular chamber. *Ascospores* 25–35 × 4–7 µm ($\overline{x}$ = 31 × 5.5 µm, n = 30), overlapping bi-seriate, fusiform, hyaline, straight or slightly curved, 1-septate, the upper cell is longer than the lower cell, deeply constricted at the septum, narrower towards both ends, smooth-walled, guttulate. **Asexual morph** Undetermined.

Culture characteristics: Ascospores germinating on PDA within 24 h and germ tubes arising from both ends. Colonies on PDA, slow growing, reaching 2 cm diam. after 4 weeks of incubation at room temperature, initially white becoming blackish brown at maturity, slightly effuse, radially with an undulate edge, reverse blackish brown.

Material examined: CHINA, Yunnan, Diqing Autonomous Prefecture, Shangri-La, Xiaozhongdianzhen (27.468883°N 99.845828°E), 2958 m, on dead wood of *Rosa* sp. (*Rosaceae*), 30 August 2020, GC Ren, DQ33 (HKAS 115782, **new host record**), living culture could not maintain.

GenBank numbers: ITS = MZ493297, LSU = MZ493311, SSU = MZ493283, TEF1-*α* = MZ508406.

Notes: Zhang et al. (2018) introduced *Lophiotrema hydei* as a saprobe on herbaceous plant from Guizhou Province, China. In this study, we found a new strain that grouped with the ex-type strain of *L. hydei* in multi-gene phylogenetic analysis with 98% MLBS support (Fig. 50). There were no nucleotide differences between these two strains in SSU, LSU, ITS and TEF1-α. The asci of the new isolate are comparatively larger (80–120 × 10–13 µm vs. 78–89(–99) × 6.9–8.8 µm), but other features are similar in dimensions (Fig. 47). Therefore, we identify our collection as a new host record of *Lophiotrema hydei* on *Rosa* sp. from Yunnan Province, China.

Lophiotrema lincangensis Wanas. & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF558584; *Facesoffungi number*: FoF 09948; Fig. 48

Etymology: The specific epithet "*lincangensis*" refers to the Lincang City, Yunnan Province, China where the type was collected.

Holotype: HKAS 115777

Saprobic on dead twigs of *Fagaceae* sp. **Sexual morph**: *Ascomata* 140–180 µm high, 120–160 µm diam. ($\overline{x}$ = 158 × 139 µm, n = 10), solitary or gregarious, immersed to erumpent through host tissue, globose to subglobose, brown to dark brown, uni-loculate, glabrous, ostiolate. *Ostiole* mostly central, minute papilla. *Peridium* 15–30 µm wide, composed of angular, pseudoparenchymatous cells, outer layer, dark brown, thick-walled cells, inner layer, hyaline with thin-walled cells. *Hamathecium* composed of numerous, 1.5–2 µm wide, filamentous, septate, cellular pseudoparaphyses. *Asci* 50–90 × 6.5–9 µm ($\overline{x}$ = 63.5 × 7.5 µm, n = 20), 8-spored, bitunicate, fissitunicate, cylindrical to cylindric-clavate, short pedicellate, apically rounded, with a minute ocular chamber. *Ascospores* 16–22 × 3–4 µm ($\overline{x}$ = 19.5 × 3 µm, n = 30), overlapping bi-seriate, fusiform, hyaline, straight or slightly curved, one-celled when young and become inconspicuously 1-septate at maturation, the upper cell is longer than the lower cell, constricted at the septum, narrower towards both end cells, smooth-walled, guttules. **Asexual morph** Undetermined.

Culture characteristics: Ascospores germinating on PDA within 24 h and germ tubes arising from both ends. Colonies on PDA, slow growing, reaching 2 cm diam. after 4 weeks of incubation at room temperature, initially white becoming blackish brown at maturity, slightly effuse, radially with a smooth edge, blackish brown.

Material examined: CHINA, Yunnan, Lincang City, Linxiang, 24.883878° N 100.092519° E, on dead twigs of *Fagaceae* sp., 10 August 2020, GC Ren, LC21-01 (HKAS 115777, **holotype**), ex-type living culture could not maintain; *ibid*. LC21-03 (HKAS 115778), living culture could not maintain.

GenBank numbers: ITS = MZ493298, MZ493299, LSU = MZ493312, MZ493313, SSU = MZ493284, MZ493285, RPB2 = MZ508416, MZ508417, TEF1-α = MZ508407, MZ508408.

Notes: During our investigation on the woody-based microfungi in Yunnan, two isolates were recovered from *Fagaceae* hosts in Lincang City. Morphological characteristics such as asci and ascospores fit well within the species concept of *Lophiotrema* (Fig. 48). In our phylogenetic study, these new strains clustered with *L. hydei* and *L. mucilaginosis* with 100% MLBS support (Fig. 50). Comparatively, our new collections had smaller asci and conidia than these two species (see notes of *L. hydei*). A nucleotide base comparison of ITS (513 bp) among our new strains, *L. hydei* and *L. mucilaginosis* reveals 23 bp (4.5%) and 24 bp (4.7%) base pair differences (Jeewon and Hyde 2016). The TEF1-α nucleotides (889 bp) comparison of the two species with our new strain reveals 29 bp (3.3%) and 24 bp (2.7%) difference respectively. The RPB2 nucleotides comparison (953 bp) of with *L. mucilaginosis* and our new strains reveals 54 bp (5.6%) base pair differences. Whereas *L. hydei* is lacking of RPB2 sequence data.

Lophiotrema neoarundinariae Y. Zhang ter, Kaz. Tanaka & K.D. Hyde [as '*neoarundinaria*'], Stud. Mycol. 64: 97 (2009)

Index Fungorum number: IF836880; *Facesoffungi number*: FoF 09949; Fig. 49

≡ *Didymosphaeria arundinariae* Ellis & Everh., N. Amer. Pyren. (Newfield): 732 (1892)

Saprobic on dead twigs of *Prunus* sp. **Sexual morph**: *Ascomata* 200–300 µm high, 150–200 µm diam. ($\overline{x}$ = 248 × 180.5 µm, n = 10), solitary or gregarious, immersed to erumpent through host tissue, subglobose or obpyriform, brown to dark brown, ostiolate. *Ostiole*

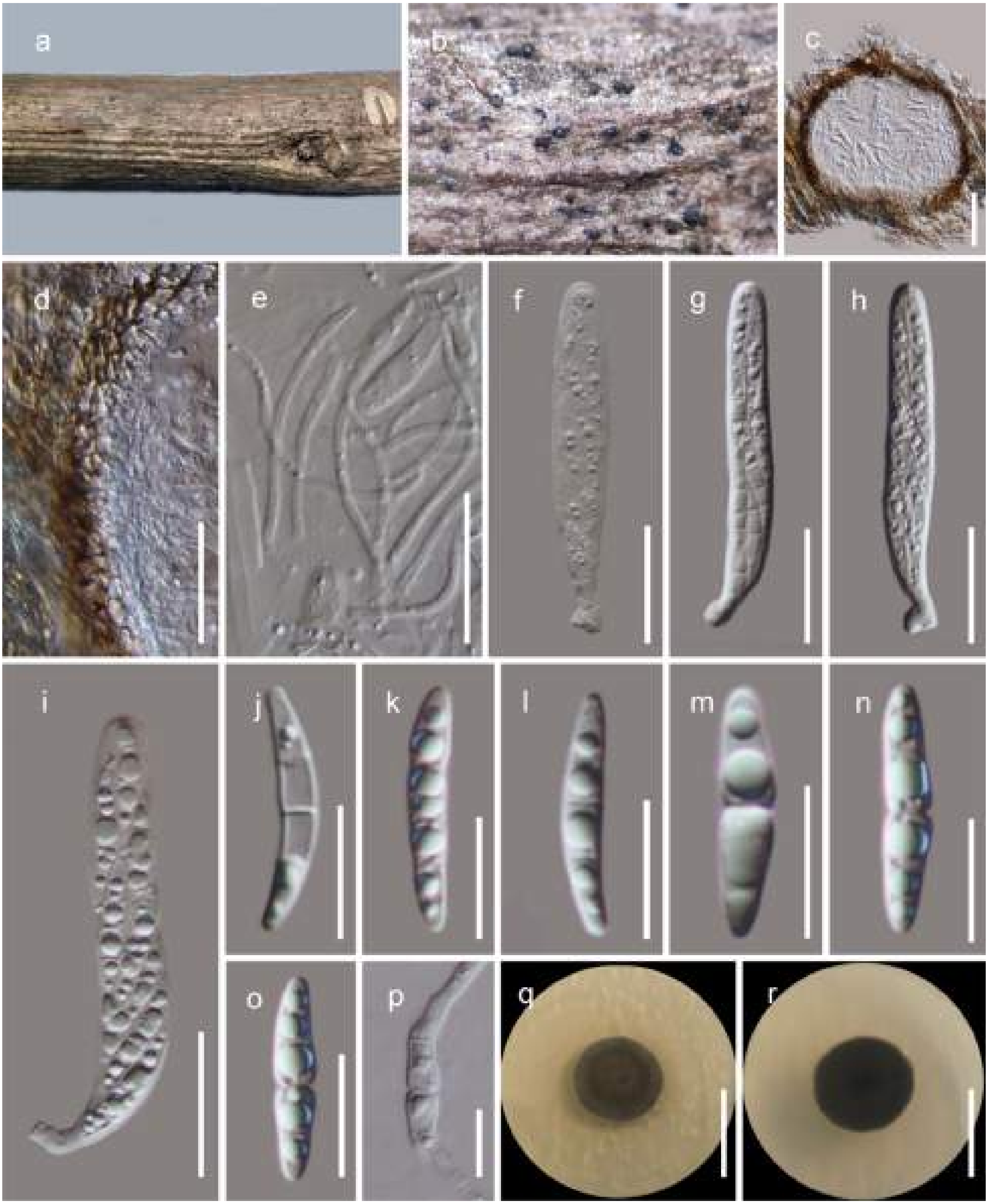


Fig. 48 ***Lophiotrema lincangensis*** (HKAS 115777, **holotype**). **a**, **b** Appearance of ascomata on host surface. **c** Longitudinal section of an ascoma. **d** Section of the peridium. **e** Pseudoparaphyses. **f**–**i** Asci. **j**–**o** Ascospores. **p** Germinated ascospore. **q**, **r** Culture characteristic on PDA (**q** = from above, **r** = from below). Scale bars: **c** = 100 μm, **d**, **f**–**i** = 20 μm, **e** = 5 μm, **j**–**p** = 10 μm, **q**, **r** = 10 mm

50–80 µm long, 40–60 µm diam., carbonaceous, mostly central, minute papilla, with crest-like opening, filled with hyaline periphysate. *Peridium* 10–15 µm wide at the base, 12–20 µm wide at sides, composed of flattened, angular, pseudoparenchymatous cells, outer layer, dark brown, thick-walled cells, inner layer, hyaline with thin-walled cells. *Hamathecium* composed of numerous, 1.5–2 µm wide, filamentous, septate, branched, cellular pseudoparaphyses. *Asci* 80–120 × 8–9 µm ($\bar{x}$ = 98 × 8 µm, n = 20), 8-spored, bitunicate, fissitunicate, cylindrical, subsessile to short pedicellate, apically rounded, with a minute ocular chamber. *Ascospores* 20–30 × 3.5–4.5 µm ($\bar{x}$ = 23 × 4 µm, n = 30), overlapping biseriate, fusiform, hyaline, straight or slightly curved, one-celled when young, becoming 3-septate at maturation, the upper cell is longer than the lower cell, constricted at the septa, narrower towards both end cells, smooth-walled, with guttules. **Asexual morph** Undetermined.

Culture characteristics: Ascospores germinating on PDA within 24 h and germ tubes arising from both end cells. Colonies on PDA, reaching 4 cm diam. after 4 weeks of incubation at room temperature, initially white becoming dirty white to creamy, flattened, with a smooth edge, reverse dark brown, with pale grey margin.

Material examined: CHINA, Yunnan, Kunming, Xiaokong Mountain, 25.171311° N 102.703690° E, on dead twigs of *Prunus* sp., 21 December 2019, CG Ren, KM007 HKAS 115779, **new host record**), living culture (KUMUCC 21-0037).

GenBank numbers: ITS = MZ493302, LSU = MZ493316, SSU = MZ493288, RPB2 = MZ508420, TEF1-α = MZ508411.

Notes: Zhang et al. (2009) introduced *Lophiotrema neoarundinariae* comb. nov. to accommodate taxon which was previously described as *Didymosphaeria arundinariae*. Schoch et al. (2009a), Tanaka et al. (2009), Hirayama and Tanaka (2011) and Hashimoto et al. (2016, 2017) provided additional DNA based sequence data for this species. In this study, a newly collected taxon is identified as *L. neoarundinariae* based on multigene phylogenetic analysis and reported as a new host record on *Prunus* sp. from Yunnan, China (Figs. 49 and 50).

Macrodiplodiopsidaceae Voglmayr, Jaklitsch & Crous

Notes: *Macrodiplodiopsidaceae* was introduced by Crous et al. (2015) to accommodate *Macrodiplodiopsis* and *Pseudochaetosphaeronema* in the suborder Massarineae. Tanaka et al. (2015) accepted the asexual genera *Camarographium*, *Macrodiplodiopsis* and *Pseudochaetosphaeronema* and Ariyawansa et al. (2015a) introduced *Pseudomonodictys*. However, *Macrodiplodiopsis* and *Pseudochaetosphaeronema* are currently accepted in *Macrodiplodiopsidaceae* (Wijayawardene et al. 2020). In this study, the sequences for phylogenetic analyses were downloaded from GenBank by following the latest treatment in Hyde et al. (2020b) and results of BLAST searches in NCBI. An updated phylogenetic tree is presented in Fig. 52. Our phylogenetic analysis is similar to that of Hyde et al. (2020b).

Pseudochaetosphaeronema Punith.

Notes: *Pseudochaetosphaeronema* was introduced by Punithalingam (1979) based on *Pseudochaetosphaeronema larense*. The whole genus was treated based on asexual morphology and sexual morphs were undetermined (Zhang et al. 2016b; Hyde et al. 2020b). The members of the genus can act as human pathogens, endophytes and saprobes (Ahmed et al. 2014; Zhang et al. 2016b; Hyde et al. 2020b). Six species epithets are listed in Index Fungorum (2021). In this study, we introduce a novel species of *Pseudochaetosphaeronema* collected from Thailand, and it is the first report of the sexual morph of the genus. The tree topology of our multigene phylogenetic analyses is similar to the latest analysis performed by Hyde et al. (2020b).

Pseudochaetosphaeronema chiangraiense Wijesinghe, Boonmee & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF558549; *Facesofungi number*: FoF 09950; Fig. 51

Etymology: The name reflects the location from which species was collected, Chiang Rai, Thailand.

Holotype: MFLU 21-0083

Saprobic on dead terrestrial branch of *Tamarindus* sp. **Sexual morph** *Ascomata* 190–255 µm high, 190–200 µm diam., ($\bar{x}$ = 223 × 197 µm, n = 10), solitary, scattered, immersed, erumpent on host, uni-loculate, black, globose to subglobose. *Peridium* 13–17 µm wide, thin-walled, composed of several layers of small, brown to pale brown cells of *textura angularis*. *Hamathecium* comprising numerous, 2–4.5 µm wide, cellular, unbranched, pseudoparaphyses that are septate, without constrictions at the septa. *Asci* 50–110 × 15–30 µm ($\bar{x}$ = 80 × 18 µm, n = 30), 8-spored, bitunicate, fissitunicate, with obovoid, short distinct pedicel with rounded end, apex rounded with a minute ocular chamber. *Ascospores* 20–45 × 7–8 µm ($\bar{x}$ = 34 × 7.5 µm, n = 30), overlapping, 2–3-seriate, hyaline, fusiform, with pointed ends, 1-septate at the center, constricted at the septa, guttulate, thick and smooth-walled. **Asexual morph** Undetermined.

Culture characteristics: Ascospores germinating on PDA within 24 h. Germ tubes produced both sides of ascospore. Colonies on PDA reaching 1–2 cm diam. after 5 days in day light at 25 °C, colonies medium dense, flat or effuse, from above, greenish gray in middle and pale brown at the margin, yellowish brown in reverse side.

Material examined: THAILAND, Chiang Rai Province, Nang Lae Village, on the dam of the pond near Lake Hill Resort, dead branch of *Tamarindus* sp. (*Fabaceae*),10 May

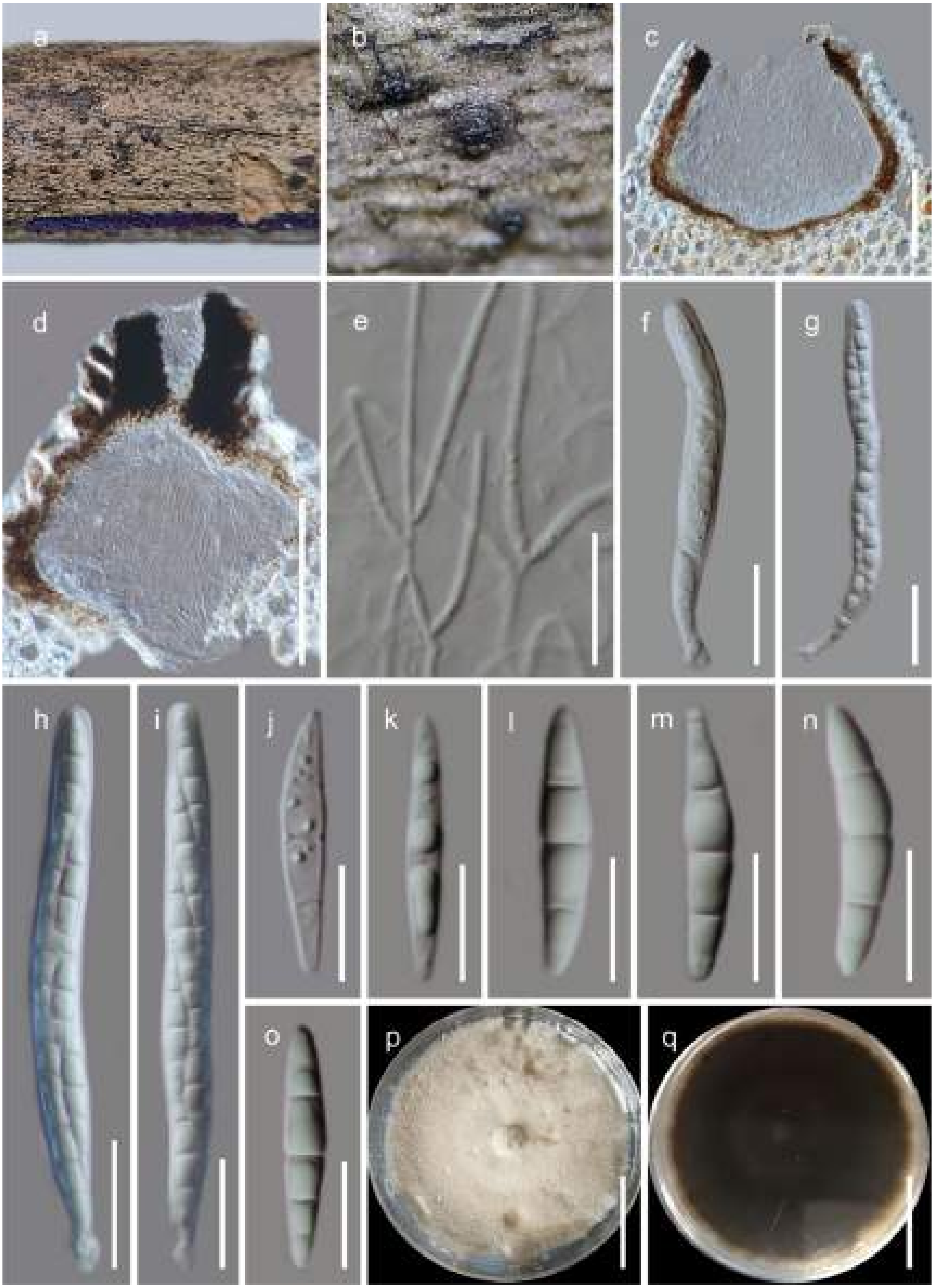


Fig. 49 ***Lophiotrema neoarundinariae*** (HKAS 115779, **new record**). **a**, **b** Appearance of ascomata on host surface. **c** Longitudinal section of an ascoma. **d** Section of peridium and papillate. **e** Pseudoparaphyses. **f–i** Asci. **j–o** Ascospores. **p**, **q** Culture characteristic on PDA (**p** = from above, **q** = from below). Scale bars: **c** = 100 µm, **d**, **h–i** = 20 µm, **e** = 5 µm, **j–o** = 10 µm, **p**, **q** = 10 mm

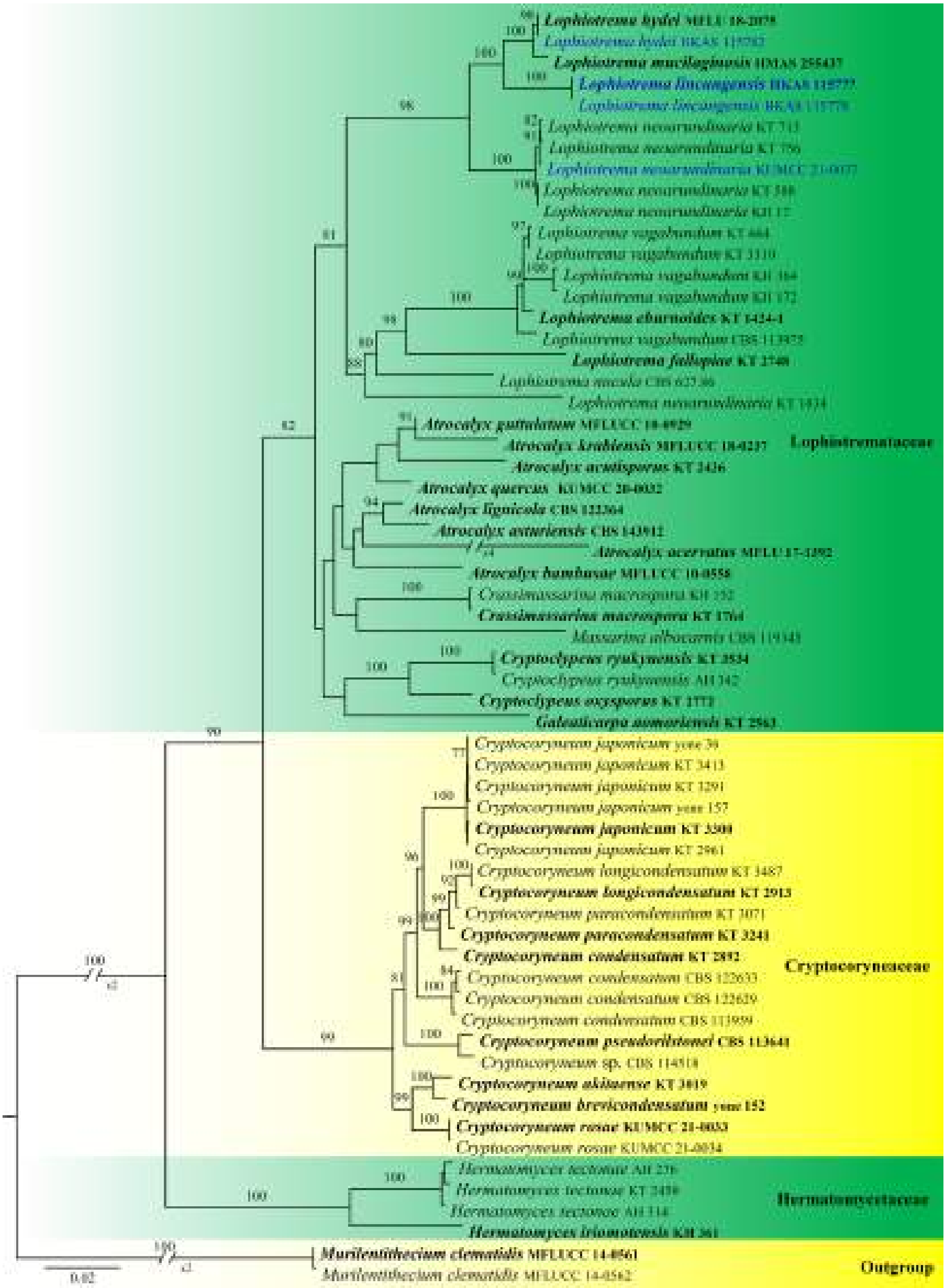


Fig. 50 Phylogram generated from maximum likelihood analysis based on combined SSU, LSU, ITS, TEF1-α and RPB2 sequence data to indicate the newly generated strains in *Lophiotremataceae*. Sixty strains are included in the combined analyses which comprise a total of 4357 characters. *Murilentithecium clematidis* (MFLUCC 14-0561 and MFLUCC 14-0562) is selected as the outgroup taxon. The best RAxML tree with a final likelihood value of − 24211.323363 is presented. RAxML analysis yielded 1272 distinct alignment patterns and 6.17% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.246394, C = 0.256619, G = 0.267068, T = 0.229919, with substitution rates AC = 1.576531, AG = 4.38051, AT = 1.49611, CG = 1.339907, CT = 10.502267, GT = 1.000000; gamma distribution shape parameter alpha = 0.450773. Bootstrap support values for maximum likelihood (MLBS, left) equal to or greater than 70% is given above the nodes. Ex-type strains are in bold and newly generated sequences are in blue

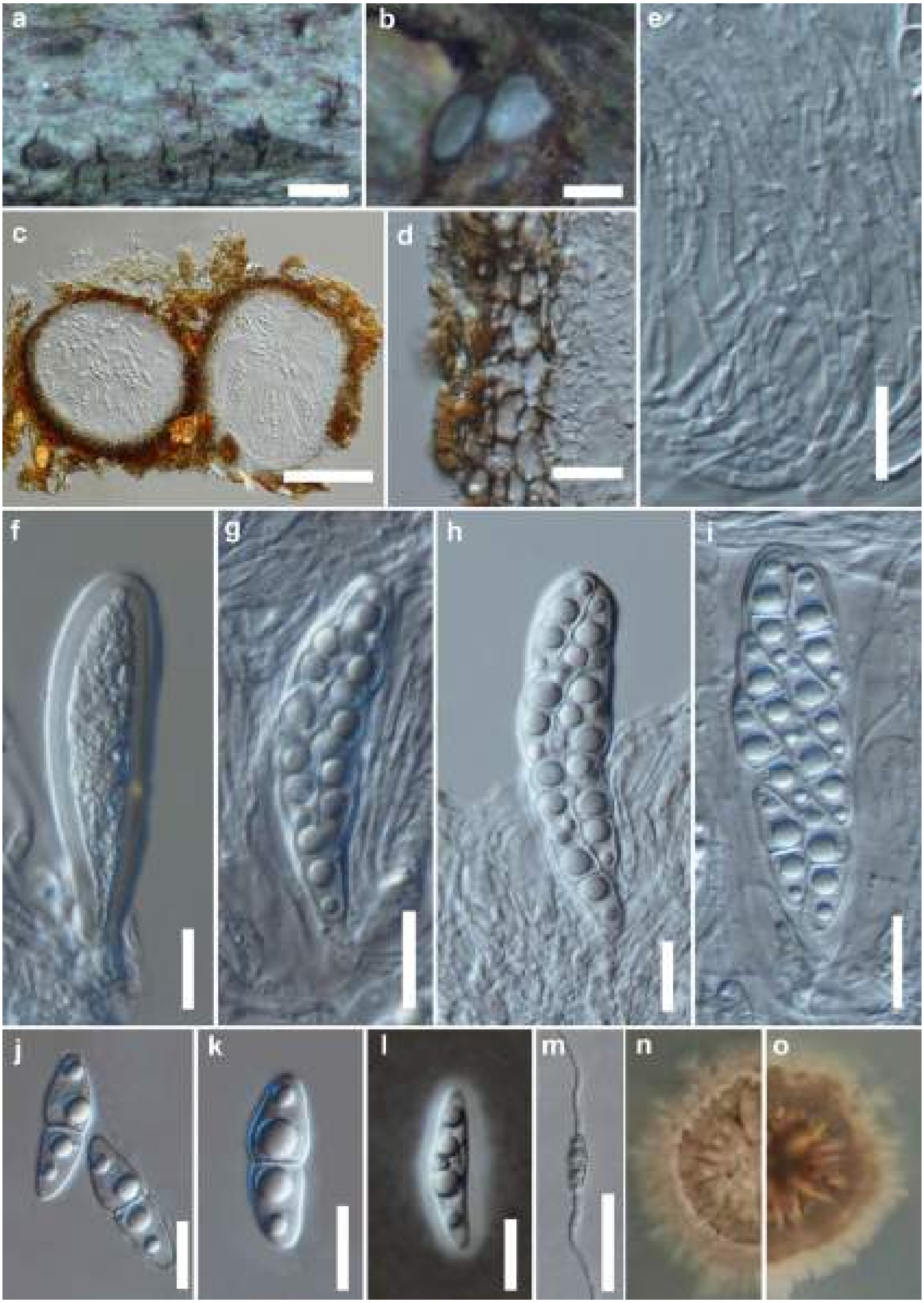


Fig. 51 ***Pseudochaetosphaeronema chiangraiense*** (MFLU 21-0083, **holotype**). **a**, **b** Appearance of ascostromata on host substrate. **c** Longitudinal section of ascomata. **d** Peridium **e** Pseudoparaphyses. **f–i** Asci. **j–l** Ascospores. **m** Germinated ascospore. **n**, **o** Cultures on PDA from surface and reverse. Scale bars: Scale bars: **a** = 500 µm, **b** = 200 µm, **c** = 100 µm, **m** = 50 µm, **e–k** = 20 µm, **d**, **l** = 10 µm

2020, S.N. Wijesinghe, N2 (MFLU 21-0083, **holotype**), ex-type living culture, MFLUCC 21-0070.

GenBank numbers: ITS = MZ457923, LSU = MZ457922, TEF1-α = MZ476770.

Notes: In our DNA sequence analysis, all reported members of *Pseudochaetosphaeronema* and closest *Camarographium* strains are grouped together in Clade A in *Macrodiplodiopsidaceae* (Fig. 52). *Pseudochaetosphaeronema chiangraiense* is only known from its sexual morph (Fig. 51) and therefore, we cannot compare it with the existing species in this genus with respect to their asexual characteristics (Punithalingam 1979; Ahmed et al. 2015; Zhang et al. 2016b; Tibpromma et al. 2018; Jayasiri et al. 2019; Hyde et al. 2020b). The BLAST searches of ITS and LSU sequence data for our new isolate indicates high similarity to *Camarographium koreanum* (CBS 117,159) and TEF1-α sequence data indicates high similarity to *Camarographium* sp. (1 NV-2015). Therefore, we include these strains in our final multigene phylogenetic analysis and our novel isolate forms a distinct lineage with an unidentified *Camarographium* sp. (B45, B46) with 88% MLBS support (Clade A; Fig. 52). According to the guidelines of Jeewon and Hyde (2016) we have analysed nucleotide differences within the rRNA gene region for further clarification. When comparing the ITS (ITS1-5.8S-ITS2) region between our isolate with the B45 and B46 strains, there were 48 and 43 bp (11.11% and 9.95%) difference respectively from 432 nucleotides in ITS. Also, in comparison of the LSU gene region of our strain with B45 and B46 strains, we have revealed (13/774) bp (1.67%) difference and 16/785 bp (2.03%) difference respectively. According to these phylogenetic results we conclude our isolate is a new species of *Pseudochaetosphaeronema*. We introduce the species as *Pseudochaetosphaeronema chiangraiense* collected from Thailand.

Massarinaceae Munk

Notes: We follow the latest treatment and updated accounts of *Massarinaceae* in Hongsanan et al. (2020a).

Helminthosporium Link

Notes: *Helminthosporium* includes mostly saprobes and pathogens on a wide range of hosts and has a worldwide distribution (Voglmayr and Jaklitsch 2017; Tian et al. 2017; Zhao et al. 2018a). Currently, an estimated 223 species are accepted for *Helminthosporium* in Hongsanan et al. (2020a). Zhao et al. (2018a) provided a recent account of *Helminthosporium* with several new isolates. In this study, we introduce *H. chiangraiensis* as a new species and provide a supporting phylogenetic tree.

Helminthosporium chiangraiense Boonmee, Huanraluek & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF558539; *Facesoffungi number*: FoF 09192; Fig. 53

Etymology: The specific epithet "*chiangraiense*" refers to it discover in Chiang Rai Province.

Holotype: MFLU 21-0064

Saprobic on dead twigs. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Colonies* 230–584 µm diam., effuse, dark brown to black, hairy. Mycelium immersed, forming stroma-like aggregations of dark brown pseudoparenchymatous cells. *Conidiophores* 168–304.5 × 5.5–12 ($\bar{x}$ = 232 × 9 µm, n = 20), mononematous, macronematous, caespitose, erect, cylindrical, straight to slightly flexuous, wide at the base, unbranched, dark brown, with apical pore, multi-septate, with dark scars, smooth-walled. *Conidiogenous cells* mono- to polytretic, integrated, terminal and intercalary, cylindrical, cicatrized, with dark scars, with distinct pores. *Conidia* 141–207 × 14–22 ($\bar{x}$ = 161 × 19 µm, n = 20), solitary, obclavate, straight to slightly curved, wider below than apex, truncate and with dark scar at base, upper cell tapering towards long apex, cylindrical, apically rostrate and pale brown, 9–13-distoseptate, smooth-walled. *Conidial secession* schizolytic.

Culture characteristics: Conidium germinating on PDA within 24 h and germ tubes produced from both ends. Colonies on PDA reaching 20 mm diam., in 7 days at room temperature, within a month covering the Petri dish, effuse, hairy, mycelium radiating outwards, fimbriate edge, dense, dark. Mycelium superficial and partly immersed, dark brown.

Material examined: THAILAND, Chiang Rai Province, Muang, Thasud, Mae Fah Lung University, Botanical garden, on dead twigs of unidentified plant, 14 June 2019, N. Huanraluek, CRB1 (MFLU 21-0064, **holotype**), ex-type living culture, MFLUCC 21-0087.

GenBank numbers: ITS = MZ538504, LSU = MZ538538.

Notes: *Helminthosporium chiangraiense* is phylogenetically related to *H. leucadendri*, but is clearly distinguished based on morphology and phylogeny. Phylogenetic analysis of the combined LSU, SSU and ITS sequence data of *Helminthosporium* taxa, our strain (MFLUCC 21-0087) clusters with the ex-type strain *H. leucadendri* (CBS 135133) with moderate support (0.95 BYPP; Fig. 54). Sequence comparison for the ITS region between *H. chiangraiense* (MFLUCC 21-0087) and *H. leucadendri* (CBS 135133) showed a 13.38% (76/568 bp) base pair difference (Jeewon and Hyde 2016). *Helminthosporium chiangraiense* is distinct from *H. leucadendri* in colony features and conidial shape, size and number of distosepta (Quaedvlieg et al. 2013; Figs. 98 and 99). Therefore, we introduce *Helminthosporium chiangraiense* as a new species (Fig. 53).

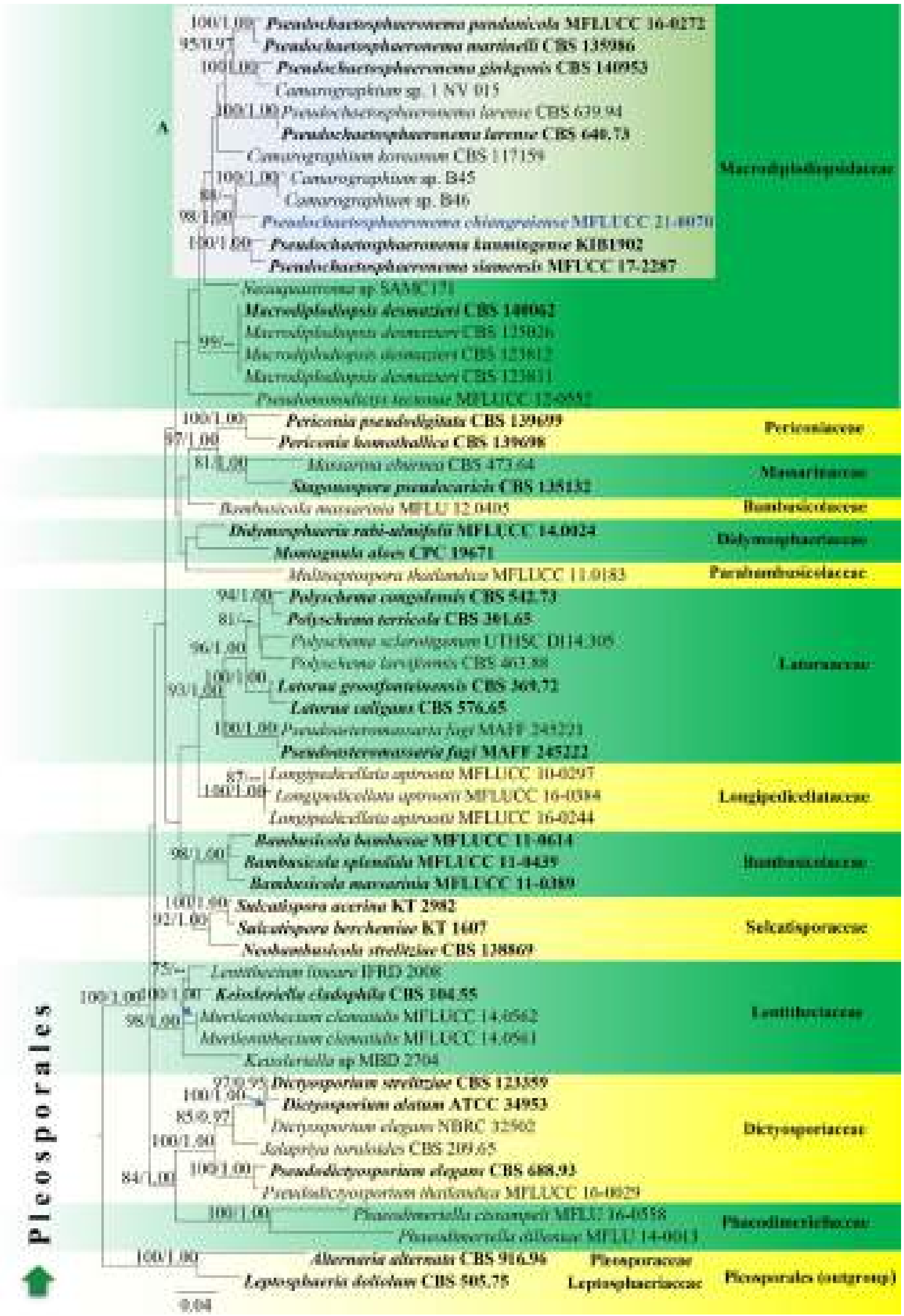


Fig. 52 Phylogram generated from maximum likelihood analysis based on combined LSU, SSU, ITS and TEF1-α sequence data representing suborder *Massarineae* in *Pleosporales*. Related sequences are taken from Hyde et al. (2020b) and additions according to the BLAST searches in NCBI. Fifty-eight strains are included in the combined analyses which comprised 3070 characters (798 characters for LSU, 961 characters for SSU, 469 characters for ITS, 842 characters for TEF1-α) after alignment. *Alternaria alternata* (CBS 916.96) and *Leptosphaeria doliolum* (CBS 505.75) in *Pleosporaceae* and *Leptosphaeriaceae* respectively (*Pleosporales*) were used as the outgroup taxa. The best scoring RAxML tree with a final likelihood value of − 18300.642497 is presented. The matrix had 1007 distinct alignment patterns, with 36.82% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.240587, C = 0.242773, G = 0.272823, T = 0.243817; substitution rates: AC = 1.614921, AG = 3.258874, AT = 1.951323, CG = 1.249772, CT = 8.508461, GT = 1.000000; gamma distribution shape parameter α = 0.183977. Bootstrap support values for ML equal to or greater than 75% are given above the nodes (left side). Bayesian posterior probabilities (BYPP) equal to or greater than 0.95 are given above the nodes (right side). Ex-type strains are in bold and newly generated sequence is in blue bold

Fig. 53 ***Helminthosporium chiangraiense*** (MFLU 21-0064, **holotype**). **a** Colonies on natural substrate. **b** Punctiform conidioma. **c** Cross section of conidioma. **d** Cross section of conidioma cells. **e** Conidiophores. **f** Conidiophore with attached conidium. **g**–**l** Conidia. **m** Germinated conidium. **n**, **o** Culture on PDA from surface and reverse. Scale bars: **a** = 500 µm, **b** = 200 µm, **c**, **e** = 100 µm, **d**, **f**–**m** = 50 µm

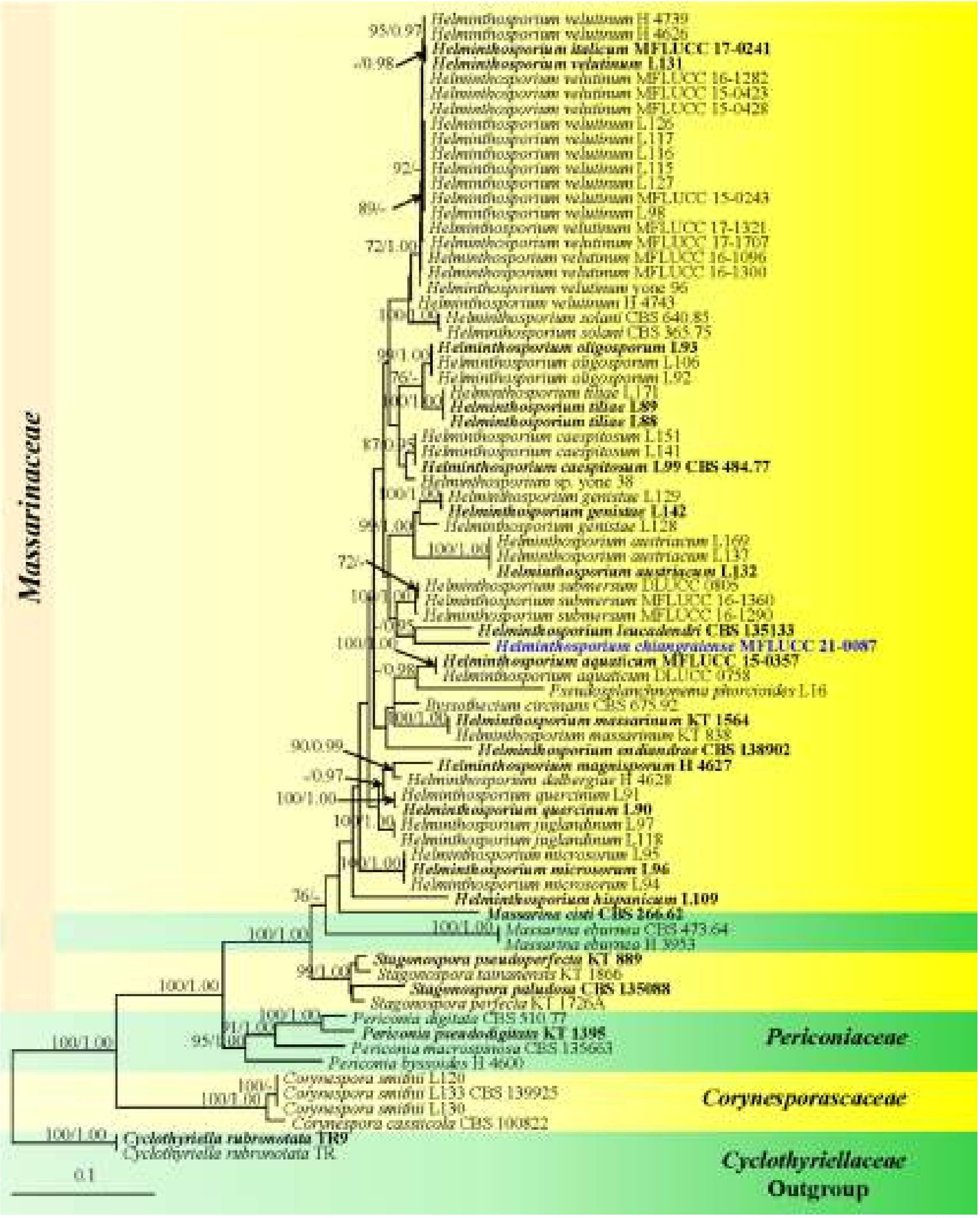


Fig. 54 Phylogram generated from maximum likelihood analysis based on combined LSU, SSU and ITS sequence data of *Helminthosporium* taxa (*Massarinaceae*) and related families. Seventy-seven strains are included in the combined analyses which comprise a total of 2567 characters. *Cyclothyriella rubronotata* (TR and TR9) are selected as the outgroup taxa. The best RAxML tree with a final likelihood value of − 11885.302979 is presented. RAxML analysis yielded 713 distinct alignment patterns and 23.08% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.246572, C = 0.227244, G = 0.274051, T = 0.252133, with substitution rates AC = 2.645156, AG = 3.449326, AT = 2.077592, CG = 1.025293, CT = 7.769520, GT = 1.000000; gamma distribution shape parameter alpha = 0.143346. Bootstrap support values for maximum likelihood (MLBS, left) equal to or greater than 70% is given above the nodes. Bayesian posterior probabilities (BYPP, right) equal to or greater than 0.95 are given above the nodes. Ex-type strains are in bold and newly generated sequence is in blue

Nigrogranaceae Jaklitsch & Voglmayr

Notes: *Nigrogranaceae* was erected by Jaklitsch and Voglmayr (2016) to accommodate three species of *Nigrograna*. The multigene phylogenetic analysis of a combined ITS, LSU, SSU, RPB2 and TEF1-α sequence data in Jaklitsch and Voglmayr (2016) revealed that *Biatriospora marina* (the type species of *Biatriosporaceae*) clusters with *Nigrograna*. Hence the latter study revamped *Biatriosporaceae* and established *Nigrogranaceae*. In addition, all the *Biatriospora* species were transferred in *Nigrograna* by Jaklitsch and Voglmayr (2016). However, it is unlikely that the strain of *Biatriospora marina* used in the analyses is this species and therefore Hongsanan et al. (2020a) maintained *Biatriosporaceae* as a distinct family. Currently *Nigrogranaceae* accommodates 16 species (both sexual and asexual morphs) with endophytic, human pathogenic and saprobic lifestyles (Hongsanan et al. 2020b; Zhang et al. 2020).

Nigrograna Gruyter, Verkley & Crous

Notes: *Nigrograna* was introduced by de Gruyter et al. (2012) with *N. mackinnonii* as the type species. Jaklitsch and Voglmayr (2016) introduced three novel taxa (viz. *N. mycophila, N. norvegica* and *N. obliqua*) to the genus and also synonymized *Melanomma fuscidulum* (≡ *Sphaeria fuscidula*) under *Nigrograna* as *N. fuscidula*. Currently the genus represents 16 species epithets in Index Fungorum (2021) which were recorded from a wide range of hosts in marine and terrestrial habitats (Hyde et al. 2017; Tibpromma et al. 2017b; Dayarathne et al. 2020). These existing taxa have also been confirmed by DNA sequence data in GenBank (Hongsanan et al. 2020b). Most of taxa in the genus *Nigrograna* exhibit saprobic lifestyles and also were recorded as human pathogens and endophytes with a cosmopolitan distribution (Kolařík 2018; Zhao et al. 2018b). *Nigrograna* is characterized by having black ascomata with clavate, short pedicellate asci and pale to chocolate brown, fusoid to narrowly ellipsoid, septate ascospores. Recently, Dayarathne et al. (2020) and Wanasinghe et al. (2020b) documented three taxonomic novelties (i.e. *N. magnolia, N. samueliana* and *N. rhizophorae*) in the genus. *Nigrograna hydei* and *N. obtusispora* are also included to the genus by Zhang et al. (2020).

Nigrograna jinghongensis Wanas. & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF558601; *Facesoffungi number*: FoF 09951; Fig. 55

Etymology: The specific epithet "*jinghongensis*" refers to the Jinghong City, Yunnan Province, China where the type was collected.

Holotype: KUN-HKAS 115776

Saprobic on woody litter. **Sexual morph**: *Ascomata* 300–400 μm high, 220–300 μm diam. ($\bar{x}$ = 347 × 259 μm, n = 10), perithecioid, solitary or gregarious, immersed to erumpent through host tissue, subglobose or obpyriform, uni-loculate, brown to dark brown, ostiolate. *Ostiole* mostly central. *Peridium* 10–15 μm wide at the base, 20–30 μm wide in sides, composed of angular cells, outer layer, dark brown, thick-walled cells, inner layer, hyaline with thin-walled cells. *Hamathecium* composed of numerous, 1.5–2.5 μm wide, filamentous, septate pseudoparaphyses. *Asci* 60–90 × 7–9 μm ($\bar{x}$ = 77 × 8 μm, n = 20), 8-spored, bitunicate, clavate to cylindric-clavate, short pedicellate, apically rounded, with a minute ocular chamber. *Ascospores* 12–15 × 4–5.5 μm ($\bar{x}$ = 14 × 4.5 μm, n = 30), overlapping bi-seriate, ellipsoid, yellowish-brown to brown, 1-septate, slightly echinulate, guttulate. **Asexual morph** Undetermined.

Culture characteristics: Ascospores germinating on PDA within 24 h and germ tubes arising from both ends. Colonies on PDA, slow growing, reaching 2 cm diam. after 4 weeks of incubation at room temperature, initially white becoming dirty white to light grey at maturity, slightly effuse, radially with an undulate edge, greyish, reverse creamy.

Material examined: CHINA, Yunnan, Xishuangbanna Dai Autonomous Prefecture, Mengla County, Menglunzhen, 21.891084° N 101.305898° E, on dead woody litter, 25 November 2020, D.N. Wanasinghe, DWX01-3 (KUN-HKAS 115776, **holotype**), ex-type living culture (KUMUCC 21-0035); *ibid*. DWX01-3-2 (KUN-HKAS 115775), living culture (KUMUCC 21-0036).

GenBank numbers: ITS = MZ493303, MZ493304, LSU = MZ493317, MZ493318, SSU = MZ493289, MZ493290, RPB2 = MZ508421, MZ508422, TEF1-α = MZ508412, MZ508413.

Notes: In the multigene phylogeny, *Nigrograna jinghongensis* (KUMUCC 21-0035 and KUMUCC 21-0036) clustered as a sister taxon to *N. yasuniana* and *Nigrograna* sp. (MFLUCC 17-2663) with 100% MLBS support (Fig. 56). The sequence comparison between our new strain and *N. yasuniana*, ITS had 0.63%, TEF1-α had 2.46% and RPB2 had 6.34% base pair variations. *Nigrograna yasuniana* was previously documented as an endophyte on *Conceveiba guianensis* (*Euphorbiaceae*) from Ecuador. Unfortunately, sufficient morphological data are not available for *N. yasuniana* to compare with our novel taxon. Based on its morphology and phylogenetic placement, we therefore, introduce *Nigrograna jinghongensis* as a new species (Fig. 55).

Occultibambusaceae D.Q. Dai & K.D. Hyde

Notes: *Occultibambusaceae* is characterized by solitary, scattered, immersed, subglobose, dark brown, uni- or multi-loculate ascostromata, bitunicate, fissitunicate, (6)–8-spored, shortly pedicellate, cylindrical to clavate asci, and 1–3-seriate, fusiform, sometimes asymmetric, hyaline or pale brown to dark brown, 1–3-septate ascospores with or without sheath (Doilom et al. 2016; Hyde et al. 2016; Jayasiri et al. 2016; Dai et al. 2017; Zhang et al. 2017; Tibpromma et al.

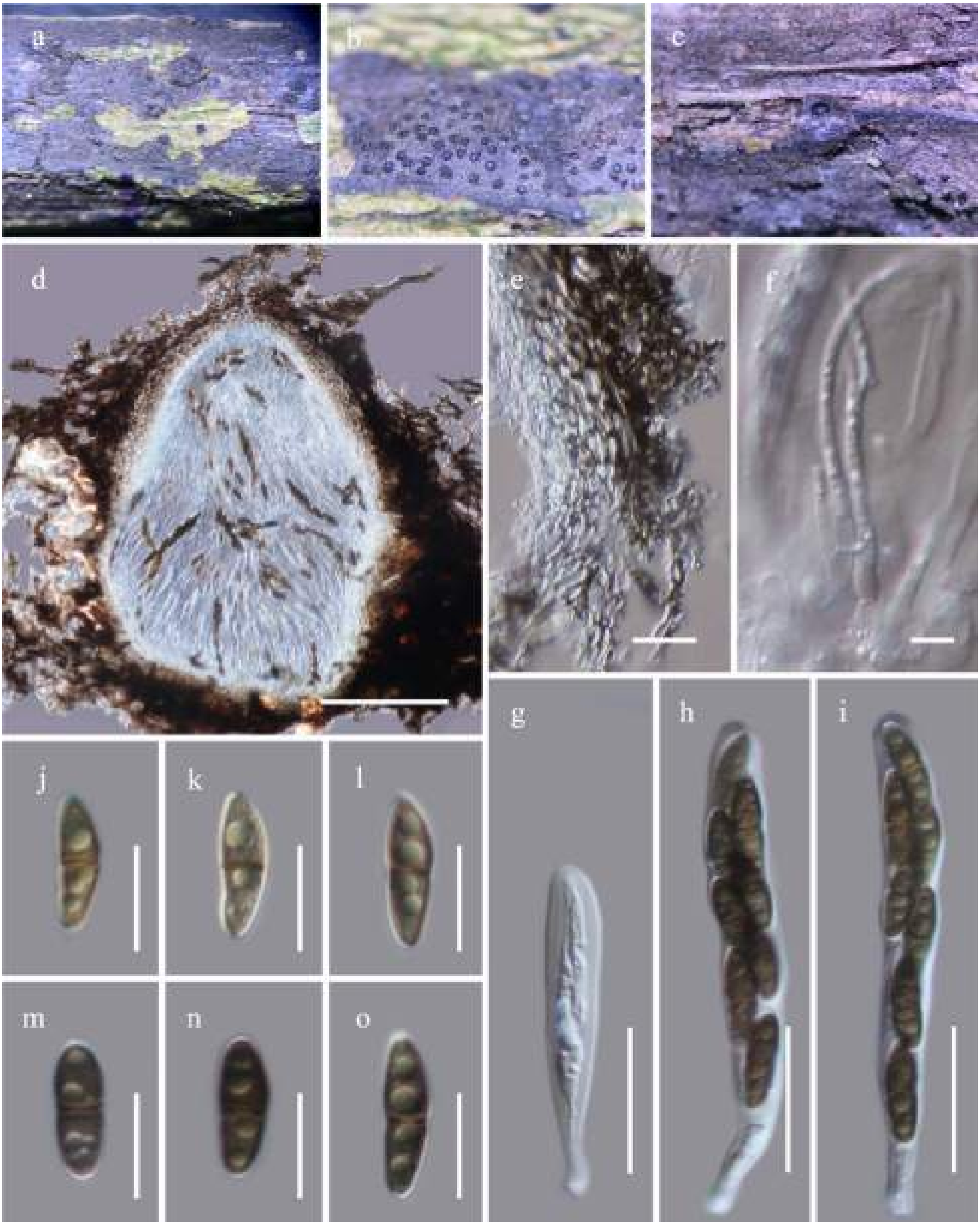


Fig. 55 ***Nigrograna jinghongensis*** (KUN-HKAS 115776, **holotype**). **a**–**c** Appearance of ascomata on host surface. **d** Longitudinal section of an ascoma. **e** Section of the peridium cells. **f** Pseudoparaphyses. **g**–**i** Asci. **j**–**o** Ascospores. Scale bars: **d** = 100 μm, **e**, **g**–**i** = 20 μm, **f** = 5 μm, **j**–**o** = 10 μm

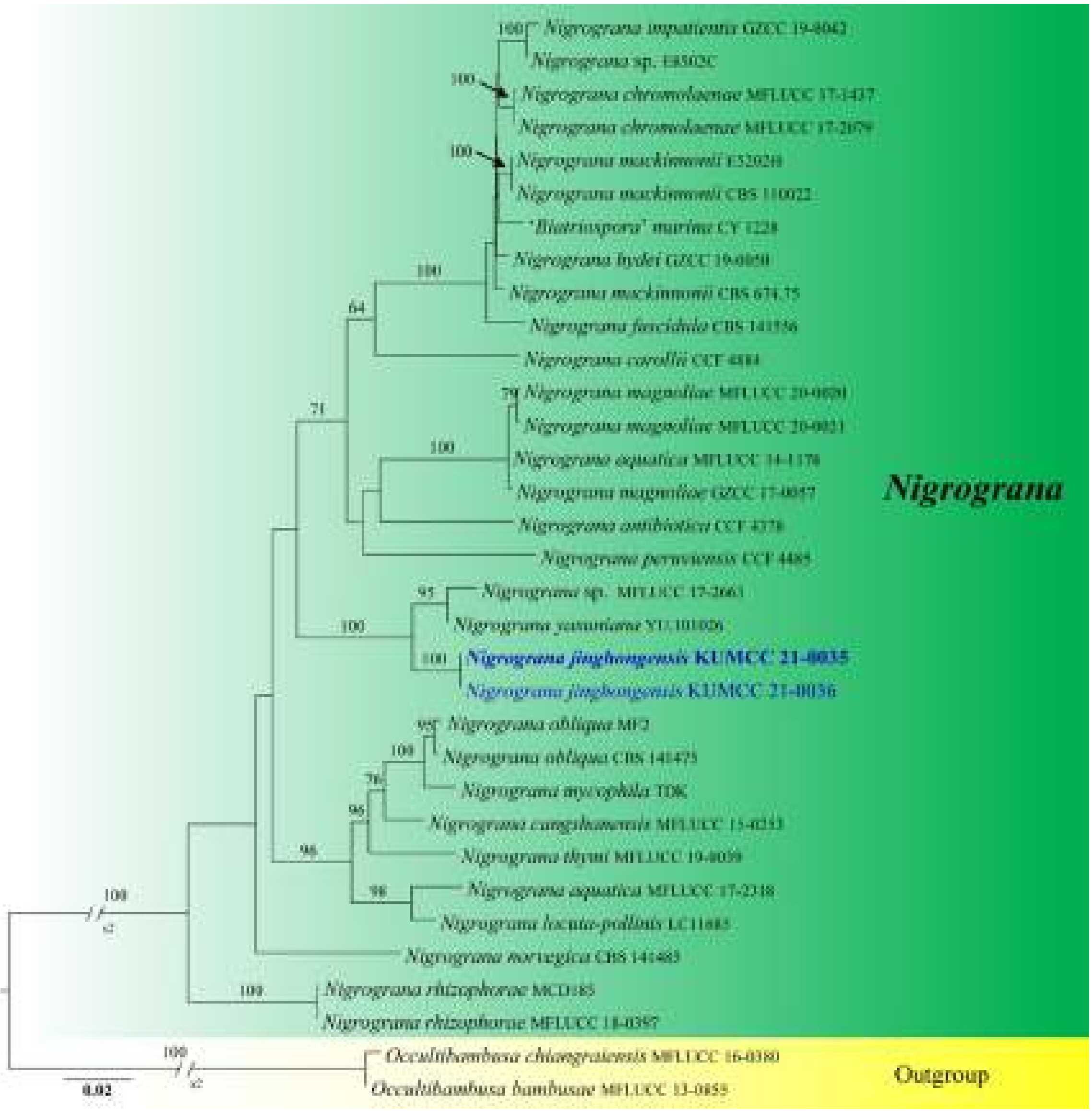


Fig. 56 Phylogram generated from the best scoring of the RAxML tree based on combined SSU, LSU, ITS, TEF1-α and RPB2 sequence dataset to indicate the new species *Nigrograna jinghongensis* and related species in *Nigrogranaceae*. Thirty-three strains are included in the combined analyses which comprise a total of 4372 characters. *Occultibambusa bambusae* (MFLUCC 13-0855) and *O. chiangraiensis* (MFLUCC 16-0380) are selected as the outgroup taxa. The best RAxML tree with a final likelihood value of − 16022.187073 is presented. RAxML analysis yielded 1068 distinct alignment patterns and 26.01% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.24908, C = 0.245478, G = 0.267145, T = 0.238298, with substitution rates AC = 1.477319, AG = 4.369095, AT = 1.2688, CG = 0.859595, CT = 11.229756, GT = 1.000000; gamma distribution shape parameter alpha = 0.579103. Bootstrap support values for maximum likelihood (MLBS, left) equal to or greater than 60% is given above the nodes. Ex-type strains are in bold and newly generated sequences are in blue

2018; Phookamsak et al. 2019; Rathnayaka et al. 2019; Dong et al. 2020b; Hongsanan et al. 2020a; Phukhamsakda et al. 2020). There are four genera accommodated in the family, viz. *Brunneofusispora*, *Occultibambusa*, *Seriascoma* and *Versicolorisporium*. *Occultibambusa*, *Seriascoma* and *Versicolorisporium* are reported to have coelomycetous asexual morphs (Hatakeyama et al. 2008; Dai et al. 2017), while *Neooccultibambusa* forms chlamydospores in culture or exists as a hyphomycetous asexual morph (Doilom et al. 2016; Jayasiri et al. 2016; Hyde et al. 2018a). However, there have not been any asexual morphs of *Brunneofusispora* reported so far (Phookamsak et al. 2019; Phukhamsakda et al. 2020).

Seriascoma Phookamsak, D.Q. Dai & K.D. Hyde

Notes: *Seriascoma* is typified with *Seriascoma didymospora*. Two species are accommodated in the genus viz. *S. didymospora* and *S. yunnanense* (Hongsanan et al. 2020a; Species Fungorum 2021). The genus is characterized by solitary or gregarious, erumpent, subglobose or elongated, uni- or multi-loculate, coriaceous ascostromata embedded under a clypeus, bitunicate, fissitunicate, 8-spored, clavate asci with short to long furcate pedicel, and 1–3-seriate, fusiform, hyaline, asymmetric, 1-septate ascospores, slightly constricted at the septum, with or without a sheath (Dai et al. 2017; Rathnayaka et al. 2019). To date, asexual morphs of the genus have only been reported for *S. didymospora* which were characterized by eustromatic, solitary to gregarious, semi-immersed to erumpent, conical, black, uni-loculate conidiomata, enteroblastic, phialidic, determinate, cylindrical to ampulliform, hyaline, aseptate, smooth conidiogenous cells bearing oblong, hyaline, aseptate, smooth conidia (Dai et al. 2017). In the present study, we introduce a novel species in *Seriascoma*.

Seriascoma honghense H.B. Jiang, Phookamsak & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF558194; *Facesoffungi number*: FoF 09765; Fig. 57

Etymology: The specific epithet "*honghense*" refers to the collection site (Honghe County), of which the new species was collected.

Holotype: KUN-HKAS 112013

Saprobic on dead bamboo branches. **Sexual morph** Undetermined. **Asexual morph** Coelomycetous. *Conidiomata* pycnidial, 60–90 µm high, 320–510 µm diam., solitary to gregarious, immersed under cortex to superficial, raised, black, elongate-conical, 1- to multi-loculate, glabrous. *Locules* 45–300 µm diam., 30–70 µm high, clustered, arranged in rows, dark brown, subglobose to ampulliform. *Peridium* 12–20 µm thick, thin- to thick-walled, of unequal thickness, thick at the sides, thin at the base, composed of host and fungal tissue, with several layers of dark brown to brown, pseudoparenchymatous cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 5.5–6.5 × 2–3 µm ($\bar{x} = 6 \times 5$ µm, n = 20), enteroblastic, phialidic, determinate, discrete, subglobose or cylindrical to conical, hyaline, aseptate, smooth-walled. *Conidia* 4.5–5 × 2 µm ($\bar{x} = 5 \times 2$ µm, n = 20), subglobose to oblong, hyaline, bi-guttulate, aseptate, smooth-walled.

Culture characteristics: Conidia germinating on PDA within 24 h. Colonies growing fast on PDA, reaching 10 mm in 1 week at room temperature, under the normal light, cottony, circular, raised, grayish to dark brown from above and below. Mycelium superficial to immersed in media, with branched, septate, smooth hyphae.

Material examined: CHINA, Yunnan Province, Honghe Autonomous Prefecture, Honghe County, a roadside bamboo (23°13′30.42″ N, 102°20′58.85″ E, altitude 1682 m), on dead branches of bamboo in a terrestrial environment, 28 October 2020, H.B. Jiang, HONGHE008 (KUN-HKAS 112013, **holotype**); HMAS 249946 (isotype), ex-type living culture, KUMCC 21-0007.

GenBank numbers: ITS = MW981351, LSU = MW981347, SSU = MZ325471, RPB2 = MZ325473, TEF1-α = MZ325472.

Notes: *Seriascoma honghense* matches the typical characteristics of the coelomycetous asexual morph of *Seriascoma* (Fig. 57). However, it differs from *Seriascoma didymospora* in its multi-loculate, flat conidiomata and a thinner peridium. Based on the present phylogeny, *S. honghense* is determined to be a sister to *S. didymospora* with 98% ML, 0.96 PP statistical support (Fig. 58). Pairwise nucleotide comparison of ITS and TEF1-α also showed that *S. honghense* differs from *S. didymospora* in 36/483 bp (7.45%) and 26/947 bp (2.75%), respectively.

Paradictyoarthriniaceae Doilom, Ariyaw., Bhat & K.D. Hyde

Notes: *Paradictyoarthriniaceae* was introduced by Liu et al. (2015a) based on its unique morphology and phylogenetic placement. Members of this family include asexual and sexual morphs as saprobes in freshwater and terrestrial habitats (Matsushima 1996; Liu et al. 2015a, 2018; Wanasinghe et al. 2018). Only two genera have been identified, namely *Paradictyoarthrinium* and *Xenomassariosphaeria* are accommodated in this family (Wijayawardene et al. 2020).

Paradictyoarthrinium Matsush.

Notes: Matsushima (1996) introduced *Paradictyoarthrinium* to accommodate hyphomycetous taxon that occurs on a dead decaying spathe of *Cocos nucifera* from South Africa. The genus is characterized by superficial, gregarious, black, powdery fruiting bodies and macronematous conidiophores with unevenly dictyoseptate, muriform, subglobose to ellipsoidal dark brown conidia (Liu et al. 2015a). Presently, only four species have been reported in *Paradictyoarthrinium* (Index Fungorum 2021). In this study, we report *Paradictyoarthrinium diffractum* as a new record from a terrestrial habitat in Thailand.

Paradictyoarthrinium diffractum Matsush., Matsush. Mycol. Mem. 9:18 (1996)

Index Fungorum number: IF415849; *Facesoffungi number*: FoF 01854; Fig. 59

Saprobic on decaying wood. **Sexual morph** Undetermined. **Asexual morph** *Colonies* on natural substrate,

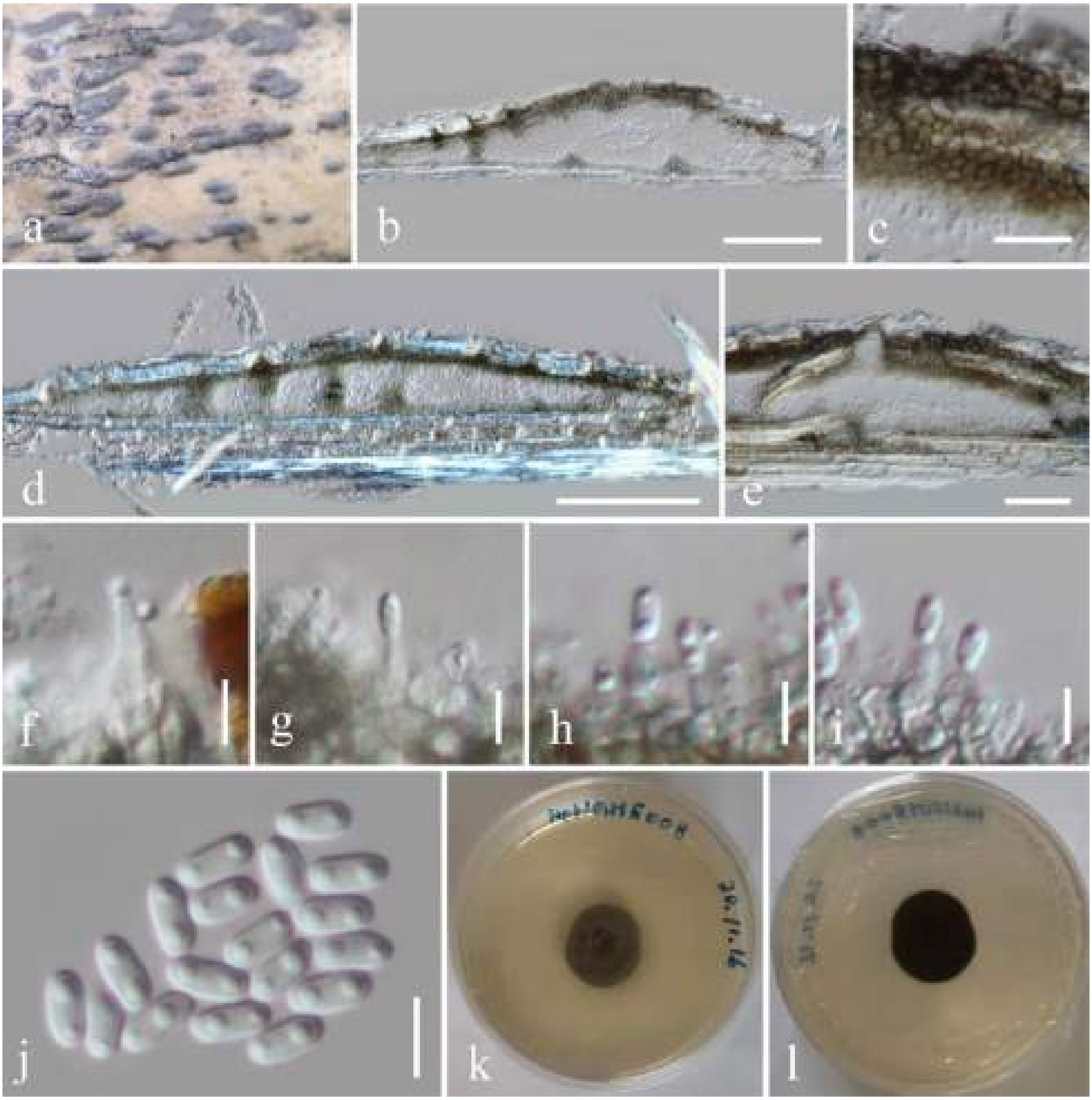


Fig. 57 ***Seriascoma honghense*** (KUN-HKAS 112013, **holotype**). **a** Conidiomata on surface of dead bamboo branches. **b**, **d** Vertical section of conidioma. **c** Wall of conidioma. **e** Ampulliform locule of conidioma. **f**–**i** Conidiogenous cells bearing conidia. **j** Conidia. **k**, **l** Culture frontage and reverse. Scale bars: **b**, **d** = 100 µm, **e** = 50 µm, **c** = 20 µm, **f**–**j** = 5 µm

superficial, effuse, gregarious, scattered, black, shiny. *Mycelium* mostly superficial, partly immersed, composed of branched, septate, brown. *Conidiophores* 5–19 µm long, 4–5 µm wide, macronematous, erect to slightly curved, arising from hyphae. *Conidiogenous cells* blastic, integrated, terminal, determinate. *Conidia* 12–20 × 11–19 ($\bar{x}$ = 15 × 16 µm, n = 10), muriform, subglobose to irregular in shape, dark brown to black solitary, developing in branched chains, with 1–2 short chains, variable in shape and size.

Culture characteristics: Conidia germinating on PDA within 24 h and germ tubes produced around conidia. Colonies on PDA reaching 5 cm diam. after 4 weeks incubated at 25 °C, superficial, dense and woolly, raised effuse, dull surface, velvety, olivaceous grey to dark grey, radiating outwards, entire edge.

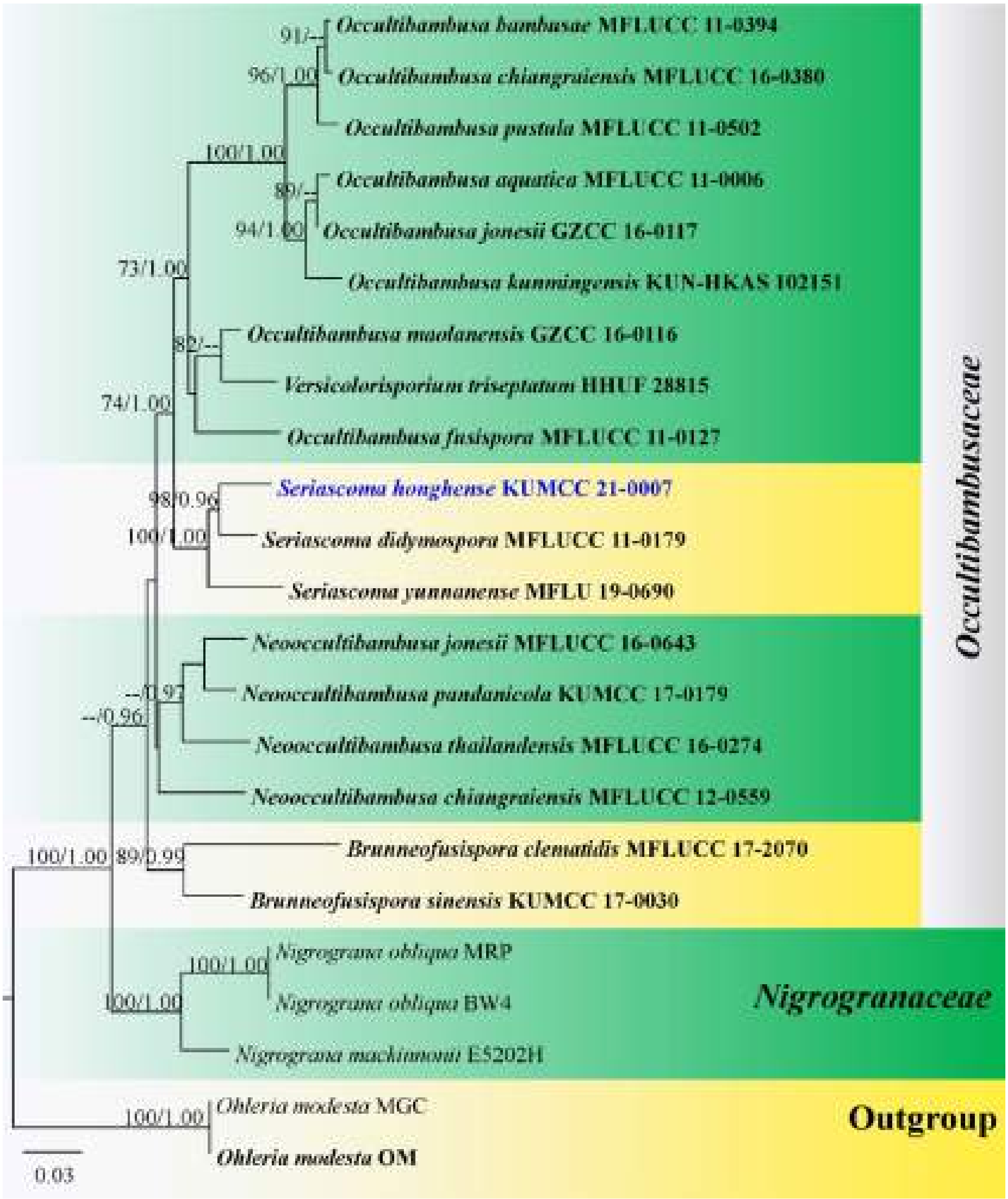


Fig. 58 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, SSU and TEF1-α sequence data. Twenty-three strains are included in the combined gene analyses comprising 3865 characters after alignment (643 characters for ITS, 853 characters for LSU, 1438 characters for SSU, 931 characters for TEF1-α). *Ohleria modesta* (MGC and OM) is used as the outgroup taxon. The tree topology of the Bayesian analysis was similar to the maximum likelihood analysis. The best RAxML tree with a final likelihood value of − 13136.916046 is presented. The matrix had 883 distinct alignment patterns, with 33.71% undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.241326, C = 0.251489, G = 0.273232, T = 0.233953; substitution rates AC = 1.629497, AG = 2.743632, AT = 1.443415, CG = 0.989741, CT = 7.278242, GT = 1.000000; gamma distribution shape parameter α = 0.150194. Bootstrap values for maximum likelihood equal to or greater than 70% and Bayesian posterior probabilities equal or greater than 0.95 BYPP are placed above or below the branches. Ex-type strains are in bold and newly generated sequence is in blue

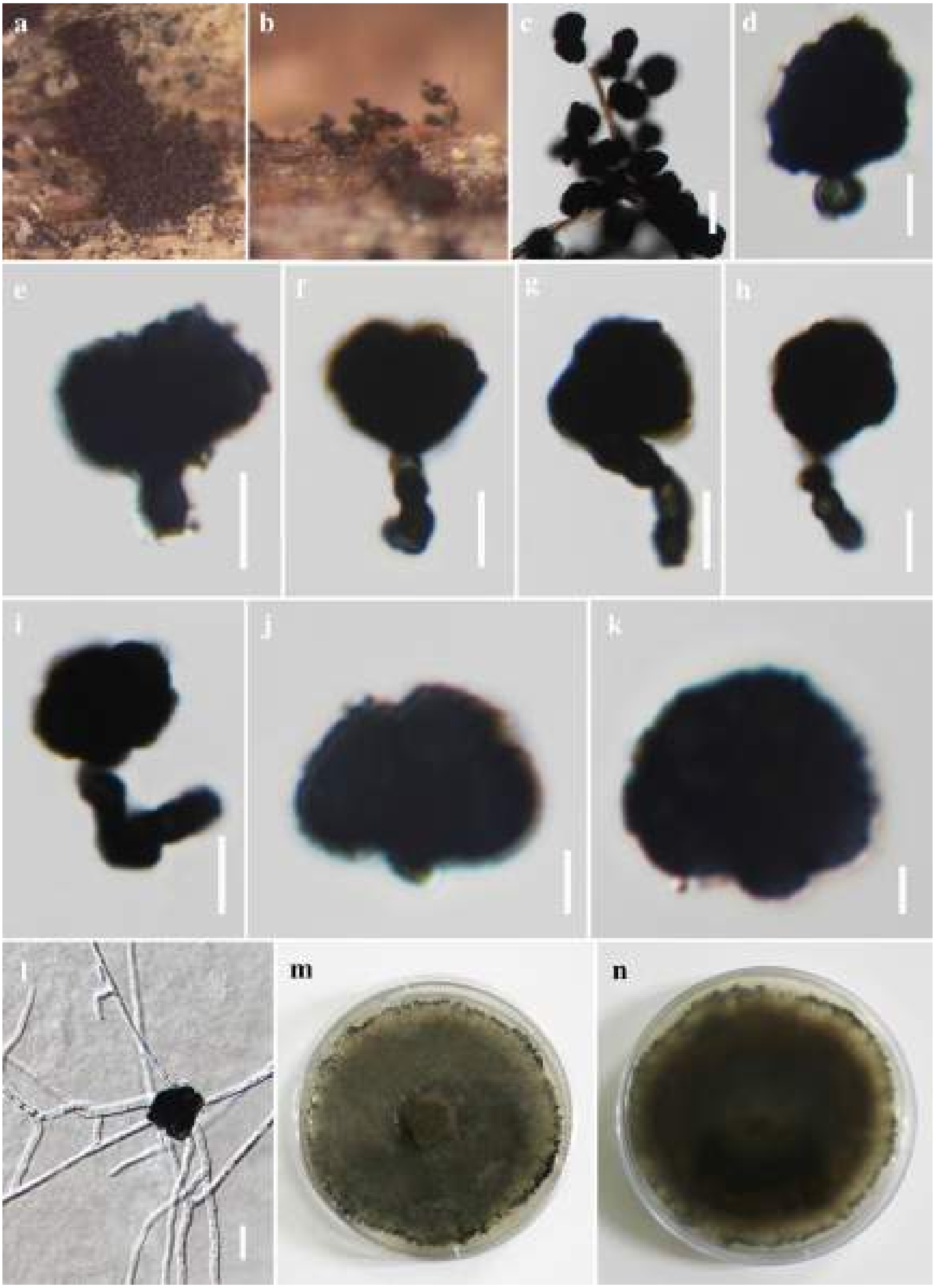


Fig. 59 ***Paradictyoarthrinium diffractum*** (MFLU 21-0065, **new record**). **a**, **b** Colonies on woody substrate. **c** Conidial masses arising from conidiogenous cells. **d**–**i** Conidiogenous cells with attached conidia. **j**, **k** Conidia. **l** Germinated conidium. **m**, **n** Culture on PDA from surface and reverse. Scale bars: **c** = 20 μm, **d**–**i**, **l** = 10 μm, **j**, **k** = 5 μm

Material examined: THAILAND, Mukdahan Province, on decaying wood, 24 July 2019, S. Boonmee, WD10 (MFLU 21-0065, **new record**), living culture MFLUCC 21-0088.

GenBank numbers: ITS = MZ538520, LSU = MZ538554, SSU = MZ538573, RPB2 = MZ567112, TEF1-α = MZ567097.

Notes: We collected a fungal strain from woody substrates in northeastern Thailand and it identified as *Paradictyoarthrinium diffractum* with the support of morphology (Fig. 59) and phylogenetic evidence (Fig. 60). Our isolate MFLUCC 21-0088 clustered among *P. diffractum* strains (MFLUCC 13-0466, MFLUCC 12-0557, 117F5C-AC, UFMG PEZEQ5, NFCCI-4665, KUMCC 19-0111, HUEFS 212651, BCC 8704, GUFCC 15514) with 82% MLBS, 0.99 BYPP support. This is a new record of *P. diffractum* reported from northeastern Thailand. This may be a species complex.

Phaeoseptaceae S. Boonmee, Thambug. & K.D. Hyde

Notes: *Phaeoseptaceae* (*Pleosporales*) was introduced as a monotypic family by Hyde et al. (2018a) with *Phaeoseptum* as the generic type. Members of *Phaeoseptaceae* are saprobic on dead wood in terrestrial and aquatic habitats (Hyde et al. 2018a; Liu et al. 2019; Phukhamsakda et al. 2020; Wanasinghe et al. 2020a). According to the treatment of Liu et al. (2019) and Phukhamsakda et al. (2020), we describe a novel species of *Pleopunctum* that is assigned to this family based on the evidence of phylogenetic analysis and morphological features.

Pleopunctum N.G. Liu, K.D. Hyde & J.K. Liu

Notes: The hyphomycetous genus *Pleopunctum* was established in *Phaeoseptaceae* by Liu et al. (2019) to accommodate two species, namely, *P. ellipticum* (type species) and *P. pseudoellipticum*. Phukhamsakda et al. (2020) introduced the third *Pleopunctum* species from dead branches of *Clematis sikkimensis*. The genus is characterized by gregarious, superficial, brown colonies, mononematous, septate conidiophores, monoblastic conidiogenous cells, multi-septate, muriform and oval to ellipsoidal conidia (Liu et al. 2019; Phukhamsakda et al. 2020). In this study, morphological characteristics and multi-gene phylogenetic analysis of a combined LSU, ITS, SSU and TEF1-α sequence data reveals a new species of *Pleopunctum* from dead branches of unidentified plant collected in Thailand (Fig. 62).

Pleopunctum thailandicum J.Y. Zhang, Y.Z. Lu & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF558394; *Facesoffungi number*: FoF 09804; Fig. 61

Etymology: The specific epithet "*thailandicum*" reflects the country, where the specimen was collected, Thailand.

Holotype: MFLU 21-0043

Saprobic on dead branches of unidentified plant. **Sexual morph** Undetermined. **Asexual morph** *Hyphomycetous*. *Colonies* on natural substrate dry forming sporodochial conidiomata, superficial, scattered, gregarious, punctiform, glistening, oval. blackish brown. *Mycelium* immersed in the substrate, composed of septate, branched, hyaline to pale-yellow. *Conidiophores* 2.5–5 µm wide micronematous or macronematous, mononematous, cylindrical or truncate, erect, unbranched, hyaline to brown, sometimes reduced to conidiogenous cells. *Conidiogenous cells*, monoblastic, holoblastic, terminal, integrated, subspherical or ampulliform, hyaline. *Conidia* 29–38 × 19–25 µm ($\bar{x}$ = 34 × 22 µm, n = 25), acrogenous, solitary, muriform, oval to ellipsoidal, multiseptate, slightly constricted at the septa, oval to ellipsoidal, thick-walled, smooth, brown to hyaline at upper and lower cells when immature, dark brown when mature, rounded at apex, truncate at base, sometimes with a hyaline, globose basal cell, 8–20 × 8.5–18.5 µm ($\bar{x}$ = 13 × 12 µm).

Culture characteristics: Conidia germinated on WA within 15 h at room temperature. Colonies reaching 15 mm at 2 weeks, convex, rough surface with edge entire, radiating outwards; reverse smooth, white to pale yellowish at the centre.

Material examined: THAILAND, Chiang Mai Province, Mae Taeng, Ki Lek, Chang Wat (19°07′52.3″ N 98°45′35.7″ E), on dead branches of unidentified plant, 8 August 2019, N. Wu, N17 (MFLU 21-0043, **holotype**); ex-type living culture, MFLUCC 21-0039.

GenBank numbers: ITS = MZ198894, LSU = MZ198896, TEF1-α: MZ172461.

Notes: The phylogenetic analysis reveals that a new species, *Pleopunctum thailandicum* belongs to *Pleopunctum*, where it is sister to *P. clematidis* with 100% MLBS, 1.00 BYPP support (Fig. 62). *Pleopunctum thailandicum* is similar to *P. clematidis* in having superficial and brown colonies, holoblastic, monoblastic conidiogenous cells and muriform, oval to ellipsoidal conidia (Liu et al. 2018; Phukhamsakda et al. 2020). However, *P. thailandicum* differs from *P. clematidis* by its black and larger conidia, and lacks dimorphic conidia (Fig. 61).

Phaeosphaeriaceae M.E. Barr

Notes: Members of *Phaeosphaeriaceae* are cosmopolitan and exhibit diverse life modes, mainly as saprobes, endophytes and pathogens of economically important plants as well humans (Phookamsak et al. 2014, 2017b; Hongsanan et al. 2020a). Apart from their cosmopolitan distribution, the family is morphologically and phylogenetically highly diverse. Thus, currently 83 genera are accommodated in this family (Hongsanan et al. 2020a). Species of *Phaeosphaeriaceae* are commonly found on monocotyledonous and herbaceous plants, as well as some other soft woody plants in both terrestrial and aquatic environments (Hongsanan

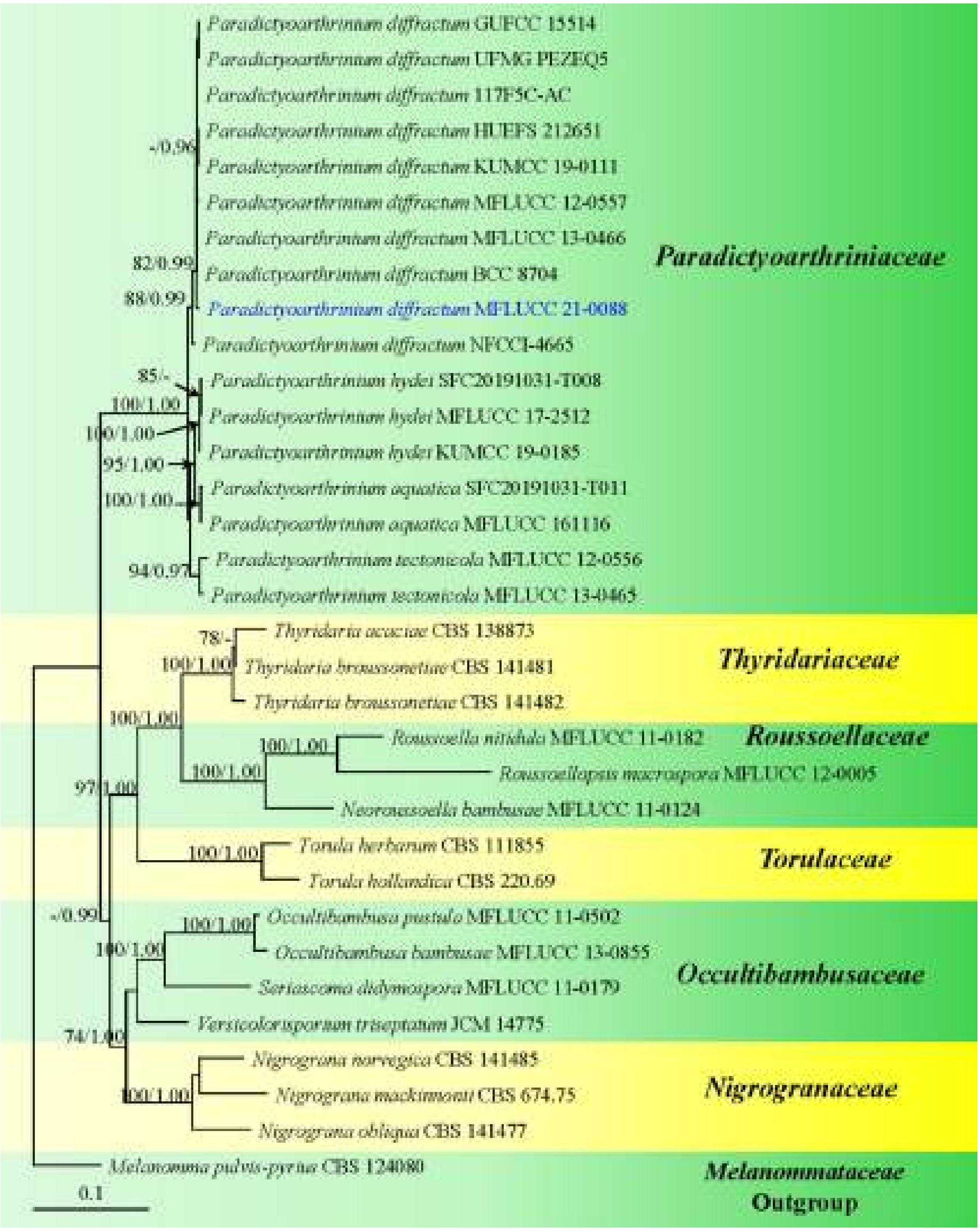


Fig. 60 Maximum likelihood phylogenetic tree based on a combined LSU, ITS, RPB2, SSU and TEF1-α sequence data of *Paradictyoarthrinium* taxa (*Paradictyoarthriniaceae*) and related families. The tree is rooted with *Melanomma pulvis-pyrius* (CBS 124080). Bootstrap support values for maximum likelihood (MLBS, left) equal to or greater than 70% is given above the nodes. Bayesian posterior probabilities (BYPP, right) equal to or greater than 0.95 are given above the nodes. Newly generated sequence is in blue

et al. 2020a). Some of the species in this family have an ability to produce secondary metabolites that are capable of antimicrobial activities (Mapook et al. 2020).

Phaeosphaeriopsis M.P.S. Câmara, M.E. Palm & A.W. Ramaley

Notes: *Phaeosphaeriopsis* is a widely distributed group of phaeosphaeriacous fungi where species are defined primarily

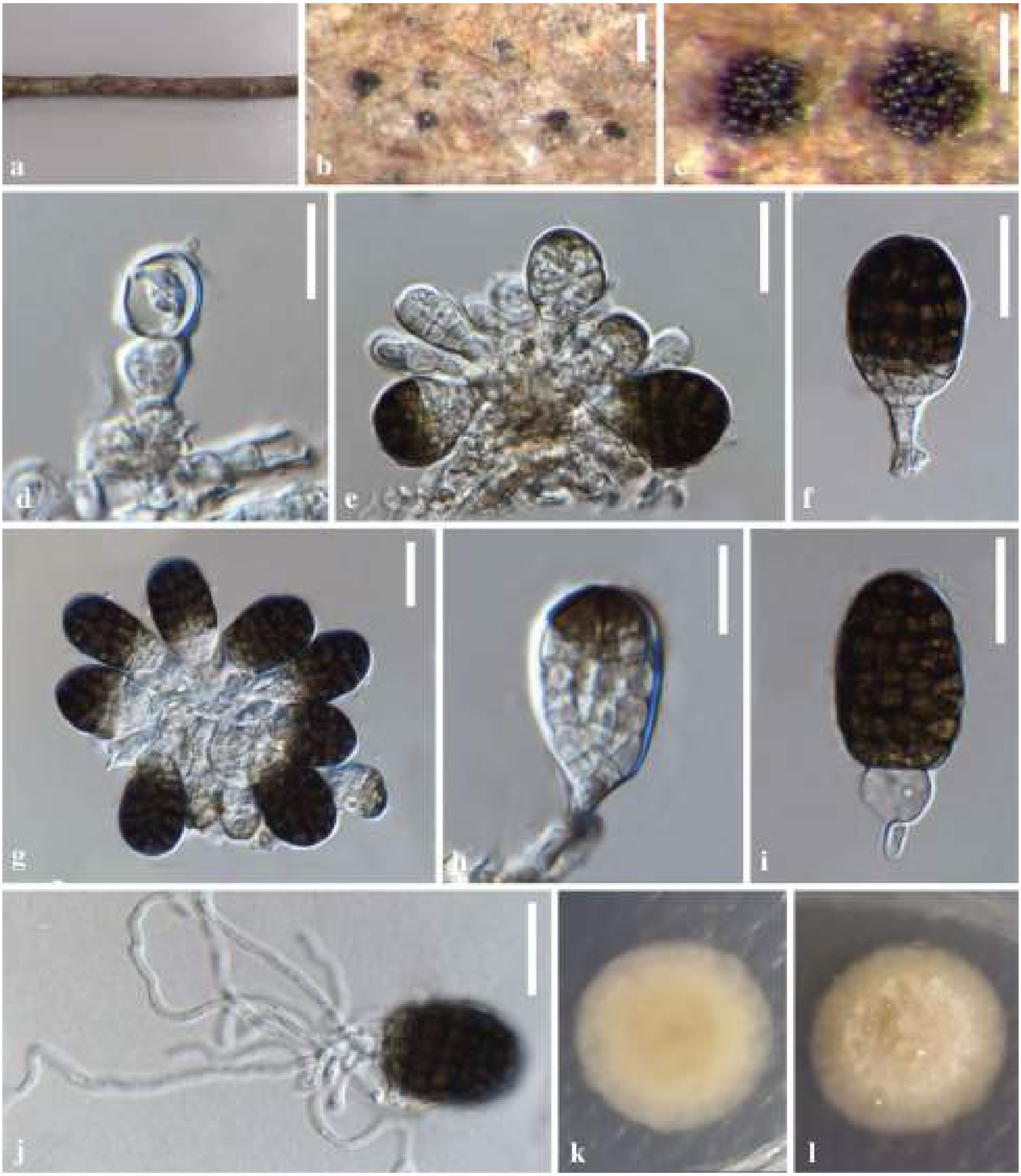


Fig. 61 ***Pleopunctum thailandcum*** (MFLU 21-0043, **holotype**). **a**–**c** Colonies on natural substrates. **d**, **e** Conidiophores with conidiogenous cells. **f**–**h** Conidiogenous cells and conidia. **i** Conidium with basal hyaline cells. **j** Germinated conidium. **k**, **l** Culture on PDA from surface and reverse. Scale bars: **b** = 250 µm, **c** = 100 µm, **e**–**g**, **i**, **j** = 20 µm, **d**, **h** = 10 µm

based on immersed, subepidermal, globose to subglobose to pyriform ascomata, cylindric asci and vertically septate, punctate or verrucose ascospores with coniothyrium-like or phaeostagonospora-like asexual morphs (Câmara et al. 2003; Thambugala et al. 2014b). Currently, 17 species are accepted in this genus in Species Fungorum (2021).

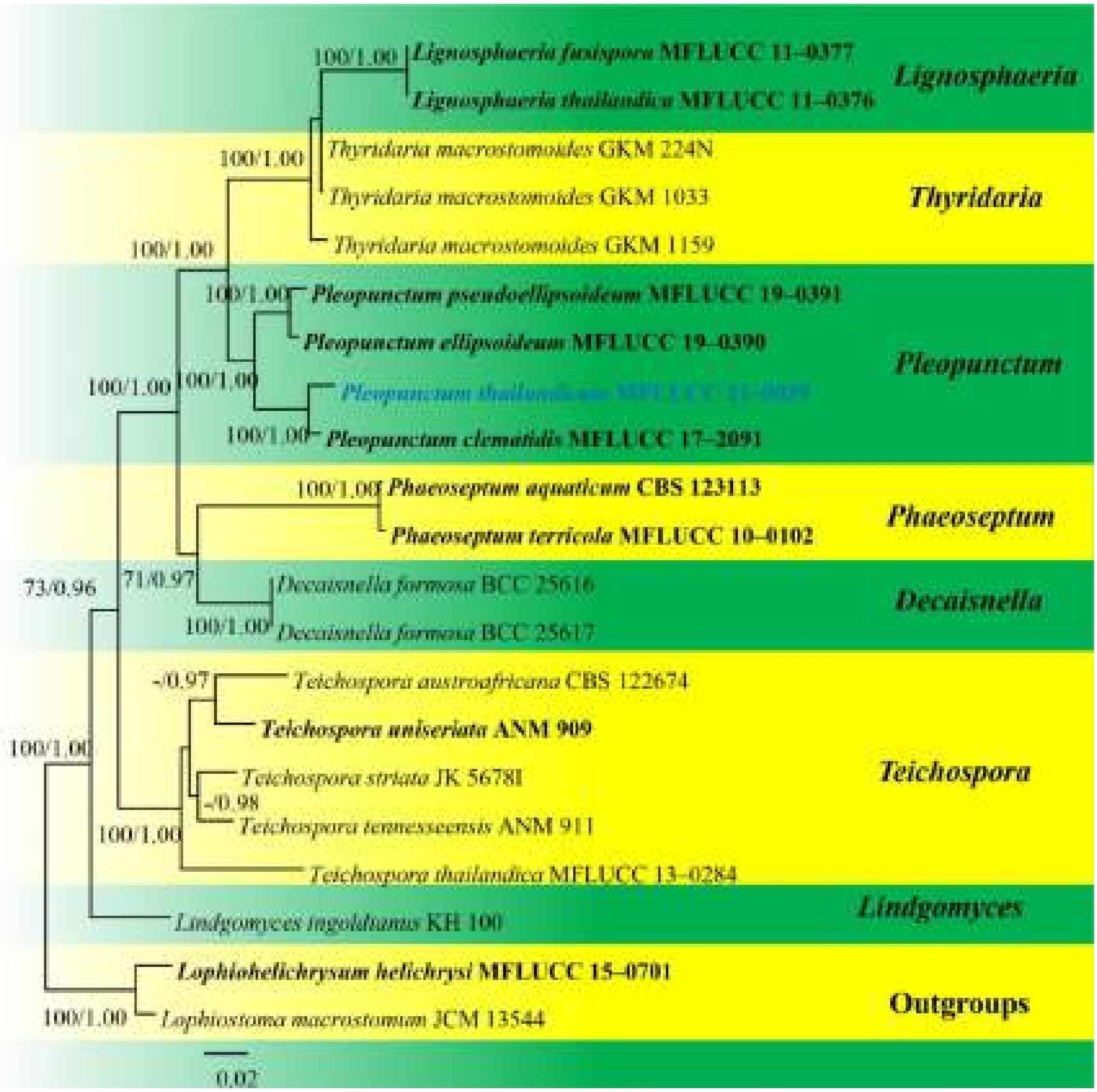


Fig. 62 Phylogram generated from Bayesian analysis based on combined LSU, SSU, ITS and TEF1-α sequence data. Twenty-one strains are included in the combined analyses which comprised 3338 characters (866 characters for LSU, 999 characters for SSU, 550 characters for ITS, 923 characters for TEF1-α) after alignment. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RAxML tree with a final likelihood value of − 11657.841536 is presented. Estimated base frequencies were as follows: A = 0.239152, C = 0.258772, G = 0.277763, T = 0.224314; substitution rates AC = 1.083541, AG = 2.347613, AT = 1.453520, CG = 1.144548, CT = 7.950168, GT = 1.000000. Bootstrap support values for ML greater than 70% and Bayesian posterior probabilities greater than 0.95 are given near nodes respectively. The tree is rooted with *Lophiohelichrysum helichrysi* (MFLUCC 15-0701) and *Lophiostoma macrostomum* (JCM 13,544). Ex-type strains are in bold and newly generated sequence is in blue

However, Thambugala et al. (2014b) synonymized *Phaeosphaeriopsis musae* under *Phaeosphaeria musae* and the accepted number of species in *Phaeosphaeriopsis* should therefore be 16 species. All *Phaeosphaeriopsis* species have available DNA sequence data for molecular comparisons, and the genus is monophyletic. The sexual morph of the majority of *Phaeosphaeriopsis* species is known and currently, *P. agapanthi* and *P. aloes* are known only from their coelomycetous asexual morph. Herein we report the sexual morph of *Phaeosphaeriopsis aloes* from dead leaves of *Yucca elephantipes* in Yunnan, China.

Phaeosphaeriopsis aloes Crous & Y. Marín, Marin-Felix et al., Stud. Mycol. 94: 61 (2019)

Index Fungorum number: IF829642; *Facesoffungi number*: FoF 09952; Fig. 63

Saprobic on dead leaves of *Yucca elephantipes*, visible as abundant black spots, scattered on entire leaf surface, **Sexual**

Fig. 63 ***Phaeosphaeriopsis aloes*** (KUN-HKAS 115783, **new host and new geographical record**). **a–d** Ascomata observed on host substrate. **e** Vertical section through an ascoma. **f** Close of an ostiole. **g** Cells of peridium. **h** Pseudoparaphyses. **j–l** Asci. **i**, **m–p** Ascospores. Scale bars: **d**, **e** = 50 μm, **g**, **i–p** = 20 μm, **h** = 10 μm

morph *Ascomata* 160–220 µm high, 140–180 µm diam. ($\bar{x}$ = 195.5 × 169 µm, n = 10), scattered, immersed, unilocular, globose, black, papillate, ostiolate. *Peridium* 10 – 40 µm wide, comprising two layers dark brown-walled cells of *textura angularis*, outer layer loosely arranged and inner layer compressed. *Hamathecium* of 1.5–2.5 µm wide, cellular, hyaline, septate, rarely branching, pseudoparaphyses anastomosing mostly above the asci, embedded in a mucilaginous matrix. *Asci* 80 – 100 × 10 – 12 µm ($\bar{x}$ = 93 × 12 µm, n = 20), 8-spored, bitunicate, fissitunicate, cylindrical, short-pedicellate, apically rounded, lacking an ocular chamber. *Ascospores* 16 – 22 × 4 – 5 µm ($\bar{x}$ = 19 × 4.5 µm, n = 25), overlapping biseriate, cylindrical, 3-septate at young stage, becoming 5-septate when mature, without constriction or slightly constricted at the basal septum, fourth cell swollen, hyaline when immature, becoming yellowish brown at maturity, verrucose, prominent guttules in each cell, surrounded by a thick mucilaginous sheath. **Asexual morph** Coelomycetous (see Marin-Felix et al. 2019a, p. 61).

Material examined: CHINA, Yunnan Province, Heilongtan, Kunming Institute of Botany, 25.137711° N 102.745185° E, on dead leaves of *Yucca elephantipes* (*Asparagaceae*), 2 February 2019, D.N. Wanasinghe, (KUN-HKAS 115783, **new host and new geographical record**).

GenBank numbers: ITS = MZ493305; LSU = MZ493319; SSU = MZ493291; TEF1-α = MZ508414.

Notes: *Phaeosphaeriopsis aloes* was introduced by Marin-Felix et al. (2019a) on leaves of *Aloe* sp. from USA, California. In this study we have acquired DNA from a sexual morph and in multi-gene phylogeny our strain and the ex-type strain of *P. aloes* (CBS 145,367) group in a well-supported monophyletic clade (Fig. 64). Even though these two isolates are not derived from the same host or locality, there was only one bp difference in the comparison of the 518 nucleotides across the ITS regions. The TEF1-α gene region of CBS 145,367 is not available for further comparison. From these molecular perspectives, taxonomically, it would be wise to consider these two strains as belonging to a single species (Jeewon and Hyde 2016). The sexual morph is similar to *Phaeosphaeriopsis agavensis*, *P. nolinae* and *P. obtusispora* in terms of its ascospore characteristics (Câmara et al. 2003). These are however, not phylogenetically closely related (Fig. 64), therefore, we introduce our taxon as the sexual morph of *Phaeosphaeriopsis aloes* (Fig. 63). We could not manage to maintain a living culture as subsequent attempts to isolate failed, and hence a living culture is unavailable. Thus, we extracted DNA directly from the fruiting bodies.

Pleosporaceae Nitschke

Notes: *Pleosporaceae* is a species rich family that distributed worldwide, especially in tropical regions (Ariyawansa et al. 2015b). The species in this family are generally found as saprobes and endophytes on various plants, or opportunistic human, and plant pathogens (Hongsanan et al. 2020a). Hyphomycetous in the asexual morph and brown muriform ascospores in the sexual morph are typical of this family. Currently there are 23 accepted genera in *Pleosporaceae*. We follow the latest treatment of this family in Hongsanan et al. (2020a) and Wijayawardene et al. (2020).

Comoclathris Clem.

Notes: *Comoclathris* was introduced by Clements (1909) which is typified by *Comoclathris lanata*. The genus is accepted as a genus in *Pleosporaceae* (Hongsanan et al. 2020a; Wijayawardene et al. 2020). Currently there are 34 accepted species in this genus, but only 18 species have been confirmed by DNA based sequence data analyses (Hongsanan et al. 2020a). We report a new record of *Comoclathris permunda* on *Achillea* sp. in Uzbekistan for the first time.

Comoclathris permunda (Cooke) E. Müll., Monogr. Biol. Soc. Pakistan 8: 68 (1979) [1978]

Index Fungorum number: IF283403; *Facesoffungi number*: FoF 03231; Fig. 65

≡ *Sphaeria permunda* Cooke, Grevillea 5(no. 35): 111 (1877)

Saprobic on dead herbaceous branches. **Sexual morph** *Ascomata* 190–250 µm high, 200–280 µm diam. ($\bar{x}$ = 226.5 × 243 µm, n = 10), semi immersed to erumpent, solitary, scattered, dark brown to black, coriaceous, cupulate when dry, with brown to reddish brown. *Peridium* 10–15 µm wide at the base, 15–30 µm wide in sides, comprising two layers, outer layer heavily pigmented, thin-walled, comprising blackish to dark brown cells of *textura angularis*, inner layer composed of hyaline, thin-walled cells of *textura angularis*. *Hamathecium* comprising numerous, 2.5–4.5 µm ($\bar{x}$ = 3 µm, n = 20) wide, filamentous, branched, septate, pseudoparaphyses. *Asci* 80–120 × 18–24 µm ($\bar{x}$ = 103 × 20 µm, n = 20), 8-spored, bitunicate, fissitunicate, cylindric-clavate, with a 10–15 µm long pedicel, thick-walled at the apex, with a minute ocular chamber. *Ascospores* 20–30 × 8–12 µm ($\bar{x}$ = 25 × 11 µm, n = 30), overlapping 1–2-seriate, muriform, mostly ellipsoidal, 3 – 4 transversely septate, with 1 vertical septum, constricted at the septa, initially hyaline, becoming brown at maturity, conically rounded at the ends, surrounded by 3–6 µm thick, hyaline, mucilaginous sheath. **Asexual morph** Undetermined.

Material examined: UZBEKISTAN, Jizzakh Province, Zaamin District, Zaamin National Nature Park, Ettisuv River, Turkestan range of Pamir-Alay Mountains, on dead aerial stem of *Achillea* sp. (*Asteraceae*), 11 July 2019, Yusufjon Gafforov, YG-Z12-1 (TASM 6159, KUN-HKAS 115786, **reference specimen**).

GenBank numbers: ITS = MZ493294, LSU = MZ493308, SSU = MZ493280, RPB2 = MZ508415.

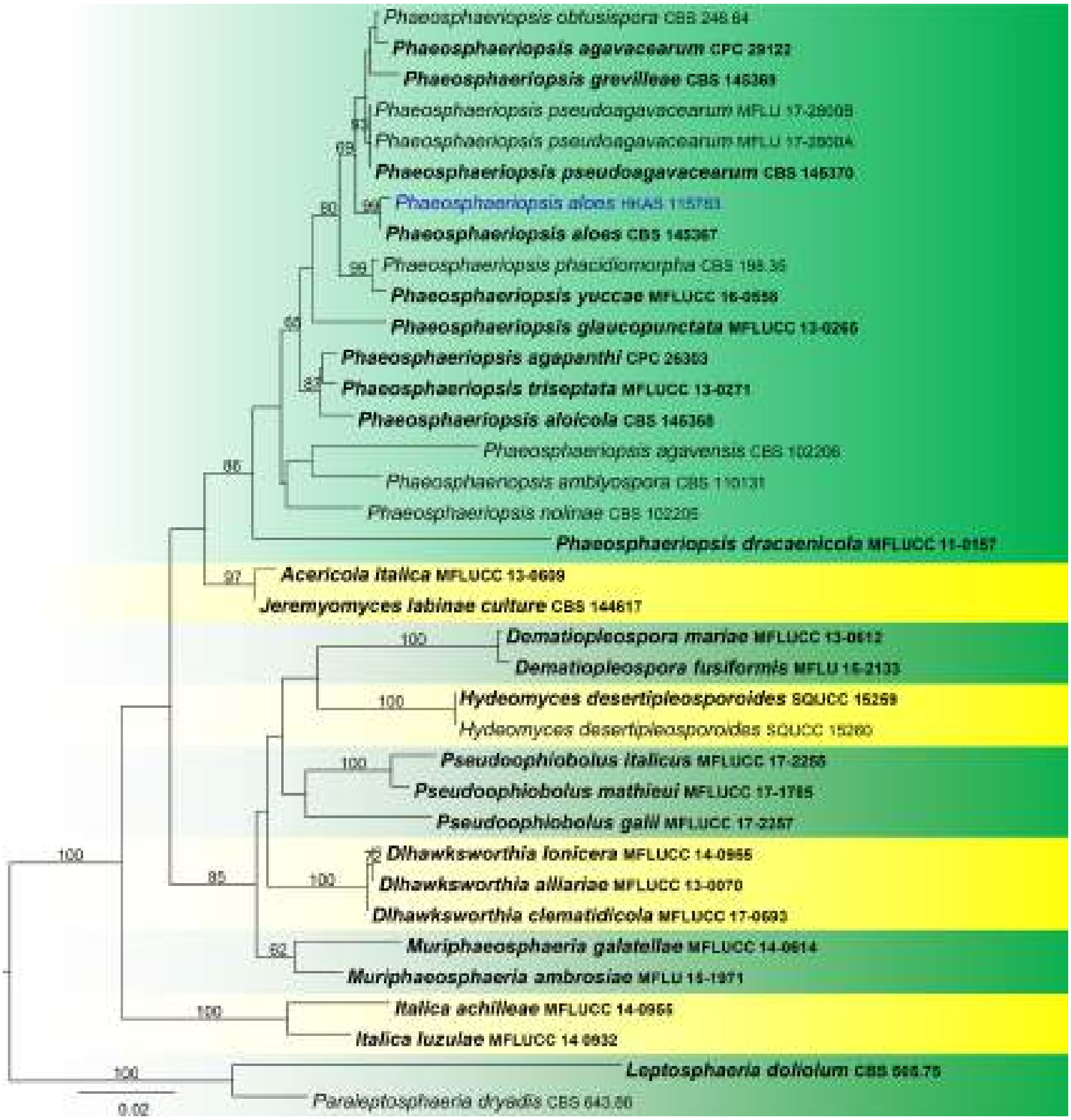


Fig. 64 Phylogram generated from the best scoring of the RAxML tree based on a combined SSU, LSU, TEF1-α and ITS sequence dataset to indicate the representative species in *Phaeosphaeriaceae*. Twenty-six strains are included in the combined analyses which comprise a total of 2930 characters. *Leptosphaeria doliolum* (CBS 505.75) and *Paraleptosphaeria dryadis* (CBS 643.86) are selected as the outgroup taxa. The best RAxML tree with a final likelihood value of − 10260.911412 is presented. RAxML analysis yielded 541 distinct alignment patterns and 25.64% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.247998, C = 0.227405, G = 0.266027, T = 0.258570; substitution rates AC = 1.142059, AG = 3.643753, AT = 2.176676, CG = 0.693405, CT = 7.632890, GT = 1.00; gamma distribution shape parameter alpha = 0.572735. Bootstrap support values for maximum likelihood (MLBS, left) equal to or greater than 60% are given above the nodes. Ex-type strains are in bold and newly generated sequence is in blue

Notes: *Comoclathris permunda* was introduced by Müller (1977) and the taxon was reported on different hosts from various countries (Table 3). Thambugala et al. (2017) collected a similar species to *C. permunda* (Müller 1977) in Italy on *Phleum pratense* and designated a reference specimen of this species. They also confirmed its phylogenetic affiliation in *Comoclathris*. Our new collection, TASM 6159 (from Uzbekistan), which fits with the original description of *Comoclathris permunda* (Müller 1977) and the description of Thambugala et al. (2017) in having solitary, dark brown to black ascomata that are cupulate when dry, cylindric-clavate, pedicellate asci with a minute ocular chamber, brown, ellipsoidal, 3–4 transversely septate, with 1 vertical septum ascospores with conically rounded ends (Fig. 65). In the phylogenetic analysis of combined SSU, LSU, ITS, and RPB2 sequence dataset to indicated that our new strain

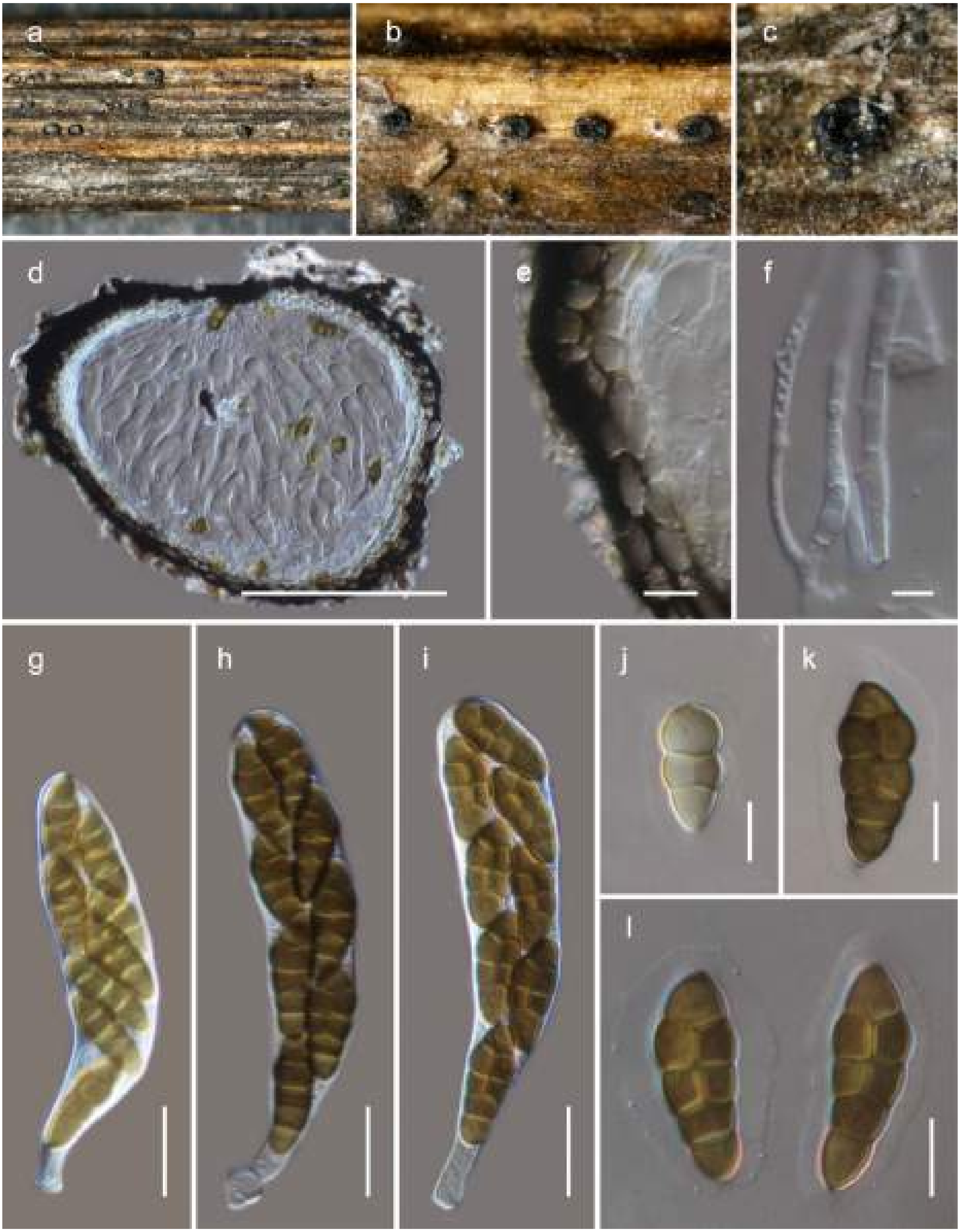


Fig. 65 ***Comoclathris permunda*** (TASM 6159, **reference specimen**). **a–c** Appearance of ascomata on host surface. **d** Longitudinal section of an ascoma. **e** Section of the peridium. **f** Pseudoparaphyses. **g–i** Asci. **j–l** Ascospores surrounded by with a mucilaginous sheath. Scale bars: **d** = 50 µm, **e**, **j–l** = 10 µm, **f** = 5 µm, **g–i** = 20 µm

Table 3 Known hosts were found for *Comoclathris permunda* and their distribution

Plant host	Host family	Country	References
Achillea sp.	*Asteraceae*	Uzbekistan	This study
Amorpha fruticosa	*Fabaceae*	USA	Cooke (1983), Thambugala et al. (2017)
Apiaceae sp.	*Apiaceae*	USA	Shoemaker and Babcock (1992)
Aquilegia vulgaris	*Ranunculaceae*	Pakistan	Ahmad (1978), Ahmad et al. (1997)
Arabis platysperma	*Brassicaceae*	California	Shoemaker and Babcock (1992)
Arenaria drypideae	*Caryophyllaceae*	Turkey	Shoemaker and Babcock (1992)
Artemisia sp.	*Asteraceae*	Pakistan	Ahmad (1978), Ahmad et al. (1997)
Asclepias sp.	*Apocynaceae*	USA	French (1989)
Atriplex halimus	*Amaranthaceae*	Portugal, Spain	Checa (2004)
Boerhavia diffusa	*Nyctaginaceae*	Pakistan	Ahmad (1978), Ahmad et al. (1997)
Bupleurum spinosum	*Apiaceae*	Portugal, Spain	Checa (2004)
Cakile maritima	*Brassicaceae*	Portugal, Spain	Checa (2004)
Castilleja miniata	*Orobanchaceae*	USA	Shoemaker and Babcock (1992)
Chlorogalum pomeridianum	*Asparagaceae*	USA	Shoemaker and Babcock (1992)
Chlorogalum sp.	*Asparagaceae*	USA	Thambugala et al. (2017)
Eryngium campestre	*Apiaceae*	Portugal, Spain	Checa (2004)
Heldreichia rotundifolia	*Brassicaceae*	Turkey	Shoemaker and Babcock (1992)
Koeleria cristata	*Poaceae*	Canada	Shoemaker and Babcock (1992)
Lactuca tenerrima	*Asteraceae*	Portugal, Spain	Checa (2004)
Linum usitatissimum	*Linaceae*	USA	Thambugala et al. (2017)
Penstemon gracilentus	*Plantaginaceae*	USA	French (1989)
Phleum pratense	*Poaceae*	Italy	Thambugala et al. (2017)
Polygonum amphibium	*Polygonaceae*	USA	Shoemaker and Babcock (1992)
Prunus cerasus	*Rosaceae*	USA	Shoemaker and Babcock (1992)
Sambucus racemosa var. *microbotrys*	*Adoxaceae*	USA	Shoemaker and Babcock (1992)
Santolina chamaecyparissus	*Asteraceae*	Portugal, Spain	Checa (2004)
Selinum papyraceum	*Apiaceae*	Pakistan	Ahmad (1978), Ahmad et al. (1997)
Selinum tenuifolium	*Apiaceae*	Pakistan	Ahmad (1978), Ahmad et al. (1997)
Senecio tournefortii var. *granatensis*	*Asteráceas*	Portugal, Spain	Checa (2004)
Solanum dulcamara	*Solanaceae*	Portugal, Spain	Checa (2004)
Stephanomeria tenuifolia	*Asteraceae*	USA	Shoemaker and Babcock (1992)
Synthyris dissecta	*Plantaginaceae*	USA	Shoemaker and Babcock (1992)
Thalictrum fendleri	*Ranunculaceae*	USA	Shoemaker and Babcock (1992)
Wisteria chinensis	*Fabaceae*	Portugal, Spain	Checa (2004)

is monophyletic with *Comoclathris permunda* (MFLUCC 14-0974) with 100% MLBS support (Fig. 66).

Testudinaceae Arx

Notes: *Testudinaceae*, currently consists of nine genera *Angustospora*, *Halotestudina*, *Lepidosphaeria*, *Lojkania*, *Muritestudina*, *Neotestudina*, *Testudina*, *Ulospora* and *Verruculina* (Hongsanan et al. 2020a). Presence of cleistothecioid ascomata, 1-septate or multi-septate, or muriform, brown, glabrous or ornamented ascospores are the characteristic features of all these genera (Hongsanan et al. 2020a). Different genera have been established under *Testudinaceae* based on the differences in size, shape and ornamentation of the ascospores (von Arx and Müller 1975; Hawksworth 1979). Recent phylogenetic studies have shown the close genetic relationship between genera of *Testudinaceae* (Hashimoto et al. 2017; Doilom et al. 2018; Hongsanan et al. 2020a).

Lepidosphaeria Parg.-Leduc

Notes: We follow the latest updated account of *Lepidosphaeria* in Hongsanan et al. (2020a).

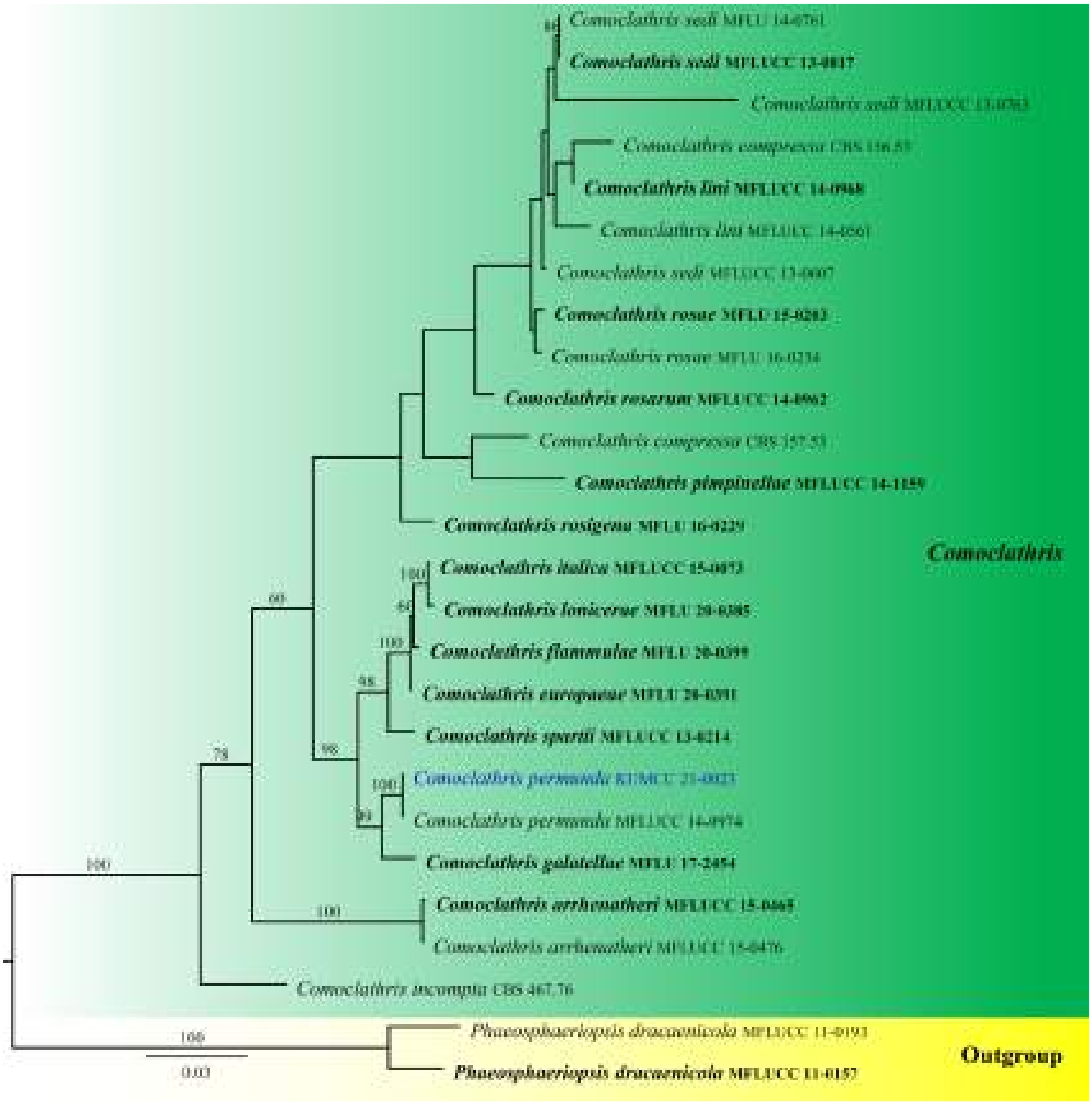


Fig. 66 Phylogram generated from the best scoring of the RAxML tree based on a combined SSU, LSU, ITS, and RPB2 sequence dataset to indicate the species in *Comoclathris*. Twenty-six strains are included in the combined analyses which comprise a total of 3318 characters. *Phaeosphaeriopsis dracaenicola* (MFLUCC 11-0157, MFLUCC 11-0193) is selected as the outgroup taxon. The best RAxML tree with a final likelihood value of – 11070.111652 is presented. RAxML analysis yielded 691 distinct alignment patterns and 19.26% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.25654, C = 0.224566, G = 0.266202, T = 0.252692, with substitution rates AC = 1.928472, AG = 4.365502, AT = 1.451146, CG = 1.060614, CT = 9.003466, GT = 1.000000; gamma distribution shape parameter alpha = 0.483396. Bootstrap support values for maximum likelihood (MLBS) equal to or greater than 60% is given above the nodes. Ex-type strains are in bold and newly generated sequence is in blue

Lepidosphaeria strobelii A.C. Lagashetti, D. Choudhary & S.K. Singh, ***sp. nov.***

MycoBank number: MB830723; *Facesoffungi number*: FoF 06120, Fig. 67

Etymology: specific epithet refers to Prof. Gary Strobel, MSU, USA to commemorate his immense contribution in the field of biology of endophytic fungi.

Holotype: AMH-10126

Colour codes follow: Methuen Handbook of Colour (Kornerup and Wanscher 1978)

Isolated as an endophyte from *Cinnemomum zeylanicum*. **Sexual morph** Undetermined. **Asexual morph** *Hyphae* septate, hyaline, thin-walled, 1–4 µm wide, simple to branched, smooth-walled, consisting of series of inflated cells (chlamydospores), globulated and hyphae showed frequent anastomosis and spirally twisting. *Hyphal cells*, cylindrical, 7–19.5 × 1.5–4 µm ($\bar{x} = 12.5 \times 2$ µm, n = 30).

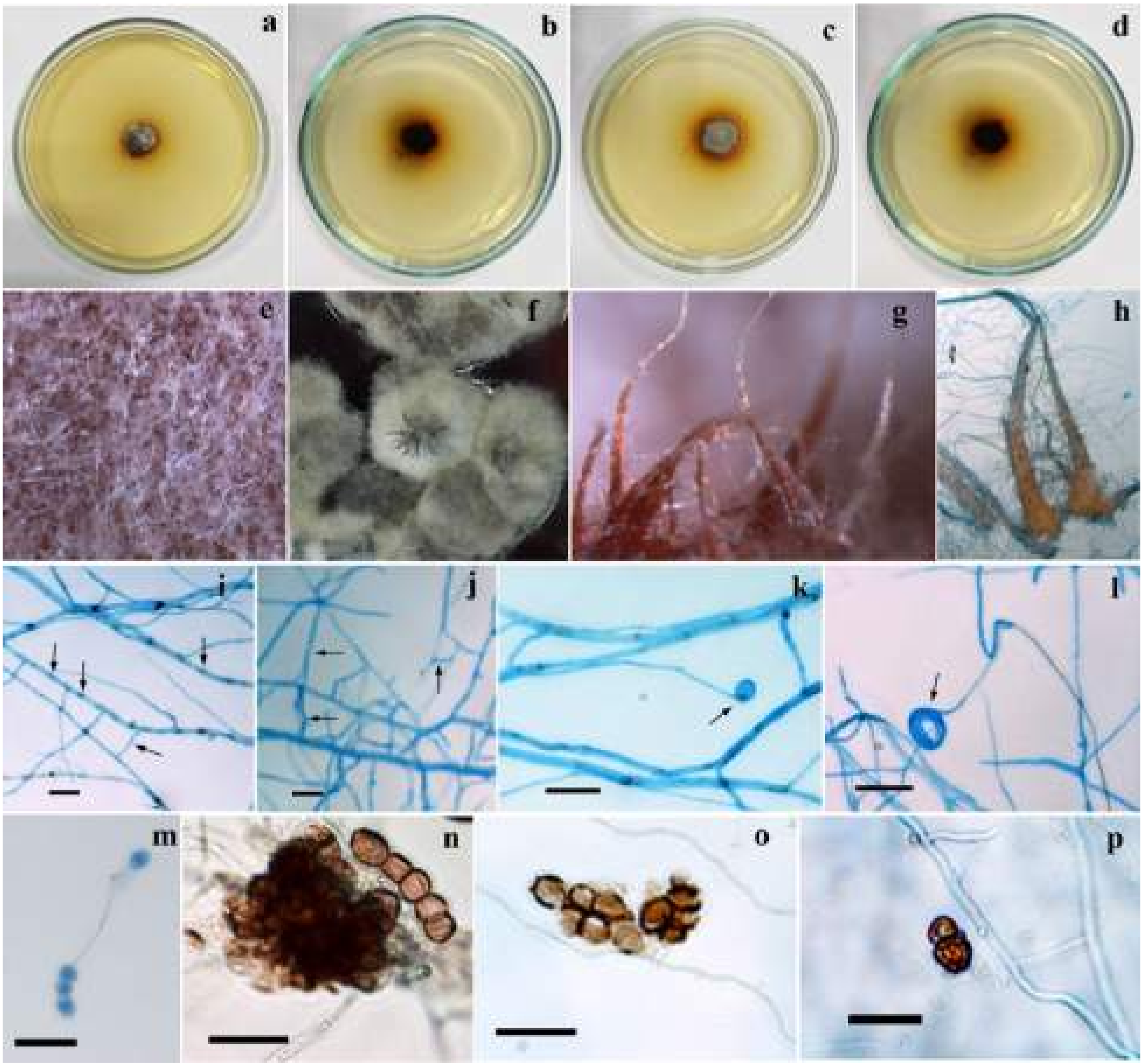


Fig. 67 ***Lepidosphaeria strobelii*** (AMH 10126, **holotype**; NFCCI 4579, **ex-type culture**). **a**, **b** Colonies morphology on potato dextrose agar (from surface and reverse views). **c, d** Colonies morphology on SDA, from surface and reverse views). **e** Stereoscopic view of colony growing on PDA. **f**, **g** Magnified view showing hyphal bundles. **h** Microscopic view of hyphal bundles. **i** Mycelia with septate hyphae (arrows). **j** Mycelia showing frequent anastomosis (arrows). **k**, **l** Mycelia with spiral twisting (arrows). **m** Young chlamydospores. **n** Mature chlamydospores in chain. **o** Mature chlamydospores in bunch. **p** Mature chlamydospore. Scale bars: **i**–**p** = 20 µm

Chlamydospores hyaline as well as light to dark olivaceous brown, observed frequently, terminal to intercalary, solitary, in branched chains and in bunches, with thickened and darkened wall, variable in shape, globose to cylindrical, 4.5–11 × 5–9 µm ($\bar{x}$ = 8.5 × 7.5 µm, n = 30).

Culture characteristics: Colonies growing slowly on PDA reaching to 12–14 mm diam. after 2 weeks at 25 °C; colonies from above grey (4D1), circular, raised, rocky, with slightly cottony aerial mycelium, synnematous, entire with irregular margin; colony from below, violet brown (10F8), sulcate, with diffusible red pigment. Colonies on Sabouraud Dextrose agar (SDA) reaching to 12–13 mm diam. after 2 weeks at 25 °C; colonies from above greyish green (28C3), circular, raised, velvety with smooth, entire and irregular margin; colony from below violet brown (10F8), sulcate and with diffusible red pigment.

Material examined: INDIA, Karnataka, Belgaum (15.8497° N 74.4977° E), on living leaves of *Cinnemomum zeylanicum*, 29 November 2011, S.K. Singh (AMH 10126, **holotype**), ex-type living culture, NFCCI 4579.

GenBank numbers: ITS = MH790217, LSU = MK749433.

Notes: The proposed a new species, *Lepidosphaeria strobelii* is phylogenetically distinct from *L. nicotiae* with 99% MLBS support (Fig. 68) based on maximum likelihood analysis of a combined ITS and LSU sequence dataset. A megablast analysis, the ITS sequence of *L. strobelii* showed 95.23% (419/440) similarity and 6 gaps (1%) with *L. nicotiae* (CBS 559.71, Ex-type) and 96.08% (441/459) similarity and 2 gaps (0%) with *L. nicotiae* (1B0102). A comparison of the ITS sequence shows that *L. strobelii* differs from *L. nicotiae*, 21/441 base positions (4.7%) without gaps. Moreover, the source of isolation of these species are different. Type strain, *L. nicotiae* (CBS 559.71) was isolated from desert soil in Algeria and *L. nicotiae* (1B0102) was from totally suspended particles of air from Bangkok, Thailand. Whereas, *L. strobelii* (NFCCI 4579) was isolated as an endophyte from the leaves of *Cinnemomum zeylanicum* in India (Fig. 67). Morphologically, the new species could not be compared

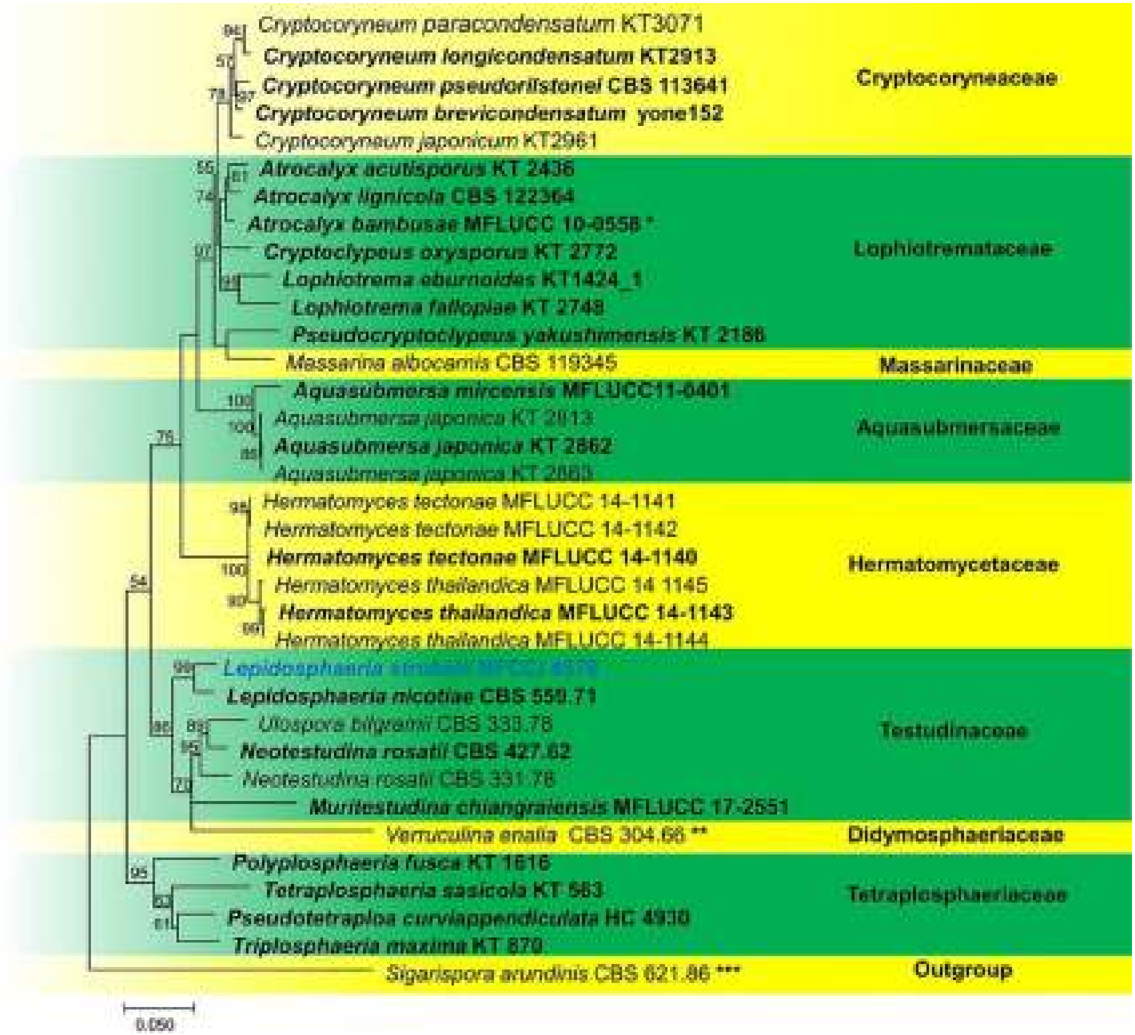


Fig. 68 Phylogram generated from maximum likelihood method for *Lepidosphaeria strobelii* (NFCCI 4579); using combined ITS and LSU sequence dataset. The evolutionary history was inferred based on the General Time Reversible model (Nei and Kumar 2000). The tree with the highest log likelihood (− 7009.2670) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. A discrete GAMMA distribution was used to model evolutionary rate differences among sites [5 categories (+G, parameter = 0.5660)]. The rate variation model allowed for some sites to be evolutionarily invariable [(+I), 58.2766% sites]. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 35 nucleotide sequences. All positions with less than 85% site coverage were eliminated. That is fewer than 15% alignment gaps, missing data, and ambiguous bases were allowed at any position. There were a total of 1322 positions in the final dataset. Evolutionary analyses were conducted in MEGA7 (Kumar et al. 2016). *Sigarispora arundinis* (formerly known as *Lophiostoma arundinis*) was used as an outgroup. Ex-type strains are in bold and newly generated sequence is in blue

with *L. nicotiae*. *Lepidosphaeria nicotiae* is characterized by its sexual morph, forming cleistothecial, black, globose to subglobose ascomata, elongate-clavate asci, with a long pedicel, embedded in filiform, hyphae-like pseudoparaphyses, and pale brown to brown, oblong, tuberculate, 1-septate, finely echinulate ascospores (Doilom et al. 2018). While the sexual morph of *L. strobelii* is undetermined.

Remarks:

**Atrocalyx bambusae* is formerly known as *Lophiotrema bambusae*,

***Veruuculina enalia* is formerly known as *Didymosphaeria enalia* and

****Sigarispora arundinis* is formerly known as *Lophiostoma arundinis*.

Tetraplosphaeriaceae Kaz. Tanaka & K. Hiray.

Notes: We follow the latest treatment and updated accounts of *Tetraplosphaeriaceae* in Hongsanan et al. (2020a).

Ernakulamia Subram.

Notes: The latest treatment and updated accounts of *Ernakulamia* were provided in Hyde et al. (2020a). Only four species are included in this genus, *E. cochinensis* (Subram.) Subram. (type species), *E. krabiensis*, *E. tanakae* and *E. xishuangbannaensis* (Dong et al. 2020b; Hyde et al. 2020b; Index Fungorum 2021) and all species have sequence data available in GenBank. *Ernakulamia cochinensis* and *E. tanakae* were found on decaying spathes of *Cocos nucifera* (*Arecacceae*) in India (Subramanian 1957, 1994; Hyde et al. 2020b), whereas *Ernakulamia krabiensis* was found on decaying pods septum of *Acacia* sp. (*Fabaceae*) in Thailand (Jayasiri et al. 2019). Unfortunately, *Ernakulamia xishuangbannaensis* was previously introduced as *Polyplosphaeria xishuangbannaensis* Tibpromma & K.D. Hyde on dead leaves of *Pandanus* in Yunnan, China (Tibpromma et al. 2018). Multilocus phylogenetic analysis demonstrated *P. xishuangbannaensis* clustered within *Ernakulamia* (Dong et al. 2020b). Thus, the species was transferred to *Ernakulamia* as *E. xishuangbannaensis* by Dong et al. (2020b). In this study, *Ernakulamia tanakae* is reported for the first time on decaying wood of an unidentified host from Thailand. The updated phylogenetic analysis is presented (Fig. 70).

Ernakulamia tanakae Rajeshkumar & K.D. Hyde, Fungal Diversity 100: 111 (2020)

Index Fungorum number: IF556700; *Facesoffungi number*: FoF 06338; Fig. 69

Saprobic on decaying wood. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Colonies* effuse, superficial, dark brown to black, sparsely hyaline hyphal network. *Conidiophores* not seen. *Conidiogenous cells* monotretic, integrated. *Conidia* 35–48 × 22–37 µm ($\bar{x}$ = 42 × 30 µm, n = 10), dictyosporous, obconical, obovoid or subglobose, dark brown, multi-septate, thick-walled, with 3–5-appendages per conidium. *Appendages* 24–68 × 4–5 µm, cylindrical stiff, straight, apical or subapical, dark brown, 3–6-septate, smooth-walled.

Culture characteristics: Conidium germinating on PDA within 24 h. Colonies on PDA reaching 3.5 cm diam. after 2 weeks at room temperature, circular, undulate edge, grey to dark grey, dense and raised on medium surface. Mycelium superficial, velvety, flossy.

Material examined: THAILAND, Phetchabun Province, Lom Sak, saprobic on decaying wood of unidentified host, 25 July 2019, S. Boonmee, LSP02 (MFLU 21-0066, **new record**), living culture, MFLUCC 21-0089.

GenBank numbers: ITS = MZ538502, LSU = MZ538536, TEF1-α = MZ567081.

Notes: *Ernakulamia tanakae* was introduced by Hyde et al. (2020a), which is reported as a second species found on the *Cocos nucifera* host from India as well as the type species *E. cochinensis*. All species of *Ernakulamia* are characterized by superficial, dictyosporous, with cylindrical stiff appendages and dark brown conidia (Fig. 69, Subramanian 1994; Jayasiri et al. 2019; Hyde et al. 2020b). Phylogenetic analysis placed our strain (MFLUCC 21-0089) close to the type strain (NFCCI 4615) and other isolates of *E. tanakae* (NFCCI 4616 and NFCCI 4617) (Fig. 70). Pairwise comparison of DNA sequences of LSU and ITS regions of these four strains reveals 2/872 bp (0.23%) and 5/528 bp (0.95%) very few base pair differences, which confirms that they are conspecific. Thus, a new geographical record of *E. tanakae* on decaying wood from Thailand is reported.

Thyridariaceae Q. Tian & K.D. Hyde

Notes: We follow the latest treatment of *Thyridariaceae* in Mapook et al. (2020) and updated accounts of taxa in Hongsanan et al. (2020a).

Thyridaria Sacc.

Notes: *Thyridaria* was introduced by Saccardo (1875) which was typified by *T. broussonetiae* (Sacc.) Traverso, where *T. incrustans* Sacc. was synonymized (Barr 1990). *Thyridaria* comprises 52 species (Wijayawardene et al. 2020) which are widely distributed. Taxa in this genus are mostly saprobes on a diverse range of plant substrates (Hyde et al. 2013; Jaklitsch and Voglmayr 2016; Hongsanan et al. 2020a; Index Fungorum 2021). Only two species *T. acaciae* and *T. broussonetiae* have sequence data available in GenBank. We follow the latest treatment of *Thyridaria* in Jaklitsch and Voglmayr (2016) and updated accounts of taxa in Wijayawardene et al. (2020).

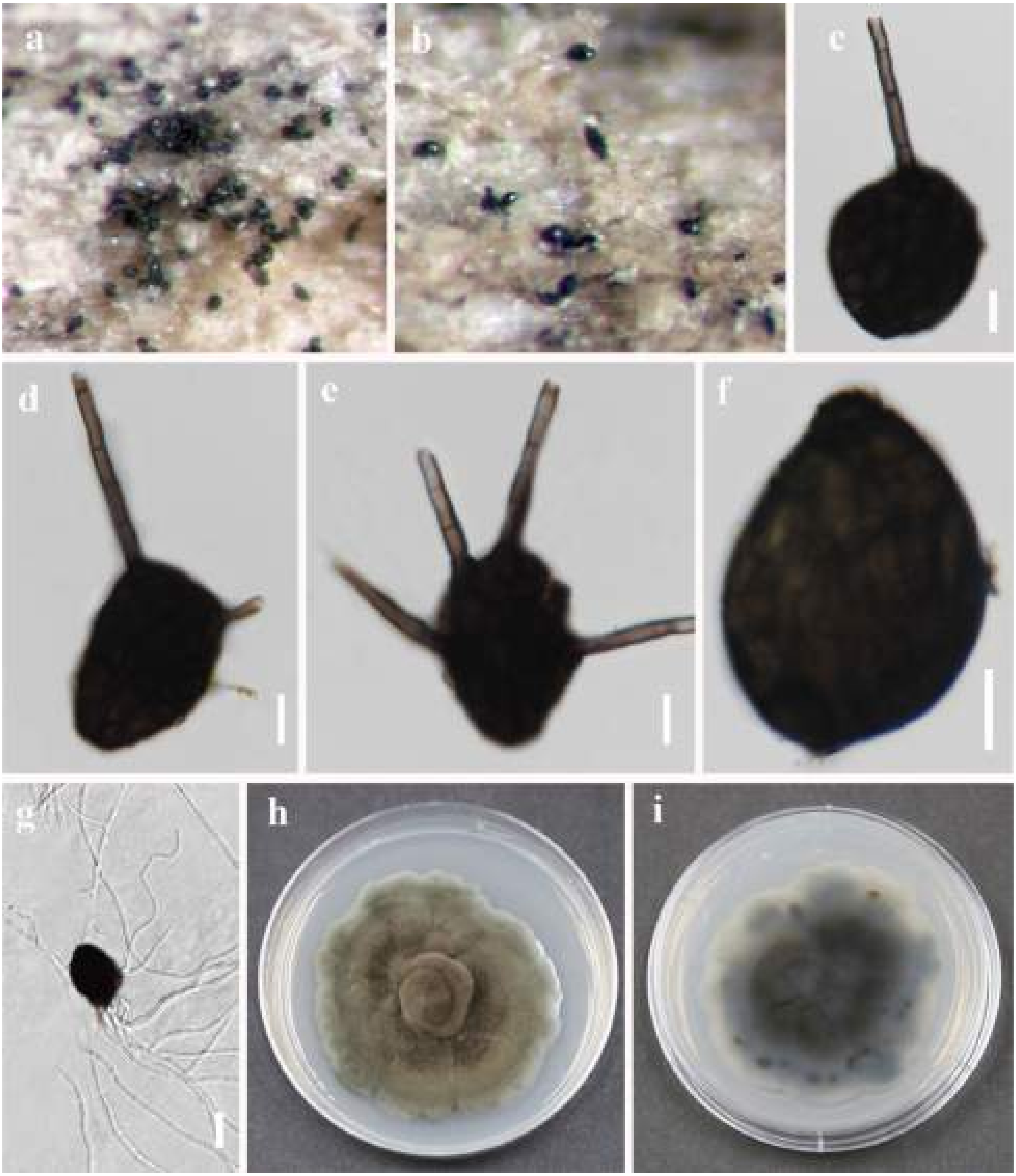


Fig. 69 ***Ernakulamia tanakae*** (MFLU 21-0066, **new record**). **a**, **b** Appearance of conidial masses on host substrate. **c**–**f** Mature conidia. **g** Germinated conidium. **h**, **i** Culture on PDA from surface and reverse. Scale bars: **c**–**f** = 10 μm, **g** = 20 μm

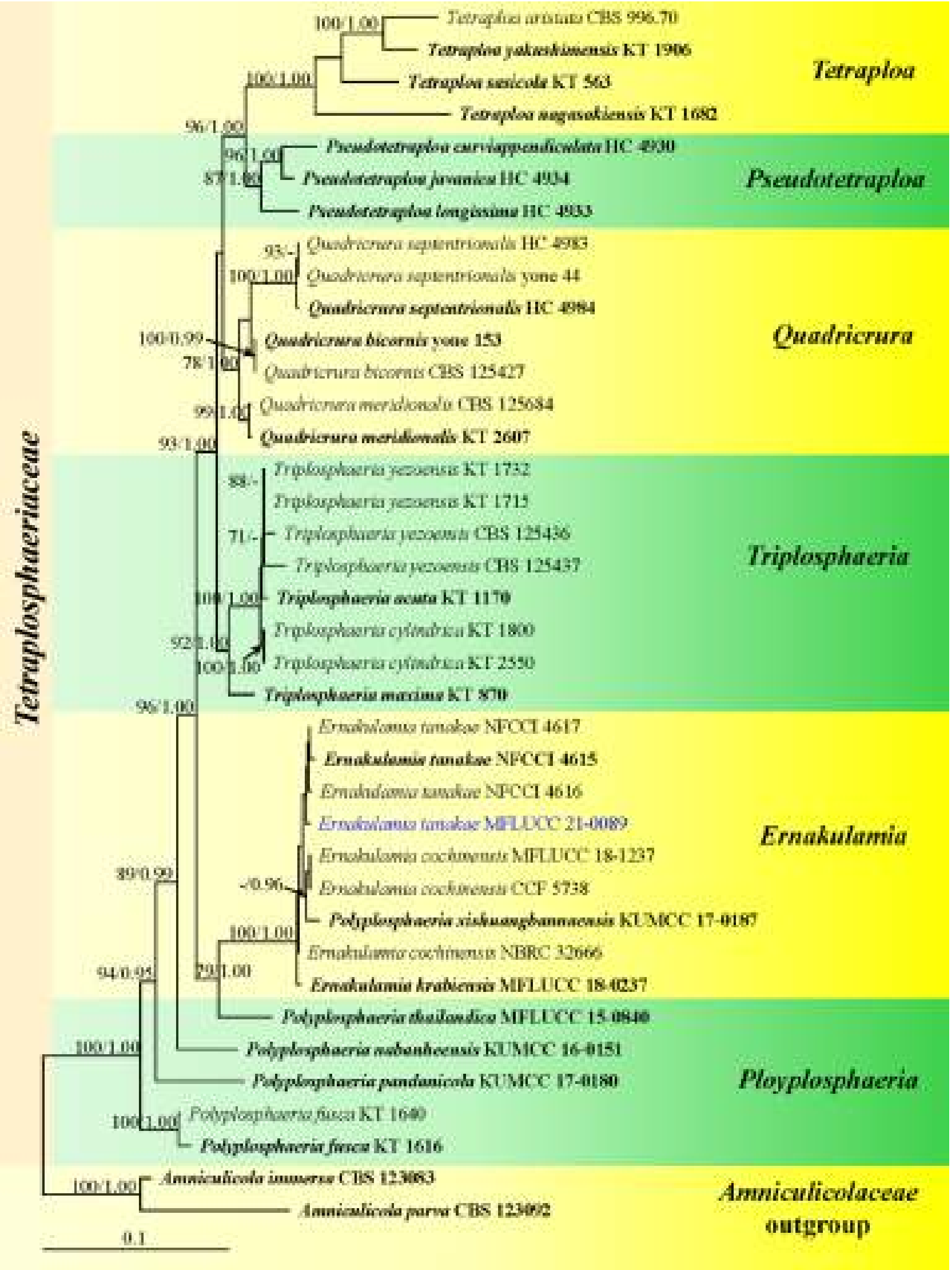


Fig. 70 Maximum likelihood phylogenetic tree based on a combined LSU and ITS sequence dataset of *Ernakulamia* taxa and related genera in *Tetraplosphaeriaceae*. Thirty-eight strains are included in the combined analyses which comprise a total of 1468 characters. *Amniculicola immersa* (CBS 12308) and *A. parva* (CBS 123092) are selected as the outgroup taxa. The best RAxML tree with a final likelihood value of − 5624.746373 is presented. RAxML analysis yielded 413 distinct alignment patterns and 15% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.236603, C = 0.245429, G = 0.293755, T = 0.224212, with substitution rates AC = 2.551620, AG = 2.407140, AT = 1.683194, CG = 0.618325, CT = 9.671311, GT = 1.000000; gamma distribution shape parameter alpha = 0.164106. Bootstrap support values for maximum likelihood (MLBS, left) equal to or greater than 70% are given above or below the nodes. Bayesian posterior probabilities (BYPP, right) equal to or greater than 0.95 are given above the nodes. Ex-type strains are in bold and newly generated sequence is in blue

Thyridaria aureobrunnea Boonmee, Huanraluek & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF558540; *Facesoffungi number*: FoF 09193; Fig. 71

Etymology: The specific epithet '*aureobrunnea*' refers to the golden brown to chestnut brown ascospores.

Holotype: MFLU 21-0067

Saprobic on decaying wood. **Sexual morph** *Ascomata* 248–294.5 µm high, 262–286.5 µm diam. ($\bar{x}$ = 330 × 367 µm, n = 4), immersed, erumpent, aggregated, clustered, globose to subglobose, uniloculate, dark brown to black, central ostiole, with minute papilla. *Ostiole*, papillate, protruding from the center of the ascomata, with a pore-like opening, yellowish around apical pore when wet. *Peridium* 18 × 33 µm wide, comprising several layers of dark brown cells of *textura angularis*. *Hamathecium* comprising 1–2 µm wide, cylindrical, filamentous, rarely branched, inconspicuously septate, anastomosed, hyaline pseudoparaphyses. *Asci*

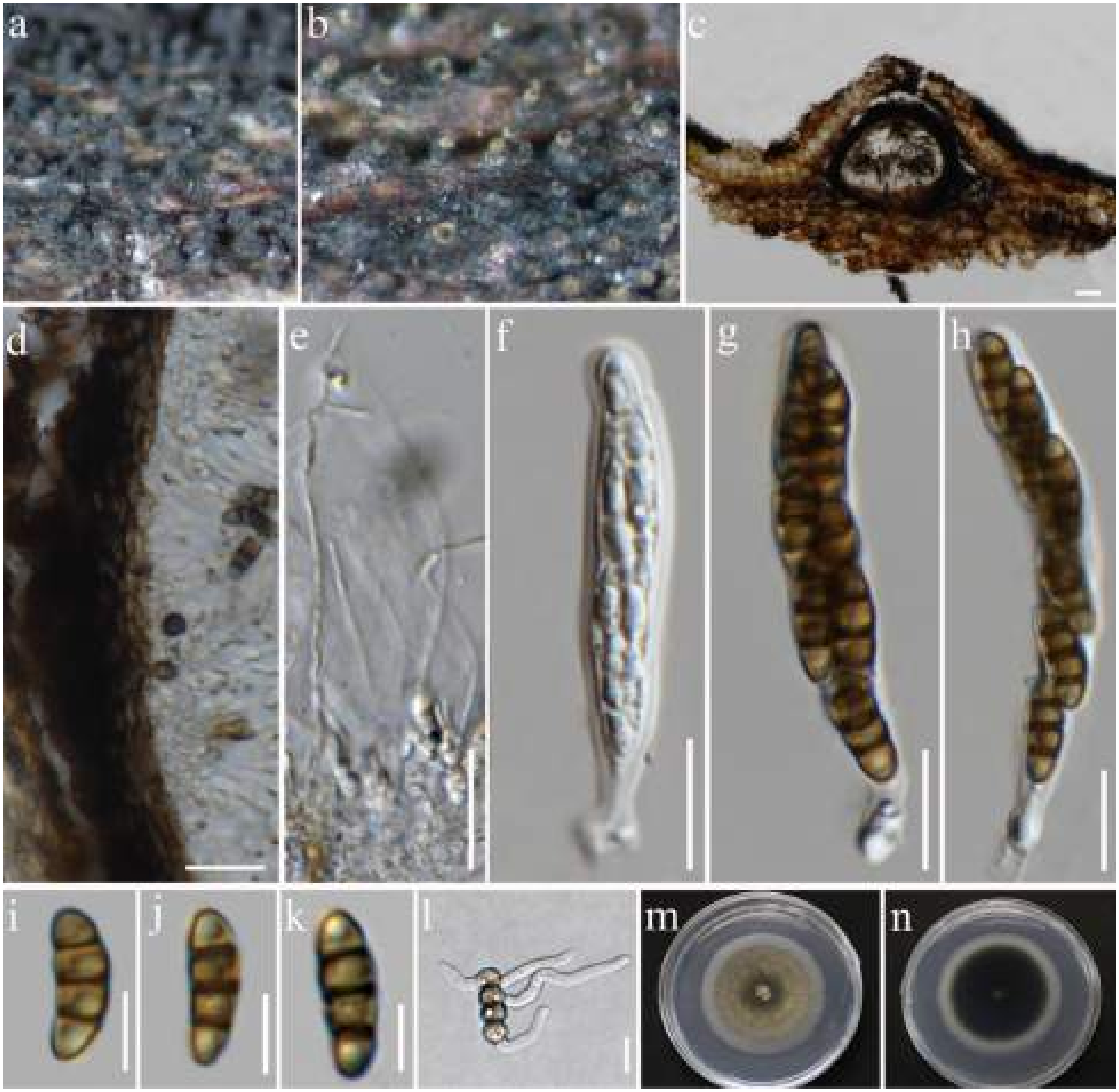


Fig. 71 ***Thyridaria aureobrunnea*** (MFLU 21-0067, **holotype**). **a**, **b** Ascomata on woody substrate. **c** Cross sections of ascoma. **d** Peridium. **e** Pseudoparaphyses. **f–h** Asci. **i–k** Ascospores. **l** Germinated ascospore. **m**, **n** Culture on PDA from surface and reverse at 1 month. Scale bars: **c** = 50 µm, **d**, **e** = 20 µm, **f–h** = 10 µm, **i–l** = 5 µm

45–61.5 × 7–8.5 µm ($\bar{x}$ = 52 × 7.5 µm, n = 10), 8-spored, bitunicate, cylindric-clavate to clavate, slightly curved, bulbous pedicellate, apically rounded. *Ascospores* 10.5–13 × 3.5–4.5 µm ($\bar{x}$ = 12 × 4 µm, n = 20), overlapping uni- to bi-seriate, ellipsoid to obovoid, slightly curved, golden brown to chestnut brown, 3-septate, strongly constricted and darkened at the septa, guttulate, smooth-walled. **Asexual morph** Undetermined.

Culture characteristics: Ascospore germinating on PDA within 24 h and germ tubes produced from each cell of the ascospores. Colonies on PDA reaching 3.5 cm diam. after 2 weeks at room temperature, circular, entire edge, olivaceous brown to brown from the center towards margin, white grey at the margin, dark brown at the reverse with surrounded by white grey at the margin. Mycelium superficial, velvety.

Material examined: THAILAND, Chiang Rai Province, Mae Yao, on decaying wood, 23 September 2019, N. Huanraluek, MY06 (MFLU 21-0067, **holotype**), ex-type living culture, MFLUCC 21-0090.

GenBank number: ITS = MZ538528, LSU = MZ538562.

Notes: In the BLASTn search of LSU and ITS sequences, *Thyridaria aureobrunnea* is most similar to *T. broussonetiae* (CBS 121895 and CBS 141481) with 99.18% and 92.21% similarities, respectively. A combined LSU, ITS and TEF1-α sequence analysis indicates that *T. aureobrunnea* forms a distinct lineage basal to *T. acaciae* and *T. broussonetiae* (type species) with 100% MLBS, 1.00 BYPP support (Fig. 72). *Thyridaria aureobrunnea* (Fig. 71) can be distinguished from the type species *T. broussonetiae* in morphological characteristics such as uniloculate ascomata, shapes and size of asci and ascospores (Jaklitsch and Voglmayr 2016). In addition, *Thyridaria acaciae* is known only as an asexual morph which is produced in culture (Crous et al. 2014b; Jaklitsch and Voglmayr 2016), and thus we cannot compare the morphology. Based on the highly supported distinct lineage and differences in DNA sequences, a new species, *Thyridaria aureobrunnea* is introduced.

Torulaceae Corda

Notes: *Torulaceae* was introduced by Corda in Sturm (1829) to accommodate *Torula* and typified by *T. herbarum* (Pers.) Link. *Torulaceae* forms a well-supported lineage in the order *Pleosporales* (Crous et al. 2015; Hyde et al. 2016, 2019, 2020a; Li et al. 2016b; Su et al. 2016, 2018). The family is circumscribed only by asexual morph characters with key distinguishing features such as; mostly immersed mycelium, erect, micro- or macronematous, straight or flexuous, subcylindrical conidiophores with or without apical branches, doliiform to ellipsoid or clavate, brown, smooth to verruculose, and mono- to polyblastic conidiogenous cells which in some cupulate after secession of conidia and subcylindrical, phragmosporous, acrogenous, brown, dry, and smooth to verrucose conidia which are often produced in branched chains (Li et al. 2016b; Hyde et al. 2019). Currently, *Torulaceae* includes six genera viz. *Dendryphion*, *Neotorula*, *Rostriconidium*, *Rutola*, *Sporidesmioides* and *Torula* (Crous et al. 2020a; Hongsanan et al 2020a). In this study, we propose a new genus *Cylindrotorula* within *Torulaceae* with evidence from morphology and multi-gene phylogenetic analyses (ITS, LSU, RPB2 and TEF1-α). *Cylindrotorula* constitutes a well-supported distinct lineage (100% MLBS, 1.00 BYPP) basal to *Neotorula*, *Dendryphion* and *Torula*.

Cylindrotorula Rajeshkumar, Wijayaw. & Bhat, ***gen. nov.***

Index Fungorum number: IF557635; *Facesoffungi number*: FoF 08026

Etymology: Named after cylindrical, elongated, verruculose primary conidia, and conidial ornamentations similar to *Torula* species.

Holotype: AMH 10228

Saprobic on decaying *Cocos nucifera* spathe. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Conidiomata* sporodochial, scattered, greyish, dark greyish brown or dark brown. *Conidiophores* micronematous, mononematous, reduced, cylindrical, smooth, erect, unbranched or rarely branched. *Conidiogenous cells* cylindrical or button-shaped, produce primary and secondary conidia. *Primary conidia* arising holoblastically, elongated, cylindrical, wavy or undulated or flexuous, smooth at base, verrucose above, pale to dark brown, unbranched, phragmo-septate. *Secondary conidia* two types, globose and cylindrical, verrucose or smooth, arising from primary conidia from intercalary, monotretic, non-cicatrized conidiogenous loci just below septa; cylindrical or finger shaped conidia slightly curved, aseptate, thin-walled, brown.

Type species: ***Cylindrotorula indica*** Rajeshkumar, Wijayaw., Bhat, N. Ashtekar & S. Lad

Notes: The proposed new genus *Cylindrotorula* is similar to *Alcornia*, *Parapericonia* and *Sporotretospora* (Ellis 1976; Monteiro et al. 2017; Whitton et al. 2012). All these genera have been described solely on morphology and are yet to be investigated based on DNA sequence analyses. The conidiophores in *Alcornia* and *Parapericonia* are illustrated and interpreted as elongated, verruculose, flexuous and with a distinct basal constriction or zone of weakness. *Sporotretophora* and *Alcornia* are similar in arrangement of conidiophores, enteroblastic tretic conidiogenesis, and unicelled conidia, but *Sporotretophora* has monotretic conidiogenous cells and schizolytic secession of conidia (Whitton et al. 2012). A detailed micro-morphological study of *Cylindroturula* on natural substrates using SEM and compound microscopy revealed its holoblastic development of

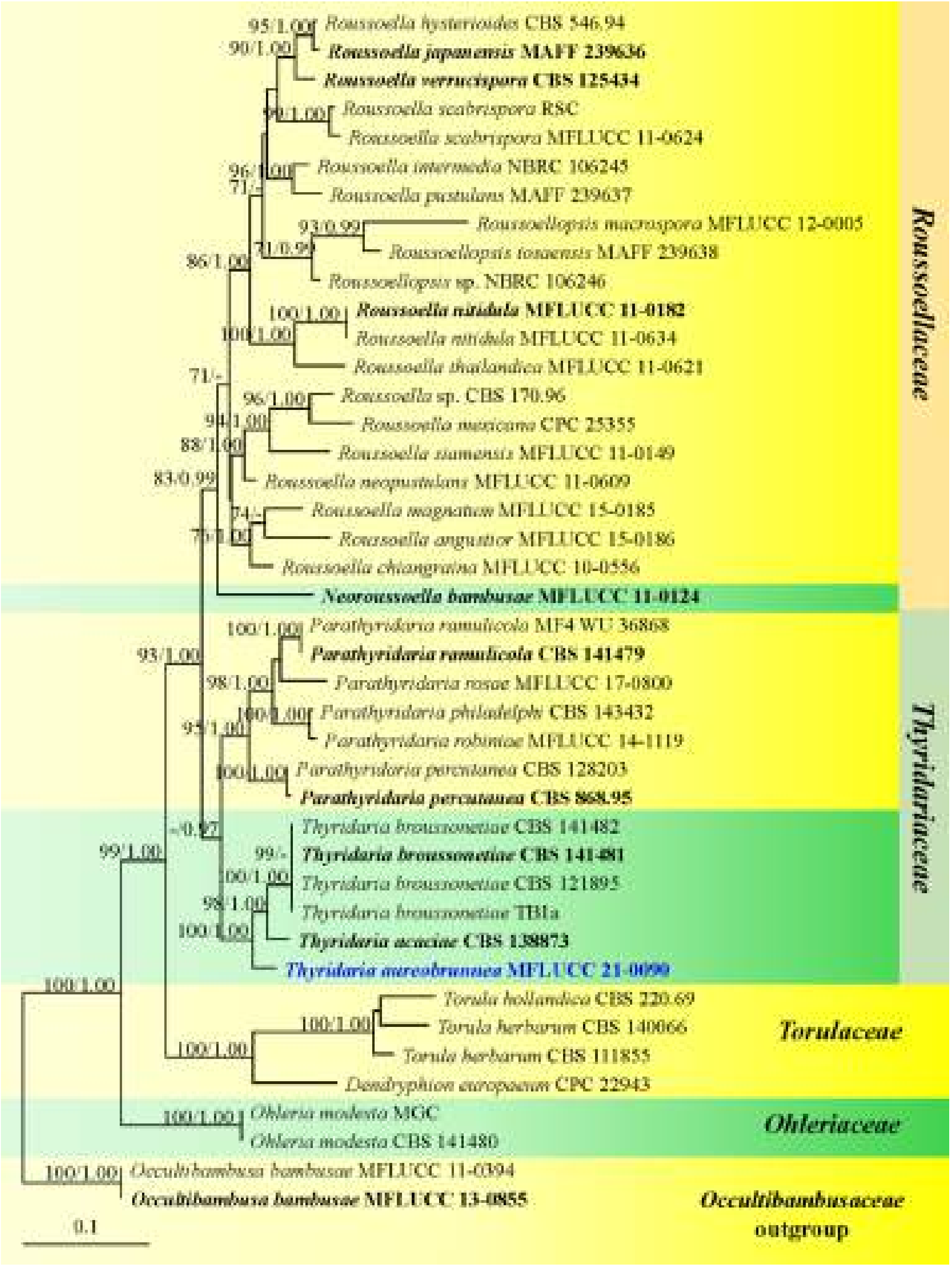


Fig. 72 Maximum likelihood phylogenetic tree based on a combined LSU, ITS and TEF1-α sequence data of *Thyridaria* taxa (*Thyridariaceae*) and related families. Forty-two strains are included in the combined analysis, which comprise a total of 2216 characters. *Occultibambusa bambusae* (MFLUCC 11-0394 and MFLUCC 13-0855) are selected as the outgroup taxa. The best RAxML tree with a final likelihood value of − 12410.223662 is presented. RAxML analysis yielded 752 distinct alignment patterns and 19.90% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.235389, C = 0.270091, G = 0.280715, T = 0.213806, with substitution rates AC = 1.372292, AG = 2.751820, AT = 1.999735, CG = 1.148507, CT = 6.478337, GT = 1.000000; gamma distribution shape parameter alpha = 0.169795. Bootstrap support values for maximum likelihood (MLBS, left) equal to or greater than 70% is given above or below the nodes. Bayesian posterior probabilities (BYPP, right) equal to or greater than 0.95 are given above the nodes. Ex-type strains are in bold and newly generated sequence is in blue

cylindrical, elongated, flexuous, verrucose primary conidia from a reduced, sporodochial, micronematous, mononematous, septate, branched, or unbranched, erect conidiophores having an apical cylindrical or button-shaped conidiogenous cells (Figs. 73, 74 and 75). Secondary conidia develop monotretic and are of two types, (1) globose, verruculose, brown to dark brown and (2) finger-shaped or narrow cylindrical, thin-walled, smooth to minutely verrucose, with an obtuse tip and truncate base.

The monotretic, secondary conidial development segregates *Cylindrotorula* from the *Parapericonia*. Whereas monotretic to polytretic globose conidia with an integrated, rhexolytic, verruculose ornamentation is the key distinguishing character in *Alcornia*. The narrowly cylindrical, curved, thin-walled secondary conidia having monotretic conidial ontogeny seen in *Cylindrotorula* is absent in *Alcornia, Parapericonia* and *Sporotretophora*. A BLASTn search using ITS, LSU, RPB2 and TEF1-α sequence data in NCBI has shown about 90% similarity of the query sequences to *Dendryphion* and *Neotorula* strains. *Dendryphion* is characterized by polytretic conidiogenous cells with pores encircled by dark scars, and chains of brown, septate (didymo- or cheiro) conidia (Crous et al. 2014a). The phylogenetic analyses based on ITS, LSU, RPB2 and TEF1-α sequence data also formed a well-supported (100% MLBS, 1.00 BYPP; Fig. 76) independent sister lineage sister to *Neotorula* and *Dendryphion* within *Torulaceae*. Thus, based on morphological characteristics and phylogenetic analyses, we accommodate *Cylindrotorula* as new genus with the type species *C. indica*.

Cylindrotorula indica Rajeshkumar, Wijayaw., Bhat, N. Ashtekar & S. Lad, ***sp. nov.***

Index Fungorum number: IF557636; *Facesoffungi number*: FoF 08025; Figs. 73, 74, 75

Etymology: Named after India, the country where this fungus is native.

Holotype: AMH 10228

Saprobic on decaying *Cocos nucifera* spathe. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Conidiomata* sporodochial, scattered, greyish, dark greyish brown or dark brown. *Conidiophores* micronematous, mononematous, reduced, cylindrical, smooth, erect, unbranched or rarely branched, 0–1-septate, 3.5–12 × 2.8–4 µm. *Conidiogenous cells* cylindrical or button-shaped, form primary and secondary conidia. *Primary conidia* arising holoblastically, elongated, cylindrical, wavy or undulated or flexuous, smooth at base, verruculose above, pale to dark-brown, unbranched, phragmo-septate, 5–10-septate, 68–125 × 3–4.5 µm. *Secondary conidia* two types, globose and cylindrical or finger-shaped, arising from primary conidia at intercalary, monotretic, non-cicatrized conidiogenous loci, globose or

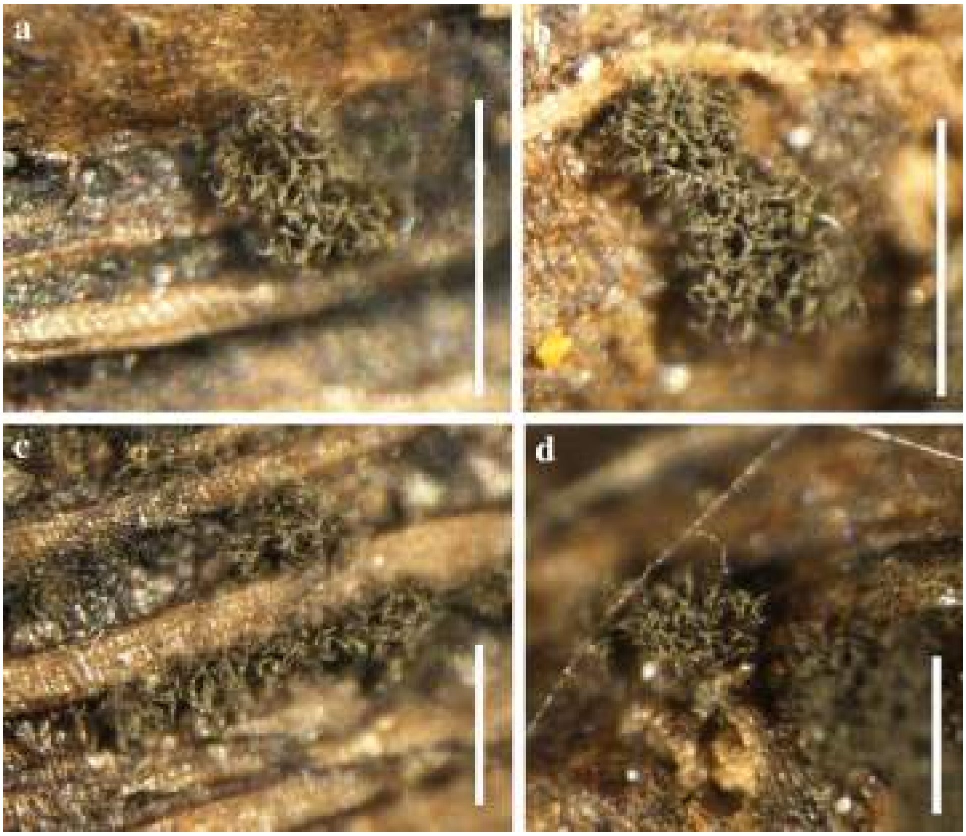


Fig. 73 ***Cylindrotorula indica*** (AMH 10228, **holotype**). **a–d** Sporodochial conidiomata on natural substrate. Scale bars: **a–d** = 100 µm

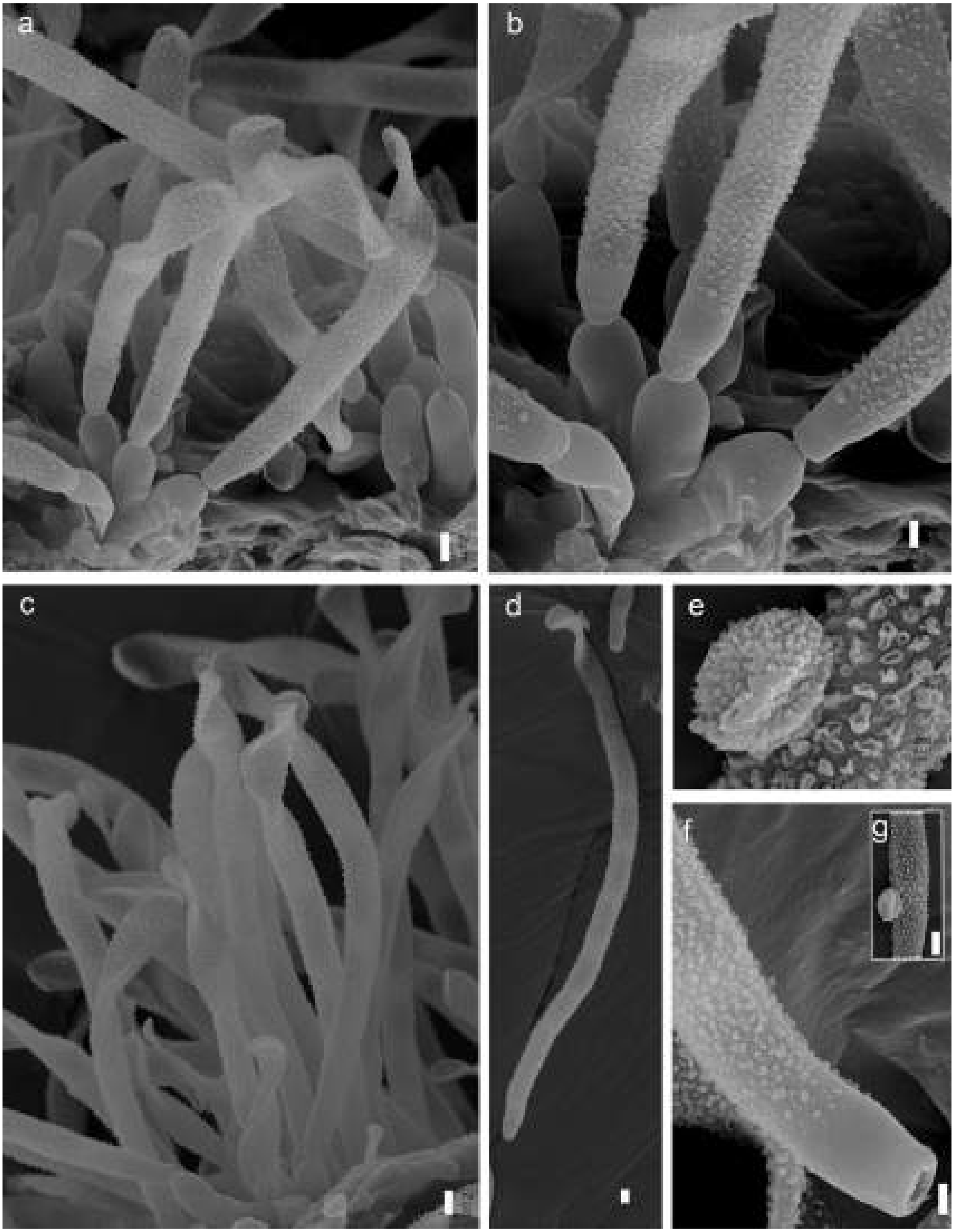


Fig. 74 *Cylindrotorula indica* (AMH 10228, **holotype**). **a**–**c** SEM of conidiomata showing conidiophores and primary conidia. **d** Cylindrical elongated primary conidium. **e** Globose secondary conidium. **f** Base of primary conidium. **g** Secondary conidial development of primary conidia. Scale bars: **a**, **c**, **d**, **g** = 2 μm, **b** = 1 μm, **e** = 200 nm, **f** = 1 μm

Fig. 75 ***Cylindrotorula indica*** (AMH 10228, **holotype**). **a**, **b** Sporodochial conidiomata. **c**–**g** Primary conidia with monotretic secondary conidia. **h**, **i** Dark thick hilum of primary conidia. **j**, **k** Pleomorphic secondary conidia. **l**, **m** Monotretic secondary conidial development. **n**, **o** Branched conidiophore with primary conidia. Scale bars: **a**–**o** = 10 μm

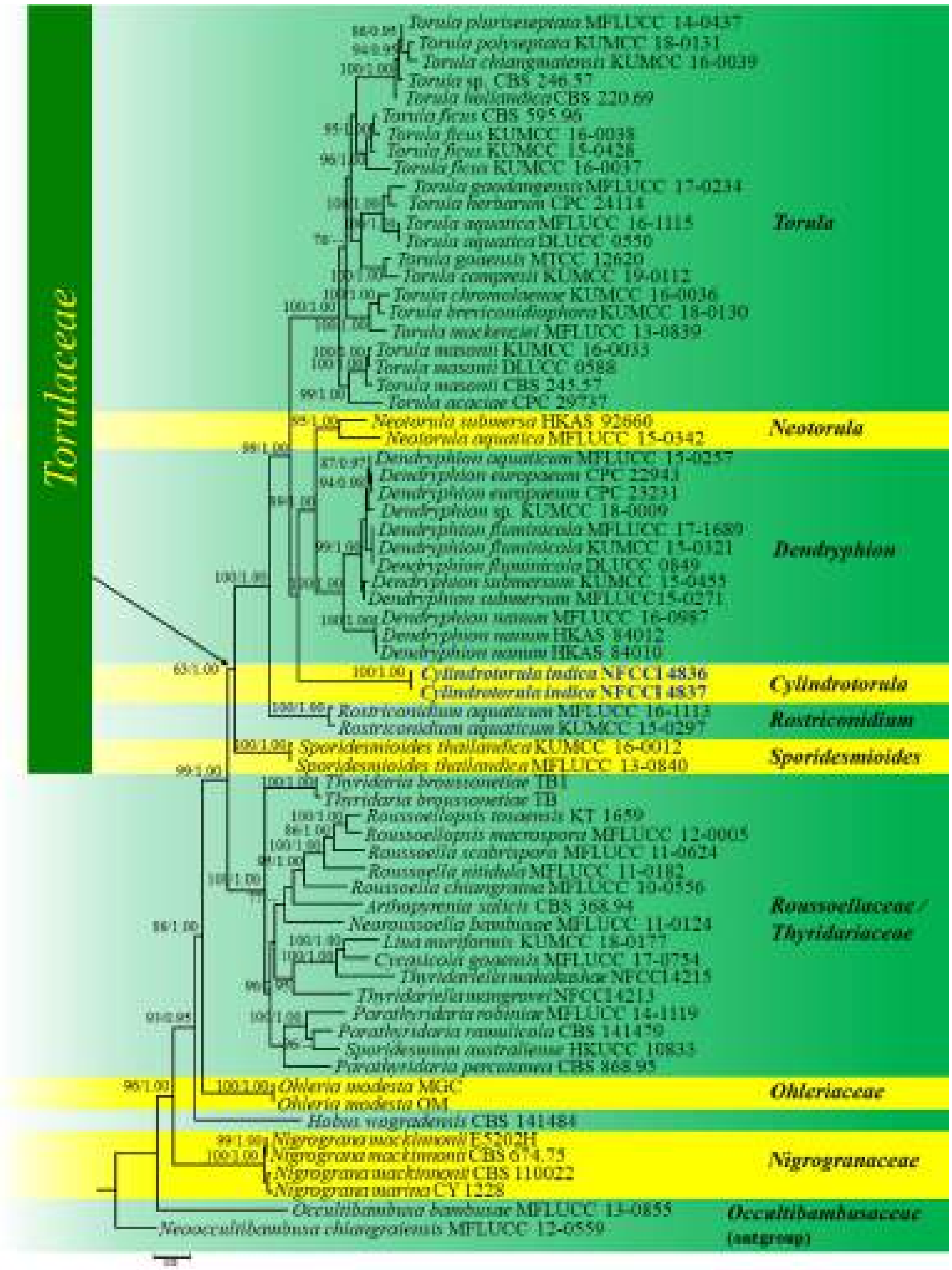


Fig. 76 Phylogram generated from maximum likelihood analysis based on LSU, RPB2, ITS, and TEF1-α sequence dataset representing *Torulaceae* and related families. Related sequences are taken from Hyde et al. (2019). Sixty-eight strains are included in the combined analyses which comprise 2807 characters and 517 characters for ITS after alignment. *Neooccultibambusa chiangraiensis* (MFLUCC 12-0559) and *Occultibambusa bambusae* (MFLUCC 12-0559) in *Occultibambusaceae* (*Pleosporales*) are used as the outgroup taxa. Single gene analyses were also performed to compare the topology and clade stability with combined gene analyses. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RAxML tree with a final likelihood values of − 25944.916075 is presented. The matrix had 1201 distinct alignment patterns, with 23.66% undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.240116, C = 0.269729, G = 0.272735, T = 0.217421; substitution rates AC = 1.567160, AG = 3.410853, AT = 1.595585, CG = 0.809155, CT = 7.747008, GT = 1.000000; gamma distribution shape parameter α = 0.645809. Bootstrap values for maximum likelihood (MLBS) equal to or greater than 60% and posterior probabilities (BYPP, right) equal to or greater than 0.95 (the rounding of values to 2 decimal places) from Bayesian inference analysis labeled on the nodes. The newly generated sequences are in blue bold

elongated, slightly curved, aseptate, smooth, verrucose or verruculose, thin-walled, brown. *Micrometry* globose secondary conidia, 3.5–5 × 3.5–5 µm, cylindrical or finger-shaped conidia, 9.5–30 × 2.5–3.5 µm.

Culture characteristics: Colonies on MEA at 25 ± 2 °C reaching 30–35 mm diam. after 1 month; initially aerial mycelium white to brownish grey (4D2), velutinous, in old cultures brownish grey (4D2) with olive grey (4E4) margin; reverse dark grey (4F1). Soluble pigments and exudates absent. Colour codes and names used in descriptions are from Kornerup and Wanscher (1978).

Material examined: INDIA, Maharashtra, Thane (19°13′13″ N 72°57′17″ E, ± 23 msl), on decaying spathe of *Cocos nucifera* (*Arecacceae*), July 2018, K.C. Rajeshkumar and S. Lad, AMH 10228 (**holotype**), ex-type living culture NFCCI 4836; *ibid*., NFCCI 4837.

GenBank numbers: NFCCI 4836: ITS = MT339444, LSU = MT339442, RPB2 = MT321490, TEF1-α = MT321492; NFCCI 4837: ITS = MT339445, LSU = MT339443, RPB2 = MT321491, TEF1-α = MT321493.

Dendryphion Wallr.

Notes: *Dendryphion* was introduced by Wallroth (1833) and is typified by *Dendryphion comosum* Wallr. The genus is characterized by having erect, solitary, polytretic conidiophores, branched in upper part, forming septate, pigmented, thick-walled, finely roughened stipe and a distinct conidiogenous apparatus, with dark scars and catenate, in simple or branched chains of brown, septate (didymo- or cheiro) conidia (Crous et al. 2015; Su et al. 2016, 2018; Li et al. 2020a). Species of *Dendryphion* are saprobic on dead stems of herbaceous plants and decaying wood, and also grows on submerged decaying wood in freshwater habitats (Su et al. 2016, 2018; Li et al. 2020a). There are 85 *Dendryphion* epithets listed in Index Fungorum (2021) but only 36 species are accepted in *Dendryphion* (Species Fungorum 2021), and only seven species have DNA sequences available in the GenBank database.

Dendryphion hydei J.F. Li, Phookamsak & Jeewon, PLoS ONE 15(2): e0228067 (2020)

Index Fungorum number: IF556746; *Facesoffungi number*: FoF 04574; Fig. 77

Saprobic on submerged wood in a freshwater habitat. **Sexual morph** Undetermined. **Asexual morph** *Colonies* on the substrate superficial, effuse, hairy, brown to dark brown. *Mycelium* partly immersed to superficial on the substrate, branched, septate, pale brown to brown hyphae. *Conidiophores* 338–428 × 10–16 µm ($\bar{x}$ = 383 × 13 µm, n = 15) (10–16 µm wide at the base, 5–7 µm wide at the apex branch) macronematous, mononematous, septate, straight or flexuous, cylindrical, thick-walled, simple branch on the top primary branches, pale brown to brown, unbranched part dark brown. *Conidiogenous cells* 5–9 × 4–5 µm ($\bar{x}$ = 7 × 4 µm, n = 25) polytretic, terminal, integrated, pale brown. *Conidia* 33–56 (–108) × 6–8 µm ($\bar{x}$ = 44 × 7 µm, n = 30) single, dry, drum to globose, pale brown to brown, slightly paler at the end cells, bead-like chains, 4–13(–21)-septate, constricted at the septa, middle cells wider than the top and bottom. *Conidial secession* schizolytic.

Culture characteristics: Conidia germinated on the PDA within 24 h, and germ tube produced from both ends. Colonies grow on the PDA, and after 2 weeks of incubation at room temperature, the diameter reaches about 4 cm. Hyphae are initially white to light grey, and then gradually become grey to dark grey, with convex middle, flocculent, grey to dark grey, smooth edges, white, and flocculent, forming a white ring about one centimeter. Reverse light yellow–brown, uniform color, smooth.

Material examined: CHINA, Yunnan Province, Puer City, (100°37′59″ E 22°36′36″ N, 919 msl), on submerged wood, 30 April 2018, H.W. Shen, Q.S. Zhou and Z.L. Luo, S-2049 (HKAS 112706, **new record**), living culture, DLUCC 2049.

GenBank numbers: ITS = MW723060, LSU = MW879527, SSU = MW774583, RPB2 = MW729781, TEF1-α: MW729786.

Notes: *Dendryphion hydei* was found on a branch litter of *Bidens pilosa* Linn. in Chiang Mai Province, Thailand (Li et al. 2020a). Phylogenetically, our isolate clustered with the ex-type strain of *Dendryphion hydei* (HKAS 97479) with low statistical support (Fig. 80). Our new isolate (Fig. 77) has some differences in size from the type species; it has longer conidiophores (338–428 × 10–16 µm vs. 260–380 × 7–14 µm) and conidia (33–56 (–108) × 6–8 µm vs. (17–)20–30(–35) µm long × 4–7 µm), and has more septa (4–13 vs. 2–4). Based on morphological data and phylogenetic analysis, we report *D. hydei* as the first record in a freshwater habitat.

Torula Pers.

Notes: *Torula* was introduced by Persoon (1795) and is typified by *T. herbarum*. Members in this genus are hyphomycetous asexual morph and characterized by superficial dark colonies and branched chains, dark brown conidia (Crane and Schoknecht 1977; Crous et al. 2015, 2020a; Hyde et al. 2020b; Su et al. 2016; Li et al. 2017, 2020a). There are 543 *Torula* epithets are listed in Index Fungorum (2021), but only 49 species have morphological studies and 17 species have molecular data support (Hongsanan et al. 2020a). In this study, based on morphological and phylogenetic analyses, *Torula lancangjiangensis* is introduced as a new species and a new record of *T. mackenziei* from a freshwater habitat in China is reported.

Torula lancangjiangensis H.W. Shen, S. Boonmee, Z.L. Luo & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF558159; *Facesoffungi number*: FoF 09753; Fig. 78

Fig. 77 ***Dendryphion hydei*** (HKAS 112706, **new record**). **a** Colonies on submerged wood. **b–d** Conidiophores with conidiogenous cells. **e**, **f** Conidiogenous cells with conidia. **g–l** Conidia. **m**, **n** Culture on PDA (surface and reverse). Scale bars: **a** = 200 µm, **b**, **c** = 50 µm, **d–f**, **h–l** = 10 µm, **g** = 20 µm

Fig. 78 ***Torula lancangjiangensis*** (HKAS 112709, **holotype**). **a**, **b** Colonies on submerged wood. **c**–**f** Conidiophores with conidiogenous cells. **g**, **h** Conidiophores, conidiogenous cells with conidia. **i**–**k** Conidia. **l** Conidia in chain. **m** Germinated conidium. **n** Culture on PDA from surface and reverse. Scale bars: **c**–**m** = 20 µm

Etymology: Referring to the collecting site from the Langcangjiang River in China.

Holotype: HKAS 112709

Saprobic on submerged wood in a freshwater habitat. **Sexual morph** Undetermined. **Asexual morph** *Colonies* sparse, hairy, dry, velvety, dark brown to black on substrate. *Mycelium* partly immersed to superficial on the substrate, septate, branched, light brown to brown hyphae. *Conidiophores* 5–15 × 3–4 µm ($\bar{x}$ = 10 × 3 µm, n = 25), macronematous to semi- macronematous, mononematous, erect, straight or slightly flexuous, without apical branches, light brown to brown, ellipsoid to subcylindrical, smooth-walled, 0–2-septate, with 1–2 doliiform to globose cells. *Conidiogenous cells* 5–7 × 5–6 µm ($\bar{x}$ = 6 × 5 µm, n = 25), polyblastic, integrated, terminal or intercalary, doliiform to subglobose, brown to dark brown, smooth to verrucose, thick-walled. *Conidia* (24–)45–74(–100) × 6–7(–8) µm ($\bar{x}$ = 60 × 7 µm, n = 40), acrogenous, catenated, composed of moniliform cells, brown to dark brown, 5–19-septate, constricted at the septa, doliiform to globose, most circular–drum form, with 1–2 cells black at the apex. Conidial secession schizolytic.

Culture characteristics: Conidia germinated on PDA within 24 h, and germ tube produced from the conidial cells at both ends or in the middle. Colonies grow on the PDA, and after incubating at room temperature for 1 month, the diameter reaches to 3.5 cm. Hyphae are initially light gray, turning dark grey at maturity, raised in the middle, flocculent, velvety, white, with edges smooth, light grey to light brown. Reverse light grey in the middle light gray to dark grey, smooth edges.

Material examined: CHINA, Yunnan Province, Xishuangbanna, (100°42′04″ E 22°05′19″ N, 680 msl), on submerged wood, 4 May 2018, H.W. Shen, Q.S. Zhou and Z.L. Luo, S-2043 (HKAS 112709, **holotype**, MFLU 21-0112, isotype), ex-type living culture, DLUCC 2043; THAILAND, Chiang Rai, Muang, Thasud, Mae Fah Lung University, Botanical garden, on dead twigs, 15 November 2018, Boonmee, B03 (MFLU 21-0076), living culture, MFLUCC 21-0099.

GenBank numbers: DLUCC 2043: ITS = MW723059, LSU = MW879526, SSU = MW774582, RPB2 = MW729780, TEF1-α = MW729785; B03: ITS = MZ538529, LSU = MZ538563, TEF1-α = MZ567104.

Notes: In a NCBI BLASTn search based on RPB2 sequences, the closest match of *Torula lancangjiangensis* was *T. camporesii* (KUMCC 19-0112; GenBank no. MN507404) with 97.67% similarity. A comparison of RPB2 nucleotide bases indicated that *T. lancangensis* differs from *T. camporesii* in 50/1055 bp (4.7%). In addition, multigene phylogenetic analysis of a combined dataset of the LSU, SSU, TEF1-α, RPB2, and ITS showed that *T. lancangjiangensis* and *T. camporesii* are close relatives with 95% MLBS, 1.00 BYPP support (Fig. 80). *Torula lancangjiangensis* resembles *T. camporesii* in having ellipsoid to subcylindrical, multi-septate conidia; and doliiform to subglobose, brown to dark brown conidiogenous cells (Fig. 78). However, conidial cells of *T. camporesii* are wide in the middle and small at the ends, while the cells of *T. lancangjiangensis* are more uniform. Therefore, *Torula lancangjiangensis* is introduced as a new species.

Torula mackenziei J.F. Li, Phookamsak & K.D. Hyde, Mycol Progress 16: 447–461 (2017)

Index Fungorum number: IF819537; *Facesoffungi number*: FoF 02714; Fig. 79

Saprobic on submerged wood in a freshwater habitat. **Sexual morph** Undetermined. **Asexual morph** *Colonies* on the substrate superficial, effuse, hairy, powdery, black. *Mycelium* immersed on the substrate, composed of septate, branched, smooth, light brown hyphae. *Conidiophores* 7–20(–48) × 3–5 µm ($\bar{x}$ = 13 × 4 µm, n = 15), macronematous, mononematous, solitary, erect, minutely verruculose, thick-walled, without apical branches, brown, ellipsoid to subglobose. *Conidiogenous cells* 5–7 × 4–6 µm ($\bar{x}$ = 6 × 5 µm, n = 15), polyblastic, terminal, dark brown to black, paler at apex, smooth to minutely verruculose, thick-walled, globose to ellipsoid, discrete. *Conidia* 13–20 × 6–7 µm ($\bar{x}$ = 16 × 7 µm, n = 50) acrogenous, catenated, yellowish brown to dark brown, minutely verruculose, 3–5-septate, rounded at both ends, paler yellowish at apex, composed of moniliform cells, slightly constricted at septa, doliiform to globose, in beadlike chains, with conidial chains in branches. Conidial secession schizolytic.

Culture characteristics: Conidia germinated on PDA within 24 h, and the germ tube produced by a certain conidial cell at either end or in the center. Colonies grow on PDA, and after incubating at room temperature for 1 month, the diameter reaches about 5 cm. Hyphae are initially white to light grey, and then gradually become grey to brown, with convex middle, flocculent, gray to brown, smooth edges and dark grey; reverse light grey in the middle, dark gray to black, smooth edges.

Material examined: CHINA, Yunnan Province, Kunming City (103°08′59″ E 24°37′53″ N, 1790 msl), on submerged wood, 13 May 2018, H.W. Shen and X. He, S-1837 (HKAS 112705, **new record**), living culture, DLUCC 1837.

GenBank numbers: ITS = MW723058, LSU = MW879525, SSU = MW774581, RPB2 = MW729779, TEF1-α: MW729784.

Notes: In the phylogenetic analyses our strain clustered with the type of *Torula mackenziei* (MFLU 16-2820) with 100% ML, 1.00 BYPP support (Fig. 80). *Torula mackenziei* was collected from a dead branch of *Bidens pilosa* in Doi Mae Salong, Chiang Rai Province, Thailand (Li et al. 2017). Compared with *T. mackenziei*, our strain has larger conidiophores (7–20 × 3–5 µm vs. 3–4.3 × 3.4–3.7 µm),

Fig. 79 ***Torula mackenziei*** (HKAS 112705, **new record**). **a** Colonies on submerged wood. **b**–**f** Conidiophores with conidiogenous cells and conidia. **g**, **h** Conidia. **i**–**k** Conidia in catenated chain. **l**–**o** Branched chains of conidia. **p** Germinated conidium. **q** Culture on PDA from surface and reverse. Scale bars: **a**–**p** = 10 µm

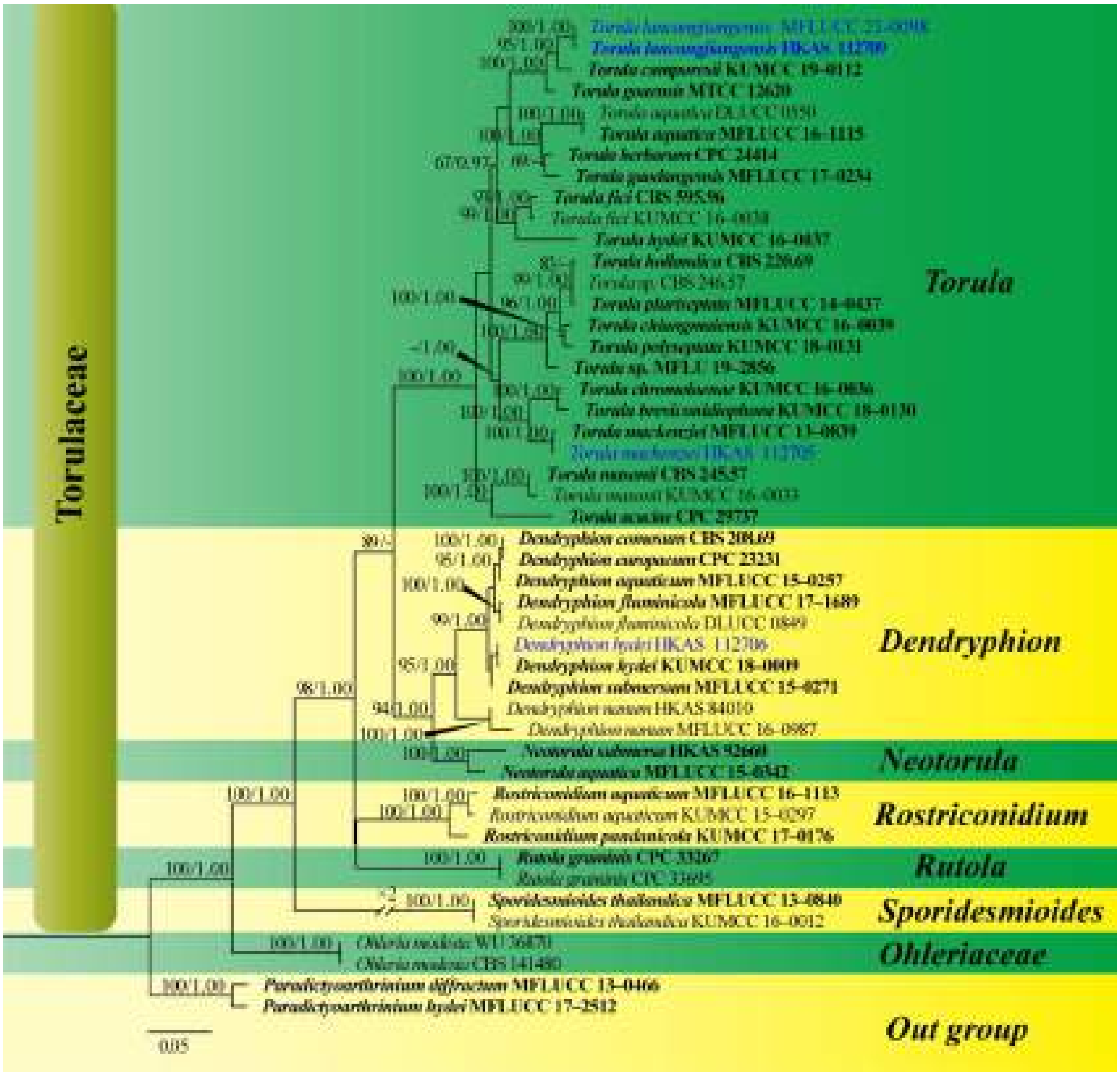


Fig. 80 Phylogram generated from maximum likelihood analysis based on combined LSU, SSU, TEF1-α, RPB2 and ITS sequence dataset representing genera of *Torulaceae* and other related families in *Pleosporales*. The updated sequence dataset was derived from Hyde et al. (2020b) and Li et al. (2020a). Forty-seven strains are included in the combined analyses which comprise a total of 4193 characters. *Paeadictyoarthrinium diffractun* MFLUCC 13-0466 and *P. hydei* MFLUCC 17-2512 are selected as the outgroup taxa. The best RAxML tree with a final likelihood value of − 20632.568415 is presented. RAxML analysis yielded 1256 distinct alignment patterns and 34.11% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.246275, C = 0.259573, G = 0.270969, T = 0.223183, with substitution rates AC = 1.544243, AG = 3.270041, AT = 1.437706, CG = 0.944551, CT = 7.854806, GT = 1.000000; gamma distribution shape parameter alpha = 0.178530. Bootstrap support values for maximum likelihood (MLBS, left) equal to or greater than 70% is given above the nodes. Bayesian posterior probabilities (BYPP, right) equal to or greater than 0.95 are given above the nodes. Ex-type strains are in bold and newly generated sequences are in blue

conidiogenous cells (5–7 × 4–6 µm vs. 4.3–4.7 × 4–4.8 µm), and conidia (13–20 × 6–7 µm vs. 9.4–18.5 × 4.4–4.7 µm). Our strains were collected from submerged wood in a freshwater habitat in Yunnan, China (Fig. 79). We suspect that different growth habitats and substrates may lead to differences in sizes of the strains. In our study, we report the new collection as a new record in a freshwater habitat.

Wicklowiaceae Ariyaw. & K.D. Hyde

Notes: We follow the latest treatment and updated accounts of *Wicklowiaceae* in Calabon et al. (2020a) and Hongsanan et al. (2020a).

Wicklowia Raja, A. Ferrer & Shearer

Notes: *Wicklowia* was introduced by Raja et al. (2010) to accommodate the freshwater taxa and was typified by *Wicklowia aquatica*. Only three species are accepted in this genus (Raja et al. 2010; Boonmee et al. 2019; Calabon et al. 2020a;

Index Fungorum 2021). In this study, *Wicklowia fusiformispora* is introduced as a new species and *W. submersa* is reported as a new record from northern Thailand.

Wicklowia fusiformispora Boonmee, Huanraluek & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF558541; *Facesoffungi number*: FoF 09954; Fig. 81

Etymology: The specific epithet "*fusiformispora*" refers to the fusiform shape of ascospores.

Holotype: MFLU 21-0068

Saprobic on decaying submerged wood in the river. **Sexual morph** *Ascomata* 212–244 × 225–274 µm ($\bar{x}$ = 231 × 253 µm), immersed, erumpent when mature, ellipsoid on the host surface, scattered, gregarious, subglobose, uni-loculate, dark brown, ostiolate. *Peridium* 32–51 µm wide, thick-walled, composed of light brown to dark brown of pseudoparenchymatous cells of *textura angularis*. *Hamathecium comprising* 1–3 µm wide, numerous, cylindrical, filiform, branched, septate, hyaline pseudoparaphyses. *Asci* 78–151 × 21–30 µm ($\bar{x}$ = 115 × 30 µm, n = 10), 8-spored, bitunicate, fissitunicate, cylindrical-clavate, apically thickened and rounded, with an ocular chamber when immature, sessile or short pedicellate. *Ascospores* 32–41 × 9–19 µm ($\bar{x}$ = 36 × 12 µm, n = 20), 2–3-seriate overlapping, fusiform to cylindrical-ellipsoid, with rounded ends, slightly inequilateral, asymmetrical, slightly curved, hyaline, 1-septate, constricted at the septum, guttulate when immature, surrounded by a thin mucilaginous sheath, smooth-walled. **Asexual morph** Undetermined.

Culture characteristics: Ascospores germinated on PDA within 12 h at room temperature. Colonies on MEA, reaching 15 mm diam. in 4 weeks at room temperature. Mycelium superficial, hairy, radiating outwards, effuse with wavy to fimbriate edge, dark brown.

Material examined: THAILAND, Chiang Mai Province, Mae Ai, Tha Ton, Kok River, on decaying submerged wood in the river shore, 9 December 2019, S. Boonmee, N-KR1 (MFLU 21-0068, **holotype**), ex-type living culture, MFLUCC 21-0091.

GenBank numbers: ITS = MZ538533, LSU = MZ538567, SSU = MZ538576, TEF1-α = MZ567108.

Notes: *Wicklowia fusiformispora* shares common characters with other described species in *Wicklowia*, but it differs from all the other species in terms of details regarding features including of shape and size of ascomata, asci and ascospores (Raja et al. 2010; Boonmee et al. 2019; Calabon et al. 2020a). Phylogenetic analysis based on a combined LSU and SSU sequence dataset indicates that *W. fusiformispora* clustered with *W. phuketensis* with 97% MLBS, 1.00 BYPP support (Fig. 83). However, *Wicklowia fusiformispora* is distinct from *W. phuketensis* by its uni-loculate ascomata and has smaller asci (78–151 × 21–30 µm vs. 86–288 × 22–32 µm) and ascospores (32–41 × 9–19 µm vs. 34–43 × 9–12 µm) (see Calabon et al. 2020a, b; Fig. 2). A comparison of LSU sequences indicates that *W. fusiformispora* differs from *W. aquatica* in 27/850 bp (3.17%), *W. phuketensis* in 10/850 bp (1.17%), and *W. submersa* 18/850 (2.11%). Sequence data of the ITS region of *W. aquatica*, *W. phuketensis* and *W. submersa* are not available in the GenBank for the comparison. We therefore, identify *W. fusiformispora* as a new species which collected from Kok River in northern Thailand (Fig. 81).

Wicklowia submersa Boonmee, Sorvongxay & K.D. Hyde, Phytotaxa 411(1): 76 (2019)

Index Fungorum number: IF556334; *Facesoffungi number*: FoF 05994; Fig. 82

Saprobic on decaying wood submerged in a freshwater canal. **Sexual morph** *Ascomata* 93–186 × 126–179 µm ($\bar{x}$ = 134 × 151 µm), immersed, erumpent when mature, raising the host tissue, dark ellipsoid or slit-like, uni-loculate, subglobose, dark brown, scattered, gregarious, ostiolate. *Peridium* 20–24 µm wide, thick-walled, composed of dark brown of pseudoparenchymatous cells of *textura angularis*. *Hamathecium* comprising 1–2 µm wide, numerous, cylindrical, filiform, branched, septate, hyaline pseudoparaphyses. *Asci* 64–95 × 21–28 µm ($\bar{x}$ = 76 × 24 µm, n = 7), 8-spored, bitunicate, fissitunicate, cylindrical-clavate, apically thickened and rounded, with an ocular chamber when immature, sessile or short pedicellate. *Ascospores* 24–28 × 7–15 µm ($\bar{x}$ = 26 × 9 µm, n = 20), 2–3-seriate, partially overlapping, ellipsoidal-oblong to broad fusiform, with rounded ends, slightly inequilateral, asymmetrical, upper cell wider, hyaline, 1-septate, constricted at the septum, guttulate when immature, surrounded by a distinctly mucilaginous sheath, smooth-walled. **Asexual morph** Undetermined.

Culture characteristics: Ascospores germinated on PDA within 12 h. Colonies on MEA, reaching 0.5–1.5 cm diam., in 2 weeks at room temperature. Mycelium superficial, dark grey to brown, hairy, radiating outwards. effuse with wavy and dark brown edge.

Material examined: THAILAND, Uttaradit Province, Phichai, Thasak, Chom Tok Village, on decaying submerged wood in a freshwater canal, 29 December 2018, S. Boonmee, CTU11 (MFLU 21-0069, **new record**), living culture, MFLUCC 21-0092.

GenBank numbers: LSU = MZ538568, TEF1-α = MZ567109.

Notes: *Wicklowia submersa* was reported from a freshwater habitat collected in Krabi Province, southern Thailand (Boonmee et al. 2019). Our new isolate of *W. submersa* (MFLUCC 21-0092) was collected from Uttaradit Province in northern Thailand. Our new collection (Fig. 82) share similar characters of ascomata, asci and ascospores identical to the ex-type strain *W. submersa* (MFLUCC 18-0373).

Fig. 81 ***Wicklowia fusiformispora*** (MFLU 21-0068, **holotype**). **a**, **b** Appearance of ascomata on decaying submerged wood. **c**, **d** Cross sections of ascomata. **e** Section of peridium. **f** Pseudoparaphyses. **g**–**k** Asci. **l**–**o** Ascospores. **p** Ascospore stained in Nigrosine reagent. **q** Germinated ascospore. **r**, **s** Culture on MEA from above and below. Scale bars: **c**, **d** = 200 µm, **e**–**k**, **q** = 20 µm, **l**–**p** = 10 µm

Fig. 82 ***Wicklowia submersa*** (MFLU 21-0069, **new record**). **a** Appearance of ascomata on substrate. **b** Cross section of ascomata. **c** Section of peridium. **d** Pseudoparaphyses. **e–h** Asci. **i–k** Ascospores (i and j = ascospores mounted in water, k = ascospore stained in Nigrosin reagent). **l** Germinated ascospore. **m**, **n** Culture on MEA from surface and reverse. Scale bars: **b** = 100 µm, **c–h**, **l** = 20 µm, **i–k** = 10 µm

Phylogenetic analysis indicates that our strain consistently clustered with the ex-type strain MFLUCC 18-0373 with 100% MLBS, 1.00 BYPP support (Fig. 83). We therefore, report our isolate MFLUCC 21-0092 as a new record of *W. submersa* in Thailand.

Tubeufiales S. Boonmee & K.D. Hyde

Notes: *Tubeufiales* currently includes three families (i.e., *Bezerromycetaceae*, *Tubeufiaceae* and *Wiesneriomycetaeae*) with 55 genera and the latest updated accounts in Hongsanan et al. (2020b).

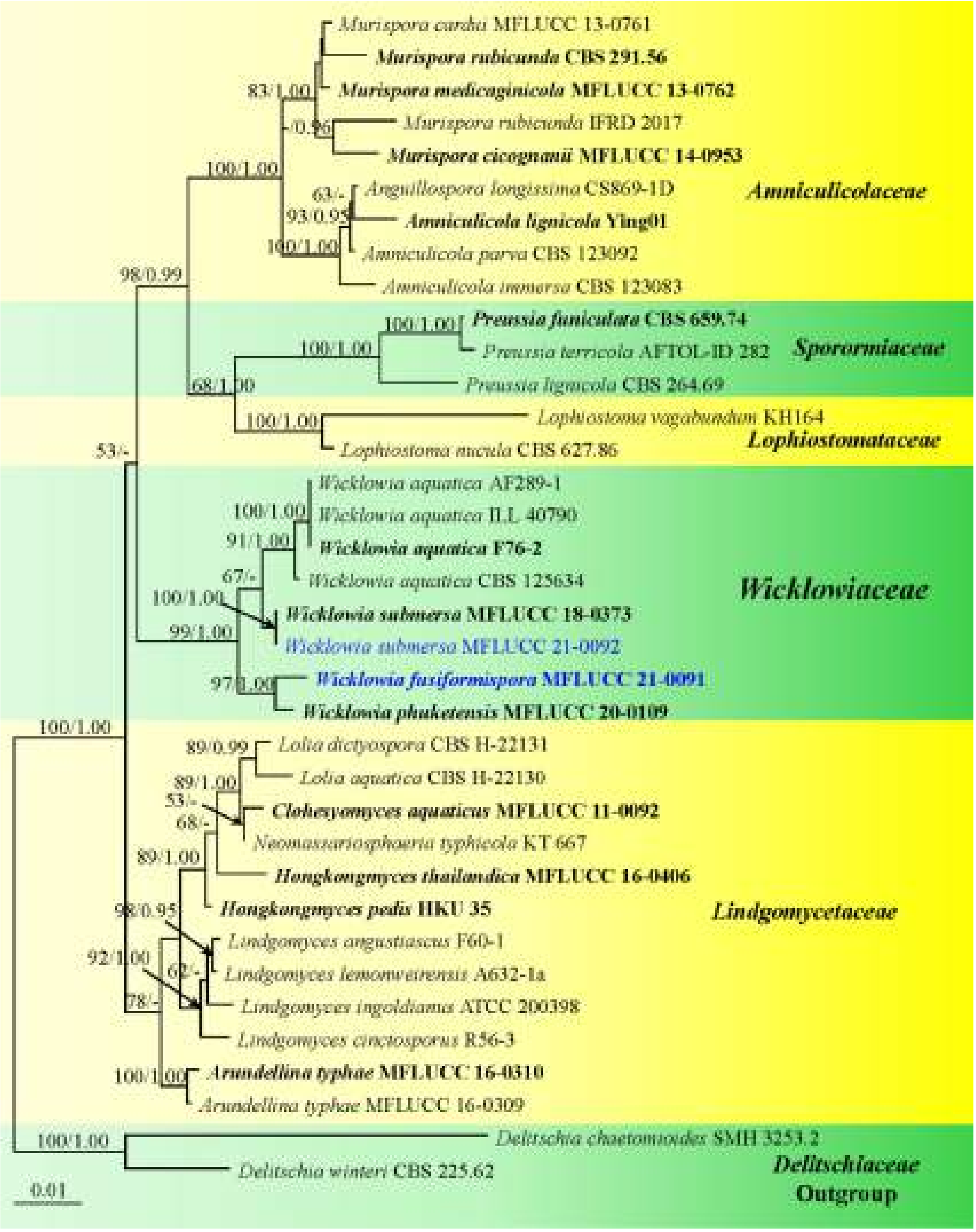


Fig. 83 Maximum likelihood phylogenetic tree based on a combined LSU and SSU sequence data of *Wicklowia* taxa (*Wicklowiaceae*) and related families. The tree is rooted with *Delitschia chaetomioides* (SMH 3253.2) and *D. winteri* (CBS 225.62). Bootstrap support values for maximum likelihood (MLBS, left) equal to or greater than 50% is given above the nodes. Bayesian posterior probabilities (BYPP, right) equal to or greater than 0.95 are given above the nodes. Ex-type strains are in bold and newly generated sequences are in blue

Tubeufiaceae M.E. Barr

Notes: We follow the latest treatments and updated accounts of *Tubeufiaceae* in Hongsanan et al. (2020b). Two new species and five new records from genera *Helicosporium*, *Neohelicosporium* and *Tubuefia* are reported in this study.

Helicosporium Nees

Notes: *Helicosporium* comprises 101 species epithets (Index Fungorum 2021) but only 20 species are accepted in the genus (Species Fungorum 2021). Its members are hyphomycetous, helisporous, with multi-coil to loosely uncoiled, multi-septate, hyaline to pale brown and smooth-walled conidia (Boonmee et al. 2014; Lu et al. 2018b). One new species and one new record are provided for this genus.

Helicosporium luteosporum Y.Z. Lu, Boonmee & K.D. Hyde, Phytotaxa 319(3): 248 (2017)

Index Fungorum number: IF552663; *Facesoffungi number*: FoF 02763; Figs. 84, 85

Saprobic on decaying wood. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous, helicosporous. *Colonies* effuse, yellow, shiny, with crowded by conidial masses. *Mycelium* composed of partly immersed to superficial, septate, branched, hyaline to brown hyphae. *Conidiophores* 142–370 µm long, 5–8 µm wide at base, micronematous, mononematous, arising from repent mycelium, tapering toward narrow subacute at apex, fuscous branching and brown at base, brownish to hyaline towards apex, septate, smooth-walled. *Conidiogenous cells* 3–7.5 × 2–3 µm, denticulate, holoblastic, monoblastic, bearing lateral minute denticles each with single conidium. *Conidia* 81–161 µm diam.,

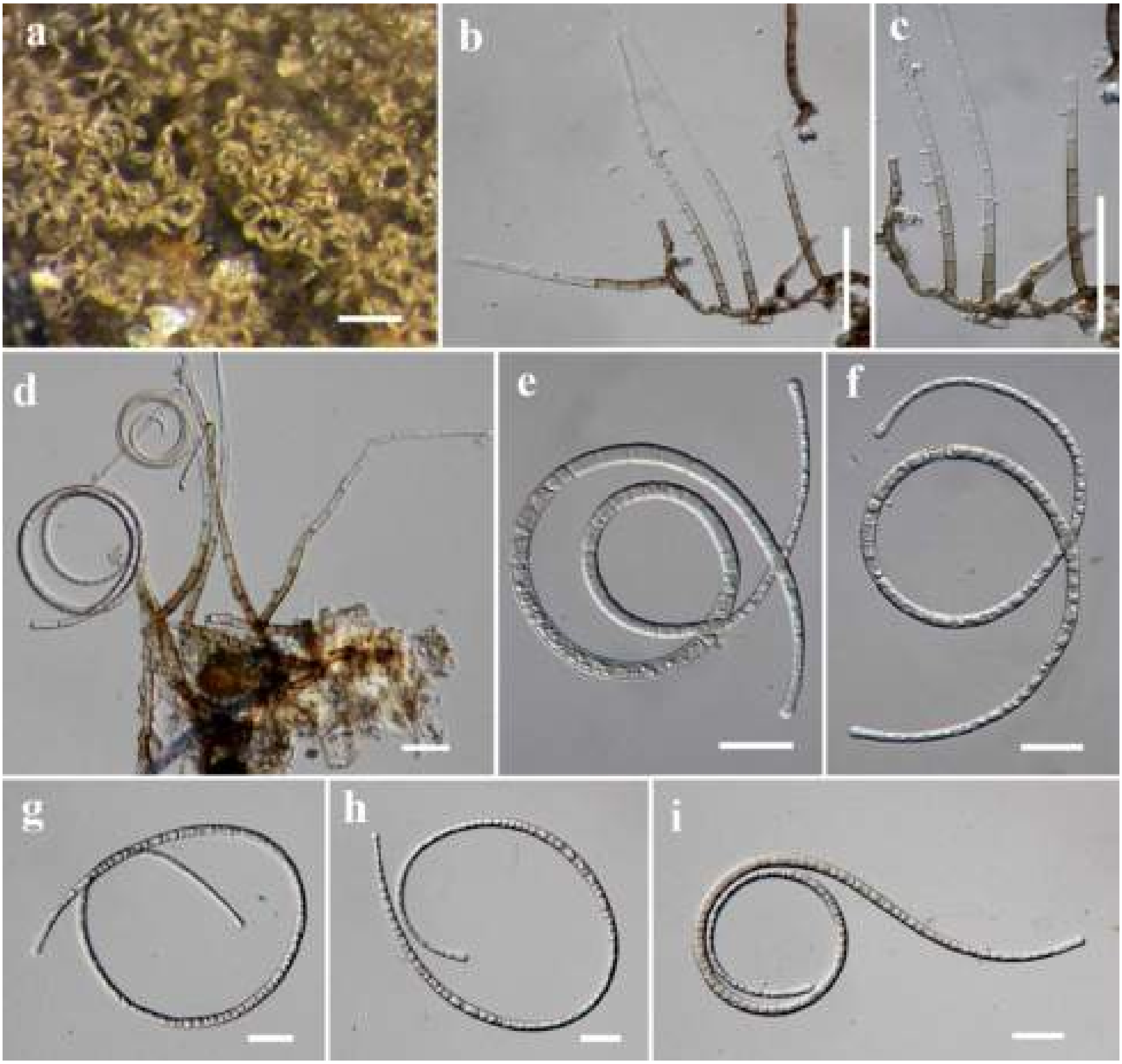


Fig. 84 ***Helicosporium luteosporum*** (MFLU 17-0502, **new record**). **a** Colony on decaying wood. **b–d** Conidiophores with lateral minute polyblastic denticles and attached conidia. **e–i** Conidia. Scale bars: **a** = 200 µm, **b, c** = 50 µm, **d–i** = 20 µm

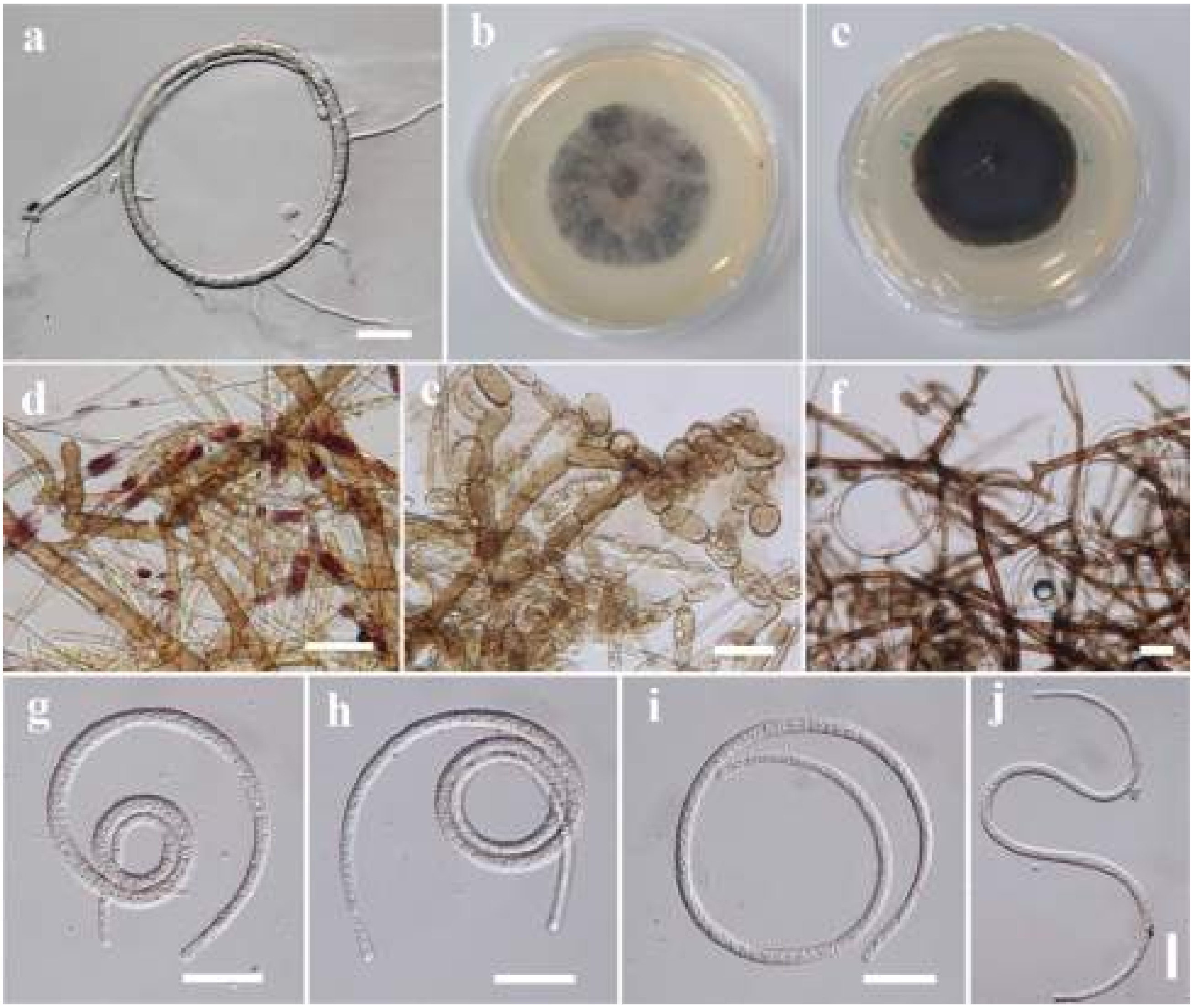


Fig. 85 ***Helicosporium luteosporum*** sporulation in culture (MFLUCC 16-1233). **a** Germinated conidium. **b**, **c** Culture on MEA from surface and reverse after 1 month. **d**–**f** Mycelium and development of conidia in culture. **g**–**j** Conidia. Scale bars: **a**, **d**–**j** = 20 µm

with conidial filament 6–8 µm wide, with 634–674.5 µm long, loosely coiled 1–2½ times, becoming loosely uncoiled in water, rounded at apical ends, indistinctly multi-septate, not constricted at the septa, bright, hyaline to pale brown, guttulate, smooth-walled.

Culture characteristics: Ascospores germinating on MEA within 24 h and many germ tubes produced from conidium cells. Colonies growing on MEA slowly, less than 5 mm diam. in 7 days at room temperature, slightly raised-radially with entire edge, brownish-gray to pale brown. *Mycelium* developing superficial, composed of branched, septate, pale brown, reddish-brown to dark brown, with red pigmented hyphal filaments, conidial spores formed on hyphae in culture at 60 days. *Conidia* 55–112 µm diam., with conidial filament 7.5–8 µm wide, with 445–448 µm long, loosely coiled 1–3½ times, becoming loosely uncoiled in water, rounded at apical ends, indistinctly multi-septate, not constricted at the septa, hyaline, with granular contents.

Material examined: THAILAND, Chanthaburi, Laem Sing, Ban Phlio, on decaying wood in a terrestrial habitat, 7 July 2016, S. Boonmee, NTP02-Ax (MFLU 17-0502, **new record**), living culture, MFLUCC 16-1233.

GenBank numbers: LSU = KY873624.

Notes: Isolate (MFLUCC 16-1233) was identified as *Helicosporium luteosporum* based on phylogenetic analysis, but morphological illustrations were not provided (Brahamanage et al. 2017; Lu et al. 2017). A nucleotide base comparison of the LSU sequence reveals that our taxon is 100% similar to the ex-type strain *H. luteosporum* MFLUCC 16-0266 (Jeewon and Hyde 2016). Further, phylogenetic analyses of a combined ITS, LSU and TEF1-α sequence dataset indicates that our strain clusters with the *H. luteosporum* strain with 100% MLBS, 1.00 BYPP support (Fig. 87). Therefore, we provide a detailed description, illustration and update phylogenetic tree for *H. luteosporum* (MFLUCC 16-1233) as a new geographical record in Thailand (Figs. 84 and 85).

Helicosporium sexuale Boonmee, Promputtha & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF558542; *Facesoffungi number*: FoF 09194; Fig. 86

Etymology: '*sexuale*' referring to sexual morph.

Holotype: MFLU 21-0104

Saprobic on decaying wood. **Sexual morph** *Ascomata* 185–235 × 116–214 µm, superficial, solitary, scattered, globose to subglobose, yellowish brown, shiny when fresh, with sparsely setae, minutely papilla, ostiolate. *Setae* 73–88 × 4–8 µm, stiff, tapering to an acute tip, septate, dark brown. *Peridium* 8–12 wide µm, composed of 2–3-layer cells of *textura angularis*, yellowish brown to hyaline cells, lacking pseudoparaphyses. *Asci* 54.5–76 × 11–20 µm, 8-spored, bitunicate, cylindric-clavate, rounded at apex, sessile. *Ascospores* 51.5–71 × 3–4 µm, fasciculate, cylindrical, narrowly fusiform, subacute ends, straight to slightly curved, 9–11-spetate, not constricted at septa, hyaline, smooth-walled. **Asexual morph** Undetermined.

Culture characteristics: Ascospores germinating on MEA within 24 h and many germ tubes produced from ascospore cells. *Colonies* growing on MEA slowly, less than 5 mm diam. in 7 days at room temperature, slightly raised-radially with entire edge, brown to dark brown, asexual conidia not formed at 60 days.

Material examined: THAILAND, Chanthaburi Province, Laem Sing, Ban Phlio, on decaying wood in a terrestrial habitat, 7 July 2016, S. Boonmee, NTP15 (MFLU 21-0104, **holotype**), ex-type living culture, MFLUCC 16-1244.

GenBank numbers: ITS = MZ538503, LSU = MZ538537, RPB2 = MZ567111, TEF1-α = MZ567082.

Notes: Phylogenetic analysis indicates that *Helicosporium sexuale* (MFLUCC 16-1244) is basal to *H. vegetum* strains (CBS 254.75, CBS 269.52, CBS 941.72, NBRC 303045 and NBRC 9014) with 96% MLBS, 1.00 BYPP support (Fig. 87); the phylogeny also shows that it is a distinct species (Fig. 87). *Helicosporium sexuale* differed from *H. vegetum* and other species by the capacity to form its sexual morphs (Fig. 86). We therefore, introduce *H. sexuale* as a new sexual species in *Helicosporium*.

Neohelicosporium Y.Z. Lu, J.C. Kang & K.D. Hyde

Notes: The latest treatments and updated accounts of *Neohelicosporium* followed herein are Lu et al. (2018a). Lu et al. (2018a) introduced *Neohelicosporium* to accommodate the taxa in having *Helicosporium*-like characters based on phylogenetic and morphological evidence, which is typified by *Ne. parvisporum*. Members of *Neohelicosporium* differ from *Helicosporium* in having acrogenous and/or acropleurogenous conidia developing from an integrated, sympodial conidiogenous cell while the latter has pleurogenous conidia and discrete, determinate conidiogenous cells (Lu et al. 2018a). Four new isolates of *Neohelicosporium irregulare* and one new isolate of *Neohelicosporium parvisporum* are reported.

Neohelicosporium irregulare Y.Z. Lu, J.C. Kang & K.D. Hyde, Fungal Diversity 92: 235 (2018)

Index Fungorum number: IF554871; *Facesoffungi number*: FoF 04739; Figs. 88, 89

Saprobic on submerged decaying wood. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous, helicosporous. *Colonies* effuse, white, shiny, with crowded by conidial masses. *Mycelium* composed of superficial and partly immersed, branched, anastomosing, septate, brown hyphae, smooth-walled. *Conidiophores* 116–229.5 × 6–8 µm, micronematous, mononematous, arising from repent mycelium, tapering toward narrow at apex, widest at base, branched, septate, brown, smooth-walled. *Conidiogenous cells* holoblastic, mono- to polyblastic, terminal or intercalary, integrated, subhyaline, bearing lateral minute denticles each with single conidium. *Conidia* 36–53 µm diam., with conidial filament 3–4.5 µm wide, with 190.5–236 µm long, loosely coiled 1–3 times, becoming loosely uncoiled in water, rounded at apical ends, indistinctly multi-septate, not constricted at the septa, hyaline, with granular contents.

Culture characteristics: Conidium germinating on MEA within 24 h and many germ tubes produced from conidium cells. Colonies growing on MEA, reaching greater than 10 mm diam. in 7 days at room temperature, irregular, slightly raised, with edge undulate to fimbriate, dark brown. *Mycelium* developing superficial, partly immersed, composed of branched, septate, light brown to dark brown hyphal filaments, conidial spores formed on hyphae in culture at 60 days. *Conidia* 29–49 µm diam., conidial filament 4–5.5 µm wide, 167–208 µm long, loosely coiled 1–3½ times, becoming loosely uncoiled in water, rounded at apical ends, indistinctly multi-septate, not constricted at the septa, hyaline to brown, with granular contents.

Material examined: THAILAND, Chiang Rai Province, Muang, Mae Yao, Huay Mae Sai, on submerged decaying wood in a small freshwater stream, 17 March 2016, S. Boonmee, HMS03 (MFLU 21-0097), living culture, MFLUCC 16-0721; HMS04 (MFLU 21-0098, **new record**) living culture, MFLUCC 16-0722; HMS05 (MFLU 21-0099), living culture, MFLUCC 16-0723; HMS17 (MFLU 21-0102), living culture, MFLUCC 16-0758.

GenBank numbers: HMS03: ITS = MZ538516, LSU = MZ538550, TEF1-α = MZ567093; HMS04:

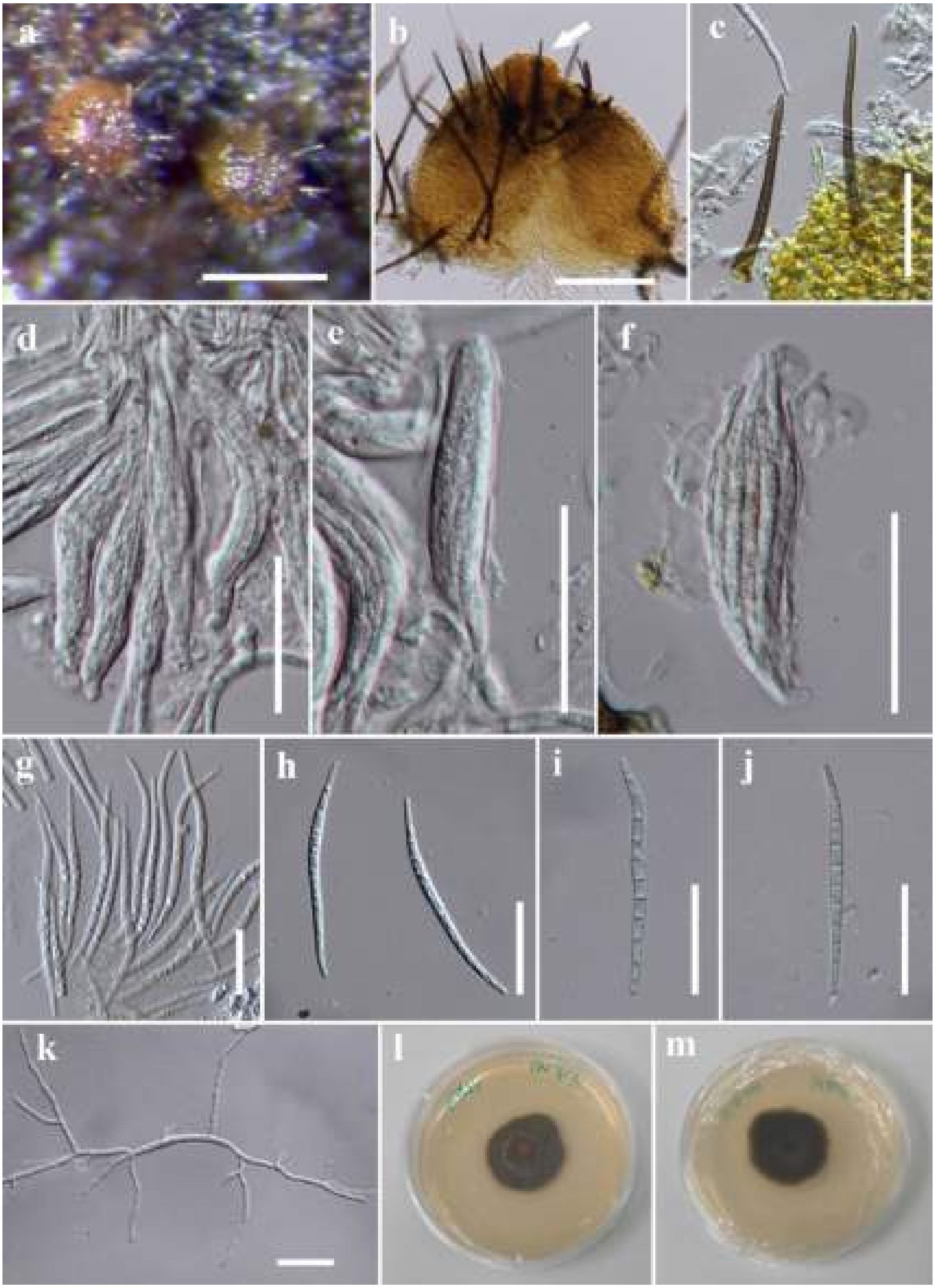


Fig. 86 ***Helicosporium sexuale*** (MFLU 21-0104, **holotype**). **a** Superficial ascomata on decaying wood substrate. **b** Squash mount of ascoma showing peridium. **c** Setae. **d**–**f** Asci. **g**–**j** Ascospores. **k** Germinated conidium. **l**, **m** Culture on MEA from surface and reverse after 1 month. Scale bars: **a** = 200 µm, **b** = 100 µm, **c**–**f** = 40 µm, **g**–**k** = 20 µm

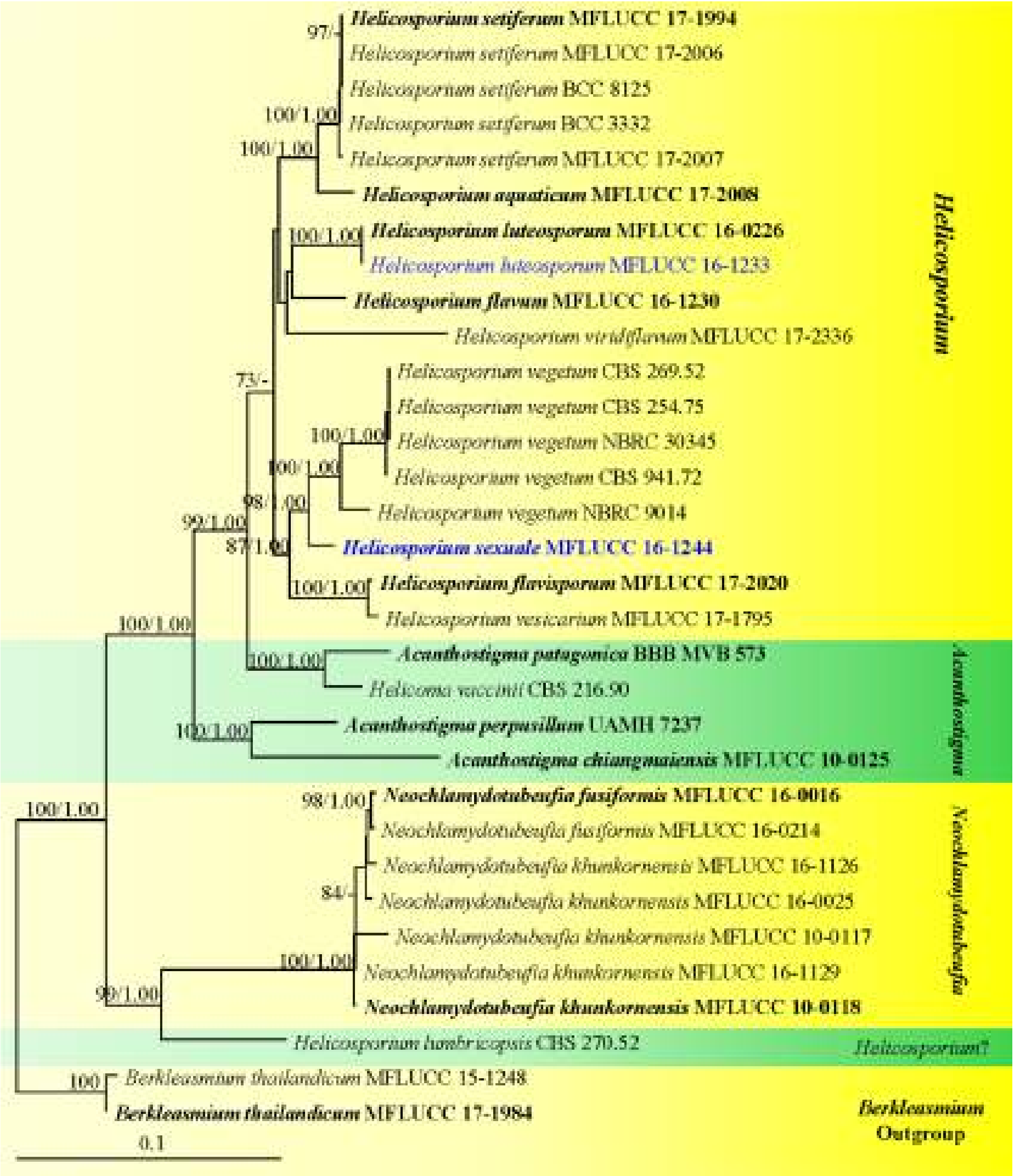


Fig. 87 Maximum likelihood phylogenetic tree based on a combined ITS, LSU and TEF1-α sequence data of *Helicosporium* taxa and related genera in *Tubeufiaceae*. Thirty-two taxa are included in the combined analyses which comprise a total of 2367 characters. *Berkleasmium thailandicum* (MFLUCC 15-1248 and MFLUCC 17-1984) are selected as the outgroup taxa. The best RAxML tree with a final likelihood value of – 8690.594891 is presented. RAxML analysis yielded 609 distinct alignment patterns and 25.02% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.231326, C = 0.266395, G = 0.273200, T = 0.229079, with substitution rates AC = 1.159455, AG = 2.641204, AT = 1.962575, CG = 0.673701, CT = 9.846706, GT = 1.000000; gamma distribution shape parameter alpha = 0.182397. Bootstrap support values for maximum likelihood (MLBS, left) equal to or greater than 70% is given above the nodes. Bayesian posterior probabilities (BYPP, right) equal to or greater than 0.95 are given above the nodes. Ex-type strains are in bold and newly generated sequences are in blue

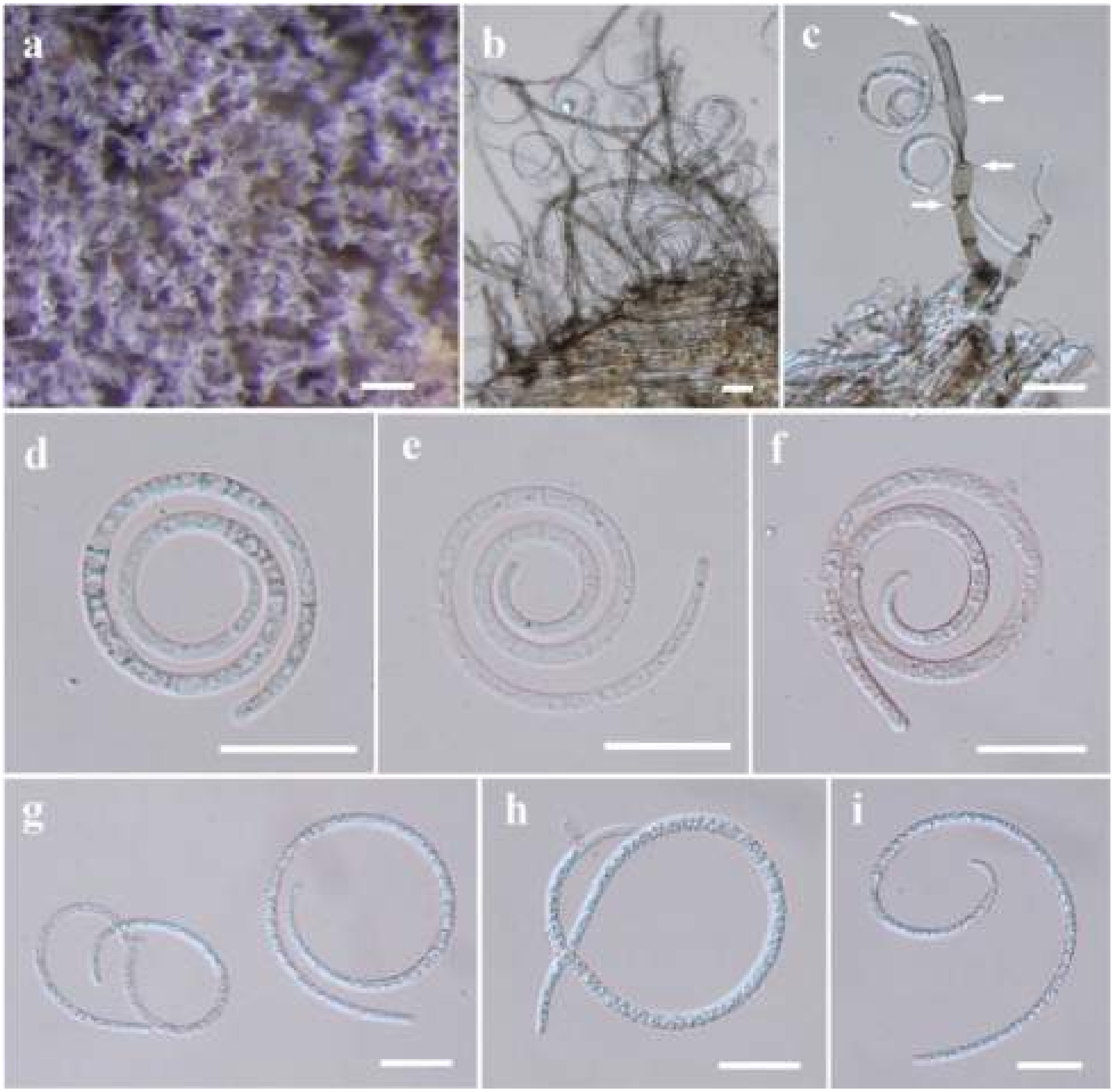


Fig. 88 ***Neohelicosporium irregulare*** (MFLU 21-0098, **new record**). **a** Colony on decaying wood. **b**, **c** Conidiophores with lateral minute polyblastic denticles and attached conidia. **d**–**i** Conidia. Scale bars: **a** = 100 μm, **b**–**i** = 20 μm

ITS = MZ538517, LSU = MZ538551, TEF1-α = MZ567094; HMS05: ITS = MZ538518, LSU = MZ538552, TEF1-α = MZ567095; HMS17: ITS = MZ538519, LSU = MZ538553, TEF1-α = MZ567096.

Notes: Four new collections of *Neohelicosporium irregulare* (MFLUCC 16-0721, MFLUCC 16-0722, MFLUCC 16-0722 and MFLUCC 16-0758) were recovered from submerged decaying wood from Chiang Rai Province. They can be identified as *Neohelicosporium* since they formed typical effuse colonies, erect conidiophores and long filamentous, multi-septate with hyaline to light pigmented helicospores (Figs. 88 and 89). They share a close phylogenetic affinity to the ex-type strain *Neohelicosporium irregulare* (MFLUCC 17-1796) in the combined LSU, ITS and TEF1-α sequenced data, which confirmed that they are the same species (Fig. 91).

Neohelicosporium parvisporum Y.Z. Lu, J.C. Kang & K.D. Hyde, Mycol. Progr. 17(5): 637 (2017)

Index Fungorum number: IF822056; *Facesoffungi number*: FoF 03571; Fig. 90

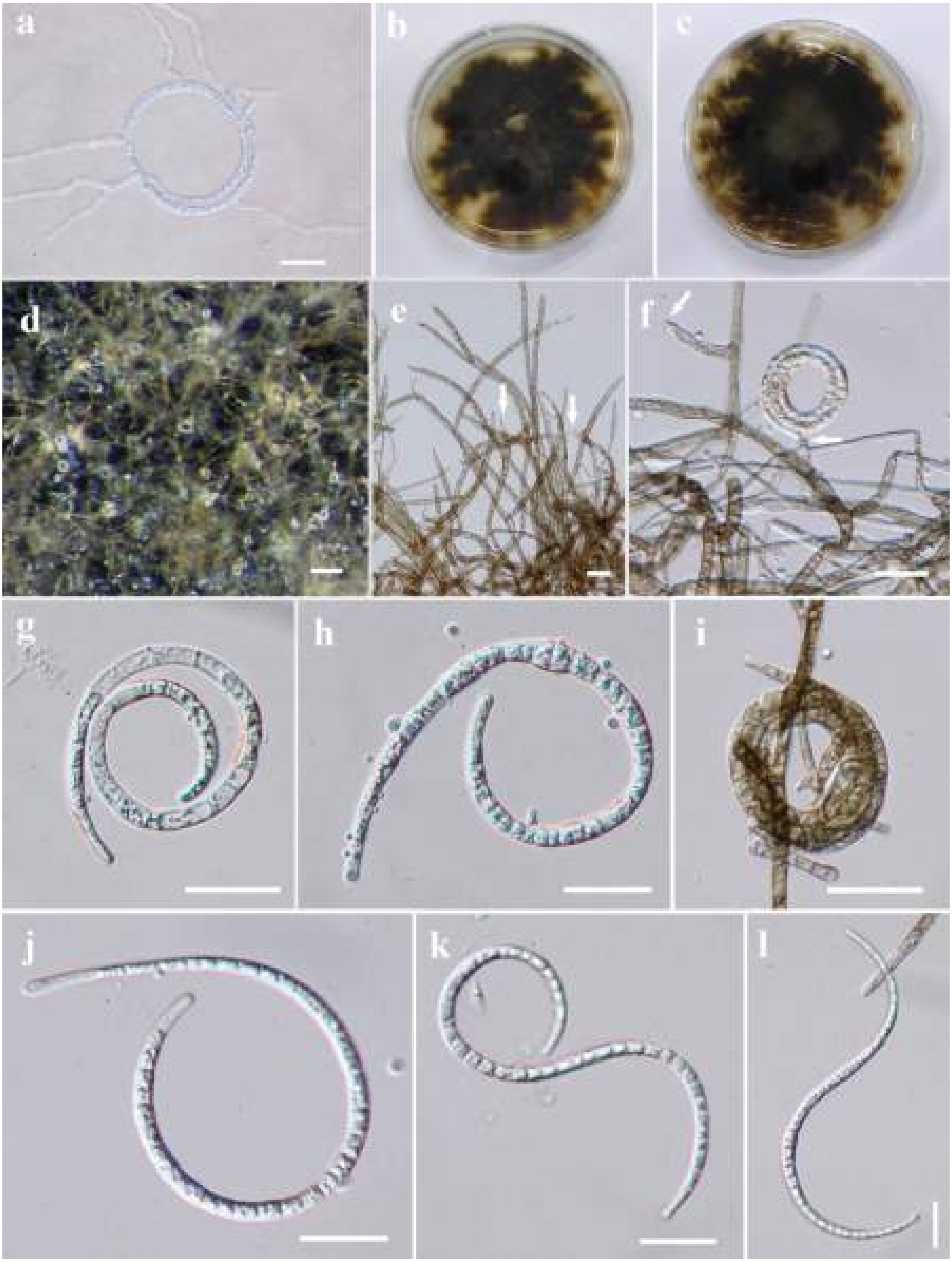


Fig. 89 ***Neohelicosporium irregulare*** sporulation in culture (MFLUCC 16-0722). **a** Germinated conidium. **b**, **c** Culture on MEA from surface and reverse. **d**–**f** Mycelium and development of conidia in culture. **g**–**l** Conidia. Scale bars: **a**, **e**–**l** = 20 µm, **d** = 100 µm

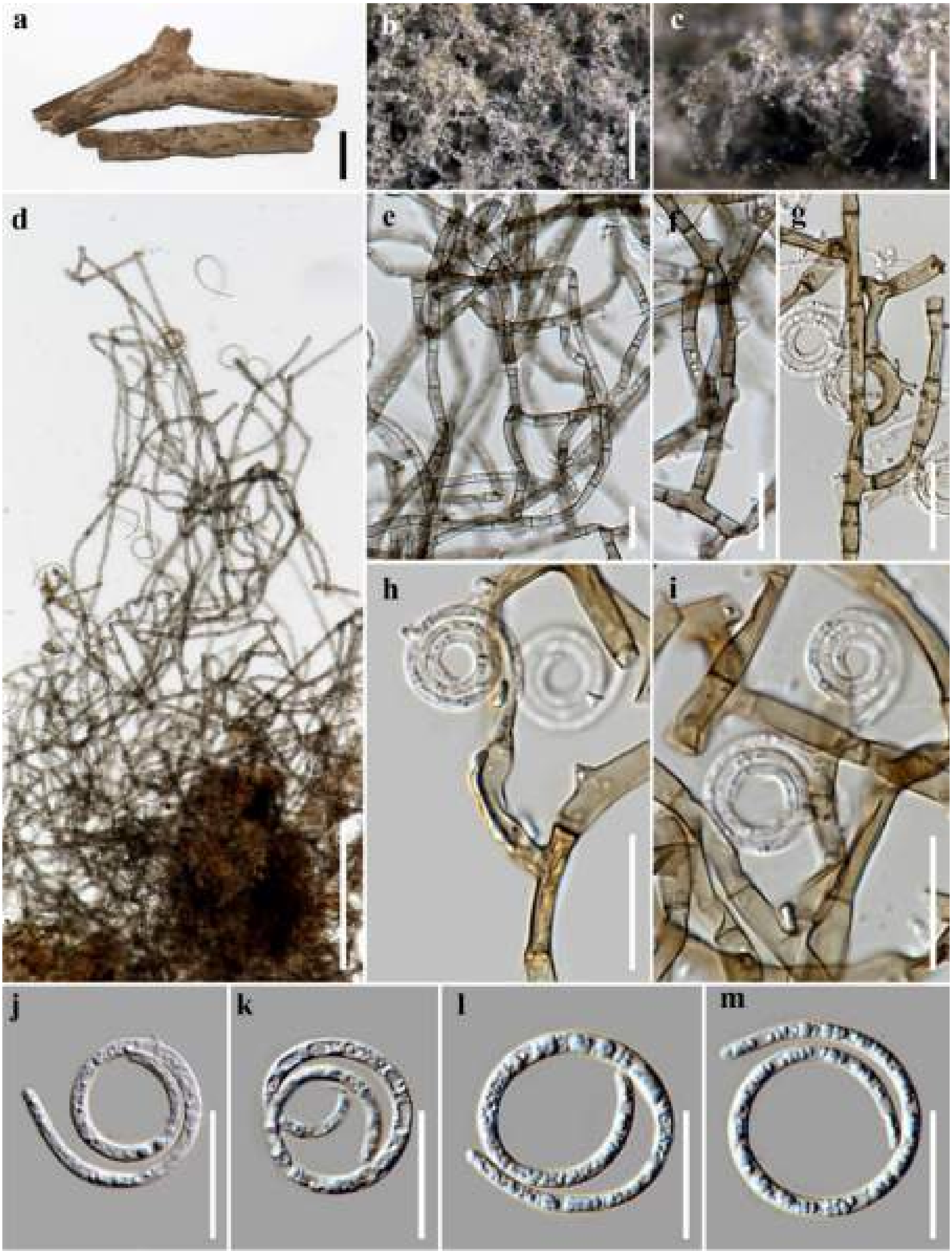


Fig. 90 ***Neohelicosporium parvisporum*** (MFLU 21-0123, **new record**). **a** Substrate. **b**, **c** Colony on decaying wood. **d**–**f** Conidiophores with conidia. **g**–**i** Conidiogenous cells. **j**–**m** Conidia. Scale bars: **a** = 20 mm, **b**, **c** = 500 µm, **d** = 100 µm; **e**–**m** = 20 µm

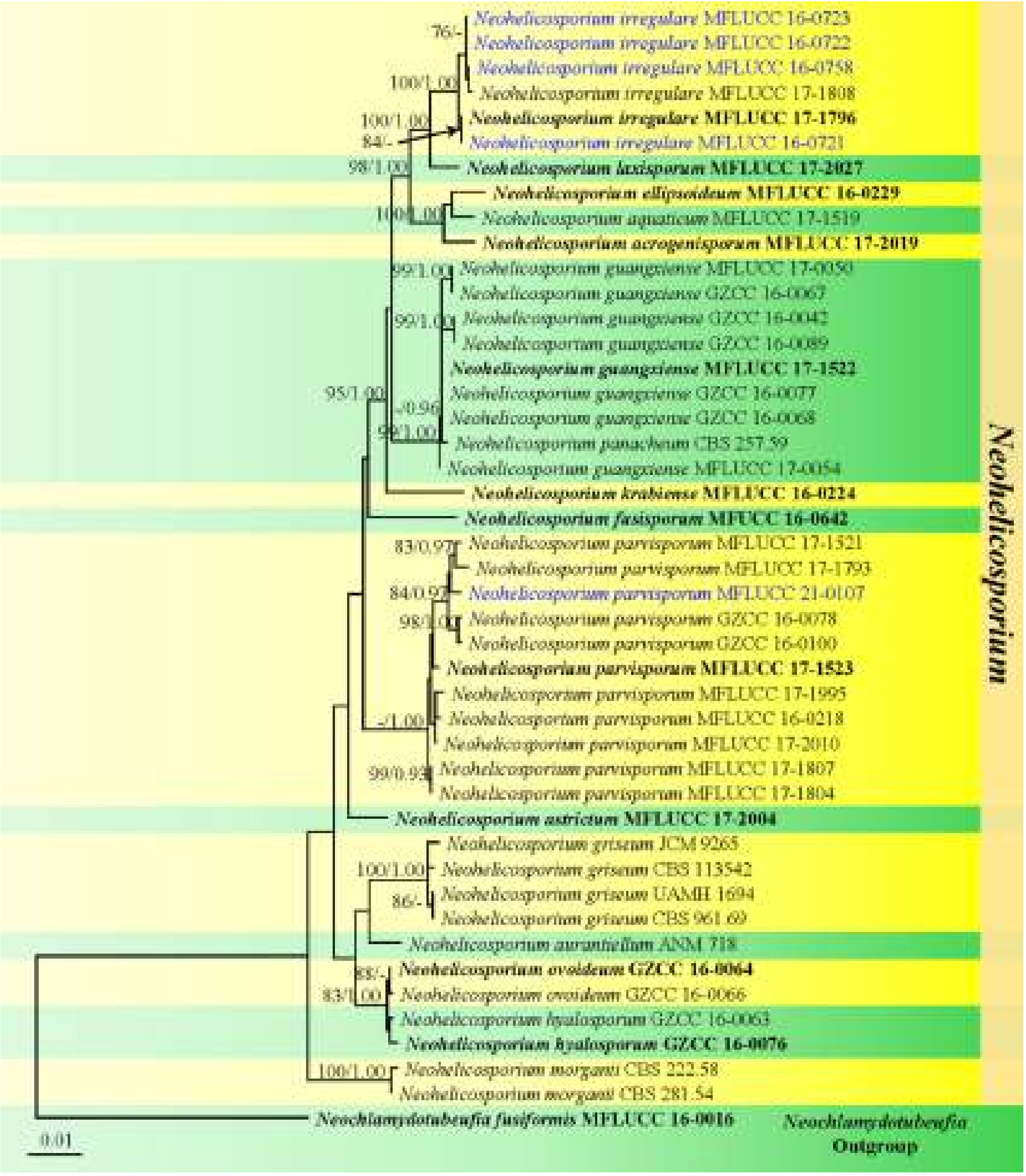


Fig. 91 Maximum likelihood phylogenetic tree based on a combined ITS, LSU and TEF1-α sequence data of *Neohelicosporium* taxa and related genera in *Tubeufiaceae*. Forty-five taxa are included in the combined analyses which comprise a total of 2348 characters. *Neochlamydotubeufia fusiformis* (MFLUCC 16-0016) is selected as the outgroup taxon. The best RAxML tree with a final likelihood value of − 5971.586719 is presented. RAxML analysis yielded 343 distinct alignment patterns and 12.46% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.230669, C = 0.271979, G = 0.266714, T = 0.230637, with substitution rates AC = 0.718733, AG = 2.140841, AT = 1.942223, CG = 0.669931, CT = 13.341832, GT = 1.000000; gamma distribution shape parameter alpha = 0.020000. Bootstrap support values for maximum likelihood (MLBS, left) equal to or greater than 70% is given above the nodes. Bayesian posterior probabilities (BYPP, right) equal to or greater than 0.95 are given above the nodes. Ex-type strains are in bold and newly generated sequences are in blue

Saprobic on submerged decaying wood. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous, helicosporous. *Colonies* on the substrate superficial, effuse, gregarious, white to light pink. *Mycelium* composed of partly immersed, partly superficial, hyaline to pale brown, septate, abundantly branched hyphae, with masses of crowded, glistening conidia. *Conidiophores* up to 400 µm long, 4–6 µm wide, micronematous, mononematous, flexuous, cylindrical, branched, septate, pale brown, smooth-walled. *Conidiogenous cells* 8–12 µm long, 2.5–5 µm wide, holoblastic, mono- to polyblastic, integrated, intercalary, cylindrical, with denticles, pale brown, smooth-walled. *Conidia* 13.5–33 µm diam., conidial filament 2–4 µm wide, 100–150 µm long, tightly coiled 3–4 times, becoming loosely coiled in water, rounded at the tip, multi-septate, verrucose, guttulate, hyaline.

Culture characteristics: Conidia germinating on MEA and producing germ tubes within 12 h. Colonies growing on PDA, circular, umbonate, surface rough and wrinkled, edge entire, reaching 10–15 mm in 2 weeks at 25 °C, pale brown to brown, mycelium superficial and partially immersed, branched, septate, hyaline to pale brown, smooth.

Material examined: THAILAND, Chiang Mai Province, Mushroom Research Center, on submerged decaying wood in a freshwater stream, 29 January 2019, S. Boonmee, SB18-3 (MFLU 21-0123, **new record**), living culture, MFLUCC 21-0107.

GenBank numbers: ITS = MT864353, LSU = MT860431.

Notes: *Neohelicosporium parvisporum* was introduced by Lu et al. (2018a), which was collected from a freshwater habitat. Based on phylogenetic analysis of combined ITS, LSU and TEF1-α sequence data showed that our isolate (MFLUCC 21-0107) clusters among isolates *N. parvisporum* without statistical support (Fig. 91). Our isolate has similar conidial and conidiophore morphology to *N. parvisporum* (MFLUCC 17-1523). However, our isolate has smaller conidiogenous cells (8–12 × 2.5–5 vs. 14.5–22.5 × 3.5–4.5 µm) and larger conidia (13.5–33 × 14–24.5 µm) (Fig. 90). A comparison of the ITS nucleotides of *N. parvisporum* (MFLUCC 17-1523 = GZCC 16-0088) and the new strain (MFLUCC 21-0107) revealed 9/550 (1.64%) nucleotide differences.

Tubeufia Penz. & Sacc.

Notes: We follow the latest treatments and updated accounts in Lu et al. (2018b), Hyde et al. (2019) and Wijayawardene et al. (2020). The members of *Tubeufia* include sexual and asexual morphs and are widely distributed in tropical regions, and they are commonly can be found on dead wood in terrestrial and freshwater habitats (Lu et al. 2018b; Hyde et al. 2019). In this study, *T. longiohelicospora* is introduced and two species (*T. chiangmaiensis* and *T. roseohelicospora*) are reported as common species records on decaying wood.

Tubeufia chiangmaiensis Boonmee & K.D. Hyde, Fungal Diversity 68: 248 (2014)

Index Fungorum number: IF550705; *Facesoffungi number*: FoF 00172; Figs. 92, 93

Saprobic on decaying wood. **Sexual morph** *Ascomata* 227.5–253 × 160–192 µm, superficial, seated on a subiculum, solitary, scattered, globose-subglobose to ovate, cream-white to yellowish when freshly, light brown to brown, collapsing when dry, slightly compressed subiculum hyphae, developing from ascomatal base onto substrate, with ambiguous ostiolate. *Peridium* 13–22.5 µm wide, composed of 2–3 layers of thick-walled, light brown cells of *textura angularis*. *Hamathecium* comprising 1–2 µm wide, numerous, septate, branched, hyaline pseudoparaphyses. *Asci* 116–123 × 12–15.5 µm ($\bar{x}$ = 118.5 × 14 µm, n = 10), 8-spored, bitunicate, fissitunicate, elongate cylindrical to slightly clavate, apedicellate, thick-walled, rounded at apex, tapering towards narrow base, sessile. *Asci* 54.5–70 × 3.5–5.5 µm ($\bar{x}$ = 63 × 5 µm, n = 10), overlapping 2–3-seriate, cylindric-fusiform, tapering toward ends, 7-septate, slightly constricted at the medium septum, hyaline, smooth-walled. **Asexual morph** Hyphomycetous, helicosporous. *Conidiophores* semi-macronematous, mononematous, borne as lateral branches from superficial hyphae, pale brown to brown, septate, simple or branched, flexuous to geniculate. *Conidiophores cells* holoblastic, terminal or intercalary, dentate, hyaline, smooth. *Conidia* 26–54 µm diam., conidial filament 4–6(–9) µm wide, (186–)265–309.5 µm long, loosely coiled 1–2½ times, becoming loosely uncoiled in water, rounded at apical ends, indistinctly multi-septate, not constricted at the septa, hyaline to brown, with granular contents.

Culture characteristics: Ascospore germinating on MEA within 24 h and many germ tubes produced from many cells. Colonies growing on MEA, reaching greater than 10 mm diam. in 7 days at room temperature, flat, sparsely hairy, radially striate, with fimbriate edge, dark brown, with yellowish pigmented in the medium after 30 days. *Mycelium* superficial, composed of branched, septate, brown to dark brown hyphal filaments, conidial spores formed on hyphae in culture at 60 days.

Material examined: THAILAND, Chiang Mai Province, Mae Taeng, Pa Pae, Mushroom Research Center, on decaying wood, 17 July 2015, S. Boonmee, MRC2 (MFLU 21-0103, **new record**), living culture, MFLUCC 16-0197.

GenBank numbers: ITS = MZ538530, LSU = MZ538564, TEF1-α = MZ567105.

Notes: *Tubeufia chiangmaiensis* was collected from Mushroom Research Center, Chiang Mai Province, Thailand. This is the third report for *T. chiangmaiensis* produced an asexual morph on culture (Fig. 93). Our isolate MFLUCC 16-0197 shares some similar morphological characters of sexual and asexual morphs (Figs. 93 and 94) to the type of *T. chiangmaiensis* MFLUCC 15-0514 and MFLUCC 17-01801 (Boonmee et al. 2014; Lu et al. 2018b). However, no outstanding differences were observed in the morphological comparison among three isolates (Fig. 97). Therefore, a record of *T. chiangmaiensis* on decaying wood, from Chiang Mai Province is reported.

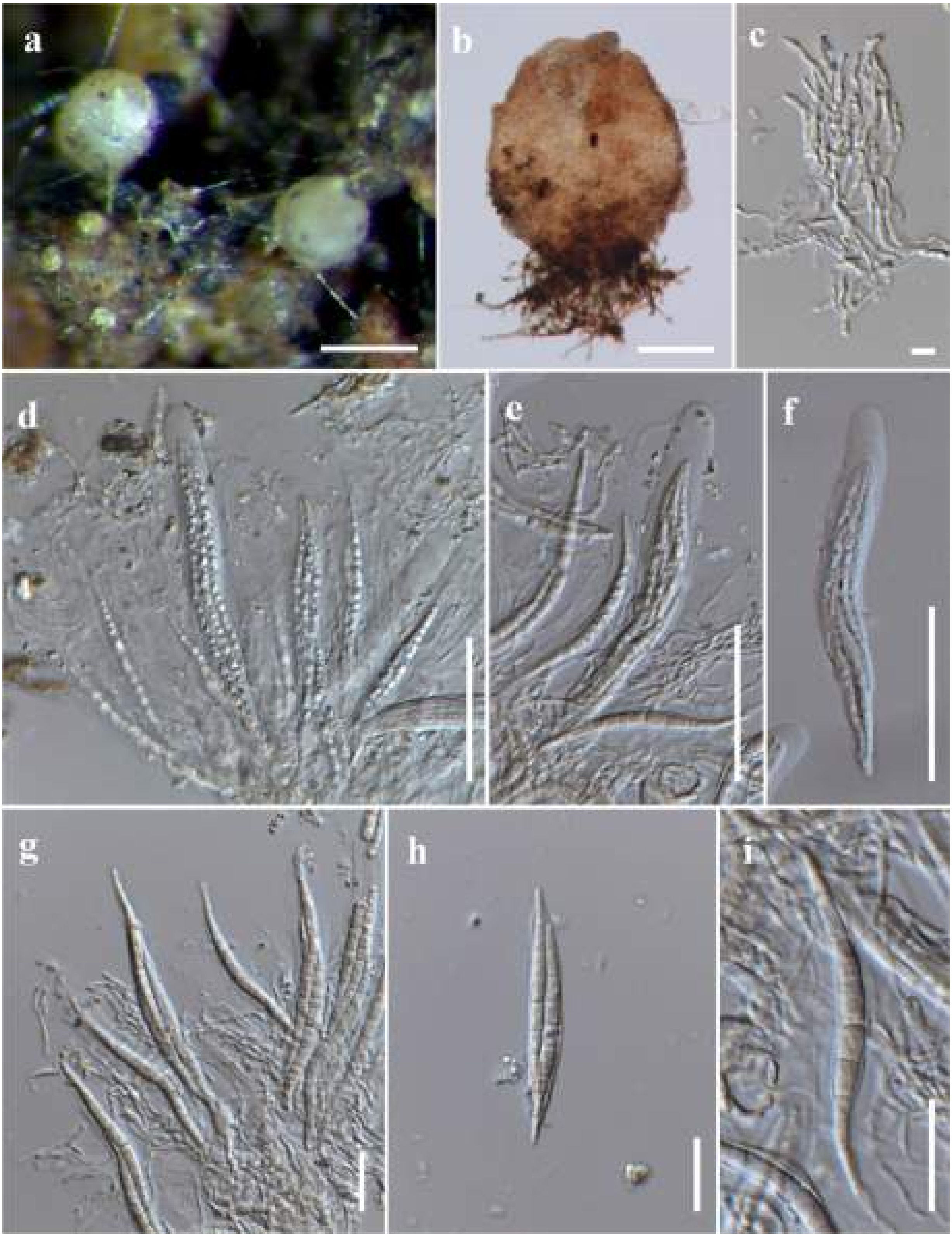


Fig. 92 ***Tubeufia chiangmaiensis*** (MFLU 21-0103, **new record**). **a** Superficial ascomata on decaying wood substrate. **b** Squash mount of ascoma showing peridium and subiculum hyphae at the base. **c** Pseudoparaphyses. **d**–**f** Asci. **g**–**i** Ascospores. Scale bars: **a** = 200 µm, **b** = 100 µm, **c** = 10 µm, **d**–**f** = 50 µm, **g**–**i** = 20 µm

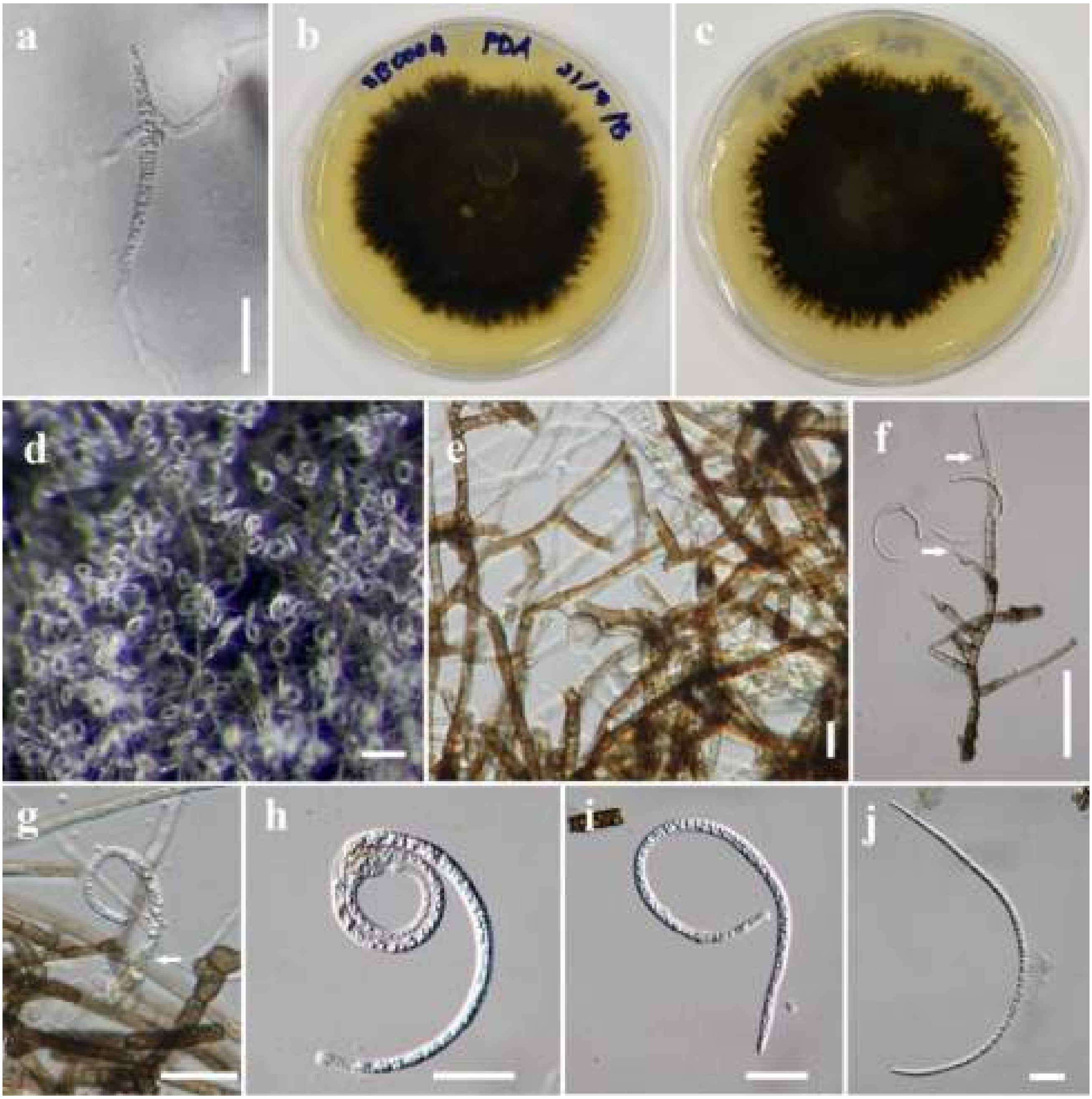


Fig. 93 ***Tubeufia chiangmaiensis*** sporulation in culture (MFLUCC 16-0197). **a** Germinated ascospore. **b**, **c** Culture on MEA from surface and reverse after 1 month. **d**–**f** Development of conidia and mycelium in culture. **g**–**j** Conidia. Scale bars: **a**, **f** = 50 μm, **d** = 100 μm, **e** = 10 μm, **g**–**j** = 20 μm

Tubeufia longihelicospora Boonmee, Promputtha & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF558543; *Facesoffungi number*: FoF 09195; Figs. 94, 95

Etymology: '*longihelicospora*' referring to the asexual characters with long filamentous helicoid conidia.

Holotype: MFLU 21-0100

Saprobic on submerged decaying wood. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous, helicosporous. *Colonies* on natural substrate effuse, superficial, shiny, hairy, hyaline to white of crowded conidiospore masses. *Mycelium* composed of superficial and partly immersed, branched at the base, septate, hyaline to brown hyphae. *Conidiophores* macronematous, thick-walled, branched at the base, septate, pale brown to brown,

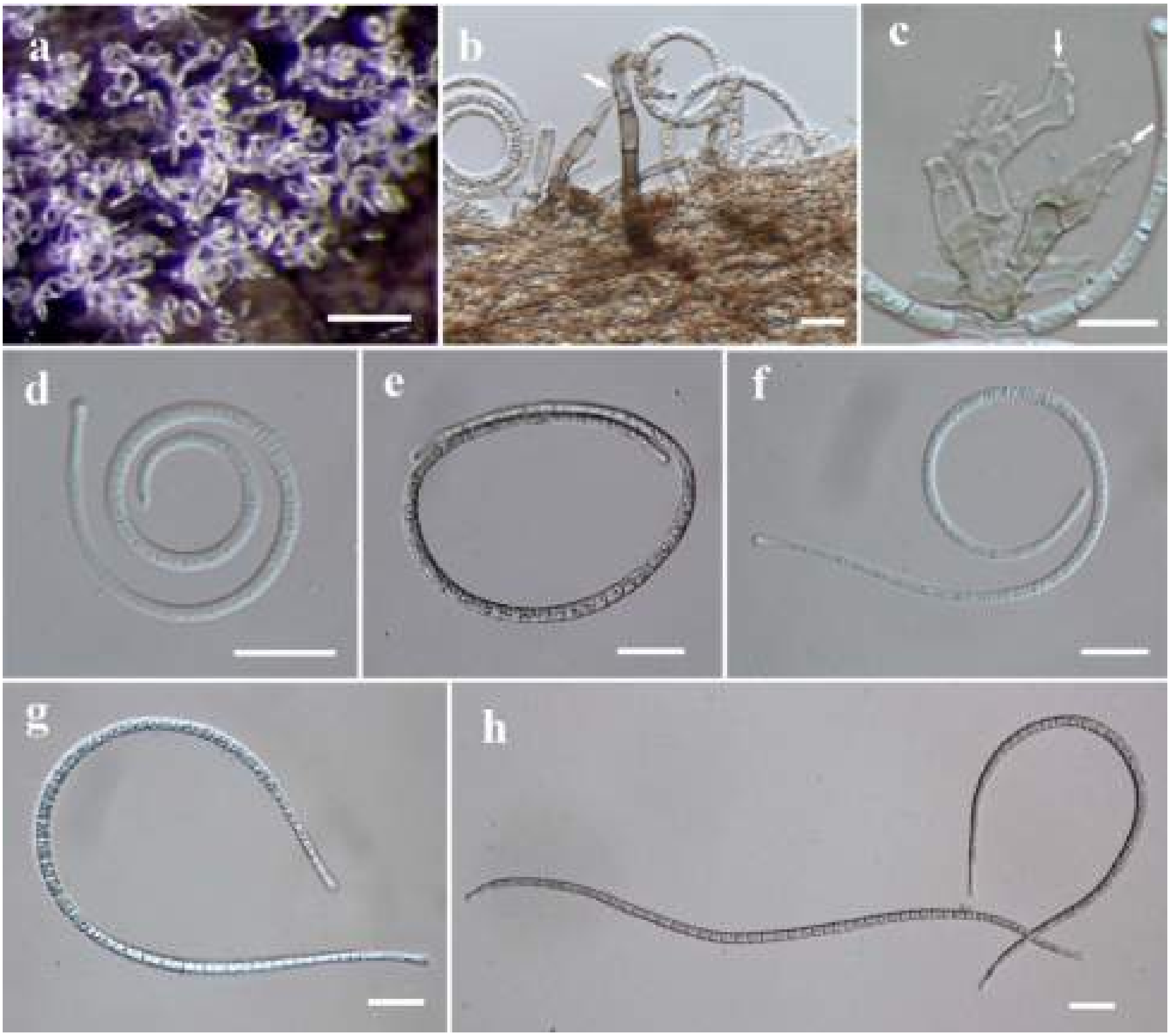


Fig. 94 ***Tubeufia longihelicospora*** (MFLU 21-0100, **holotype**). **a** Colony on decaying wood. **b**, **c** Conidiophores and lateral minute denticles. **d**–**h** Conidia. Scale bars: **a** = 200 µm, **b**, **c** = 10 µm, **d**–**h** = 20 µm

smooth-walled. *Conidiogenous cells* monoblastic, terminal or intercalary, integrated, subhyaline, bearing lateral minute denticles. *Conidia* 36–52 µm diam., with conidial filament 4–5.5 µm wide, 252–360 µm long, loosely coiled 1–3½ times, becoming loosely uncoiled in water, rounded at apical ends, multi-septate, 33–45-septate, slightly constricted at the septa, hyaline to subhyaline, with granular contents.

Culture characteristics: Conidium germinating on MEA within 24 h and many germ tubes produced from conidium cells. Colonies growing on MEA, reaching greater than 10 mm diam. in 7 days at room temperature, effuse, sparsely hairy, radially striate, slightly fimbriate edge, dark brown, with yellow brown pigmented in the medium after 30 days. *Mycelium* superficial, partly immersed, branched, septate, hyaline, brown to dark brown hyphal filaments, asexual conidia not formed at 60 days.

Material examined: THAILAND, Chiang Rai Province, Muang, Mae Yao, Huay Mae Sai, on submerged decaying wood in a small freshwater stream, 17 March 2016, S. Boonmee, HMS07 (MFLU 21-0100, **holotype**), ex-type living culture, MFLUCC 16-0753.

GenBank numbers: ITS = MZ538531, LSU = MZ538565, TEF1-α = MZ567106.

Notes: *Tubeufia longihelicospora* is introduced as a new species based on morphological characters and phylogenetic evidence. Our new taxon forms a separate lineage basal to *T. brunnea*, *T. hechiensis* and *T. taiwanensis* with 100% MLBS, 1.00 BYPP support (Fig. 97). *Tubeufia longihelicospora*

Fig. 95 ***Tubeufia longihelicospora*** (MFLUCC 16-0753, **ex-type**). **a** Germinated conidium. **b**, **c** Culture on MEA from surface and reverse after 1 month. **d**–**f** Mycelium and development on culture (Note: the formation of chlamydospores). Scale bars: **a**, **d**–**f** = 20 μm

shares similar characteristics with *T. hechiensis* in having white colonies on natural woody substrates and multi-septate, hyaline, loosely coil conidia, but it differs in conidiophore and conidiogenous cell characters (Figs. 94 and 95). Furthermore, *T. longihelicospora* is distinguished from *T. brunnea* and *T. taiwanensis* by its macronematous, thick-walled, conidiophores and smaller, cylindrical filamentous conidia. A comparison of ITS nucleotide bases shows that *T. longihelicospora* differs from *T. brunnea* in 29/584 bp (5.3%), *T. hechiensis* in 28/546 bp (5.1%) and *T. taiwanensis* in 28/546 bp (5.1%) following the guidelines of Jeewon and Hyde (2016).

Tubeufia roseohelicospora Y.Z. Lu, Boonmee & K.D. Hyde, Fungal Diversity 80: 128 (2016)

Index Fungorum number: IF552222; *Facesoffungi number*: FoF 02362; Fig. 96

Saprobic on submerged decaying wood. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous, helicosporous. *Colonies* on wood substrate superficial, effuse, hyaline to white of crowded conidiospore masses. *Mycelium* composed of superficial and partly immersed, anastomosing, branched, septate, brown hyphae, smooth-walled. *Conidiophores* (19–)59–90(–158) × 3–7.5 μm, macronematous, mononematous, erect, arising from repent mycelium, flexuous, branched, septate, brown, smooth-walled. *Conidiogenous cells* (8–)18–40 × 3–6 μm, holoblastic, mono- to polyblastic, terminal or intercalary, integrated, subhyaline, bearing lateral minute denticles each with single conidium. *Conidia* 20–44 μm diam., with conidial filament 3–6 μm wide, with 318–563 μm long, loosely coiled 1½–4½ times, becoming loosely uncoiled in water, rounded at apical ends, indistinctly multi-septate, not constricted at the septa, hyaline, guttulate, smooth-walled.

Culture characteristics: Conidium germinating on MEA within 24 h and many germ tubes produced from conidium cells. Colonies growing on MEA, reaching greater than 10 mm diam. in 7 days at room temperature, effuse, sparsely hairy, radially striate, with fimbriate edge, dark brown, with yellow brown pigmented in the medium after 45 days. *Mycelium* superficial, composed of branched, septate, brown to dark brown hyphal filaments, conidial spores formed on hyphae in culture at 60 days.

Material examined: THAILAND, Chiang Rai Province, Muang, Mae Yao, Huay Mae Sai, on submerged decaying wood in a small freshwater stream, 17 March 2016, S. Boonmee, HMS14 (MFLU 21-0101, **new record**), living culture, MFLUCC 16-0729.

GenBank numbers: ITS = MZ538532, LSU = MZ538566, TEF1-α = MZ567107.

Notes: *Tubeufia roseohelicospora* was introduced by Hyde et al. (2016) to accommodate a taxon that is characterized by tightly helicoid with light pink conidia. Phylogenetic analysis of the combined LSU, ITS and TEF1-α dataset

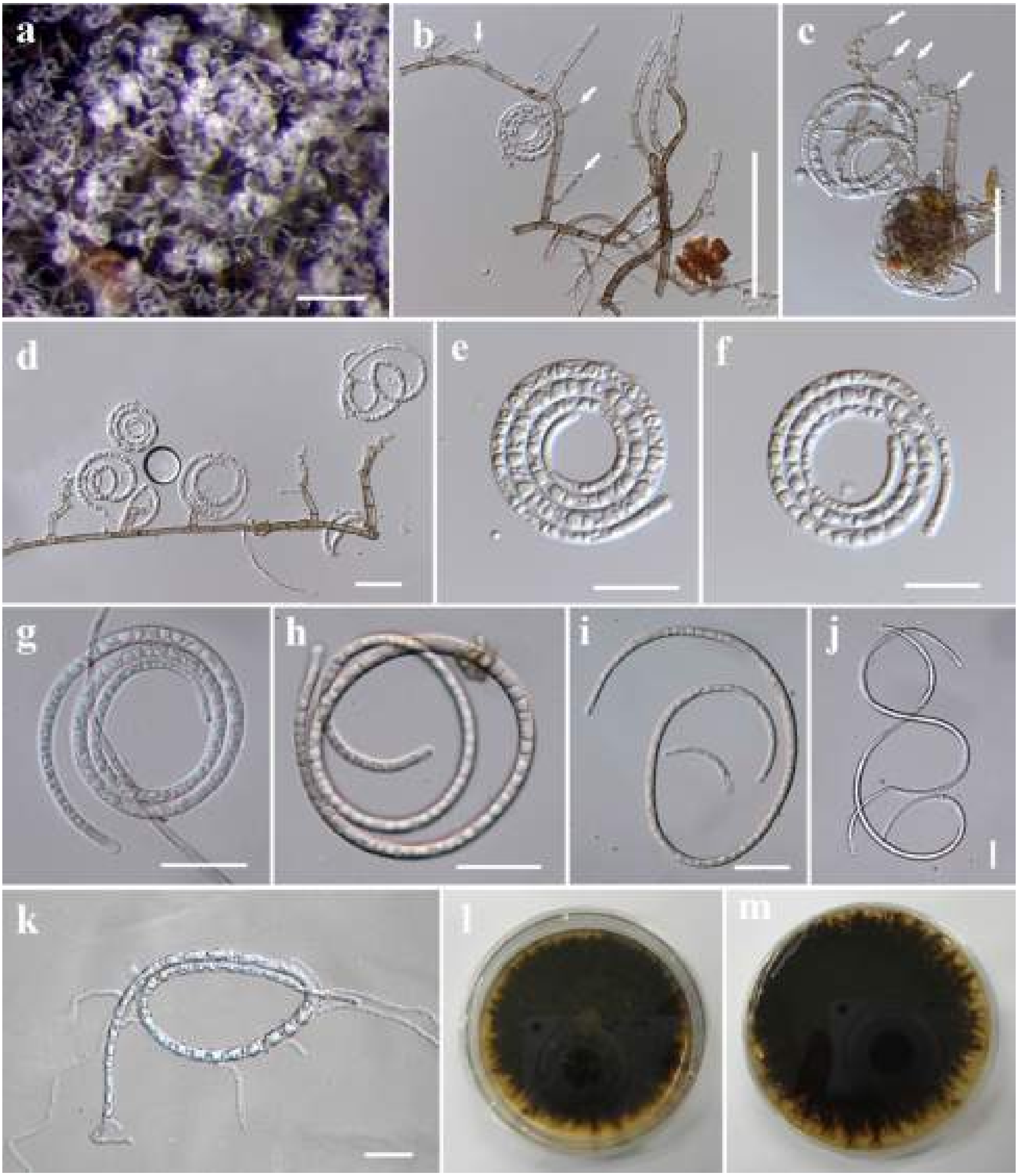


Fig. 96 ***Tubeufia roseohelicospora*** (MFLU 21-0101, **new record**). **a** Colony on decaying wood. **b–d** Conidiophores with lateral minute polyblastic denticles and attached conidia. **e–j** Conidia. **k** Germinated conidium. **l**, **m** Culture on MEA from surface and reverse after 1 month. Scale bars: **a** = 200 µm, **b**, **c** = 50 µm, **d**–**k** = 20 µm

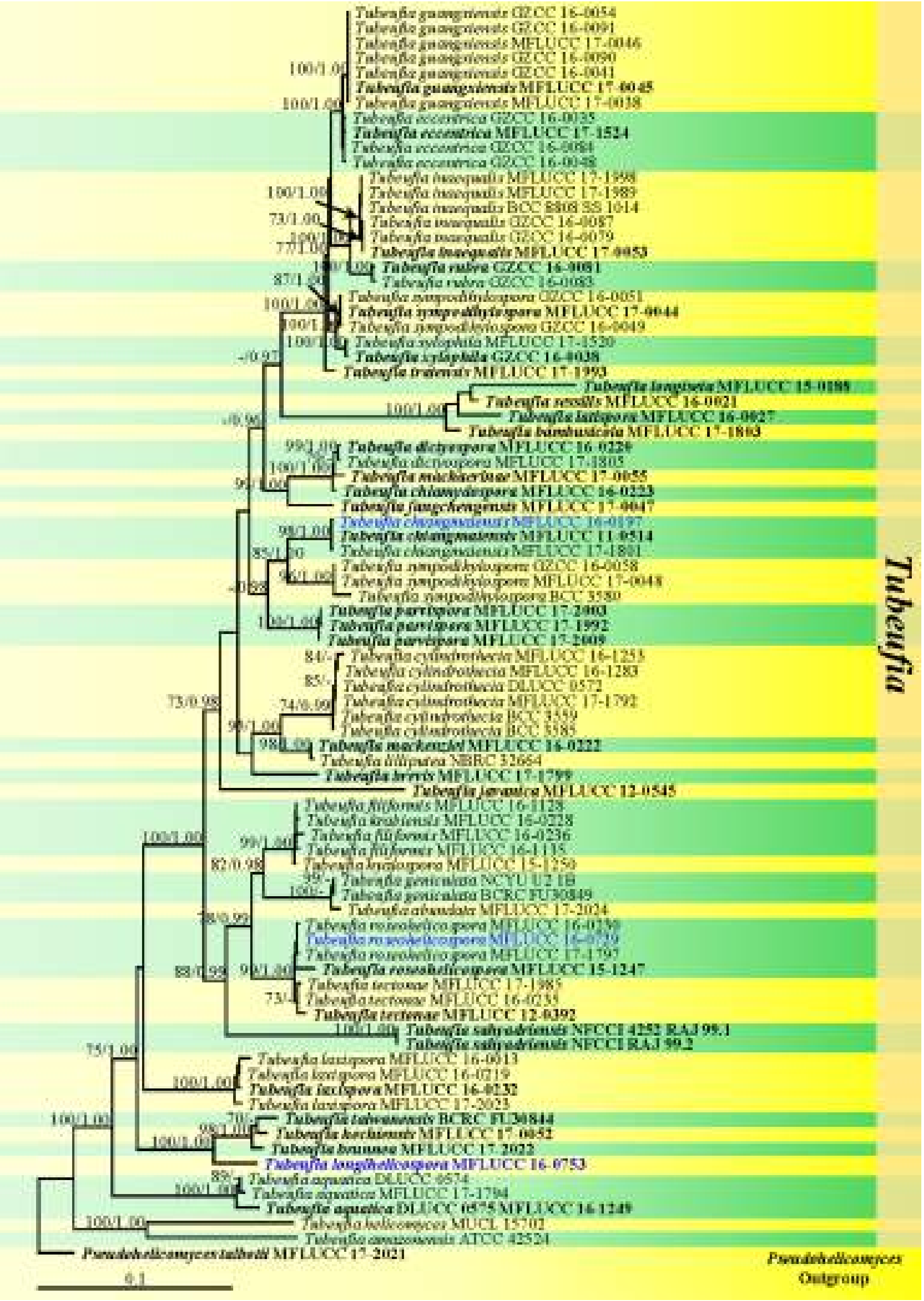


Fig. 97 Maximum likelihood phylogenetic tree based on a combined LSU, ITS and TEF1-α sequence dataset of *Tubeufia* taxa and related genera in *Tubeufiaceae*. Eighty-four strains are included in the combined analyses which comprise a total of 2395 characters. *Pseudohelicomyces talbotii* (MFLUCC 17-2021) is selected as the outgroup taxon. The best RAxML tree with a final likelihood value of − 11543.960875 is presented. RAxML analysis yielded 680 distinct alignment patterns and 15.58% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.238955, C = 0.251270, G = 0.256785, T = 0.229079, with substitution rates AC = 0.670086, AG = 4.164732, AT = 3.398524, CG = 0.528840, CT = 7.628422, GT = 1.000000; gamma distribution shape parameter alpha = 0.148685. Bootstrap support values for maximum likelihood (MLBS, left) equal to or greater than 70% is given above the nodes. Bayesian posterior probabilities (BYPP, right) equal to or greater than 0.95 are given above the nodes. Ex-type strains are in bold and newly generated sequences are in blue

indicates that our strain MFLUCC 16-0721 is related to *T. roseohelicospora* isolates (MFLUCC 15-1247, MFLUCC 17-1797 and MFLUCC 17-2024) with 99% MLBS, 1.00 BYPP support (Fig. 97). Furthermore, our taxon also shares similar morphological characters (Fig. 96) with the ex-type strain MFLUCC 15-1247 provided in Hyde et al. (2016). We therefore, identify our taxon as *Tubeufia roseohelicospora* a new record from Chiang Rai Province, Thailand.

Pleosporales*, genus *incertae sedis

Megacapitula J.L. Chen & Tzean

Notes: *Megacapitula* was introduced to accommodate a single species *M. villosa* which was found on an unidentified fallen decayed petiole in Taiwan by Chen and Tzean (1993). There is no sequence data available. The genus is characterized by obclavate or ellipsoidal to obpyriform, darkly pigmented conidia, crowned with densely packed hairy, brown apical appendages (Chen and Tzean 1993; Delgado 2010). Prabhugaonkar and Bhat (2011) later provided ITS sequence for an isolate of *M. villosa* collected from dead fronds of palm *Caryota urens* (*Arecaceae*) in India. Phylogenetic analysis with only ITS sequence data indicated that *M. villosa* (GUFCC 15515) clustered with an unidentified endophyte strain P1802A and basal to other genera of *Pleosporales* (Prabhugaonkar and Bhat 2011). In addition, there are two unpublished sequences of *M. villosa* AL4 and cp053a that are available in GenBank databases but no morphological descriptions. In this study, we introduce the new record *Megacapitula villosa* which was isolated from submerged decaying wood in a small freshwater stream in Thailand and provide an updated phylogenetic tree for *Megacapitula* (Fig. 100).

Megacapitula villosa J.L. Chen & Tzean, Mycol. Res. 97(3): 347 (1993)

Index Fungorum number: IF359484; *Facesoffungi number*: FoF 09196; Figs. 98, 99

Saprobic on submerged decaying wood. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Mycelium* superficial, partly immerged, composed of a loose network of repent, septate, branched, hyaline to light brown hyphae connected with conidia. *Colonies* on natural substrate effuse, solitary, dark brown to black. *Conidiophores* reduce to conidiogenous cells. *Conidiogenous cells* monoblastic, semi-macronematous, integrated, terminal or intercalary on mycelial extensions, branched, almost sessile. *Conidia* 139–321.5 × 42.5–94 µm ($\bar{x}$ = 231 × 77 µm, n = 15), holoblastic, solitary, scattered, oblong to ovoid, obclavate, ellipsoidal or obpyriform, internally with bundles of narrow cylindrical hyphae, together emerging as brown apical appendages from the top, disappearing when dry, faintly septate, dark brown to black, smooth-walled.

Culture characteristics: Conidia germinating on malt extract agar (MEA) within 12 h. Colonies growing on MEA, reaching 18 mm in 2 weeks at 28 °C, low convex, round with scalloped from middle to margin, radiating, slightly wavy, greyish brown to dark brown in surface, dark brown to black in reverse. Mycelium superficial and partly immersed, branched, septate, with hyaline to dark brown, pigmented verrucose, rough-walled, conidia produced on mycelium in culture at 45 days, 117–314 × 48–91 µm ($\bar{x}$ = 213 × 70 µm, n = 10), oblong to ovoid, obclavate, ellipsoidal or obpyriform, muriform, internally with bundles of narrow of cylindrical hyphal appendages emerging from the top, faintly septate, dark brown to black, smooth-walled.

Material examined: THAILAND, Chanthaburi Province, Laem Sing, on submerged decaying wood in a small freshwater stream, 7 July 2015, S. Boonmee, LS03 (MFLU 19-0257, ***new geographical record***), living culture, MFLUCC 16-1231.

GenBank numbers: ITS = MZ538513, LSU = MZ538547, TEF1-α = MZ567115.

Notes: *Megacapitula* comprises a single species *M. villosa* as the type species (Wijayawardene et al. 2020; Index Fungorum 2021). Our new collection is a typical of *Megacapitula*, and it shares similar conidial morphology to *Megacapitula villosa* (PPH17E: ex-type species) from Taiwan (Chen and Tzean 1993), and strain GUFCC 15515 from India (Prabhugaonkar and Bhat 2011). Phylogenetic analysis of a combined LSU and ITS sequence dataset showed that our newly obtained strain MFLUCC 16-1231 clustered among *Megacapitula villosa* strains (AL4, cp053a), and basal to unidentified endophytic and saprobic strains with 100% MLBS and 1.00 BYPP support (Fig. 100). Comparison of ITS sequences showed that *Megacapitula villosa* (MFLUCC 16-1231) has 100% similarity with strain GUFCC 15,515. Two unidentified morphological strains AL4 and cp053a have only 1/459 (0.21%) base pair different from our taxon. Therefore, we identify our collection as *M. villosa* isolated from submerged decaying wood in a small freshwater stream and it is reported here as a new geographical record from Thailand (Figs. 98 and 99). *Megacapitula villosa* is likely to comprise more than one species and may represent a distinct family.

Eurotiomycetes O.E. Erikss. & Winka

Chaetothyriales M.E. Barr

Notes: *Chaetothyriales* was introduced by Barr (1987) based on the presence of periphysoids (apical paraphyses) in the ascomata and eight families were accepted in the order viz. *Chaetothyriaceae*, *Coccodiniaceae*, *Herpotrichiellaceae*, *Metacapnodiaceae*, *Microtheliopsidaceae*, *Pyrenotrichaceae*, *Strigulaceae* and *Trichopeltidaceae*. The

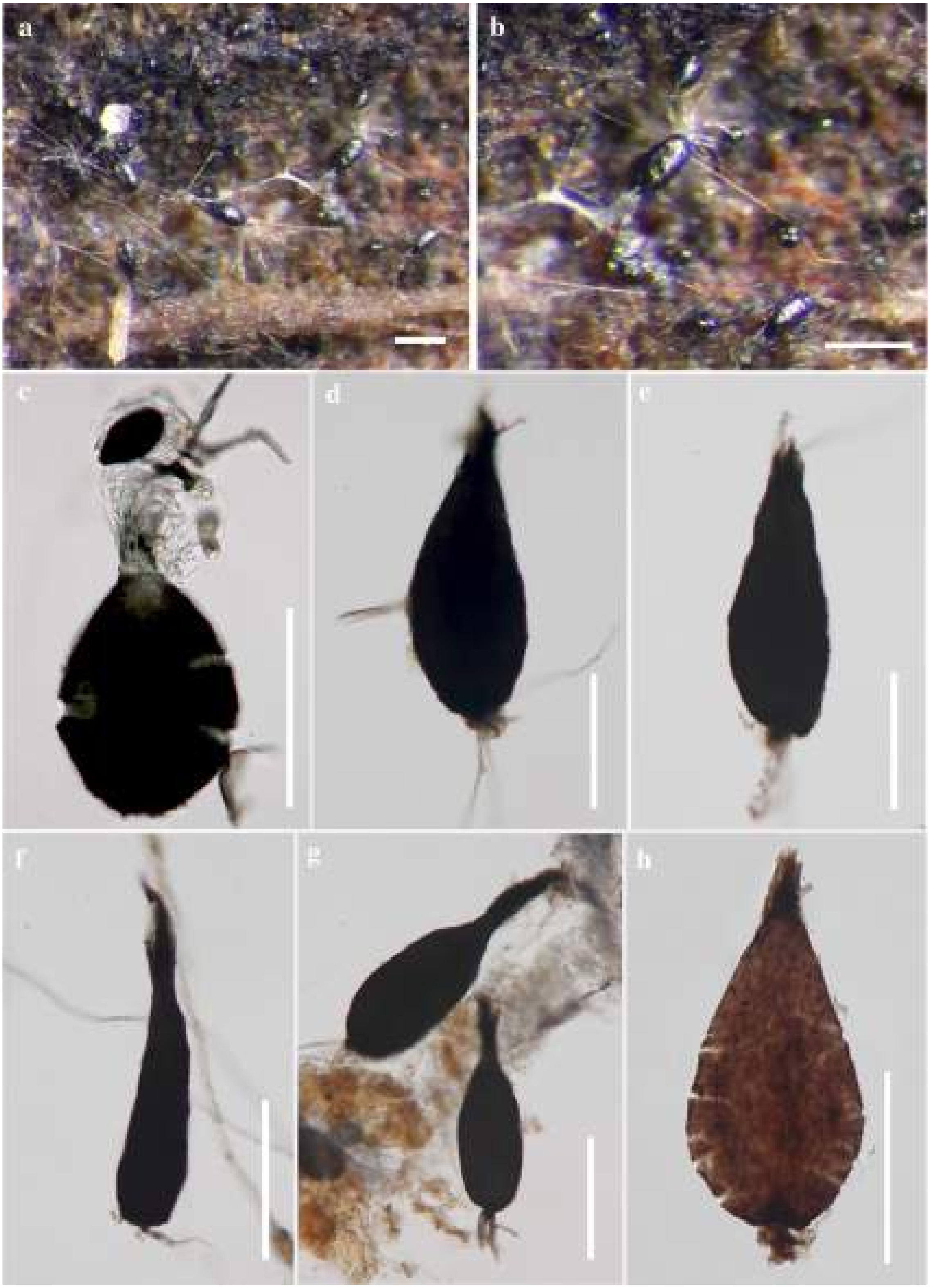


Fig. 98 ***Megacapitula villosa*** (MFLU 19-0257, ***new geographical record***). **a**, **b** Appearance of conidia with hyphal-like appendages and habit on wood substrate. **c** Immature conidium with hyphal-like appendages. **d**–**g** Mature conidia with apical hyphal-like appendages. **h** Conidium changed to brown in lactoglycerol and composed of compressed prosenchyma cells. Scale bars: **a**, **b** = 200 µm, **c**–**h** = 100 µm

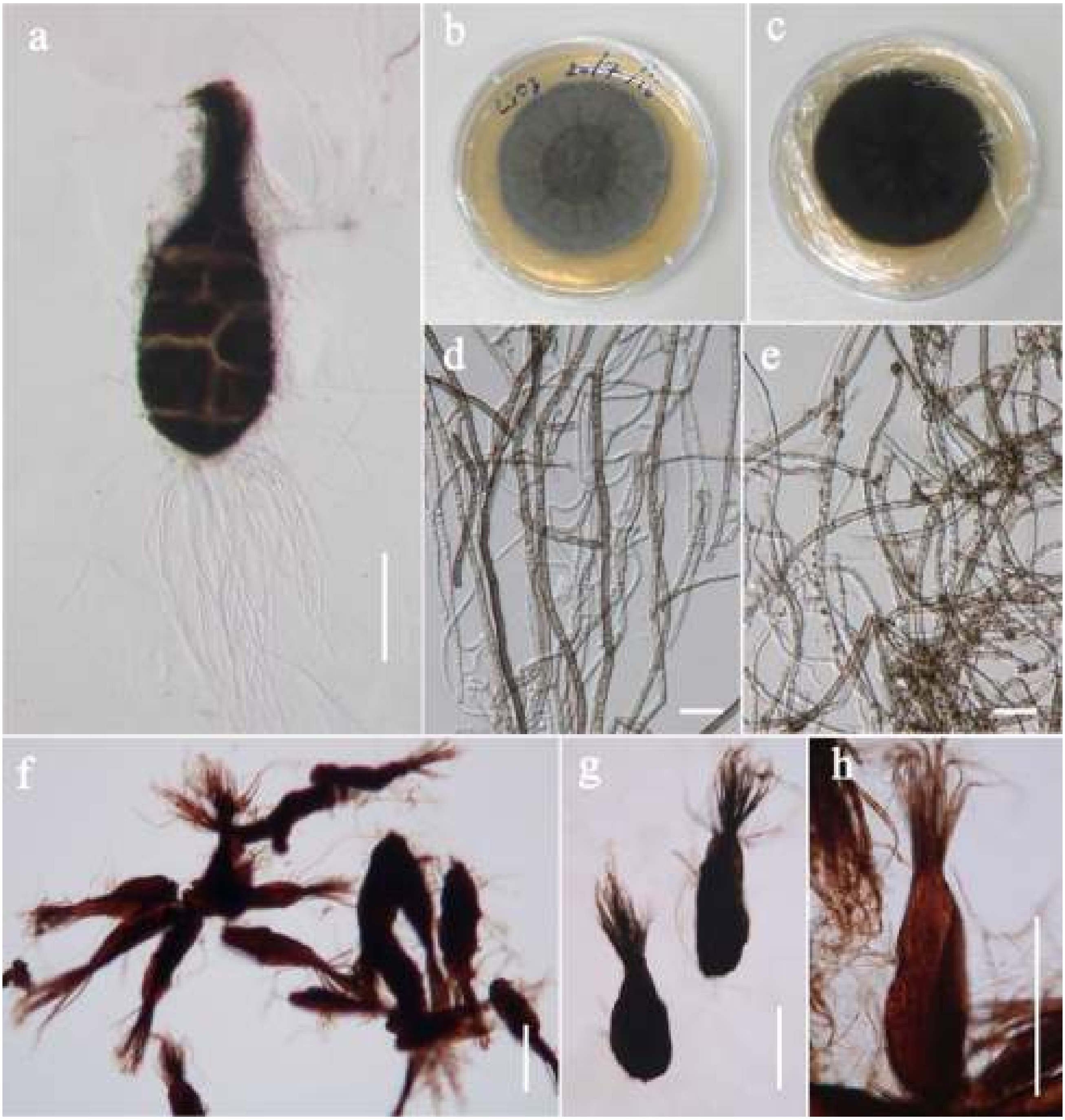


Fig. 99 ***Megacapitula villosa*** sporulated in culture (MFLUCC 16-1231). **a** Germinated conidium with germ tubes surrounded. **b**, **c** Cultures on MEA after 1 month. **d**, **e** Mycelium development in culture. **f**–**h** Conidia. Scale bars: **a**, **f**–**h** = 100 μm, **d**, **e** = 10 μm

latest classification of Wijayawardene et al. (2020), placed ten families in the order wherein *Strelitzianaceae* was synonymized as *Trichomeriaceae*, and *Paracladophialophoraceae* was added. Members of *Chaetothyriales* exhibit complex ecological variation and are common in tropical and temperate ecosystems (Chomnunti et al. 2012; Réblová et al. 2013; De Hoog 2014; Liu et al. 2015b; Hongsanan et al. 2016; Hyde et al. 2016; Teixeira et al. 2017; Dong et al. 2018).

Herpotrichiellaceae Munk

Notes: Munk (1953) established *Herpotrichiellaceae* that includes loculoascomycetes with small, superficial, inconspicuous, setose ascomata, bitunicate asci with a thickened

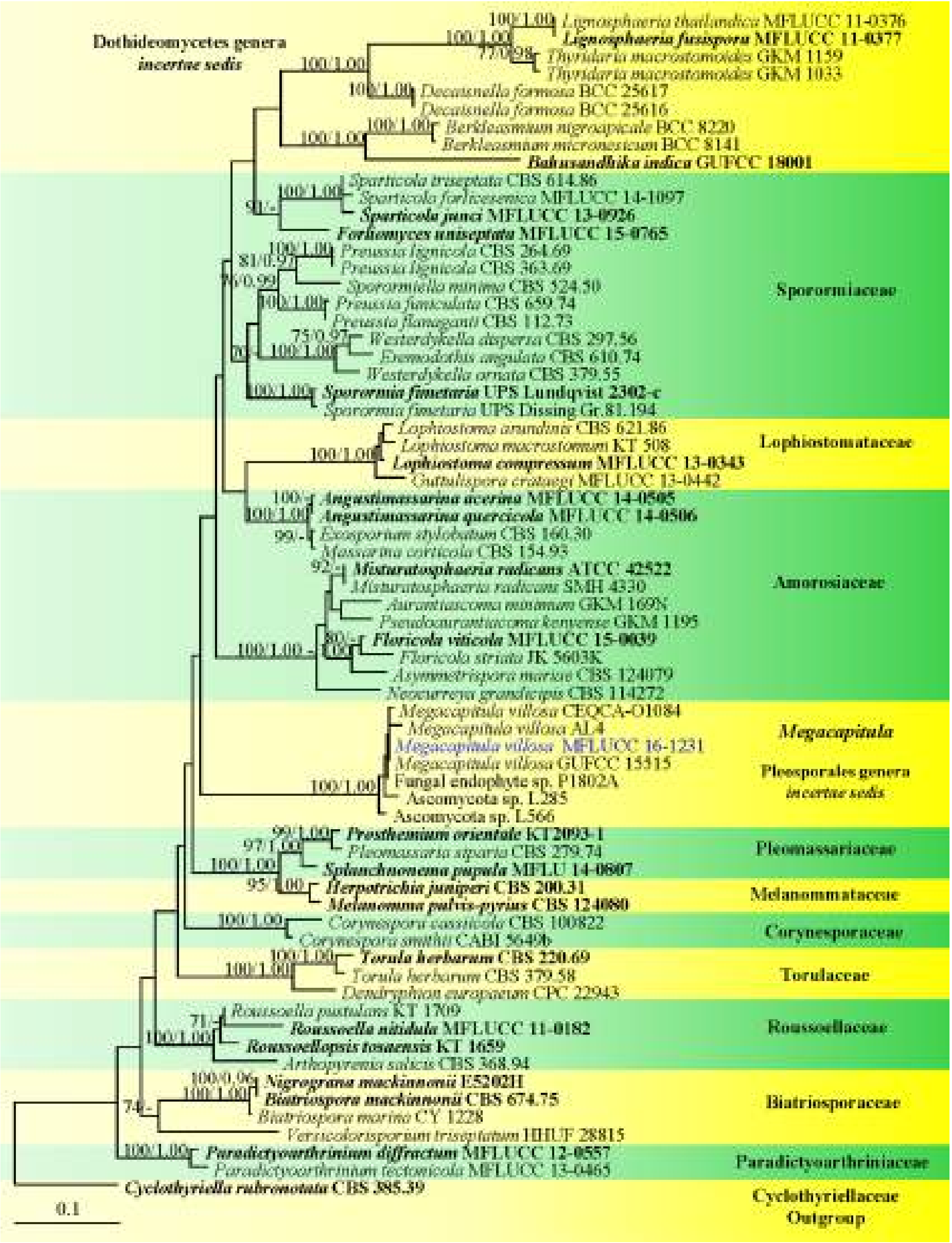


Fig. 100 Maximum likelihood phylogenetic tree based on a combined LSU and ITS sequence dataset of *Megacapitula* taxa and related families in *Pleosporales*. Sixty-seven strains are included in the combined analyses which comprise a total of 1456 characters. *Cyclothyriella rubronotata* CBS 385.39 is selected as the outgroup taxon. The best RAxML tree with a final likelihood value of − 12939.878192 is presented. RAxML analysis yielded 723 distinct alignment patterns and 29.63% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.242721, C = 0.238518, G = 0.291320, T = 0.227442, with substitution rates AC = 1.943333, AG = 2.988826, AT = 2.324598, CG = 1.416039, CT = 8.575259, GT = 1.000000; gamma distribution shape parameter alpha = 0.245601. Bootstrap support values for maximum likelihood (MLBS, left) equal to or greater than 70% is given above the nodes. Bayesian posterior probabilities (BYPP, right) equal to or greater than 0.95 are given above the nodes. Ex-type strains are in bold and newly generated sequence is in blue

endotunica and greenish-grey to brown, septate ascospores. The genera *Beriesiella, Capronia, Dictyotrichiella, Didymotrichiella* and *Herpotrichiella* were included by Munk (1953) in *Herpotrichiellaceae*. *Acanthostigmella* and *Polytrichiella* were added by Barr (1972, 1977). In the latest outline of fungal classification of Wijayawardene et al. (2020), 16 genera: *Aculeata*, *Brycekendrickomyces*, *Capronia*, *Cladophialophora*, *Exophiala*, *Fonsecaea*, *Marinophialophora*, *Melanoctona*, *Metulocladosporiella*, *Minimelanolocus*, *Phialophora*, *Pleomelogramma*, *Rhinocladiella*, *Sorocybe*, *Thysanorea* and *Veronaea* were placed in the family. Members of *Herpotrichiellaceae* have a cosmopolitan distribution and are often found in extreme environments. Most species are saprobic in nature, others are opportunistic human and animal pathogens (Müller et al. 1987; Braun and Feiler 1995; Haase et al. 1999; Crous et al. 2007).

Cladophialophora Borelli

Notes: *Cladophialophora*, typified by *C. carrionii* (Trejos) de Hoog, Kwon-Chung & McGinnis (= *C. ajelloi* Borelli), was introduced by Borelli (1980) to accommodate species exhibiting a cladosporium-like form of sporulation and phialophora-like conidiogenous cells (Borelli 1980; Badali et al. 2008; Bensch et al. 2012). *Cladophialophora* is characterized by 1-celled, globose to elongate, dry conidia arising through blastic, acropetal conidiogenesis, and arranged in branched chains, as melanized conidia with inconspicuous scars (Borelli 1980; Ho et al. 1999; De Hoog et al. 2000; Badali et al. 2008). Thirty-eight species constitute *Cladophialophora* and based on phylogenetic analysis, they are polyphyletic within *Chaetothyriales*. The generic type, *C. carrionii* and most species of this genus belong in *Herpotrichiellaceae*, but a few species are related to other chaetothyrialean families, such as *Epibryaceae* (e.g., *C. humicola, C. minutissima*) and *Trichomeriaceae* (*C. modesta*) (Gueidan et al. 2008, 2014). The genus occurs as opportunistic or pathogens of plants, animals and humans, and even as saprobes and endophytes (De Hoog et al. 2007; Crous et al. 2007; Badali et al. 2008; Feng et al. 2014).

Cladophialophora abundans P. Feng, V.A. Vicente, Najafz., van den Ende, Stielow, Badali, Boeger & de Hoog, Mycol. Progr. 13(2): 386 (2013) [2014]

Index Fungorum number: IF803489; *Facesoffungi number*: FoF 09157; Fig. 101

Saprobic on submerged decaying wood in a freshwater. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Hyphae* 2.5–4.5 µm wide, irregularly septate, straight or bent, smooth, thin-walled, hyaline to pale brown, guttulate, branched, with formation of hyphal strands, and differentiated ellipsoidal to cylindrical conidiophores with conidial chains. *Conidiophores* semi-macronematous, pale olivaceous to brown, septate, oblong to cylindrical. *Conidiogenous cells* holoblastic, mono- or polyblastic, terminal or intercalary. *Conidial chains* forming laterally or terminally on undifferentiated hyphae, with profuse, strongly coherent conidial chains. *Conidia* 4.5–7 × 3.5–5.5 µm ($\bar{x}$ = 5.9 × 4.5 µm, n = 30), pale olivaceous to brown, smooth and thin-walled, globose, ovoidal and ellipsoidal, aseptate, guttulate; conidial scars slightly pigmented. Chlamydospores and yeast cells absent.

Culture characteristics: Colonies growing on MEA, reaching 30–35 mm in 2 weeks at 25 °C. Mycelia superficial, irregularly circular, with entire to undulate margin, flat, smooth, from above pale brown, from below dark brown. Sporulation produced in culture within 2 weeks.

Material examined: THAILAND, Phuket Province, Thalang District, Mai Khao, on submerged decaying wood in a mangrove habitat, 5 May 2019, M.S. Calabon, 0506HY3 (MFLU 21-0118, ***new geographical record***), living culture, MFLUCC 21-0105.

GenBank numbers: ITS = MT864354, LSU = MT860432.

Notes: *Cladophialophora abundans* was introduced by Feng et al. (2014) to accommodate cladophialophora-like isolates from a Brazilian mangrove environment. The species was isolated from the thorn of *Dioscorea multiflora* and muddy burrows of the mangrove-land crab *(Ucides cordatus)* (Pie et al. 2011; Feng et al. 2014). The phylogenetic analysis of a combined LSU and ITS sequence data shows that *C. abundans* (MFLUCC 21-0105) clusters with the ex-type strain of *C. abundans* (CBS 126736) with 100% MLBS, 100% MPBS, 1.00 BYPP support (Fig. 103). *Cladophialophora abundans* (MFLUCC 21-0105; Fig. 101) resembles *C. abundans* when it comes to the shapes and sizes of conidia (4.5–7 × 3.5–5.5 µm vs. 4.5–6 × 2–3.5 µm) and hyphal width (2.5–4.5 µm vs. 2–3.5 µm). There are no base pair differences of the ITS nucleotides which indicates that the new strain is *C. abundans* (Jeewon and Hyde 2016). Thus, a record of *C. abundans* from Thailand is reported.

Cladophialophora aquatica M.S. Calabon, Boonmee, E.B.G. Jones & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF558644; *Facesoffungi number*: FoF 09153; Fig. 102

Etymology: Name reflects the aquatic habitat from where this species was collected.

Holotype: MFLU 21-0119

Saprobic on submerged decaying wood in a freshwater. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Hyphae* 1.2–4 µm wide, septate, hyaline to lightly pigmented. *Chlamydospores* 8–13.5 × 3.5–9 µm ($\bar{x}$ = 10.5–6 µm, n = 30), numerous, mostly in chains, intercalary or solitary, globose to subglobose, smooth, olivaceous brown to dark brown.

Culture characteristics: Colonies growing on MEA, reaching 20–30 mm in 2 weeks at 25 °C. Mycelia superficial,

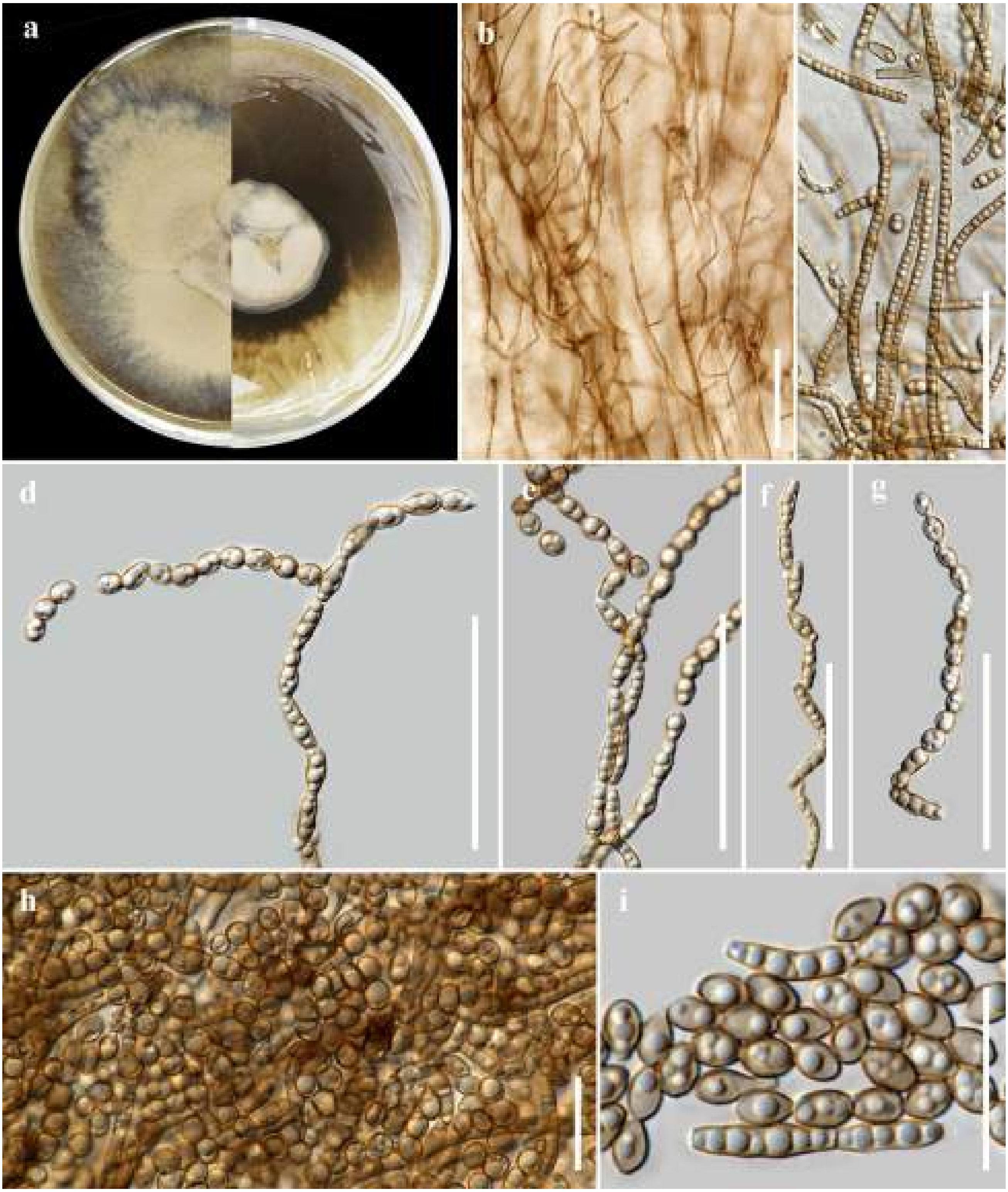


Fig. 101 ***Cladophialophora abundans*** (MFLUCC 21-0105, ***new geographical record***). **a** Culture on MEA from surface and reverse. **b**, **c** Long strongly coherent conidial chains. **d**–**g** Conidiophores and conidia. **h**, **i** Conidia. Scale bars: **b** = 100 μm, **c**–**g** = 50 μm, **h**, **i** = 20 μm

Fig. 102 ***Cladophialophora aquatica*** (MFLUCC 21-0108, **ex-type**). **a** Culture on MEA from surface and reverse. **b**–**m** Chlamydospores. Scale bars: **b** = 300 µm, **c**, **d** = 50 µm, **e**–**m** = 20 µm

circular, with entire margin, flat, smooth, from above gray, from below dark brown. Chlamydospores produced in culture and induced with plant tissues within 30 days.

Material examined: THAILAND, Chiang Mai Province, Mushroom Research Center, on submerged decaying wood in a freshwater habitat, 11 February 2019, M.S. Calabon, MC03 (MFLU 21-0119, **holotype**), ex-type living culture, MFLUCC 21-0108.

GenBank numbers: ITS = MT864355, LSU = MT860433.

Notes: Unlike other species of *Cladophialophora*, *C. aquatica* did not produce conidial chains in culture but chlamydospores were prominent and numerous (Fig. 102). One strain of *Cladophialophora immunda* CBS 109797 and *C. tortuosa* produced chlamydospores in culture infrequently (Badali et al. 2008; Obase et al. 2016). In the phylogenetic analysis of LSU and ITS sequence data, *Cladophialophora aquatica* clustered with *C. exuberans*, *C. matsushimae* and *C. mycetomatis* with only 1.00 BYPP support (Fig. 103). *Cladophialphora matsushimae* differs in having conidial chains that resembles septate vegetative hyphae and subcylindrical conidia, ramoconidia, and microconidia (Koukol 2010). *Cladophialphora exuberans* and *C. mycetomatis* differ from *C. aquatica* in having conidiogenous cells that sympodially proliferate with a few conidiogenous loci, and the presence of ramoconidia and conidia (Badali et al. 2008; Nascimento et al. 2017).

Eurotiales G.W. Martin ex Benny & Kimbr.

Notes: We follow the latest treatment and updated accounts of *Eurotiales* in Hyde et al. (2019).

Aspergillaceae Link (= *Monascaceae* J. Schröt.)

Notes: We follow the latest treatment and updated accounts of *Aspergillaceae* in Hyde et al. (2019).

Aspergillus P. Micheli ex Haller.

Notes: *Aspergillus* is the largest genus in *Aspergillaceae* contains more than 700 accepted species and divided into 25 sections (Houbraken et al. 2020; Species Fungorum 2021). *Aspergillus* section *Sparsi* is typified by *A. sparsus* and comprised four species were isolated from soil substrate (Raper and Thom 1944). Members of *Aspergillus* section *Sparsi* are commonly found in soil and their characterized by produced large globose conidia and irregular split with age (Smith 1956; Mares et al. 2008; Chen et al. 2016). Most species in this section are identified by pigment ranging from light grey to olive-buff (Varga et al. 2010). We follow the latest treatment and update accounts of *Aspergillus* in (Houbraken et al. 2020).

Aspergillus lannaensis N. Suwannarach, S. Khuna & S. Lumyong, ***sp. nov.***

MycoBank number: MB838058; *Facesoffungi number*: FoF 09955; Fig. 104

Etymology: "*lannaensis*" referring to Lanna, the old name of the region including Chiang Mai Province, northern Thailand, where soil containing the new fungus was collected.

Holotype: SDBR-CMUO8

Culture characteristics: *Colonies* growing after 7 days at 25 °C on the following agar: CYA 45–48 mm, MEA 46–49 mm, and CREA 41–43 mm. Slow growth was observed on CYA, MEA, and CREA are 18–20, 12–14 and 13–15 mm, respectively after 7 days at 37 °C. On all agar media the colonies first white, gradually becoming light yellow from entre outwards, then conidiophores are produced, conidial areas are light yellow to olive drab on MEA and CREA; light yellow to dark yellow on CYA. Reverse yellowish-brown on CYA and CREA; light yellow on MEA. On CREA thin colonies with poor sporulation and no acid production. *Conidiophores* produced abundantly on MEA. *Conidial heads* 35–137 µm diam., globose, light yellow when young, olive drab in age, radiate, commonly splitting into columns with age. *Stipes* 190–800 × 7–15 µm wide near vesicle, short, smooth, thick walled, hyaline (light yellowish-brown pigment on upper portion near vesicle). *Vesicles* globose or nearly so, 14–46 µm in diam.; uni-seriate. *Phialides* 8–15 × 2–3 µm, pyriform and covering the entire surface of the vesicle. *Conidia* 3–6 × 2–3 µm wide, oval or ellipsoidal, light yellow, with smooth-walled, and arranged in long chains.

Material examined: THAILAND, Chiang Mai Province, Mae Wang District, (18°36′46″ N 98°46′30″ E), isolated from soil of longan orchard, 8 August 2017, S. Khuna, dried culture: SDBR-CMUO8, **holotype**; Chiang Mai Province, Mae Wang District, (18°36′46″ N 98°46′30″ E), isolated from soil of longan orchard, 8 August 2017, S. Khuna, living culture, SDBR-CMUO6.

GenBank numbers: SDBR-CMUO6: *Cam* MW219780, *BenA* = MW219782, RPB2 = MW219784; SDBR-CMUO8: *Cam* = MW219781, *BenA* = MW219783, RPB2 = MW219785.

Notes: A concatenated phylogenetic tree (*cam*, *benA*, and RPB2) revealed that *Aspergillus lannaensis* forms distinct lineages sister to *A. funiculosus* with 100% MLBS, 1.00 BYPP support (Fig. 105). However, *A. lannaensis* can be distinguished from *A. funiculosus* in shapes and sizes of conidia and phialides (Smith 1956). Therefore, we introduce a new species *Aspergillus lannaensis* (Fig. 104) based on morphology coupled with phylogenetic evidence.

Sclerococcales Réblová, Unter. & W. Gams

Notes: Réblová et al. (2017) introduced *Sclerococcales* with *Sclerococcum* Fr. as type genus. *Dactylosporaceae* (= *Sclerococcaceae*) constitutes the order with five known genera: *Cylindroconidiis*, *Fusichalara*, *Longimultiseptata*, *Rhopalophora* and *Sclerococcum* (= *Dactylospora*) (Wijayawardene et al. 2020). *Sclerococcales* comprises ca. 80 species that dwell in terrestrial and aquatic environments as wood

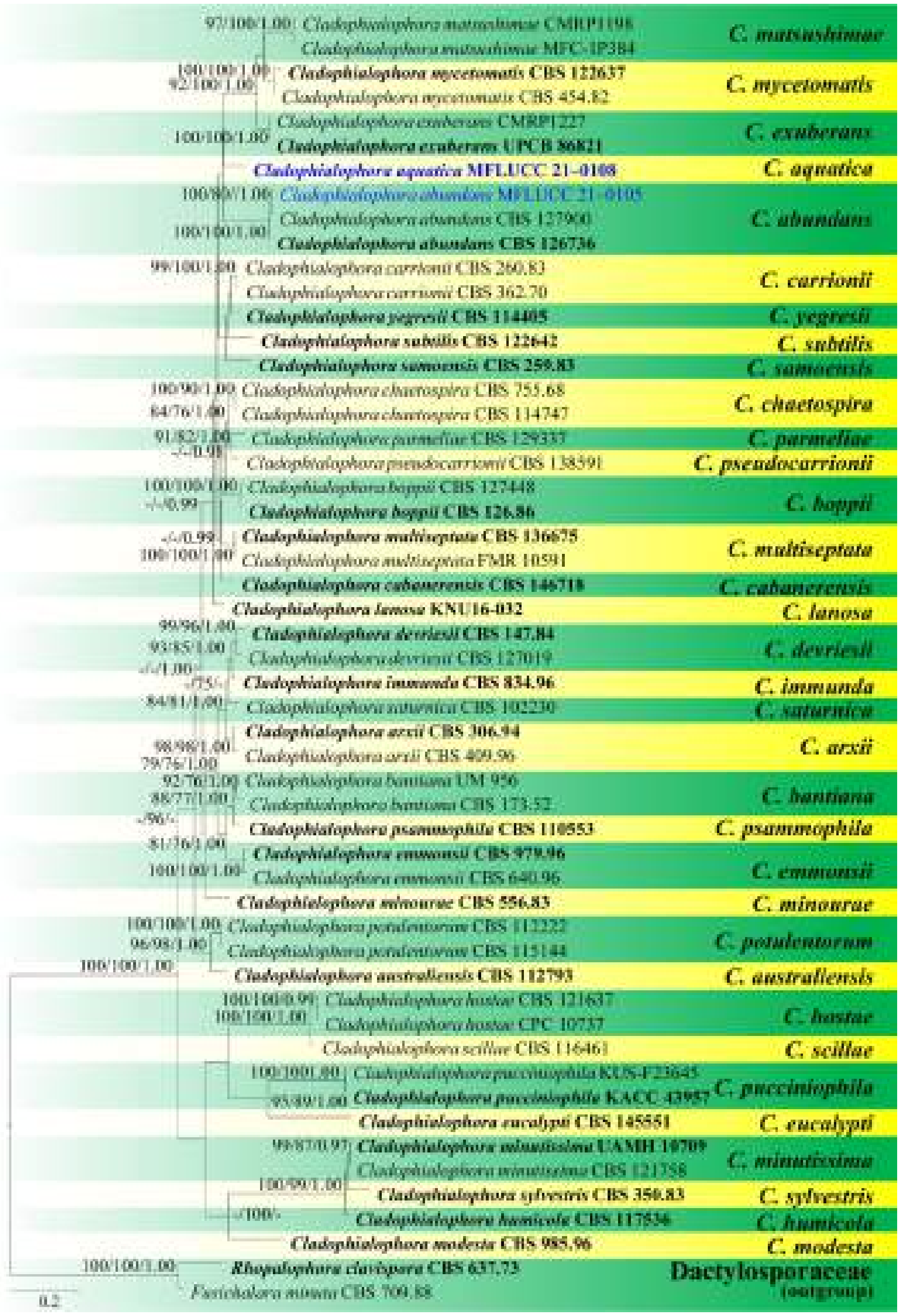


Fig. 103 Phylogram generated from maximum likelihood analysis based on combined LSU and ITS sequence data representing the species of *Cladophialophora*. Related sequences are taken from Kiyuna et al. (2018). *Rhopalophora clavispora* (CBS 637.73) and *Fusichalara minuta* (CBS 709.88) were used as the outgroup taxa. Fifty-three taxa are included in the combined analyses which comprised 1041 characters (502 characters for LSU, 539 characters for ITS) after alignment. The best scoring RAxML tree with a final likelihood value of − 9519.130038 is presented. The matrix had 524 distinct alignment patterns, with 16.53% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.236745, C = 0.249453, G = 0.269107, T = 0.244695; substitution rates: AC = 1.891141, AG = 3.179450, AT = 1.427526, CG = 0.913317, CT = 6.628918, GT = 1.000000; gamma distribution shape parameter α = 0.260996. The MP analysis resulted a single most parsimonious tree (TL = 1789, CI = 0.455, RI = 0.710, RC = 0.323, HI = 0.545). Bootstrap support values for MLBS and MPBS equal to or greater than 75% and BYPP equal to or greater than 0.95 are given above the nodes. Ex-type strains are in bold and newly generated sequences are in blue

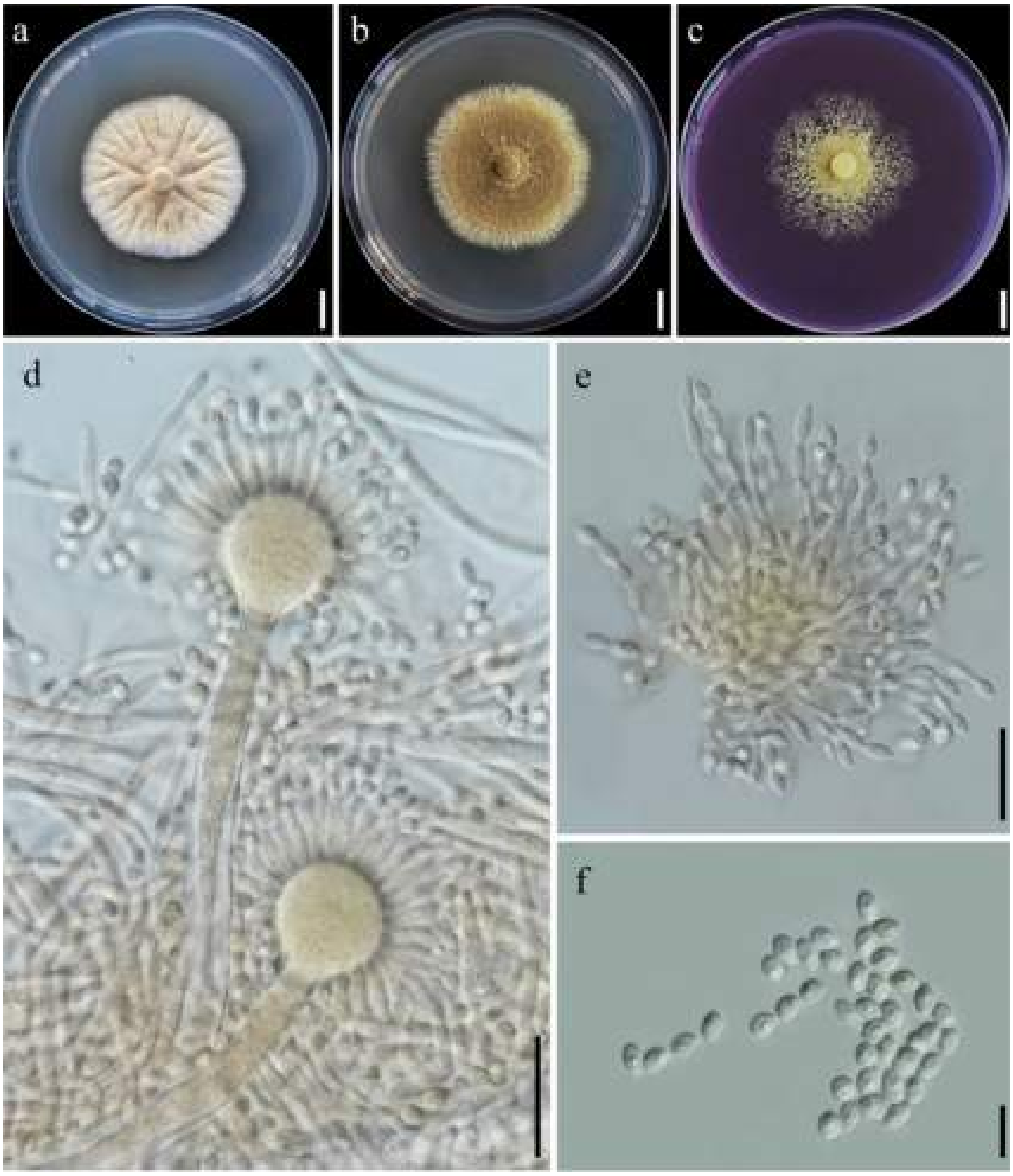


Fig. 104 ***Aspergillus lannaensis*** (SDBR-CMUO8, **holotype**). Colonies incubated at 25 °C for 7 days. **a** Colony on CYA. **b** Colony on MEA. **c** Colony on CREA. **d** Conidiophores. **e** Conidia arranged in long chains. **f** Oval or ellipsoidal conidia. Scale bars: **a**–**c** = 10 mm, **d**, **e** = 20 μm, **f** = 10 μm

saprobes, lichenized species on lichens, non-lichenized fungi or leafy liverworts, or associated with beetles as a part of intestinal microbiota (Diederich et al. 2018; Olariaga et al. 2019).

Dactylosporaceae Bellem. & Hafellner (= *Sclerococcaceae* Réblová, Unter. & W. Gams)

Notes: *Dactylosporaceae* was established by Bellemère and Hafellner (1982) with various placements based on morphology and phylogenetic studies: Eurotiomycetes (Schoch et al. 2009b; Diederich et al. 2013; Pang et al. 2014; Ekanayaka et al. 2019b; Wijayawardene et al. 2020), Lecanoromycetes (Miadlikowska et al. 2014; Pino-Bodas et al. 2017), Pezizomycotina *incertae sedis* (Jaklitsch et al. 2016) and Eurotiomycetes *incertae sedis* (Wijayawardene et al. 2020). Réblová et al. (2017) introduced *Sclerococcaceae* as type family of *Sclerococcales* but Diederich et al. (2018)

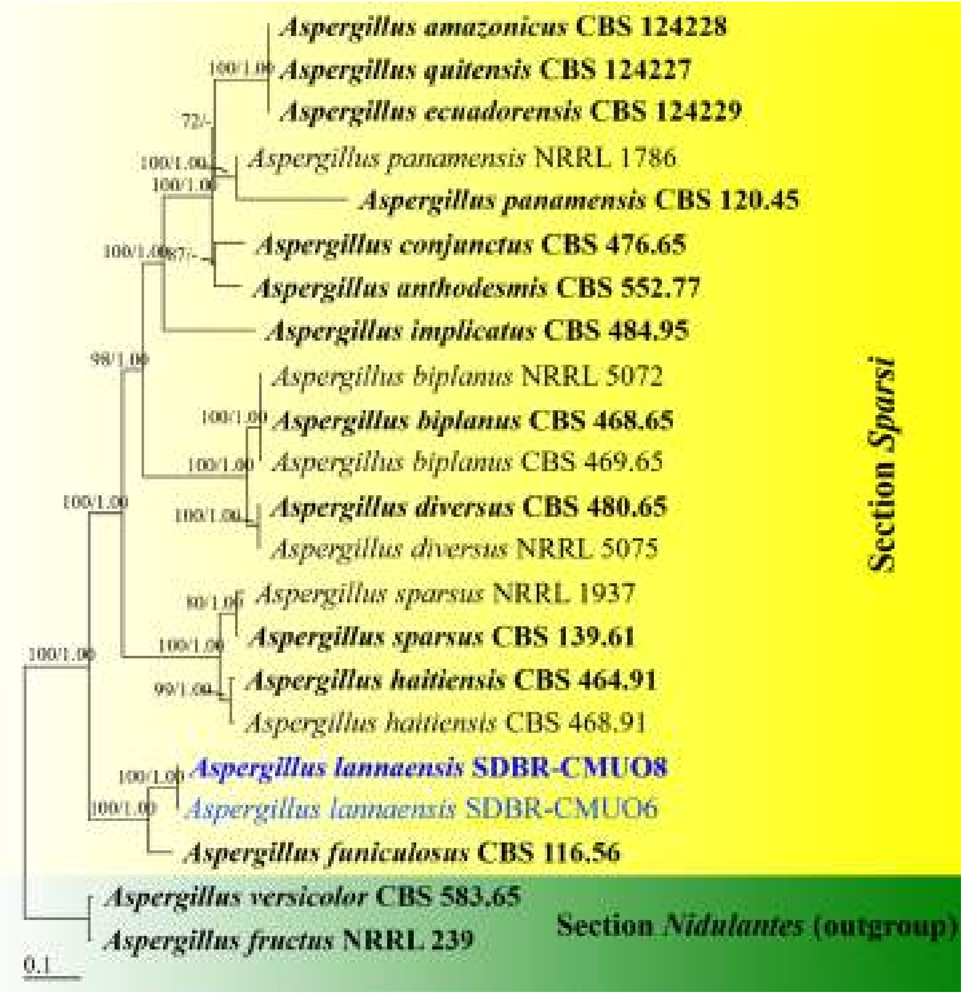


Fig. 105 Phylogenetic tree derived from maximum likelihood analysis of a combined *Cam*, *BenA* and *RPB2* genes of 22 sequences and the aligned dataset was comprised of 2360 characters including gaps (*Cam*: 1–792, *BenA*: 793–1310 and RPB2: 1311–2360). The average standard deviation of the split frequencies of the BI analysis was 0.004276. A best scoring RAxML tree was established with a final ML optimization likelihood value of – 13462.8650. The matrix had 1055 distinct alignment patterns with 21.67% undetermined characters or gaps. Estimated base frequencies were found to be: A = 0.2500, C = 0.2468, G = 0.2390, T = 0.2642; substitution rates AC = 1.0520, AG = 3.4446, AT = 1.0037, CG = 0.6646, CT = 5.3732, GT = 1.0000; proportion of invariable sites = 0.1320 and gamma distribution = 0.6870. *Aspergillus fructus* NRRL 239 and *Aspergillus versicolor* CBS 583.65 were used as outgroup. Numbers above branches are the bootstrap statistics percentages (left) and Bayesian posterior probabilities (right). Branches with bootstrap values equal to or greater than 70% are shown at each branch and the bar represents 0.1 substitutions per nucleotide position. Hyphen (-) represents support values equal to or greater than 70%/0.95. Ex-type strains are in bold and newly generated sequences are in blue

reinstated *Dactylosporaceae* to replace *Sclerococcaceae*. Five genera are included in the family and species are mostly lignicolous, lichenicolous or associated with beetles as a part of intestinal microbiota (Pang et al. 2014; Jaklitsch et al. 2016; Réblová et al. 2017; Wijayawardene et al. 2020).

Pseudobactrodesmium H. Zhang, W. Dong & K.D. Hyde

Notes: *Pseudobactrodesmium* was introduced by Dong et al. (2020a) with *P. longisporum* (≡ *Bactrodesmium longisporum*) as the type species. *Pseudobactrodesmium aquaticum, P. chiangmaiensis* and *P. longisporum* were included in the genus. *Pseudobactrodesmium longisporum* was formerly placed in *Bactrodesmium* (Dothideomycetes genera *incertae sedis*), but multigene phylogenetic analysis revealed it was unrelated to *Bactrodesmium* and clustered within *Sclerococcales* (Eurotiomycetes) (Ellis 1976; Pem et al. 2019b; Dong et al. 2020a; Wijayawardene et al. 2020).

Pseudobactrodesmium stilboideum (R. F. Castañeda & G.R.W. Arnold) M.S. Calabon, Boonmee, E.B.G. Jones, K.D. Hyde, ***comb. nov.***

≡ *Bactrodesmium stilboideum* R. F. Castañeda & G. R. W. Arnold, Revta Jardín bot. Nac., Univ. Habana 6(1): 48 (1985)

Fig. 106 ***Pseudobactrodesmium stilboideum*** (MFLU 21-0120). **a** Substrate. **b–e** Synnemata on submerged wood. **f–h** Synnemata and densely branched conidiophores, conidiogenous cells and attached conidia. **i–l** Conidia and mucilaginous cap at the apex. **m** Germinated conidium. **n** Culture on MEA from surface and reverse. Scale bars: **b**, **c** = 500 µm, **d–f** = 200 µm, **g–m** = 50 µm

= *Stigmina longispora* var. *stilboidea* (R.F. Castañeda & G.R.W. Arnold) J. Mena & Mercado, Reporte de Investigacion del Instituto de Ecología y Sistemática 17: 10(1987).

Index Fungorum number: IF558643; *Facesoffungi number*: FoF 09154; Fig. 106

Saprobic on submerged decaying wood in a freshwater habitat. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Colonies* on natural substrate 415–635 × 14–40.5 µm ($\bar{x}$ = 494.5 × 28 µm, n = 15), synnematous, superficial, effuse, scattered, dark brown to dark olivaceous brown. *Mycelium* mostly immersed, composed of white, septate, branched and guttulate hyphae. *Conidiophores* 15–30 × 2–4 µm ($\bar{x}$ = 25 × 3 µm, n = 15) macronematous, fasciculate, synnematous, compact, erect, subcylindrical, septate, slightly constricted at the septa, unbranched or branched, brown, smooth. *Conidiogenous cells* monoblastic, terminal, discrete, subcylindrical, pale brown, elongating percurrently. *Conidia* 48–65 × 7–8 µm ($\bar{x}$ = 55 × 7.5 µm, n = 50), solitary, dry, subcylindrical to narrowly fusiform, usually straight or slightly curved, euseptate, 9–13-phragmoseptate, thin and smooth-walled, slightly constricted and darker at septa, brown, paler towards both ends, obscurely guttulate, wedge-shaped at basal cell, with tapering apical cells, often enveloped by a hyaline, spherical, thin, mucilaginous cap at the apex, 8–10 µm diam. *Apical cells* elongated, up to 12 µm long, tapering gradually toward apex, hyaline to subhyaline, with subglobose tuberculate ends, secession schizolytic.

Culture characteristics: Conidia germinating on malt extract agar (MEA) within 24 h. Germ tubes produced from the basal and apical cell of conidia. Colonies growing on MEA, reaching 20–25 mm in 2 weeks at 25 °C. Mycelia superficial, circular, with entire margin, flat, smooth, from above white, from below smoke grey.

Material examined: THAILAND, Tak Province, Tha Sing Yang, Ban Mae Ja Wang, on submerged decaying wood in a freshwater river, 17 October 2019, N. Padaruth, CC44 (MFLU 21-0120), living culture, MFLUCC 21-0101.

GenBank numbers: ITS = MT864357, LSU = MT860435.

Notes: Dong et al. (2020a) synonymized *Pseudobactrodesmium stilboideum* under *P. longisporum* but based on the phylogenetic analysis of LSU and ITS sequence dataset (Fig. 107), it did not group with strains of *P. longisporum* but clustered with *P. stilboideum* MHR 18017. The aggregation of conidiophores distinguished the two species wherein *P. stilboideum* has synnematous formation but in *P. longisporum*, it is sporodochial with mononematous, fasciculate conidiophores (Ellis 1976; Castañeda-Ruiz and Arnold 1985; Dong et al. 2020a). Moreover, *P. stilboideum* has shorter and narrower (48–65 × 7–8 µm) and 9–13-septate conidia (Fig. 106), while *P. longisporum* has longer and wider (85–119 × 8–9.5 µm) and 16–21-septate conidia (Ellis 1976). *Pseudobactrodesmium stilboideum* was isolated on decaying unidentified wood and dead leaves of *Calyptronoma plumeriana* and is distributed in Cuba, Puerto Rico, South Africa, Taiwan, Thailand and UK (Ellis 1976; Castañeda-Ruiz and Arnold 1985; Hu et al. 2010a; this study).

Laboulbeniomycetes Engl.

Laboulbeniales Lindau

Notes: see Hyde et al. (2019).

Laboulbeniaceae G. Winter

Notes: see Hyde et al. (2019).

Hydrophilomyces Thaxt.

Notes: This genus includes to date 16 species associated with aquatic beetles. It is characterized by a long "accessory" cell flanking the perithecial venter and by a multicellular axis extending above the insertion of the perithecium. A single sequence is available for species in this genus (Goldmann and Weir 2018).

Hydrophilomyces hydraenae W. Rossi & M. Leonardi, ***sp. nov.***

Index Fungorum number: IF557383; *Facesoffungi number*: FoF 07847; Fig. 108

Etymology: Named after the host insect.

Holotype: FI WR2462

Thallus hyaline or nearly so. Receptacle consisting of 11–12 superposed cells, of which the basal is irregularly rhomboid, the following 2–3 cells, small, each producing laterally an elongate and variably curved buffer cell, the others gradually increasing in length from almost flattened to slightly longer than broad. *Appendage* usually curving outwards and downwards, consisting of 8–10 subequal cells, each separating a small corner cell on the anterior side; these corner cells give rise to short branchlets bearing distally 2–4 elongate antheridia soon displaced by long and slender sterile branchlets, which are repeatedly divided in the distal portion of the appendage. *Perithecial* venter ovoid, relatively short, tapering without abrupt transition to the broad neck; the latter almost isodiametric, up to three times longer than the venter, with an elongate and undistinguished tip ending in rounded apex. Total length from foot to perithecial apex 300–345 µm; length of perithecium 205–250 µm; perithecial venter 35 × 60 µm.

Material examined: USA, CA, Santa Barbara Co., W Camino Cielo (rd.) at Hwy. 154, 590 msl, 34°30.273′ N 119°48.806′ W, edge of a stream in hardwood forest, 19 July 2000, A. Newton and M. Thayer, at the base of the legs of *Hydraena vandykei* Orchymont (Coleoptera, Hydraenidae) (FI WR2462, **holotype**; FI WR2477, paratype).

Notes: The species of *Hydrophilomyces* described so far are 16, of which 8 are reported on Hydraenidae (genera *Ochtebius* and *Limnebius*), the other 8 on Hydrophilidae. These species can be distinguished from *Hydrophilomyces hydraenae* (Fig. 108) by the following characteristics: *H. gracilis*, *H. lumbricoides*, *H. major*, *H. reflexus* and *H. rhynchophorus* (all parasitic on Hyrophilidae) lack any buffer

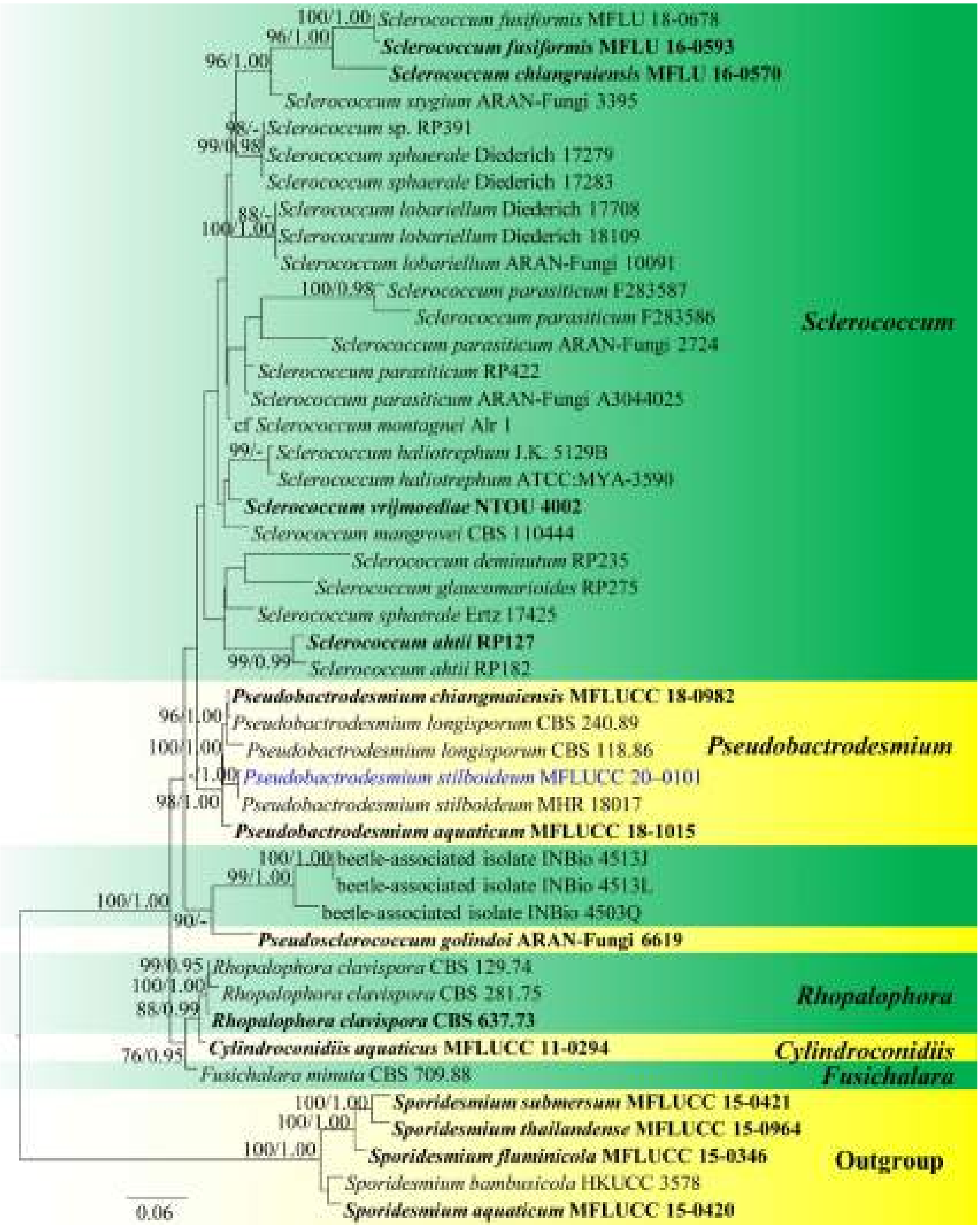


Fig. 107 Phylogenetic tree generated from maximum likelihood (ML) analysis based on combined LSU and ITS sequence data for the species from *Dactylosporaceae*. Five species of *Sporidesmium aquaticum, S. bambusicola, S. fluminicola, S. submersum* and *S. thailandense* (*Sporidesmiaceae*) are used as outgroup taxa. The dataset comprised and 1222 characters after alignment including gaps (LSU = 793 bp, ITS = 429 bp). The RAxML analysis of the combined dataset yielded a best scoring tree with a final ML optimization likelihood value of − 3662.794208. The matrix had 1053 distinct alignment patterns, with 51.86% undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.266384, C = 0.211364, G = 0.273019, T = 0.249233; substitution rates AC = 1.261100, AG = 2.304874, AT = 1.337644, CG = 1.220148, CT = 5.907736, GT = 1.000000; gamma distribution shape parameter α = 0.284689. Support values for maximum likelihood (MLBS) above than 75% and Bayesian posterior probabilities (BYPP) greater than 0.95 are given at the nodes. Ex-type species are in bold and newly generated sequence is in blue

Fig. 108 ***Hydrophilomyces hydraenae*** (FI WR2462, **holotype**). **a** Thallus from the type slide stained with acid fuchsin. **b** Thallus from the paratype slide stained with acid fuchsin. Scale bars: **a**, **b** = 100 µm

cells and have a very elongate receptacle consisting of 20 or more cells; *H. coneglianensis* has the perithecial neck about as long as the venter; *H. arcuatus*, *H. pusillus*, *H. rhytidopus* have the perithecial neck much shorter than the venter; *H. aduncus*, *H. deflexus*, *H. hamatus*, *H. limnebii* have a distinctly curved perithecial neck; *H. atroseptatus* has a stout and tapering appendage, consisting of flattened cells bearing corner cells separated by constricted dark septa from antheridia or sterile branchlets; *H. riberae* has a shorter receptacle and a broader perithecial neck; *H. digitatus* has the receptacle consisting of more or less isodiametric cells, a more elongate perithecial venter, a slenderer and shorter perithecial neck distinctly broadened at the junction with the tapering and truncate tip (Spegazzini 1917; Thaxter 1908; Huldén 1983; Majewski 1994; Santamaria 2003, 2006; Santamaria et al. 2020).

Laboulbenia Mont. & C.P. Robin

Notes: *Laboulbenia* is by far the largest genus among the *Laboulbeniales* with about 650 described species, which represent almost one third of all the known species. Besides the accepted species, several subspecific taxa have also been described as subspecies, varieties and forms. The species of *Laboulbenia* occur on various families of beetles (Coleoptera), but are also found on flies (Diptera), bugs (Hemiptera), ants, (Hymenoptera), termites (Isoptera), cockroaches (Blattodea), crickets (Orthoptera) and mites (Acarina) (Kong et al. 2020). Very few sequences are available, and is still lacking, among many others, are those of the type species.

Laboulbenia divisa W. Rossi & M. Leonardi, ***sp. nov.***

Index Fungorum number: IF557384; *Facesoffungi number*: FoF 07846; Fig. 109

Etymology: From Latin: divided, because of the lower portion of the receptacle unusually divided into many cells.

Holotype: FI WR3479a

Perithecium pale greyish brown; antheridia dark brown; appendages brown to blackish, with paler tips; the rest of the fungus is pale yellowish grey. *Thallus* very long and slender. Basal and suprabasal cells of the receptacle (cells I & II) replaced by a series of 6–9 gradually longer cells originated by secondary divisions. Cell III + IV stout, about one and half times, or less, longer than its maximum width, with the outer margin straight or slightly concave. Cell V relatively large, irregularly trapezoidal or wedge-shaped. *Insertion cell* narrow and thick, free from the base of the perithecium. *Outer appendage* consisting of a large, erect

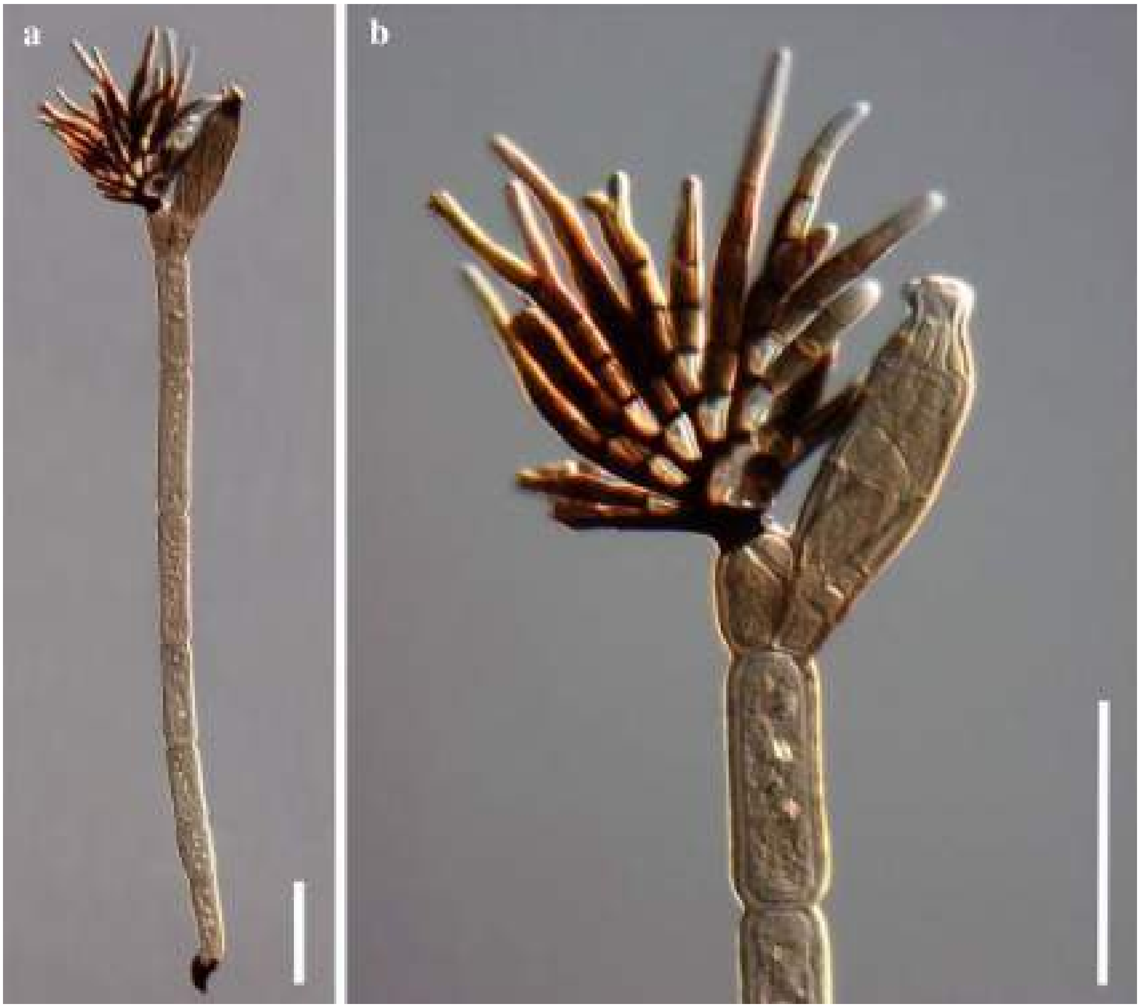


Fig. 109 ***Laboulbenia divisa*** (FI WR3479a, **holotype**). **a** Whole thallus from the type slide. **b** Upper portion of an immature thallus from the type slide. Scale bars: **a**, **b** = 100 µm

basal cell, blackish on the outer side and almost hyaline on the inner, from which arise outwardly five branches, each dividing dichotomously once or twice above the lower cell, which is hyaline and bordered with black on the outer side, the following cells being smaller and brownish; as whole the outer appendage appears as a dense, fan-shaped tuft of branchlets slightly exceeding in length the apex of the perithecium. *Inner appendage* consisting of a very small and hyaline basal cell distinctly shorter than its maximum width, from which arise two short bicellular branchlets, the lower cell of which is almost rounded, grayish brown, contrasting, separated from the smaller, paler, greyish and slenderer upper cell by a marked constriction and a thick, black septum; each of the two branchlets bear apically a tuft of (2–)3–4, elongate, bottle-shaped antheridia. Cell VI relatively small, rectangular in outline, about one and half times longer than broad. Perithecium almost entirely free, the venter slightly and evenly inflated, the wall-cells spirally twisted, describing a half turn from the base to the tip, which is rather abruptly distinguished, much darker, slightly bent inward, ending with four larges, rounded, subequal lips with hyaline margins. Length from foot to perithecial apex 880–1575 µm; perithecium 45–65 × 140–170 µm; antheridia 35 µm; longest appendages 225 µm.

Material examined: COSTA RICA, Prov. Cartago, Turrialba, P. N. Barbilla, Sendero el Felino, LN—217000 N 595000E, alt. 400–500 msl, 18.VII.2002, E. Rojas, upper surface of the tip of the abdomen of a female specimen of *Richardia telescopica* Gerdstacker (Diptera, Richardiidae) (FI WR3479a, **holotype**; WR3479b in InBIO, isotype). Costa Rica, Prov. Cartago, P. N. Barbilla, Dantas River, LN—218100 N 593600E, alt. 500–600 msl, Malaise trap, 9 December 1999—8 January 2000, E. Rojas, tip of the abdomen of *R. telescopica* (FI WR2700a and FI WR2700b, paratypes).

Notes: The division of the lower cells of the receptacle was observed so far in only two species of the large genus *Laboulbenia*: *L. partita* reported from various African and Asian countries on Chrysomelidae Alticini (Rossi and Bernardi 2018), and *L. hingstonii* described on a Carabidae from India (as *Misgomyces hingstoni*: Balazuc 1971) and known only from the type collection. *Laboulbenia divisa* is distinct from and not allied with these two latter species. Likely, the division of the cells of the receptacle is a rare feature arisen independently in species of *Laboulbenia* occurring on very different host-insects in different continents.

The species of *Laboulbenia* occurring on the Diptera are relatively few and clearly polyphyletic (Rossi and Kirk-Spriggs 2011). The new species seems to be allied with *L. richardiana* described on *Richardia teevani* Curran from French Guinea (Rossi and Kotrba 2004). *Laboulbenia divisa* shares with *L. richardiana* the undivided cells III and IV, the perithecium being wholly free and the inner appendage lacking sterile branches. *L. richardiana* has been described as a polymorphic species, but recent molecular analysis carried out on *Laboulbeniales* of other genera suggests that the different "morphotypes" may be different phylogenetic species (Goldmann and Weir 2012; Goldmann et al. 2013).

With a length greater than 1.5 mm in length, *Laboulbenia divisa* is one of the tallest species of *Laboulbenia* (Fig. 109). In this ranking is surpassed only by *L. kunkelii*, occurring on a large ground beetle from tropical Asia, and by *L. caprae* (which is likely a synonym of *L. gigantea*, occurring on large ground beetles from Europe).

Laboulbenia triarthronis W. Rossi & M. Leonardi, ***sp. nov.***

Index Fungorum number: IF558362; *Facesoffungi number*: FoF 09956; Fig. 110

Etymology: Referring to the host genus, *Triarthron*.

Holotype: SYRF RKB 601a

Thallus tinged with pale yellow, rather stocky, regularly enlarging from below upwards. Basal cell of the receptacle (cell I) slender, twice (or slightly more) longer than broad. Cell II slightly longer and distinctly broader than cell I, divided from cell III by a short transverse septum and from cell VI by a much longer, oblique and concave septum. Cell III broadly quadrangular, distinctly longer than broad. Cell IV about as long as cell III but broader. Cell V relatively large, shaped like an inverted tringle. Insertion cell oblique, narrow and thick, distinctly free from the perithecium. *Basal cell* of the outer appendage relatively large, longer than broad, bearing two branches in mature thalli; one of these branches is erect, relatively short, consisting of a linear series of small cells subtended by a contrasting blackish, constricted and elongate collarette; the second branch is produced after the former from the outer, upper angle of the basal cell: it is usually longer than the former and its cells are gradually longer towards the tip. In immature thalli the inner appendage consists of two superimposed subequal cells slightly longer than broad bearing distally a single, short antheridium, which is later displaced laterally by the growth of a branch longer than the branches of the outer appendage; sometimes this latter branch divides in two from the base. Cell VI longer than broad, irregularly shaped. Perithecium adnate to the receptacle for 2/3 to 3/4 of its length, slightly inflated, almost three times longer than maximum width, tapering without abrupt constriction to the truncate, dark brown tip slightly oriented outwards and ending in an almost flattened, hyaline apex. Length from foot to perithecial apex 190–300 µm; longest appendage 175 µm; perithecium 95–140 × 35–60 µm.

Material examined: USA, Illinois, Champaign Co., Brownfield Woods, 3 mi NE of Urbana, 14 August 1950, R.K. Benjamin, on all parts of the body of *Triarthron lecontei* Horn (= *T. pennsylvanicum* Horn) (Coleoptera, Leiodidae) collected on *Armillariella mellea*., (SYRF RKB 601a, **holotype**; SYRF RKB 601b, 601c, 601d, 601e, and FI WR4485, **paratypes**).

Notes: The appendages of *Laboulbenia triarthronis* easily distinguish the new species from the many others described so far (Fig. 110). As to the rest of the thallus, it might be compared with *L. madeirae*, described on a ground beetle, which however bears a single, robust and elongate outer appendage (Thaxter 1908, Plate LIV; Fig. 7). *Laboulbenia triarthronis* is the first species of *Laboulbenia* reported on Coleoptera Leiodidae. The beetles of this family of insects are the hosts of the other 14 genera in the *Laboulbeniales*, 4 of which are found only on Leiodidae (Benjamin 1955; Rossi and Santamaria 2012; Haelewaters and Rossi 2017).

Mimeomyces Thaxt.

Notes: Most of the 16 species recognized at present in this genus were described as *Corethromyces* Thaxt. or *Sphaleromyces* Thaxt. One species made the move in both directions: *Corethromyces bicolor* Thaxt. was first transferred to *Mimeomyces* (Tavares 1985), but was later brought back to *Corethromyces* (Weir and Hughes 2002). Only two of the species described so far were reported outside the American continent. No DNA sequence is available for any of the species in *Mimeomyces*.

Mimeomyces digitatus W. Rossi & M. Leonardi, ***sp. nov.***

Index Fungorum number: IF557385; *Facesoffungi number*: FoF 07845; Fig. 111

Etymology: From Latin: bearing a finger, because of the finger-like preapical outgrowth.

Holotype: FI WR3388

Receptacle almost wholly blackened, with the basal cell pale yellow to almost hyaline above the foot; the rest of the thallus is yellowish brown, darker just above the receptacle and paler in the distal portion of the branchlets of the

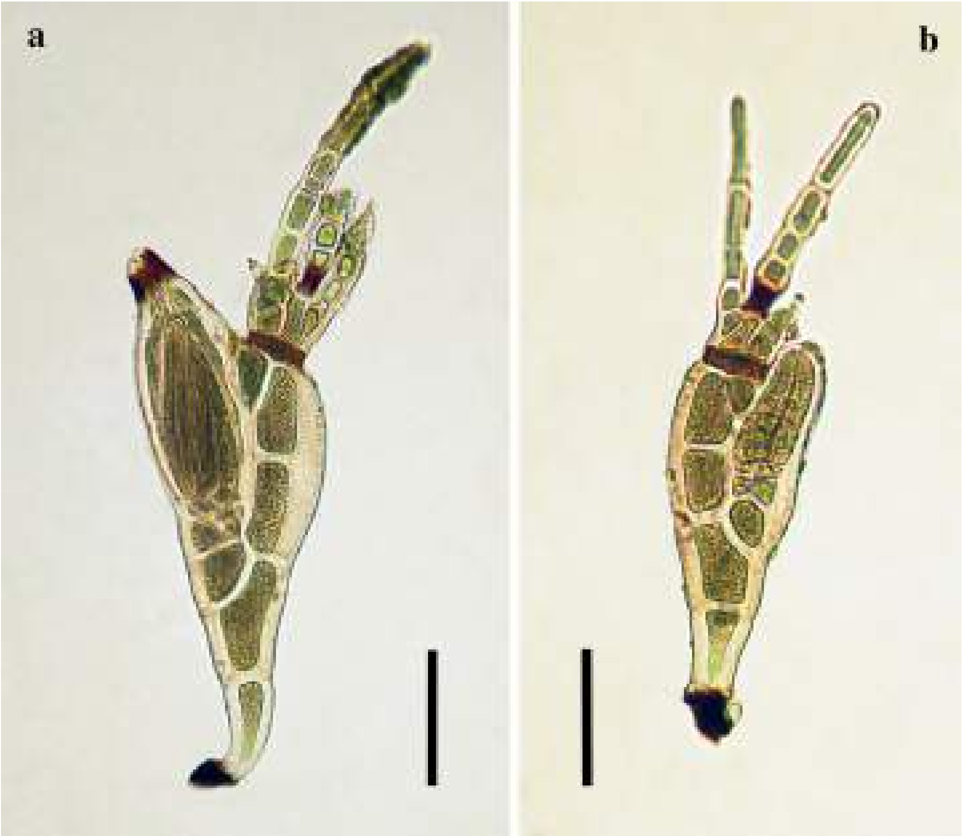


Fig. 110 ***Laboulbenia triarthronis*** (SYRF RKB 601a, **holotype**). **a** Thallus from the type slide stained with cotton blue. **b** Immature thallus from a paratype slide stained with cotton blue. Scale bars: **a**, **b** = 50 µm

appendages; the preapical outgrowth of the perithecium is chestnut brown. *Basal cell* of the receptacle relatively large, obconical, slightly inflated above the foot. *Suprabasal cell* very short, irregularly pentagonal. *Axis* of the appendage consisting of five superimposed cells subequal in length but progressively narrower, bearing on the inner side short, erect, relatively stout branchlets, most of which are bifurcate from the base. *Antheridia* not seen. Stalk cell of the perithecium oblique, distinctly broader than long. *Basal cells* of the perithecium relatively large, subequal, distinctly longer than the stalk cell. *Perithecium* oblong, nearly symmetrical, slightly inflated below, the septa between the wall cell tiers marked by slight elevations, the tip rather abruptly tapering to a subtuncate apex bearing tiny hyaline lips and a subapical long, slender, straight outgrowth pointing obliquely upwards. Length from foot to perithecial apex 295–310 µm; from foot to tip of longest appendages 160 µm; perithecium 35–37 × 195–205 µm; perithecial outgrowth 35 µm.

Material examined: ECUADOR, Napo, near Papallacta, Rio Guango, 2714 msl, 00°22′35″ S 78°04′29″ W, 29 July 2009, W. Rossi and J.A. Torres Celi, on styla of *Philonthus* sp. (Coleoptera, Staphylinidae, Staphilininae, Philonthini) (FI WR3388, **holotype**).

Notes: Because of the long, straight and nearly erect preapical outgrowth, the new species can be easily distinguished from the 16 others in the same genus, 9 of which bear no outgrowth at all (Fig. 111). To date, the only species of *Mimeomyces* reported from Ecuador were *M. latonae* (Proaño Castro and Rossi 2008) and *M. gregarius* (Rossi 2010), both of which lack any preapical outgrowth; the latter is also the only species associated with *Philonthus*, all the others being parasitic on Staphylininae Quediini, except *M. latonae* occurring on Paederinae (Tavares 1985).

Synandromyces Thaxt.

Notes: This genus includes ten species characterized mostly by a short appendage bearing a few antheridia forming a compact group and by the arrangement of cells II and III. A single sequence is available for species in this genus (Goldmann and Weir 2018).

Synandromyces makranczyi W. Rossi & M. Leonardi, ***sp. nov.***

Index Fungorum number: IF557386; *Facesoffungi number*: FoF 07844; Fig. 112

Etymology: Named after the Hungarian entomologist György Makranczy, who provided the material utilized for the description of the new species.

Holotype: FI WR3154

Receptacle, appendage and antheridia dark brown; stalk cell of perithecium and basal cells of the same light yellow; perithecium brownish red. Cell I elongate, distinctly tapering

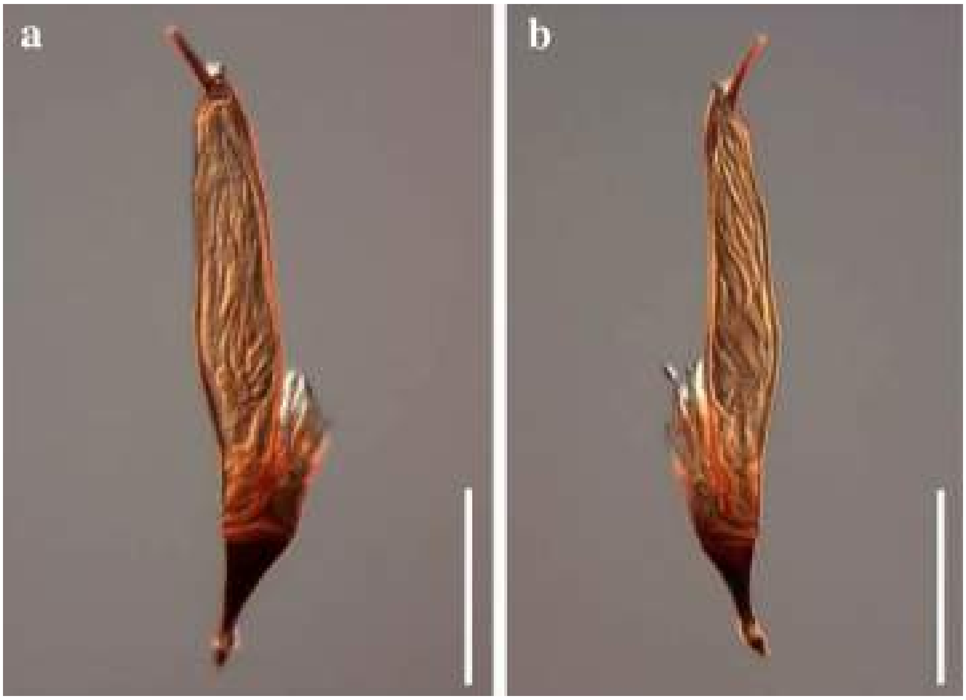


Fig. 111 ***Mimeomyces digitatus*** (FI WR3388, **holotype**). **a**, **b** Thalli from the type slide. Scale bars: **a**, **b** = 100 µm

to the foot. The arrangement of cell II and III is hidden by the dark tinge: together with cell I they form a club-shaped structure. *Antheridiiferous* axis short, consisting of five superposed and gradually smaller cells: the lower two sterile, the others bearing on the inner side single antheridia with falcate and gradually shorter efferent necks, the apexes of which reach the same height. *Stalk cell* of the perithecium about as long as the free appendage, gradually broader from below upwards. *Perithecial basal cells* large and unequal: the lower two are longer then broad, distinctly longer than the upper, which bulge externally. *Perithecial venter* symmetrically inflated, passing without abrupt transition to the tapering tip and rounded apex. Total length from foot to perithecial apex 305–370 µm; length from foot to apex of free appendage 120–140 µm; perithecium 50–55 × 135–175 µm; ascospores about 32 µm.

Material examined: PERU, Cuzco Dept., Pillahuata, Manu rd. km 128, leaf litter, 22.IX.1982, L.E. Watrous & G. Mazurek, on the upper side of the abdomen of a paratype of *Parosus major* Makranczy (Coleoptera, Staphylinidae, Oxytelinae) (FI WR3154, **holotype**).

Notes: *Synandromyces makranczyi* is the first species in the genus found occurring on Staphylinidae. It shares with *S. platydemae*, described from Cameroon on *Platydema tomentosum* (Tenebrionidae), by the dark tinge of receptacle, appendage and antheridia and the peculiar shape and arrangement of the latter (Fig. 112). However, *S. platydemae* differs from the new species by a shorter appendage, a much smaller stalk cell of the perithecium, and the very pale colour of the latter, which also bears a much shorter and less tapering tip (Thaxter 1931).

Leotiomycetes O.E. Erikss. & Winka

Notes: The class Leotiomycetes was introduced by Eriksson and Winka (1997) to accommodate non-lichenized ascomycetes which initially included only the inoperculate apothecial discomycetes having unitunicate asci that released their ascospores by pore or apical perforation (Eriksson 2005; Ekanayaka et al. 2017, 2019a; Johnston et al. 2019). The taxonomic concept of the class has been revised from the last decade based on the molecular-phylogeny approach, resulting in the class to now be considered more diverse (Johnston et al. 2019). Updated taxonomic classification of Leotiomycetes have been proposed by Ekanayaka et al. (2019a) and Johnston et al. (2019) based on different morpho-molecular criteria. Wijayawardene et al. (2020) followed the Leotiomycetes classification provided by Johnston et al. (2019) and used the Leotiomycetes's classification of Ekanayaka et al. (2019a) as an alternative classification. They accepted 13 orders, with 52 families and 626 genera in Leotiomycetes (Wijayawardene et al. 2020).

Erysiphales Gwynne-Vaughan

Notes: See an updated account of *Erysiphales* in Wijayawardene et al. (2020).

Erysiphaceae Tul. & C. Tul.

Notes: *Erysiphaceae* is a family with species that cause powdery mildew diseases on about 10,000 species of angiosperms including many cultivated crops, vegetables, fruits and ornamentals (Takamatsu et al. 2015). This family comprises about 873 species belonging to 17 genera (Braun and

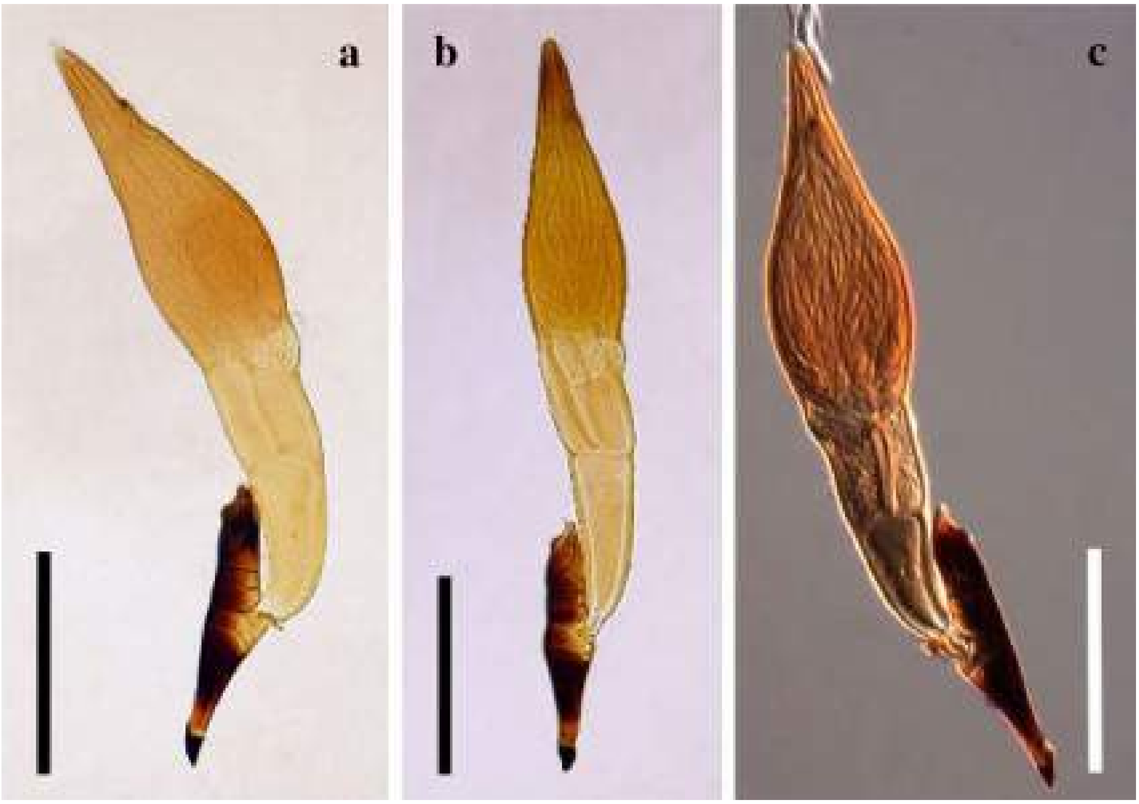


Fig. 112 ***Synandromyces makranczyi*** (FI WR3154, **holotype**). **a**, **b** Thalli from the type slide (BF). **c** Thallus from the type slide (DIC). Scale bars: **a**–**c** = 100 µm

Cook 2012). All species are obligate biotrophic parasites of plants (Takamatsu 2013).

Erysiphe R. Hedw. ex DC.

Notes: *Erysiphe* is the largest genus in the *Erysiphaceae* and contains 450 species (Takamatsu et al. 2015). It includes five tribes and two basal genera, which have been described by Mori et al. (2000) and Takamatsu et al. (2015). Some species cause serious diseases on cultivated plants, such as cereals, flowers, ornamentals (Glawe 2008; Braun and Cook 2012; Takamatsu et al. 2015). In this study, a new species of *Erysiphe* found on *Salix gracilistyla* var. *melanostachys* (black pussy willow) in Korea is described and illustrated based on morphological characters and molecular evidence (Figs. 113 and 114).

Erysiphe salicicola Hyang B. Lee, P.M. Kirk & T.T.T. Nguyen, ***sp. nov.***

Index Fungorum number: IF557324; *Facesoffungi number*: FoF 09197; Fig. 113

Etymology: Referring to the host plant.

Holotype: CNUFC PWS1

Sexual morph *Chasmothecia* scattered, 98.5–139.5(–152.5) µm diam., containing 3–13 asci. Each chasmothecium had 26–56 appendages. Appendages hyaline, aseptate, straight to curved, (0.85–)1–1.4 times as long as the cleistothecial diam., 4.5–6.5 µm wide at the base, slightly increasing towards the apex, with single septum at the base, hyaline, sometimes slightly brown at the base, 6–7.5 µm wide at the apex, circinate at the near apex. *Asci* sessile or short-stalked, 48.5–68.5 × 27.5–43 µm, obovoid or clavate, with 3–5 ascospores. *Ascospores* ellipsoidal to obovoid, 15–25(–26.5) × 10.5–15 µm. **Asexual morph** *Appressoria* developed, nipple-shaped to slightly lobed, solitary or in opposite pairs. *Conidiophores* arising from the upper part of mother cells, short, cylindrical, 57–95.5 × 7.5–9.5 µm. *Foot cells* cylindrical, straight to slightly curved near the base, followed by two shorter cells. *Conidia* oval, cylindrical, 27–35.5(–38.5) × 13.5–18.5(–21) µm.

Material examined: REPUBLIC OF KOREA, Jeonnam Province, garden of the Chonnam National University located in Gwangju (35°10′20.3″ N 126°53′56.9″ E), on *Salix gracilistyla* var. *melanostachys*, 17 September 2018, collected by H.B. Lee (CNUFC PWS1, **holotype**).

GenBank numbers: ITS = MT192530, MT192531, LSU = MT192534, MT192535.

Notes: *Erysiphe salicicola* belongs to *Erysiphe* sect. *Uncinula* and is phylogenetically related to *E. adunca*.

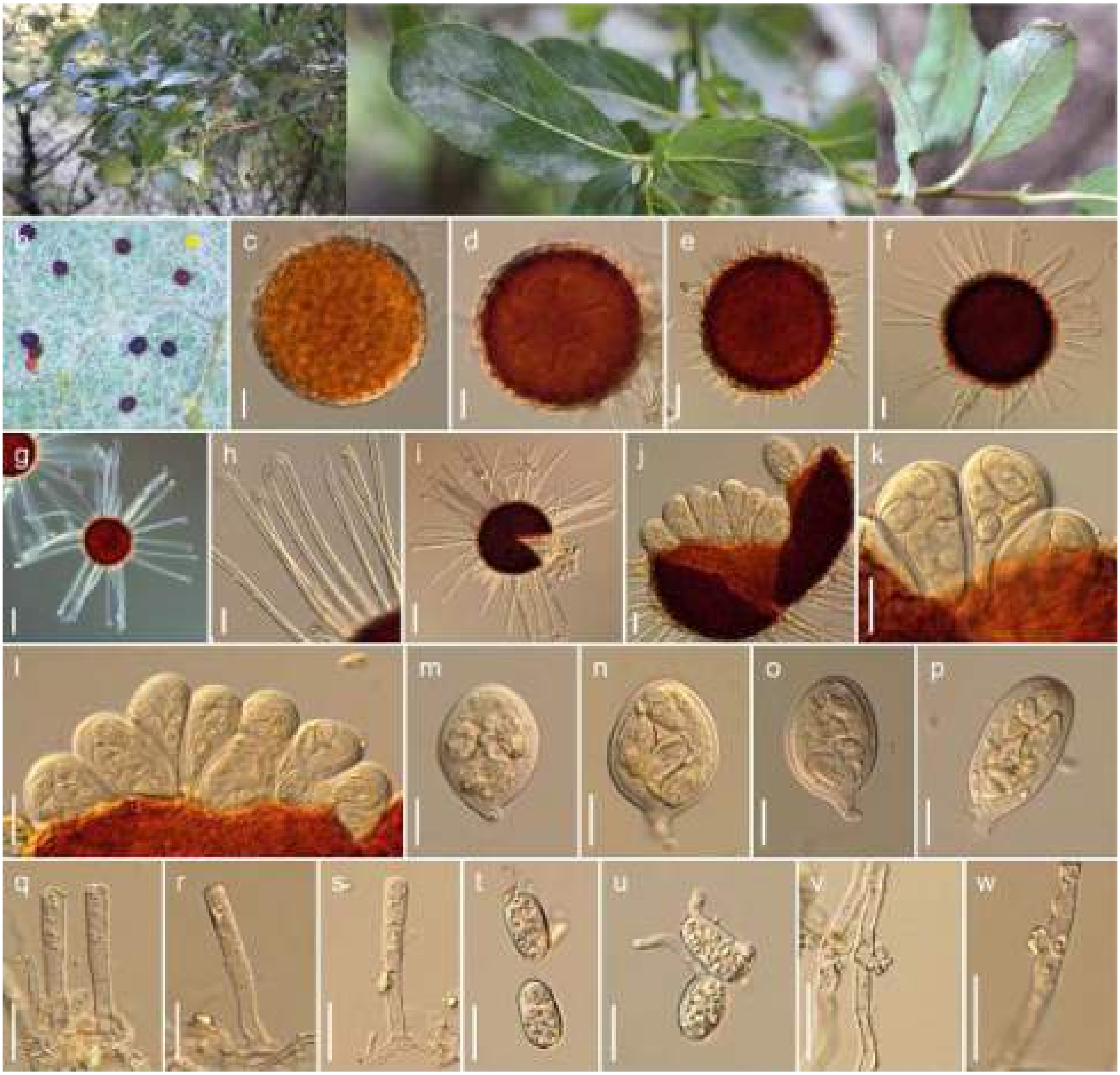


Fig. 113 ***Erysiphe salicicola*** (CNUFC PWS1, **holotype**). **a** Symptoms of powdery mildew on black pussy willow (*Salix gracilistyla* var. *melanostachys*). **b** Chasmothecia on the leaf-surface. **c–g**, **i** Young and mature chasmothecium with appendages. **h** Appendages. **j–p** Asci containing ascospores. **q–s** Conidiophores. **t**, **u** Conidia and conidial germ tubes. **v**, **w** Appressoria (Fig. b: observed under a stereomicroscope; Figs. c–w: light microscope). Scale bars: **c–f**, **h**, **j–w** = 20 µm, **g**, **i** = 50 µm

However, *E. salicicola* differs from *E. adunca* in having smaller conidia and ascospores. The number of ascospores in the asci (chasmothecium), and appendages are less than *E. adunca*. Furthermore, phylogenetic analyses indicate that *E. salicicola* forms a separate branch distinct from *E. adunca*, confirming it represents a new species. A BLASTn search of the ITS sequences indicated that *Erysiphe salicicola* was closest to *Erysiphe* sp. (MH358357) and *E. adunca* (KY660862) with similarity values of 99.2% and 93.1%, respectively. The species most closely related to *E. salicicola*, with 97.9% similarity based on LSU sequences was *E. adunca* (KR048118).

Leotiales, genus *incertae sedis*

Notes: *Leotiales* was introduced by Korf and Lizoň (2001) to accommodate a single family *Leotiaceae*. Based on multi-gene phylogenetic analyses, Ekanayaka et al. (2019a) included the other two families in this order viz.

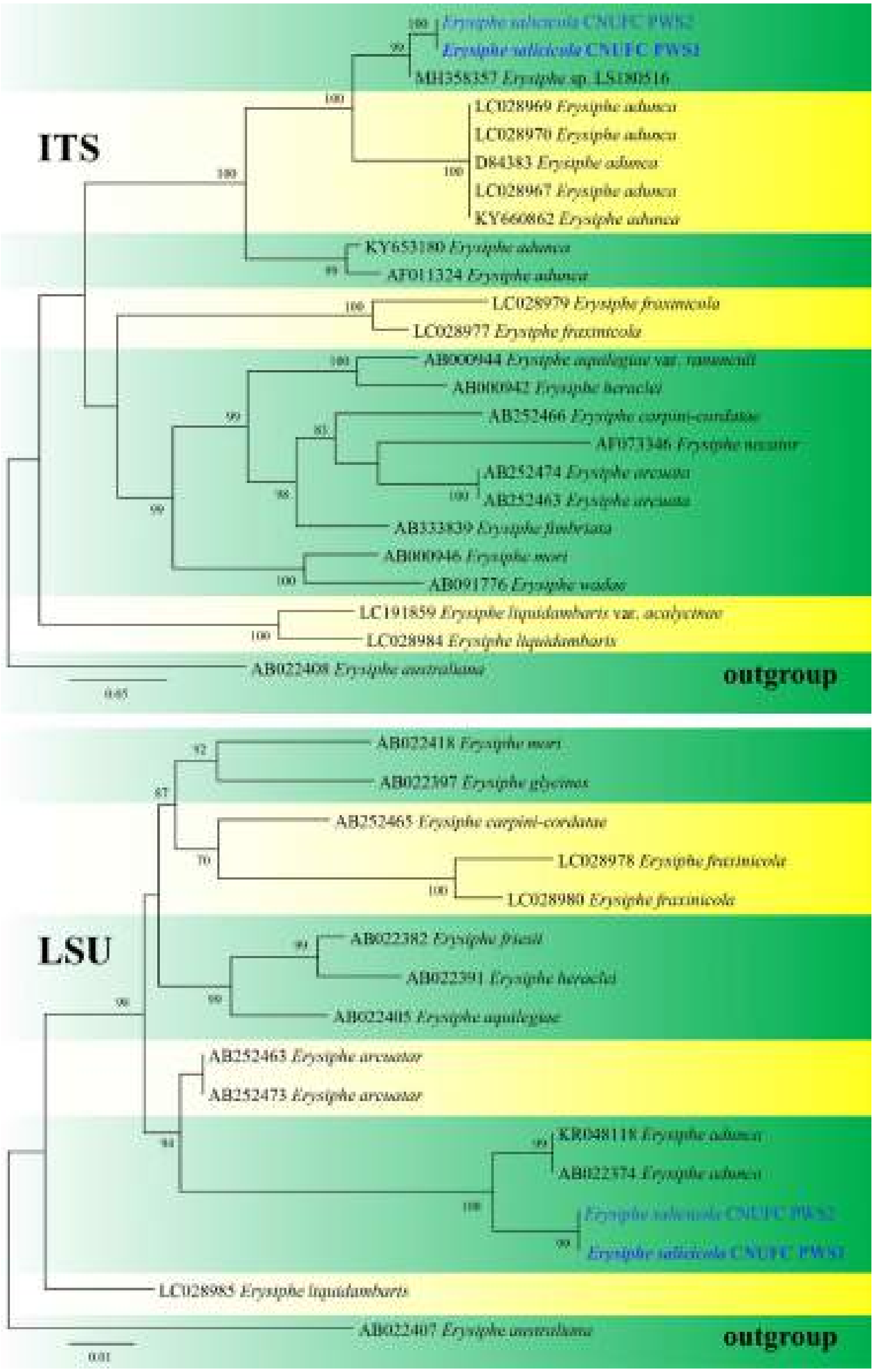


Fig. 114 Phylogram generated from maximum likelihood analysis based on ITS and LSU sequence data for species of *Erysiphe*. Bootstrap value equal to or greater than 70% for ML analyses is presented at the nodes. *Erysiphe australiana* was used as outgroup. Type strains are in bold and newly generated sequences are in blue

Cochlearomycetaceae and *Tympanidaceae* as well as including *Gelatinomyces* in *Leotiales* genera *incertae sedis*. Johnston et al. (2019) introduced a new family *Mniaeciaceae* to accommodate *Mniaecia* and also treated *Alatospora*, *Aotearoamyces*, *Claussenomyces*, and *Flagellospora* in *Leotiales*. Johnston et al. (2019) also presumed that *Gorgomyces*, *Miniancora*, *Mycosymbioses*, and *Satchmopsis* possibly belong to *Leotiales* based on phylogenetic analyses of the ITS region. Wijayawardene et al. (2020) listed four families (*Cochlearomycetaceae*, *Leotiaceae*, *Mniaeciaceae* and *Tympanidaceae*) and three genera *incertae sedis* (*Aotearoamyces*, *Alatospora* and *Flagellospora*) in *Leotiales*. In this study, we introduce a monotypic genus *Scelecoleotia* to accommodate a coelomycetous asexual species, namely *Scelecoleotia eriocamporesi* sp. nov. in *Leotiales* based on multi-gene phylogenetic analyses coupled with morphological characteristics. However, the current phylogenetic status of the new genus could not be classified as any of the families in *Leotiales*. We, hence, tentatively place the genus in *Leotiales* genera *incertae sedis* pending further studies.

Scolecoleotia H.B. Jiang, Phookamsak & K.D. Hyde, ***gen. nov.***

Index Fungorum number: IF558192; *Facesofungi number*: FoF 09763.

Etymology: The generic epithet "*Scolecoleotia*" refers to taxa in *Leotiales* having scolecosporus conidia.

Saprobic on dead aerial fronds of *Pteridium aquilinum*. **Sexual morph** Undetermined. **Asexual morph** Coelomycetous, visible as black, raised, elongate area on the host. *Conidiomata* dull, black, pycnidial, solitary to gregarious, scattered, sometimes arranged in rows on host substrates, immersed, slightly raised, elongate, hemisphaerical to subconical, with wedge-shaped at the basal angles, uniloculate, glabrous, apapillate, with inconspicuous ostiolate. *Pycnidial wall* thin-wall of equally thickness, composed of 3–5 layers, of brown to dark brown pseudoparenchymatous cells, arranged in *textura angularis* to *textura globulosa*, difficult to distinguish from the hymenium. *Hymenium* composed of 2–3 strata, of hyaline polygonal cells. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* phialidic, determinate, discrete, hyaline, ampulliform to subcylindrical, aseptate, smooth-walled, arising from innermost later of the cavity of conidioma. *Conidia* acrogenous, scolecosporous, solitary, cylindrical to filiform, curved, hyaline, aseptate, smooth-walled.

Type species: ***Scolecoleotia eriocamporesi*** H.B. Jiang, Phookamsak & K.D. Hyde,

Notes: The monotypic genus *Scolecoleotia* is introduced herein to accommodate the asexual taxon, *Scolecoleotia eriocamporesi* which was collected from *Pteridium aquilinum* (eagle fern) in Italy. The genus can be distinguished from the other genera in *Leotiales* in having elongate, hemisphaerical to subconical conidiomata, holoblastic, phialidic conidiogenous cells, with hyaline, scolecosporous, cylindrical to filiform aseptate conidia. Most genera in *Leotiales* have hyphomycetous asexual morphs (Wijayawardene et al. 2017; Ekanayaka et al. 2019a). *Scolecoleotia* has a pycnidial coelomycetous asexual morph and resembling *Collophorina*, *Epithamnolia*, *Gelatinosporium*, and *Satchmopsis* (Funk 1979; Suija et al. 2017; Wijayawardene et al. 2017; Li et al. 2020b). *Scolecoleotia* is most similar to the asexual morph of *Gelatinosporium* in having phialidic conidiogenous cells, with acrogenous, hyaline, cylindrical to filiform, aseptate conidia (Funk 1979). Species of *Gelatinosporium* are varied in terms of the shape of the conidiomata such as globose to discoid, elongate subsphaerical, or irregular-shaped which is also typical with *Scolecoleotia* in having elongate subsphaerical conidiomata (Funk 1979). *Gelatinosporium* has no molecular data to confirm their phylogenetic placements in *Leotiales*. Therefore, we introduced the new genus *Scolecoleotia* as a distinct genus from *Gelatinosporium*. Phylogenetic analyses of a combined LSU, SSU and ITS sequence dataset showed that *Scolecoleotia* forms an independent lineage basal to *Leotiales* and is not related to any families in *Leotiales*. Therefore, the genus is tentatively placed in *Leotiales* genus *incertae sedis*.

Scolecoleotia eriocamporesi H.B. Jiang, Phookamsak & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF558193; *Facesofungi number*: FoF 09764; Fig. 115

Etymology: Named after Erio Camporesi who has contributed many fungal collections from Italy.

Holotype: MFLU 16-2133

Saprobic on dead aerial fronds of *Pteridium aquilinum*. **Sexual morph** Undetermined. **Asexual morph** Coelomycetous, visible as black, raised, elongate area on the host. *Conidiomata* 75–145 µm high, 600–1100 µm long, black, pycnidial, solitary to gregarious, scattered, sometimes arranged in rows on host substrates, immersed, slightly raised, elongate, hemisphaerical to subconical, with wedge-shaped at the basal angles, uniloculate, glabrous, apapillate, with inconspicuous ostiolate. *Pycnidial wall* 10–30 µm wide, thin-wall of equally thickness, composed of 3–5 layers, of brown to dark brown pseudoparenchymatous cells, arranged in *textura angularis* to *textura globulosa*, difficult to distinguish from the hymenium. *Hymenium* composed of 2–3-strata, of hyaline polygonal cells, polygonal cells 3–6 × 3–6 µm ($\bar{x}$ = 5 × 5 µm, n = 30). *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* (5.5–)7–10(–12) × 2–3(–4) µm ($\bar{x}$ = 9 × 3 µm, n = 50), holoblastic, phialidic, determinate, discrete, hyaline, ampulliform to subcylindrical, aseptate, smooth-walled, arising

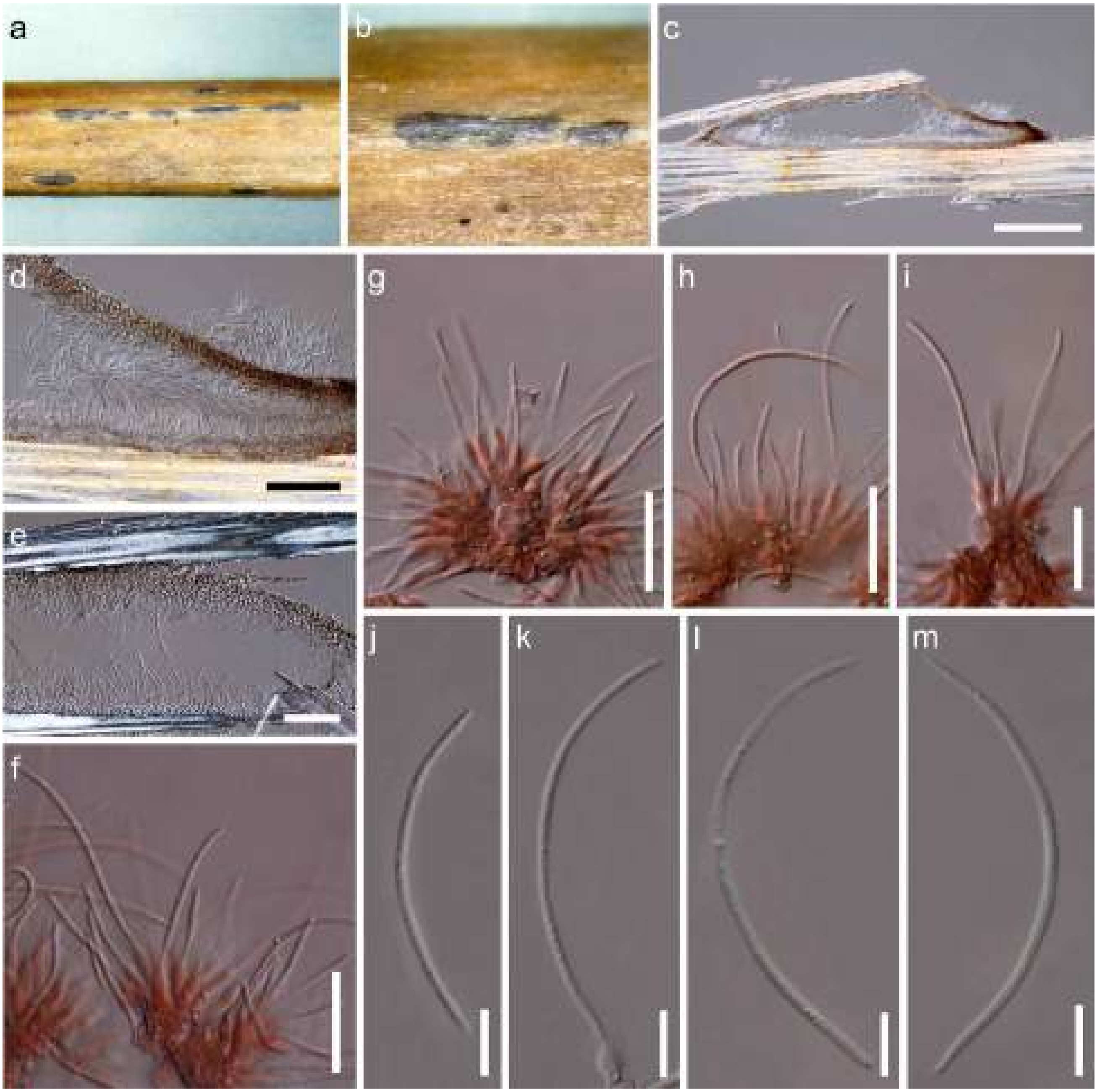


Fig. 115 ***Scolecoleotia eriocamporesi*** (MFLU 16-2133, **holotype**). **a**, **b** Appearance of conidiomata on host surface. **c** Section through conidioma. **d**, **e** Section through pycnidial wall. **f**–**i** Conidiogenous cells with attached conidia stained in Congo red. **j**–**m** Conidia. Scale bars: **c** = 500 µm, **d**, **e** = 50 µm, **f**–**i** = 20 µm, **j**–**m** = 10 µm

from the innermost layer of cavity of conidioma. *Conidia* (23–)40–65(–75) × 1.5–2.5 µm ($\bar{x}$ = 57 × 2 µm, n = 50), acrogenous, scolecosporous, solitary, cylindrical to filiform, curved, hyaline, aseptate, smooth-walled.

Material examined: ITALY, Province of Arezzo, Montemezzano-Stia, on dead aerial fronds of *Pteridium aquilinum*, 7 July 2016, E. Camporesi, IT3027A (MFLU 16-2133, **holotype**); *ibid.*, MFLU 16-2133 (isotype).

GenBank numbers: ITS = MW981448, MW981449, LSU = MW981450, MW981451, SSU = MW981452, MW981453.

Notes: Based on the NCBI BLASTn search results of the ITS, LSU and SSU sequences, *Scolecoleotia eriocamporesi* (strains IT3027A and IT3027B) showed 92% similarity with *Urceolella carestiana* (CBS 319.71), 96.26% similarity with Leotiomycetes sp. (BY-2018b) and 99.36% similarity with *Dicephalospora rufocornea* (MFLU 18-1827), respectively.

Vu et al. (2019) obtained the sequence data of *Unguicularia carestiana* (= *Urceolella carestiana* strain CBS 319.71) from Müller's collection (ETH 755, Switzerland). However, this specimen is not the type specimen of *Unguicularia carestiana* and Vu et al. (2019) did not provide a description and illustration of *U. carestiana* in their study. Therefore, we could not compare the morphological characteristics of *S. eriocamporesi* (Fig. 115) with *U. carestiana*. *Dicephalospora rufocornea* (MFLU 18-1827) was obtained by Ekanayaka et al. (2019a). The asexual morph of *D. rufocornea* has not yet been determined; thus, the morphological characteristics of *S. eriocamporesi* could not be compared with *D. rufocornea*. Whereas Leotiomycetes sp. (BY-2018b) is unpublished. DNA sequences of two strains of *S. eriocamporesi* (strains IT3027A and IT3027B) were directly obtained from the fruiting bodies and the two strains share the same branch length on the phylogenetic tree with 100% MLBS, 1.00 PP support (Fig. 116).

Sordariomycetes O.E. Erikss. & Winka

Notes: We follow the latest treatment and updated accounts of Sordariomycetes in Yuan et al. (2020).

Diaporthales Nannf.

Notes: *Diaporthales*, introduced by Nannfeldt (1932), forms a well-supported, monophyletic clade within Diaporthomycetidae (Senanayake et al. 2018). Based on molecular data, Senanayake et al. (2017a) accepted 21 families in the order, while Yang et al. (2017a), Braun et al. (2018) and Fan et al. (2018) introduced five new families. Senanayake et al. (2018) re-introduced *Tirisporellaceae* in *Diaporthales* after its exclusion by Jones et al. (2015). Thus, currently, *Diaporthales* comprises 27 families, namely *Apiosporopsidaceae*, *Apoharknessiaceae*, *Asterosporiaceae*, *Auratiopycnidiellaceae*, *Coryneaceae*, *Cryphonectriaceae*, *Cytosporaceae*, *Diaporthaceae*, *Diaporthosporellaceae*, *Diaporthostomataceae*, *Erythrogloeaceae*, *Gnomoniaceae*, *Harknessiaceae*, *Juglanconidaceae*, *Lamproconiaceae*, *Macrohilaceae*, *Melanconidaceae*, *Melanconiellaceae*, *Prosopidicolaceae*, *Pseudomelanconidaceae*, *Pseudoplagiostomaceae*, *Schizoparmaceae*, *Stilbosporaceae*, *Sydowiellaceae*, *Synnemasporellaceae*, *Tirisporellaceae* and *Tubakiaceae*.

Coryneaceae Corda (= *Pseudovalsaceae* M.E. Barr)

Notes: *Coryneaceae* includes two genera i.e., *Coryneum* and *Hyaloterminalis*, the most recent treatments for the family is Rathnayaka et al. (2020).

Coryneum Nees

Notes: *Coryneum* was the genus of *Coryneaceae* and formed a distinct phylogenetic lineage in *Diaporthales* (Senanayake et al. 2017a, 2018; Fan et al. 2018; Jiang et al. 2020). Members of this genus were easily distinguished from the other diaporthalean species in having black perithecia, often immersed in wood, asci that deliquesce at maturity, and an asexual morph with transversely distoseptate brown conidia (Senanayake et al. 2017a, 2018). *Coryneum* was recommended to be adopted as the generic name due to priority rather than *Pseudovalsa* (Rossman et al. 2015). Most *Coryneum* species were considered strongly host-specific and associated with tree branch cankers (Jiang et al. 2018, 2019; Senwanna et al. 2018).

Coryneum fagi C.M. Tian & N. Jiang, ***sp. nov.***

Index Fungorum number: IF558647; *Facesoffungi number*: FoF 09957; Fig. 117

Etymology: Named after the host genus, *Fagus*.

Holotype: BJFC-S1782

Saprobic or weak *pathogenic* branches of *Fagus* sp. **Sexual morph** Undetermined. **Asexual morph** *Conidiomata* 0.2–0.6 mm wide, 0.2–0.8 mm high, acervular, solitary, erumpent through the outer periderm layers of the host, scattered, surface tissues above slightly domed, formed of brown cell, thick-walled *textura angularis*. Conidiophores 60–125 µm long, 4–7 µm wide, cylindrical, apically pale brown, paler at the base, smooth, septate, unbranched, arising from basal stroma. *Conidiogenous cells* annellidic, integrated, terminal, cylindrical, expanding towards the apices, pale brown, smooth, with 1–3 slightly percurrent proliferations. *Conidia* 45–75 × 10–15.5 µm ($\overline{x}$ = 62.5 × 12 µm, n = 20), variable in shape, curved, broadly fusiform to fusiform, cylindrical or clavate, dark brown, smooth-walled, 6–12-distoseptate, apical cell with a hyaline tip, truncate and black at the base.

Material examined: CHINA, Sichuan Province, Yaan City, on dead branches of *Fagus* sp., 10 September 2020, N. Jiang (BJFC-S1782, **holotype**), *ibid*. BJFC-S1783 (isotype).

GenBank numbers: BJFC-S1782: ITS = MW144761, LSU = MW144953; BJFC-S1783: ITS = MW144762, LSU = MW144954.

Notes: *Coryneum* species were mainly named based on host associations and morphology, especially conidial characters, due to the absence of molecular data for most species (Jiang et al. 2018). In the present study, we discovered *Coryneum* species from a new host genus, *Fagus* (Fig. 117). The DNA was extracted directly from the conidiomata on branches and ITS and LSU sequences were amplified, sequenced and compared with known species (Fig. 118). *Coryneum fagi* was phylogenetically close to *C. ilicis*, but they can be distinguished by the wider conidia of *C. fagi* (*C. fagi* = 45–75 × 10–15.5 µm vs. 82–105 × 9.5–12.5 µm in *C. ilicis*) (Jiang et al. 2019).

Diaporthaceae Höhn. ex Wehm.

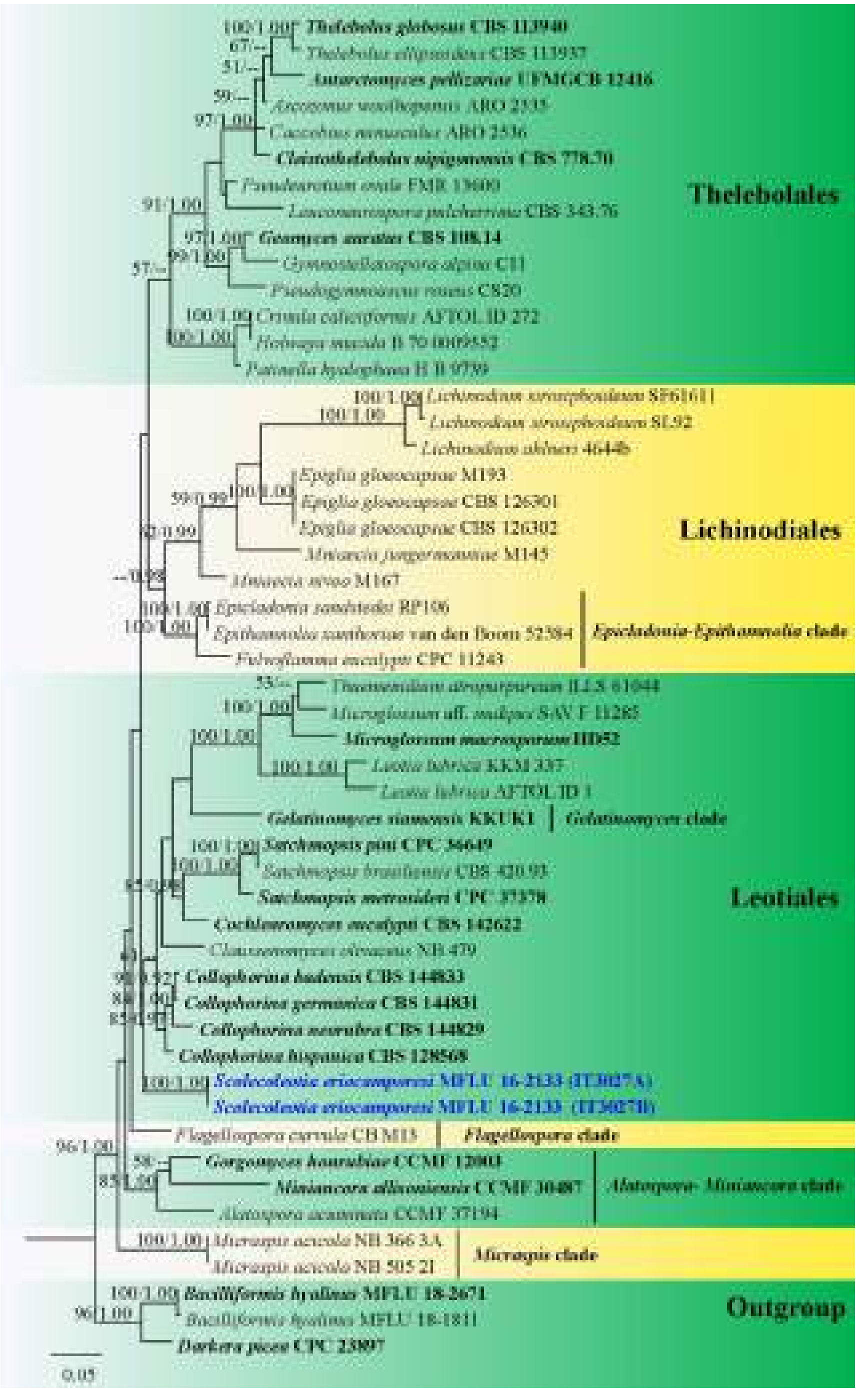


Fig. 116 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, SSU and RPB2 sequence data. Fifty-one strains are included in the combined gene analyses comprising 3907 characters after alignment (632 characters for ITS, 1019 characters for LSU, 1283 characters for SSU, 973 characters for RPB2). *Bacilliformis hyalinus* (MFLU 18-2671 and MFLU 18-1811) and *Darkera picea* (CPC 23897) are used as outgroup taxa. The tree topology of the Bayesian analysis was similar to the maximum likelihood analysis. The best RAxML tree with a final likelihood value of − 19994.043154 is presented. The matrix had 1424 distinct alignment patterns. Estimated base frequencies were as follows: A = 0.256835, C = 0.219258, G = 0.273899, T = 0.250008; substitution rates AC = 2.087920, AG = 4.320672, AT = 2.285635, CG = 1.273283, CT = 9.026514, GT = 1.000000; gamma distribution shape parameter α = 0.216097. The final average standard deviation of split frequencies at the end of total MCMC generations calculated as 0.006795 in BI analysis. Bootstrap values for maximum likelihood equal to or greater than 50% and Bayesian posterior probabilities equal or greater than 0.90 BYPP are placed above or below the branches. Ex-type strains are in bold and newly generated sequences are in blue

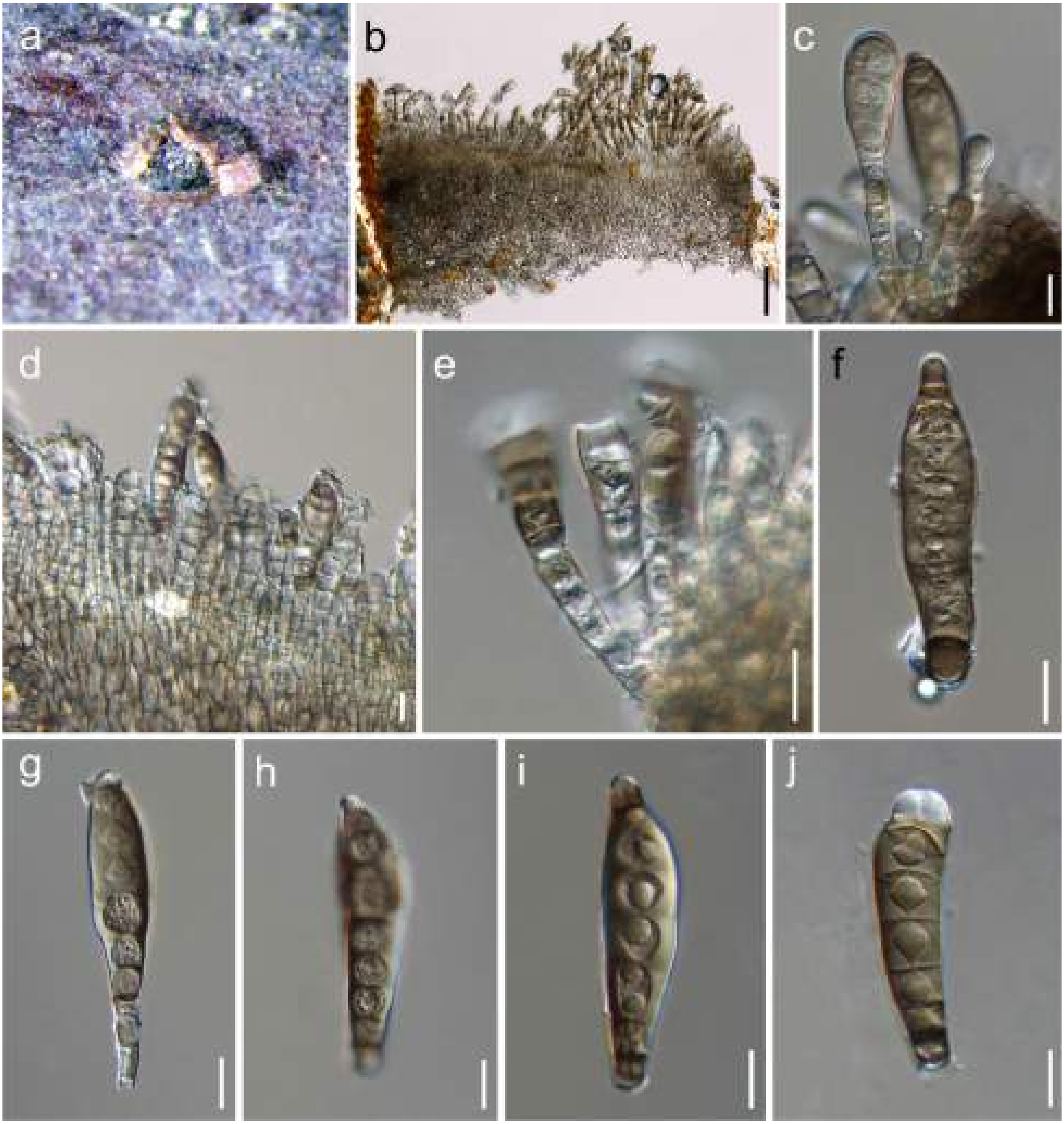


Fig. 117 ***Coryneum fagi*** (BJFC-S1782, **holotype**). **a** Conidiomata on the dead branch of *Fagus* sp. **b** Cross section of conidioma. **c**–**e** Developing conidia from conidiogenous cells. **f**–**j** Conidia. Scale bars: **b** = 100 μm, **c**–**j** = 10 μm

Notes: *Diaporthaceae*, introduced by von Höhnel (1917), is represented by species of saprobes, endophytes and phytopathogens (Dai et al. 2014; Udayanga et al. 2014a, b), including *Diaporthe*, which is the most species-rich genus (Liu et al. 2015a). The taxonomy of this family has been revised several times over the last decade based on both morphology and phylogeny (e.g., Maharachchikumbura et al. 2015, 2016; Senanayake et al. 2017b; Wanasinghe et al. 2018). Currently, *Diaporthaceae* comprises 14 genera. These include 10 genera accepted by Maharachchikumbura et al. (2016), namely *Allantoporthe*, *Apioporthella*, *Clypeoporthella*, *Diaporthe*, *Diaporthella*, *Leucodiaporthe*, *Mazzantia*, *Mazzantiella*, *Ophiodiaporthe* and *Pustulomyces*, three genera accepted by Senanayake et al. (2017a), namely

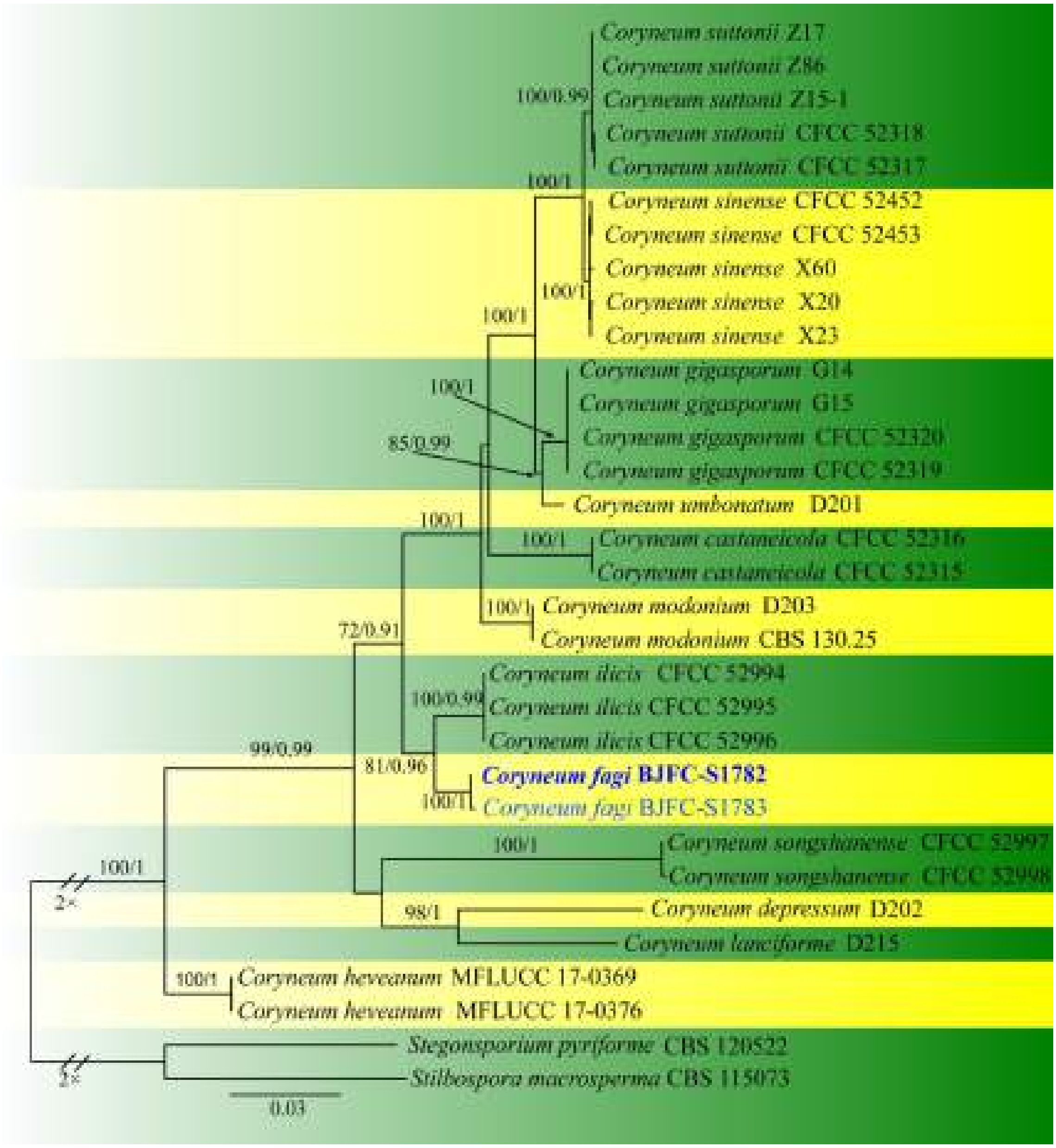


Fig. 118 Phylogram generated from RAxML analysis based on combined LSU, ITS, TEF1-α and RPB2 sequence data of *Coryneum*. Related sequences were obtained from GenBank. Thirty-two strains are included in the combined analyses, which comprise 4690 characters (1500 characters for ITS-LSU, 232 characters for TEF1-α, 1079 characters for RPB2) after alignment. *Stilbospora macrosperma* (CBS 115073) and *Stegonsporium pyriforme* (CBS 120522) are used as the outgroup taxa. The tree topology of the ML analysis was similar to the BI. The best scoring RAxML tree with a final likelihood value of − 12745.413163 is presented. The matrix had 817 distinct alignment patterns, with 18.15% of undetermined characters or gaps. Maximum likelihood bootstrap support values equal to or greater than 50% (MLBS, left), and Bayesian posterior probabilities equal to or greater than 0.90 (BYPP, right) are given at the nodes. The newly generated sequences are in blue bold

Chiangraiomyces, *Hyaliappendispora* and *Paradiaporthe*, and *Chaetoconis* accepted by Senanayake et al. (2017b).

Diaporthe Nitschke

Notes: *Diaporthe* was introduced by Nitschke (1870) based on *Diaporthe eres* collected in Germany from *Ulmus* sp. This genus is represented by endophytes, saprobes and plant pathogens on a variety of economically important crops, ornamentals and trees (Santos et al. 2017; Dissanayake et al. 2015, 2017; Guarnaccia et al. 2018). Although revised several times (e.g., Gomes et al. 2013; Gao et al. 2017; Marín-Félix et al. 2019b; Hyde et al. 2019), the taxonomy of *Diaporthe* continues to be confused and the genus urgently needs to be reassessed. Circumscription of the *Diaporthe* species relies on molecular phylogenies based on ITS and partial sequences of TEF1, TUB2, CAL and HIS3 genes (Yang et al. 2018b; Hyde et al. 2019). Marín-Félix et al. (2019b) accepted 213 species in *Diaporthe* supported by ex-type cultures and molecular data. Hyde et al. (2019) introduced two new species, *Diaporthe italiana* and *Diaporthe rumicicola*. Thus, currently *Diaporthe* comprises 215 species. We introduce a new species, *Diaporthe chamaeropicola*, from palms (*Arecaceae*) in Lisbon, Portugal, based on morphological characters and phylogenetic analyses of ITS, TEF1, TUB2 and CAL sequence data. The phylogenetic tree is presented in Fig. 124. Four new records of *Diaporthe* species from palms are presented. These include the isolates of *D. foeniculina* and *D. pyracanthae* from *Chamaerops humilis* and *D. foeniculina* from *Trachycarpus fortunei*, along with the isolate of *D. pseudophoenicicola* from *C. humilis*.

A survey of the literature reveals that no intensive study supported by molecular data has been carried out to resolve the complex nature of *Diaporthe* species occurring on palms. Although several *Diaporthe* species have been recorded on palms, most of them were based mainly on their unique palm hosts but without molecular data to confirm their phylogenetic position. As a result, most of these species have not been transferred to *Diaporthe* and remain in *Phomopsis*. Fröhlich et al. (1997) provided a synopsis of *Diaporthe* (as *Phomopsis*) species known from palms and several other species that have been reported by Taylor and Hyde (2003). Herein, a new synopsis of *Diaporthe* species from palms is presented considering the currently accepted and phylogenetically validated *Diaporthe* names (Table 4). A search of the US National Fungus Collections Fungus-Host Database (Farr and Rossman 2019) revealed 31 species of *Diaporthe*/*Phomopsis* associated with hosts in the *Arecaceae*. These names were verified against MycoBank and Index Fungorum as well as the literature, which reduced the number to five *Diaporthe* species. Table 4 lists all currently accepted names of *Diaporthe* species associated with *Arecaceae*, their respective hosts and the countries from which they were recorded. *Diaporthe arctii* was described from *Trachycarpus fortunei* by Taylor and Hyde (2003) in Switzerland and the United Kingdom based solely on morphology. However, since morphology is of limited value in defining species in *Diaporthe*, the validity of this name for these isolates cannot be confirmed and therefore, the report was excluded from the list. *Diaporthe eres* was recorded from diseased leaves of *Rhapis subtilis* by Gao et al. (2016). Nevertheless, Gao et al. (2016) regarded its phylogenetic position as a species complex since many isolates evaluated revealed ambiguous clades with short branches and moderate bootstrap support. Thus, the correct name for the species recorded on *R. subtilis* needs to be clarified and this record was excluded. Udayanga et al. (2012a, b) recorded another *Diaporthe* species from *Rhapis* sp. in Thailand. Although molecular data support this species, no morphological information was included, the species remained unnamed and was simply regarded as *Diaporthe* sp. Consequently, this species was also disregarded from the present listing of *Diaporthe* names reported from *Arecaceae*.

Table 4 Accepted *Diaporthe* species associated with *Arecaceae*

Species	Host	Country	References
Diaporthe arecae	*Areca catechu*	India	Gomes et al. (2013)
Diaporthe arengae	*Arenga engleri*	China	Gomes et al. (2013)
Diaporthe chamaeropis	*Chamaerops humilis*	Greece	Gomes et al. (2013)
Diaporthe chamaeropicola sp. nov	*Chamaerops humilis*	Portugal	Present study
Diaporthe eres	*Rhapis subtilis*	China	Gao et al. (2016)
Diaporthe foeniculina	*Chamaerops humilis*	Portugal	Present study
	Trachycarpus fortunei	Portugal	Present study
Diaporthe pseudophoenicicola	*Chamaerops humilis*	Portugal	Present study
	Phoenix canariensis	China	Gao et al. (2017)
	Phoenix dactylifera	Spain	Gomes et al. (2013)
	Phoenix dactylifera	Portugal	Present study
Diaporthe pyracanthae	*Chamaerops humilis*	Portugal	Present study

The *Diaporthe* species considered were only those described with both morphological and molecular data. Currently valid *Diaporthe* names that were described on palms based solely on morphological data were disregarded

Diaporthe chamaeropicola D.R.S. Pereira & A.J.L. Phillips, ***sp. nov.***

Index Fungorum number: IF557847; *Facesoffungi number*: FoF 09160; Fig. 119

Etymology: Named after the host genus from which it was collected, *Chamaerops humilis*.

Holotype: AVE-F-8

Associated with foliar lesions. **Sexual morph** Undetermined. **Asexual morph** *Conidiomata* pycnidial, solitary, occasionally aggregated, subglobose, dark-brown to black, thick-walled, up to 4 mm diam., covered with hyphal outgrows, superficial, lacking an ostiole, dehiscent by irregular fissures on pycnidial wall, exuding a creamy mucoid mass

Fig. 119 ***Diaporthe chamaeropicola*** (AVE-F-8, **holotype**). **a** Conidiomata formed on 1/2 PDA with conidia oozing in creamy mucoid masses. **b**–**d** Short conidiogenous cells (white arrows point to collarettes, black arrows point at periclinal thickenings). **e**, **g** Long conidiogenous cells. **f**, **h** Paraphyses (black arrow indicates a branch that is functioning as a conidiogenous cell). **i** Conidia. Scale bars: **a** = 1 mm, **b**–**i** = 5 µm

of conidia. *Pycnidial wall* pseudoparenchymatous of dark-brown *textura angularis*, cells thick-walled in outer layers, becoming thin-walled and hyaline towards the inner layers. *Conidiophores* absent. *Conidiogenous cells* lining the entire cavity, straight, hyaline, smooth-walled, thin-walled, cylindrical, occasionally ampulliform, tapering towards the apex, aseptate or 1–3-septate, unbranched or branched, collarette up to 1 µm long, variable in length, dimorphic, *short conidiogenous cells*, 4.9–19.4 × 0.9–2.6 µm (mean ± SD = 13.66 ± 3.68 × 1.75 ± 0.39 µm), *long conidiogenous cells*, 15.2–49.2 × 1.1–2.7 µm (mean ± SD = 29.54 ± 7.28 × 1.75 ± 0.36 µm), mostly phialidic, proliferating at the same level giving rise to periclinal thickenings, enteroblastic, occasionally proliferating percurrently giving rise to 1–2 annellations, often intermingled with paraphyses. *Paraphyses* straight, flexuous, hyaline, smooth- and thin-walled, cylindrical, tapering towards the apex, with 1–2–(3) basal septa, unbranched or branched below, often one of the branches later functioning as a conidiogenous cell, extending above conidiogenous cells, 26.6–78.8 µm (mean ± SD = 53.57 ± 12.72 µm) long. *Alpha conidia* cylindrical to ellipsoidal, mostly with rounded apex and obtuse to truncate base, hyaline, smooth- and thin-walled, aseptate, bi-guttulate, with a conspicuous guttule at each end, occasionally with several minute scattered guttules, straight to slightly curved, 5.6–9.4 × 1.7–3 µm (mean ± SD = 7.53 ± 0.89 × 2.31 ± 0.30 µm); mean ± SD conidium length/width ratio = 3.33 ± 0.73. *Beta* and *gamma conidia* not seen.

Culture characteristics: Colonies on 1/2 PDA, reaching 60 mm diam. after 7 d at 20 ℃. Surface flat, sparse aerial mycelium, often growing with concentric zones, with filiform margin, circular, pearl white to dirty white, opaque to slightly translucent. Reverse luteous, pale brown towards the centre. No diffusible pigment. *Conidiomata* black, scattered over the surface of the colony.

Material examined: PORTUGAL, Lisbon, Parque das Nações, Jardins da Água, near Oceanário de Lisboa, on foliar lesions of segments of *Chamaerops humilis* (*Arecaceae*), 16 October 2018, D.R.S. Pereira, HDP 034 (AVE-F-8 a dried culture of CDP 460, **holotype**), ex-type living culture, CBS XXXX = CDP 460/01.

GenBank Numbers: CAL = MT011068, ITS = MT022111, TEF1-α = MT011074, TUB2 = MT011080.

Distribution: Lisbon, Portugal.

Notes: *Diaporthe chamaeropicola* was found associated with foliar lesions of *Chamaerops humilis* (Fig. 123), but pathogenicity has not been tested. The phylogenetic position of *D. chamaeropicola* among accepted *Diaporthe* species has not clearly been resolved. Nevertheless, this species is phylogenetically related to but distinct from *D. ceratozamiae*, *D. phyllanthicola* and *D. loropetali* (Fig. 123). *Diaporthe chamaeropicola* is similar to *D. ceratozamiae* (Fig. 119), producing globose pycnidia, whose internal cavity is lined with cylindrical conidiogenous cells intermingled with long cylindrical, septate and branched paraphyses (Crous et al. 2011). However, *D. chamaeropicola* has larger conidiomata than *D. ceratozamiae* (up to 4 mm diam. vs. 300 µm diam.), lacks conidiophores, and alpha conidia have a different shape (cylindrical/ellipsoidal vs. fusiform). In addition, the two species differ in 13 nucleotide positions in ITS. *Diaporthe chamaeropicola* differs from *D. phyllanthicola* and *D. loropetali* in 9 and 13 nucleotide positions in ITS, respectively. No TUB2, TEF1 and CAL sequences are available for *D. ceratozamiae*, *D. phyllanthicola* or *D. loropetali*.

Diaporthe foeniculina (Sacc.) Udayanga & Castl., Persoonia 32: 95 (2014)

Index Fungorum number: IF803929; *Facesoffungi number*: FoF 02183; Fig. 120

≡ *Phoma foeniculina* Sacc., Michelia 2: 95 (1880)

= *Diaporthe foeniculacea* Niessl, Instituto de Coimbra 27: 168 (1879)

= *Phomopsis californica* HS Fawc., Phytopathology 12: 419 (1922)

= *Diaporthe theicola* Curzi, Atti dell'Istituto Botanico della Università e Laboratorio Crittogamico di Pavia 3: 60 (1927)

= *Phomopsis theicola* Curzi, Atti dell'Istituto Botanico della Università e Laboratorio Crittogamico di Pavia 3: 64 (1927)

≡ *Phomopsis foeniculina* (Sacc.) Sousa da Câmara, Agronomia Lusitanica 9: 104 (1947)

= *Diaporthe neotheicola* AJL Phillips & JM Santos, Fungal Diversity 34: 120 (2009)

= *Diaporthe rhusicola* Crous, Persoonia 26: 135 (2011)

Associated with foliar lesions. **Sexual morph** Undetermined. **Asexual morph** *Conidiomata* pycnidial, stromatic, uni- to multi-locular, solitary or aggregated, black, thick-walled, of variable morphology and dimensions, up to 1.3 mm diam., subglobose to pulvinate, glabrous or covered with hyphal outgrows, superficial, 1–3-ostiolate, mostly 3-ostiolate, exuding a creamy, yellowish mass or cirri of conidia. *Pycnidial locules* uni-chambered, often with a globose base and a long neck. *Pycnidial wall* pseudoparenchymatous, composed of oblong to isodiametric thin-walled cells, outer cell layers of *textura epidermoidea*, pigmented, dark-brown, inner cell layers of *textura angularis*, hyaline. *Conidiophores* arising all around the cavity of conidioma from the innermost wall layer, rarely absent, straight, sometimes curved, hyaline, smooth- and thin-walled, cylindrical, subcylindrical or doliiform, rarely with a globose base, aseptate, unbranched, rarely with a small branch, 3.7–13.2 × 1.3–4.12 µm (mean ± SD = 7.77 ± 1.90 × 2.17 ± 0.52 µm). *Conidiogenous cells* lining the entire cavity, straight, hyaline, smooth- and thin-walled, dimorphic, *short conidiogenous cells*, on *Populus* sp. twigs 9.2–19.6 × 1.4–2.5 µm (mean ± SD = 12.91 ± 1.88 × 1.84 ± 0.26 µm), producing mostly

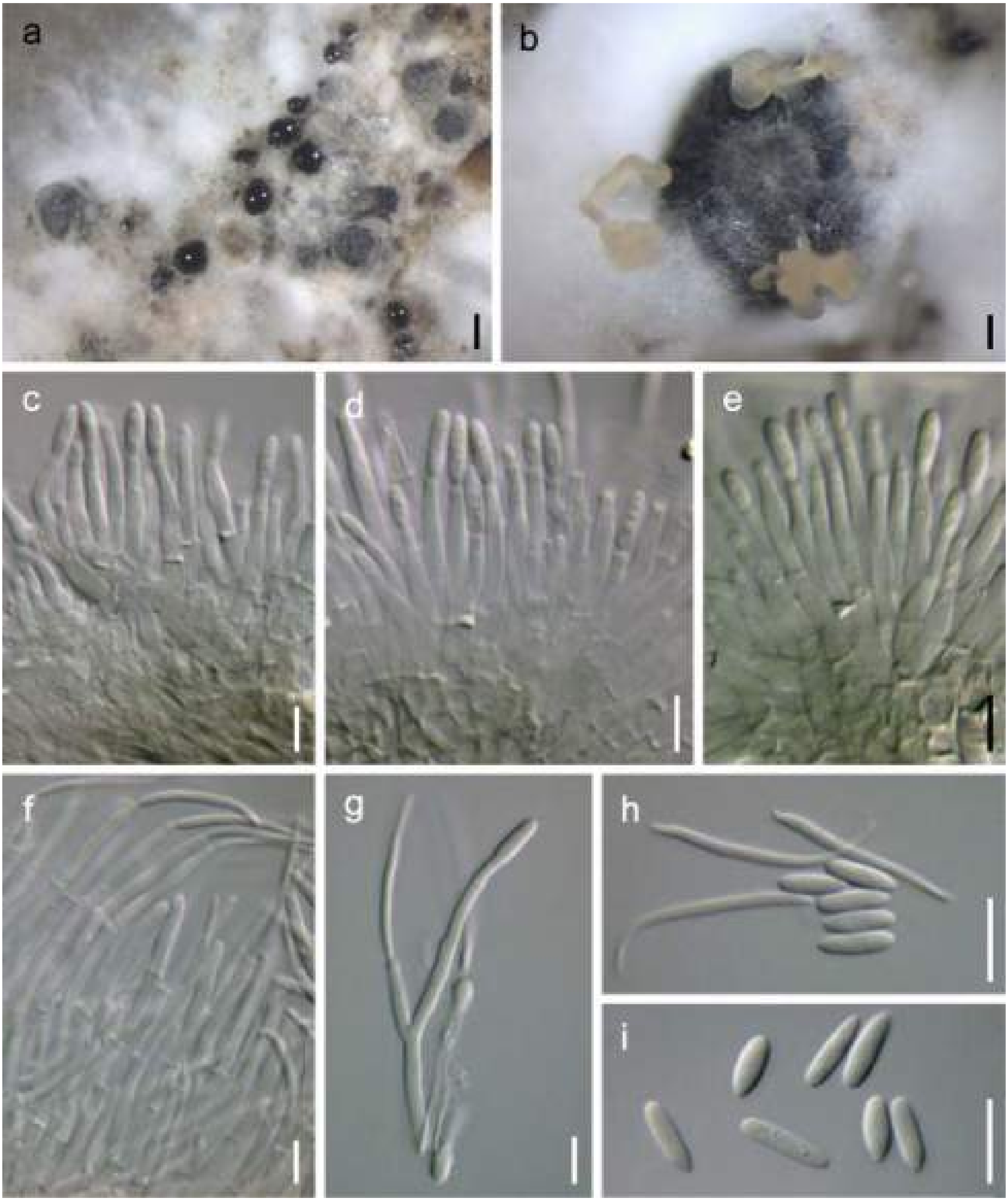


Fig. 120 ***Diaporthe foeniculina*** (CDP 022, **new record**). **a**, **b** Conidiomata formed on 1/2 PDA. Conidia are oozing in yellowish cirri. **c**–**e** Conidiophores and short conidiogenous cells. **f, g** Long conidiogenous cells. **h** Alpha and beta conidia. **i** Alpha conidia. Scale bars: **a** = 0.5 mm, **b** = 0.1 mm, **c**–**i** = 5 μm

alpha conidia, cylindrical, subcylindrical, occasionally ampulliform, tapering towards the apex, aseptate, unbranched, rarely branched, small collarette rarely present, *long conidiogenous cells*, on *Populus* sp. twigs up to 60 µm long, 1.1–2.1 µm (mean ± SD = 1.55 ± 0.20 µm) wide, producing mostly beta conidia, filiform or cylindrical, mostly 3-septate, branched, phialidic, enteroblastic, proliferating at the same level giving rise to periclinal thickenings. *Alpha conidia* obovoid, with one end rounded and the other obtuse or truncate, hyaline, smooth- and thin-walled, aseptate, aguttulate or bi-guttulate, rarely with more than 2 guttules at each end, not produced on 1/2 PDA, on *Populus* sp. twigs 5.8–9 × 1.5–2.7 µm (mean ± SD = 7.18 ± 0.66 × 2.09 ± 0.27 µm); mean ± SD conidium length/width ratio = 3.49 ± 0.62. *Beta conidia* filiform, hamate, sometimes slightly sigmoid, base rounded or truncate, apex acute and tapered, hyaline, smooth- and thin-walled, aseptate, aguttulate, on *Populus* sp. twigs 19.5–24.6 × 1.1–1.7 µm (mean ± SD = 22.13 ± 1.33 × 1.33 ± 0.22 µm); mean ± SD conidium length/width ratio = 17.04 ± 2.77. *Gamma conidia* infrequent, fusiform, with both ends acute or slightly truncate, hyaline, smooth- and thin-walled, aseptate, aguttulate or with several minute guttules.

Culture characteristics: Colonies on PDA, reaching 38 mm diam. after 7 at 20 ℃. Surface flat, glabrous to velvety, with sparse aerial mycelium, with filamentous or filiform margin, irregular, whitish, orange- to brownish, gold- to brownish, opaque. Reverse yellowish to pale, becoming brownish towards the centre. No diffusible pigment. *Conidiomata* black, scattered over the surface of the colony, often exuding orange or black droplets.

Material examined: PORTUGAL, Lisbon, Parque das Nações, Jardins Garcia d'Orta, Talhão do Coloane, on foliar lesions of segments of *Trachycarpus fortunei* (*Arecaceae*), 5 October 2018, D.R.S. Pereira (specimen HDP 013/02, living culture CDP 022); PORTUGAL, Lisbon, Marvila, Ferreira de Castro Street, near Casa dos Direitos Sociais, on foliar lesions of segments of *Chamaerops humilis* (*Arecaceae*), 13 October 2018, D.R.S. Pereira (specimen HDP 025/02, living culture CDP 209); PORTUGAL, Lisbon, Parque das Nações, Jardins da Água, near Oceanário de Lisboa, on foliar lesions of segments of *Chamaerops humilis* (*Arecaceae*), 16 October 2018, D.R.S. Pereira (specimen HDP 035/02, living culture CDP 315).

Distribution: Argentina, Australia, Europe (Greece, Portugal, Spain, Italy), New Zealand, South Africa, USA (California) (Udayanga et al. 2014b; Lawrence et al. 2015; Annesi et al. 2016; Guarnaccia et al. 2016; present study).

Hosts: *Acacia* spp., *Acer* spp., *Actinidia deliciosa*, *Aspalathus linearis*, *Bougainvillea spectabilis*, *Camellia sinensis*, *Castanea* spp., *Chamaerops humilis*, *Citrus limon*, *C. limonia*, *Crataegus* spp., *Diospyros* spp., *Foeniculum vulgare*, *Fuchsia* spp., *Hydrangea* spp., *Juglans* spp., *Malus* spp., *Olea* spp., *Persea americana*, *Prunus* spp., *Pyrus* spp., *Quercus* spp., *Rhus* spp., *Ribes* spp., *Salix* sp., *Trachycarpus fortunei*, *Vitis vinifera*, *Wisteria sinensis* (Udayanga et al. 2014b; Lawrence et al. 2015; Annesi et al. 2016; Guarnaccia et al. 2016; present study).

GenBank number: CDP 022: ITS = MT000992, TEF1-α = MN990208, TUB2 = MN990209; CDP 209: ITS = MT004913, TEF1-α = MT011071, TUB2 = MT011077; CDP 315: ITS = MT004914, TEF1-α = MT011072, TUB2 = MT011078.

Notes: *Diaporthe foeniculina* was first reported on *Foeniculum vulgare* from Madeira, Portugal (Phillips 2003) and has since then been recorded on more than 20 different hosts in nine countries around the world. The taxonomic and phylogenetic position of this species has been unclear in the past, but it is now well-resolved (see Udayanga et al. 2014b). Three isolates of *D. foeniculina* were recorded from foliar lesions of palms (Fig. 123), but pathogenicity has not been tested. This is the first time this *Diaporthe* species is reported from *Arecaceae*, representing a new host record. Two of the isolates were recorded from *Chamaerops humilis*, another was recorded from *Trachycarpus fortunei*, thus giving new insight into the wide host range already reported for *D. foeniculina* (Fig. 120).

Diaporthe pseudophoenicicola R.R. Gomes, Glienke & Crous, Persoonia 31: 30 (2013)

Index Fungorum number: IF803839; *Facesoffungi number*: FoF 09161; Fig. 121

Associated with foliar lesions. **Sexual morph** Undetermined. **Asexual morph** *Conidiomata* pycnidial, stromatic, uni- to multi-locular or convoluted, solitary, black, thick-walled, of variable morphology and dimensions, up to 3.5 mm diam., subglobose to pulvinate, sometimes conical or discoid, glabrous or covered with some hyphal outgrows, superficial to semi-immersed, inostiolate, dehiscent by irregular fissures on pycnidial wall, exuding a creamy, pale-luteous mucoid mass of conidia. *Pycnidial locules* uni- to multi-chambered, subdivided by invaginations of common pycnidial walls. *Pycnidial wall* pseudoparenchymatous, composed of oblong to isodiametric thin-walled cells, outer cell layers of *textura globulosa*, pigmented, dark-brown, inner cell layers of *textura angularis*, hyaline. *Conidiophores* absent. *Conidiogenous cells* lining the entire cavity, 11.7–49.7 × 1.1–3.1 µm (mean ± SD = 21.99 ± 9.09 × 1.83 ± 0.44 µm), intermingled with paraphyses, straight, hyaline, smooth- and thin-walled, cylindrical, ampulliform, aseptate to 1-septate at the base, unbranched, rarely with 1 branch below the septum, phialidic, collarette rarely present, enteroblastic, proliferating at the same level giving rise to periclinal thickenings, occasionally proliferating percurrently giving rise to 1–2 distinct annellations or enteroblastic proliferating percurrently after the formation of a new conidiogenous cell by apical wall-building. *Paraphyses* straight or curved at the apex, hyaline, smooth- and

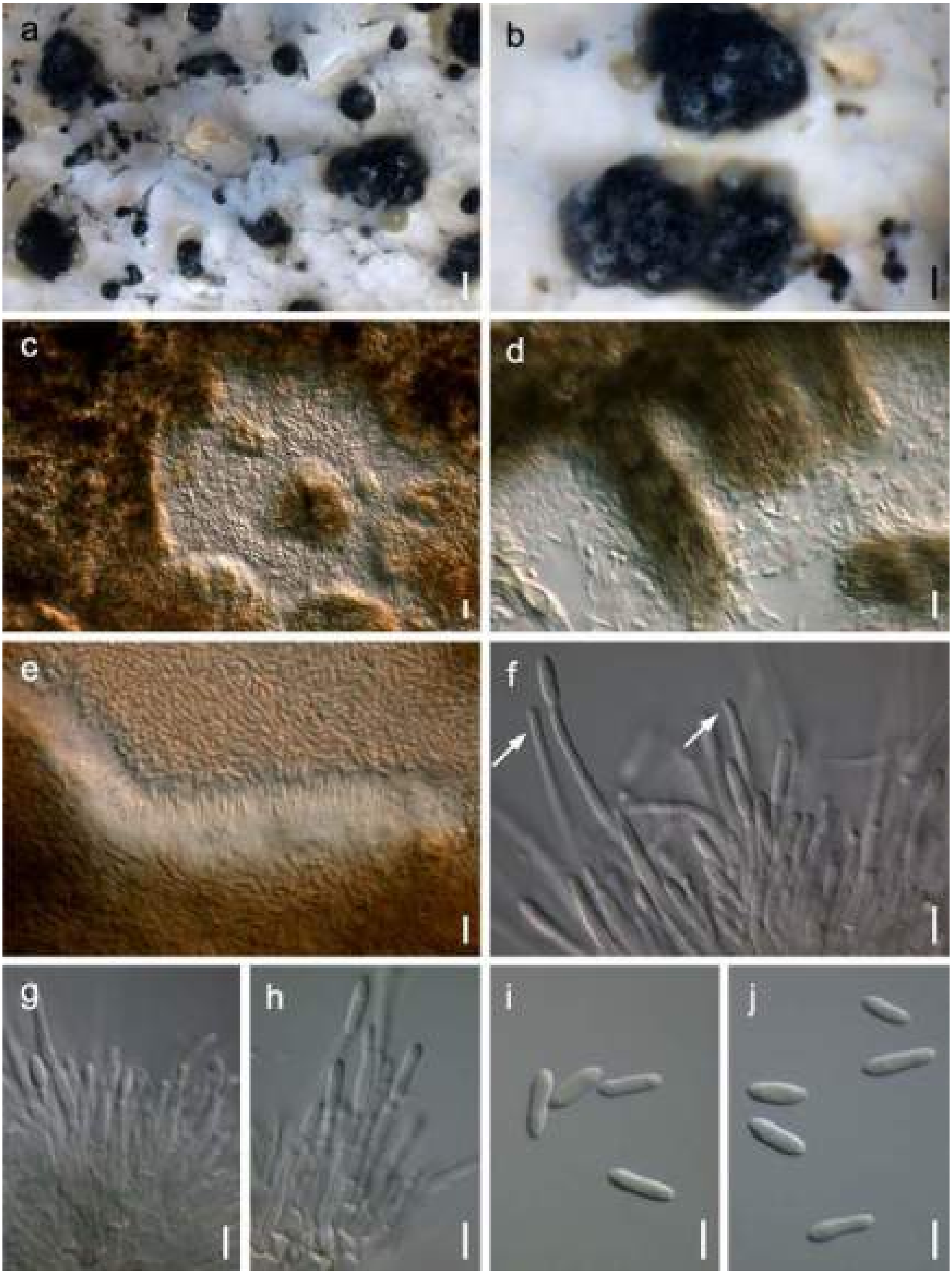


Fig. 121 ***Diaporthe pseudophoenicicola*** (CDP 047, **new record**). **a**, **b** Conidiomata formed on 1/2 PDA. Conidia are oozing in creamy mucoid masses. **c** Section through conidioma loculus. **d** Section through conidioma loculus showing wall invaginations. **e** Section through conidiogenous layer. **f**–**h** Conidiogenous cells and paraphyses (white arrows). **i**, **j** Conidia. Scale bars: **a** = 1 mm, **b** = 0.5 mm, **c**–**e** = 10 µm, **f**–**j** = 5 µm

thin-walled, aseptate to 1–2-septate, unbranched or rarely branched at the base, extending above conidiogenous cells, up to 60 µm long. *Alpha conidia* cylindrical to allantoid, often mediumly narrowed, mostly with one end rounded and the other acute or slightly truncate, hyaline, smooth-walled, thin-walled, aseptate, bi-guttulate, with an inconspicuous guttule at each end, 6.4–9.4 × 2.9–1.5 µm (mean ± SD = 8.07 ± 0.80 × 2.11 ± 0.31 µm); mean ± SD conidium length/width ratio = 3.91 ± 0.70. *Beta* and *gamma conidia* not seen.

Culture characteristics: Colonies on PDA, reaching 42 mm diam. after 7 at 20 ℃. Surface flat to velvety, with filiform margin, circular, whitish to pale, opaque to slightly translucent. Reverse yellowish to pale, becoming buff towards the centre. No diffusible pigment. *Conidiomata* black, formed in poorly defined concentric rings.

Material examined: PORTUGAL, Lisbon, Parque das Nações, Jardins da Água, Pomar do Mediterrâneo, on foliar lesions of segments of *Chamaerops humilis* (*Arecaceae*), 16 October 2018, D.R.S. Pereira (specimen HDP 039/02, living culture CDP 047); PORTUGAL, Lisbon, Parque das Nações, on foliar lesions of leaflets of *Phoenix dactylifera* (*Arecaceae*), 16 October 2018, D.R.S. Pereira (specimen HDP 044/01, living culture CDP 358).

Distribution: China (Gao et al. 2017), Iraq (Shalt El Arab), Spain (Mallorca) (Gomes et al. 2013), Portugal (Lisbon) (present study).

Hosts: *Chamaerops humilis* (present study), *Mangifera indica*, *P. canariensis* (Gao et al. 2017), *Phoenix dactylifera* (Gomes et al. 2013; present study).

GenBank number: CDP 047: CAL = MT011065, ITS = MT002357, TEF1-α = MT011069, TUB2 = MT011075; CDP 358, CAL = MT011067, ITS = MT004743, TEF1-α = MT011073, TUB2 = MT011079.

Notes: *Diaporthe pseudophoenicicola* was first reported on *Phoenix dactylifera* from Mallorca, Spain (Gomes et al. 2013). Two isolates of *D. pseudophoenicicola* were recorded from foliar lesions of palms (Fig. 123), but pathogenicity has not been tested (Figs. 121 and 123). This is the first report of this species from Portugal. One of the isolates was recorded from *C. humilis* and represented a new host record. The other isolate was recorded from *P. canariensis*, a host it has already been reported on in China (Gao et al. 2017).

Diaporthe pyracanthae L. Santos & A. Alves, Mycosphere 8: 493 (2017)

Index Fungorum number: IF820224; *Facesoffungi number*: FoF 09198; Fig. 122

Associated with foliar lesions. **Sexual morph** Undetermined. **Asexual morph** *Conidiomata* pycnidial, stromatic, solitary, subglobose to pyriform, dark-brown to black, thick-walled, 600 µm diam., mostly glabrous, but often covered with hyphal outgrows, superficial, opening via a central ostiole, internal cavity heart-shaped, exuding a pearl mucoid mass of conidia. *Pycnidial wall* pseudoparenchymatous of dark-brown, paler on the apex or around the ostiole, thin-walled *textura angularis*, becoming hyaline towards the inner layers. *Conidiophores* absent. *Conidiogenous cells* lining the entire cavity, lining the entire cavity, 5.9–22.6 × 1.5–3.4 µm (mean ± SD = 12.54 ± 3.47 × 2.09 ± 0.42 µm), straight or curved, hyaline, smooth- and thin-walled, cylindrical, occasionally ampulliform, tapering towards the apex, aseptate, rarely 1-septate, with a small branch below the septum, phialidic, collarette minute, enteroblastic, proliferating at the same level giving rise to periclinal thickenings. *Alpha conidia* fusiform to ellipsoidal, with both ends rounded or one end subobtuse, hyaline, smooth- and thin-walled, aseptate, mostly aguttulate, often with two inconspicuous guttules, not produced on PDA, on autoclaved palm leaf pieces 5–6.4 × 1.8–2.9 µm (mean ± SD = 5.77 ± 0.34 × 2.39 ± 0.22 µm); mean ± SD conidium length/width ratio = 2.43 ± 0.26. *Beta conidia* filiform, mostly hooked at the apex, base truncate, apex acute and tapered, hyaline, smooth- and thin-walled, aseptate, aguttulate, 21.6–32.1 × 0.9–1.8 µm (mean ± SD = 27.47 ± 1.91 × 1.28 ± 0.17 µm); mean ± SD conidium length/width ratio = 21.82 ± 3.34. *Gamma conidia* not seen.

Culture characteristics: Colonies on PDA, reaching 55 mm diam. after 7 d at 20 ℃. Surface flat, sparse aerial mycelium in raised concentric circles, with irregular margin, circular to irregular, white, pale-brown to yellowish towards the centre, opaque. Reverse luteous, buff to marron towards the centre. No diffusible pigment. *Conidiomata* black, scattered over the surface of the colony.

Material examined: PORTUGAL, Lisbon, Parque das Nações, Jardins Garcia d'Orta, Talhão do Coloane, on foliar lesions of segments of *Chamaerops humilis* (*Arecaceae*), 16 October 2018, D.R.S. Pereira (specimen HDP 039/02, living culture CDP 052).

Distribution: Portugal, Aveiro (Santos et al. 2017), Lisbon (present study).

Hosts: *Pyracantha coccinea* (Santos et al. 2017), *Chamaerops humilis* (present study).

GenBank number: CAL = MT011066, ITS = MT002843, TEF1-α = MT011070, TUB2 = MT011076.

Notes: *Diaporthe pyracanthae* was introduced by Santos et al. (2017) for a collection on *Pyracanthus coccinia* in Portugal and since then it has not been reported on any other hosts. One isolate of *D. pyracanthae* was recorded from foliar lesions of palms, but pathogenicity has not been tested (Figs. 122 and 123). This is the first time that *D. pyracanthae* is reported from *Arecaceae*, namely *Chamaerops humilis*, representing a new host record.

Phaeocytostroma Petr.

Notes: *Phaeocytostroma* was introduced by Petrak (1921) with the type species *P. istrica* isolated from rotting culms

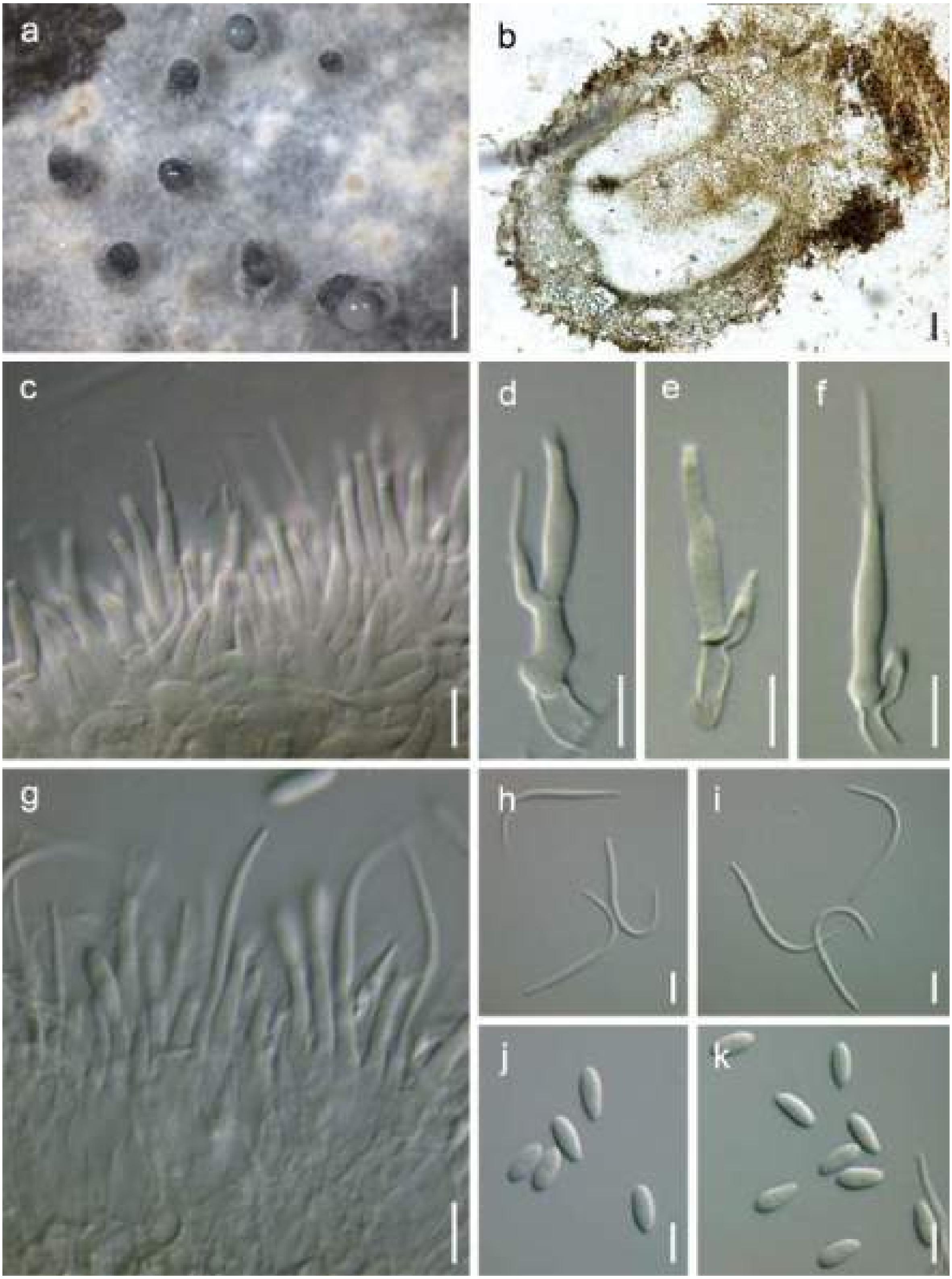


Fig. 122 ***Diaporthe pyracanthae*** (CDP 052, **new record**). **a** Conidiomata formed on 1/2 PDA. Conidia are oozing in pearl mucoid masses. **b** Vertical section of conidioma, showing its heart-shaped internal cavity. **c**–**g** Conidiogenous cells. **h**, **i** Beta conidia. **j**, **k** Alpha conidia. Scale bars: **a** = 0.5 mm, **b** = 20 µm, **c**–**k** = 5 µm

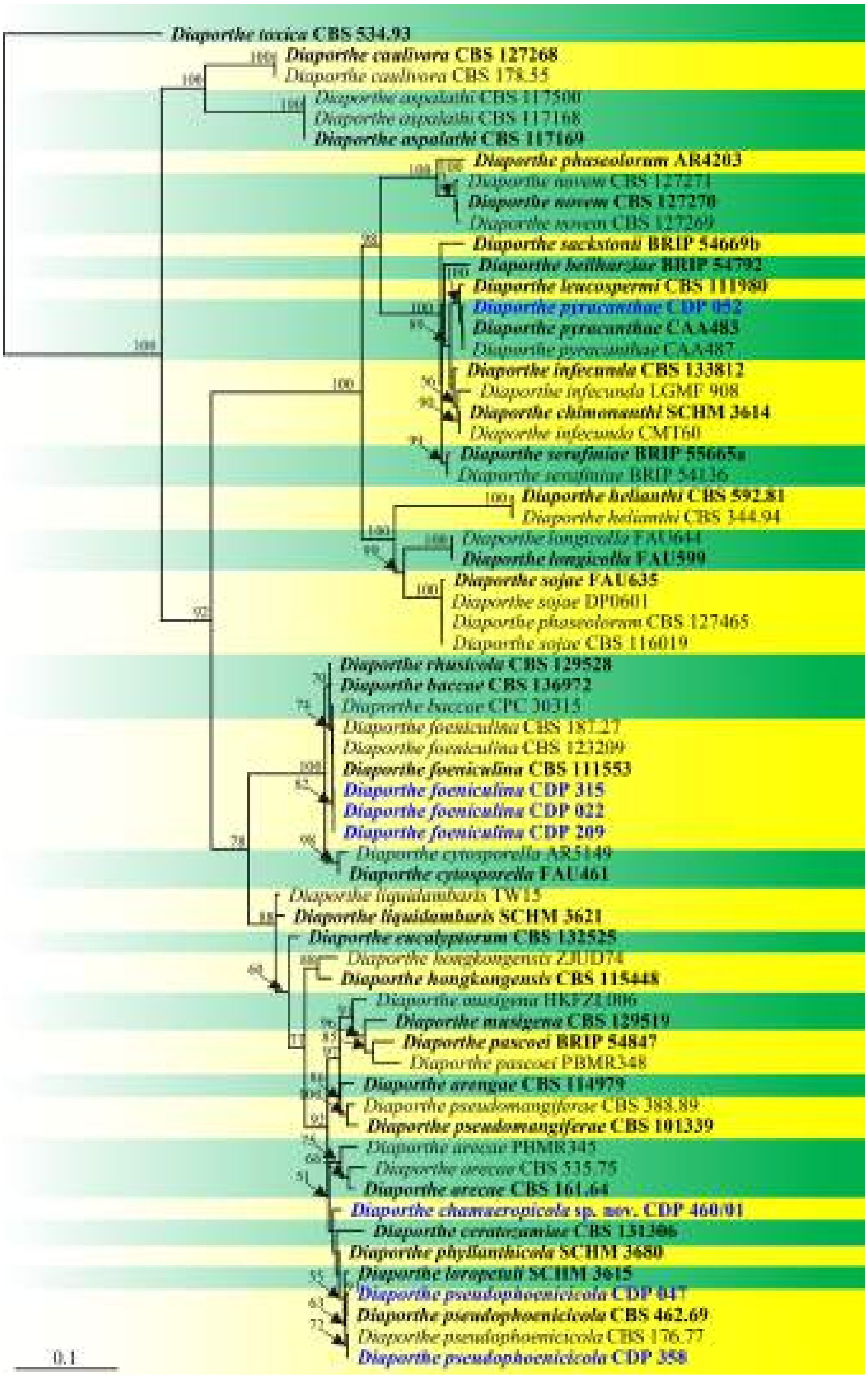


Fig. 123 Maximum Likelihood tree generated by RAxML with GTR + G + I nucleotide substitution model using the combined four loci ITS, TEF1-α, TUB and CAL. The sequences were retrieved from GenBank according to BLAST searches with the ITS locus and by reference to the recent literature. Sixty-four strains are included in the combined analyses that comprise 2248 characters (including gaps) (502 characters for ITS, 669 for TUB, 411 for TEF1-α and 554 for CAL) after alignment and manual adjustment. The final likelihood score for the ML tree was − 15269.024241. The matrix had 1121 distinct alignment patterns, with 27.31% undetermined characters or gaps. ML bootstrap support values (> 50%) are shown above the branches. The scale bar represents the expected number of nucleotide changes per site. *Diaporthe toxica* (CBS 534.93) was included as an outgroup. Ex-type/ex-epitype/ex-isotype/ex-neotype cultures are in bold and newly generated sequences are in blue

of *Zea mays* in Croatia. Sutton (1964) re-circumscribed *Phaeocytostroma* and synonymized *Pleocyta* and *Phaeocytosporella* under *Phaeocytostroma*. Lamprecht et al. (2011) provided additional collections and phylogenetic placement of species in *Phaeocytostroma* and included in *Diaporthaceae*. Our phylogenetic taxon sampling *Phaeocytostroma* were retrieved from Lamprecht et al. (2011) and the GenBank database. Six species have been included in *Phaeocytostroma* (Index Fungorum 2021). This study introduces a new species *Phaeocytostroma yomense* as a saprobic taxon isolated from decaying submerged wood in a freshwater habitat (Fig. 123).

Phaeocytostroma yomense Boonmee, Chandrasiri & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF558544; *Facesoffungi number*: FoF 09958; Fig. 124

Etymology: In reference to the Yom River where the holotype was collected.

Holotype: MFLU 21-0070

Saprobic on decaying submerged wood in the river. **Sexual morph** Undetermined. **Asexual morph** Coelomycetous. *Conidiomata* 337–452 μm high, 246–393 μm diam., pycnidial, white cream, superficial, scattered, gregarious, covered by massy brown hyphal mats, subglobose, uniloculate, transparent when fresh, simply fragile when dry, ostiole, dehiscence by breakdown of upper wall of conidiomata. *Conidiomata walls* easily fragile, difficult to observe, conidiophores and conidiogenous cells not seen. *Conidia* 14–23 × 3–6 μm ($\bar{x}$ = 18 × 4.5 μm, n = 20), cylindrical-ellipsoid, oblong allantoid, asymmetrical with obtuse ends, aseptate, pale brown, smooth-walled.

Culture characteristics: Conidium germinating on water agar within 12 h at room temperature. Colonies on PDA, fast growing, reaching 5 cm diam., in 2 weeks, slightly effuse, entire edge, brown to dark brown in surface, dark brown in reverse, mycelium superficial, partially immersed, brown, radiating outwards.

Material examined: THAILAND, Phayao Province, Pong, Yom River, on decaying submerged wood in the river shore, 18 December 2019, S. Boonmee and K.S.U. Chandrasiri, YR2 (MFLU 21-0070, **holotype**), ex-type living culture, MFLUCC 21-0093.

GenBank numbers: ITS = MZ538521, LSU = MZ538555.

Notes: *Phaeocytostroma yomense* shares similar conidial features such as cylindrical-ellipsoid to oblong shapes and pale brown colour to species *Ph. sacchari* (Sutton 1964, 1980), but *Ph. yomense* differs from *Ph. sacchari* in conidiomatal features such as superficial, bright pigmented and covered by hyphal mats. Phylogenetically, *Ph. yomense* is position in a distinct lineage basal to the strain of *Ph. plurivorum* (CBS 113835) with 98% MLBS, 1.00 BYPP support (Fig. 125). A comparison of the ITS sequence between *Ph. yomense* (MFLUCC 21-0093) and *Ph. plurivorum* (CBS 113835) showed 1.54% (9/581 bp with 7 gabs difference). However, *Ph. yomense* differs from *Ph. plurivorum* (Sutton 1980) in having white cream and smaller conidiomata (337–452 × 246–393 μm vs. up to 700 × 300–400 μm). *Phaeocytostroma yomense* differs from other species by its current occurrence as an aquatic taxon in a freshwater habitat and having superficial, white cream pigmented, covered by massy hyphal mat conidiomata and pale brown conidia (Fig. 124). We therefore, introduce a new species *Ph. yomense* based on its morphological distinctness and phylogenetic affinity.

Fuscosporellales Jing Yang, Bhat & K.D. Hyde

Notes: Yang et al. (2016) introduced the new order *Fuscosporellales* based on the evidence of multigene phylogenetic analysis to accommodate a monotypic family *Fuscosporellaceae*.

Fuscosporellaceae Jing Yang, Bhat & K.D. Hyde

Notes: *Fuscosporellaceae* was introduced by Yang et al. (2016) to accommodate six genera *Bactrodesmiastrum*, *Fuscosporella*, *Mucispora*, *Parafuscosporella*, *Plagiascoma* and *Pseudoascotaiwania* and 14 species all of which were described from lignicolous substrates in freshwater habitats. The type species of the family is *Fuscosporella pyriformis* Jing Yang, Bhat & K.D. Hyde (Boonyuen et al. 2016; Yang et al. 2016). The family is characterized by macronematous, mononematous, branched, hyaline conidiophores; holoblastic, globose to clavate conidiogenous cells; obovate to obpyriform, with a septum near the base, smooth, brown to dark brown conidia. Based on morphology and the combined phylogenetic analyses of ITS and SSU sequence data, a novel species *Parafuscosporella nilotica* is introduced.

Parafuscosporella Jing Yang & K.D. Hyde

Notes: *Parafuscosporella* currently comprises three species described from freshwater habitats in Thailand. The genus is characterized by sphaerical to cushion-shaped, erumpent to superficial, black, gelatinous sporodochia, with a jelly-like cover; semi-macronematous, mononematous, compact, flexuous, simple or branched, mostly moniliform, conidiophores with globose to subglobose, ellipsoidal or clavate cells; monoblastic, integrated, sometimes discrete, terminal, globose, subglobose, ellipsoidal or clavate conidiogenous cells and acrogenous, ellipsoidal to broadly obpyriform, smooth, dark brown to black conidia, with a septum near the base, sometimes with a small protuberance, with pale brown basal cells (Boonyuen et al. 2016; Yang et al. 2016). In this study, a new species *Parafuscosporella nilotica* is introduced based on evidence of morphology and phylogenetic placement (Figs. 126 and 127).

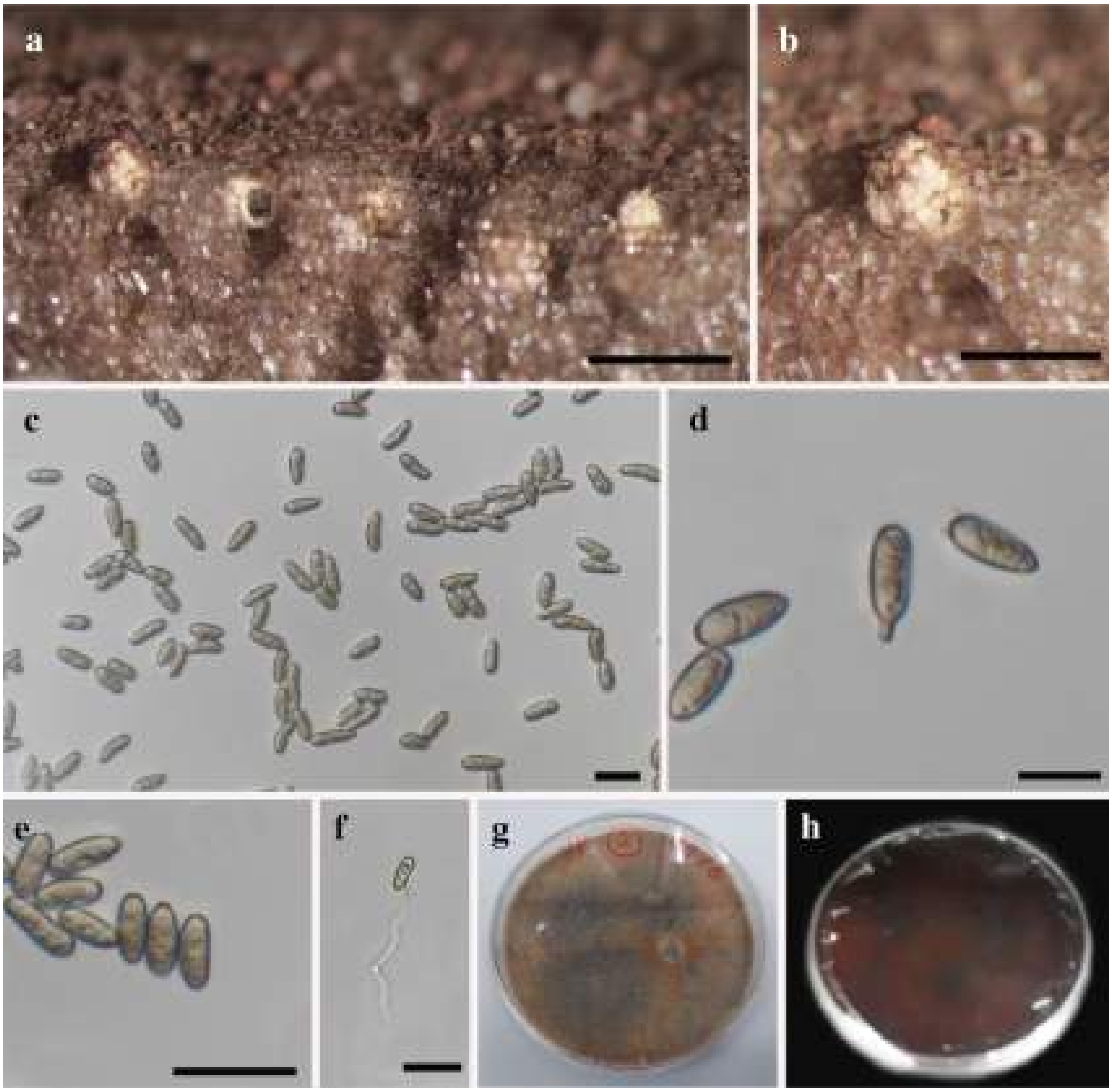


Fig. 124 ***Phaeocytostroma yomense*** (MFLU 21-0070, **holotype**). **a**, **b** Appearance of white conidiomata on decaying submersed wood substrate. **c**–**e** Conidia. **f** Germinated conidium. **g**, **h** Culture on PDA from surface and reverse. Scale bars: **a** = 100 µm, **b** = 50 µm, **c**, **e**, **f** = 20 µm, **d** = 10 µm

Parafuscosporella nilotica Abdel-Aziz ***sp. nov.***

Index Fungorum number: IF557838; *Facesoffungi number*: FoF 09199; Fig. 126

Etymology: Named after the River Nile, where this fungus was collected.

Holotype: CBS H-22128

Saprobic on the surface of decaying submerged wood in a freshwater river. **Sexual morph** Undetermined. **Asexual morph** *Colonies* on natural substrate, effuse, black. *Mycelium* partly immersed, partly superficial, composed of septate, hyaline hyphae, 1.5–3 µm wide. *Conidiomata* 300–600 µm diam. ($\bar{x}$ = 421 µm, n = 10), sporodochial, scattered, sphaerical to cushion-shaped, with jelly-like cover, gelatinous. *Conidiophores* micronematous, mononematous, either reduced to conidiogenous cells and conidia born directly on hyphae or when present unicellular, cylindrical to clavate, smooth-walled, hyaline, 3–7 µm long, 1.5–3 µm wide. *Conidiogenous cells* holoblastic, monoblastic, integrate. *Conidial secession* rhexolytic. *Conidia* 18–22 × 11–15 µm ($\bar{x}$ = 21 × 13.5 µm, n = 50), acrogenous, obpyriform, with a septum near the base, smooth, brown to dark brown, basal cell paler.

Culture characteristics: Conidia germinating on PDA within 24 h at 25 °C and germ tubes produced from both ends. Colonies on PDA reaching 1–1.5 cm diam. after 1 month at 25 °C, dark-brown, same from below.

Material examined: EGYPT, Sohag City, the River Nile, on decaying submerged wood, 14 August 2012, F.A.

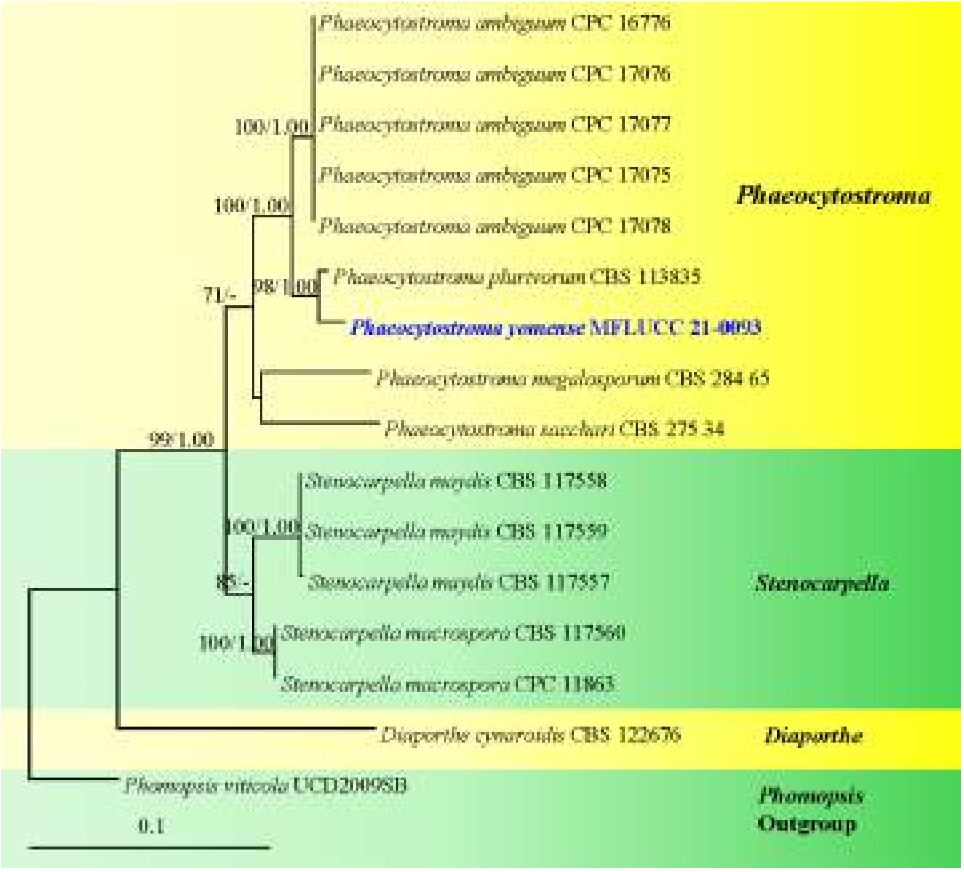


Fig. 125 Maximum likelihood phylogenetic tree based on a combined ITS, LSU and TEF1-α sequence data of *Phaeocytostroma* taxa and some related genera in *Diaporthaceae*. The tree is rooted with *Phomopsis viticola* (UCD2009SB). Bootstrap support values for maximum likelihood (MLBS, left) equal to or greater than 70% is given above the nodes. Bayesian posterior probabilities (BYPP, right) equal to or greater than 0.95 are given above the nodes. The newly generated sequence is in blue bold

Abdel-Aziz (CBS H-22128, **holotype**), ex-type living culture (MF 1312).

GenBank numbers: ITS = MN921198, SSU = MN921199.

Notes: Phylogenetic analyses of ITS placed *Parafuscosporella nilotica* as distinct novel species within the *Parafuscosporella* clade with 87% MLBS, 95% MPBS, 0.98 BYPP support (Fig. 127). *Parafuscosporella nilotica* differs from the other *Parafuscosporella* species in having simple, micronematous, cylindrical to clavate conidiophores, whereas other species have macronematous, mostly moniliform, with globose to subglobose, ellipsoidal or clavate cells (Fig. 126). *Parafuscosporella nilotica* has much smaller conidial sizes than all species; 18–22 × 11–15 µm vs 20–29 × 13–19 µm for *P. aquatica*; (37.5–)40–47.5 × (25–)27.5–42.5 µm for *P. garethii*; 28–37 × 14–21 µm for *P. moniliformis*; 26.5–36 × 12–26 µm for *P. mucosa* and 23–30 × 16–26 µm for *P. pyriformis* (Boonyuen et al. 2016; Yang et al. 2016, 2020).

Hypocreales Lindau

Notes: The recent treatments for *Hypocreales* in Hyde et al. (2020d) and Yuan et al. (2020).

Nectriaceae Tul. & C. Tul. [as 'Nectriei']

Notes: *Nectriaceae* was introduced by Tulasne and Tulasne (1865) and accepted as a family in *Hypocreales*, based on stromatic and perithecial characters (Seaver 1909; Petch 1938; Kreisel 1969; Rossman et al. 1999). Presently, *Nectriaceae* comprised 46 genera (Wijayawardene et al. 2020). Asexual morphs are mainly hyphomycetous, less commonly coelomycetous (Hyde et al. 2020b, d). *Nectriaceae* members are cosmopolitan in distribution as saprobes, endophytes or pathogens of various host species (Rossman et al. 1999; Lombard et al. 2015).

Fusarium Link

Notes: *Fusarium* species are economically important fungi including, many well-known plant pathogens, which cause blights, cankers, root and stalk rots and wilts of broad-acre, horticultural, ornamental and forest plants, and cause human infections worldwide (Jayawardena et al. 2019; Summerell 2019). We describe a new species of *Fusarium* isolated from grain sorghum (*Sorghum bicolor*) in Queensland, Australia, and introduce new records of *F. atrovinosum* and *F. clavum* on *S. bicolor* based on morphological characters and multi-locus phylogenetic analyses.

Fusarium atrovinosum L. Lombard & Crous, Fungal Systematics and Evolution 4: 190 (2019)

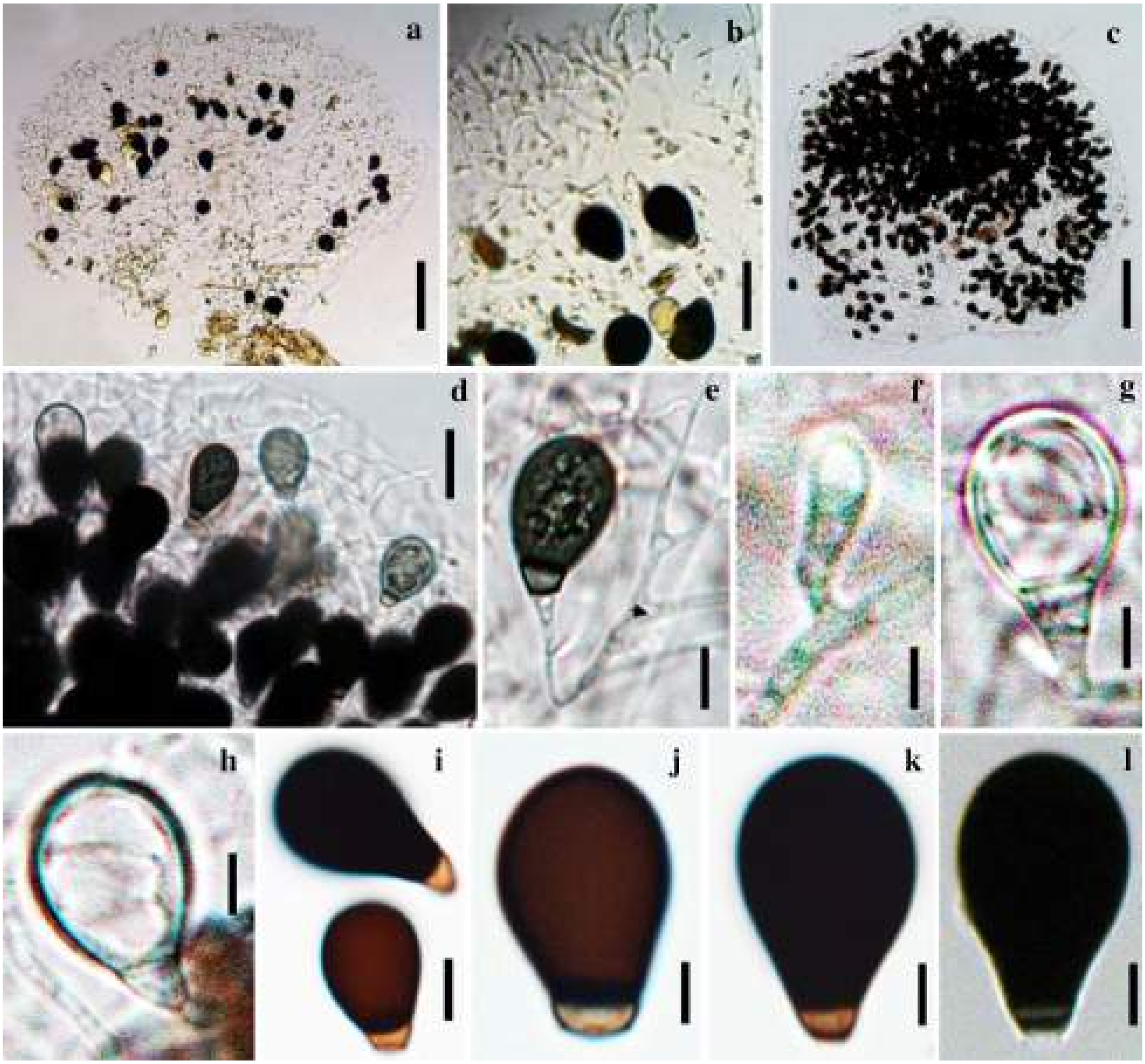


Fig. 126 ***Parafuscosporella nilotica*** (CBS H-22128, **holotype**). **a**, **b** Vertical section through sporodochium. **c**, **d** Squash of sporodochium. **e**–**l** Conidia at different stages of development. Scale bars: **a**, **c** = 120 µm, **b**, **d** = 20 µm, **e**, **i** = 10 µm, **f**–**h**, **j**–**l** = 5 µm

Index Fungorum number: IF831559; *Facesoffungi number*: FoF 09577; Fig. 128

Saprobic on dead stalk of *Sorghum bicolor*. **Sexual morph** Undetermined. **Asexual morph** *Conidiophores* 20–50 µm tall, carried on aerial mycelium, unbranched or irregularly or sympodially branched, bearing a terminal single phialide or whorl of 2–3 phialides. *Conidiogenous cells* 9–23 × 2–4 µm, polyphialides, subulate to subcylindrical, smooth. *Conidia* 4–14 × 2–3 µm, formed in false heads on the phialide tips, hyaline, fusiform to ellipsoidal to obovoid, smooth and thin-walled, mostly 0-septate, rarely 1–2-septate then larger. *Chlamydospores* 5–22 µm diam., abundant, globose to subglobose, smooth to slightly verrucose, formed terminally or intercalarily in chains of three or more; wall 1–1.5 µm.

Culture characteristics: Colonies on PDA reaching 90 mm at 24 °C after 28 d in the dark; surface vinaceous, mycelium dense to woolly, without odour; reverse livid red to dark vinaceous. On SNA colonies sparse, white to pale rosy buff in the centre, powdery due to abundant; reverse pale rosy buff. On CLA aerial mycelium abundant, white, lacking sporodochia on the carnation leaf pieces. On WA colonies sparse and powdery; pale rosy vinaceous in the centre; reverse pale rosy vinaceous.

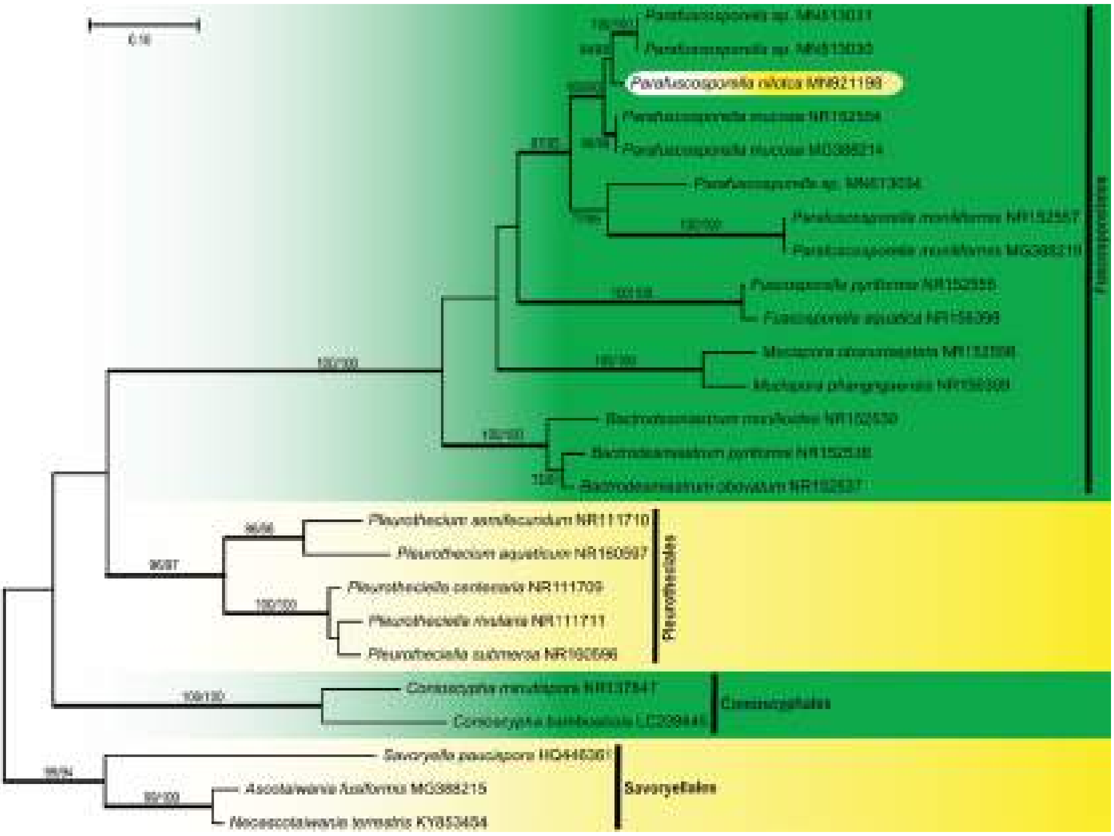


Fig. 127 Phylogenetic relationship of *Parafuscosporella nilotica* with related taxa in *Fuscosporellaceae* based on the nucleotide sequences of the ITS. The maximum likelihood (ML) tree (-ln likelihood = 4928.50) was constructed in MEGA X (Kumar et al. 2018). The maximum parsimonious data set of the combined genes consisted of 25 taxa with 3 representatives of *Savoryellales* are used as the outgroup taxa. The dataset includes 503 total characters, of which 175 were constant, 30 parsimony-uninformative and 298 parsimony-informative. The parsimony analyses of the data matrix yielded 3 equally most parsimonious trees with a tree length of 1021 steps [consistency index (CI) = 0.6298, homoplasy index (HI) = 0.3702, retention index (RI) = 0.7816, rescaled consistency index (RC) = 0.4923]. Phylogenetic trees obtained from ML, maximum parsimony (MP) and Bayesian inference posterior probabilities (BIPP) were similar in topology. Bootstrap support on the nodes represents MLBS and MPBS equal to or greater than 50%. Branches with a BYPP of equal to or greater than 95% are in bold. The new taxon is in yellow box

Material examined: AUSTRALIA, Goondiwindi, on dead stalk of *Sorghum bicolor*, 19 February 2018, N. Vaghefi, BRIP 70767a, **new record**.

GenBank numbers: CAL = MW403492, RPB2 = MW403493, TEF1-α = MW403494.

Notes: *Fusarium atrovinosum* belongs to the *Fusarium chlamydosporum* species complex (O'Donnell et al. 2009; Lombard et al. 2019b). In a four-locus phylogeny (Fig. 129), the isolate (BRIP 70767a) was recovered in a well-supported clade (98% MLBS, 1.00 BYPP) that contained the type strain of *F. atrovinosum* (CBS 445.67). This isolate (BRIP 70767a) was morphologically and culturally similar to the type strain of *F. atrovinosum* (CBS 445.67) described in Lombard et al. (2019b). *Fusarium atrovinosum* was described on *Triticum aestivum* (wheat) in Australia (Lombard et al. 2019b). Subsequently, *F. atrovinosum* has been reported from Brazil in association with rice seed and other hosts (Costa 2020). These studies indicate that *F. atrovinosum* may have an association with grass (*Poaceae*) hosts. This is the first record of *F. atrovinosum* on *Sorghum* (Fig. 128).

Fusarium clavum J.W. Xia, L. Lombard, Sand.-Den., X.G. Zhang & Crous, Persoonia 43: 199 (2019)

Index Fungorum number: IF833468; *Facesoffungi number*: FoF 09578; Fig. 130

Saprobic on dead stalk of *Sorghum bicolor*. **Sexual morph** Undetermined. **Asexual morph** *Sporodochia* salmon to orange, formed abundantly on carnation leaf pieces. Conidiophores densely and irregularly branched. *Conidiogenous cells* monophialides, subulate to subcylindrical, smooth, thin

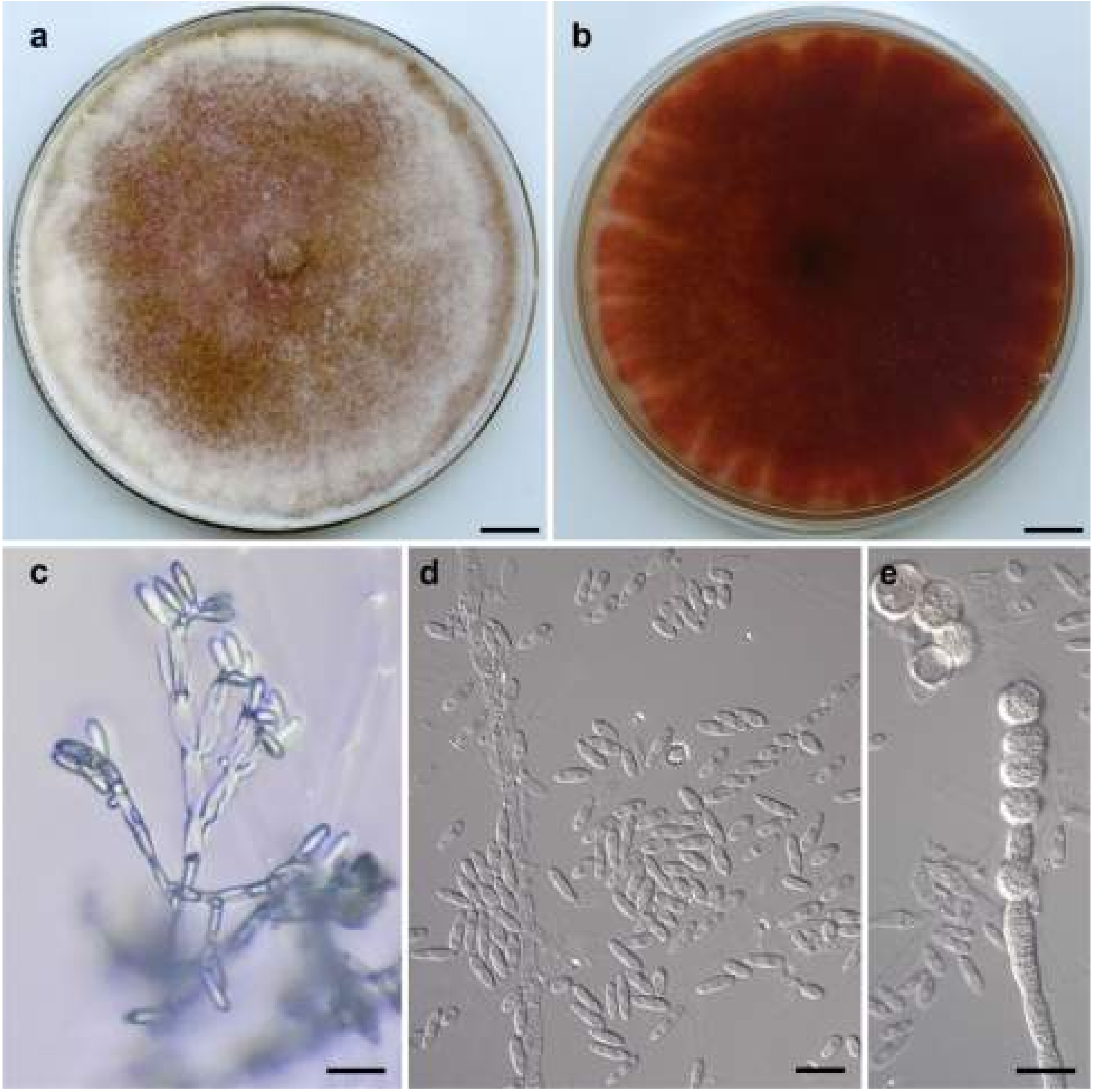


Fig. 128 ***Fusarium atrovinosum*** (BRIP 70767a, **new record**). **a**, **b** Culture on PDA from surface and reverse. **c** Conidiophores. **d** Conidia. **e** Chlamydospores. Scale bars: **a**, **b** = 1 cm, **c**–**e** = 10 µm

walled. *Conidia* 25–35 × 3–4 µm, falcate, slender, curved dorsiventrally, tapering towards both ends, with elongated or whip-like curved apical cells, mostly 3-septate, hyaline, smooth-walled. *Chlamydospores* 6–12 µm diam., abundant, globose, subglobose to oval, subhyaline to yellowish-brown, smooth-walled, terminal or intercalary, solitary, in pairs or forming chains.

Culture characteristics: Colonies on PDA reaching 90 mm at 24 °C after 28 d; surface cinnamon, flat, velvety, with scant aerial mycelium; reverse cinnamon. On SNA and WA colonies sparse and flat, without colour, sporulation moderate on the surface of the agar and the carnation leaf pieces.

Material examined: AUSTRALIA, Brookstead, on dead stalk of *Sorghum bicolor*, 19 February 2018, N. Vaghefi, BRIP 70756a, **new record**.

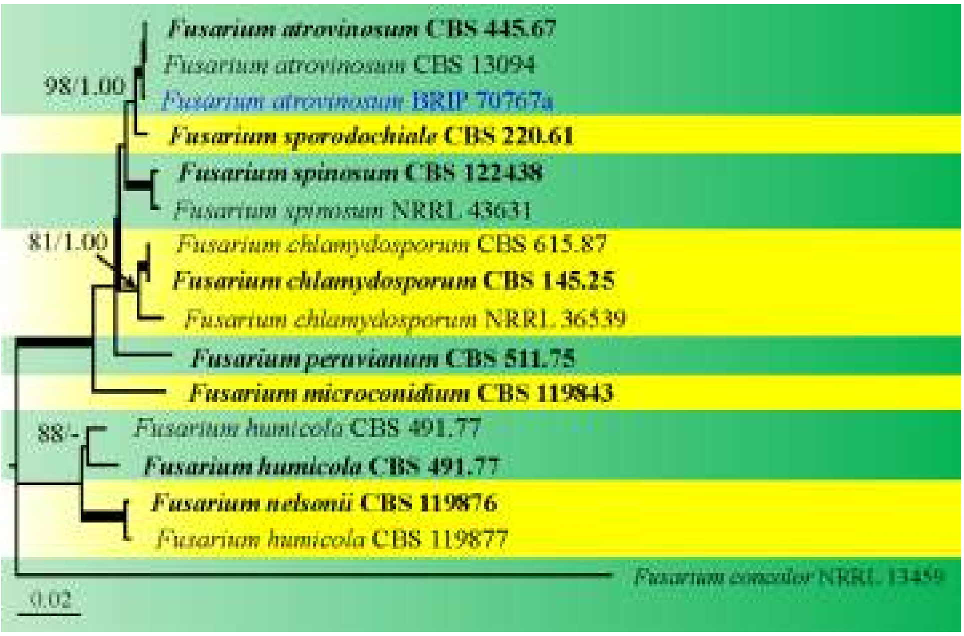


Fig. 129 Phylogram generated from Bayesian analysis based on combined CAL, RPB1, RPB2 and TEF1-α sequence data representing *Fusarium chlamydosporum* species complex and related taxa. The second measure of branch support was obtained through Maximum Likelihood (ML) analysis of the same alignment using RAxML v. 8 (Stamatakis 2014) based on the GTR substitution model with gamma-distribution rate variation for each partition. Reference strains were obtained from Lombard et al. (2019b). The tree is rooted to *Fusarium concolor* (NRRL 13459). The analysis was performed using MrBayes v. 3.2.4 (Ronquist et al. 2012) based on the K80, K80+G, and HKY+G nucleotide substitution models selected for CAL, RPB2, and TEF1-α, respectively, using PAUP v. 4.0 (Swofford 2003) and MrModeltest v. 2.3. (Nylander 2009). Maximum likelihood bootstrap support values (MLBS) greater than 80% are placed above the nodes and Bayesian posterior probabilities (BYPP) equal to or greater than 0.95. Branches with MLBS = 100% and BYPP = 1.00 are thickened. Scale bar indicates the number of substitutions per nucleotide. Ex-type strains are in bold and newly isolate is in blue

GenBank numbers: CAL = MW403051, RPB1 = MW403052, RPB2 = MW403053, TEF1-α = MW403054.

Notes: *Fusarium clavum* belongs to the *Fusarium incarnatum-equiseti* species complex (Wang et al. 2019a; Xia et al. 2019). In a three-locus phylogeny (Fig. 131), the isolate (BRIP 70756a) was recovered in a well-supported clade (99% MLBS, 1.00 BYPP) with the type strain *F. clavum* (CBS 126202). *Fusarium clavum* has been reported from various plants, human organs, and soil in Africa, Europe, Asia, and the USA (Xia et al 2019; Matic et al. 2020). Although the isolate (BRIP 70756a) was isolated from stalk rot on *S. bicolor*, the pathogenicity of this isolate has not been established (Fig. 130). This is the first record of *F. clavum* on *S. bicolor*, and the first record of this fungus in Australia.

Fusarium queenslandicum T.B. Potter, A.H. Sparks, Vaghefi & R.G. Shivas, ***sp. nov.***

MycoBank number: MB837495; *Facesoffungi number*: FoF 09579; Fig. 132

Etymology. The name refers to the State of Queensland, from where this fungus was collected.

Holotype: BRIP 70769a

Saprobic on dead stalk of *Sorghum bicolor*. **Sexual morph** Undetermined. **Asexual Morph** *Conidiophores* abundant on aerial mycelium, unbranched, lateral or terminal. *Conidiogenous cells* monophialides, subcylindrical. *Microconidia* in false heads on aerial mycelium, 4–25 × 3–4.5 µm, narrowly ellipsoidal or reniform, hyaline, aseptate. Sporodochia and macroconidia not seen. *Chlamydospores* 7–13 × 7–9 µm, abundant, globose to ellipsoidal, intercalary or terminal, single or in pairs, rough-walled.

Culture characteristics: Colonies on PDA reaching 90 mm at 24 °C after 28 d, surface appressed with velvety cream patches of aerial mycelium up to 1 cm diam., subhyaline on the agar; reverse pale buff; on SNA with sparse aerial mycelium, cream becoming pale violet in the central part; sporulation abundant on PDA, SNA, WA and carnation leaf pieces.

Material examined: AUSTRALIA, Goondiwindi, on dead stalk of *Sorghum bicolor*, 19 February 2018, *N. Vaghefi*, BRIP 70769a (**holotype**), includes an ex-type living culture.

GenBank numbers: RPB1 = MW038832, RPB2 = MW038833, TEF1-α = MW038834, TUB2 = MW403138.

Notes: *Fusarium queenslandicum* belongs to the *F. oxysporum* species complex (Lombard et al. 2019a) based

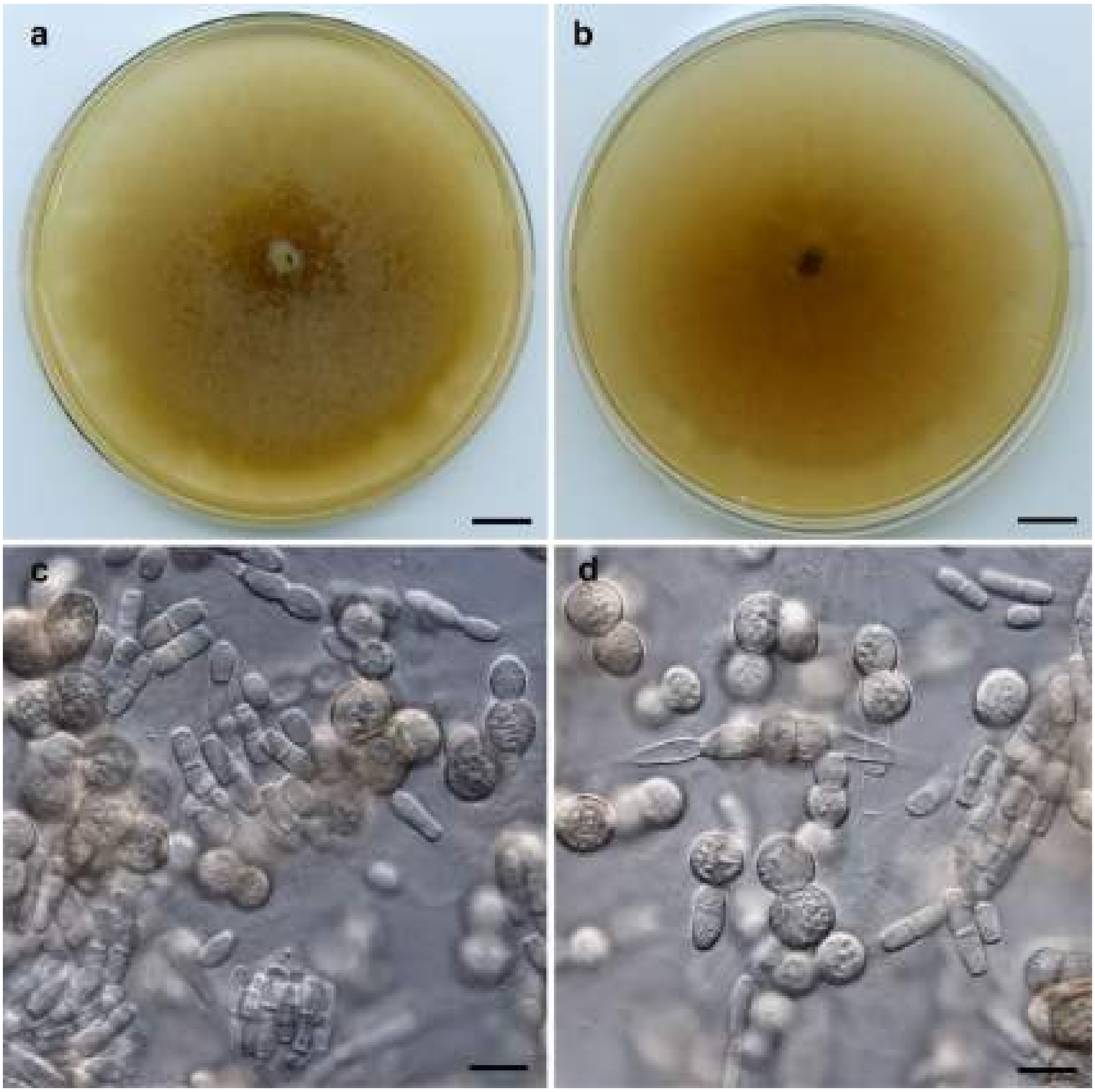


Fig. 130 ***Fusarium clavum*** (BRIP 70756a, **new record**). **a**, **b** Culture on PDA from surface and reverse. **c**, **d** Conidia and chlamydospores. Scale bars: **a**, **b** = 1 cm, **c**, **d** = 10 µm

on sequence comparisons of the RPB1, RPB2, TEF1-*α* and TUB2 loci with those available in the *Fusarium* MLST database (http://www.cbs.knaw.nl/fusarium). The TEF1-α sequence of *F. queenslandicum* was identical to a culture (CBS 412.90 = NRRL 36464) collected from tomato in Israel that was identified as *F. languescens*. A pairwise comparison revealed 10 nucleotide variations between the TEF1-*α* sequence of *F. queenslandicum* and that of the ex-type culture of *F. languescens* (CBS 64578 = NRRL 36531). The four-locus phylogeny based on sequences of CAL, RPB2, TEF1-α, and TUB2 clearly separated *F. queenslandicum* from *F. languescens* and other species within the FOSC (Fig. 133). *Fusarium queenslandicum* was isolated from an asymptomatic stalk of cultivated *Sorghum bicolor* (Fig. 132).

Mariannaea G. Arnaud ex Samson

Notes: We follow the latest treatment and updated accounts of *Mariannaea* in Hyde et al. (2020b).

Mariannaea camelliae N. Suwannarach & J. Kumla, ***sp. nov.***

Mycobank number: MB838938, *Facesoffungi number*: FoF 09959; Fig. 134

Etymology: The specific epithet "*camelliae*" refers to generic name of the host plant, *Camellia*.

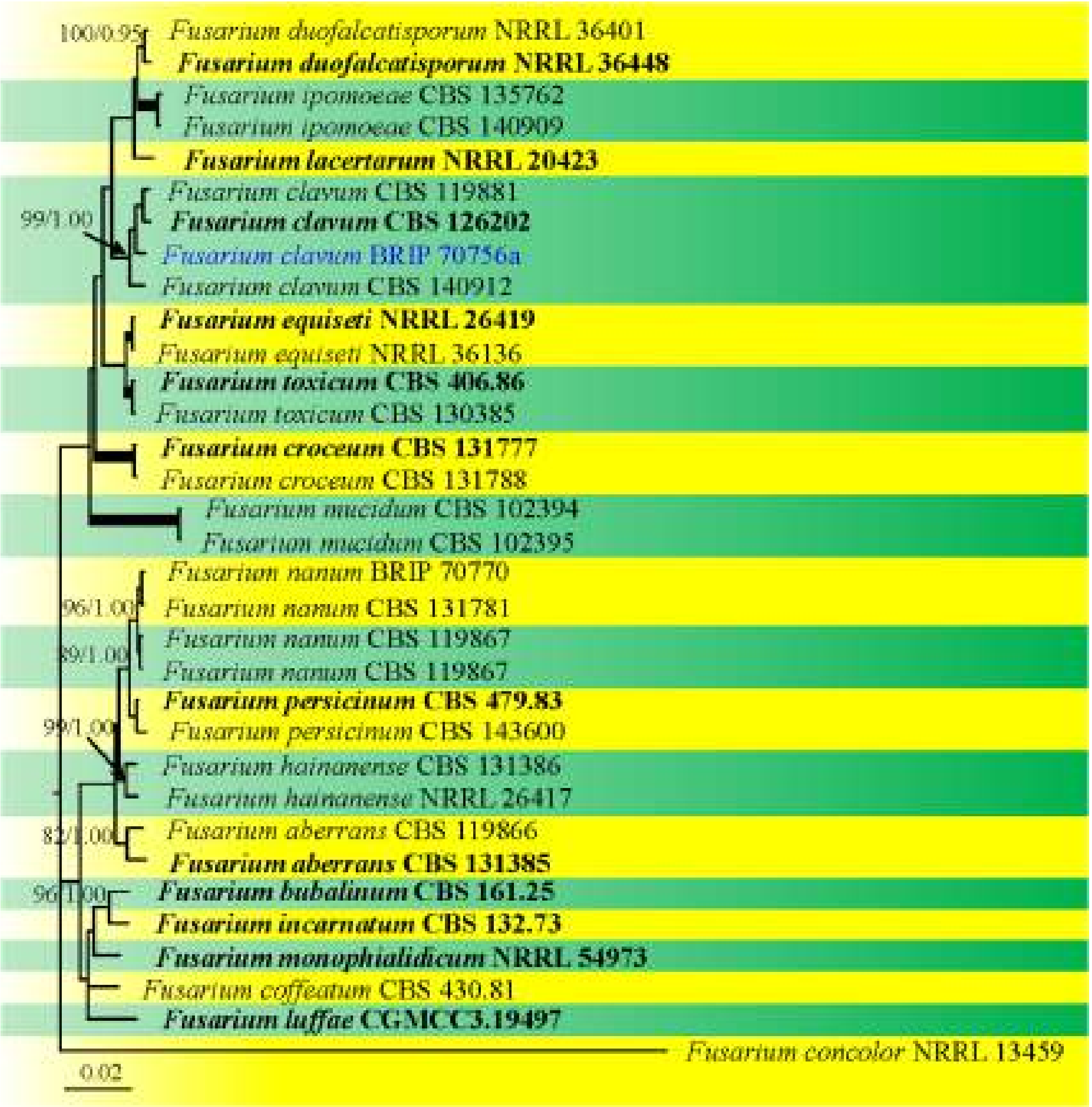


Fig. 131 Phylogram generated from Bayesian analysis based on combined CAL, RPB2, and TEF1-α sequence data representing *Fusarium incarnatum-equiseti* species complex and related taxa. The second measure of branch support was obtained through Maximum Likelihood (ML) analysis of the same alignment using RAxML v. 8 (Stamatakis 2014) based on the GTR substitution model with gamma-distribution rate variation for each partition. Reference sequence were obtained from Xia et al. (2019). The tree is rooted to *Fusarium concolor* (NRRL 13459). The analysis was performed using MrBayes v. 3.2.4 (Ronquist et al. 2012) based on the K80, K80 + G, and HKY + G nucleotide substitution models selected for CAL, RPB2, and TEF1-α, respectively, using PAUP v. 4.0 (Swofford 2003) and MrModeltest v. 2.3. (Nylander 2009). Maximum likelihood bootstrap support values (MLBS) greater than 80% are placed above the nodes and Bayesian posterior probabilities (BYPP) equal to or greater than 0.95. Branches with MLBS = 100% and BYPP = 1.00 are thickened. Scale bar indicates the number of substitutions per nucleotide. Ex-type strains are in bold and newly isolate is in blue

Holotype: SDBR-CMU329

Endophyte from leaves of *Camellia sinensis* var. *assamica*. **Sexual morph** Undetermined. **Asexual morph** *Colonies* growing on PDA growing moderately fast, 30–50 cm diam., within 1 week at 25 °C, consisting of a matted felt with velutinous appearance, in age becoming funiculose to fasciculate, slightly powdery upon sporulation, surface of the colonies pale yellowish, with age brown, margin regular or irregular; reverse yellowish brown. *Colonies* growing on MEA growing moderately fast, 30–4.7 cm diam., within 1 week at 25 °C, consisting of a flat, homogeneous, mycelium loose, surface of the colonies white, margin regular or irregular; reverse white. *Colonies* growing on OA growing moderately fast, 30–50 cm diam., within 1 week at 25 °C, consisting of a matted felt with velutinous appearance, slightly powdery upon sporulation, surface of the

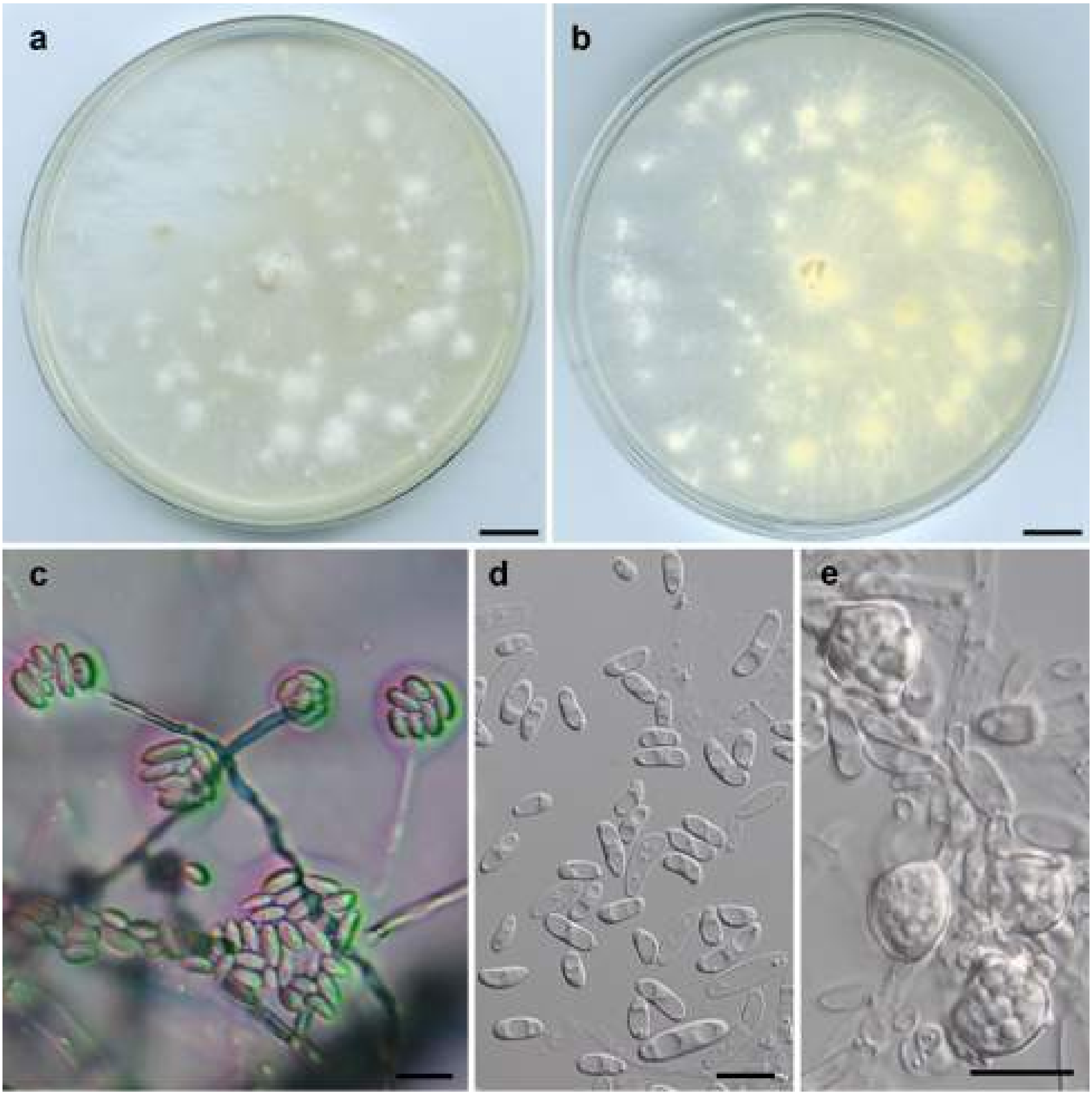


Fig. 132 ***Fusarium queenslandicum*** (BRIP 70769a, **holotype**). **a**, **b** Culture on PDA from surface and reverse. **c** Conidiophores with false heads. **d** Microconidia. **e** Chlamydospores. Scale bars: **a**, **b** = 1 cm, **c**–**e** = 10 µm

colonies grayish white, margin regular or irregular; reverse grayish white. *Hyphae* hyaline to slightly pale brown, smooth-walled, up to 5 µm wide, margin regular or irregular. *Conidial* formation was observed in PDA, MEA and OA. *Conidiophores* 105–225 µm long, axis 3.5– 7.5 mm wide, usually macronematous, mononematous, erect, septate, bearing short branches with whorls of 1–4 phialides, or whorls of phialides in verticils along the main stalk; Axis and branches usually terminating into a longer phialide. *Phialides* 13–17.5 × 2–4.5 µm, flask-like, hyaline, smooth. *Conidia* 4–7 × 3–5 µm, globose to subglobose, aseptate, hyaline, smooth-walled, produced in imbricatechains. *Chlamydospores* present, 6–11 × 4–9 µm, intercalary or terminal, produced in short chains, thick-walled, yellowish white, globose to ellipsoidal or lageniform.

Material exminated: THAILAND, Nan Province, Skad, Pua District, 19°15′42″ N 101°0′16″ E, isolated as an endophyte from leaves of *Camellia sinensis* var. *assamica*,

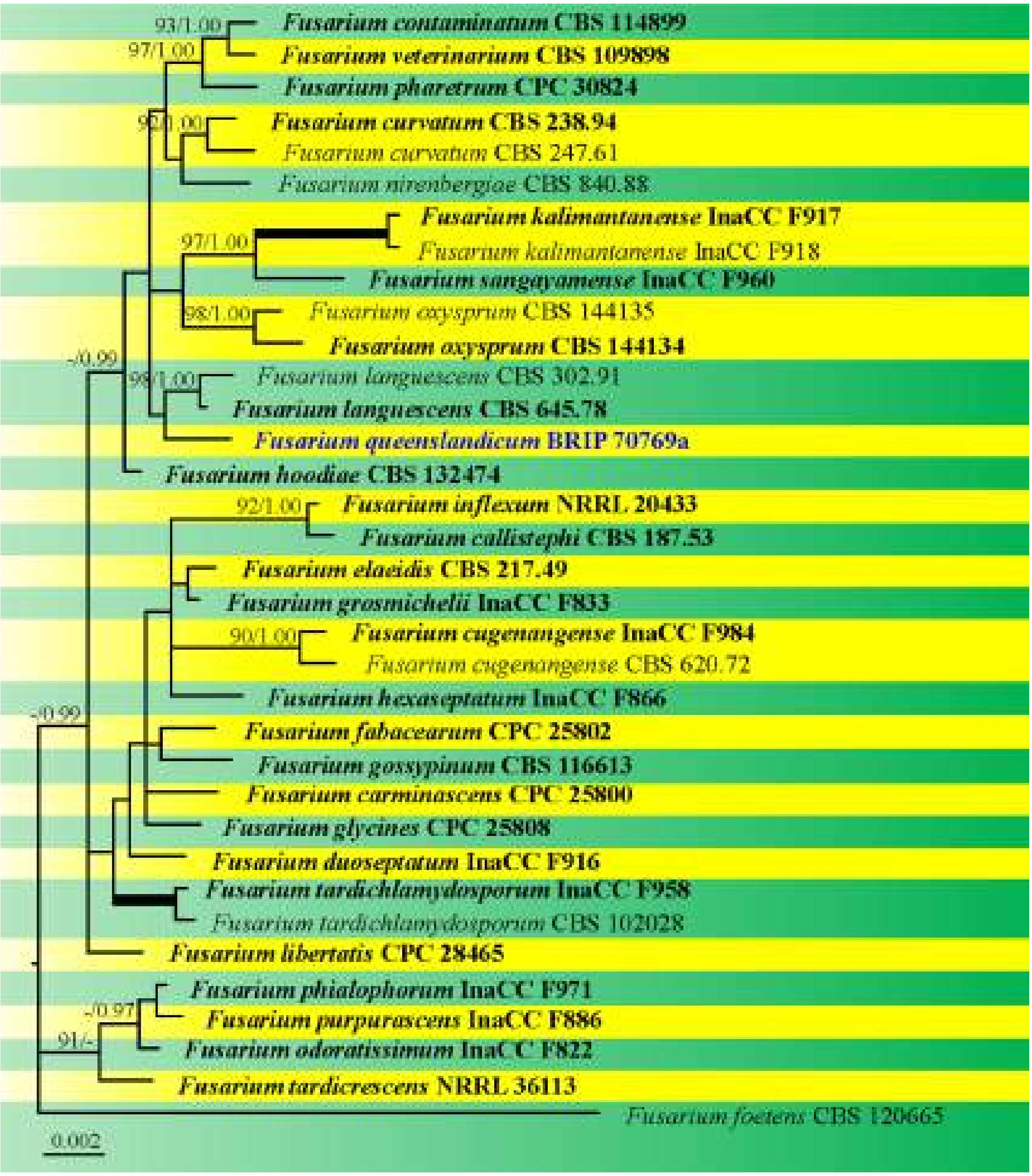


Fig. 133 Phylogram generated from Bayesian analysis based on combined CAL, RPB2, TEF1-α, and TUB2 sequence data representing *Fusarium oxysporum* species complex and related taxa. The second measure of branch support was obtained through Maximum Likelihood (ML) analysis of the same alignment using RAxML v. 8 (Stamatakis 2014) based on the GTR substitution model with gamma-distribution rate variation for each partition. Reference sequence were obtained from Lombard et al. (2019a) and Maryani et al. (2019). The tree is rooted to *Fusarium foetens* (CBS 120665). The analysis was performed using MrBayes v. 3.2.4 (Ronquist et al. 2012) based on the K80, K80 + G, HKY + G, and SYM + I + G nucleotide substitution models selected for CAL, RPB2, TEF1-α, and TUB2, respectively, using PAUP v. 4.0 (Swofford 2003) and MrModeltest v. 2.3. (Nylander 2009). Maximum likelihood bootstrap support values (MLBS) greater than 80% are placed above the nodes and Bayesian posterior probabilities (BYPP) equal to or greater than 0.95. Branches with BYPP = 1.00 and MLBS = 100% are thickened. Scale bar indicates the number of substitutions per nucleotide. Ex-type strains are in bold and newly sequence is in blue

September 2017, N. Suwannarach, SDBR-CMU329 (dried culture, **holotype**), ex-type living culture, TBRC13889.

GenBank number: ITS = MH734517, LSU = MH734518, TEF1-α = MH734520, TUB-2 = MH734519.

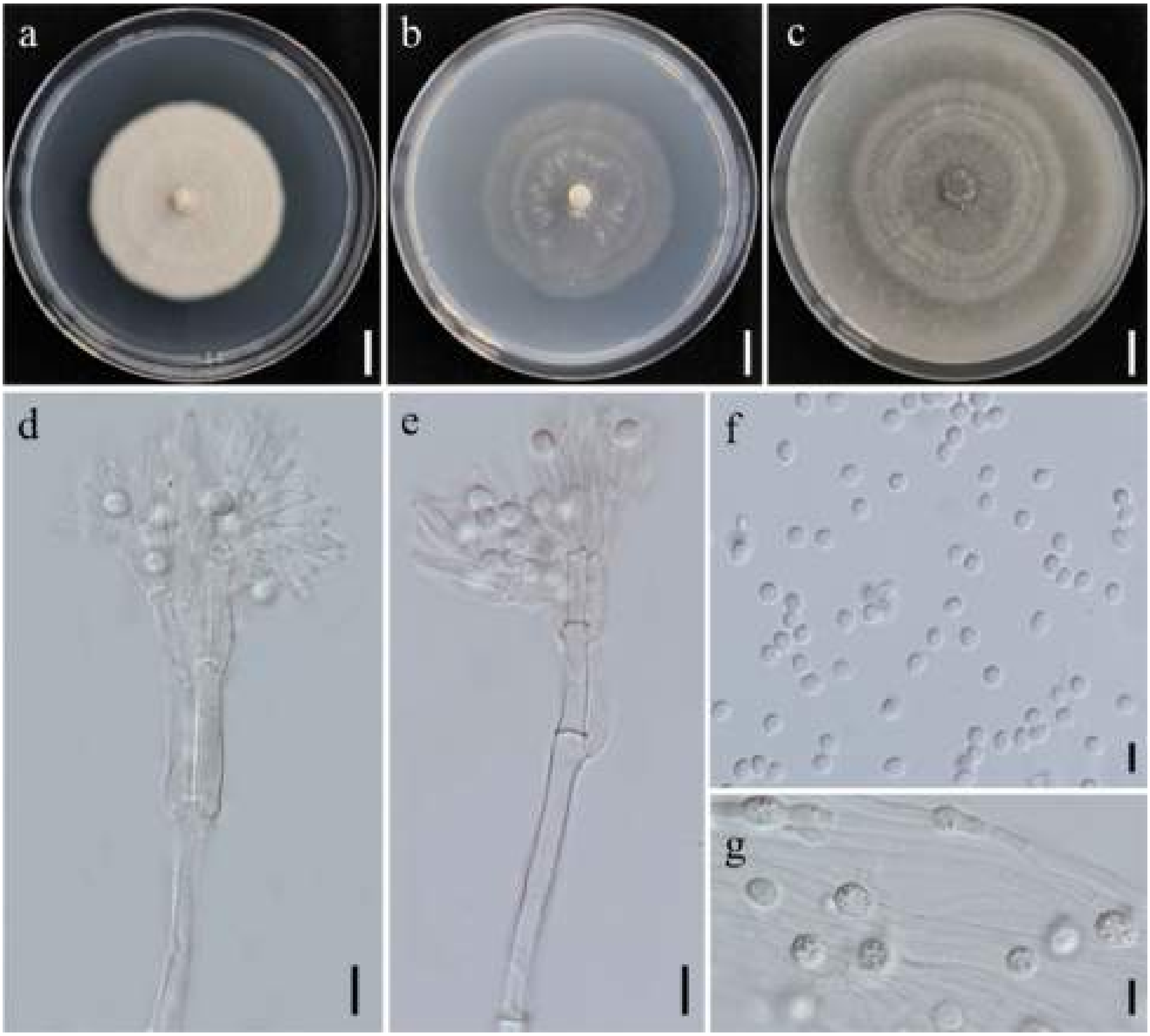


Fig. 134 ***Mariannaea camelliae*** (SDBR-CMU329, **holotype**). **a** Culture on PDA. **b** Culture on MEA. **c** Culture on OA. **d**, **e** Conidiophores and phialides. **f** Conidia. **g** Chlamydospores. Scale bars: **a**–**c** = 1 cm, **d**–**g** = 10 μm

Notes: *Mariannaea camelliae* was isolated as an endophytic fungus from leaves of *Camellia sinensis* var. *assamica* collected in northern Thailand. *Mariannaea camelliae* is characterized by pale yellowish colonies on PDA, globose to subglobose conidia and presenting chlamydospores (Fig. 134), and shares resemblance to *M. chlamydospora* (Hu et al. 2016). However, *M. camelliae* differs from *M. chlamydospora* in size of conidia and chlamydospores. Phylogenetically, *M. camelliae* forms a well-supported lineage basal to *M. atlantica*, *M. fusiformis* and *M. punicea* (100% MLBS, 1.00 BYPP; Fig. 135), the phylogeny also indicates that they are distinct species. Therefore, *Mariannaea camelliae* introduce as a new species based on morphology and phylogenetic evidence.

Thyronectria Sacc.

Notes: *Thyronectria* was introduced by Saccardo (1875) to accommodate *T. patavina* (Sacc.) as the type species. This species was later synonymized under *Pleonectria* (Hirooka et al. 2012). Therefore, Seeler (1940) introduced *Thyronectria rhodochlora* as the type species of *Thyronectria*. Recently, *Pleonectria* was synonymized with *Thyronectria* (Jaklitsch and Voglmayr 2014). Jaklitsch and Voglmayr (2014) accepted 42 *Thyronectria* species based on morphology and phylogenetic based evidence. In our

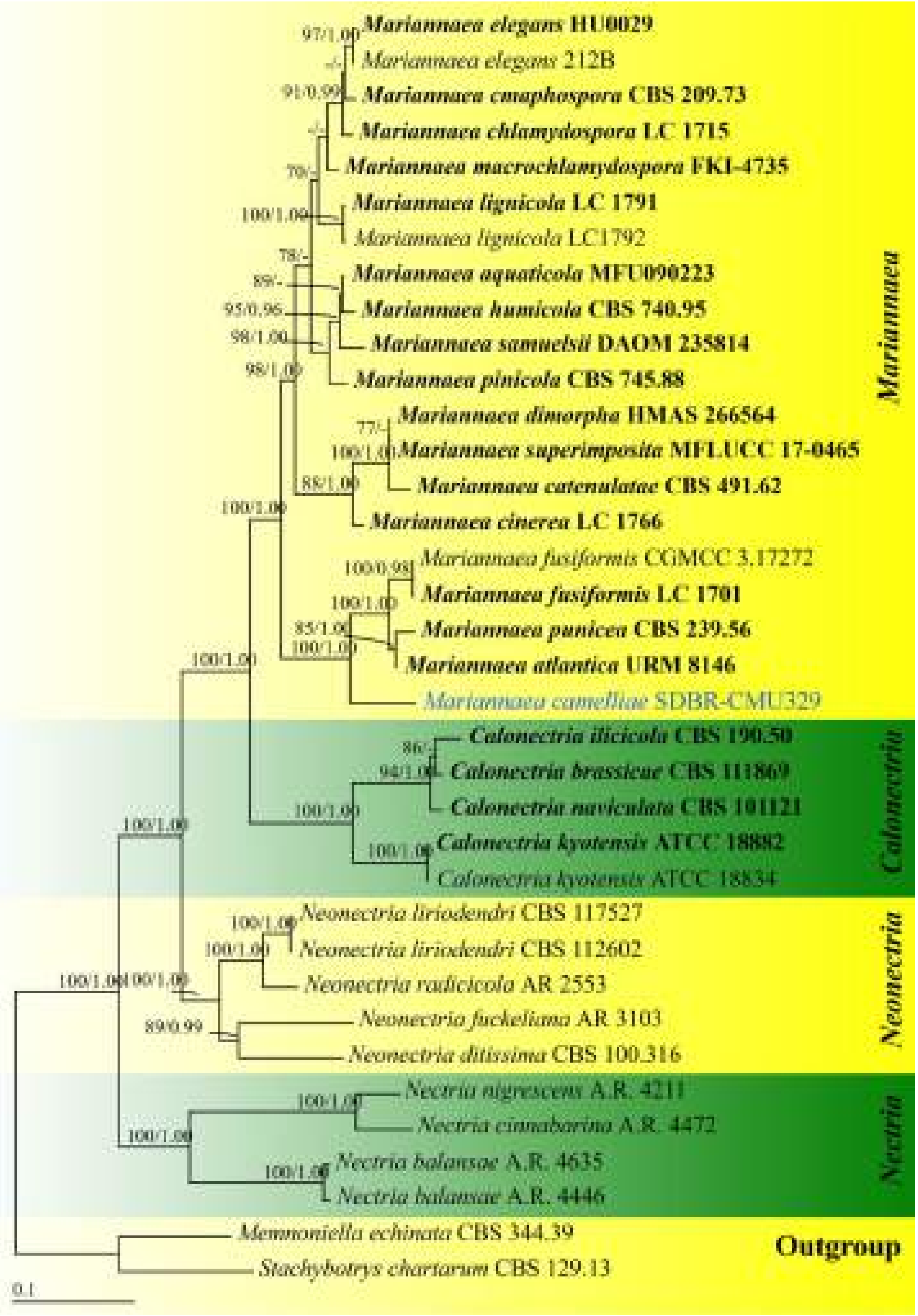


Fig. 135 Phylogenetic tree derived from maximum likelihood analysis of a combined ITS, LSU, TUB-2 and TEF1-α genes of 37 sequences and the aligned dataset was comprised of 2360 characters including gaps (ITS: 1–602, LSU: 603–1437, TUB-2: 1437–2061 and TEF1-α: 2062–2645). The average standard deviation of the split frequencies of the BI analysis was 0.002106. A best scoring RAxML tree was established with a final ML optimization likelihood value of − 14705.9596. The matrix had 1180 distinct alignment patterns with 33.94% undetermined characters or gaps. Estimated base frequencies were found to be: A = 0.2219, C = 0.2777, G = 0.2538, T = 0.2466; substitution rates AC = 1.4433, AG = 2.8971, AT = 1.5532, CG = 0.7904, CT = 5.2827, GT = 1.0000; proportion of invariable sites = 0.4850 and gamma distribution = 0.6770. *Memnoniella echinata* CBS 344.39 and *Stachybotry chartarum* CBS 129.13 were used as outgroup. Numbers above branches are the bootstrap statistics percentages (left) and Bayesian posterior probabilities (right). Branches with bootstrap values equal to or greater than 70% are shown at each branch and the bar represents 0.1 substitutions per nucleotide position. Hyphen (-) represents support values equal to or less than 70%/0.95. Ex-type strains are in bold and newly generated sequence is in blue

study, we introduce a record of *Thyronectria caudata* from Uzbekistan.

Thyronectria caudata (Malençon) Jaklitsch & Voglmayr, Persoonia 33: 195 (2014)

Index Fungorum number: IF808296; *Facesoffungi number*: FoF 09960; Fig. 136

≡ *Thyronectria lamyi* var. *caudata* Malençon, Bull. Trimestriel Soc. Mycol. France 95: 99 (1979)

Saprobic on woody twigs. **Sexual morph** *Ascomata* 280–380 µm high, 300–400 µm diam. ($\bar{x}$ = 329 × 356 µm, n = 15), superficial on the hypostroma, not surrounded by bark flaps, aggregated in round or elongated clusters, rarely solitary, globose to obovoid, rarely cupulate when dry, reddish brown. *Ostiole* central, slightly papillate or flat-umbilicate, periphysate. *Peridium* 30–60 µm wide, widest at the apex, composed of several layers of yellowish-brown cells of *textura angularis*. *Hamathecium* comprising numerous, 1.5–3.5 µm wide, filamentous, rarely branched, hyaline, paraphyses. *Asci* 90–120 × 15–25 µm ($\bar{x}$ = 103.5 × 19 µm, n = 15), 8-spored, unitunicate, cylindrical to clavate, pedicellate, rounded at the apex, mostly filled with ascoconidia when mature. *Ascospores* 20–28 × 4–6 µm ($\bar{x}$ = 24 × 5 µm, n = 30), 1–2-seriate, overlapping, narrowly clavate, with 6–10 transverse septa and 1 longitudinal or oblique septum in 1 or few cells of, all cells budding to produce oblong, 1-celled, hyaline, straight to slightly curved ascoconidia 3.5–5 × 1–1.5 µm ($\bar{x}$ = 4 × 1 µm, n = 40). **Asexual morph** Undetermined.

Material examined: UZBEKISTAN, Jizzakh Province, Zaamin District, Zaamin National Nature Park, river of Uriklisoy, Turkestan range of Pamir-Alay Mountains, on dead stems of *Berberis oblonga* (Regel) C.K. Schneid (*Berberidaceae*), 13 July 2019, Yusufjon Gafforov YG-Z54-1 (TASM 6160, KUN-HKAS 115784, **new record**); *ibid*., 13 July 2019, Y. Gafforov and T. Kholmuradova, YG-Z54-2 (TASM 6161, KUN-HKAS 115785).

GenBank numbers: ACT = MZ508400, MZ508401, ITS = MZ493292, MZ493293, LSU = MZ493306, MZ493307, TEF1-α = MZ508402, MZ508403.

Notes: *Thyronectria caudata* was initially introduced as *Thyronectria lamyi* var. *caudate* by Malençon (1979). Jaklitsch and Voglmayr (2014) synonymized this as the *Thyronectria caudata*. Morphological features (Fig. 136) of TASM 6160 and TASM 6161 are similar to those in the holotype of *Thyronectria caudata*. These collections were all made from the same host genus (*Berberis*) but in different locations. Phylogenetically, TASM 6160 and TASM 6161 are closely related to *Thyronectria berberidicola* (Ma et al. 2020) in the multi-gene concatenated tree (Fig. 137). However, this species does not deposit in MycoBank or Index Fungorum. Ma et al. (2020) introduced *Thyronectria berberidicola* from the Xinjiang Uygur Autonomous Region in China and the morphological features between *Thyronectria caudata* and this species results in no outstanding differences. We reckon the collections made by Ma et al. (2020) should also belong to *Thyronectria caudata*.

Pleurotheciales Réblová & Seifert

Notes: We follow the latest treatment and updated accounts of *Pleurotheciales* in Réblová et al. (2016) and Hyde et al. (2019, 2020b, d).

Pleurotheciaceae Réblová & Seifert

Notes: Réblová et al. (2016) introduced a single family *Pleurotheciaceae* in *Pleurotheciales* and introduced two genera in this family viz. *Adelosphaeria* and *Melanotrigonum*. Based on their multi-gene phylogenetic analyses, taxa in eleven genera formed six monophyletic clades within this family (Réblová et al. 2016). However, only eight genera were listed in this family by Wijayawardene et al. (2018) which was updated to 11 genera by Wijayawardene et al. (2020) and Hyde et al. (2020b). *Pleurotheciaceae* is known from both sexual and asexual morphs which are characterized by perithecial, immersed to superficial, ascomata, with papillate or with a central rarely eccentric neck, leathery to fragile, carbonaceous peridial walls, unitunicate, 8-spored, cylindrical or cylindrical-clavate asci, with a J-, apical ring, abundant paraphyses and ellipsoidal to fusiform, hyaline or versicolorous, septate ascospores, with polar cells, hyaline to brown at the central cell (Réblová et al. 2016; Luo et al. 2018; Hyde et al. 2020d). The asexual morphs of genera in this family have been reported as hyphomycetes forming loose fascicles or indeterminate synnemata. Conidiophores are macronematous or semi-macronematous, or sometimes forming percurrently conidiophores. Conidiogenous cells produce holoblastic conidia, with rhexolytic conidial secession on short denticles or extending polyblastically on a sympodial rachis, or schizolytic on monoblastic or solitary thallic conidiogenous cells. Conidia are hyaline to brown or versicolorous, varied in shape, aseptate or septate (Réblová et al. 2016; Luo et al. 2018; Hyde et al. 2020b, d). Taxa of this family can be found on a wide range of hosts and substrates from terrestrial and freshwater habitats (Farr and Rossman 2020).

Phaeoisaria Höhn.

Notes: *Phaeoisaria* was introduced by von Höhnel (1909) to accommodate a hyphomycetous taxon which was found on a bamboo substrate with *Phaeoisaria bambusae* as the type species. The genus was characterized by indeterminate synnemata with aseptate or septate ellipsoidal, obovoidal, fusiform-cylindrical to falcate, hyaline conidia (Réblová et al. 2016; Luo et al. 2019; Hyde et al. 2019). For the latest

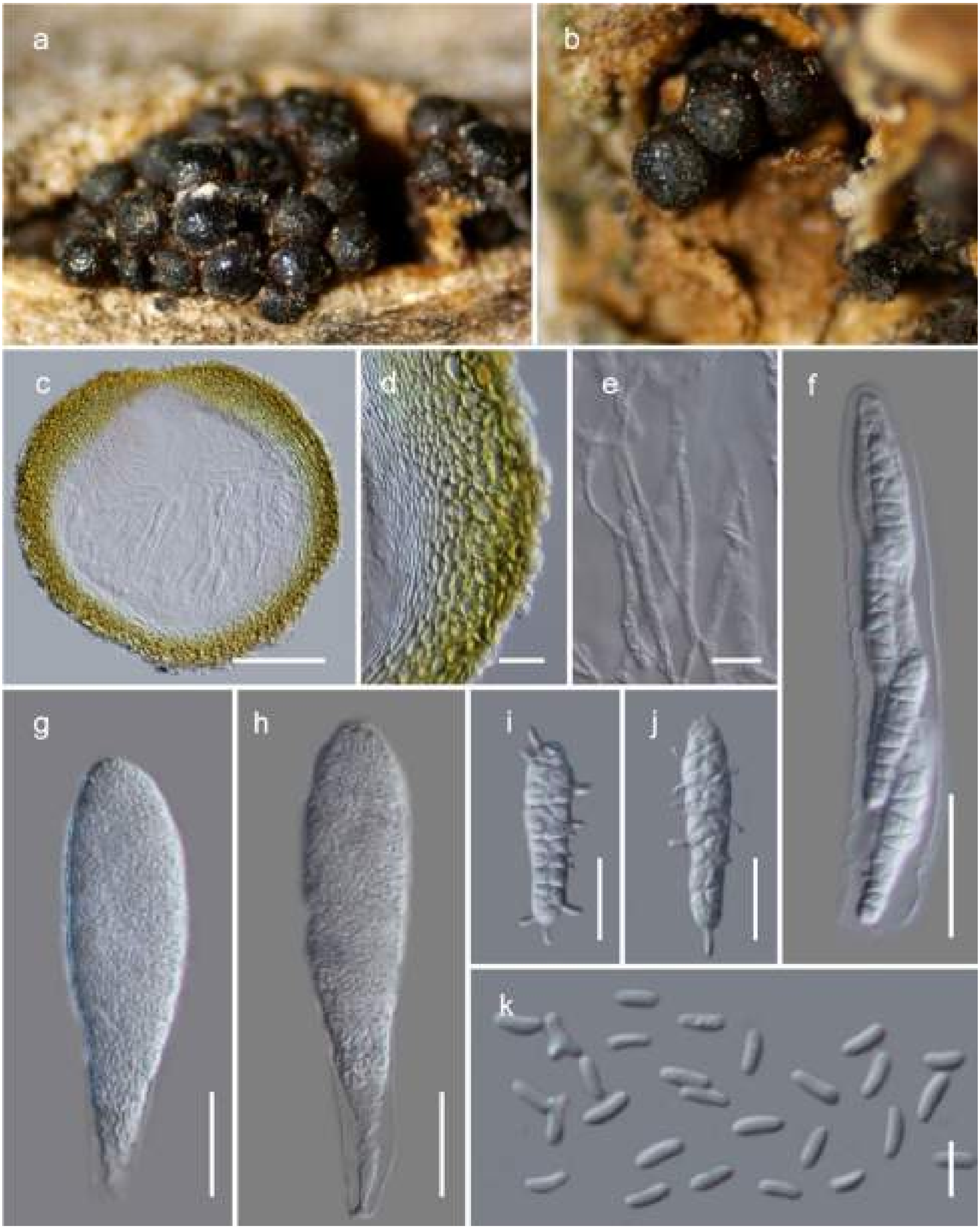


Fig. 136 ***Thyronectria caudata*** (TASM 6160, KUN-HKAS 115784, **new record**). **a**, **b** Perithecial aggregates on host surface. **c** Longitudinal section of a perithecium. **d** Section of the peridium cells. **e** Paraphyses. **f**–**h** Asci. **i**, **j** Ascospores. **k** Ascoconidia. Scale bars: **c** = 100 µm, **d**, **f**–**h** = 20 µm, **e**, **i**, **j** = 10 µm, **k** = 5 µm

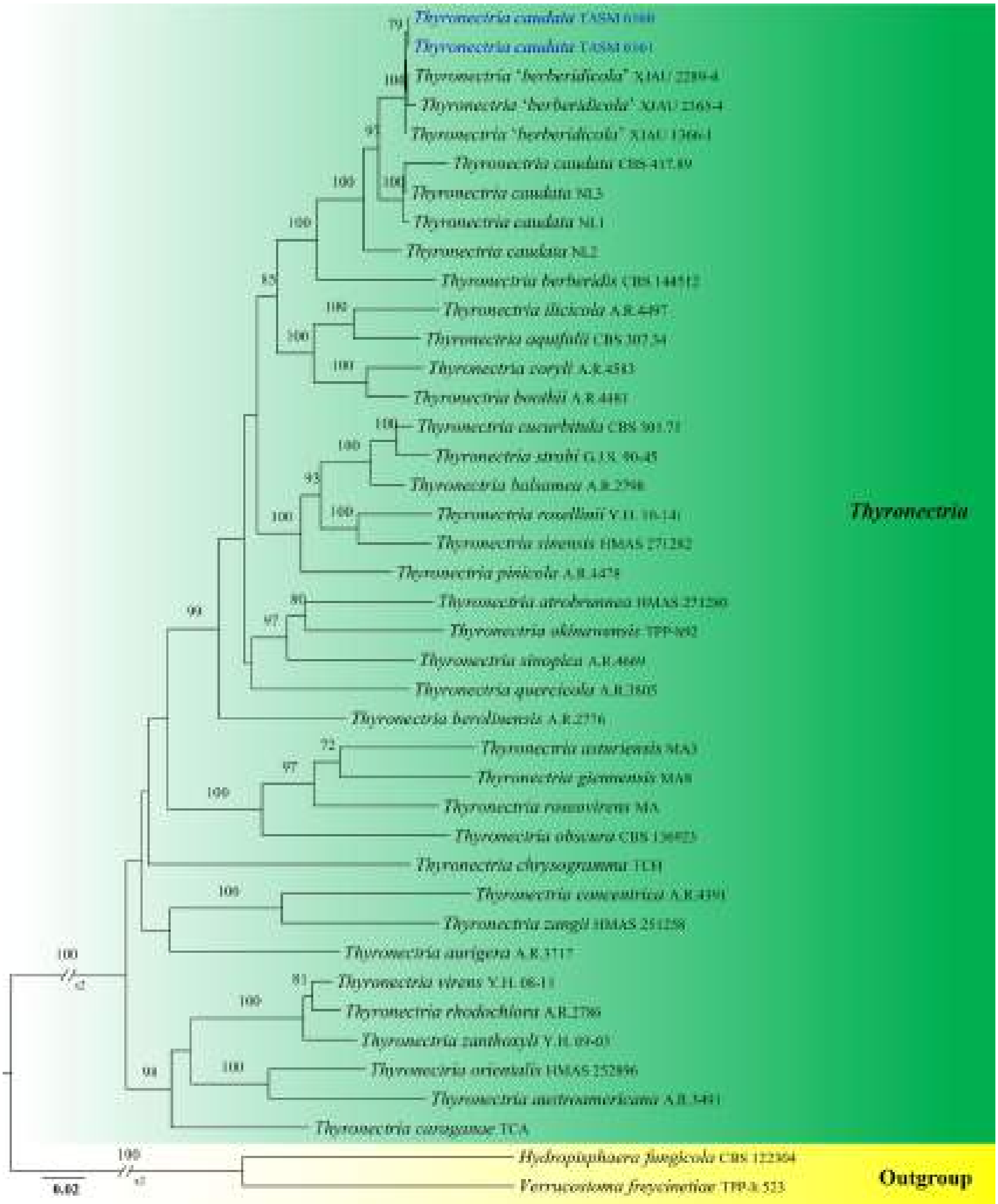


Fig. 137 Phylogram generated from the best scoring of the RAxML tree based on combined LSU, ITS, ACT, BTUB and TEF1-α sequence dataset to indicate the taxa in *Thyronectria*. Forty-one strains are included in the combined analyses which comprise a total of 4040 characters. *Hydropisphaera fungicola* (CBS 122304) and *Verrucostoma freycinetiae* (TPP-h 523) are selected as the outgroup taxa. The best RAxML tree with a final likelihood value of − 28737.934247 is presented. RAxML analysis yielded 1441 distinct alignment patterns and 21.81% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.218868, C = 0.290291, G = 0.260083, T = 0.230759, with substitution rates AC = 0.91049, AG = 2.312893, AT = 1.471029, CG = 0.955498, CT = 5.294875, GT = 1.000000; gamma distribution shape parameter alpha = 0.629127. Bootstrap support values for maximum likelihood (MLBS) equal to or greater than 70% is given above the nodes. Newly generated sequences are in blue

treatment and updated accounts of *Phaeoisaria*, we follow Luo et al. (2019), Hyde et al. (2020a) and Wijayawardene et al. (2020).

Phaeoisaria aquatica Z.L. Luo, X.J. Su & K.D. Hyde, Mycol. Progr. 17(5): 514 (2018)

Index Fungorum number: IF821837; *Facesoffungi number*: FoF 03411; Fig. 138

Saprobic on submerged decaying wood. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Colonies* effuse, solitary, dark brown to black, hairy, covered by white conidial mass. *Mycelium* immersed in the substrate. *Synnemata* 313–727 × 11–23 µm ($\bar{x}$ = 470 × 16 µm, n = 5), erect, straight to flexuous, dark brown to black, composed of compact parallel conidiophores, wide at the base, wide at the apical fertile region. *Conidiophores* macronematous, synematous, septate, branched, dark brown, smooth. *Conidiogenous cell* 12–21 × 2–5 µm ($\bar{x}$ = 17 × 3.5 µm, n = 10), polyblastic, integrated, terminal and intercalary, sympodial, cylindrical or attenuated towards tip, hyaline to light brown, denticulate, denticle conspicuously cylindrical. *Conidia* 4.5–8 × 2–3 µm ($\bar{x}$ = 5.5 × 2 µm, n = 30), ellipsoid to obovoid or sub-spatulate, straight, aseptate, hyaline, smooth-walled.

Culture characteristics: Conidia germinating on PDA within 24 h and germ tubes arising from both ends. Colonies on malt extract agar (MEA), reaching 2 cm diam. after 2 weeks at room temperature, flat, circular, surface slightly rough with crenated edge, white mist at the middle region, surrounded by greenish brown towards white grey at the margin, olivaceous dark green at the reverse with surrounded by white grey at the margin.

Material examined: THAILAND, Chiang Rai Province, Muang, Mae Yao Village, saprobic on submerged decaying wood, 23 September 2019, N. Huanraluek, MY01 (MFLU 21-0071, **new record**), living culture, MFLUCC 21-0094.

GenBank number: ITS = MZ538522, LSU = MZ538556, TEF1-α = MZ567098.

Notes: *Phaeoisaria aquatica* was introduced as a new species by Luo et al. (2018), which was found on decaying submerged wood in Jinsh River in China. The strain MFLUCC 21-0094 that was isolated and described in this study, is phylogenetically related to the type strain MFLUCC 16-1298 with 94% MLBS, 1.00 BYPP support (Fig. 141). Furthermore, our strain (Fig. 138) shares similar features of dark brown synematous, compact parallel conidiophores and ellipsoid to obovoid, aseptate, hyaline conidia with *Ph. aquatica* (MFLUCC 16-1298), the type strain and both strains were found in freshwater habitats. Therefore, based on morphology and phylogenetic affinity, our strain MFLUCC 21-0094 is identified as *Ph. aquatica* and it is reported here as a new geographical record from Thailand.

Phaeoisaria synnematicus P.N. Singh & S.K. Singh ***sp. nov.***

MycoBank number: MB830711; *Facesoffungi number*: FoF 06138; Fig. 139

Etymology: specific epithet ‘*synnematicus*’ refers to the formation of synnemata.

Holotype: AMH 10055

Color Codes Follow: Methuen Handbook of Colour (Kornerup and Wanscher 1978).

Saprobic on dead bark of *Azadirachta indica* Juss., in a terrestrial habitat. **Sexual morph** Undetermined. **Asexual morph** *Vegetative hyphae* septate, branched, smooth-walled, subhyaline to light olivaceous, up to 2.35 µm wide. *Chlamydospores* 8.5–25.5 × 6–10.5 µm, produced abundantly from submerged and superficial mycelium, intercalary, lateral to terminal, globose, sub-globose, clavate to ampulliform, solitary to catenate, dark brown, smooth walled, wall thickened and darkened, sessile, persistent to caducous, aseptate (rarely with one or two septa). *Synnemata* up to 960 µm long and 12–30 µm diam., synnematal, erect, rigid, dark brown to olivaceous brown, composed of compact parallel appressed conidiophores, cylindrical to clavate. *Conidiogenous cells* 1.5–18 × 0.5–2 µm, polyblastic, integrated, acropleurogenous, terminal or intercalary, sympodial, cylindrical to denticulate, hyaline, smooth walled, denticles simple to rarely branched, hyaline, up to 2 µm long and 1 µm wide. *Secession* schizolytic. *Conidiophores* 1.5–960 µm long, 1–3.5 µm wide, macronematous to semi-macronematous, highly geniculate, dark brown to olivaceous brown, synnematous, simple to dichotomously branched, emerging out at the apex and along the sides of the upper half or two thirds of each synnema, dark brown at the base, brown to pale brown towards the apex. Sometimes conidiophores reduced to a single conidiogenous cell, arising from aerial hyphae. *Conidia* 4–11 × 2–5 µm ($\bar{x}$ = 6 × 2.5 µm, n = 30), dimorphic, clavate to ellipsoidal, cylindrical to falcate, base narrowly truncate, tip obtuse, variable in size, sometimes constricted near septa, 1–2-guttulate, hyaline, aseptate to one septate, smooth-walled.

Culture characteristics: on MGYP (Malt Extract Glucose Yeast Peptone agar), slow growing, floccose, pale yellow (4A3), 37 × 37 diam. in 37 days at 25 °C, periphery light grey, floccose (1C1), margin regular, reverse dark brown (7F-4). *Hyphae* septate, unbranched to branched, smooth walled subhyaline to light olivaceous, 1.8–2.3 µm wide.

Material examined: INDIA, Maharashtra, Pune District, dead bark of *Azadirachta indica* (*Meliaceae*), 4 June 2017, P.N. Singh, AMH 10055 (**holotype**), ex-type living culture, NFCCI 4479.

GenBank Numbers: ITS = MK391494, LSU = MK391492.

Notes: The present taxon was isolated in pure culture from dead bark of *Azadirchta indica*. The overall morphological and cultural characteristics are distinct from other species in the genus. Though in having prominent synnemata

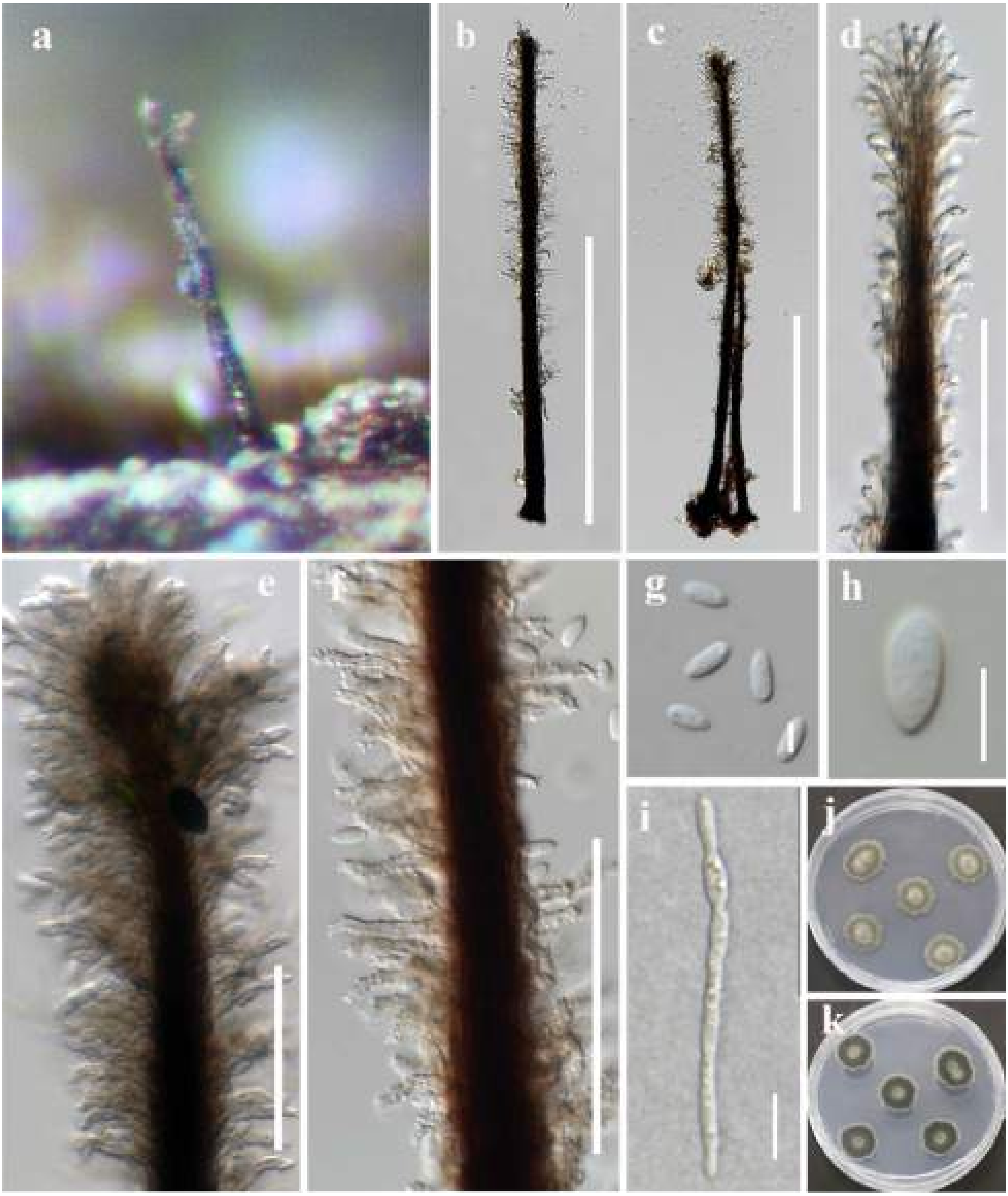


Fig. 138 ***Phaeoisaria aquatica*** (MFLU 21-0071, **new record**). **a** Conidiomata synnemata on wood. **b**, **c** Conidiophores. **d**–**f** Conidiogenous cells. **g**, **h** Conidia. **i** Germinated conidium. **j**, **k** Culture on MEA from surface and reverse. Scale bars: **b**, **c** = 300 μm, **d**–**f** = 50 μm, **g**, **h** = 5 μm, **i** = 10 μm

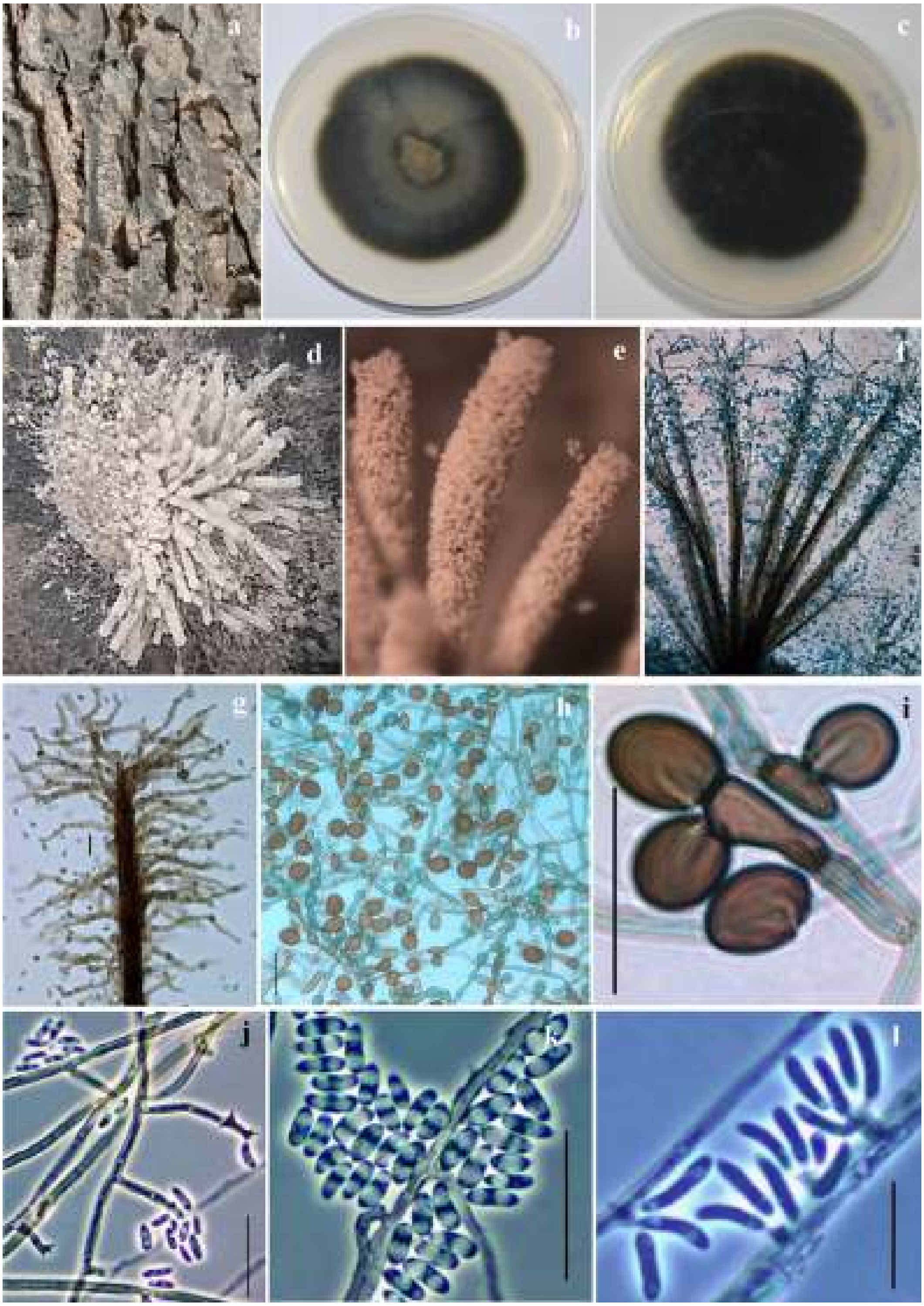


Fig. 139 ***Phaeoisaria synnematicus*** (AMH 10055, **holotype**). **a** Substrate (Bark of *Azadirchta indica*). **b** Colony morphology (front view). **c** Reverse view of colony. **d**, **e** Stereoscopic view of synnemata (in culture). **f** Numerous synnemata (slide culture microscopic view). **g** Synnema showing splaying conidiophores. **h** Numerous simple to catenate chlamydospores. **i** Persistent lateral to terminal produced sub-globose chlamydospores. **j** Enlarged view of conidiophores showing acropleurogenous conidiogenous cells and conidia. **k** Enlarged microscopic view of fusoid to clavate conidia and hyphae. **l** Curved and cylindrical guttulate conidia produced from small conidiophores. Scale bars: **g**–**l** = 20 µm

the morphological characters are comparable with some species, like *Phaeoisaria clematidis* (Hughes 1958) and *P. aquatica* (Luo et al. 2018). The new species is different in having smaller synnemata (399–960 × 12–30 µm) as against to larger (1000–1500 × 20–80 µm) in *P. clematidis*. Conidia in present taxon are significantly larger (4–11 × 2–5 µm) as compared to smaller conidia in *P. annesophiae* (4.5–9 × 2–3.5 µm) (Crous et al. 2017), *P. clematidis* (4–10 × 1.5–2.5 µm), *P. aquatica* (6.5–7.5 µm long) and *P. guttulata* (3.5–5.5 × 2.5–4.8 µm) (Hyde et al. 2018a). Our new taxon is distinct from *P. annesophieae* (Crous et al. 2017) in the presence of synnemata, which is absent in the latter taxon. Similarly, the new taxon is also different from *P. guttulata* (Hyde et al. 2018a) in having larger synnemata (480–700 × 2–5 vs. 399–960 × 12.35–30 µm) and conidia (3.5–5.5 × 2.5–4.8 vs. 4–11 × 2–5 µm). As such, in overall morphological features, the present taxon is distinct from allied taxa.

Based on the sequence analysis, the proposed *Phaeoisaria synnematicus* is different from other known species. For the megablast analysis, the ITS sequence of *P. synnematicus* showed 97.58% (526/539) similarity and 2 gaps with *P. annesophieae* (CBS 143235, ex-type), 93.85% (519/553) similarity and 12 gaps (2.17%) with *P. clematidis* (CBS 113340), 92.67% (506/546) similarity and 15 gaps (2.74%) with *P. pseudoclematidis* (MFLUCC 11-0393, type), 92.62% (465/502) similarity and 14 gaps (2.78%) with *P. sedimenticola* (CGMCC 3.14949, ex-type), 92.81% (439/473) similarity and 11 (2.32%) gaps with *P. aquatica* (MFLU 17-0918, ex-type) and 93.76% (511/545) similarity and 9 (1.65%) gaps with *P. guttulata* (MFLUCC 17-1965, ex-type). The distinct morphological features and phylogenetic analysis confirm the proposed taxon to be a new species, *Phaeoisaria synnematicus* (Figs. 139 and 141).

Pleurotheciella Réblová, Seifert & J. Fourn.

Notes: *Pleurotheciella* was introduced by Réblová et al. (2012) and is typified by *P. rivularia* Réblová, Seifert & Fournier. The genus was introduced to accommodate pleurothecium-like taxa, which are characterized by non-stromatic, perithecial, semi-immersed to superficial, subglobose, heavily pigmented, glabrous ascomata, with bi-layered, leathery to fragile peridium, with abundant apically tapering paraphyses, unitunicate, 8-spored, cylindrical-clavate asci with a J-, apical ring, and ellipsoidal-fusiform, hyaline to subhyaline, septate ascospores lacking mucilaginous sheath or appendages (Réblová et al. 2012). The hyphomycetous asexual morph is characterized by subhyaline unbranched to sparingly branched, septate conidiophores, often reduced to the conidiogenous cells, with integrated, subhyaline to hyaline, minute denticles, and ellipsoidal to obovoidal, hyaline, aseptate to septate conidia (Réblová et al. 2012).

Réblová et al. (2012) initially included two species in this genus. Subsequently, Réblová et al. (2016) included another new combination, *Pleurotheciella uniseptata* (Matsush.) Seifert in this genus. Luo et al. (2018) introduced other six lignicolous freshwater species of *Pleurotheciella* from the Greater Mekong Subregion. Hyde et al. (2018a) introduced *Pleurotheciella krabiensis* and *P. tropica* from submerged dead and decaying wood in Thailand. Currently, there are 11 species accommodated in this genus. Based on phylogenetic analyses coupled with morphological characteristics, we introduce a novel species *P. dimorphospora* occurring on dead branches of *Malus* sp. from a terrestrial environment in Yunnan, China.

Pleurotheciella dimorphospora H.B. Jiang, Phookamsak & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF558191; *Facesoffungi number*: FoF 09762; Fig. 140

Etymology: The specific epithet "*dimorphospora*" refers to the fungus forming two types of conidia.

Holotype: MFLU 20-0138

Saprobic on dead branches of *Malus* sp. **Sexual morph** Undetermined. **Asexual morph** *Natural substrate* visible as small, black, shiny dots on host substrate. *Mycelium* immersed to partly immersed, sparse, brown, composed of septate, branched hyphae. *Conidiophores* 9–15(–21) × 2–4 µm ($\bar{x}$ = 10.5 × 2 µm, n = 30), difficult to distinguish on host, macronematous, mononematous, subhyaline to brown, septate, unbranched to branched, erect on host surface. *Conidiogenous cells* holoblastic, terminal, integrated. *Conidia* (16.5–)20–27(–32) × (15–)20–25(–28) µm ($\bar{x}$ = 23 × 20.5 µm, n = 30), dark brown to black, muriform, variedly shaped, ellipsoidal, subglobose, or irregular in shape, sectored, inconspicuously septate. In vitro: *Dimorphic*, with two types of conidial morphology. Type I: *Conidiophores* 4.5–6 × 2.5–4 µm ($\bar{x}$ = 5–3 µm, n = 20), semi-macronematous or macronematous, mononematous, straight or flexuous, hyaline to brown, cylindrical, septate, unbranched. *Conidiogenous cells* holoblastic, terminal or intercalary, integrated, brown. *Conidia* 20–29 × 14–19 µm wide ($\bar{x}$ = 24.5 × 17 µm, n = 30), brown, muriform, varied in shape, subglobose to cordiform, or irregular in shape, with a protuberant hilum. Type II: *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 6–8 µm long ($\bar{x}$ = 8 µm, n = 20), 2–3 µm wide ($\bar{x}$ = 2 µm, n = 20), holoblastic, terminal, hyaline, ellipsoidal, aseptate, unbranched. *Conidia* 8.5–10.8 µm long ($\bar{x}$ = 9.7 µm, n = 20), 4–5 µm wide ($\bar{x}$ = 4 µm, n = 20), hyaline, ellipsoidal, 0–1-septate, 2-guttulate, smooth-walled.

Culture characteristics: Conidia germinating on WA within 24 h and germ tubes produced in all directions. Colonies on PDA, reaching 20–25 mm diam. after 14 days

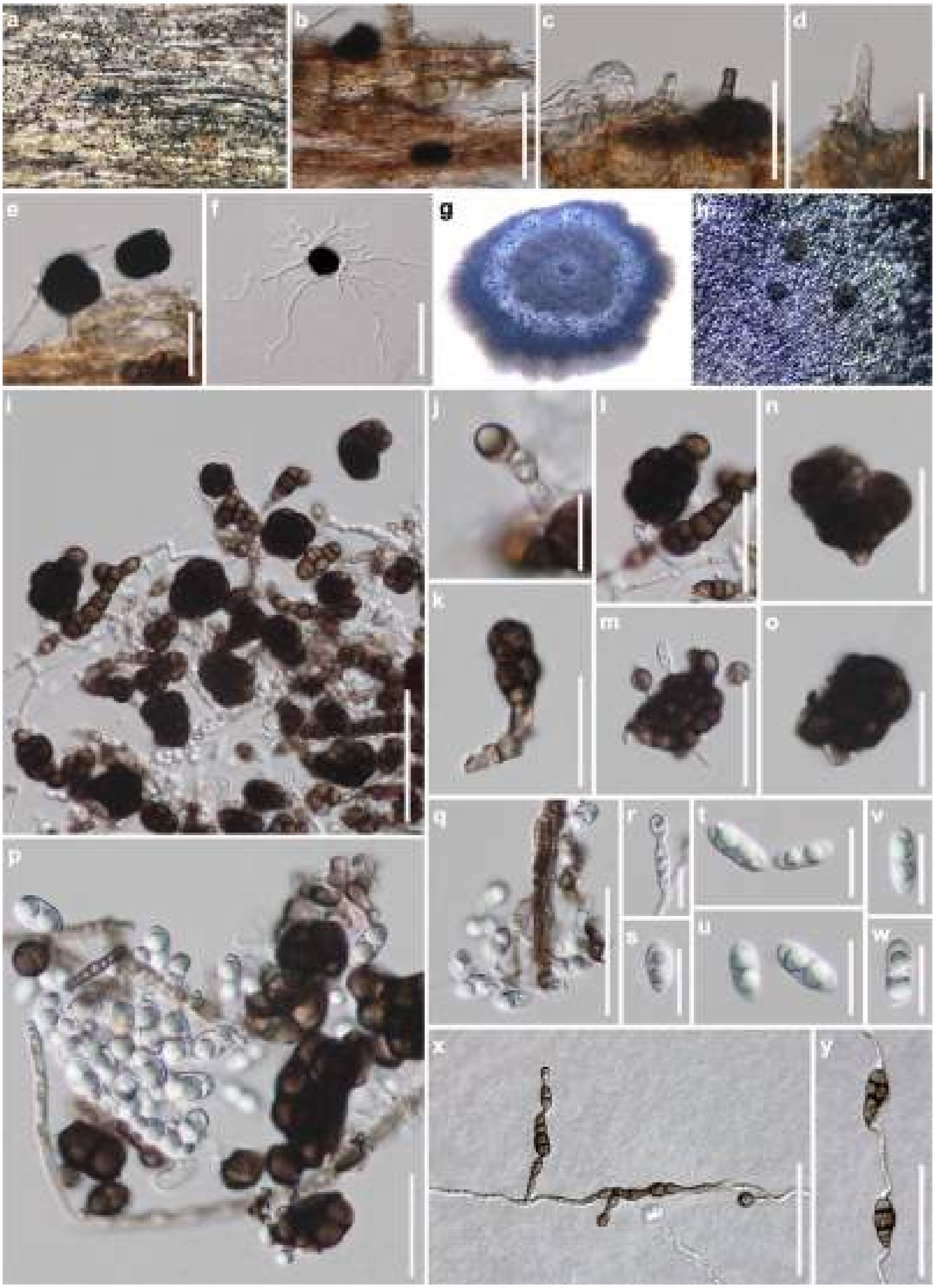


Fig. 140 ***Pleurotheciella dimorphospora*** (MFLU 20-0138, **holotype**; KUMCC 20-0185, **ex-type**). **a** Appearance of black, shiny conidia on host substrate. **b** Squash mount showing mycelia partly immersed in host substrate. **c**, **d** Conidiophores erect on host surface. **e** Black, muriform conidia on natural substrate. **f** Germinated conidium on WA. **g** Colony on PDA after 4 weeks. **h** Conidial masses induced on culture growing on PDA after 4 weeks. **i**, **m**–**o** Dark brown, muriform conidia on PDA. **j**–**l** Conidiogenous cells with attached conidia. **p** Hyaline, didymosporous conidia associated with dark brown, muriform conidia. **q**, **r** Conidiogenesis of hyaline conidia. **s**–**w** Hyaline conidia. **x**, **y** Lateral and intercalary conidia. Scale bars: **b**, **f**, **i**, **x** = 50 μm, **c**, **l**–**n**, **q**, **y** = 30 μm, **d**, **e**, **k**, **o**, **p** = 20 μm, **j**, **r**–**w** = 10 μm

at room temperature, with subglobose, dense, humid, dark brown mycelium on the frontage, convex at the entre, dark brown to black in reverse. Mycelium 1.5–3 µm ($\bar{x}$ = 2 µm, n = 20) wide, superficial to immersed in media, with dark brown, composed of septate, branched, smooth hyphae.

Material examined: CHINA, Yunnan Province, Kunming City, Kunming Institute of Botany Kunming Institute of Botany (102°44′19″ E 25°8′27″ N; 1951 msl ± 3 msl), on dead branch of *Malus* sp. (*Rosaceae*), 18 August 2018, R. Phookamsak, KIB049 (MFLU 20-0138, **holotype**), ex-type living culture, KUMCC 20-0185.

GenBank Numbers: ITS = MW981446, MW981447, LSU = MW981444, MW981445, SSU = MW981454, MW981455, TEF1-α = MZ509663, MZ509664, RPB2 = MZ509665, MZ509666.

Notes: In this study, we observed a terrestrial fungus occurring on dead branches of *Malus* sp. in Kunming, Yunnan, China. The species forms dark brown to black, shiny conidia on the host tissue in nature. We obtained a pure culture of this fungus by single conidia isolation from these dark brown to black conidia and the species formed black conidial masses and hyaline conidial masses on PDA after 1 month. We re-isolated hyaline and brown conidia, and obtained DNA sequence data for both hyaline and brown conidia. Based on DNA sequence data analyses, the sample forming hyaline conidia (KUMCC 20-0185H) are supported to be conspecific to the sample forming brown conidia (KUMCC 20-0185).

Pleurotheciella dimorphospora can be distinguished from other *Pleurotheciella* species in forming two types of conidia and lacking sympodially conidia on conspicuous denticles (Fig. 140). The species formed a distinct clade, clustering with *P. saprophytica* with 100% MLBS, 1.00 BYPP (Fig. 141). *Pleurotheciella saprophytica* differs from *P. dimorphospora* in having polyblastic, sympodial, denticulate conidiogenous cells, with conspicuous denticles (Luo et al. 2018). A comparison of ITS and RPB2 nucleotide bases between *P. dimorphospora* and *P. saprophytica* shows that *P. dimorphospora* is different from *P. saprophytica* in 23/519 bp (4.4%) of ITS and 56/723 bp (7.7%) of RPB2. According to the recommendation of Jeewon and Hyde (2016), we introduce *P. dimorphospora* as a new species from the terrestrial environment.

Pseudodactylariales Crous

Notes: We follow the latest treatment and updated accounts of *Pseudodactylariales* in Hyde et al. (2020b).

Pseudodactylariaceae Crous

Notes: *Pseudodactylariaceae* is a monotypic family introduced by Crous et al. (2017) to accommodate a monotypic genus *Pseudodactylaria*. We follow the latest treatment and updated accounts of *Pseudodactylariaceae* in Hyde et al. (2020b).

Pseudodactylaria Crous

Notes: Crous et al. (2017) introduced *Pseudodactylaria* to accommodate species *P. hyalotunicata* and *P. xanthorrhoeae* (type species). *Pseudodactylaria* is characterized by white erect conidiophores, fusoid-dllipsoid conidia that are surrounded by a thin mucilaginous sheath. Four species are presently included in *Pseudodactylaria* has presently included four species (Index Fungorum 2021).

Pseudodactylaria albicolonia R.J. Xu, Boonmee & K.D. Hyde, *sp. nov.*

Index Fungorum number: IF558548; *Facesoffungi number*: FoF 09961; Fig. 142

Etymology: '*albicolonia*' referring to the white colonies of this fungus.

Holotype: MFLU 21-0095

Saprobic on decaying submerged wood in a freshwater stream. **Sexual morph** Undetermined. **Asexual morph** *Colonies* effuse, gregarious, plentiful, white. *Mycelium* partly superficial, partly immersed in the substrate, consisting of branched, septate, smooth, hyaline hyphae. *Conidiophores* 43–85 × 3–5.5 µm ($\bar{x}$ = 62 × 4 µm, n = 11), macronematous, mononematous, unbranched, solitary, erect, subcylindrical, straight, or slightly flexuous, hyaline, sometimes light brown at the base 1–4-septate, smooth, sometimes expands at the base and slightly constricted at the septa of the apex. *Conidiogenous cells* 18–51 × 3–6 µm ($\bar{x}$ = 34 × 4 µm, n = 14), holoblastic, polyblastic, integrated, terminal, sympodial, subcylindrical, straight or flexuous, hyaline, rough-walled, apical part forming a rachis with numerous, denticles, sometimes percurrently regenerating. *Conidia* 14–19.5 × 2.5–4 µm ($\bar{x}$ = 17 × 3 µm, n = 30), acropleurogenous, solitary, fusiform, 0–1-septate, rarely slightly constricted at septum, hyaline, guttulate.

Culture characteristics: Conidia germinated on MEA media within 12 h and germ tubes were produced from both ends. Colony reached 3 cm at 28 °C in the dark for 1 week, on MEA media, circular, flat, with fluffy, dense, white mycelium, edge entire.

Material examined: THAILAND, Chiang Rai Province, Mueang, Ban Du, (99°49′18.12″ E 20°06′36″ N), on decaying submerged wood in a freshwater stream, 18 August 2020, R.J. Xu, MD-85 (MFLU 21-0095, **holotype**), ex-type culture, MFLUCC 21-0073.

GenBank number: ITS = MW751848, LSU = MZ493341.

Notes: *Pseudodactylaria albicolonia* shares several characters in common with *P. fusiformis* and *P. camporesiana* such as unbranched conidiophores, holoblastic, polyblastic conidiogenous cells and fusiform, hyaline conidia (Lin et al. 2018; Lu et al. 2020; Hyde et al. 2020b). Phylogenetically,

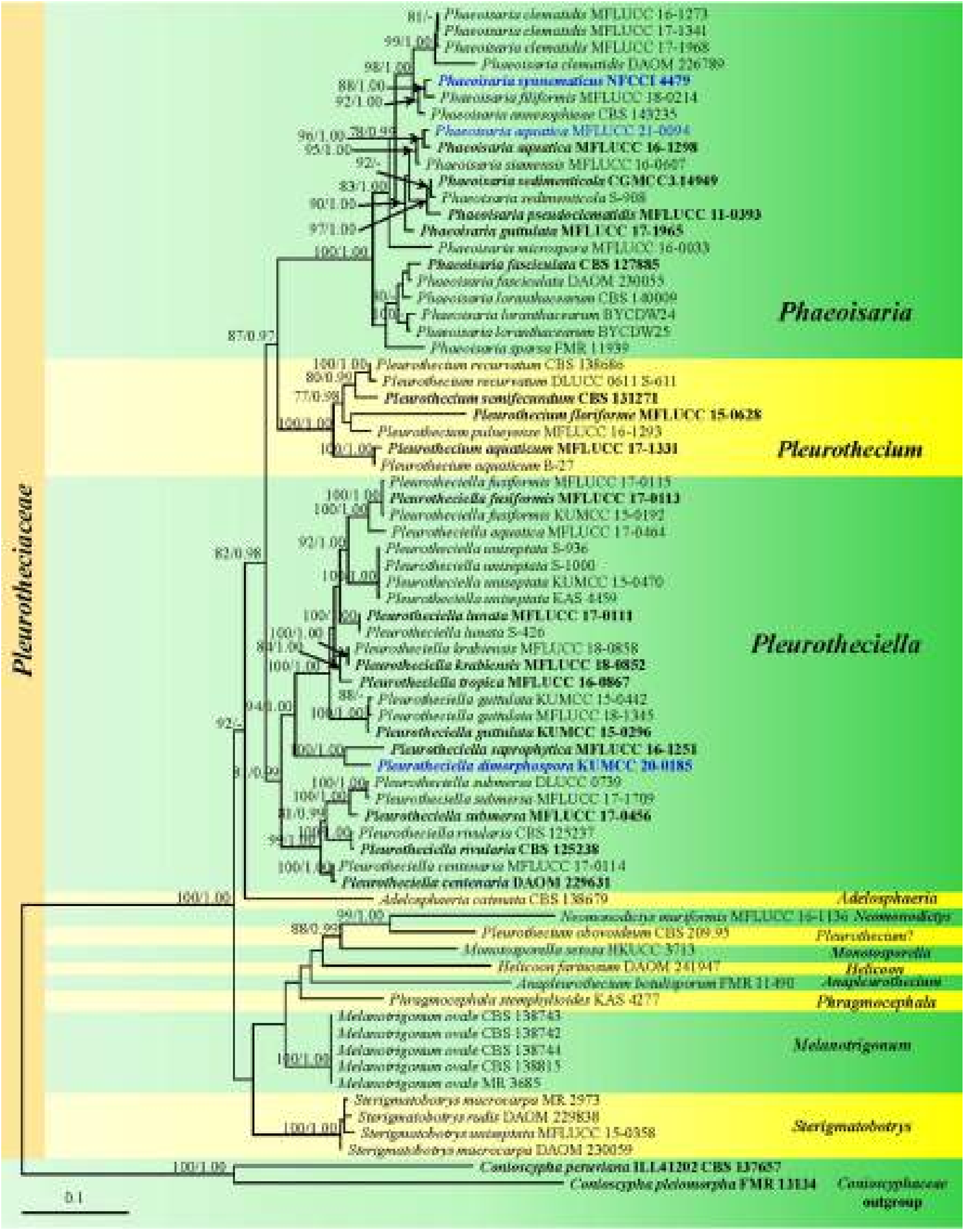


Fig. 141 Maximum likelihood phylogenetic tree based on a combined LSU, ITS, SSU and RPB2 sequence data of genera in *Pleurotheciaceae*. *Conioscypha peruviana* CBS 137657 and *C. pleiomorpha* FMR 13,134 were selected as the outgroup taxa. Bootstrap support values for maximum likelihood (MLBS, left) equal to or greater than 70% is given above the nodes. Bayesian posterior probabilities (BYPP, right) equal to or greater than 95% are given above the nodes. Ex-type strains are in bold and newly generated sequences are in blue

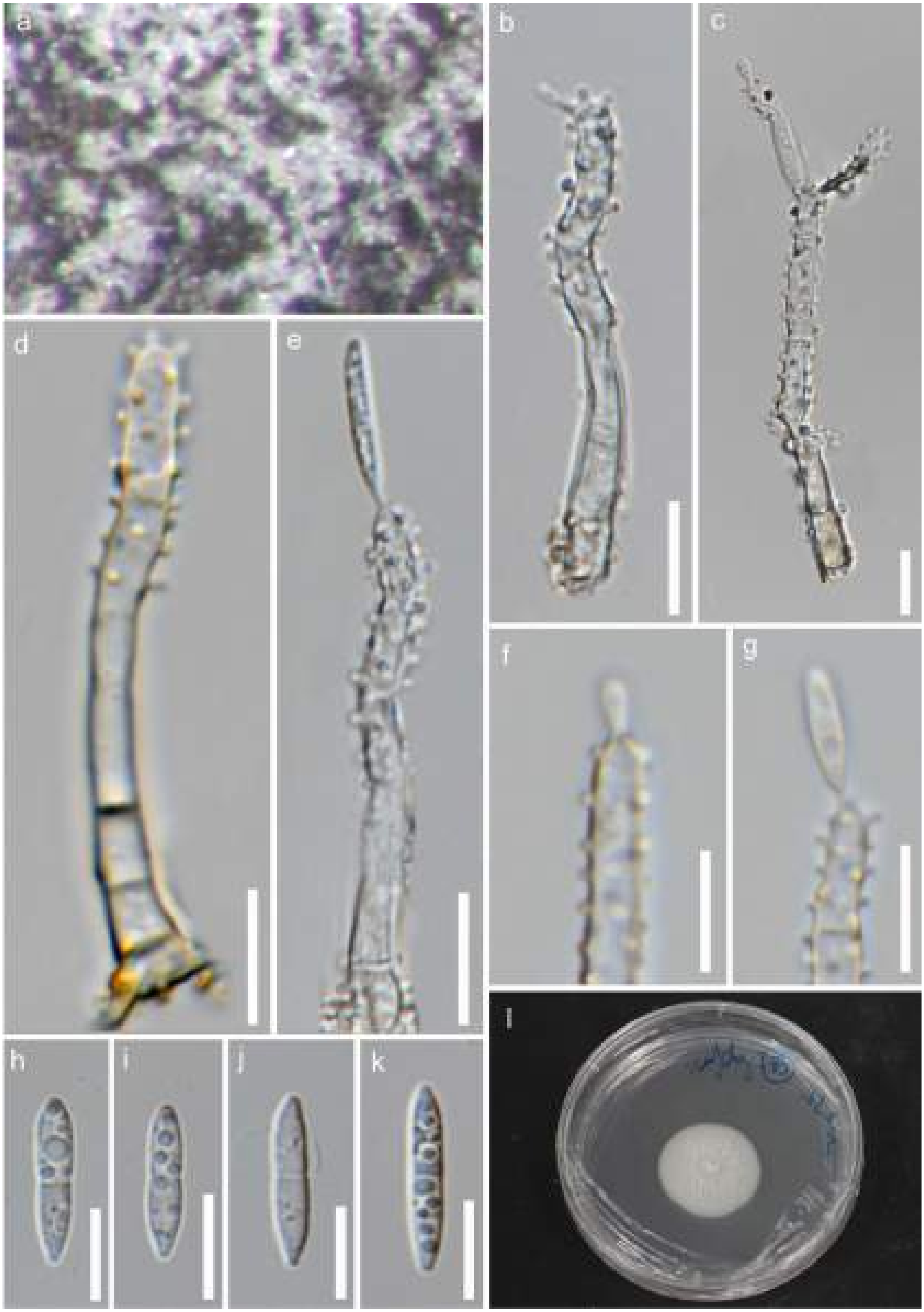


Fig. 142 ***Pseudodactylaria albicolonia*** (MFLU 21-0095, **holotype**). **a** Colony on decaying wood. **b–d** Conidiophores with conidia. **e–g** Conidiogenous cells with attached conidia. **h–k** conidia. **l** Colony on MEA medium. Scale bars: **b–k** = 10 μm

P. albumcoloniam formed a distinct lineage basal to *P. hyalotunicata* and *P. xanthorrhoeae* with 86% MLBS, 1.00 BYPP support (Fig. 143). *Pseudodactylaria albicolonia* differs from *P. hyalotunicata* and the type species *P. xanthorrhoeae* in having shorter conidia (14–19.5 × 2.5–4 µm vs. 20–25 × 2.5–3 µm and (20–)22–27(–33) × (3–)3.5(–4) µm, respectively) and lacking a mucilaginous sheath (Tsui et al. 1997; Crous et al. 2017). Therefore, we introduce a new species *P. albumcoloniam* (Fig. 142) from a freshwater habitat in Thailand based on morphological differences and phylogenetic evidence.

Savoryellales Boonyuen, Suetrong, Sivichai, K.L. Pang & E.B.G. Jones

Notes: *Savoryellales* (Boonyuen et al. 2011) comprises a single family *Savoryellaceae*. We follow the latest treatment and updated accounts of *Savoryellales* in Hyde et al. (2020b).

Savoryellaceae Jaklitsch & Réblová

Notes: *Savoryellaceae* comprises five genera viz. *Ascotaiwania*, *Canalisporium*, *Neoascotaiwania*, *Rhexoacrodictys* and *Savoryella* (Wijayawardene et al. 2020). For the latest treatment and updated accounts of *Savoryellales*, we follow in Hyde et al. (2019, 2020b) and Réblová et al. (2020).

Canalisporium Nawawi & Kuthub. (=*Ascothailandia* Sri-indr., Boonyuen, Sivichai & E.B.G. Jones)

Notes: *Canalisporium* was introduced to accommodate a taxon in having dark brown and muriform conidia and is typified by *Canalisporium caribense* (Sri-indrasutdhi et al.

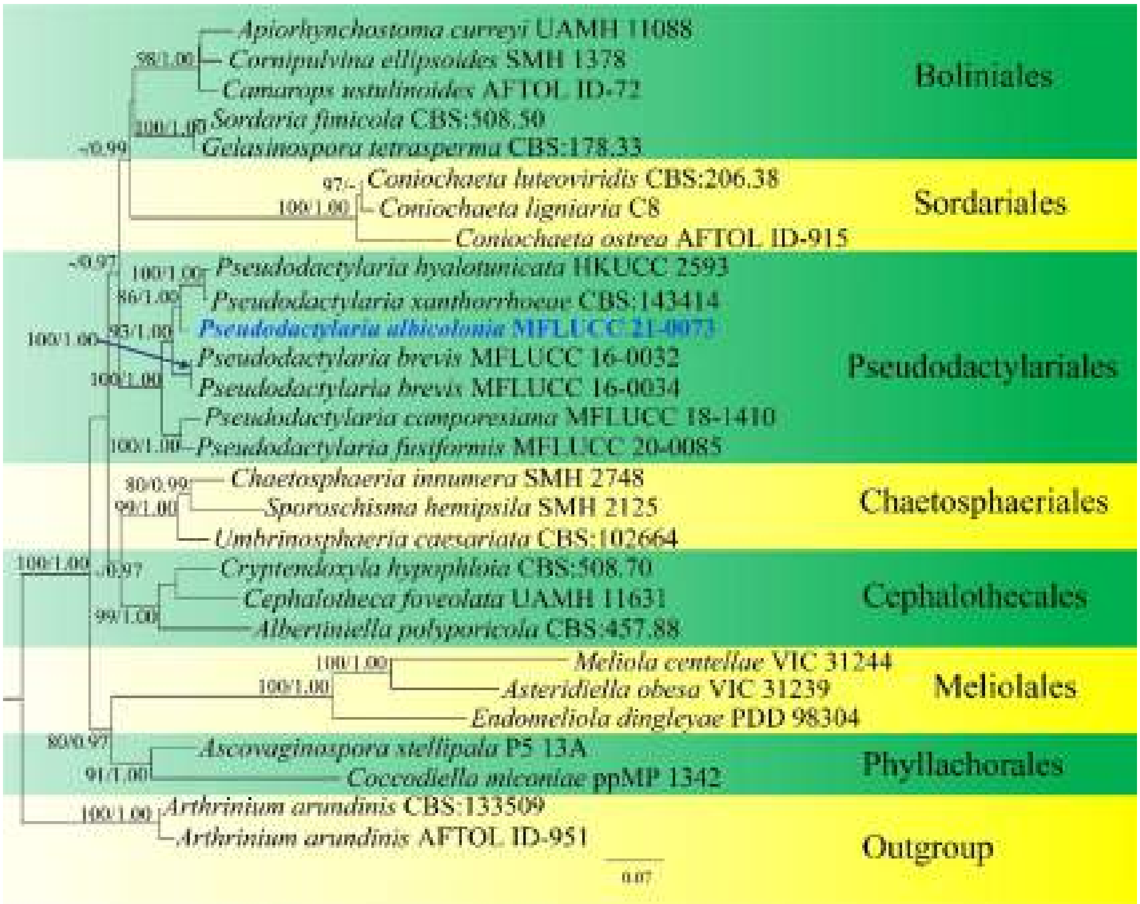


Fig. 143 Phylogram generated from the best scoring of the RAxML tree based on combined LSU, ITS, sequence dataset to indicate the new species *Pseudodactylaria albicolonia* and related genera in *Pseudodactylariales*. Twenty-eight strains are included in the combined analysis, which comprise a total of 1306 characters. *Arthrinium arundinis* CBS 133509 and *A. montagnei* AFTOL ID-951 are selected as the outgroup taxa. The best RAxML tree with a final likelihood value of − 10010.943263 is presented. RAxML analysis yielded 664 distinct alignment patterns and 21.66% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.246125, C = 0.236142, G = 0.297752, T = 0.219981, with substitution rates AC = 0.978864, AG = 2.183946, AT = 1.688622, CG = 0.686434, CT = 5.976862, GT = 1.000000; gamma distribution shape parameter alpha = 0.403195. Bootstrap support values for maximum likelihood (MLBS, left) equal to or greater than 70% is given above the nodes. Bayesian posterior probabilities (BYPP, right) equal to or greater than 0.95 are given above the nodes. Newly generated sequences are in blue and bold

2010; Hyde et al. 2020b). Members of *Canalisporium* are saprobes commonly found on dead or decaying wood and dead plants in different habitats such as freshwater and terrestrial (Sri-indrasutdhi et al. 2010; Dayarathne et al. 2019; Hyde et al. 2019, 2020b; Index Fungorum 2021). Sixteen species are included in *Canalisporium* based on morphological and phylogenetic analyses (Hyde et al. 2020b).

Canalisporium caribense (Hol.-Jech. & Mercado) Nawawi & Kuthub., Mycotaxon 34(2): 479 (1989)

≡ *Berkleasmium caribense* Hol.-Jech. & Mercado 1984

Index Fungorum number: IF125432; *Facesoffungi number*: FoF 05486; Fig. 144

Saprobic on submerged decaying wood in the river. **Sexual morph** Undetermined. **Asexual morph** *Colonies* on natural substrate sporodochial, scattered, punctiform, granular, black, shining. *Mycelium* immersed, composed of branched, septate, pale brown to brown. *Conidiophores* micronematous or semi-macronematous, mononematous, fasciculate, simple or sometimes branched, septate, hyaline to very pale brown. *Conidiogenous cells* monoblastic, integrated, terminal, determinate, hyaline or pale brown. *Conidia* 21–42 × 18–26 µm ($\bar{x}$ = 32.5 × 24 µm, n = 30), acrogenous, muriform, solitary, broadly ellipsoidal to obovoid, fusiform to obclavate, flattened, brown to dark brown, one longitudinal column septum, thick and dark at the septum, 9–13-transverse septate, constricted at the septa, smooth-walled.

Culture characteristics: Conidia germinating on water agar and germ tubes produced from basal conidium within 24 h at room temperature. Colonies growing on PDA, circular, umbonate, slightly fimbriate to entire edge, olivaceous grey in the middle, with dark brown at the margin, dark in reverse. Mycelium superficial and partially immersed, branched, septate, hyaline to pale brown.

Material examined: THAILAND, Phayao Province, Pong District, Yom River, on decaying submerged wood in the river shore, 18 December 2019, S.K.U. Chandrasiri and S. Boonmee, YR1 (MFLU 21-0072, **new record**), living culture, MFLUCC 21-0095.

GenBank numbers: ITS = MZ538501, LSU = MZ538535, TEF1-α: MZ567080.

Notes: A new collection of *Canalisporium caribense* (MFLUCC 21-0095) was collected from a freshwater river in northern Thailand (Fig. 144). Our collection shares identical morphology to the type species *C. caribense* (Holubová-Jechová and Mercado 1984; Nawawi and Kuthubutheen 1989). Further, phylogenetic analysis based on a combined LSU, ITS, SSU, TEF1-α and RPB2 sequences place our isolate MFLUCC 21-0095with strains of *C. caribense* (SS03683 and SS03839; Sri-indrasutdhi et al. 2010) with 99% MLBS, 1.00 BYPP support (Fig. 146). Therefore, a new additional record of *C. caribense* is reported from northern Thailand.

Rhexoacrodictys W.A. Baker & Morgan-Jones

Notes: *Rhexoacrodictys* was introduced to accommodate hyphomycetous taxa presence of acrodictys-like structures (Baker et al. 2002). The latest treatment and updated accounts of *Rhexoacrodictys* consists of five species (Luo et al. 2019; Wijayawardene et al. 2020).

Rhexoacrodictys nigrospora Boonmee, D.F. Bao & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF558545; *Facesoffungi number*: FoF 09200; Fig. 145

Etymology: The specific epithet "*nigrospora*" refers to the black conidia.

Holotype: MFLU 21-0073

Saprobic on decaying bark. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Colonies* superficial, dark brown to black. *Mycelium* superficial and immersed, composed of branched, septate, pale brown to brown hyphae, 1–2 µm wide, verruculose or finely echinulate-walled. *Conidiophores* micronematous or semi-macronematous, mononematous, cylindrical filamentous, flexuous, scattered to grouped, simple, single or a loose cluster brown to dark brown, smooth-walled. *Conidiogenous cells* monoblastic, polyblastic, integrated, terminal and intercalary or discrete, determinate. *Conidia* 15–31 × 16–33 µm ($\bar{x}$ = 22 × 23 µm, n = 20), holoblastic, solitary, dry, acrogenous, simple, globose to subglobose, truncate at the base, multi-septate, dark brown when immature, becoming black and faintly septate at maturity, thick and smooth-walled.

Culture characteristics: Conidia germinating on PDA within 24 h and germ tubes arising from terminal end cell. Colonies on malt extract agar (MEA), reaching 3.5 cm diam. after 2 weeks at room temperature, colonies circular, low convex, surface slightly rough with entire edge, around the white to greyish brown, dark green to black at the reverse.

Material examined: THAILAND, Phetchabun Province, Lom Sak, on decaying bark, 25 July 2019, S. Boonmee, LSP03 (MFLU 21-0073, **holotype**), ex-type living culture, MFLUCC 21-0096; Mukdahan Province, on decaying wood, 24 July 2019, S. Boonmee, WD09 (MFLU 21-0074), living culture MFLUCC 21-0097.

GenBank number: LSP03: ITS = MZ538524, LSU = MZ538558, TEF1-α = MZ567100; WD09: ITS = MZ538525, LSU = MZ538559, SSU = MZ538574, RPB2 = MZ567113, TEF1-α = MZ567101.

Notes: *Rhexoacrodictys nigrospora* differs from the type *Rh. erecta* and other species in having cylindrical filamentous, flexuous conidiophores and globose to subglobose, faintly septate, dark brown to black conidia (Baker et al. 2002; Xiao et al. 2018). Phylogenetically, *Rh. nigrospora*

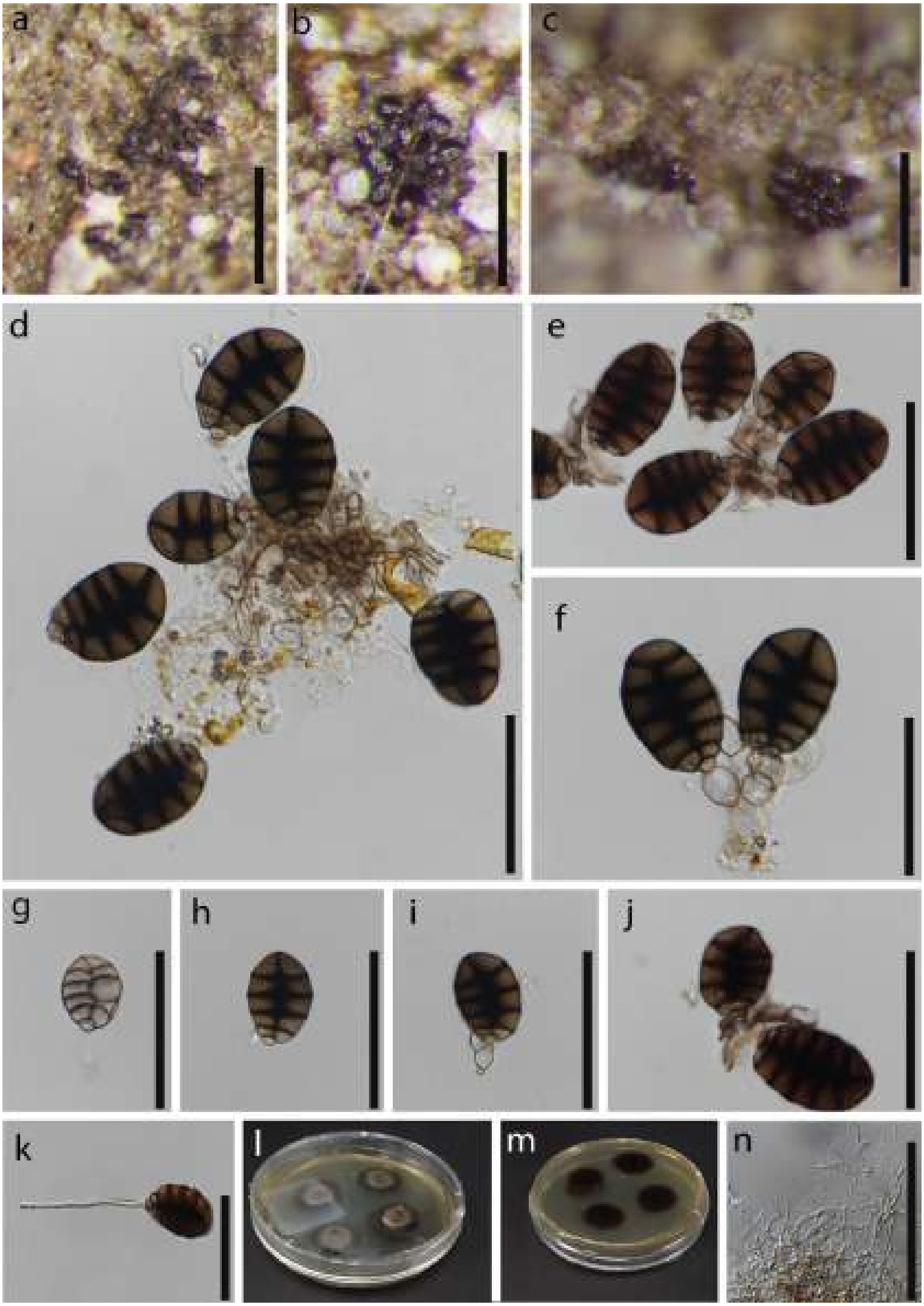


Fig. 144 ***Canalisporium caribense*** (MFLU 21-0072, **new record**). **a**–**c** Sporodochia on wood. **d**, **e** Squash mount of sporodochia. **f** Conidiogenous cells with conidia. **g**–**j** Conidia. **k** Germinated conidium. **l**, **m** Culture on PDA from surface and reverse. **n** Mycelium on PDA. Scale bars: **a**–**c** = 20 µm, **d**–**n** = 5 µm

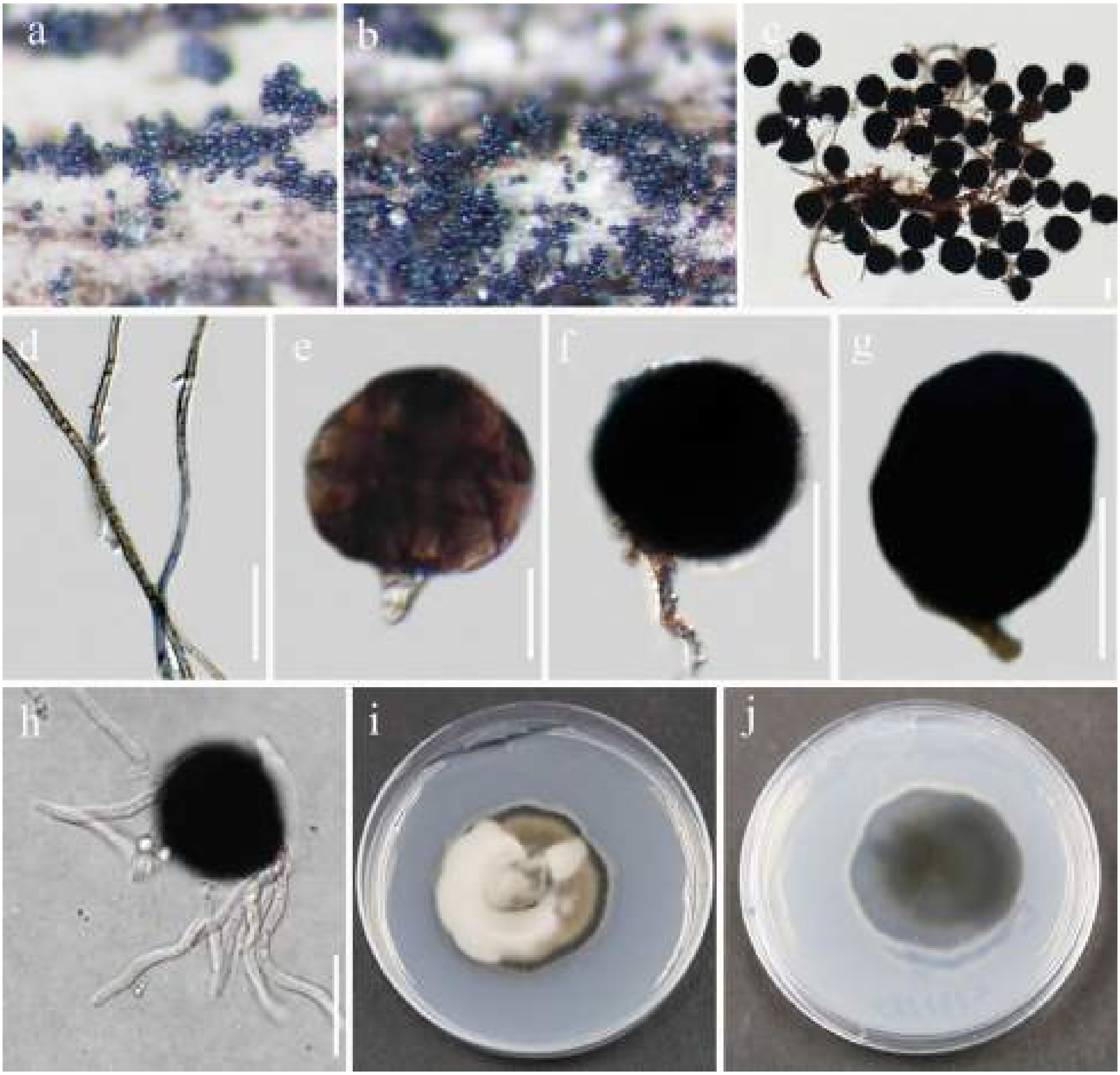


Fig. 145 ***Rhexoacrodictys nigrospora*** (MFLU 21-0073, **holotype**). **a**, **b** Conidiomata on the substrate. **c** Squash of mount of conidia. **d** Conidiophores with minutely conidiogenous cells. **e**–**g** Conidia. **h** Germinated conidium. **i**, **j** Culture on PDA from surface and reverse. Scale bars: **c**, **e**, **f** = 10 µm, **d**, **g** = 20 µm

forms a distinct lineage basal to *Rhexoacrodictys* species with 100% MSBS, 1.00 BYPP support (Fig. 146). Currently, only four species listed in this genus (Species Fungorum 2021). We, therefore introduce *Rh. nigrospora* (Fig. 145) as the fifth species in *Rhexoacrodictys* based on morphological and phylogenetic analyses.

Lasiosphaeriaceae Nannf.

Notes: *Lasiosphaeriaceae*, typified by *Lasiosphaeria* Ces. & De Not, was introduced by Nannfeldt (1932). The family is highly polyphyletic with several paraphyletic genera (Huhndorf et al. 2004; Miller and Huhndorf 2004, 2005; Cai et al. 2006; Kruys et al. 2015). Furthermore, *Lasiosphaeriaceae* consists of morphologically diverse taxa being the most diverse genera in *Sordariales* (Huhndorf et al. 2004; Miller and Huhndorf 2005). The latest treatment of the family followed Hyde et al. (2020d).

Cercophora Fuckel

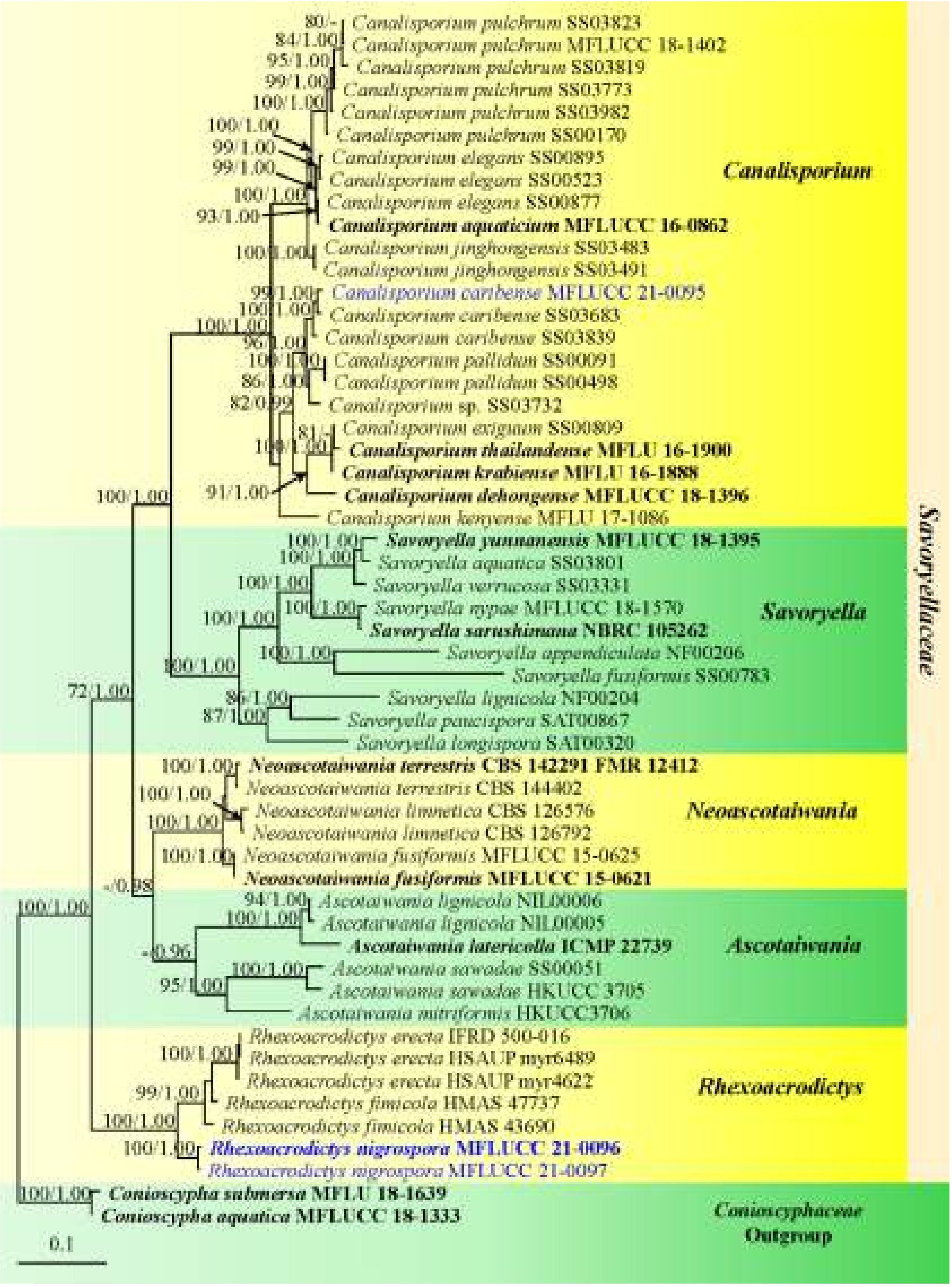


Fig. 146 Maximum likelihood phylogenetic tree based on a combined LSU, ITS, SSU, TEF1-α and RPB2 sequence data of genera in *Savoryellaceae*. *Conioscypha aquatica* MFLUCC 18-1333 and *C. submersa* MFLU 18-1639 are selected as the outgroup taxa. Bootstrap support values for maximum likelihood (MLBS, left) equal to or greater than 70% is given above the nodes. Bayesian posterior probabilities (BYPP, right) equal to or greater than 0.95 are given above the nodes. Ex-type strains are in bold and newly generated sequences are in blue

Notes: Fuckel (2011) established *Cercophora* with three species: *C. conica*, *C. fimiseda,* and *C. mirabilis* (type species). Multi-loci phylogenetic analyses of *Cercophora* species clustered in the lasiosphaeriaceous complex (Huhndorf et al. 2004; Kruys et al. 2015; Hyde et al. 2020d). Sixty-four morphologically distinct *Cercophora* species are listed in Species Fungorum (2021) wherein 27 species have molecular data. The latest treatment of *Cercophora* is Hyde et al. (2020d).

Cercophora dulciaquae M.S. Calabon, E.B.G. Jones & K.D. Hyde, ***sp.nov.***

Index Fungorum number: IF558645; *Facesoffungi number*: FoF 09962; Fig. 147

Etymology: The specific epithet "*dulciaquae*" reflects the origin in a freshwater habitat.

Holotype: MFLU 21-0122

Saprobic on submerged decaying wood. **Sexual morph** *Ascomata* 390–700 µm high, 350–475 µm diam., perithecial, mostly solitary, superficial, with base immersed in the hyphae, subglobose to obpyriform with conical neck, black, centrally located ostiole, without periphyses. *Peridium* 30–40 µm thick, slightly thicker at apex, 2-layers, outer layer composed of dark brown, thick-walled, irregular, brown cells of *textura angularis*; inner layer thin-walled, composed of elongated, flattened, light brown to hyaline cells. *Hamathecium* 2–3 µm wide, filiform, septate, unbranched, abundant, hyaline paraphyses. *Asci* 110–180 × 15–25 µm ($\bar{x}$ = 135 × 16 µm, n = 20), 8-spored, unitunicate, cylindrical with premature ascospores, cylindric-clavate at later stages, apex rounded, narrow, apical ring, thin-walled, with a short pedicel. *Ascospores* 35–60 × 6–8 µm ($\bar{x}$ = 45 × 7 µm, n = 20), 2-seriate, premature, hyaline, aseptate, cylindrical, slightly sigmoid to geniculate, numerous oil droplets, curved, rounded at both ends, with a lash-like appendage attached to both ends, 8–15 µm long; becoming differentiated into a swollen head and pedicel, 1-transversely septate, head 10–20 × 9–11 µm ($\bar{x}$ = 17 × 10 µm, n = 30), conical at the apex, truncate at the base, hyaline to dark brown, with several oil globules, *pedicel* 19–27 × 4–6 µm ($\bar{x}$ = 23 × 5 µm, n = 30), hyaline to pale brown, curved; appendages disappear with age. **Asexual morph**: Undetermined.

Culture characters: Conidia germinated on MEA within 24 h. Colonies on MEA reaching 1–2 cm diam. after 4 weeks at room temperature, slow growing, colonies irregular, medium dense, flat with smooth and filiform margins; brown to dark brown in top view, reverse brown.

Material examined: THAILAND, Chiang Mai Province, Mushroom Research Center, on decaying wood submerged in a freshwater stream, 29 January 2019, S. Boonmee, SB17-10 (MFLU 21-0122, **holotype**), ex-type living culture, MFLUCC 21-0104.

GenBank numbers: ITS = MZ497331, LSU = MZ497335.

Notes: *Cercophora dulciaquae* is the seventh species from *Cercophora* (*C. appalachianensis*, *C. aquatica*, *C. caudata*, *C. costariensis*, *C. squamulosa*, *C. vinosa*) observed from freshwater habitats (Luo et al. 2019; Calabon et al. 2020b). It closely resembles *C. aquatica* and *C. costariensis*. Still, it differs in ascomata (390–700 µm high vs. 400–600 µm high vs. 350–500 µm high), asci (110–180 × 15–25 µm vs. 180–250 × 13–16 µm vs. 135–186 × 13–16 µm) and ascospore size (35–60 × 6–8 µm vs. 36–51 × 4–6 µm vs. 40–49 × 4–5 µm) (Chaudhary et al. 2007; Catania et al. 2011). Furthermore, *C. dulciaqaue* (Fig. 147) has aseptate ascospores while *C. aquatica* has up to 5-septate ascospores after liberation from the ascus. Immature ascospores of *C. dulciaquae* have bipolar appendages, but these are absent in *C. costariensis* (Catania et al. 2011). Based on the phylogenetic analysis of combined LSU and ITS sequence data, *C. dulciaquae* clustered with *Zopfiella marina* (CBS 155.77) with low bootstrap support (Fig. 148). The two species are morphologically different and the novel species fits the generic description of *Cercophora*. *Cercophora dulciaquae* is phylogenetically close to *C. tuberculata.* The former species differs in ascomatal morphology (short neck vs. neck up to 150 µm high, with basal tubercles) and ascospore size (35–60 × 6–8 µm vs. 37.5–40 × 2.5–5 µm) (Chang and Wang 2005). Blast results of ITS sequence data revealed a 99.44% similarity to *Apodus oryzae* (E-219) while LSU sequence data showed a 99.88% similarity with *Apodus oryzae* (ATCC 38847), *Triangularia mangenotii* (CBS 419.67; ATCC 38847) and *Zopfiella pilifera* (CBS 413.73).

Torpedosporales E.B.G. Jones, Abdel-Wahab & K.L. Pang

Notes: see latest update account of *Torpedosporales* in Wijayawardene et al. (2020).

Juncigenaceae E.B.G. Jones, Abdel-Wahab & K.L. Pang

Notes: *Juncigenaceae* was introduced by Jones et al. (2014) to accommodate three genera *Fulvocentrum*, *Juncigena* and *Marinokulati* with *Juncigena adarca* as the type species. Another two new genera *Elbamycella* and *Khaleijomyces* were described (Abdel-Wahab et al. 2018; Poli et al. 2019). The family is characterized by small-sized, coriaceous, immersed to superficial ascomata with apricot colour either in the peridium, neck or ascospores; periphysate neck; numerous, septate paraphyses that are embedded in gel and attached to the top and base of the ascomatal venter; cylindrical, clavate or fusiform asci and ellipsoidal, fusiform to clavate, septate, hyaline to pigmented ascospores, with or without sheath, smooth- to rough-walled. Currently, five genera i.e., *Elbamycella*, *Fulvocentrum*, *Juncigena*, *Khaleijomyces*, and *Marinokulati* and eight species are included in *Juncigenaceae* (Kohlmeyer et al. 1997; Jones et al. 2014; Abdel-Wahab et al. 2018, 2019; Poli et al. 2019). The eight species were described from lignicolous substrates in marine

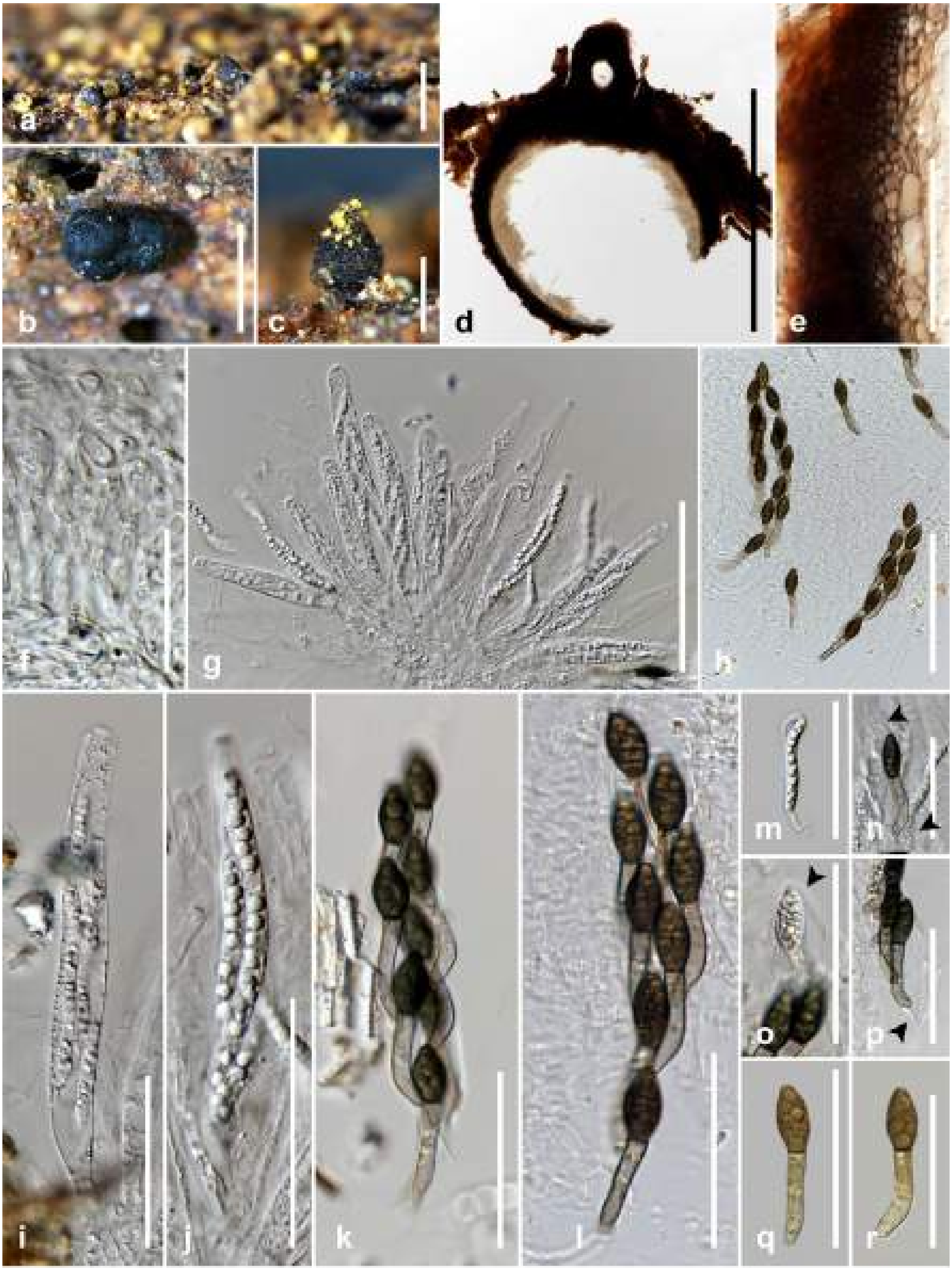


Fig. 147 ***Cercophora dulciaquae*** (MFLU 21-0122, **holotype**). **a**–**c** Appearance of ascomata on host substrate. **d** Vertical section through ascoma. **e** Section of pycnidial wall. **f** Paraphyses. **g**–**l** Asci. **m**–**r** Ascospores with bipolar appendages (arrow). Scale bars: **a**, **b** = 1 mm, **c**, **d** = 500 µm, **e**, **i**–**r** = 50 µm, **f** = 20 µm, **g**, **h** = 100 µm

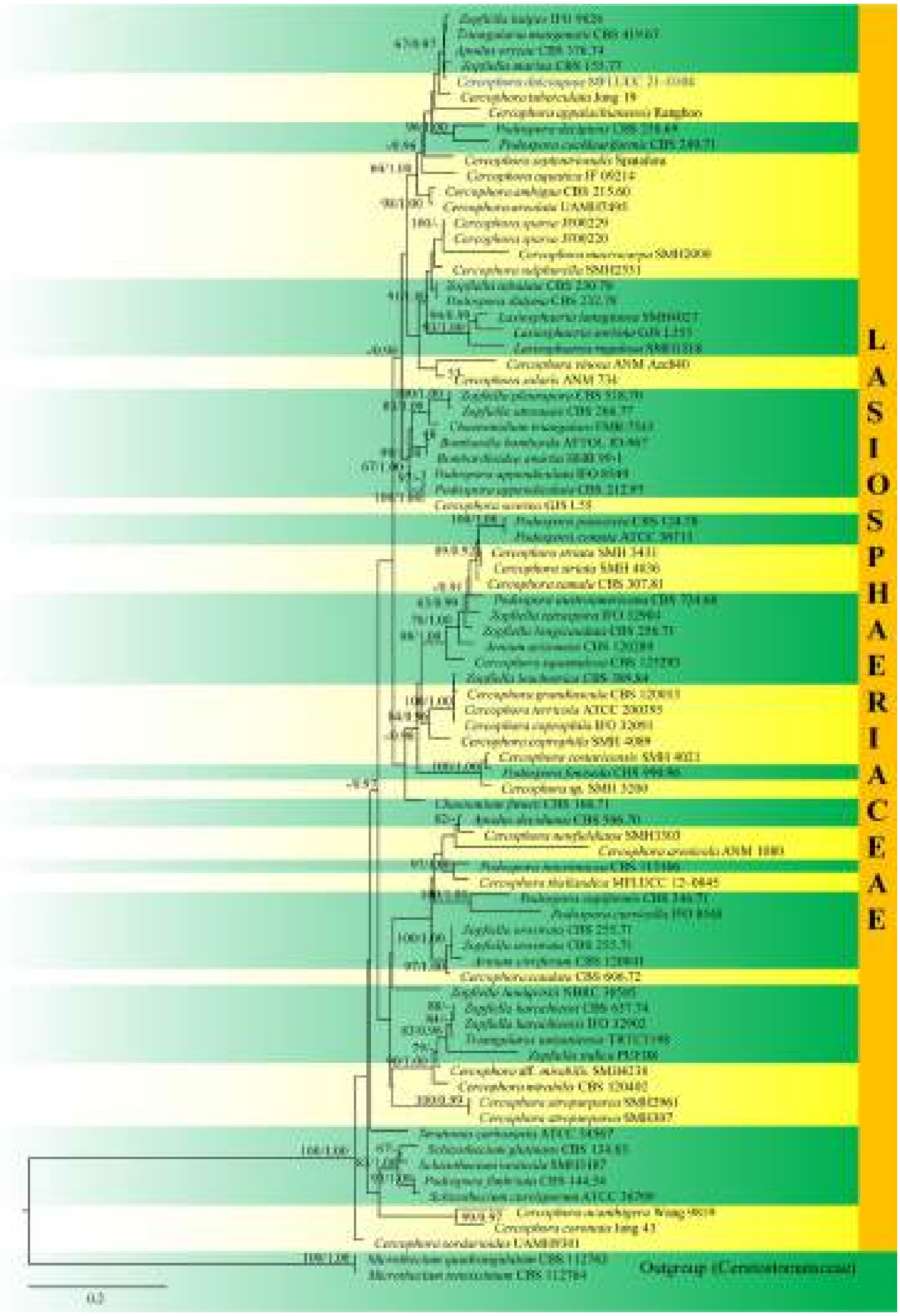


Fig. 148 Phylogenetic tree generated from maximum likelihood (ML) analysis based on combined LSU and ITS sequence data for the species from *Lasiosphaeriaceae*. *Microthecium quadrangulatum* (CBS 112763) and *M. tenuissimum* (CBS 112764) were used as outgroup taxa. The dataset comprised and 1243 characters after alignment including gaps (LSU = 828 bp and ITS = 415 bp). The RAxML analysis of the combined dataset yielded a best scoring tree with a final ML optimization likelihood value of − 4540.010304. The matrix had 520 distinct alignment patterns, with 17.16% undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.243204, C = 0.239086, G = 0.300179, T = 0.217531; substitution rates AC = 1.598327, AG = 1.651124, AT = 2.172105, CG = 0.801233, CT = 6.709684, GT = 1.000000; gamma distribution shape parameter α = 0.254987. Bootstrap support values for ML and MP equal to or greater than 60% and BYPP equal to or greater than 0.90 are given above the nodes. The newly generated sequence is in blue and bold

habitats. Based on morphology and the combined phylogenetic analyses of SSU and LSU rDNA sequence data, a novel species *Khaleijomyces umikazeanus* is introduced.

Khaleijomyces Abdel-Wahab

Notes: *Khaleijomyces* is a monotypic, marine genus that was described from driftwood in the intertidal zone, Arabian Gulf, Saudi Arabia (Abdel-Wahab et al. 2018). The genus is characterized by apricot to reddish-brown, membranous to coriaceous, superficial to immersed ascomata, surrounded by dense brown, septate hyphae, with long, periphysate necks that are apricot in colour, a common character in members of *Torpedosporales*, cymbiform to fusiform, thin-walled asci, without an apical apparatus; hyaline to brown, unicellular to septate ascospores that are 1–3 seriate in the asci (Abdel-Wahab et al. 2018). In this study, a new species *Khaleijomyces umikazeanus* is introduced based on evidence of morphology and phylogenetic placement (Figs. 149 and 150).

Khaleijomyces umikazeanus Abdel-Wahab ***sp. nov.***

Index Fungorum number: IF557837; *Facesoffungi number*: FoF 09201; Fig. 149

Etymology: Named after Umikaze Beach, where this fungus was collected.

Holotype: CBS H-23860

Saprobic on the surface of driftwood in the intertidal zone. **Sexual morph** *Ascomata* 110–200 µm diam. ($\bar{x}$ = 144 µm, n = 8), superficial, solitary, scattered on substrate, subglobose to globose, coriaceous, apricot reddish-brown. *Necks* 130–180 µm long, 40–50 µm wide, hyaline to apricot in colour, periphysate. *Peridium* 18–28 µm wide, forming *textura angularis*, two-layered; outer layer 11–16 µm wide, 4 to 11 layers of apricot to reddish-brown, thick-walled, polygonal to flattened cells; inner layer 9–13 µm wide, 4 to 10 layers of hyaline, thick-walled, polygonal to flattened cells. *Paraphyses* 2–4 µm wide, septate with swollen cells, constricted at the septa, embedded in gel, attached to the top and the base of the ascomatal venter. *Asci* 73–83 × 9–11 µm ($\bar{x}$ = 81 × 10 µm, n = 20), 8-spored, unitunicate, thin-walled, persistent, fusiform, curved, developing from ascogenous tissue at the base of the ascomata. *Ascospores* 19–24 × 5–6 µm ($\bar{x}$ = 22 × 6 µm, n = 40), 1-3-seriate, fusiform to clavate, with rounded ends, 3-septate, not constricted at the septa, hyaline to faint apricot in colour, surrounded by a deciduous amorphous material. **Asexual morph** Undetermined.

Culture characteristics: Ascospores germinating on PDA within 24 h at 25 °C and germ tubes produced from the ends of the ascospore. Colonies on PDA reaching 2 cm diam. after 3 weeks, at 25 °C, white to yellow–brown, white from below.

Material examined: JAPAN, Yokosuka City, Umikaze Beach, on decaying driftwood in the intertidal zone, 4 August 2008, M.A. Abdel-Wahab (CBS H-23860, **holotype**), ex-type living culture, NBRC 105287.

GenBank numbers: LSU = MN921253, SSU = MN921252.

Notes: Combined phylogenetic analyses of SSU and LSU rDNA placed *Khaleijomyces umikazeanus* as a distinct species. It grouped with *K. marinus* in phylogenetic analysis but with low statistical support. *Khaleijomyces umikazeanus* differs from *K. marinus* in having 3-septate, hyaline ascospores, while those in the latter species are unicellular when young that become 1–4-septate and yellow–brown to brown in older specimens. The outer layer of the peridium in *K. umikazeanus* is *textura angularis* while *K. marinus* is *textura epidermoidea*. The hamathecium in *K. umikazeanus* forms persistent paraphyses, embedded in gel and attached to the top and the bottom of the ascomatal venter, while it is pseudoparenchymatous in *K. marinus* that fills the young ascomatal venter and breaks down into catenophyses that become deliquescent early (Abdel-Wahab et al. 2018). *Khaleijomyces umikazeanus* differs from *Fulvocentrum* species in having asci without an apical apparatus and wide and septate paraphyses (2–4 µm wide). The asci in *Fulvocentrum* species either have apical thickening in *F. aegyptiacum* and *F. clavatisporum*, and apical ring in *F. rubrum*. The hamathecium in *Fulvocentrum* species are narrow (1–2 µm wide), numerous and aseptate (Abdel-Wahab et al. 2001, 2019). *Khaleijomyces umikazeanus* also differs from *Fulvocentrum* species in the morphology of ascomata, asci and ascospores and are phylogenetically distant (Figs. 149 and 150).

Xylariales Nannf.

Notes: Xylariomycetidae consists of two main orders, namely *Amphisphaeriales* and *Xylariales*. *Xylariales* was considered the second largest order among the Sordariomycetes and a detailed description is provided by Maharachchikumbura et al. (2016) and Hyde et al. (2020b). This order has been revised based on both morphology and phylogenetic data and many families were either newly introduced or transferred (Hongsanan et al. 2017; Daranagama et al. 2018; Voglmayr et al. 2018; Wendt et al. 2018). Currently, 148 genera (Wijayawardane et al. 2020) are accepted in *Xylariales*, which are distributed in 22 families and 12 families *incertae sedis*. Similarly, *Cainiaceae* and *Calceomyces* were placed in Xylariomycetidae *incertae sedis*. Major contributions in the order *Xylariales* such as monographs, checklists and keys along with detailed descriptions and illustrations were provided by different mycologists (Miller 1961; Lowen 1991; Petrini 2013; Stadler et al. 2014; Shang et al. 2018; Niranjan and Sarma 2020; Hyde et al 2020a). In the recent times chemotaxonomic inputs have been widely

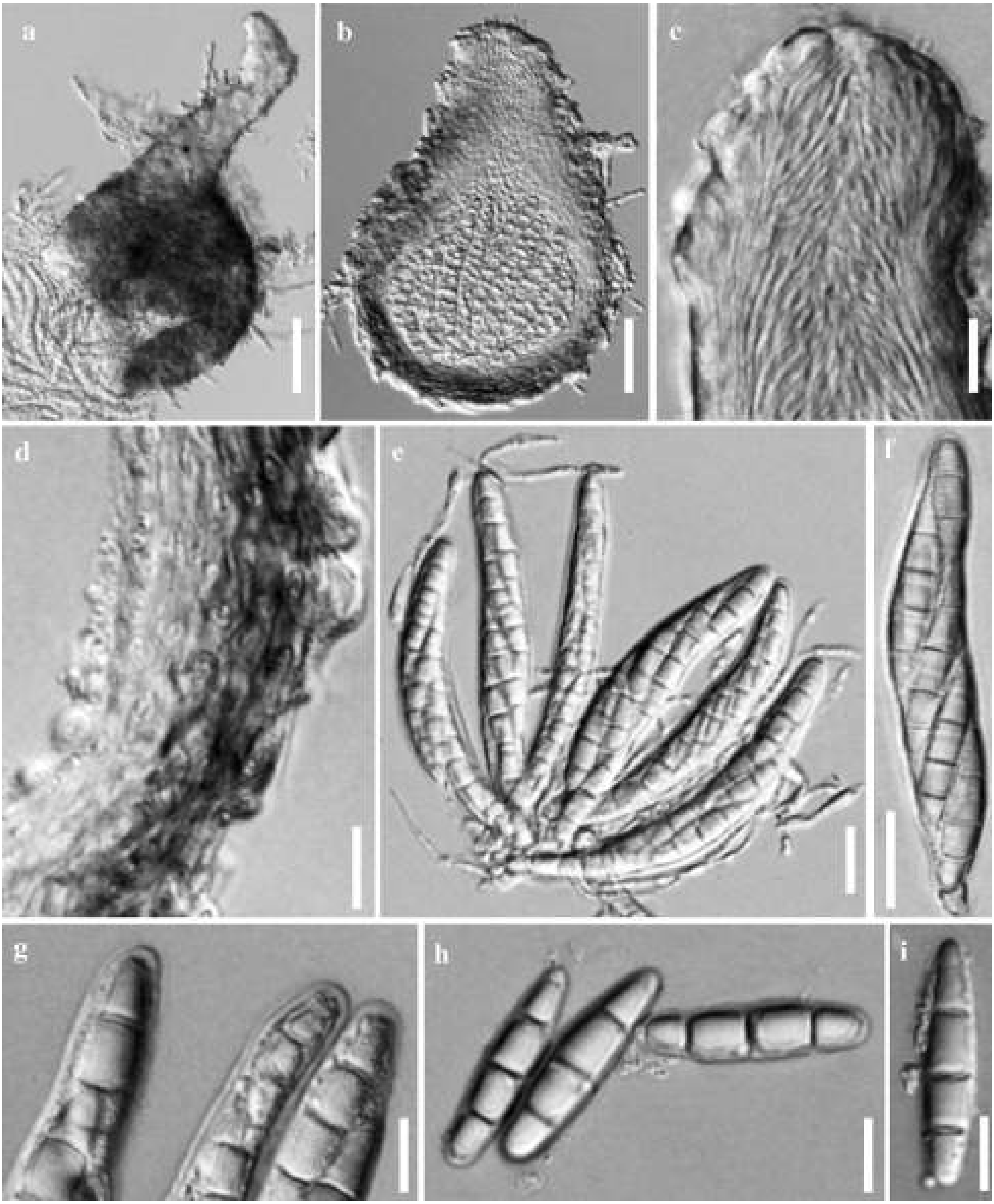


Fig. 149 ***Khaleijomyces umikazeanus*** (CBS H-23860, **holotype**). **a** Squash of ascoma. **b** Vertical section through ascoma. **c** Close up of neck show periphyses. **d** Close up of peridium. **e**, **f** Asci and paraphyses. **g** Ascal tips. **h**, **i** Ascospores with amorphous material. Scale bars: **a**, **b** = 60 μm, **c**, **d**, **g**–**i** = 10 μm, **e**, **f** = 15 μm

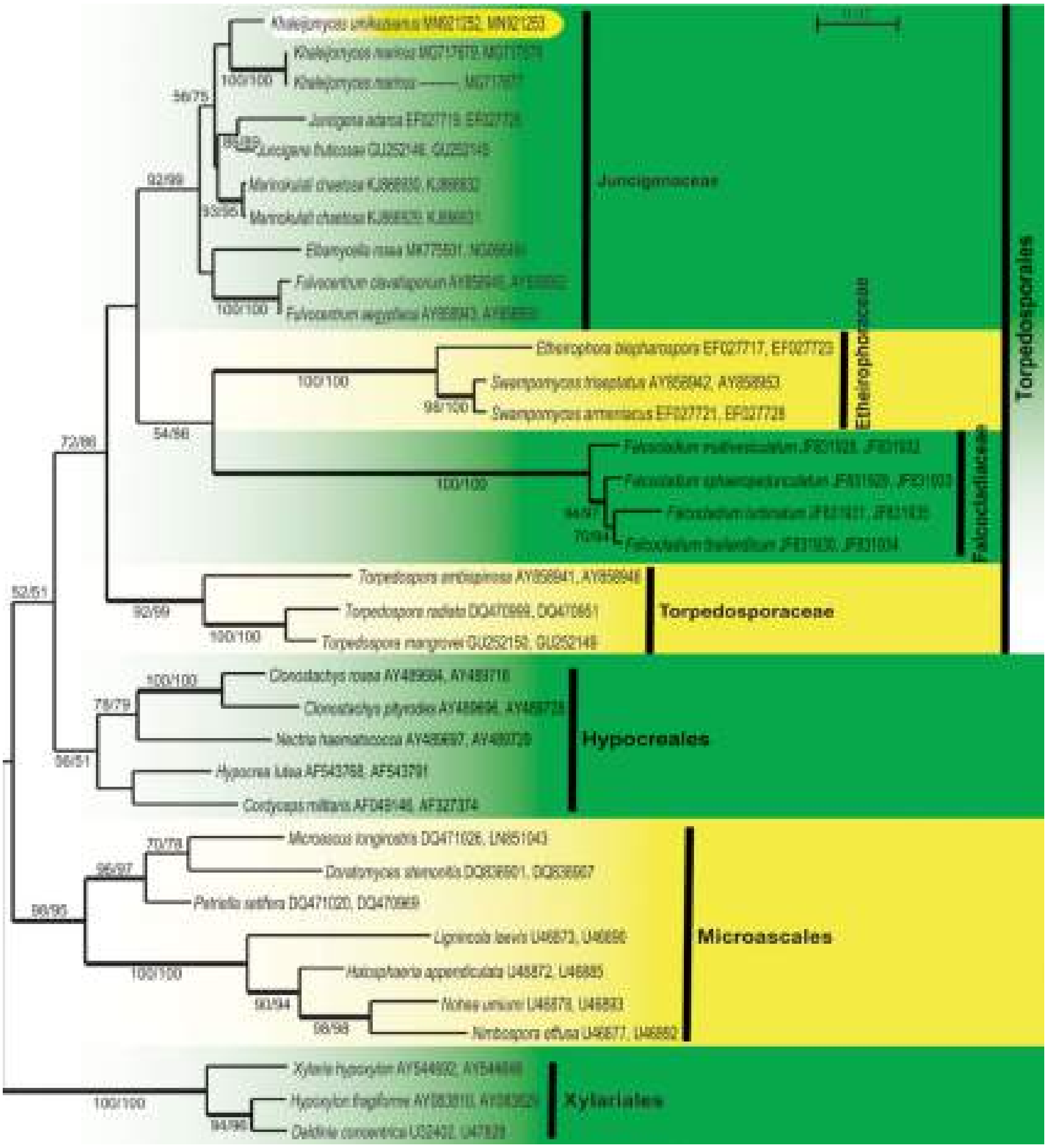


Fig. 150 Phylogenetic relationship of *Khaleijomyces umikazeanus* with related taxa in *Juncigenaceae* based on the nucleotide sequences of the combined SSU and LSU rDNA. The maximum likelihood (ML) tree (-ln likelihood = 14429.06) was constructed in PAUP 4 (Swofford 2002). The maximum parsimonious data set of the combined genes consisted of 35 taxa with 3 representatives of *Xylariales* used as outgroup. The combined dataset includes 1116 total characters, of which 712 were constant, 89 parsimony-uninformative and 315 parsimony-informative. The parsimony analyses of the data matrix yielded 2 equally most parsimonious trees with a tree length of 1084 steps [consistency index (CI) = 0.5424, homoplasy index (HI) = 0.4576, retention index (RI) = 0.7385, rescaled consistency index (RC) = 0.4005]. Phylogenetic trees obtained from ML, maximum parsimony (MP) and Bayesian inference posterior probabilities (BYPP) were similar in topology. Bootstrap support on the nodes represents MLBS and MPBS equal to or greater than 50%. Branches with a BYPP of equal to or greater than 0.95 are in bold. The newly taxon is in yellow box

used in *Hypoxylaceae* (Kuhnert et al. 2017a, b; Helaly et al. 2018; Wendt et al. 2018; Becker et al. 2020), while other mycologists made molecular taxonomy and morphological observations in the order *Xylariales* including the establishment of a web portal (Niranjan and Sarma 2018; Wijayawardene et al. 2017, 2018; Basnet et al. 2019; Bundhun et al. 2020; Hyde et al. 2020a; Stadler et al. 2020).

Diatrypaceae Nitschke

Notes: *Diatrypaceae* was introduced by Nitschke (1869) and it is typified by *Diatrype* (Augusto et al. 2016; Hyde et al. 2020d). In the past, this family belonged to *Diatrypales* and in current classification *Diatrypaceae* belongs to *Xylariales* (Augusto et al. 2016; Hyde et al. 2020d; Wijayawardene et al. 2020). Diatrypaceous taxa are most likely colonise any kind of ecosystem with woody plants in both aquatic and terrestrial habitats and some are pathogens of economic crops as well as forest trees (Chacón et al. 2013; Senanayake et al. 2015; Dayarathne et al. 2016; Hyde et al. 2020d; Konta et al. 2020). There are 20 genera accounted to *Diatrypaceae* (Wijayawardene et al. 2020). In this study we discuss two *Eutypa* species collected from Italy.

Eutypa Tul. & C. Tul.

Notes: *Eutypa* was established by Tulasne and Tulasne (1863) and typified by *Eutypa lata* which is a serious pathogen of grape cankers (Rolshausen et al. 2004, 2008). The genus consists of both pathogenic and saprobic members, and pathogens are reported as the causal agents for *Eutypa* dieback of apricots, cherries and grapevine (Camps et al. 2014; Hyde et al. 2020d; Lolas et al. 2020). There are 219 epithets listed in Index Fungorum (2021) however, 131 species are accounted for in the genus (Wijayawardene et al. 2020). We follow the latest treatment for *Diatrypaceae* in Konta et al. (2020) to resolve the taxonomic placements of our newly isolated strains. An updated phylogenetic tree is presented in Fig. 153. This study reports two new host records of *Eutypa flavovirens* and *E. lata* from two different Italian sites.

Eutypa flavovirens (Pers.) Tul. & C. Tul., Select. fung. carpol. (Paris) 2: 57 (1863)

Index Fungorum number: IF122506; *Facesoffungi number*: FoF 00692; Fig. 151

Saprobic on dead land branch of *Quercus* sp. **Sexual morph** *Stromata* 0.7–1 mm diam., gregarious, aggregates are solitary to scattered, erumpent on the bark, black, outer thin carbonaceous layer, pustulate, with numerous ascomata in a single stroma. *Ascomata* 350–650 μm high, 300–450 μm diam., ($\bar{x}$ = 360 × 490 μm, n = 10) length with ostiole neck, immersed in the stroma, globose to broadly ovoid, narrowing towards the apex, very narrow at the base of papilla, ostiolate, papillate. *Ostiole neck* 100–130 × 250–275 μm ($\bar{x}$ = 90 × 260, n = 5), opening to outer surface, appearing as black spots, comprising outer dark brown and inner pale brown to yellowish parenchymatous cell layers, with periphyses oriented towards apical direction. *Peridium* 15–25 μm thick, with two layers, outer layer comprising 4–6 layers with thick-walled, dark brown to pale brown cells of *textura angularis* to *textura prismatica* cells, inner layer comprising 2–3 layers with thin-walled, hyaline cells of *textura prismatica*. *Hamathecium* 1–1.5 μm wide, filiform, longer than the asci, septate, unbranched, guttulate, hyaline paraphyses. *Asci* 80–120 × 8–10 μm ($\bar{x}$ = 105 × 8.5 μm, n = 20), 8-spored, unitunicate, thin-walled, clavate, with a J- apical ring, long, thin-walled pedicel, with cylindrical, thick-walled, swollen upper portion, apically flat. *Ascospores* 7–9.5 × 2–2.5 μm ($\bar{x}$ = 8.5 × 1.5 μm, n = 40), overlapping, 1–3-seriate, yellowish to brown, unicellular, ellipsoidal to cylindrical or elongate-allantoid, aseptate, straight to slightly curved, with or without guttules, smooth-walled. **Asexual morph** See Senanayake et al. (2015) and Niranjan et al. (2018).

Culture characteristics: Ascospores germinating on PDA within 24 h and germ tubes arising from one end of the ascospore. Colonies on PDA, reaching 4–5 cm diam. after 7 days at 25 °C, colonies medium dense, flat or effuse, slightly raised, cottony, white, margin rough.

Material examined: ITALY, Province of Bologna, Calistri—Porretta Terme, on the dead land branch of *Quercus* sp. (*Fagaceae*), 9 April 2019, E. Camporesi, IT 4287 (MFLU 19-0911, **new record**), living culture, MFLUCC 21-0069.

GenBank numbers: ITS = MZ456005, TUB2 = MZ476771.

Notes: In the multigene phylogeny (ITS and TUB2) of this study, our isolate (MFLUCC 21-0069) and *Eutypa flavovirens* (E48C, CBS 272) clustered together with relatively high support (98% MLBS, 1.00 BYPP; Fig. 153). *Eutypa flavovirens* strains MFLUCC 12-0052, MFLUCC 13-0625 and PUFNI 310 were studied by Senanayake et al. (2015) and Niranjan et al. (2018) and they did not provide TUB2 DNA sequences to support. However, in our phylogenetic analyses, *Eutypa flavovirens* strains are grouped within *Allodiatrype* clade (Fig. 153) introduced by Konta et al. (2020). In our study *Eutypa* shown to be polyphyletic genus which are presently reside in A, B, C and D clades. According to Niranjan et al. (2018) several strains of *Eutypa flavovirens* have been identified with few differences in size of the asci and ascospores. Also, Senanayake et al. (2015) reported, the specimen collection in Thailand (MFLUCC 13-0625) may not be identical to species collected from Europe. Likewise, our isolate collected from Italy having ascomata, ostiole neck, peridium thickness are larger than previously studied and differs in having thinner paraphyses (Fig. 151). However, our isolate showed that the distinct yellowish green stromatic tissues the same as other *Eutypa flavovirens* isolates from Senanayake et al. (2015) and Niranjan et al. (2018). Based on the morpho-molecular analyses we conclude that our new collection is another record of *Eutypa flavovirens* and also a new host record on *Quercus* sp. (*Fagaceae*) in Italy.

Eutypa lata (Pers.) Tul. & C. Tul., Select. fung. carpol. (Paris) 2: 56 (1863)

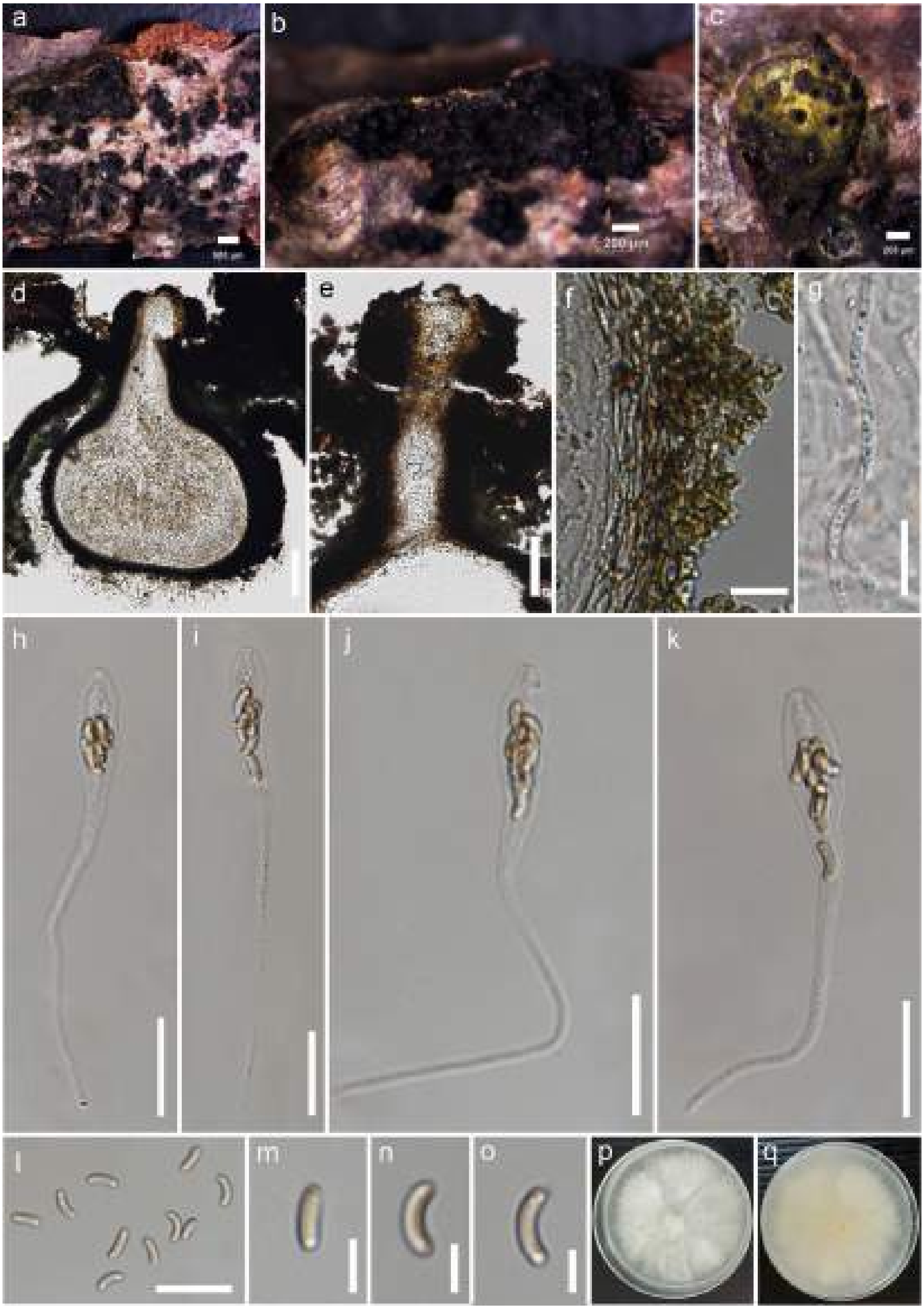


Fig. 151 ***Eutypa flavovirens*** (MFLU 19-0717, **new record**). **a**, **b** Stromata on substrate. **c** Cross-section of stroma. **d**, **e** Vertical section through stromata showing ostiolar canals. **f** Peridium. **g** Paraphyses. **h**–**k** Asci. **l**–**o** Ascospores. **p**, **q** Culture on PDA from above and below. Scale bars: **a** = 500 µm, **b**, **c** = 200 µm, **d** = 100 µm, **e** = 50 µm, **h**–**l** = 20 µm, **f**–**g** = 10 µm, **m**–**o** = 5 µm

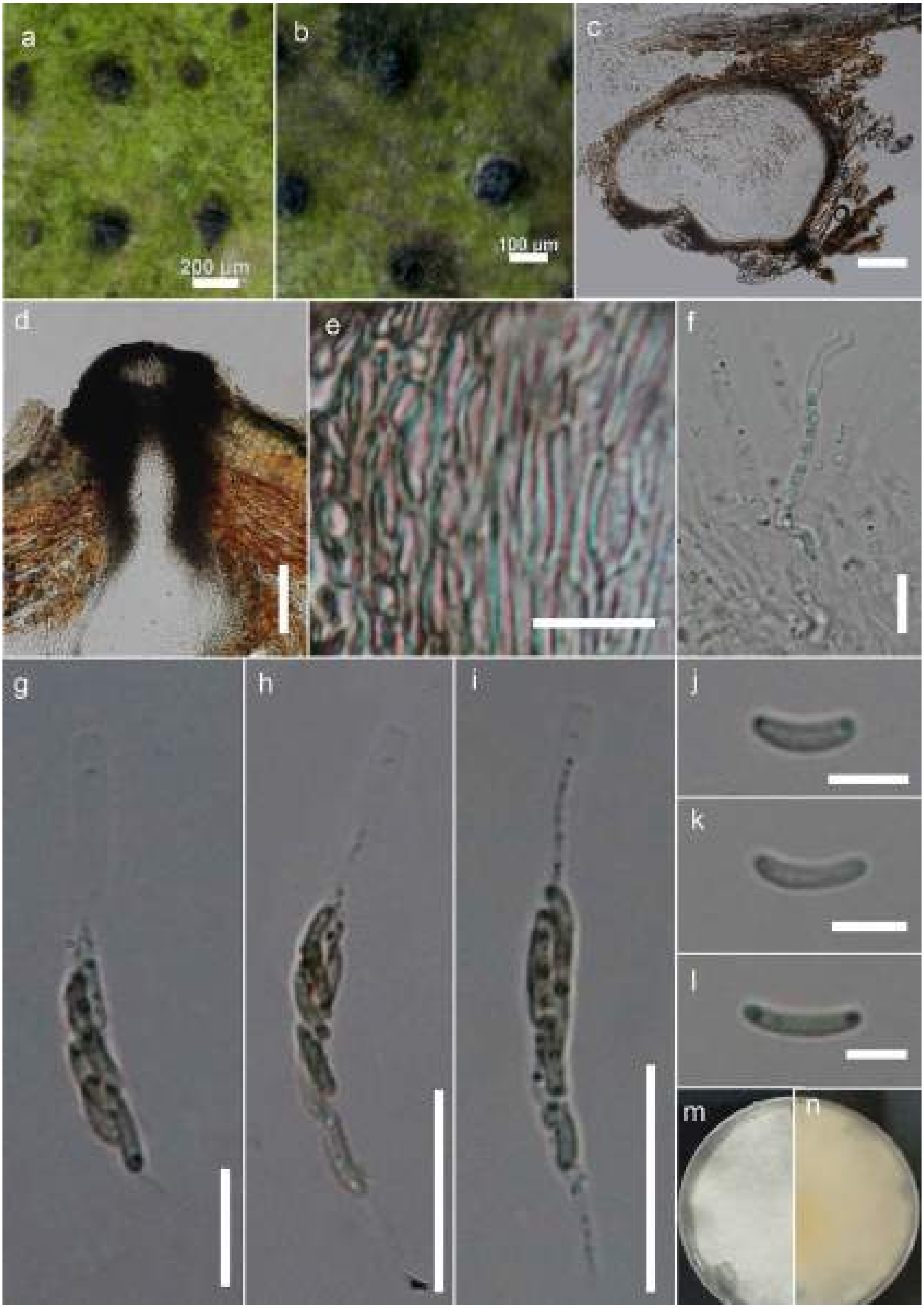


Fig. 152 ***Eutypa lata*** (MFLU 19-0501, **new record**). **a**, **b** Stromata on substrate. **c** Cross-section of ascoma. **d** Ostiole. **e** Peridium. **f** Paraphyses. **g**–**i** Asci. **j**–**l** Ascospores. **m**, **n** Culture on PDA from above and below. Scale bars: **a** = 200 µm, **b**, **c** = 100 µm, **d** = 50 µm, **f**, **h**, **i** = 20 µm, **e**, **g** = 10 µm, **j**–**l** = 5 µm

Index Fungorum number: IF140211; *Facesoffungi number*: FoF 09963; Fig. 152

Saprobic on the dead aerial branch of *Corylus avellana*. **Sexual morph** *Ascostromata* 400–600 µm high, 350–450 µm diam. ($\bar{x}$ = 380 × 490 µm, n = 10) length with ostiole neck, solitary, scattered semi-immersed, erumpent on the bark, subglobose to irregular, black, ostiolate. *Ostiole* individual, central, ostiole neck 150–200 µm high ($\bar{x}$ = 165 µm, n = 5). *Peridium* 20–30 µm wide, composed of two layers, outer layer comprising 4–5 layers of thick-walled, brown to pale brown cells of *textura angularis* to *textura prismatica*, thin inner layer comprising 3–5 layers of thin-walled, hyaline cells of *textura prismatica*. *Hamathecium* 1.8–3 µm wide, filiform, longer than the asci, septate, guttulate, unbranched, hyaline paraphyses. *Asci* 40–65 × 4–5 µm ($\bar{x}$ = 53 × 4.5 µm, n = 10), 8-spored, unitunicate, thin-walled, clavate, long pedicillate, apically truncate. *Ascospores* 5–9 × 1–2 µm ($\bar{x}$ = 7 × 1.5 µm, n = 30), overlapping bi-seriate, aseptate, hyaline, ellipsoidal to cylindrical or allantoid, slightly curved, smooth-walled, mostly with small guttules at the edges. **Asexual morph** sees (Moyo et al. 2018).

Culture characteristics: Ascospores germinating on PDA within 24 h and germ tubes arising from both ends of the ascospore. Colonies on PDA, reaching 4–5 cm diam. after 7 days at 25 °C, colonies medium dense, flat or effuse, slightly raised, cottony, white, margin rough.

Material examined: ITALY, Province of Forlì-Cesena, Teodorano—Meldola, on the dead aerial branch of *Corylus avellana* (*Betulaceae*), 20 January 2019, E. Camporesi, IT 4212 (MFLU 19-0501, **new record**), living culture, MFLUCC 21-0068.

GenBank numbers: ITS = MZ453405, TUB2 = MZ476772.

Notes: The multigene phylogeny (ITS and TUB2) of this study, our strain (MFLUCC 21-0068) and *Eutypa lata* (EP18, RGA01 and ATCC 28120) strains clustered together with 89% MLBS, 0.96 BYPP support (Clade B; Fig. 153). Comparing the ITS (ITS1-5.8S-ITS2) and TUB2 rDNA regions between EP18 and RGA01 strains, only 1 bp (0.19%) difference was found from 526 nucleotides in the ITS and no base pair differences in the TUB2. Comparison of the same gene regions between our strain and RGA01 strain, there are only 1 bp (0.18%) difference that could in the ITS and within the 350 bp of the TUB2 region, there are 7 bp (2.0%) difference. In comparison of the same gene regions between our strain and ATCC 28,120 strain there were no base pair differences in the ITS and 7 bp (1.88%) of difference from 372 bp in the TUB2. When morphological characters of our species were examined, they were similar with the genus description provided by Vasilyeva and Stephenson (2006) and Senanayake et al. (2015). The species description of *Eutypa lata* provided by Moyo et al. (2018) is morphologically similar to our isolate MFLUCC 21-0068 (Fig. 152). According to morpho-molecular analyses we conclude that our new collection is another record of *Eutypa lata* and also a new host record on *Corylus avellana* (*Betulaceae*) in Italy.

Xylariaceae Tul. & C. Tul.

Notes: Members of *Xylariaceae* are occur throughout the world as saprobes, pathogens or endophytes in dead and decaying logs, leaves and fruits, or insect vectors. The family has been covered extensively in several recent treatises including Maharachchikumbura et al. (2016); Daranagama et al. (2018) and Xie et al. (2020). Several new genera and new species have been added into this family in recent times (Tibpromma et al. 2017a, b; Heredia et al. 2020; Voglmayr and Beenken 2020) into this family. Maharachchikumbura et al. (2016) accepted more than 80 genera. The family has also been broadly divided into two sub families Xylaroideae and Hypoxyloideae, the latter became *Hypoxylaceae* (Wendt et al. 2018). After the separation of *Hypoxylaceae*, the number of genera in *Xylariaceae* reduced to 37 genera (Daranagama et al. 2018). In a recent paper only 32 genera were accepted (Wijayawardane et al. 2020). *Xylariaceae* is known to produce different kinds of secondary metabolites (Helaly et al. 2018) and these are used as markers by some authors (Song et al. 2014). For example, the following genera could be delineated through the chemotaxonomic data by incorporating the secondary metabolite profiles: *Coniolariella*, *Entoleuca*, *Hypocopra*, *Kretzschmaria*, *Rosellinia* and *Xylotumulus* (Shang et al. 2018; Helaly et al. 2018; Becker et al. 2020).

Xylaria Hill ex Schrank

Notes: *Xylaria* members are mostly macroscopic in nature in that they can be seen by the unaided eye, and consist of members with different lifestyles including saprobic, pathogenic or endophytic in plant tissues, fallen leaves, fruits, seeds, manure and insects. *Xylaria* species are characterized by superficial, massive or sometimes reduced stroma in different shapes and size, unitunicate, cylindrical and pedicellate asci with or without a J + apical ring and ellipsoidal, dark ascospores with germ pores or germ slits, as well as geniculosporium, nodulisporium-like or libertella-like asexual morphs (Maharachchikumbura et al. 2016; Hyde et al. 2020a, b). There are more than 600 species known in this family and this number has been increasing with recent additions from different parts of the world (Husbands et al. 2018; Ju et al. 2018; Fournier et al. 2018; Ma and Li 2018; Crous et al. 2019; Hsieh et al. 2020; Ibrahim et al. 2020).

Xylaria apiospora M. Niranjan & V.V. Sarma, ***sp. nov.***

Index Fungorum number: IF557848; *Facesoffungi number*: FoF 08683; Fig. 154

Etymology: The ascospores having the apical cell.

Holotype: AMH-10071

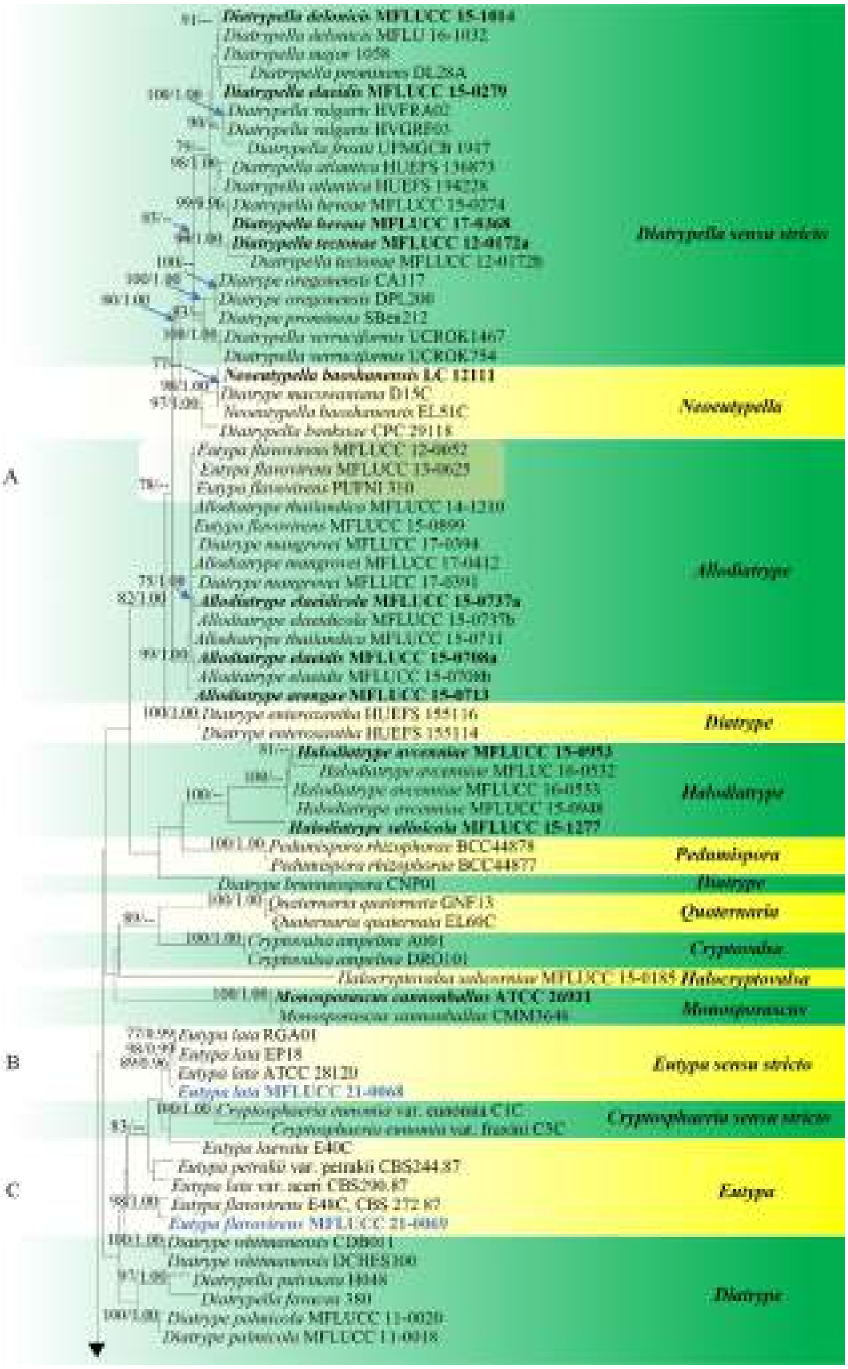


Fig. 153 Phylogram generated from maximum likelihood analysis based on combined ITS and TUB2 sequence data representing *Diatrypaceae* in *Xylariales*. Related sequences are taken from Konta et al. (2020) and additions according to the BLAST searches in NCBI. Hundred and twenty-nine strains are included in the combined analyses which comprised 1180 characters (665 characters for ITS and 515 characters for TUB2) after alignment. *Kretzschmaria deusta* (CBS 826.72) and *Xylaria hypoxylon* (CBS 122620) in *Xylariaceae* (*Xylariales*) were used as the outgroup taxa. The best scoring RAxML tree with a final likelihood value of − 17362.853779 is presented. The matrix had 906 distinct alignment patterns, with 37.13% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.224946, C = 0.263658, G = 0.237000, T = 0.274396; substitution rates: AC = 1.093989, AG = 3.037146, AT = 1.238822, CG = 0.814851, CT = 4.048082, GT = 1.000000; gamma distribution shape parameter α = 0.183977. Bootstrap support values for ML equal to or greater than 75% are given above the nodes (left side). Bayesian posterior probabilities (BYPP) equal to or greater than 0.95 are given above the nodes (right side). Ex-type strains are in bold and newly generated sequences are in blue

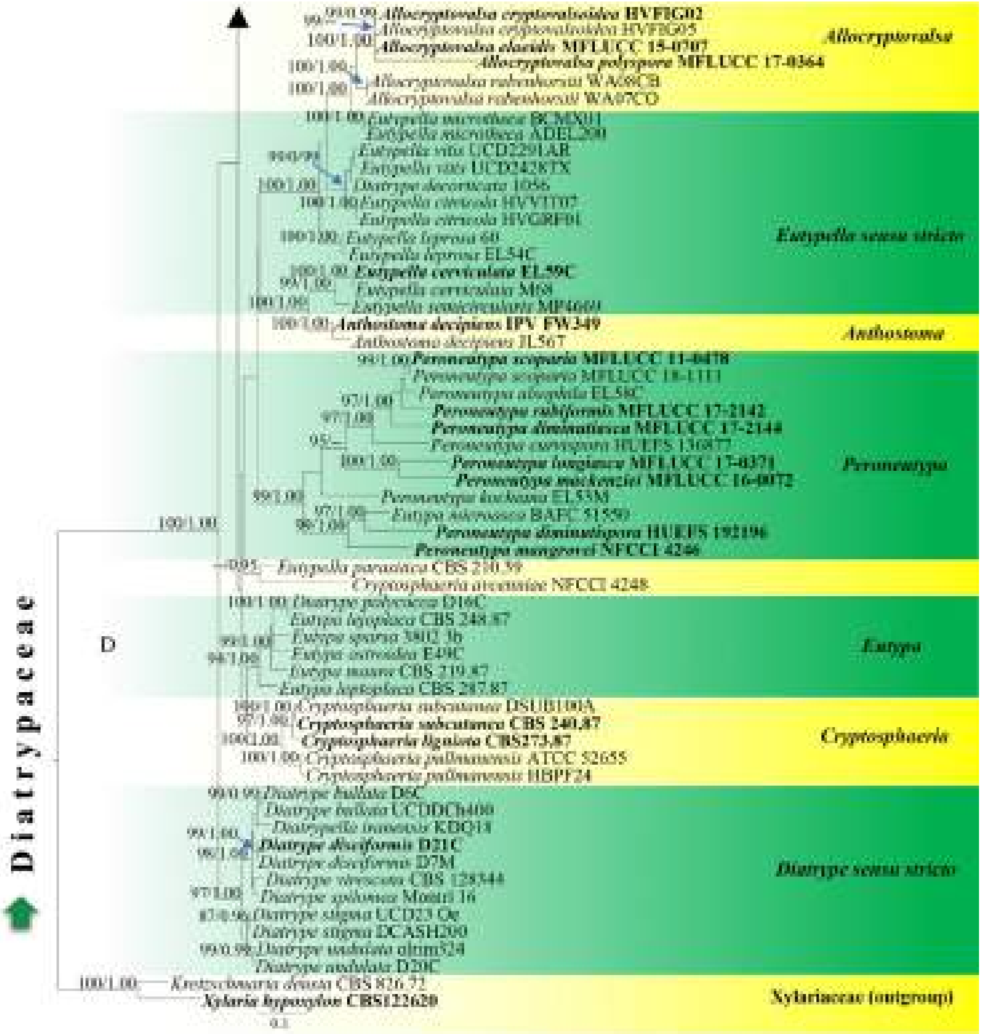


Fig. 153 (continued)

Saprobic on decaying twig. **Sexual morph** *Ascostromata* superficial, solitary, black, crust 95 µm high, with brown hyphae on surface, loosely connected, hyaline, filamentous tissue and central brown tissue. *Ascomata* (193–)285–460 × (180–)215–260 µm ($\bar{x}$ = 242 × 233 µm, n = 8), globose, erumpent, pullvinate, clypeate, periphysate. *Necks* 82–120 µm high. *Peridium* 39 µm wide, with brown to hyaline cell layers of *textura porrecta*. *Hamathecium* comprising 5.9 µm wide, septate, branched, longer than asci, sparsely paraphyses. *Asci* 91–126 × 4.5–6 µm ($\bar{x}$ = 108 × 5 µm, n = 25), 8–spored, unitunicate, cylindrical, apically rounded, cylindrical, with a J + an apical ring, rings 1.5–2 × 1.5–2 µm ($\bar{x}$ = 2 × 2 µm, n = 25), long pedicellate, persistent. *Ascospores* 12–14.5 × 4–5 µm ($\bar{x}$ = 13 × 4 µm, n = 25), overlapping uni-seriate, fusiform, hyaline to brown at maturity, germ slit curved, obtuse ends, with hyaline apical cell at one end, smooth walled. **Asexual morph** Undetermined.

Material examined: INDIA, Andaman and Nicobar Islands, South Andaman, Chidiya Tapu, Viewpoint Area (11°48′10″ N 92°71′08″ E). Recorded on a decaying log, 9 December 2017, M. Niranjan and V.V. Sarma (PUFNI 1766). Herbarium specimen submitted to Ajrekar Mycological Herbarium-AMH (AMH-10071, **holotype**) and ex-type living culture (NFCCI-4370) deposited at National Fungal Culture Collection of India (NFCCI), Agarkhar Reserch Institute, Pune, Maharasthra, India.

GenBank numbers: ITS = MT572916.

Notes: *Xylaria apiospora* slightly differs from *X. longipes* (Rogers 1983) in having smaller ascomata (285–460 × 215–260 vs. 450–650 × 400–600 µm) and asci (91–126 × 4.5–6 vs. 130–180 × 7–9 µm), and larger ascospores (12–14.5 × 4–5 vs. 13–15 × 5–7 µm) with hyaline smaller, apical cells. While *X. apiospora* has fusiform ascospores with hyaline, smaller cells, *X. longipes* has ellipsoid-inequilateral, aseptate ascospores. Phylogenetically,

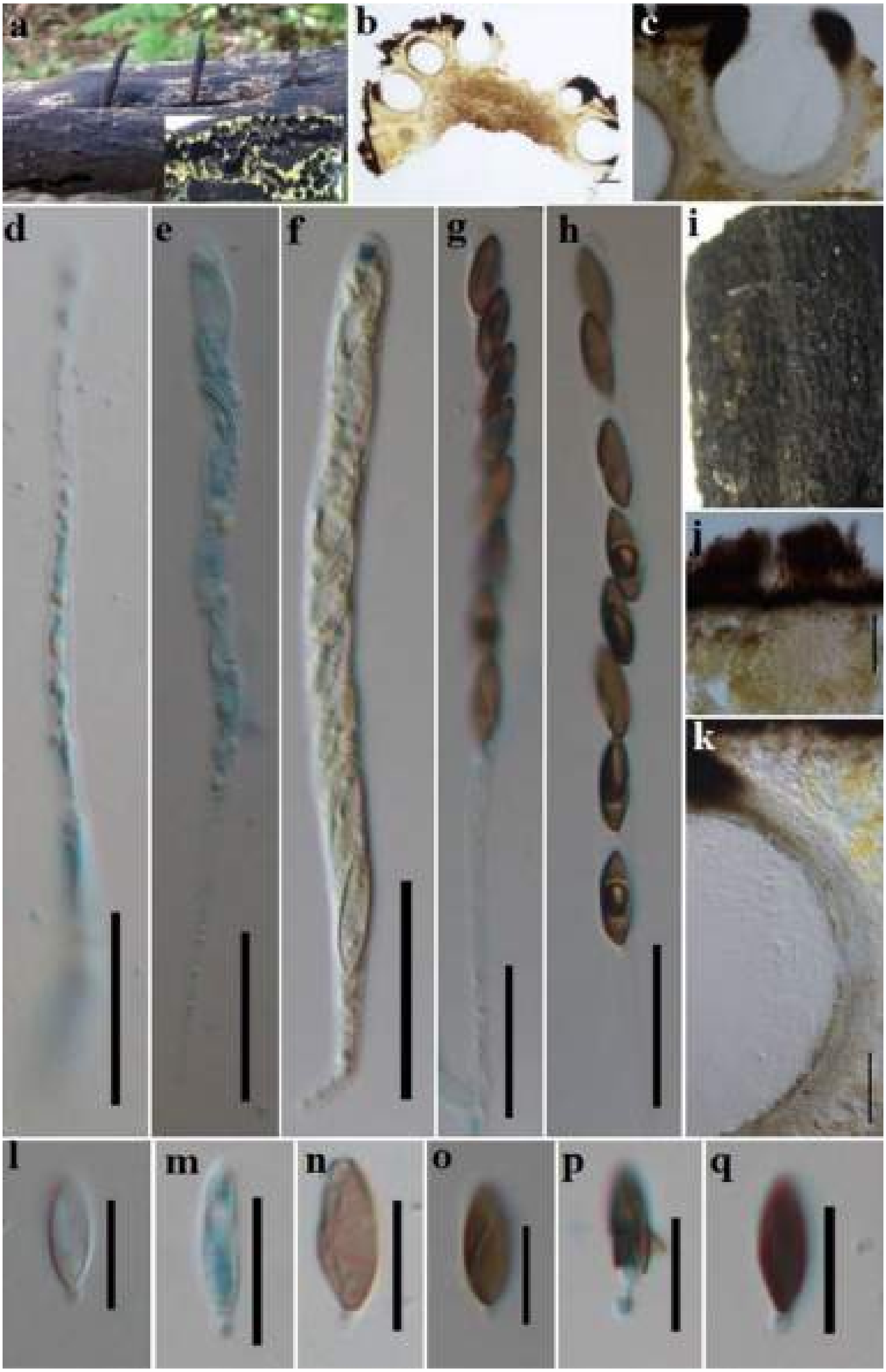


Fig. 154 ***Xylaria apiospora*** (NFCCI-4370, **holotype**). **a** Stromata on decaying host. **b**, **c** Horizontal section of stromata. **d** Paraphyses. **e**–**h** Asci. **i** Striations on stromatal surface. **j** Cross section of stroma. **k** Peridium. **l**–**q** Ascospores. Scale bars: **b** = 100 µm, **c**, **j**, **k** = 50 µm, **d**–**h** = 20 µm, **l**–**q** = 10 µm

X. apiospora constitutes a distinct basal lineage to *Xylaria multiplex* (1010). Therefore, we introduce *X. apiospora* as a new species based on morphology and phylogenetic evidence (Figs. 154 and 156).

Xylaria haemorrhoidalis Berk. & Broome. Journal of the Linnean Society. Botany 14: 117 (1875).

Index Fungorum number: IF224410; *Facesoffungi number*: FoF 08682; Fig. 155

Saprobic on decaying twig. **Sexual morph** *Stromata* 1.2–1.5 cm long, 0.3 cm wide, 0.9 long at stipes, upright, aggregated, unbranched, obclavate, fertile apices, surface pulvinate, black, soft with scattered brown hairs emerging from grooves, internally has white thick hyphae, stalks long very distinct from stroma. *Ascomata* perithecial 478–630 × 495–580 µm ($\bar{x}$ = 567 × 542 µm, n = 5), globose, clypeate. *Necks* 152–210 µm high ($\bar{x}$ = 182.5 µm, n = 5), periphysate. *Peridium* 34–41 µm wide, with outer brown cell layers of *textura porrecta*, inner thin cell layers of *textura angularis*. *Hamathecium* comprising 8.5–12 µm wide, septate, branched, longer than asci, sparsely paraphyses. *Asci* 140–206 × (10–)12–18(–21) µm ($\bar{x}$ = 167 × 14 µm, n = 25), 8-spored, unitunicate, cylindrical, apically rounded, urn-shaped J + an apical ring 6–10 × 4–5(–6) µm ($\bar{x}$ = 8 × 5 µm, n = 25), long pedicellate, persistent. *Ascospores* (21–)23–26 × 10–12 µm ($\bar{x}$ = 25 × 10.5 µm, n = 25), overlapping uni-seriate, hyaline to brown at maturity, ovoid, straight germ slit, obtuse ends, smooth walled. **Asexual morph** Undetermined.

Material examined: INDIA, Andaman and Nicobar Islands, South Andaman, Mount Harriet, (11°71′09.8″ N 92°73′30.6″ E). Recorded from a decaying log, 7 December 2017, M. Niranjan and V.V. Sarma (PUFNI 1765). Herbarium specimen submitted to Ajrekar Mycological Herbarium-AMH (AMH-10070, **new record**) and living culture (NFCCI-4369) deposited at National Fungal Culture Collection of India (NFCCI), Agarkhar Research Institute, Pune, Maharashtra, India.

GenBank numbers: ITS = MT572915.

Notes: *Xylaria haemorrhoidalis* is poorly known due to the fact that very few reports are available on its occurrence (Ju et al. 2009). Dade (1940) synonymized this fungus with *X. allantoidea* but recent molecular data show that it is distinct (Fig. 156). In the NCBI database, sequence data of only six accessions of *X. haemorrhoidalis* are available of which three are of ITS and one each of α-actin, *β-tubulin* and RPB2 genes. It has earlier been reported from Taiwan and the present record from Andaman forests, India extends its geographical range (Fig. 155).

Xylariales*, genus *incertae sedis

Melanographium Sacc.

Notes: *Melanographium* was introduced by Saccardo (1913) to accommodate the hyphomycetous taxon and is typified by *M. spleniosporum*. *Melanographium* taxa are saprobes and commonly found on dead or decaying wood, leaves, stems, culms or petioles, mostly on palms (Ellis 1963; Goh and Hyde 1997; Somrithipol and Jones 2005). The genus is characterized by having superficial colonies, unbranched and erect brown conidiophores, polyblastic conidiogenous cells with sympodial proliferation, and holoblastic, reniform, aseptate, brown to dark brown conidia (Ellis 1963, 1971). *Melanographium* includes 14 accepted species mostly based on morphology, but only one species, namely *Melanographium phoenicis* (MFLUCC 18-1481), have sequence data (Hyde et al. 2020b; Index Fungorum 2021). In this study, we introduce a new species *Melanographium smilacis* based on morphological and phylogenetic analyses.

Melanographium smilacis Boonmee, Huanraluek & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF558546; *Facesoffungi number*: FoF 09964; Fig. 157

Etymology: The specific epithet "*smilacis*" reflects the host genus *Smilax*.

Holotype: MLFU 21-0075

Saprobic on dead stems of *Smilax perfoliate*. **Sexual morph** Undetermined. **Asexual morph** *Colonies* on natural substrate superficial, effuse, velvety, tufted, dark brown. *Mycelium* immersed, composed of branched, septate, smooth, brown hyphae. *Conidiophores* 270–561 × 2–7 µm ($\bar{x}$ = 460 × 5 µm, n = 20), macronematous, loosely or densely, fascicle, panicle or tufted, unbranched, multiseptate, straight below, slightly flexuous, geniculate near the apex, brown to dark brown below, brown to pale brown towards the apex, subhyaline at the tip, thick-walled, rarely with percurrent proliferations. *Conidiogenous cells* polyblastic, integrated, terminal, sympodial, cylindrical or slightly clavate, with minutely protruding conidiogenous scars. *Conidia* 11–17 × 4–13 µm ($\bar{x}$ = 14 × 9 µm, n = 50), holoblastic, acropleurogenous, solitary, reniform or broad obovoid to semicircular, slightly curved, olivaceous brown to dark brown, aseptate, large guttulate when immature, verrucose or smooth-walled. *Conidial secession* schizolytic.

Culture characteristics: Conidia germinated on MEA, colony circular and flat, reaching 3.5 cm in 2 weeks at 25 °C, dense, effuse, velvety, radially with fimbriate edge, white grey to pale brown in surface, reddish brown to brown in reverse, with orangish yellow pigmented in media, with radiating outwards mycelium with dull white margin.

Material examined: THAILAND, Chiang Rai, Muang, Doi Lan, on dead stems of *Smilax perfoliate* L. (*Smilacaceae*), 27 March 2019, S. Boonmee, DL1 (MFLU 21-0075, **holotype**), ex-type living culture, MFLUCC 21-0098.

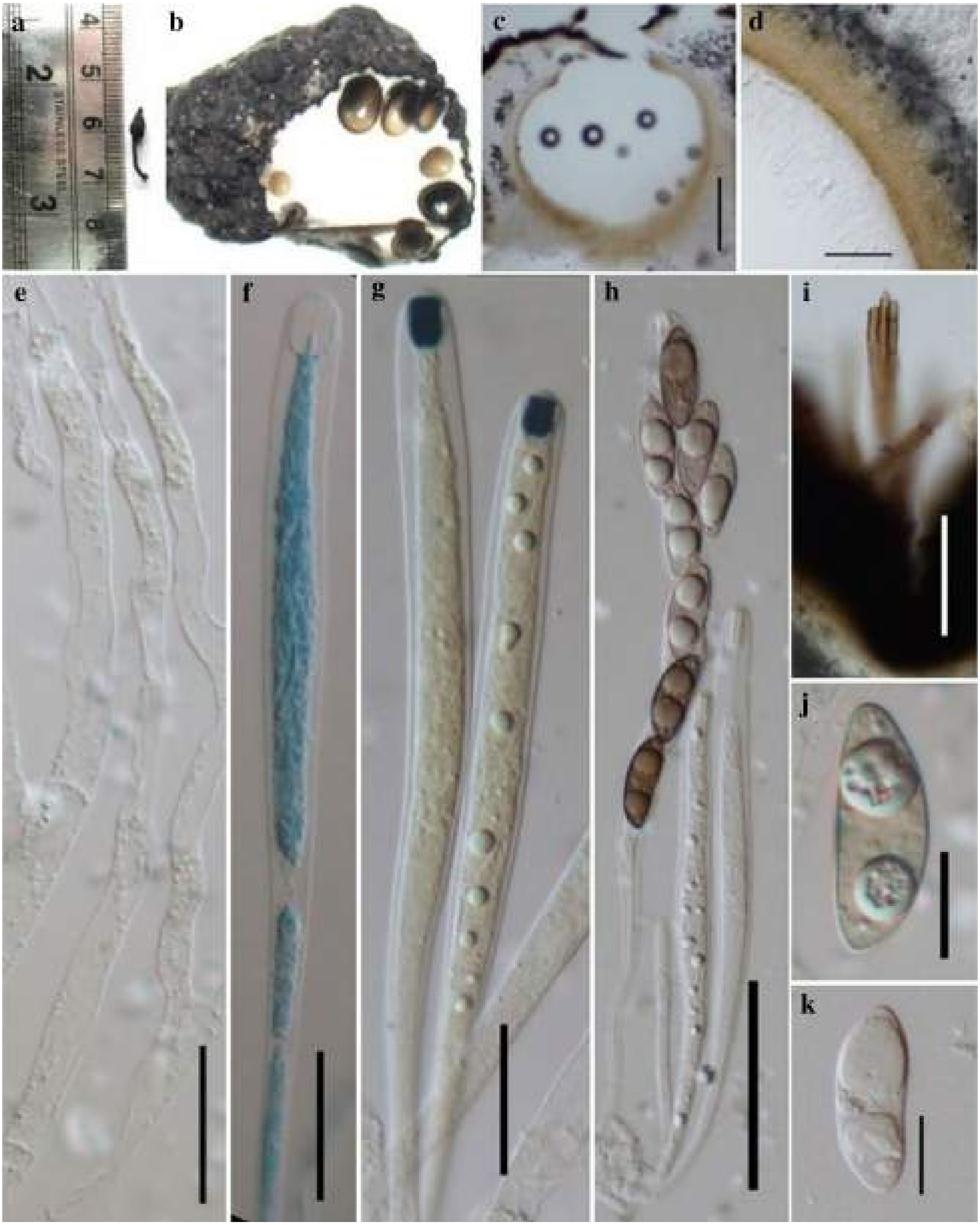


Fig. 155 ***Xylaria haemorrhoidalis*** (NFCCI-4369, **new record**) **a** Stromata on decaying host. **b**, **c** Horizontal section of ascoma. **d** Peridium. **e** Paraphyses. **f**–**h** Asci. **i** Hyphae on stromata surface. **j**, **k** Ascospores. Scale bars: **c** = 200 µm, **d**, **h**, **i** = 50 µm, **e**–**g** = 20 µm, **k**, **n** = 10 µm

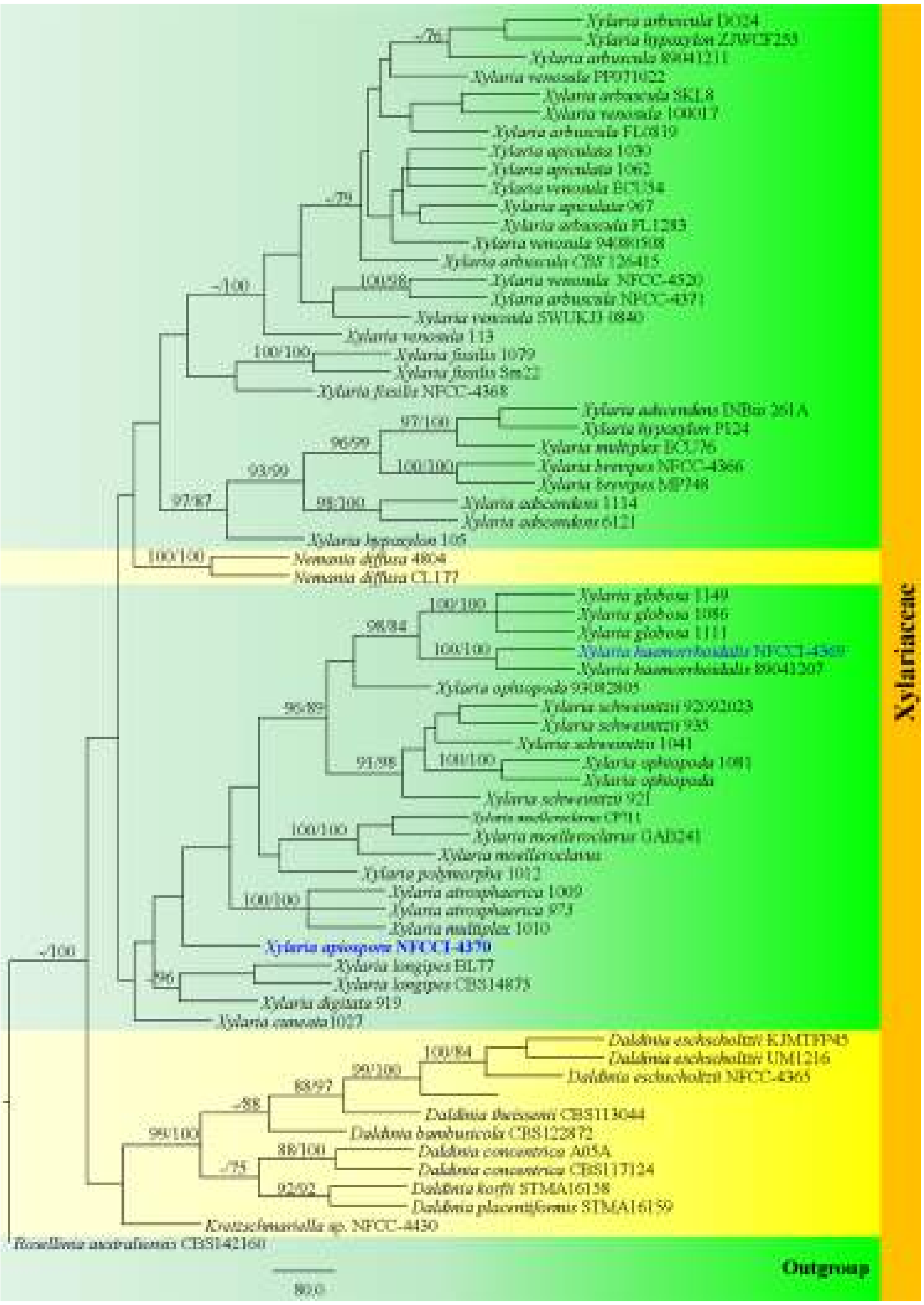


Fig. 156 Maximum parsimony tree of *Xylariaceae* constructed by using the ITS sequence. The tree includes both ML and MP values. *Rosellinia australiensis* is selected as an outgroup taxon. RAxML analysis yielded a minimum scoring tree with a final ML optimization likelihood value of – 5854.053127. The matrix had 393 distinct alignment patterns with 10.20% of undetermined characters or gaps. The maximum parsimonious dataset consists of 626 characters of which 278 were constant, 233 parsimony-informative and 115 parsimony-uninformative. The parsimony analysis of the data matrix resulted in one thousand equally parsimonious trees with a length of 1041 steps (CI 0.540, RI = 0.829, RC 0.447, HI = 0.460) in the first tree. The overall topology of the phylogenetic trees resulted from ML and MP were similar and incongruent in with earlier studies. The phylogenetic analysis showed that *Xylaria haemorrhoidalis* NFCC-4369 nested with *Xylaria haemorrhoidalis* 89041207 with 100% MLBS and 100% MPBS support. Similarly, *Xylaria apiospora* NFCC-4370 branched with *Xylaria multiplex* 1010 with week bootstrap support of MPBS. The newly generated sequences are indicated in blue bold

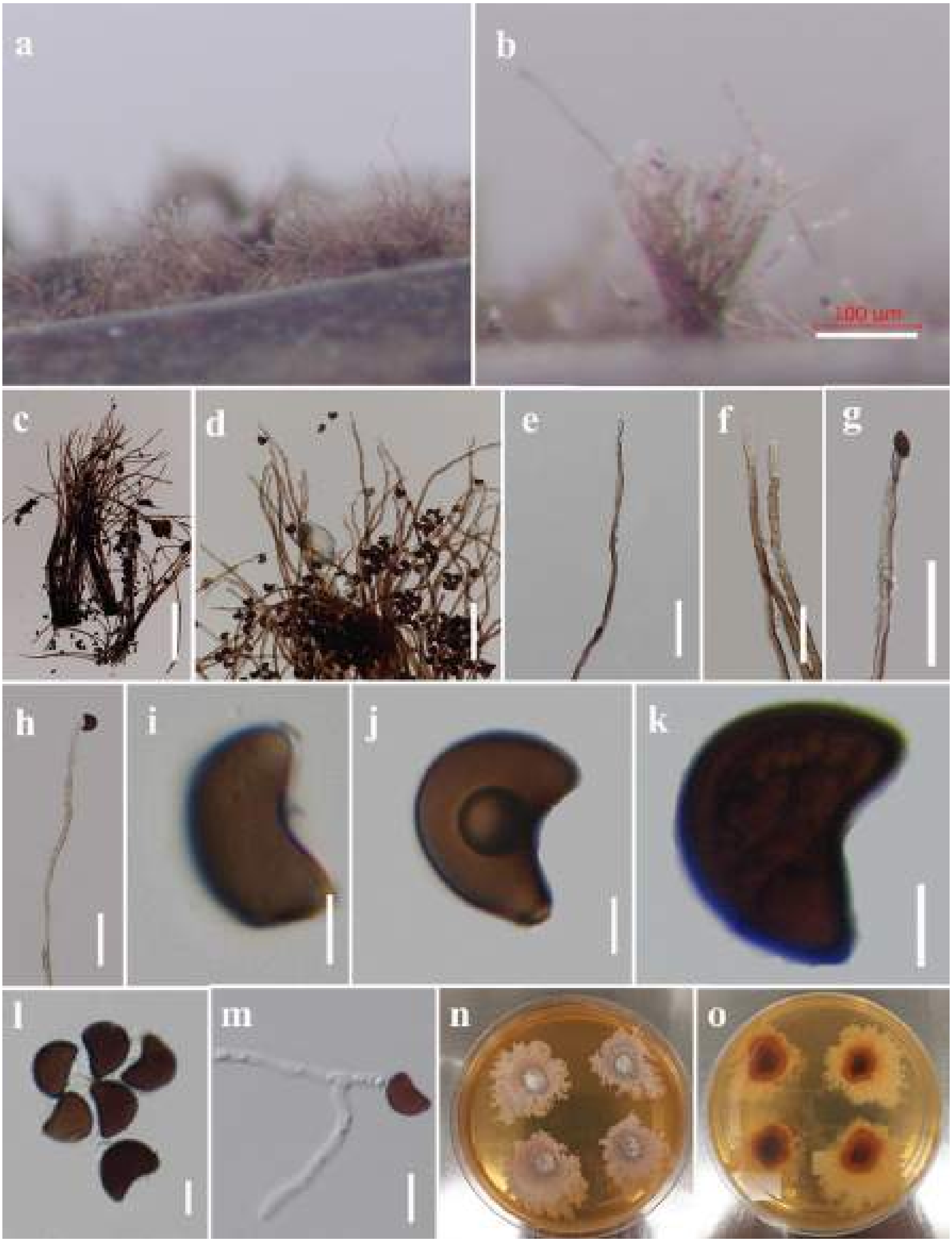


Fig. 157 ***Melanographium smilacis*** (MFLU 21-0075, **holotype**). **a**, **b** Appearance of colonies on natural substrate. **c**, **d** Squash mount of conidiophores with attached conidia. **e**, **f** Close-up of conidiophores showing septation with paler at the apex. **g**, **h** Apex of conidiophores with developing conidia. **i**–**l** Conidia with a basal scar. **m** Germinated conidium. **n**, **o** Culture on MEA from surface and reverse. Scale bars: **b** = 100 µm, **c**, **d** = 200 µm, **e**–**h** = 50 µm, **i**–**l** = 5 µm, **m** = 10 µm

GenBank numbers: ITS = MZ538514, LSU = MZ538548, SSU = MZ538572, TEF1-α = MZ567091.

Notes: *Melanographium smilacis* was found on dead stems of *Smilax perfoliate* (*Smilacaceae*). *Melanographium smilacis* shares common characters with species in *Melanographium* such as effused and tufted colonies, loosely or densely fascicle and brown conidiophores and reniform shape, aseptate with dark pigmented conidia (Saccardo 1913; Trotter 1931; Ellis 1963, 1971; Goh and Hyde 1997; Somrithipol and Jones 2005; Hyde et al. 2020b). Phylogenetically, *Melanographium smilacis* is as a sister lineage with the ex-type strain of *M. phoenicis* (MFLUCC 18-1481) with 100% MLBS, 1.00 BYPP support (Fig. 158). However, *M. smilacis* differs from *M. phoenicis* and other species in terms of the conidial features such as reniform or broad obovoid to semicircular shapes and lacking a slit (Fig. 157). According

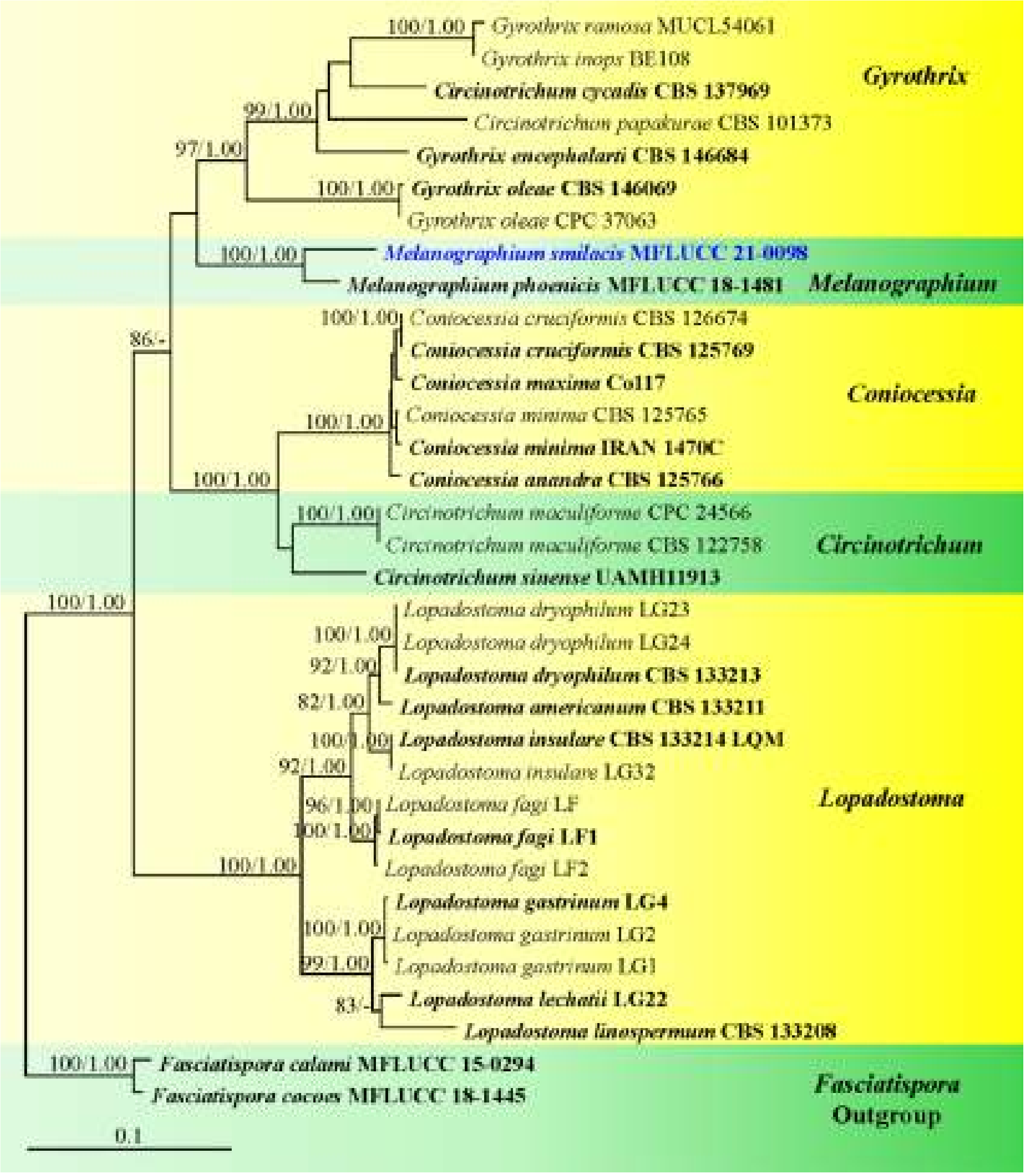


Fig. 158 Maximum likelihood phylogenetic tree based on a combined LSU and ITS sequence data of *Melanographium* taxa and related genera. The tree is rooted with *Fasciatispora calami* (MFLUCC 15-0294) and *F. cocoes* (MFLUCC 18-1445). Bootstrap support values for maximum likelihood (MLBS, left) equal to or greater than 70% is given above the nodes. Bayesian posterior probabilities (BYPP, right) equal to or greater than 0.95 are given above the nodes. Ex-type strains are in bold and newly generated sequence is in blue

to the morphological and phylogenetic analyses, we introduce a new species, *Melanographium smilacis*.

Basidiomycota R.T. Moore

Notes: The modern classification of Basidiomycota is adopted in this note following Zhao et al. (2017) and He et al. (2019).

Agaricomycetes Doweld

Notes: The classification of the families in Agaricomycetes is adopted herein following Hibbett et al. (2014), Zhao et al. (2017) and He et al. (2019).

Agaricales Underw.

Notes: *Agaricales* includes six well-accepted clades, viz. Agaricoid, Tricholomatoid, Marasmioid, Pluteoid, Hygrophoroid and Plicaturopsidoid (Matheny et al. 2006). He et al (2019) listed around 17,291 species belonging to 508 genera of 38 families in *Agaricales.* Some genera in this order have uncertain positions at the family level. Several genera are even polyphyletic. Therefore, it is necessary to construct a comprehensive phylogenetic frame for *Agaricales* to properly establish the position of the taxa.

Agaricaceae Chevall.

Notes: According to the recent study of He et al. (2019), *Agaricaceae* is a large group of Basidiomycota consisting of approximately 54 genera. Several studies established the genus classification under different families based on the molecular data (Vellinga 2004; Vellinga et al. 2011; Matheny et al. 2006).

Chlorophyllum Massee

Notes: *Chlorophyllum* belongs to *Agaricaceae* comprising 19 species (Vellinga 2004; He et al. 2019) distributed in both tropical and temperate regions. This genus has six accepted sections namely *Chlorophyllum*, *Ellipsoidospororum*, *Endoptychorum*, *Parvispororum*, *Rhacodium* and *Sphaerospororum* (Ge et al. 2018). *Chlorophyllum molybdites* is the sole species recorded from Laos (Læssøe et al. 2019). In this study, we propose another three species of *Chlorophyllum* first recorded in Laos.

Chlorophyllum demangei (Pat.) Z.W. Ge & Zhu L. Yang, MycoKeys 33: 80 (2018)

Index Fungorum number: IF823863; *Facesoffungi number*: FoF 07067; Figs. 159, 160

Fig. 159 Basidiomata of ***Chlorophyllum demangei*** (HNL502498, **new record**)

Pileus 40–80 mm diam., convex-hemispherical to umbonate, expanding to applanate when fully mature, with straight margin, center glabrous, with brown to brown (5D4, 6D7–8) calotte, with concolourous with tufted patches to suamules around umbo toward margin, on white background and becoming orange white (5A2) when mature, margin sulcate and striate, with exceeding lamellae when mature. *Lamellae* free, ventricose, 4–7 mm wide, white and becoming yellowish white (4A2) with age, crowded, with concolorous eroded lamella-edge. Stipe 80–130 × 6–12 mm, cylindrical to downward base; surface smooth, covered with white fibrils at base zone. *Annulus* superonate, moveable, with brown to brown (5D4, 6D7–8) surface. *Context* in pileus white, in stipe white and hollow, turning orange white (5A2) in both stipe and pileus context. *Taste* peanut-liked. Smell mild. Spore print white. *Basidiospores* [50,2,2] 6–8 × 4–6.5 µm, avl × avw = 7 × 5 µm, Q = 1–1.5, Qav = 1.5, ellipsoid to oblong-amygdaliform in side-viewed, ellipsoid to oblong in frontal view, without germ pore, hyaline, thick-walled, dextrinoid, congophilous. *Basidia* 15–25 × 8–12 µm, clavate, hyaline, thin-walled, 2-spored and 4-spored. *Cheilocystidia* abundant, 20–60 × 5–11 µm, clavate to narrowly clavate, sometimes lageniform, cylindrical with papillate apex, hyaline, thick-walled. Pleurocystidia absent. *Pileus* covering a trichoderm made up of cylindrical to narrowly clavate elements with long stalk, 60–140 × 5–16 µm, hyaline to pale brown parietal pigment, sometimes encrusted. *Stipe* covering a cutis made up of cylindrical hyphae and elements, up to 7–15 µm wide. *Clamp connections* absent.

Material examined: LAOS, Oudomxay Province, Xay, Houay Houm Village, 18 August 2014, P. Sysouphanthong, PS2014-827 (HNL502498); Oudomxay Province, Beng, Na Pa Village, 19 July 2014, P. Sysouphanthong, PS2014-467 (HNL502138, **new record**).

GenBank numbers: ITS = MW193055, MW040572.

Notes: Lao specimens of *Chlorophyllum demangei* are solitary to gregarious. *Chlorophyllum demangei* is saprotrophic, growing on rotten wood and decayed leaves. It is found in various habitats (Figs. 159 and 160). This species was described as *Lepiota demangei* Pat. in sect.

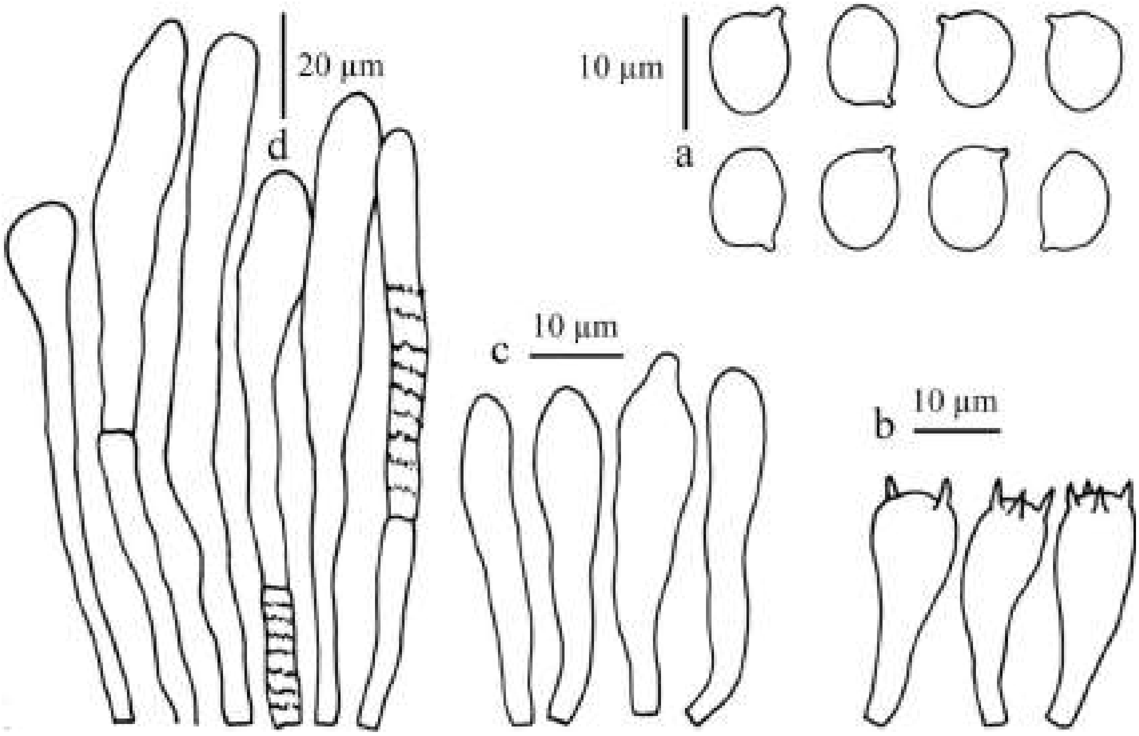


Fig. 160 Microcharacters of ***Chlorophyllum demangei*** (HNL502498). **a** Basidiospores. **b** Basidia. **c** Cheilocystidia. **d** Element cells at pileus covering. Scale bars: **a**–**c** = 10 µm, **d** = 20 µm

Ellipsoidospororum, including other species with white basidiospores (Ge et al. 2018). *Chlorophyllum demangei* can be distinguished from *C. hortense* (Murrill) Vellinga *by having* 4-spored basidia while the latter has 2-spored basidia. Multigene phylogeny showed that they are two different species (Ge et al. 2018). ITS gene tree shows that the two Lao specimens clustered with other *Chlorophyllum demangei* collections in GenBank (Fig. 165). *Chlorophyllum demangei* in this study is a first record for Laos.

Chlorophyllum globosum (Mossebo) Vellinga, Mycotaxon 83: 416 (2002)

Index Fungorum number: IF823863; *Facesoffungi number*: FoF 07069; Figs. 161, 162

Pileus up to 150 mm diam., first subglobose, expanding to convex and plano-concave when mature, with straight margin, when young glabrous, brownish grey to light brown (7D3–8), soon surface broken and leaving concolorous glabrous at center, with concolorous patches spreading towards margin, on white to yellowish-white (4A2) fibrillose background, margin white, sulcate and exceeding lamellae when mature. Lamellae free, white to orange-white (5A2) at first, becoming grayish green (29B4) with age, very crowded, ventricose, 10–16 mm wide, with eroded lamellae-edge. Stipe 140–180 × 10–20 mm, tapering to apex, with wide bulb at base, 25–30 mm wide; smooth and white background, becoming orange grey to greyish orange (6B2-3) with age. *Annulus* cuff-like, moveable, white in upper part, with brownish grey to light brown (7D3–8) squamules at underside. *Context* thick and white in pileus, white in stipe, turning pastel red (9A4) in both pileus and stipe when cut. Smell and oduor not observed. Spore print grayish-green (29D5–6). *Basidiospores* [25,1,1] 8.5–12.5 × 6.5–8.5 µm, avl × avw = 10–11.5 × 7.5–8 µm, Q = 1–1.5, avQ = 1, broadly ellipsoid to ellipsoid-amygdaliform in side-view, broadly ellipsoid or amygdaliform in frontal view, apex truncate and with germ pore, thick-walled, hyaline, dextrinoid, congophilous. *Basidia* 18–350 × 8–16 µm, clavate, hyaline, slightly thick-walled, 4-spored. *Cheilocystidia* abundant, 35–62 × 8–15 µm, clavate to narrowly clavate, slightly thick-walled, hyaline. *Pleurocystidia* absent. *Pileus* covering a hymenoderm made up of several layers of cylindrical hyphae, terminal elements cylindrical to narrowly clavate with rounded or attenuate apex 50–950 × 4–13 µm, slightly thick-walled, hyaline or with pale yellow intracellular pigment. *Clamp connections* absent.

Material examined: LAOS, Vientiane Capital, Xaythany, Houay Yang Preserve Forest, 16 June 2017, P. Sysouphanthong, PS2017-7 (HNL503445, **new record**).

GenBank numbers: ITS = MN317315.

Notes: We observed the specimens of *Chlorophyllum globosum* from young to mature stages. *Chlorophyllum*

Fig. 161 ***Chlorophyllum globosum*** (HNL503445, **new record**). **a**–**c** Basidiomata

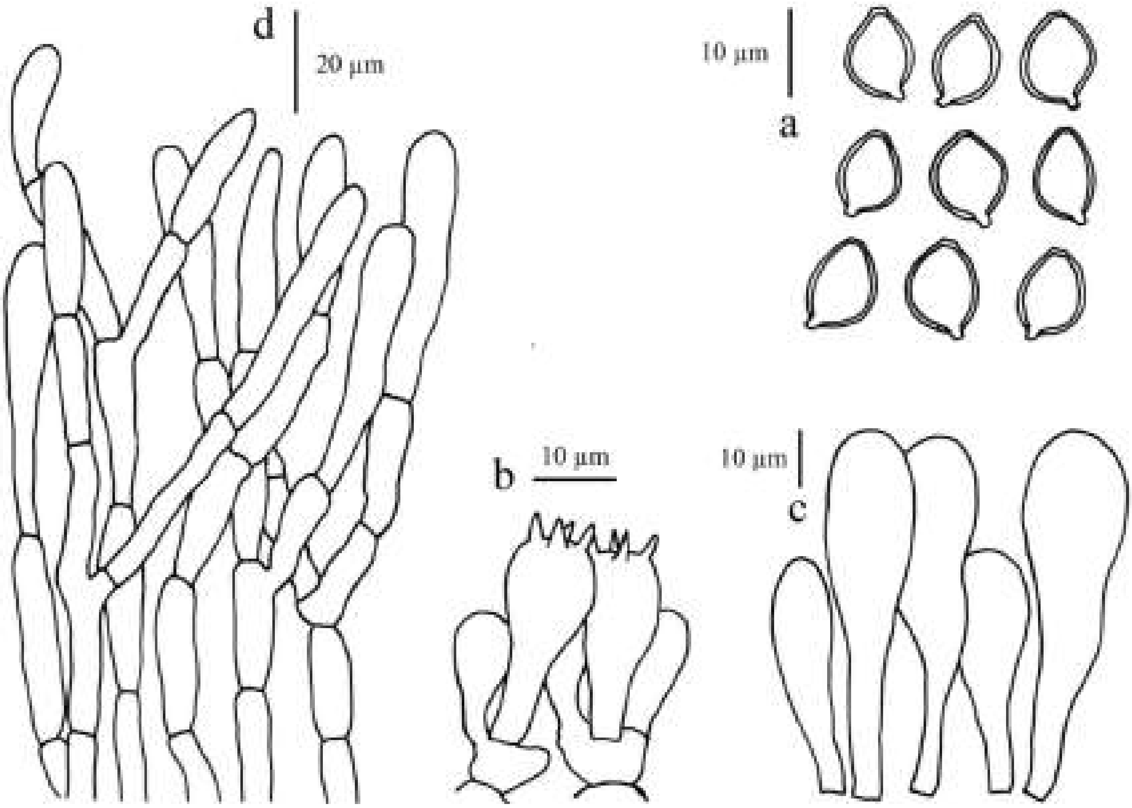


Fig. 162 Microcharacters of ***Chlorophyllum demangei*** (HNL503445). **a** Basidiospores. **b** basidia. **c** Cheilocystidia. **d** Element cells at pileus covering. Scale bars: **a**–**c** = 10 µm, **d** = 20 µm

Fig. 163 ***Chlorophyllum hortense*** (HNL502149, **new record**). **a**, **b** Basidiomata

globosum is a tropical species originally described from Cameroon (Mossebo et al. 2000). It is distributed in other tropical countries such as China, India, South Africa and Thailand (Ge et al. 2018). It closely resembles *C. molybdites* in morphology, but the phylogenetic analysis showed that they are two different species (Vellinga 2003). This study suggests the first record of *Chlorophyllum globosum* for Laos (Figs. 161, 162 and 165).

Chlorophyllum hortense (Murrill) Vellinga, Mycotaxon 83: 416 (2002)

Index Fungorum number: IF374396; *Facesoffungi number*: FoF 03444; Figs. 163, 164

Pileus 72–98 mm, convex, expanding to umbonate with distinctly umbo, with straight margin, surface covered with light brown to yellow brown (5D4–5) glabrous

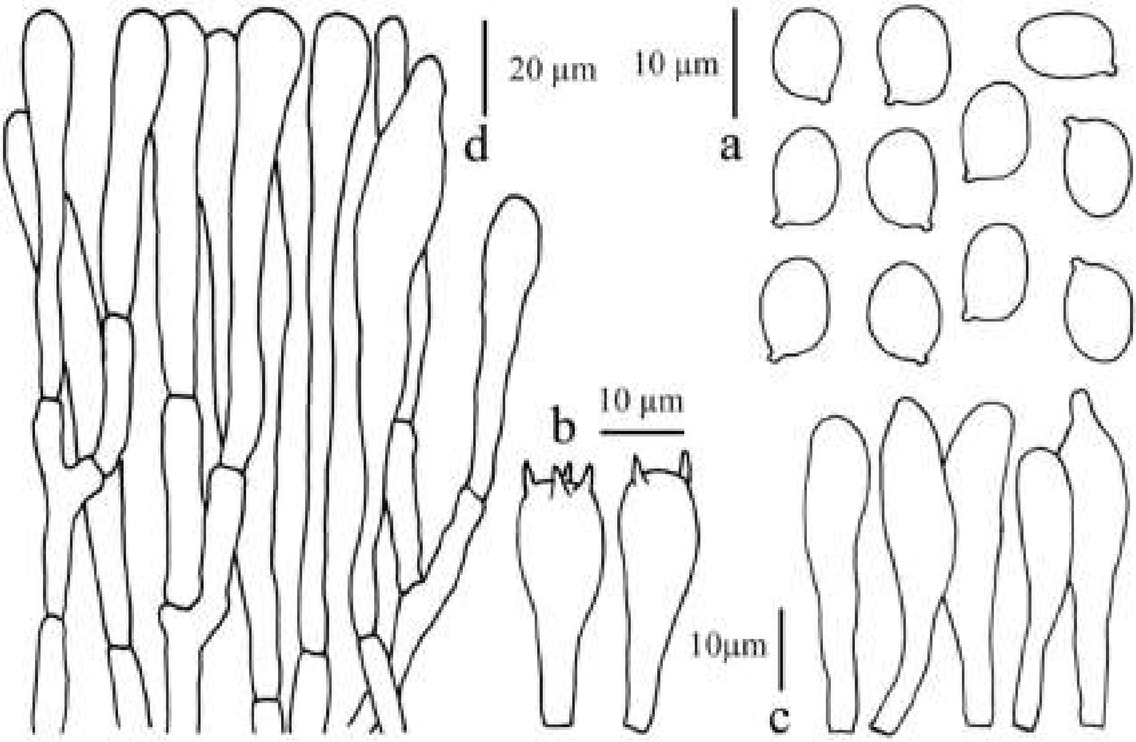


Fig. 164 Microcharacters of ***Chlorophyllum hortense*** (HNL502149). **a** Basidiospores. **b** Basidia. **c** Cheilocystidia. **d** Element cells at pilus covering. Scale bars: **a**–**c** = 10 µm, **d** = 20 µm

calotte at center, with brownish yellow (5C7–8) irregular patches or squamules toward margin, on orang white to light orange (5A2–4) background, margin sulcate or slightly striate, white. *Lamellae* free, narrowly fusiform, up to 7 mm wide, white, crowded, lamella-edge eroded. *Stipe* 60–110 × 6–7 mm, cylindrical, slightly wider to base; surface smooth, white. *Annulus* superonate, moveable, white, with brownish yellow (5C7–8) on upper part. *Context* white in pileus, white in stipe and hollow. All parts of basidiomata turning orange-white (5A2) when touched. *Taste* peanut-like. Smell mild. Spore print white. *Basidiospores* [50,2,1] 6–8.5 × 5–6.5 µm, avl × avw = 7.5 × 6 µm, Q = 1–1.5, Qav = 1, in side-view broadly ellipsoid to ellipsoid amygdaliform, in frontal view ellipsoid, oblong, without germ pore, hyaline, dextrinoid, congophilous, cyanophilous, metachromatic. *Basidia* 25–30 × 8–11.5 µm, clavate, hyaline, 2-spored, occasionally 1-spored. *Lamella* edge sterile, with abundant cheilocystidia. *Cheilocystidia* 35–50 × 7–9 µm, narrowly clavate, cylindrical, sometimes with short apical excrescence or appendage, colorless. *Pleurocystidia* absent. *Pileus* covering of scales a trichoderm made up of cylindrical, narrowly clavate elements with long stalk, 30–155 × 6–16 µm, colorless or with pale brown parietal pigment, with encrusted wall in some elements and lower hyphae. *Stipe* covering a cutis made up of cylindrical hyphae and elements, colorless, 10 µm wide. *Clamp connections* not observed.

Material examined: LAOS, Oudomxay Province, Xay District, Houay Houm Village, 19 July 2014, P. Sysouphanthong, PS2014-478 (HNL502149, **new record**).

GenBank numbers: ITS = MW040573.

Notes: Two basidiomata of *Chlorophyllum hortense* were found in grasslands in Laos. *Chlorophyllum hortense* is characterized by white to yellowish brown pileus, free and white lamellae, and the presence of annulus (Fig. 163). Microcharacters are oblong ovoid and white basidiospores without a germ pore, basically 2-spored basidia, clavate to cylindrical cheilocystidia, trichodermal pileus covering made up of narrowly clavate elements, without clamp-connection in all tissue (Fig. 164). *Chlorophyllum hortense* is distributed amongst tropical countries, mostly found on grassland, dung or compost (Vellinga 2004). This species is similar to *C. demangei* except that the latter has 4-spored basidia. Phylogenetic tree confirmed that they are different species (Fig. 165).

Micropsalliota Höhn.

Notes: *Micropsalliota* is a genus of *Agaricaceae* with 70 species distributed worldwide. This genus is highly diversity in tropical regions (Zhao et al. 2010; He et al. 2019). It is related to *Xanthagaricus* and has a tiny to medium sized, brown basidiospores (Zhao et al. 2010; Vellinga et al. 2011). Twenty-three species have been reported from Thailand, a neighboring country of Laos (Zhao et al. 2010). Based on morphology and molecular-phylogenetic analysis, we report the first records of *M. globocystis* Heinem. and *M. gracilis* Heinem. in Laos.

Micropsalliota globocystis Heinem., Bull. Jard. Bot. natn. Belg. 50(1–2): 57 (1980)

Index Fungorum number: IF113558; *Facesoffungi number*: FoF 09760; Figs. 166, 167

Pileus 30–70 mm diam., when young subglobose to broadly conical, expanding to convex or umbonate, applanate to plano-concave when mature, with straight margin, surface fibrillose to squamules fibrillose, reddish brown (9D4-8), darker at center, on white to pale yellow (5A3) fibrillose background, turning orange white (5A2) when touched, margin with sulcate marginal zone, with exceeding lamellae when mature. *Lamellae* free, ventricose, up to 5 mm wide, white to yellowish white (4A2) at first, becoming orange grey to greyish orange (6B2-3) when mature, crowded, with white eroded lamella-edge. Stipe 50–100 × 5–8 mm, cylindrical, or slightly wider at base; surface covered with white fibrillose, crowded, on white fibrillose background, turning orange-white (5A2) when touched. *Annulus* superior, persistent, white. *Context* in pileus white, in stipe white and hollow, when cut turning orange white (5A2) in both stipe and pileus context. *Taste* and oduor not observed. Spore print orange grey (6B2). *Basidiospores* [50,2,2] 5.5–8.5 × 3–4 µm, avl × avw = 6 × 4 µm, Q = 1–2, Qav = 1.5, ellipsoid in side-view, ellipsoid to oblong in frontal view, without germ pore, slightly thick-walled, hyaline to pale brown. *Basidia* 15–23 × 7–10 µm, clavate, hyaline and slightly thick-walled, 4-spored. *Cheilocystidia* abundant, 28–65 × 7–16 µm, narrowly clavate to broadly clavate, sometimes with median constriction and 1–2-septate, hyaline, thick-walled. *Pleurocystidia* absent. *Pileus* covering a cutis made up of cylindrical elements, 60–110 × 10–23 µm, encrusted, with reddish brown parietal and intracellular pigment, with encrusted hyphae in lower layer, hyaline or with reddish brown parietal and intracellular pigment. *Stipe* covering not observed.

Material examined: LAOS, Xiangkhouang Province, Koun District, Om Village, 27 May 2016, P. Sysouphanthong, PS2016-69 (HNL501440); Oudomxay Province, Beng District, Na Pa Village, 23 June 2014, P. Sysouphanthong, PS2014-106 (HNL501777, **new record**).

GenBank numbers: ITS = MW073388, MW073389.

Notes: *Micropsalliota globocystis* is a saprotrophic species found in the northern part of Laos (Figs. 166 and 167). Zhao et al. (2010) indicated that the species is very common in Thailand. Molecular analysis showed that *M. globocystis* is sister to *M. megarubescens*, but they are quite different in morphology. Another species, *M. pseudoglobocystis* also resembles to *M. globocystis*, but the cheilocystidia vary in shape. Molecular analysis confirmed that they are distinct

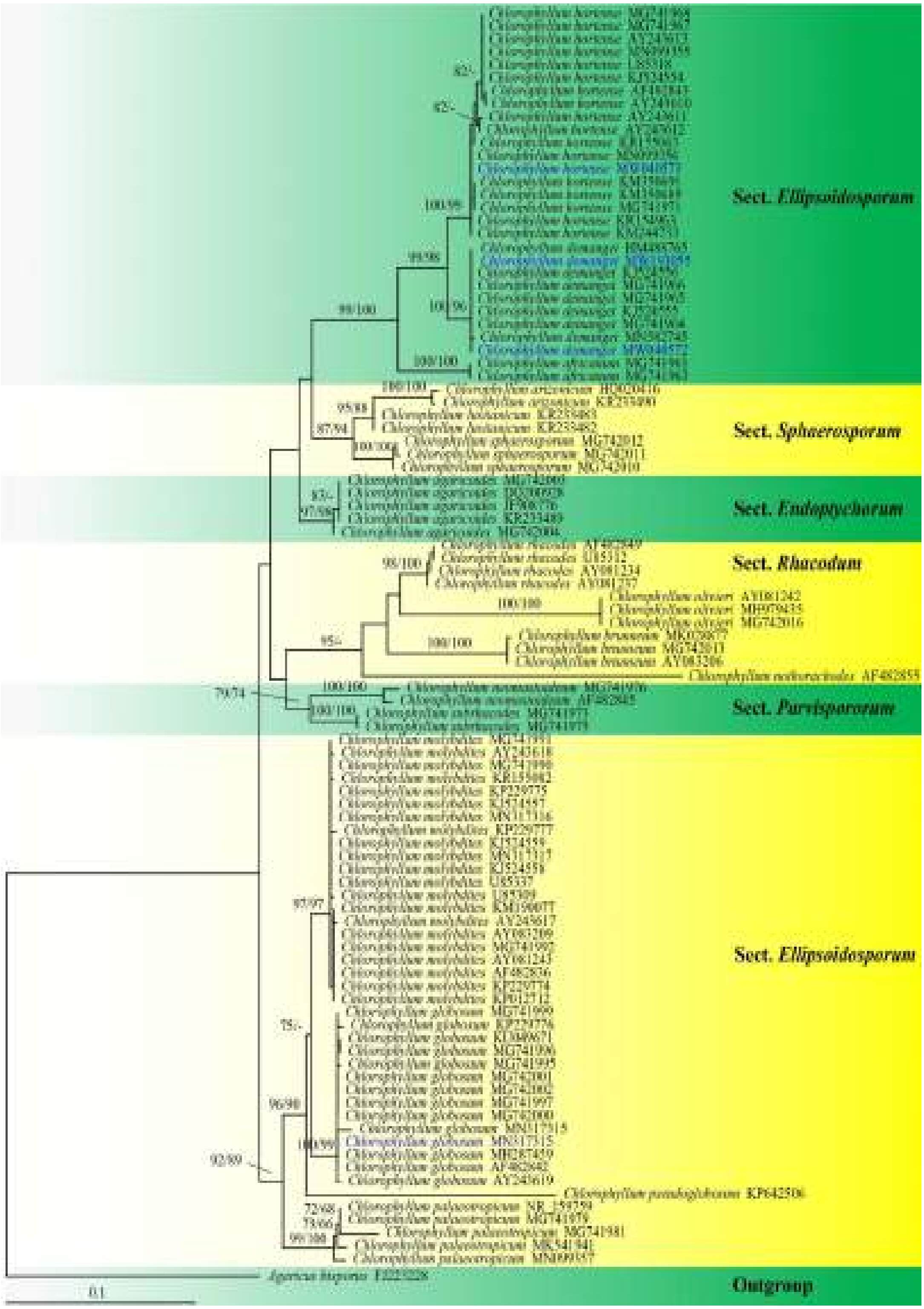


Fig. 165 Maximum likelihood phylogenetic tree of *Chlorophyllum* based on nrITS sequences. The maximum likelihood (ML) analysis was performed in RAxML 7.2.6 (Stamatakis et al. 2008) and maximum parsimony (MP) analysis was performed the program PAUP* 4.0 b10 (Swofford 2004). Bootstrap values of ML/MP equal to or greater than 70% are given above branches. GenBank accession number is indicated after species name. *Agaricus bisporus* (FJ223228) is an outgroup. The three shows six different sections. Newly sequences generated from Laos are in blue

Fig. 166 ***Micropsalliota globocystis*** (HNL501777, **new record**). **a**, **b** Basidiomata

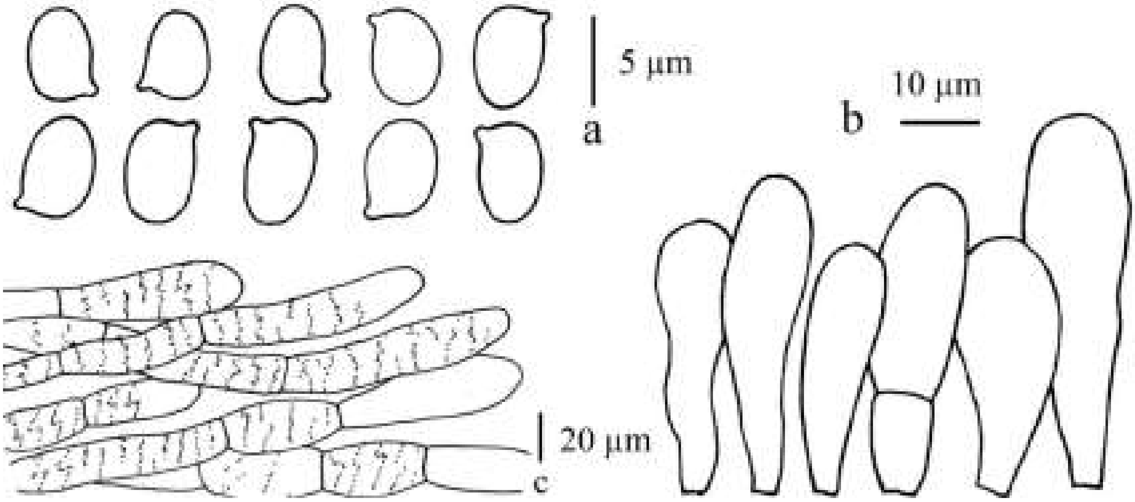


Fig. 167 Microcharacters of ***Micropsalliota globocystis*** (HNL501777). **a** Basidiospores. **b** Cheilocystidia. **c** Element cells at pileus covering. Scale bars: **a** = 5 µm, **b** = 10 µm, **c** = 20 µm

species (Wei et al. 2015). According to the nrITS analysis, the *M. globocystis* complex includes *M. globocystis*, *M. pseudoglobocystis* and *M. pseudoglobocystis*. Lao specimens of *M. globocystis* grouped well with those from Thailand and China (Fig. 170). Both morphology and molecular data derived from Lao and Thai specimens indicate that they are conspecific.

Micropsalliota gracilis Heinem., Bull. Jard. Bot. natn. Belg. 50(1–2): 60 (1980)

Index Fungorum number: IF113559; *Facesoffungi number*: FoF 09761; Figs. 168, 169

Pileus 10–30 mm, first conical, expanding to umbonate, applanate when mature, completely covered with crowded fibrillose when young, brownish red to violet brown (10 D6-8 to (10E6-8), with paler colour when mature, fibrillose, sometimes striate, with white background, margin appendiculate, with white and short velar remnants, fragile when mature. *Lamellae* free, white when young, becoming orange grey to greyish orange (6B2-3) when mature, ventricose 4–6 mm wide, moderately crowded, with eroded lamella-edge. Stipe 25–60 × 2–4 mm, cylindrical, wider at base (5–7 mm wide); surface covered with white fibrillose, on white background, turning orange-white (5A2) when

Fig. 168 ***Micropsalliota gracilis*** (HNL503436, **new record**). **a**–**c** Basidiomata

touched. *Annulus* superior, persistent, white. *Context* in pileus white and thin, in stipe white and hollow, turning orange white (5A2) in both stipe and pileus when touched. Taste and oduor not observed. Spore pint orange grey (6B2). *Basidiospores* 5–6.5 × 3–4.5 µm, avl × avw = 6 × 3.5 µm, Q = 1.5–2, Qav = 1.6, in side-view amygdaliform to ellipsoid, in frontal view ellipsoid to oblong, slightly thick-walled, hyaline to pale brown. *Basidia* 13–17 × 6–8 µm, clavate, hyaline and thin-walled, 4-spored. *Cheilocystidia* 25–50 × 7–12 µm, various in shape, versiform, narrowly utriform, narrowly lageniform, lecythiform, with a long neck and capitulum at apex. *Pleurocystidia* absent. *Pileus* covering a cutis composed of cylindrical to oblong to fusiform elements, up to 25 µm, with brownish red parietal and intracellular pigment. *Clamp connections* absent.

Material examined: LAOS, Vientiane Capital, Xaythany District, Houay Yang Preserve Forest, 17 November 2015, P. Sysouphanthong, PS205 (HNL503432); Chiang Rai Province, Muang District, Campus of Mae Fah Luang University, 08 Jun 2019, P. Sysouphanthong, PS2019-45 (MFLU 19-2358); *ibidem*, 17 November 2015, P. Sysouphanthong, PS209 (HNL503436, **new record**).

GenBank numbers: ITS = MW192914, MW192915.

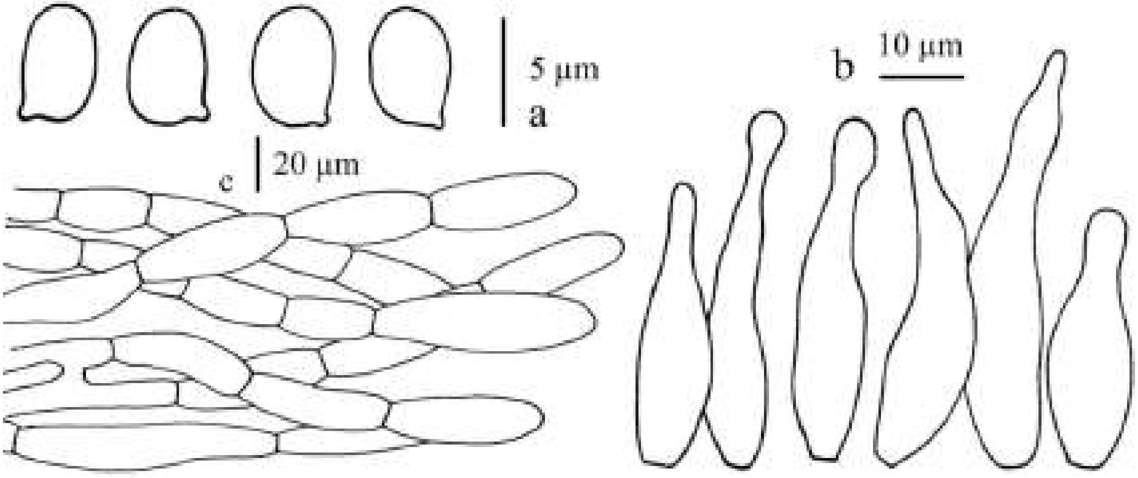


Fig. 169 Microcharacters of ***Micropsalliota grcilis*** (HNL503436). **a** Basidiospores. **b** Cheilocystidia. **c** Element cells at pileus covering. Scale bars: **a** = 5 µm, **b** = 10 µm, **c** = 20 µm

Notes: Two specimens of saprotrophic *Micropsalliota gracilis* were found on rich humus soil of deciduous forest growing in solitary or in large groups from central Laos. This species has tiny basidiomata with brownish red to violet brown fibrillose pileus (Figs. 168 and 169). The taxonomic details have been well discussed by Zhao et al. (2010). Lao specimens are similar to Thai specimens based on morphology and nrITS sequence analysis (Fig. 170) indicating that they are conspecific. This is the first record of *Micropsalliota gracilis* in Laos.

Xanthagaricus (Heinem.) Little Flower, Hosag. & T.K. Abraham

Xanthagaricus, a tropical genus of *Agaricaceae*, consists of 12 species with the type species *X. flavidorufus* (He et al. 2019). Molecular-phylogenetic analysis showed that *Xanthagaricus* is related to *Micropsalliota* (Villinga et al. 2011; Zhao et al. 2010). In this study showed that *X. necopinatus* is a new record from Laos.

Xanthagaricus necopinatus Iqbal Hosen, T.H. Li, & G.M. Gates, MycoKeys 28: 9 (2017)

Index Fungorum number: IF822731; *Facesoffungi number*: FoF 07070; Figs. 171, 172

Pileus 08–18 mm diam., convex to plano-convex, sometimes umbonate, with straight margin; covered with greyish yellow (3B5–6) crowded squamules, with brownish orange to brownish yellow (5C6–8) at center, with yellowish white (3A2) background; margin covered with greyish orange (6B4) appendiculate velar remnants, sometimes absent. *Lamellae* free, 2–3 mm wide, yellowish white to orange white (4A2) at first, greyish orange (5B5) when mature, ventricose to broadly ventricose, with eroded edge. *Stipe* 25–50 × 2–3 mm, cylindrical, with wider at base (4–5 mm wide), covered with greyish yellow (3B5–6) crowded squamules, with orange white (5B2) background, turning greyish red (7B5) when touched. *Annulus* membranous, greyish orange (6B4), fragile or absent with age. *Context* orange white to pale orange (5A2-3) in pileus, thin, up to 2 mm, hollow in stipe, concolorous with surface, turning greyish red (7B5) when cut. Odour and taste not observed. Spore pint orange grey (6B2). *Basidiospores* 4–5.5 × 2.5–3.7 µm, Q = 1.40–1.78, avQ = 1.64, ellipsoid to oblong-ovoid in frontal view, slightly thick-walled, smooth, hyaline to pale brown. *Basidia* 18–22 × 5–10 µm, short clavate to clavate, slightly thick-walled, hyaline, 4-spored, rarely 2-spored. *Pleurocystidia* absent. *Cheilocystidia* 15–23 × 6–12 µm, short clavate to clavate, hyaline, thick-walled. *Pileus* irregular epithelium, element cells oblong to short clavate, 8–23 × 4–17 µm, thick-walled, encrusted, with pale brown to brown parietal and intracellular pigments. *Stipe* covering similar to pileus covering. *Clamp connections* absent.

Material examined: LAOS, Oudomxay Province, Xay District, Houay Houm Village, 16 July 2014, P. Sysouphanthong, PS2014-412 (HNL502083, **new record**); Oudomxay Province, Beng District, Na Pa Village, 19 July 2014, P. Sysouphanthong, PS2014-463 (HNL502134).

GenBank numbers: ITS = MW040548.

Notes: *Xanthagaricus necopinatus* is saprotrophic on humus-rich soil and normally grows in large groups in various forest types. *Xanthagaricus necopinatus* is recognized by small and pale yellow to brownish yellow basidiomata, abundant appendiculate velar remnants at the pileus margin, ellipsoid to oblong-ovoid and hyaline to pale brown basidiospores, clavate cheilocystidia, and irregular epithelium of pileus and stipe covering (Figs. 171 and 172). The species was first described from Bangladesh by Hosen et al. (2017). Lao specimens resembled with the type material in terms of

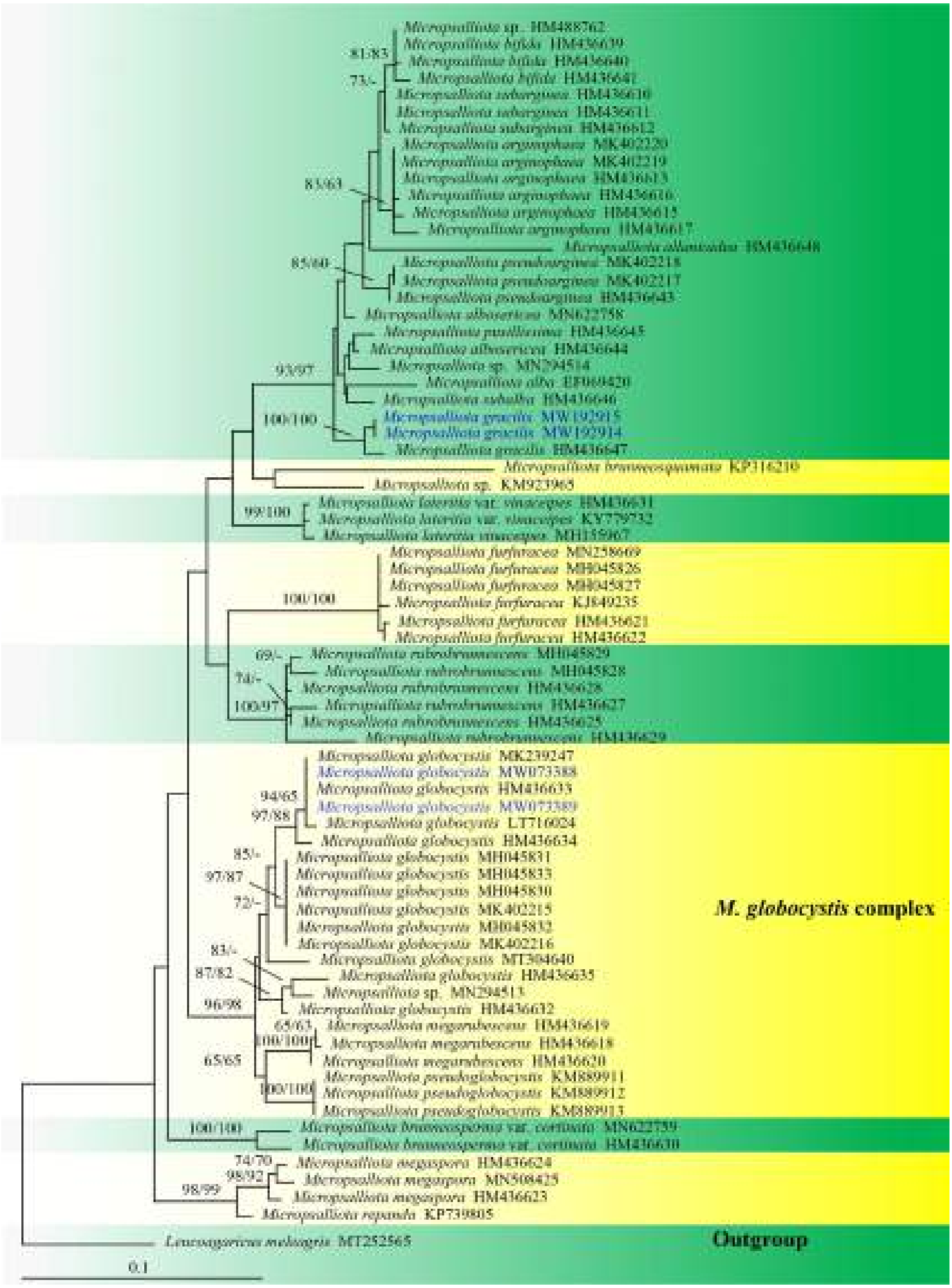


Fig. 170 Maximum likelihood phylogenetic tree of *Micropsalliota* based on nrITS sequences. The maximum likelihood (ML) analysis was performed in RAxML 7.2.6 (Stamatakis et al. 2008) and maximum parsimony (MP) analysis was performed the program PAUP* 4.0 b10 (Swofford 2004). Bootstrap values of ML/MP equal to or greater than 70% are given above branches. GenBank accession number is indicated after species name. *Leucoagaricus meleagris* (MT252565) is an outgroup. Newly sequences generated from Laos are in blue

Fig. 171 ***Xanthagaricus necopinatus*** (HNL502083, **new record**). **a**, **b** Basidiomata

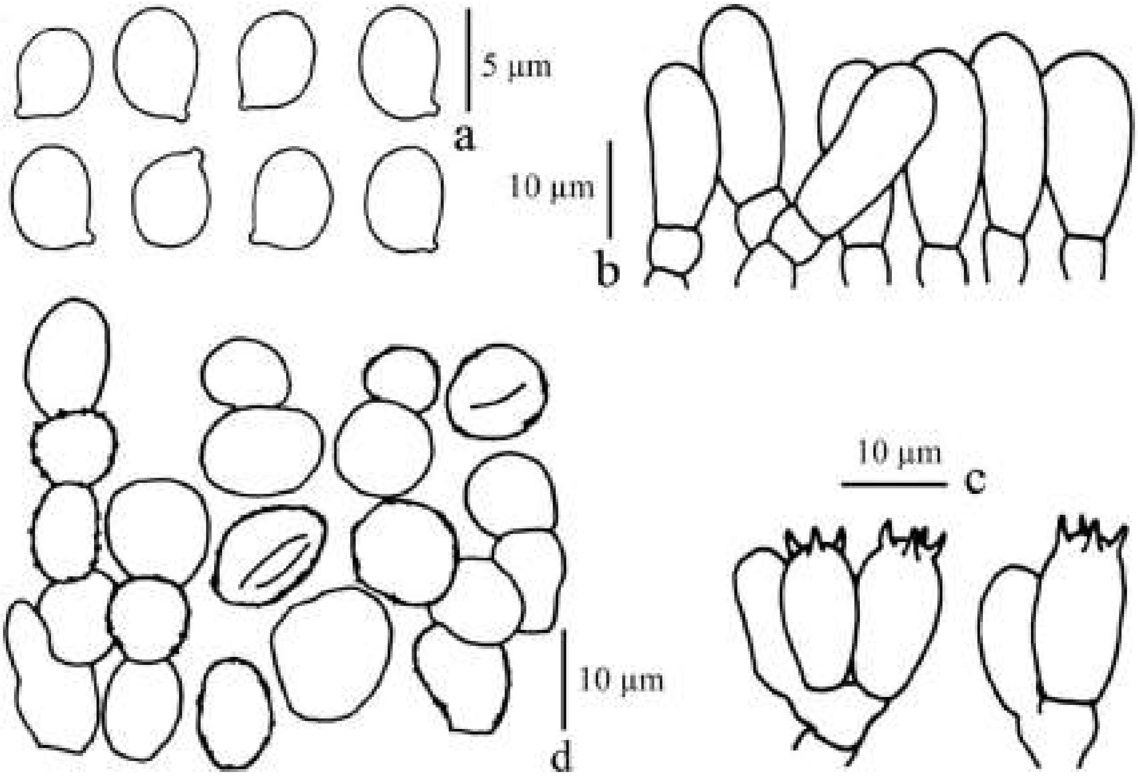


Fig. 172 Microcharacters of ***Xanthagaricus necopinatus*** (HNL502083). **a** Basidiospores. **b** Cheilocystidia. **c** Basidia. **d** Element cells at pileus covering. Scale bars: **a** = 5 µm, **b**–**d** = 10 µm

morphology and nrITS sequences of Lao specimens grouped with the type specimens (Fig. 173), thus confirming they are conspecific. This is the first record of *Xanthagaricus necopinatus* in Laos and outside of Bangladesh.

Amanitaceae E.-J. Gilbert

Notes: Updated accounts are provided in Phookamsak et al. (2019).

Saproamanita Redhead, Vizzini, Drehmel & Contu

Notes: *Amanita* has been divided into two monophyletic units, *Amanita* (ectomycorrhizal) and *Aspidella* (saprotrophic) (Gilbert 1940; Bas 1969; Vizzini et al. 2012; Wolfe

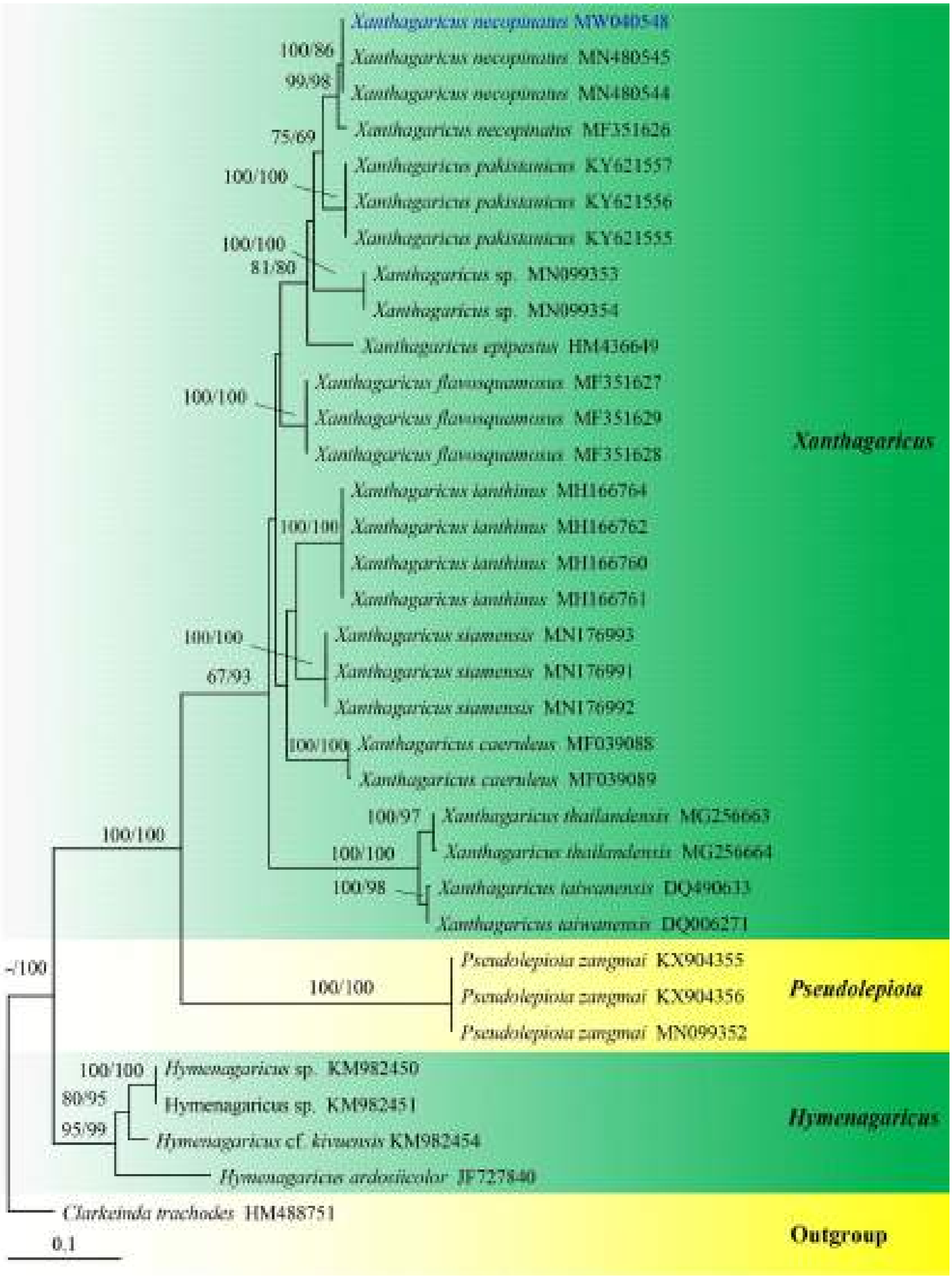


Fig. 173 Maximum likelihood phylogenetic tree of *Xanthagaricus* based on nrITS sequences. The maximum likelihood (ML) analysis was performed in RAxML 7.2.6 (Stamatakis et al. 2008) and maximum parsimony (MP) analysis was performed the program PAUP* 4.0 b10 (Swofford 2004). Bootstrap values of ML/MP equal to or greater than 70% are given above branches. GenBank accession number is indicated after species name. *Clarkeinda trachodes* (HM488751) is an outgroup. Newly sequences generated from Laos is in blue

et al. 2012). *Saproamanita* was introduced by Redhead et al. (2016) to replace *Aspidella* and typified by *S. vittadinii* (syn. *A. vittadinii*). Based on the morphology, *Saproamanita* was placed in *Amanitaceae* (*Agaricales*, Agaricomycetes). *Saproamanita* is most similar to that of the *Amanita* subgenus *Lepidella*, characterized by volval elements dominated by cylindrical to slender clavate inflated cells together with elongated stipes in which these elements are mostly scattered mid-stipe. The species in this genus can grow in open fields and grass land steppes (Beauseigneur 1926; Bas 1969). The multi-locus phylogenetic studies also support the contention that *Saproamanita* should be placed in *Amanita* subgen. *Lepidella* (Davison et al. 2013; Cui et al. 2018; Yang et al. 2018c). Currently, 24 taxa of *Saproamanita* are listed in the species Fungorum (2021). However, only two species, *S. praegraveolens* and *S. thiersii* have been reported in Thailand (Chandrasrikul et al. 2011).

Saproamanita manicata (Berk. & Broome) Redhead, Vizzini, Drehmel & Contu IMA Fungus 7: 123 (2016)

Index Fungorum number: IF816358; *Facesoffungi number*: FoF 09965; Fig. 174

Pileus 5–12 cm wide, at first hemispherical then convex-campanulate; surface pale orange (5A3) to brownish orange (6C7), initially covered by universal veil which disrupts into soft, detessile, floccoso-verucose squamules; margin initially curved, appendiculate with large, vela floccose fragments, not striate, finally revolute. *Lamellae* free, up to 12 mm wide, whitish to pinkish tint, with 2–4 series of lamellulae. *Stipe* 8–15 × 1–2 cm, cylindic, sometimes slightly inflated at the base, solid; surface white (5A1) becoming pale orange (5A3) to brownish orange (6C7), densely floccoso-squamose above, white but bruising ochraceous buff. *Annulus* superior, densely floccoso-squamose. *Volva* reduced to remnants concentrated over the middle of stipe and forming tawny brown squamules, covering the friable annular zone of the partial veil. *Context* up to 10 mm thick, white, soft spongy, consisting of loosely woven, thin-wall hyphae, 5–20 µm in diam. *Odour* strong, sweet, and unpleasant. *Basidiospores* 7–8.5 × 5.5–8 µm, $Q = 1$, $Q_m = 1 \pm 0.5$, subglobose, hyaline, amyloid. *Basidia* 35–50 × 9–13 µm, clavate, bearing four sterigmata. *Lamell-edge* not recovered. *Hymenophoral trama* bilateral, hyaline, with inflated, divergent hyphae 3–6 µm wide. *Subhymenial layer* pseudoparenchymatous. *Pileipellis* composed of radially arranged, filamentous hyphae 4–7 µm wide. *Velar squamules* formed by chains of detersile elements, up to 35 µm in diameter, cylindric to fusoid, hyaline, thin-walled. *Stipe trama* composed of longitudinally arranged, clavate terminal cells, 85–125 × 15–25 µm, filamentous hyphae scattered to abundant, 4–8 µm wide; vascular hyphae scarce. *Clamp connections* absent in all issue types.

Habitat: scattered on the ground in grassland and forest.

Distribution: Known from Dominican Republic, New Zealand Sri Lanka, Thailand, and USA (Hawaiian Islands) (Petch 1910; Pegler 1986; Hemmes and Desjardin 2008; Vizzini et al. 2016).

Material examined: THAILAND, Chiang Mai Province, Muang District, Chiang Mai University, 18°48′9″ N 98°57′5″ E, 339 msl, on the ground in grassland, 4 May 2019, J. Kumla and N. Suwannarach, SDBR-CMU-NK0356, **new record**.

GenBank number: ITS = MW648326, LSU = MW648589, TEF1-α = MW659711.

Notes: The multigene phylogenetic analysis of ITS, LSU and TEF1-α sequence data (Fig. 175) indicate that *S. manicata* was clearly distinguishable from other *Saproamanita* species forming a monophyletic clade with 100% MLBS, 1.00 BYPP support. It formed a sister taxon to *S. flavofloccosa* and *S. foetidissima* with 88% MLBS, 0.98 BYPP support. *Saproamanita flavofloccosa* (Fig. 174) can be distinguished from *S. manicata* by its subglobose to broadly ellipsoid basidiospores (6.5–13 × 5.5–9 µm, $Q_m = 1$) (Purushothama and Natarajan 1987; Senthilarasu 2014). *Saproamanita foetidissima* has broadly ellipsoid to ellipsoid basidiospores (8–11.5 × 7–9 µm, $Q_m = 1$) which is quite different from *S. manicata* (Reid and Eicker 1991).

Cortinariaceae R. Heim ex Pouzar 1983

Notes: The limits of the large, species-rich family *Cortinariaceae* remain unclear. Most species in this family belong to *Cortinarius*. Many genera formerly placed in the *Cortinariaceae*, e.g., *Phaeocollybia*, *Hebeloma* and *Galerina* have been moved to other families in the *Agaricales*. Conversely, the sequestrate genera, *Thaxterogaster*, *Quadrispora*, *Protoglossum* and *Hymenogaster* as well as *Cuphocybe*, *Rapacea* and species of *Rozites*, once thought to belong to the *Cortinariaceae*, are currently included in *Cortinarius* (Peintner et al. 2001, 2002).

Cortinarius (Pers.) Gray

Notes: Cortinarius is the largest genus of *Agaricales*, comprising over 3,000 species worldwide. They are important ectomycorrhizal partners of trees and shrubs from the families *Fagaceae*, *Salicaceae*, *Caesalpiniaceae*, *Cistaceae*, *Dipterocarpaceae*, *Myrtaceae*, *Rhamnaceae*, *Rosaceae* and *Pinaceae*, as well as some herbaceous plants from the *Cyperaceae* and *Polygonaceae* in boreal, temperate and subtropical ecosystems in both the northern and southern hemispheres (Frøslev et al. 2006; Willis 2018). The basidiomata range from agaricoid to sequestrate and usually have poorly to well-developed universal and partial veils. The basidiospore shape vary from subglobose to fusiform, they are weakly to strongly verrucose and rusty brown in deposit. Most of the *Cortinarius* species are difficult to identify based on macro- and micromorphological features and, usually,

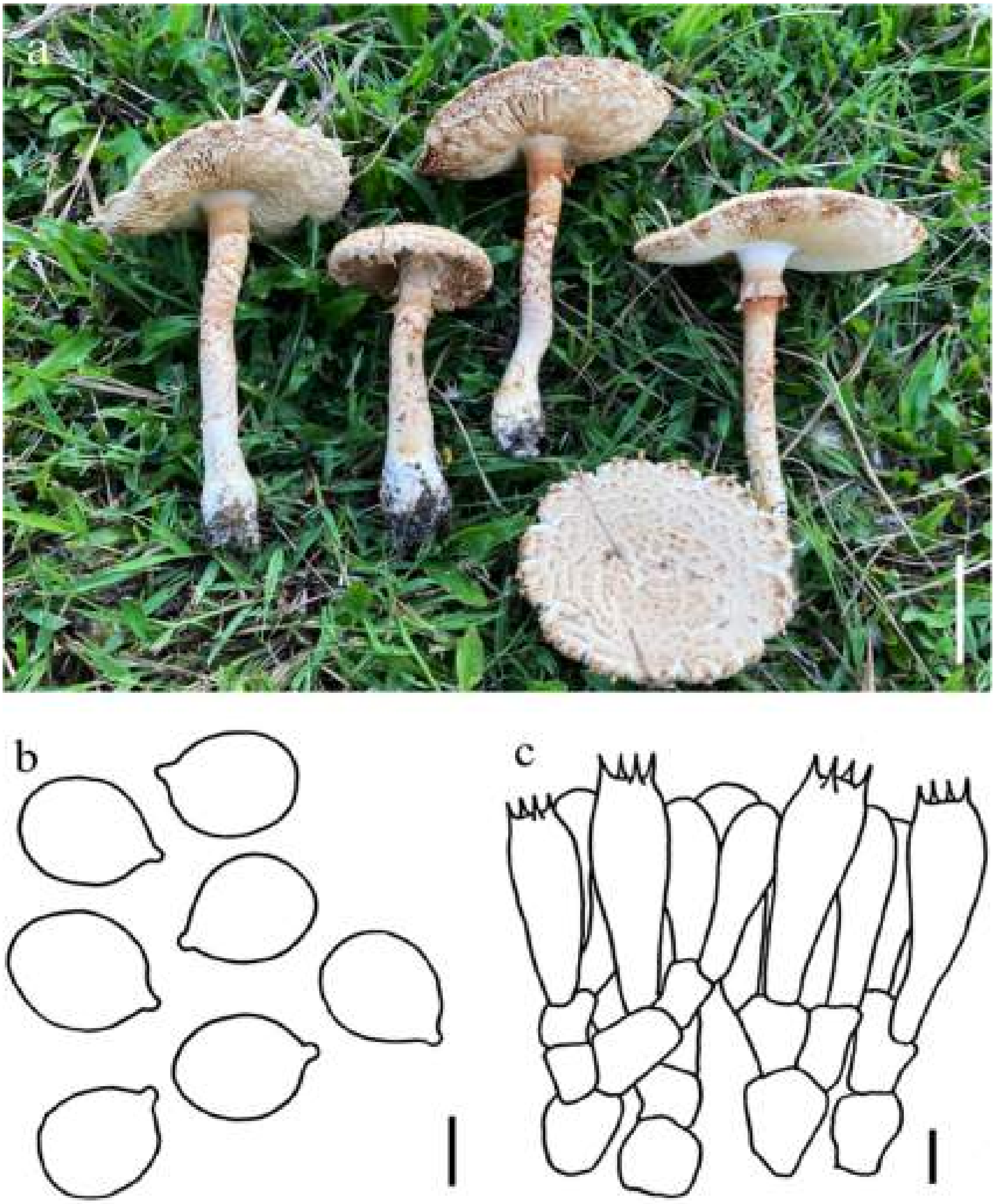


Fig. 174 ***Saproamanita manicata*** (SDBR-CMU-NK0356, **new record**). **a** Basidiomata. **b** Basidiospores. **c** Basidia. Scale bars: **a** = 5 cm, **b** = 5 µm, **c** = 10 µm

molecular analyses are essential for species delimitation. Still, many species of *Cortinarius* remain undescribed. In this study, three new species of this genus are introduced based on evidence of morphology and phylogenetic placement (Figs. 176, 177, 178, 179 and 180); two of them were found in a specific habitat of reclamation forests on lignite mine spoil heaps in Europe, the third one is known to occur in boreal and mountainous coniferous forests of the northern hemisphere.

Cortinarius alutarius Kałucka & Liimat., ***sp. nov.***

Index Fungorum number: IF558552; *Facesoffungi number*: FoF 09966; Fig. 176

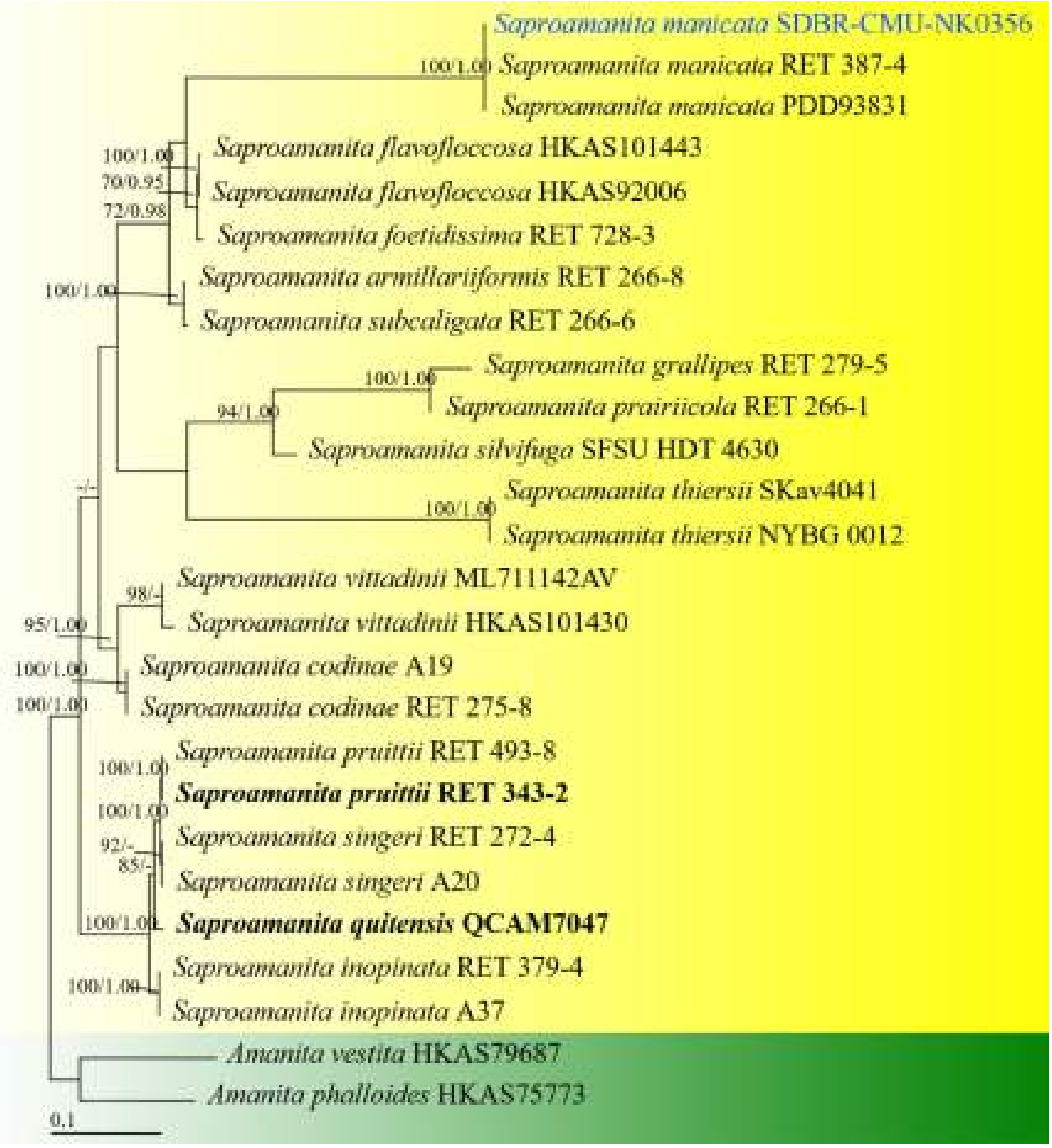


Fig. 175 Phylogenetic tree derived from maximum likelihood analysis of a combined ITS, LSU and TEF1-α genes of 26 sequences and the aligned dataset was comprised of 2352 characters including gaps (ITS: 1–923, LSU: 924–1788 and TEF1-α: 1789–2352). The average standard deviation of the split frequencies of the BI analysis was 0.00535. A best scoring RAxML tree was established with a final ML optimization likelihood value of – 10465.4175. The matrix had 949 distinct alignment patterns with 48.95% undetermined characters or gaps. Estimated base frequencies were found to be: A = 0.2711, C = 0.2011, G = 0.2422, T = 0.2850; substitution rates AC = 1.2478, AG = 2.7197, AT = 1.6015, CG = 0.6534, CT = 3.9595, GT = 1.0000; proportion of invariable sites = 0.0700 and gamma distribution = 1.0010. *Amanita phalloides* HKAS75773 and *Amanita vestita* HKAS75773 were used as outgroup. Numbers above branches are the bootstrap statistics percentages equal to or greater than 70% (MLBS, left) and Bayesian posterior probabilities equal to or greater than 0.95 (BYPP, right). Ex-type strains are in bold and newly generated sequence is in blue

Etymology: The name is based on a Latin adjective *alutarius* (made of soft leather), referring to the suede-like cap surface.

Holotype: LOD(F):47001

Pileus 1.5–2.5 cm in diam., at first conical, later low conical to almost plane, with ± distinct umbo, tomentose, floccose to finely scaly, dark rusty brown, cinnamon brown, usually darker at the centre and paler, ochraceous to buff, towards the margin, light brown or ochraceous when dry; hygrophanous. *Lamellae* fairly distant to medium spaced, adnate to emarginate, medium brown to dark brown, the edge may be paler, at least when young. *Stipe* 3–4 cm

Fig. 176 ***Cortinarius alutarius*** (LOD(F):47001, **holotype**). **a** Basidiomata. **b** Basidiospores. **c** Pileipellis structure. **d**, **e** Ascending elements of pileipellis. Scale bars: **a** = 20 mm, **b** = 10 µm, **c**–**e** = 20 µm

long, 0.2–0.4 cm thick, cylindrical, fibrillose, ochraceous buff-brown, becoming brownish to dark brown from base upwards with age or after handling. *Context* brown, darkening when old or bruised. *Universal veil* white to cream buff, distinct on the cap margin, forming fine stripes and incomplete girdles on the stipe. *Odour* not recorded. *Basidiospores* 6.5–7.5 × 4.5–5 µm, av. = 7 × 5 µm, Q = 1–1.5, Qav. = 1.5, ellipsoid to somewhat obovoid, finely to moderately verrucose, especially at the apex, indextrinoid to weakly dextrinoid (developing dextrinoid reaction very slowly to dextrinoid after a few hours), fulvous brown in 10% KOH, spore deposit rusty brown. *Basidia* 19–25 × 6–9 µm, clavate, with four sterigmata; sterile cells distinct on the gill edge, clavate, apex 5–12 µm wide, av. = 8 µm. *Lamellar trama hyphae* light ochraceous brown, smooth, with parallel streaks of parietal to encrusting dark brown, amber-like pigment, at places with pigment lumps in the corners near septa. *Pileipellis*: Epicutis thin, of hyaline, pale, ± parallel hyphae 4–11 µm, av. = 7 µm, smooth, with yellowish parietal pigment, with frequent ascending bundles consisting of appressed thick-pigmented hyphae or/and thin-walled hyphae slightly constricted at septate, mixed with hypoderm elements, some with end cells swollen, 13–23 µm wide, av. = 16.5 µm (bundles visible as fine flocs under the dissecting microscope). *Hypoderm* consisting of inflated elements 21–52 × 10–21 µm, av. = 31 × 14 µm, smooth, some thin-walled and some with parietal pigment, in deeper parts with fine, spot-like encrustations. *Trama* pale brown, consisting of parallel hyphae 3–7(–8) µm wide, av. = 5 µm, smooth with numerous spots and streaks of parietal to encrusting dark brown, amber-like pigment and lumps of pigment near the septate, in deeper layers of subcellular elements 37–44 × 13.5–23.5 µm, av. = 41 × 18 µm, with much less distinct spot-like encrustations and yellowish pigment. ITS sequence (GenBank MZ648197, holotype) differing from the most similar sequences available with at least 9 substitutions and indels. Distinct from other members of *Cortinarius* sect. *Rubricosi* and deviating from them with at least 17 substitutions and indels.

Ecology and distribution: In temperate (possibly also boreal) pine forests on acid soil, growing in groups of sporocarps; basidiomata found in August. So far known from one locality and one collection only.

Material examined: POLAND, Mt Kamieńsk lignite mine spoil heap near Bełchatów, young *Pinus sylvestris* plantation on strongly to slightly acid loamy sand, 0–0.45% $CaCO_3$, 2 August 2011, *leg*. I.L. Kałucka 00220 (LOD(F):47001, **holotype**), K(M), isotype.

GenBank number: ITS = MZ648197.

Notes: This species is only known from one locality in Poland, on Mt Kamieńsk, the outer spoil heap of the Bełchatów opencast lignite mine, in ca. 20 year old pine plantation (*Pinus sylvestris* L.), on mineral soil among short mosses, lichens and pine needles, on strongly to slightly acid loamy sand, 0–0.45% $CaCO_3$. The presence of *Betula* or *Salix* in the vicinity cannot be excluded. As at the same locality many rare species of northern distribution have been found (Kałucka et al. 2016), we suspect that the species can occur also in Northern Europe. *Cortinarius alutarius* has finely tomentose-floccose dark rusty brown cap drying to light ochraceous brown, ochraceous brown stipe darkening from base upwards and ellipsoid-obovoid moderately verrucose spores (Fig. 176). It is distinct from known closely related species, like *C. subscotoides*, *C. scotoides, C. minusculus, C. rubricosus* and *C. comptulus* and can be relatively easily distinguished based on the combination of the basidiomata habit, spore measurements and habitat type. *Cortinarius alutarius* fits well in the C. sect. *Rubricosi* Bidaud, Moenne-Locc. & Reumaux (Fig. 180). Based on the molecular and morphological data, the species is described here as new.

Cortinarius mammillatus Kałucka, Kytöv., Niskanen & Liimat., ***sp. nov.***

Index Fungorum number: IF558553; *Facesoffungi number*: FoF 09967; Figs. 177, 178

Etymology: The name is based on a Latin adjective *mammillatus* (having the form of a bluntly rounded protuberance) referring to a distinct nipple-like umbo.

Holotype: LOD(F):48001

Pileus 1.5–3 cm in diam., distinctly umbonate, with pronounced, ± acute to bluntly rounded umbo, glabrous, finely tomentose-fibrillose towards the margin, fulvous brown, ochraceous orange brown, drying mat with radial lighter stripes to pale grayish/yellowish/orange ochraceous; hygrophanous, striate. *Lamellae* medium spaced, adnate to emarginate, medium rusty brown, edge concolour or slightly paler, especially near the margin and when young. *Stipe* 5–9(–11) cm long, 0.2–0.5 cm thick at apex, cylindrical, sometimes slightly wider at the base, whitish silky fibrillose to sparsely flocculose on ochraceous to rusty brown background. *Context*: in pileus brown, in stipe paler, ochraceous brown. *Universal veil* white, fibrous to floccose. *Odour* in lamellae of cedar wood, sometimes with raphanoid note; at the base of stem iodoform-like, best observed when slightly dried. *Basidiospores* 7.5–8.5(–9) × 4.5–5.5 µm, av. = 8 × 5 µm, Q = 1–2, Qav. = 1.5, narrowly ellipsoid to ellipsoid to ellipsoid-amygdaloid, finely to moderately evenly verrucose, dextrinoid to distinctly dextrinoid, olive yellowish brown in 10% KOH, spore deposit medium brown. *Basidia* 24–34 × 6–7 µm, narrowly clavate, with four sterigmata. In KOH, many basidia and basidioles yellowish olivaceous or amber brown. *Lamellae edge* mostly fertile, with sterile cells close to the cap margin; sterile cells broadly clavate to balloon-shaped, apex 7–13 µm wide, av. = 10 µm, usually on short basal cells. *Lamellar trama hyphae* pale olive yellowish, yellowish to orange brown in KOH, yellowish to orange yellow parietally encrusted, with streaks and lumps of amber-like pigment, numerous hyphae densely finely scabrous. *Pileipellis*: *Epicutis* of hyaline, pale, parallel hyphae 5–11 µm, av. = 8 µm, smooth, some with yellowish parietal encrustation. *Hypoderm* consisting of inflated subcellular elements and inflated hyphae, (24–)28–58(–80) × 13–25(–26) µm, av. = 41.5 × 18.5 µm, smooth, some yellowish, yellowish ochraceous parietally encrusted, some with fine, spot-like encrustations to scabrous, and some with small lumps of olive ochraceous pigment, especially in deeper parts. *Trama* ochraceous brown, olive brown, consisting of ± parallel hyphae, 6–14 µm wide, av. = 10.2 µm, smooth to finely scabrous, with thin to thick parietal encrustation, some with olive brown to amber brown, spot-like encrustations or lumps of pigment, especially near the septa, in deeper layers of subcellular elements 45–68 × 12–19 µm, av. = 56 × 16 µm with similar pigmentation. ITS sequence (GenBank MZ648201, holotype) differs from other sequences of C. sect. *Obtusi* known to occur in the Northern hemisphere with more than 20 substitutions and indels.

Ecology and distribution: In boreal and mountainous coniferous forests of the northern hemisphere, growing in groups of sporocarps; basidiomata found in September and October.

Fig. 177 ***Cortinarius mammillatus*** (LOD(F):48001, **holotype**). **a** Basidiomata. **b** Basidiospores. **c** Pileipellis structure. Scale bars: **a** = 20 mm, **b** = 10 µm, **c** = 20 µm

Material examined: POLAND, Sudetes, Stołowe Mountains National Park, Czerwona Woda River valley, *Picea abies* old-growth forest, among *Polytrichum* moss, 15 September 2017, *leg*. I.L. Kałucka 17–140, (LOD(F):48001, **holotype**; K(M), isotype); loc. cit., among *Sphagnum* and *Polytrichum* mosses, 19 October 2017, *leg*. I.L. Kałucka 17–153 (LOD(F):48002); loc. cit., among *Sphagnum* and *Polytrichum* mosses, 18 September 2017, *leg*. I.L. Kałucka 17–159 (LOD(F):48003); loc. cit., among litter, grass and mosses, 7 September 2017, *leg*. I.L. Kałucka 17–160 (LOD(F):48004). FINLAND, Uusimaa, Sipoo, Paippinen, 14 Sep 2004, *leg*. K. Liimatainen and T. Niskanen 04–814 (H:6030110); Satakunta, Säkylä, Virttaankangas, Porsaanharju, pine (*Pinus sylvestris*) heath forest on sandy soil, 19 October 2006, *leg*. K. Liimatainen and T. Niskanen 06–249 (H:6029329). UK, Scotland, Woodcock Hill Plantation, in conifer plantation, under *Picea*, 21 October 2018, *leg*. D.J. Savage 488/18 (K(M):262938). CANADA, Ontario, Nipissing, Algonquin Provincial Park, Wildlife research station, chit lake trail, mixed forest of deciduous (e.g. *Betula*) and

Fig. 178 ***Cortinarius mammillatus***—additional collections (basidiomata). **a** H:7000935. **b** H:7000963. **c** LOD(F):48003. **d** LOD(F):48004. **e** LOD(F):48002. **f** LOD(F):48002a. Notes: Photographs: **a**, **b** K. Liimatainen, **c**–**f** I.L. Kałucka

coniferous trees (e.g. *Abies balsamea*), 13 September 2007, *leg*. K. Liimatainen and T. Niskanen 07–172 (H:7000834); Newfoundland, west coast Gros Morne National Park, N end of the Bonne Bay's Eastern Arm, James Callaghan hiking trail to Gros Morne Mountain, mesic to moist *Abies balsamea* dominated forest with some *Picea, Alnus*, and *Betula*, collected under *Alnus*, 21 September 2007, *leg*. K. Liimatainen and T. Niskanen 07–272 (H:7000935); Newfoundland, Avalon Peninsula, Salmonier Nature Park, mesic to moist *Picea* dominated forest with some *Abies, Betula* and *Larix*, 26 September 2007, *leg*. K. Liimatainen and T. Niskanen 07–299 (H:7000963); Newfoundland, 26 September 2007, *leg*. A. Voitk 2–101 (K(M)); Newfoundland, west coast Gros Morne National Park, N end of the Bonne Bay's Eastern Arm, James Callaghan hiking trail to Stuckless Pond, mesic to moist *Abies balsamea* dominated forest with some *Picea, Alnus*, and *Betula*, 19 September 2010, *leg*. K. Liimatainen and T. Niskanen 10–106 (H). USA. Washington, Snohomish county, Barlow past, Mt. Baker Snoqualmie National Forest, mixed coniferous forest, mainly *Tsuga heterophylla* with some *Pseudotsuga menziesii* and *Abies amabilis*, 10 October 2009, *leg*. K. Liimatainen and T. Niskanen 09–077 (H).

GenBank number: LOD(F):48001: ITS = MZ648201; LOD(F):48002: ITS = MZ648202; (LOD(F):48003): ITS = MZ648203; LOD(F):48004: ITS = MZ648204;

H:6030110: ITS = MZ648205; H:6029329: ITS = MZ648206; H:7000834: ITS = MZ648208; H:7000935: ITS = MZ648209; H:7000963: ITS = MZ648210; K(M): A. Voitk 2–101: MZ648211; H: K. Liimatainen and T. Niskanen 10–106: MZ648212; H: K. Liimatainen and T. Niskanen 09–077: MZ648213; K(M):262938: ITS = MZ648207.

Notes: The type collection and other three collections from Poland come from the mossy old-growth spruce (*Picea abies*) forest growing along the mountain stream (Pielech et al. 2018). In Finland, the species was found in pine (*Pinus sylvestris*) heath forest on sandy soil. All the North American collections are from mixed coniferous forests, with *Abies*, *Picea* and *Betula* on the east coast and *Tsuga*, *Pseudotsuga* and *Abies* on the west coast. A number of sequences available in GenBank and UNITE repositories, which do not differ from the type sequence by more than 3 substitutions and indels, come from the ECM roots of *Pinus sylvestris* (AY641464, Scotland) and *Picea rubens* (MK131478, MK131479, Canada), soil DNA from Cedar-Hemlock and Hemlock-Amabilis Fir Forests (KP889457, Canada) as well as sporocarps identified as *C. obtusus* from *Picea abies* forests (KY287715, KY287718, KY287698, Tatra Mts, Slovakia; AJ238035 = UDB000127, Norway). *Cortinarius mammillatus* has distinctly umbonate, fulvous brown, striate hygrophanous cap, glabrous with tomentose margin, slender, whitish silky fibrillose stipe and narrowly ellipsoid to ellipsoid-amygdaloid, verrucose spores (Figs. 177 and 178). It most resembles *C. obtusus* and *C. acutus*. The former is somewhat fleshier and has more slender spores with coarser ornamentation; the latter has a usually more conical cap with pointed umbo, lighter gills and thinner, more brittle stipe; both species have a greater proportion of gill edge whitish fimbriate. *C. fulvescens* has darker cap centre, pale pink universal veil and slightly longer spores. *Cortinarius mammillatus* formed a well-supported clade (100% MLBS; Fig. 180) and based on the molecular and morphological data is described here as new.

Cortinarius quercoflocculosus Kałucka & Liimat., ***sp. nov.***

Index Fungorum number: IF558554; *Facesoffungi number*: FoF 09968; Fig. 179

Etymology: The name refers to the association of the species with oak (*Quercus*) as well as flocculose cap and stipe.

Holotype: LOD(F):47002

Pileus 2–4 cm in diam., convex, not umbonate or with obtuse umbo, later broadly truncate or even with a shallow depression in the centre, with margin incurved downwards, finely fibrillose to sparsely flocculose, especially towards the margin, rusty medium brown, cinnamon brown, honey brown, beige brownish, ochraceous, frequently with darker centre; hygrophanous, margin striate, paler. *Lamellae* distant, adnate, rusty brown, bluish brown when young, with paler edge. *Stipe* 3.5–7 cm long, 0.4–0.8 cm thick at apex, 0.5–1 cm thick at the base, cylindric or frequently slightly wider at the base, solitary or cespitose, whitish silky fibrillose to sparsely flocculose, greyish white, light brownish, with bluish/lilac or rosy tinge (usually present more at the apex, but sometimes visible only at the base). *Context*: not checked. *Universal veil* white, fibrous to floccose, abundant. *Odour* in lamellae indistinct or of cedar wood. *Basidiospores* (8–)8.5–9.5(–10) × 5–6 µm, av. = 9 × 5.5 µm, Q = 1.5–2, Qav. = 1.5, ellipsoid to somewhat amygdaloid, moderately verrucose, moderately to fairly strongly dextrinoid, ochre brown in 10% KOH, spore deposit relatively bright, light rusty brown. *Basidia* 26–32 × 8–9 µm, narrowly clavate, with four sterigmata. In KOH, some basidia with dark brown amorphous pigment. *Lamellar trama hyphae* weakly pigmented, light yellowish ochre, smooth, with infrequent fine granular or spot-like encrustations. *Pileipellis*: Epicutis very thin, of 2–3 layers of parallel hyphae 4–10 µm, av. = 6.5 µm, smooth, with cementing yellow parietal pigment, with a few ascending, slightly inflated hyphae with ends 8–17 µm, av. = 12.7 µm. *Hypoderm elements* pale, consisting of 5–6 rows of ± parallel subcellular elements, 28–57(78) × 14–25 µm, av. = 41.5 × 19 µm, hyaline with yellowish cementing parietal pigment. *Trama* yellowish, consisting of parallel hyphae, 7–15(19) µm wide, av. = 11 µm, in the upper part tightly cemented with yellowish parietal pigment, with infrequent, scattered spot-like encrustations, parietal streaks and lumps of amber-like pigment, gradually transitioning to the more loose layer of subcellular elements, 42–74 × 16–24 µm, av. = 20 × 57 µm, with very few fine spot-like encrustations. *Oleiferous* hyphae present. ITS sequence (GenBank MZ648198, holotype) different from the most similar sequence available in GenBank (FJ946918; Spain, *Quercus* ectomycorrhizal root) with only 1 substitution so probably represents the same species. *C. quercoflocculosus* is distinct from the closest known species, *C. fulvopaludosus*, and deviating with 12–14 substitutions and indels.

Ecology and distribution: In European oak forests, growing in groups of sporocarps and frequently cespitose; basidiomata found in October and November.

Material examined: POLAND, Mt Kamieńsk lignite mine spoil heap near Bełchatów, young *Quercus robur* plantation with some solitary *Betula pendula* and *Pinus sylvestris*, on slightly acid to slightly alkaline clay, 1.17–5.96% $CaCO_3$, 12 November 2011, *leg*. I.L. Kałucka 00260 (LOD(F):47002, **holotype**; K, isotype); loc. cit., 2 October 2013, *leg*. I.L. Kałucka 00270 (LOD(F):47003); Adamów lignite mine spoil heap near Turek, in *Q. robur* stand, 10 October 2012, *leg*. I.L. Kałucka 00523 (LOD(F):47004).

GenBank number: LOD(F):47002: ITS = MZ648198; LOD(F):47003: ITS = MZ648199; LOD(F):47004: ITS = MZ648200.

Notes: The two collections from Mt Kamieńsk, which is the outer spoil heap of the Bełchatów opencast lignite mine, including the holotype, come from the same young oak stand; the third Polish collection was found in oak

Fig. 179 ***Cortinarius quercoflocculosus*** (LOD(F):47002, **holotype**). **a** Basidiomata. **b** Basidiospores. **c** Oleiferous hypha in trama. **d** Pileipellis structure. Scale bars: **a** = 20 mm, **b** = 10 µm, **c, d** = 20 µm

stand on a lignite mine spoil heap Adamów, 110 km apart (Kałucka et al. 2016). The ITS region of this species seems to match a single sequence known from a *Quercus* ectomycorrhizal root from Spain. Thus, the species is expected to occur at least throughout the oak forests of Europe. The closest known species, *Cortinarius fulvopaludosus*, differs in having acute umbo, slenderer stipe with very sparse veil fibrils, with a lack of blueish tinge in lamellae and stipe and narrower spores (Fig. 179). In our phylogenetic analysis, *Cortinarius quercoflocculosus* formed a well-supported clade (100% MLBS; Fig. 180) within other telamonioid ITS sequences and based on the molecular and morphological data, the taxon is described here as new.

Hydnangiaceae Gäum. & C.W. Dodge

Notes: *Hydnangiaceae* (Gäumann and Dodge 1928) is a family of *Agaricales* and currently comprises two genera, *Hydnangium* and *Laccaria* (Kirk et al. 2008). The family is characterized by basidiomata stipitate and pileate or gasteroid, epigeous or hypogeous basidiomata. When pileate, the fruitbodies are generally orange-brown or violet in coloration, lamellae thick and waxy; in gasteroid forms, fruit body shape is irregular, with or without columella, the peridium is sometimes evanescent and the hymenium is not gelatinized, and formed in locules. Hyphal system monomitic; hyphae with clamp-connections; pleurocystidia generally absent; basidia 4- or 2-spored; cheilocystidia sometimes present; basidiospores globose to cylindrical, rarely elongate with spines or slightly roughened. The spines are composed of

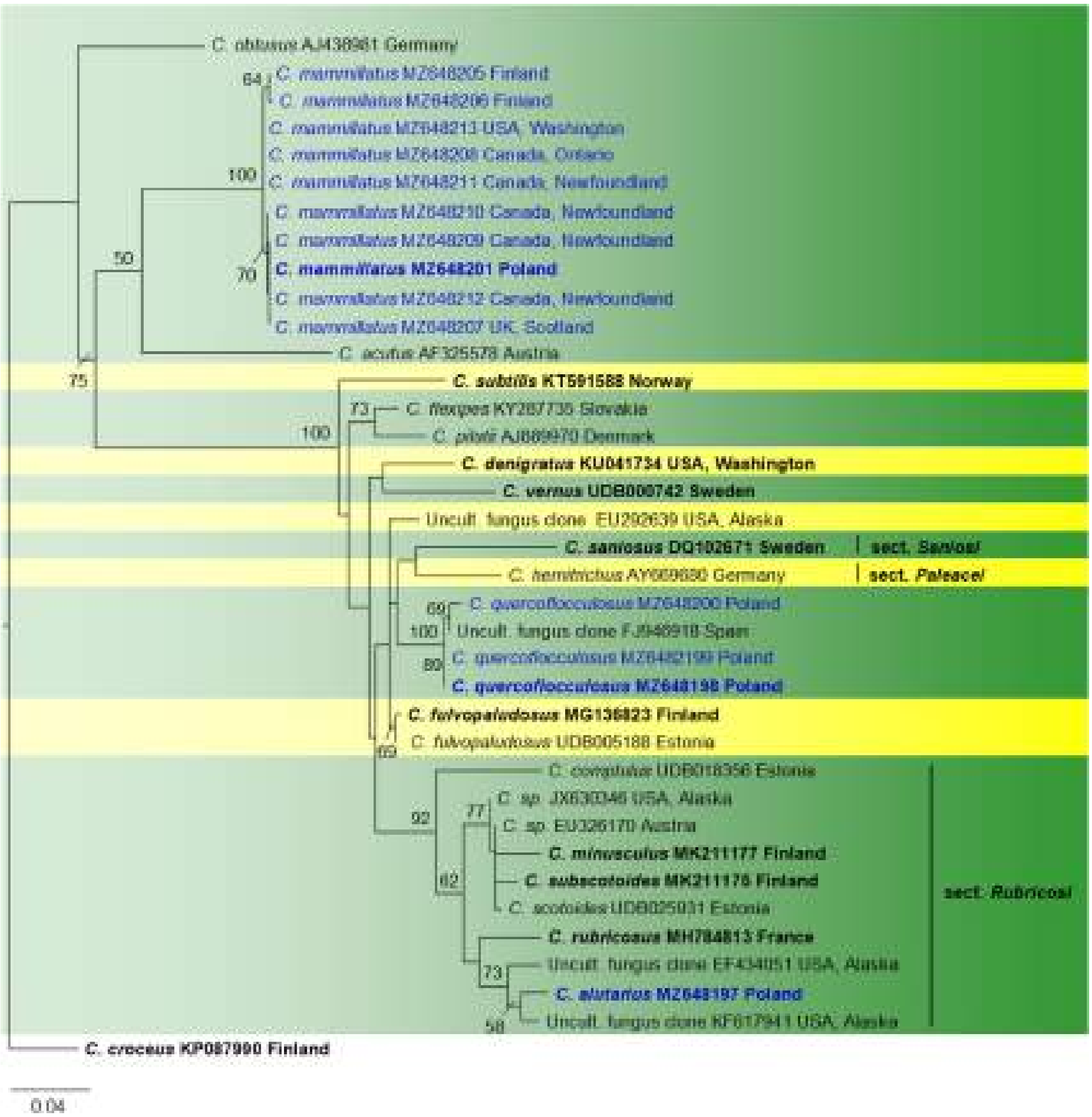


Fig. 180 Phylogram resulting from the RAxML (Stamatakis 2014) analysis of ITS region. Bootstrap values equal to or greater than 50% are indicated above the nodes. The specimens in boldface represent the type specimens of the species. The newly generated sequences are in blue

parallel microtubules converging at the tip of the cones (Cannon and Kirk 2007).

Laccaria Berk. & Broome

Notes: *Laccaria* currently comprises about 85 species (He et al. 2019), but numerous new species have been described in recent years (Wilson et al. 2013, 2016; Popa et al. 2014; Luo et al. 2016; Ramos et al. 2017; Vincenot et al. 2017; Cho et al. 2018; Wang et al. 2019b), a clear indication that the exact number of species in this genus is still undetermined. *Laccaria* species form mutualistic symbioses with many shrubs and forest tree species and are widely distributed over geographical areas from the tropics to the boreal regions (Gardes et al. 1990; Mueller 1992; Vincenot et al. 2011; Popa et al. 2014). *Laccaria* is easily recognized by having distinctive characters: basidiocarps are orange, purple, brown or flesh-coloured; pileus dry to subhygrophanous, lamellae rather thick and rather distant, from adnate to slightly decurrent; generally, with echinulate basidiospores; spore print white or pale violet (Singer 1986; Mueller 1992; Osmundson et al. 2005). In this study, a new species *Laccaria populina* is introduced based on morphological evidence and phylogenetic placement (Figs. 181 and 182).

Laccaria populina Dovana, ***sp. nov.***

Fig. 181 ***Laccaria populina*** (GDOR 411, **holotype**). **a** Basidiomata in the field. **b** Section of stem. **c** Stipitipellis in KOH 3%. **d** Section of gills in Phloxin B. **e** Pileipellis in Phloxin B. **f** Basidiospore in KOH 3%. **g** Basidia in Phloxin B. **h** terminal elements of pileipellis in KOH 3%. Scale bars: **c**, **e**, **g**, **h** = 50 µm, **d** = 100 µm, **f** = 10 µm

Index Fungorum number: IF557832; *Facesoffungi number*: FoF 09202; Fig. 181

Etymology: The specific epithet *populina* is in reference to the genus *Populus*, because it was collected under poplar trees.

Holotype: GDOR411

Pileus 15–35 mm diam., convex to plane-convex centrally depressed to subumbilicate; surface glabrous when moist, on drying slightly squamulose at center, slightly translucent-striate, hygrophan, orange, brown–red at disk transitioning to pale orange toward margin, often with wine red areas; paler with age; margin striate and crenate. *Lamellae* up to 5 mm broad, moderately distant, emarginate, sinuate to adnate with

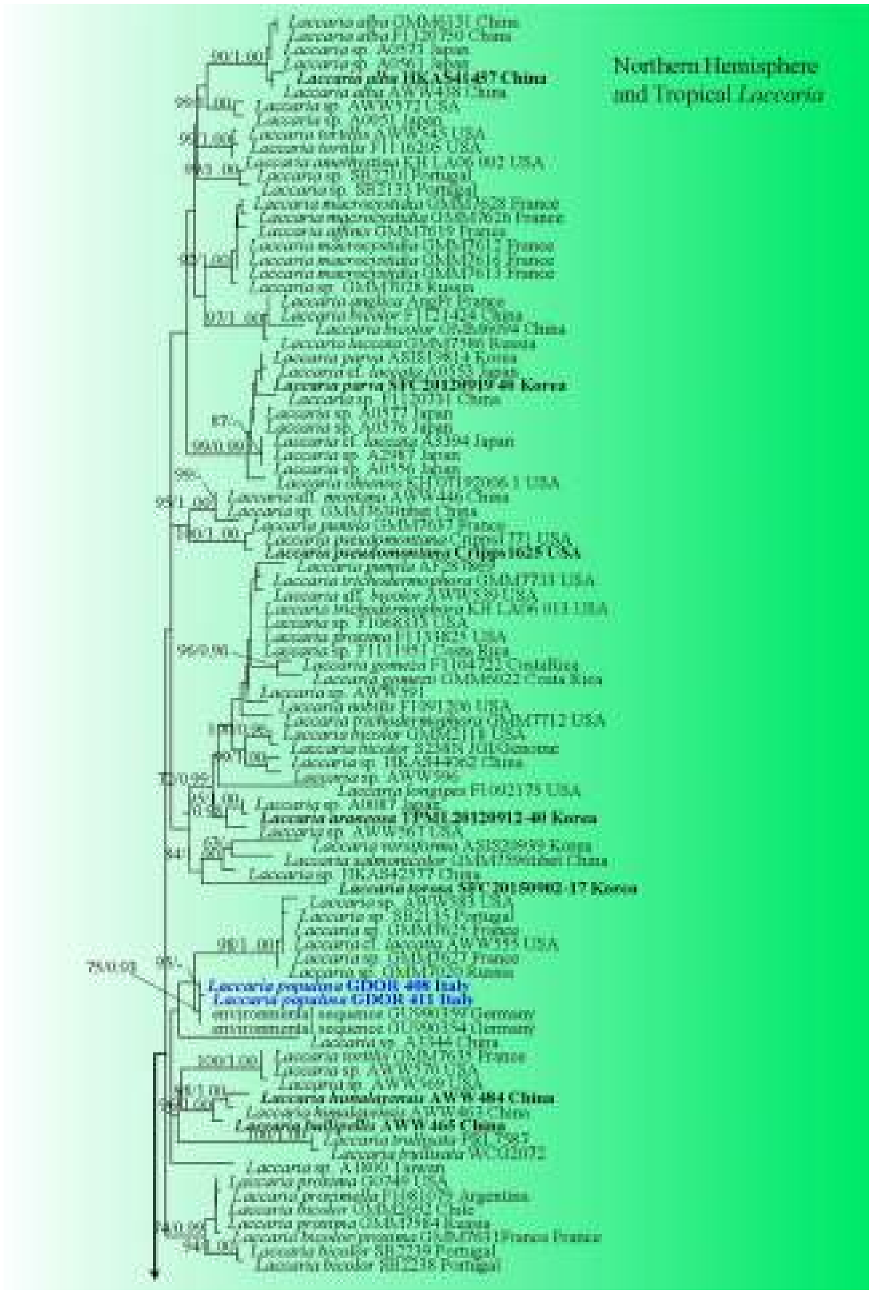


Fig. 182 Phylogram generated from maximum likelihood analysis based on LSU and ITS sequence data representing *Laccaria* of northern hemisphere and tropical areas. Related sequences aretaken from previous studies (Wilson et al. 2013; Popa et al. 2014; Luo et al. 2016; Ramos et al. 2017; Vincenot et al. 2017; Cho et al. 2018; Wang et al. 2019b). One hundred fifty-six strains are included in the combined analyses which comprise 1624 characters. *Mythicomyces corneipes* (AFTOL ID972) is used as the outgroup taxa. Single gene analyses were also performed to compare the topology and clade stability with combined gene analyses. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RaxML tree with a final likelihood values of − 9283.670199 is presented. Estimated base frequencies for the two partitions were as follows: the ITS partition A = 0.248432, C = 0.203290, G = 0.210151, T = 0.338126; substitution rates AC = 1.729861, AG = 6.506286, AT = 2.326472, CG = 0.685905, CT = 5.294619, GT = 1.000000, gamma distribution shape parameter α = 0.357610; the LSU partition A = 0.269370, C = 0.185989, G = 0.290996, T = 0.253645; substitution rates AC = 1.151721, AG = 25.007835, AT = 2.282933, CG = 0.751032, CT = 11.631350, GT = 1.000000, gamma distribution shape parameter α = 0.144016. Bootstrap values for maximum likelihood (MLBS) equal to or greater than 70% and clade credibility values greater than 0.95 (the rounding of values to 2 decimal proportions) from Bayesian-inference analysis labeled on the nodes. Ex-type strains are in bold and newly generated sequences are in blue

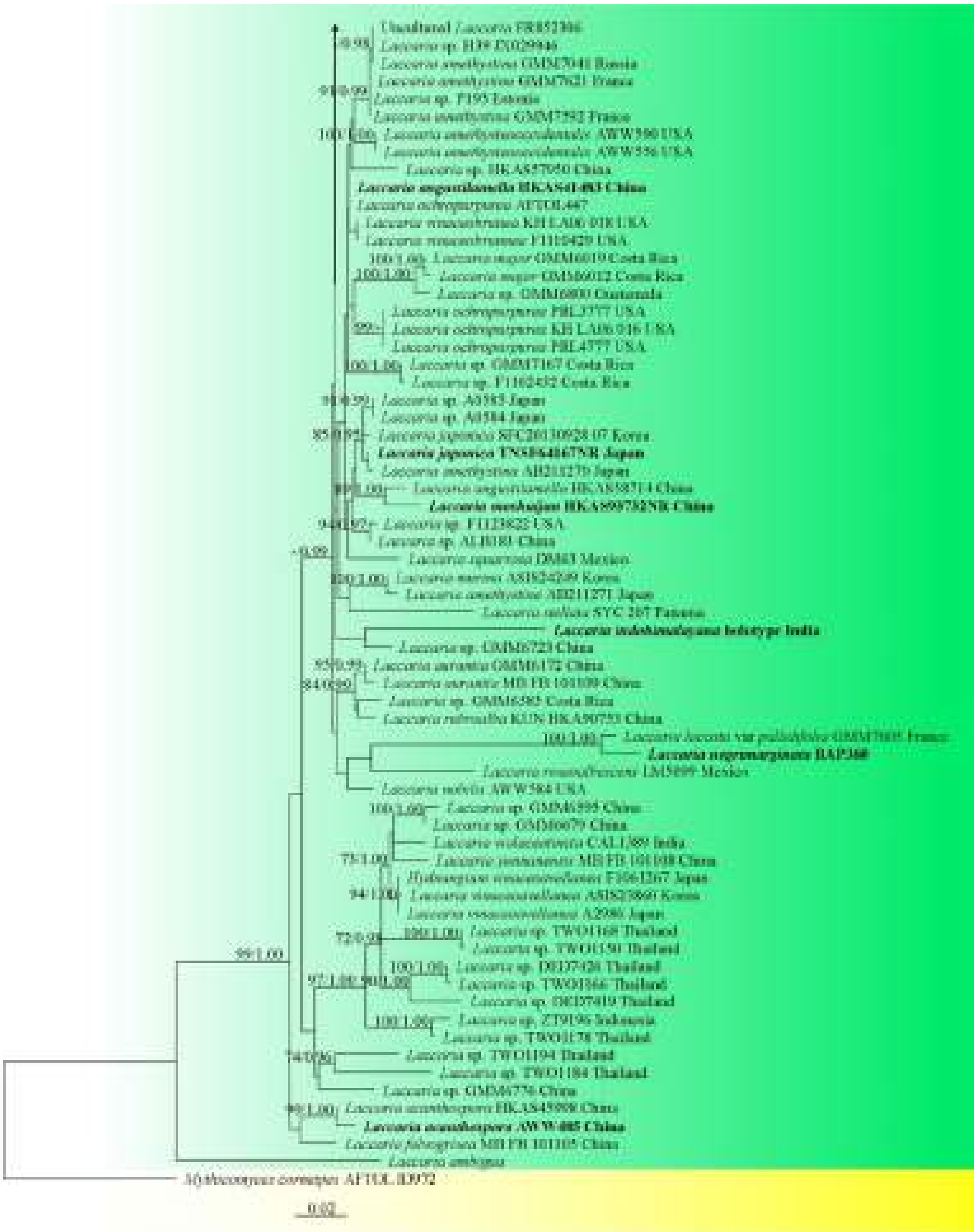


Fig. 182 (continued)

decurrent tooth, with 2–4(–5) lamellulae between two lamellae of different size, sometimes anastomosing or forked, from flesh-pink to dark orange, when old often with wine red tinge. *Stipe* 10–60 × 2–6 mm, cylindrical, centrally inserted, solid to fistulose with age, generally darker than the pileus, orange to red-brown, when moist from glabrous to fibrillose, on drying generally squamulose to squarrose overall, squamules white to ochraceous. *Context* concolorous with surface, sometimes with red-vinaceous tinge, generally vinaceous in the base of stipe. Taste mild and fungoid. Basal mycelium white. *Basidiospores* (6.6–)7.2–8.8(–9.6) × (6.4–)7.1–8.8(–9.6) µm, Q = (0.98–)0.99–1.03(–1.06) µm, globose, hyaline, moderately echinulate, 1–2 µm long, 0.8–1.5 µm broad at the base. *Basidia* 40–50 × 11–13 µm, 4-spored, clavate, containing a yellow–brown pigmentation in 3% KOH. *Pleurocystidia* 40–50 × 3–7 µm, flexuous to narrowly-cylindrical. *Cheilocystidia* rare, similar to pleurocystidia. *Hymenophoral trama*, subregular, consisting of 15–56 × 3–6 µm subparallel hyphae. *Pileipellis* of interwoven hyphae with scattered fascicles of ± perpendicular hyphae; terminal elements variable in shape, from cylindrical to clavate, sometimes with median constriction, rarely with lobed to coralloid terminal elements. *Stipitipellis* a cutis consisting of thin, parallel, 18–40 × 4–9 µm hyphae. *Clamp-connections* frequent everywhere.

Habitat: Associated with *Populus alba*, *Populus nigra*, *Populus* spp. and *Salix* spp.

Material examined: ITALY, Province of Alessandria, Mombello, locality Casalino, 220 m a.s.l., in a grassland with scattered Poplars (*Populus alba*, *Populus nigra, Populus spp.*) and Willows (*Salix* spp.) nearby, 11 November 2019, F. Dovana (GDOR 411, **holotype**); *ibidem*, 3 September 2010, F. Dovana (GDOR 408).

GenBank numbers: GDOR 411: ITS = MN871895, LSU = MN873017; GDOR 408: ITS = MN871894, LSU = MN873018.

Notes: Macroscopically, *Laccaria populina* is characterized by its medium-sized basidiomata, with brown–red or orange pileus, crenulate at the margin, context concolour with pileus, with irregular red-wine spots especially near the base of stem and copious white basal mycelium (Fig. 181a, b). *Laccaria populina* observed appeared to be associated with *Salicaceae*. Microscopically, it can be recognized by the four-spored basidia, basidiospores echinulate with spines up to 2 µm long, and pileipellis with terminal elements variable in shape and size (Fig. 181c–h). A megablast search of GenBank nucleotide database at NCBI (24 Dec. 2019) using LSU sequence of *L. populina* (holotype) showed that the best hits were *L. tortilis* (GMM7635), *L. proximella* (F1081079), *L. proxima* (GMM7631) and *L. bicolor* (GMM2692), all with 98.71% similarity and 6 gaps. As for megablast analysis (24 Dec. 2019), ITS sequence of *L. populina* showed 99.86% (708/709) similarity and no gaps with two german environmental sequences (GenBank GU990359 and GU990354) that come from *Salix viminalis* and *Populus maximowiczii* x *Populus nigra* root respectively that probably are the same species and 98.71% similarity, and 1 gap with two *Laccaria amethystina* samples (GMM7592 and GMM7621). *Laccaria proximella* and *L. proxima* differ from *L. populina* mainly by their larger ellipsoidal basidiospores (Mueller 1992). *Laccaria bicolor* differs mainly in its remarkable violet basal mycelium and presence of subglobose to broadly ellipsoid basidiospores with smaller echinulae (1–1.8 in length and ≤ 1 µm wide at base) (Mueller 1992). Compared to *L. populina*, *L. tortilis* has a smaller basidiocarp, 2-sterigmate basidia and larger globose basidiospores (9.2–)10–14.5(–16) × (8.3–)10–14.5(–16) µm (Mueller 1992). *Laccaria amethystina* is distinguished from *L. populina* by the bright grayish purple basidiomata and abundant filamentous, clavate or ventricose-rostrate conspicuous cheilocystidia (Mueller 1992). In the combined phylogenetic analysis of LSU and ITS sequences, the two collections of *L. populina* (holotype included) clustered in a supported clade (75% MLBS, 0.93 BYPP; Fig. 182) with two environmental sequences (GenBank GU990359 and GU990354) sister to the *L. cf. laccata* clade but lacking in statistical support. *Laccaria laccata* differs from *L. populina* mainly by their subglobose to ellipsoid basidiospores (Mueller 1992); *Laccaria laccata* var. *pallidifolia* is very similar to *L. populina* from which it can be distinguished by its slightly larger globose to subglobose spores (6.4–)7.4–10(–13) × (6–)7–10(–11.5) µm, with smaller echinulae (≤ 1 µm wide at base), context concolorous with pileus without a wine-red spot (Mueller 1992).

Hygrophoraceae Lotsy

Notes: *Hygrophoraceae* was validly established by Lotsy (1907). It is one of the larger families in the *Agaricales* and comprises 26 genera and more than 600 species (Lodge et al. 2014). It contains agarics, basidiolichens and corticoid fungi. We follow the treatment and updated accounts of *Hygrophoraceae* in Lodge et al. (2014). Based on morphological characteristics and phylogenetic analysis of ITS sequence data, a novel species, *Hygrocybe boertmannii* is introduced.

Hygrocybe (Fr.) P. Kumm.

Notes: *Hygrocybe* is distributed worldwide and characterized by brilliant colours of basidiomata with waxy, widely-spaced lamellae; absence of veil remnants on stipe; white, smooth, inamyloid basidiospores; presence of clamp-connections; lack of true pleurocystidia and wide, regular to subregular or parallel lamellar trama (Boertmann 1995; Babos et al. 2011; Lodge et al. 2014; Hosen et al. 2016; Singh et al. 2017). In this study, a new species *Hygrocybe boertmannii* is introduced based on evidence of morphology and phylogenetic placement (Figs. 184 and 185).

Hygrocybe boertmannii U. Singh & R.P. Bhatt, ***sp. nov.***

Index Fungorum number: IF557840; *Facesoffungi number*: FoF 07737; Fig. 183

Etymology: In recognition to David Boertmann for his contribution to the wild mushrooms.

Holotype: CAL 1802

Pileus 12–52 mm in diam., convex when young, becoming planoconvex to applanate or slightly depressed with age, non-striated, non-perforate, dry, non-viscid, orange to deep orange (5A7-5A8), with maize yellow to sunflower yellow (4A6-4A7) fibrillose-squamules on the surface; margin decurved to plane, crenate; context up to 2 mm wide, fragile, concolorous towards cap surface and pastel yellow to light yellow (3A4-3A5) towards lamellae. *Lamellae* up to 7 mm wide, sub-decurrent to decurrent or sometimes sinuate, distant, white when young, becoming yellowish white (2A2-2A3), edges concolorous but white near the stipe attachment, with about 3 complete lamellae (at margin)

Fig. 183 ***Hygrocybe boertmannii*** (US 1552, **holotype**). **a** Fresh basidiomata in the field. **b** Pileus surface with fine squamules. **c** Lamellae with lamellulae **d** Cystidia-like hyphoid elements. **e** Transverse section through hymenium showing basidia and basidiospores. **f** Terminal elements of pileipellis. Scale bars: **a** = 25 mm, **d**, **e** = 10 µm, **f** = 20 µm

per cm, and usually with 3 lamellulae of different lengths between the two complete lamellae, often interveined. *Stipe* $51-116\times6-11$ mm, central, tapered towards apex, curved near base in mature specimen, smooth, maize yellow to sunflower yellow (4A6-4A7), yellowish white (2A2) at base, hollow; context thin, concolorous to surface, fragile. Spore deposit white. *Taste* and *odour* indistinct. *Spore print* not obtained. *Basidiospores* (8–)8.7 − 9.8 − 10.9(− 11) × (6 −)6.8 − 7.6 − 8.4(− 9) µm (Q = (1.1 −)1.2 − 1.3 − 1.4 µm, n = 30), broadly ellipsoid to ellipsoid, rarely subglobose, smooth, thin-walled, hyaline, inamyloid, single to multi-guttulate, with apicules up to 1 µm long. *Basidia* 62–78 × 11–13 µm, clavate to narrowly clavate, thin-walled, turning light yellowish brown with KOH, with a basal clamp connection, 4-spored; sterigmata up to 13 × 4 µm. *Lamellar* edge non-fertile. *Cystidia-like hyphoid elements* 22–38 × 4–5 µm, emanating from the lamellar context, clavate to cylindro-clavate, fusiform, rarely ventricose; frequently clamped at bases. *Hymenophoral trama* subregular, composed of hyaline, thin-walled (up to 1 µm), cylindrical elements (26–51 × 5–7 µm) intermixed with inflated cells (30–75 × 10–16 µm), rarely with clamp connections. *Pileipellis* a trichoderm, made up of erect to semi-erect septate, thin-walled, unbranched hyphae; terminal elements 74–118 × 10–20 µm, with round apex, rarely pointed apex, clamp connections absent; underlying hyphae repent, cylindrical, rarely clamped, devoid of any pigments. *Stipitipellis* composed of septate, thin-walled, unbranched hyphae, up to 21 µm wide; clamp connection present.

Material examined: INDIA, Uttarakhand, Rudraprayag district, Baniyakund forest, growing scattered on ground under *Quercus* sp. in mixed temperate forest, 2653 msl, N30°28.998′ E079°10.658′, 08 August 2017, U. Singh, US 1552 (CAL 1802, **holotype**); 2617 msl, N30°28.926′ E079°10.615′, 25 August 2016, U. Singh, US 1358 (CAL 1803, paratype).

GenBank numbers: ITS = MT127548, MT127549.

Notes: *Hygrocybe boertmannii* is characterized by orange to deep orange pileus with yellowish fibrillose-squamules all over the pileus, crenate margin, white to yellowish distant lamellae, smooth yellow stipe, broadly ellipsoid to ellipsoid basidiospores, presence of cystidia-like hyphoid elements and a trichoderm nature of pileipellis (Fig. 183). Based on a combination of characters, e.g., dry basidiomata, squamulose pileus, smooth stipe, subregular hymenophoral trama and a trichoderm pattern of the pileipellis, it is referable to *H.* subsect. *Squamulose* (Borgen and Arnolds 2004; Boertmann 2010; Lodge et al. 2014). This placement was further confirmed by our ITS-based molecular phylogeny (Fig. 184). *Hygrocybe boertmannii* shares some similarities with *H. cantharellus* (originally described from USA) including having orange pileus with crenate margin, the presence of squamulose on pileus, yellow distant lamellae and a smooth stipe surface but the latter can be distinguished by smaller basidiomata (pileus 7–30 mm; stipe 18–67 × 1.8–4 mm), weakly to strongly arcuate decurrent lamellae, ellipsoid to ovoid basidiospores, smaller basidia (35–54 × 7.5–9.5 µm) and absence of cheilocystidia (Arnolds 1995).

Phylogenetically, *Hygrocybe boertmannii* appeared as sister to another Indian species, *H. rajendrae*, however our novel species of *Hygrocybe* is separated from *H. rajendrae* with very strong nodal support (100% MLBS, 1.00 BYPP). *Hygrocybe rajendrae* is clearly distinct from *H. boertmannii* on the basis of larger basidiomata (pileus 37–69 mm diam.; stipe $109-218\times8-14$ mm), yellowish pileus and absence of cystidia-like hyphoid elements (Singh et al. 2017). The ITS dataset consisting of 41 sequences (including our isolates: US 1552, represented by GenBank acc. no. MT12631 and US 1358, represented by GenBank acc. no. MT12634) of *Hygrocybe* and *Hygroaster* was analysed (Fig. 184). Two sequences isolated from these Indian materials appear to be nested amongst other sequences of *Hygrocybe* subg. *Pseudohygrocybe* sect. *Coccineae* subsect. *Squamulosae* and form a distinct clade that is sister to *H. rajendrae* (another Indian species) with 100% MLBS, 1.00 BYPP support. The combination of morphological features and phylogenetic analysis corroborates the proposed taxon *Hygrocybe boertmannii* as a new species distinct from all the known taxa of *Hygrocybe*.

Marasmiaceae Roze ex Kühner

Notes: *Marasmiaceae* is one of the most diverse family consisting of ca. 54 genera and 1590 species (Kirk et al. 2008). Most members of the family are commonly found to grow on decayed leaves, twigs, branches, trunks and hence are saprophytic in nature. As a saprobe, these fungi play an important role for the sustenance of forest ecosystem by recycling of nutrients.

Marasmius Fr.

Notes: *Marasmius* was proposed by Fries (1836). This is a world-wide distributed genus which has been a topic of interest by researchers all around the globe. Presently, India hosts a record of ca. 75 species of *Marasmius* among which most of them have been reported from the southern Indian regions (Dutta et al. 2015). In this study, three new species of the *Marasmius* viz. *M. benghalensis*, *M. jinfoshanensis* and *M. subtropicus* are described from China and India based on evidence of morphology and phylogenetic analysis (Figs. 185, 186, 187, 188, 189, 190, 181, 192 and 193). The present study follows the latest treatment on *Marasmius* by Shay et al. (2017) and He et al. (2019).

Marasmius benghalensis A.K. Dutta & K. Acharya, ***sp. nov.***

Index Fungorum number: IF557845; *Facesoffungi number*: FoF 07864; Figs. 185, 186

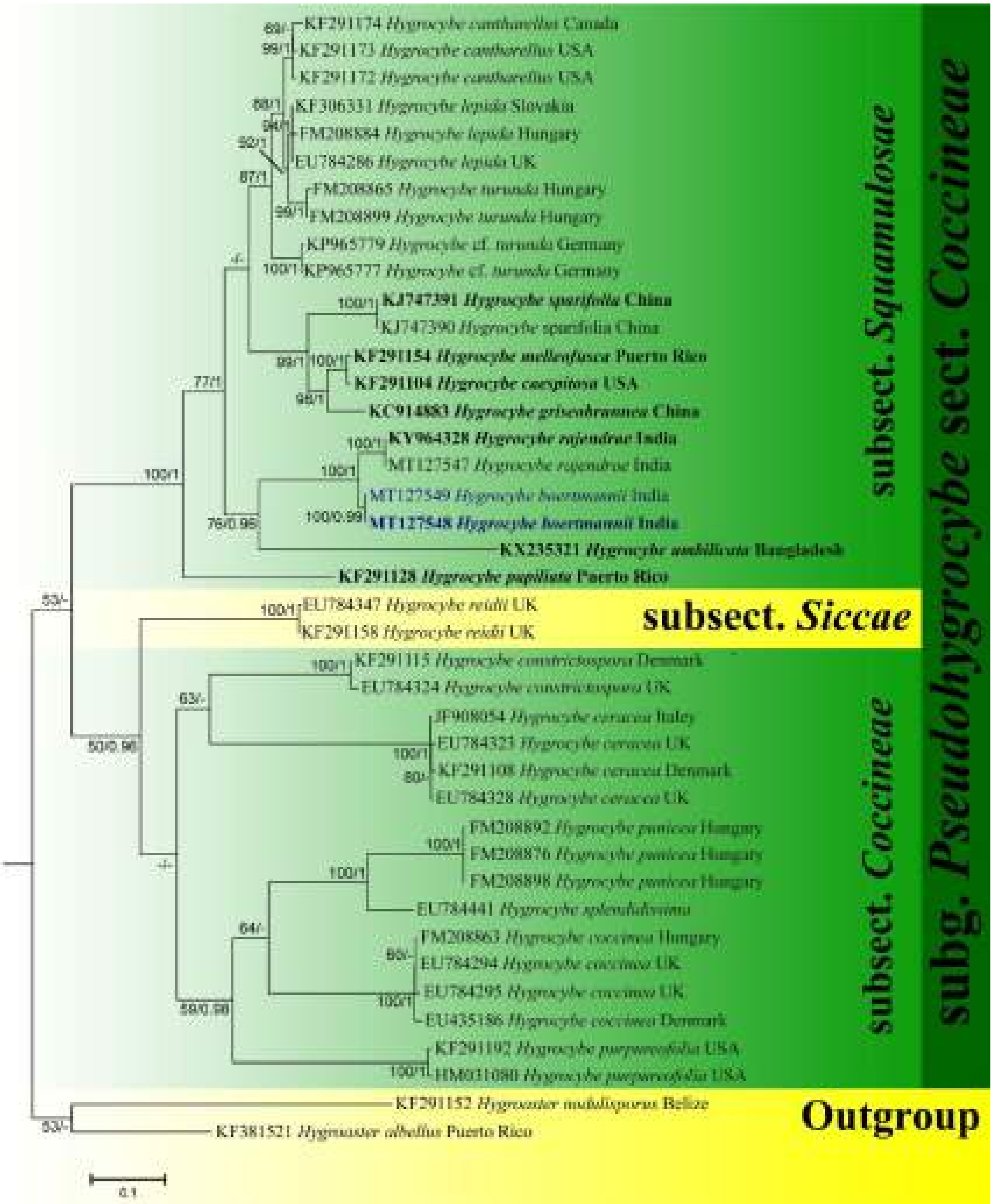


Fig. 184 Phylogenetic analyses were based on data set of nrITS sequences. Reference sequences were selected from relevant literature (Lodge et al 2014; Singh et al. 2017), BLAST searches (Altschul et al. 1997) and data retrieved from GenBank (Clark et al. 2016). Species of *Hygroaster* are selected as the outgroup taxa (Lodge et al 2014; Singh et al. 2017). Multiple sequence alignment was performed using MAFFT v.7 (Katoh and Standley 2013). Alignments were manually edited in BioEdit v 7.2.5 (Hall 1999). To change the multiple alignment format, Alignment Transformation Environment (ALTER) was used (Glez-Peña et al. 2010). Maximum Likelihood analysis was performed with the programme RAxML GUI 1.5 (Silvestro and Michalak 2012). One thousand bootstrap replicates were analysed to obtain nodal support values. Bayesian inference was computed independently twice in MrBayes v.3.2.2 (Ronquist et al. 2012), under different models. The best-fit substitution model of nucleotide evolution was carried out in MrModeltest 3.7 (Posada and Crandall 1998). Bayesian posterior probabilities (BPP) were calculated in two simultaneous runs with Markov chain Monte Carlo (MCMC) algorithm (Larget and Simon 1999). Markov chains were run for 10 million generations, saving a tree every 100th generation. Default settings in MrBayes were used for the incremental heating scheme for the chains (3 heated and 1 cold chain), unconstrained branch length [unconstrained: exponential (10.0)] and uniformative topology (uniform) priors. The first 25% of trees was discarded as burnin (Hall 2004). Ex-type strains are in black bold and newly generated sequences are indicated in blue

Fig. 185 Field pictures of the basidiomata. **a**, **b** ***Marasmius benghalensis*** (CUH AM214, **holotype**), habitats of basidiomata and lower side of the pileus showing lamellae features. Scale bars: **a**, **b** = 10 mm

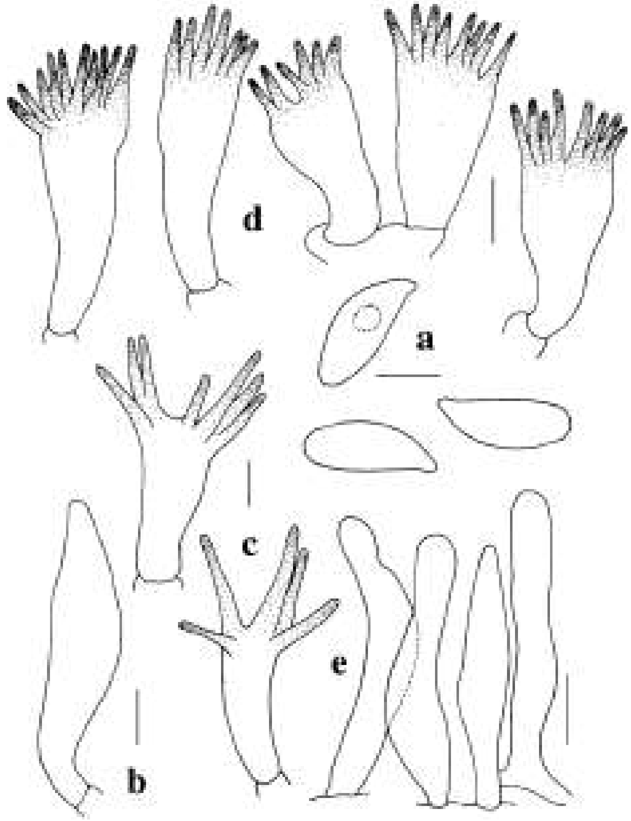


Fig. 186 ***Marasmius benghalensis*** (CUH AM214, **holotype**). **a** Basidiospores. **b** Basidioles. **c** Cheilocystidia. **d** *Siccus*-type pileipellis cells. **e** Caulocystidia. Scale bars: **a**–**c** = 5 µm, **d**–**e** = 10 µm

Etymology: '*benghalensis*' refers to West Bengal, India, the region from where the type species was collected.

Holotype: CUH AM214

Pileus 21–56 mm diam., convex when young, becoming broadly convex to undulate when old, with or without a small central depression, wrinkled, glabrous, semidry to moist, light orange (5A5), orange (5A6) to greyish orange (5B5-6) or brownish orange (5C6) or golden yellow (5B7), margin greyish yellow (4B3-4) to pale orange (5A3) or light orange (5A4), becoming yellowish with KOH, hygrophanous, non-striate. *Context* very thin, pale orange (5-6A3) to light orange (6A4) or orange grey (6B2) to greyish orange (6B3). *Lamellae* narrow, non-collariate, adnexed, subdistant (L = 11–14) with 2–4 series of lamellulae, vein-like, non-intervenose, sometimes forked from the middle towards margin, white, concolorous, smooth, even, often not reaching to the margin of pileus. *Stipe* well-developed, 52–75 × 2–4 mm, central, cylindrical, equal, hollow, dry, minutely pruinose, shiny, greyish orange (5B6) to golden yellow (5B7) or brownish orange (6C8) to brown (7D7-8) towards base, light yellow (3-4A5) to olive yellow (3C6-7) from the middle towards apex, non-insititious, strigose, basal mycelium white. *Taste* mild. *Odour* sweet.

Basidiospores (7.2–)8.5–10(–10.8) × 3.5–4(–4.5) µm ($\bar{x}$ = 9.5 × 3.8 µm, n = 30), Q = 1.8–2.7 µm ($\bar{x}$ = 2.5 µm, n = 30), ellipsoid to lacrymoid, hyaline, inamyloid, one guttate when viewed with KOH, thin-walled. *Basidia* not observed. *Basidioles* 24–27(–29) × 5–6(–7.5) µm, fusoid to clavate, hyaline, thin-walled. *Pleurocystidia* absent. *Lamellae-edge* sterile, with crowded cystidia. *Cheilocystidia* composed of *Siccus*-type broom cells; main-body (11–)14–16(–18) × (3.5–)4.5–5.5(–7.5) µm, cylindrical to clavate, hyaline, thin- to thick-walled; apical setulae (6–)9–10(–11.5) µm long, cylindrical, less dense, often with obtuse apex, pale yellowish, thick-walled. *Pileipellis* a hymeniform layer, consists of *Siccus*-type of broom cells; main-body (18–)21–25(–36) × (5–)7.5–9(–15) µm, cylindrical to clavate or subclavate, hyaline, thin- to thick-walled walled; apical setulae 3.5–6(–11) µm long, cylindrical, pale yellowish, acute to obtuse, thick-walled. *Lamellae trama* hyphae 3.5–6(–7.5) µm broad, interwoven, cylindrical, hyaline, smooth, dextrinoid, thin- to slightly thick-walled. *Pileus trama* hyphae 6.5–7(–9) µm broad, interwoven, cylindrical to irregularly cylindrical, sometimes branched, hyaline, dextrinoid, thin- to slightly thick-walled. *Stipitipellis* hyphae 3.5–4.5(–6.5) µm broad, parallel to subparallel, cylindrical, hyaline, dextrinoid, moderately thick-walled. *Stipe trama* hyphae 5–7(–11) µm broad, parallel, cylindrical, hyaline, strongly dextrinoid, moderately thick-walled (up to 0.9 µm). *Caulocystidia* (21–)39–60(–76) × (5–)6.5–7.5(–8.5) µm, abundant, non-setulose, cylindrical to irregular in outline, hyaline, inamyloid, moderately thick-walled.

Material examined: INDIA, West Bengal, Darjeeling district, near Lebong Cart road, 27°04′07.9″ N 88°15′07.2″ E, 1836 msl, on decomposed leaf litter among *Gleichenia* sp., 24 June 2016, S. Paloi (CUH AM214, **holotype**); Darjeeling district, near Lebong Cart road, 27°04′07.9″ N 88°15′07.2″ E, 1836 msl, 25 June 2016, S. Paloi (CUH AM221).

GenBank numbers: ITS = MF189043, MF189044, LSU = MT255002, MT255001.

Notes: Diagnostic features of the present taxon include: a non-striate, wrinkled, greyish yellow to pale orange pileus with orange to brownish orange or golden yellow disc; narrow, vein-like, adnexed, subdistant (11–14), white lamellae that often do not reach the pileus margin; a minutely pruinose, strigose stipe with white basal mycelium; presence of a sweetish odour; ellipsoid to lacrymoid basidiospores with mean 9.5 × 3.8 µm; absence of pleurocystidia; presence of *Siccus*-type broom cells in the pileipellis and form of cheilocystidia; and simple cylindrical caulocystidia ranging 21–76 × 5–8.5 µm (Figs. 185 and 186). These combinations of features undoubtedly place *Marasmius benghalensis* under ser. *Atrorubentes* of the sect. *Sicci* (Tan et al. 2009; Wannathes et al. 2009).

Among similar species within ser. *Atrorubentes* of the sect. *Sicci*, *Marasmius xestocephalous* Singer has a striate pileus, a greater number of lamellae (15–18), shorter stipe (18–35 mm long), much longer basidiospores (10–15 µm), and caulocystidia that is forked or apically lobed (Wannathes et al. 2009). *Marasmius inthanonensis* described for the first time from Northern Thailand (Wannathes et al. 2009), differs by its pileus-coloured, dark olive to olive at disc, close and much broader lamellae (3–6 mm) coloured light brown at the edge, much longer stipe (up to 102 mm long), and relatively shorter caulocystidia (up to 48 µm long).

Among other similar species within the sect. *Sicci*: *Marasmius hypochroides*, one of the frequently encountered taxon in India, primarily differs by the absence of caulocystidia and belongs to a different ser. *Leonini* of the sect. *Sicci* (Pegler 1986; Wannathes et al. 2009). The Brazilian taxon *Marasmius cladophyllus* (Singer 1976; Pegler 1983) has adnate, close reticulately interveined, crowded lamellae coloured pale buff, a stipe-coloured purplish brown towards base with pale buff apex, and less broad basidiospores (2.5–3.5 µm, Q = 2.0). *Marasmius ruber* (Pegler 1983) differs by its sulcate pileus, crowded lamellae coloured yellow to orange with scarlet red towards edge, relatively shorter stipe (15–50 mm) with glabrous surface, and less broad basidiospores (2.5–3.5 µm). The Mexican taxon, *Marasmius leoninus* Berk. has somewhat differently coloured pileus with white context, much broader lamellae (3–4.5 mm), glabrous stipe surface coloured white towards apex, absence of any sweetish odour, and presence of *Siccus*-type broom cells in the form of caulocystidia (Singer 1976).

In the phylogenetic tree, *Marasmius benghalensis* appears to be close to *M. luteolus* (60% MLBS, 0.99 BYPP; Fig. 187). However, *M. luteolus* has minutely velutinous to pruinose pileus surface, adnate attachment of lamellae, presence of pleurocystidia of the *Siccus*-type, and two types viz. *Siccus*-type as well as non-setulose caulocystidia (Wannathes et al. 2009).

Marasmius jinfoshanensis Chun Y. Deng & Gafforov ***sp. nov.***

MycoBank number: MB836094; *Facesoffungi Number*: FoF 09969; Figs. 188, 189

Etymology: Referring to the Jinfoshan National Nature Reserve, the location where the type specimen was collected.

Holotype: HGASMF 01–4344

Pileus 3–5 mm, convex to broadly conical, umbonate; glabrous; greyish orange (5B4, 5B5, 6B5), light brown (7D5), brownish orange (6C6, 7C6, 7C4), at center with a surrounding white dot. *Lamellae* subdistant, L = 12–16, l = 0, collariate, pale cream, with a concolorous edge. *Stipe* up to 60–80 mm long, filiform, insititious, smooth, glabrous, white at apex, reddish brown (7E8, 8E8) to dark brown (7F7, 8F8) to black. *Basidiospores* (6.5–)7–8(–9.8) × 4–5 µm, E = 1.6–2, Q = 1.7, ellipsoid, sublacrymoid, ellipsoid-fusoid, thin-walled, smooth, hyaline, inamyloid. *Basidia* 19–27 × 9–11 µm, 4-spored, clavate. *Basidioles* 12–28 × 4–9 µm, clavate, cylindrical, fusoid. *Cheilocystidia* in the form of broom-cells of the Rotalis-type, 20–30 × 5–8 µm, clavate, subcylindrical, thin-walled, with ± thin-walled or slightly thick-walled, projections. *Pleurocystidia* absent. *Trama hyphae* cylindrical to subinflated, thin-walled, hyaline, dextrinoid, up to 12 µm wide. *Pileipellis* a hymeniderm consisting of broom-cells of the Rotalis-type, 13–18 × 7–14 µm, clavate, subvesiculose, pyriform, thin-walled, sometimes with slightly thick-walled apex, with cylindrical to warty, up to 2 × 1 µm large projections. *Stipitipellis* a cutis composed of cylindrical, parallel, slightly thick-walled, smooth, up to 5 µm wide hyphae with yellowish walls in KOH; medulla hyphae slightly dextrinoid. *Caulocystidia* absent. *Clamp connections* present in all tissues.

Material examined: CHINA, Chongqing, Nanchuan district, Jinfoshan National Nature Reserve, N107.182222, E29.030152, 2 037 m alt., 6 Apr. 2020, C.Y. Deng, DCY 2409 (HGASMF 01–4344, **holotype**); *ibid*., 6 Apr. 2020, C.Y. Deng, DCY 2413, (HGASMF 01–4345, **paratype**).

GenBank numbers: HGASMF 01–4344: ITS = MT556448, LSU = MW237220; HGASMF 01–4345: ITS = MT556449, LSU = MW237221.

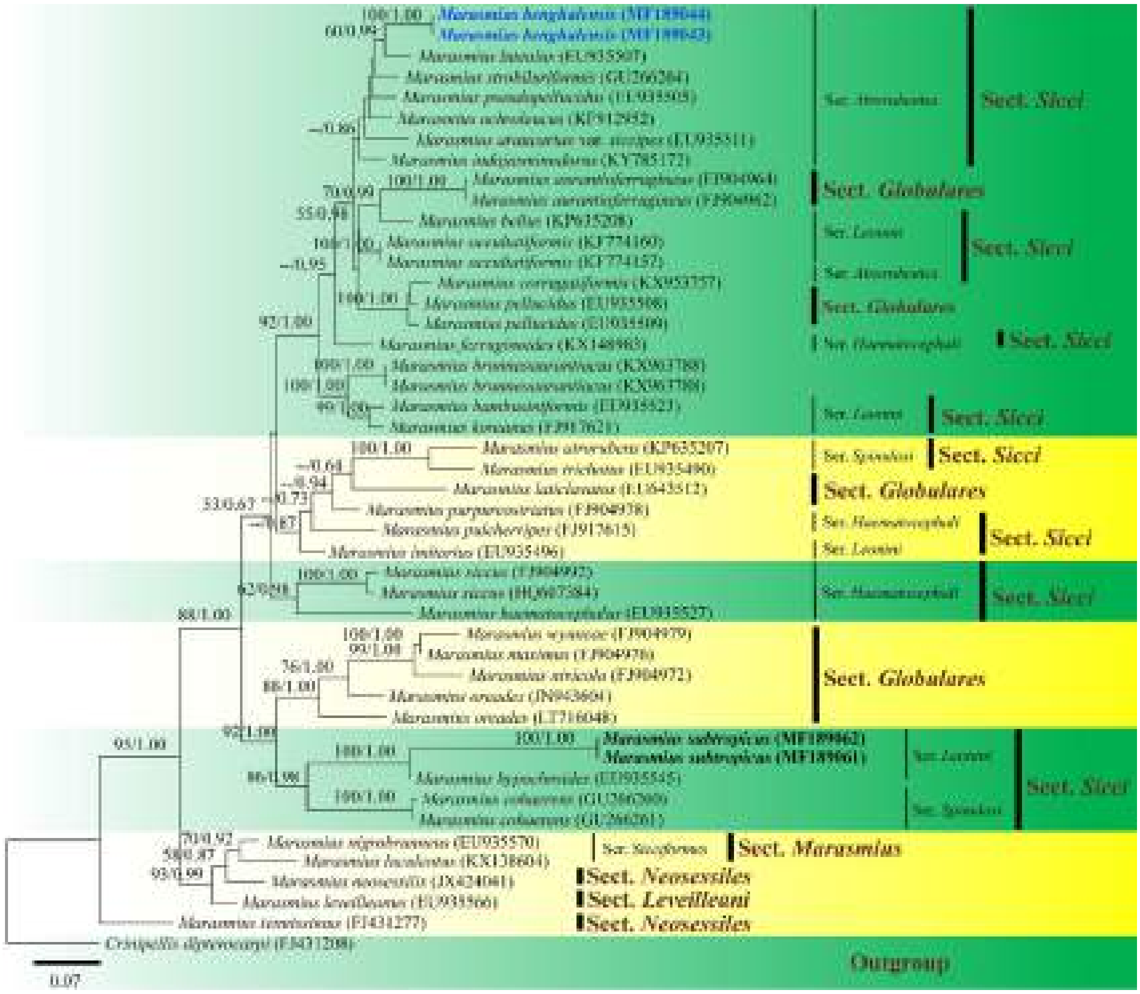


Fig. 187 Phylogram generated from maximum likelihood (ML) analysis based on nrDNA ITS sequence data of *Marasmius* species using best-fit model (HKY + G) with Bayesian Information Criterion (BIC) value of 14371.193718. Related sequences are mostly taken from Wannathes et al. (2009) and Antonín et al. (2012). Thirty-six taxa of *Marasmius* and one outgroup taxon are included in the analyses comprising 742 characters after alignment. *Crinipellis dipterocarpi* is used as the outgroup taxon following Wannathes et al. (2009). Bayesian analysis (BA) reached a standard deviation of split frequencies of 0.004984 after 10^6 generations and produced 11210 credible set of trees after discarding initial 3,792 trees as burnin phase. Tree topology of the ML analysis is similar to the BA. The best RaxML tree with a final likelihood values of − 6870.939953 is presented. The matrix had 483 distinct alignment patterns, with 17.46% proportion of gaps and completely undetermined characters. Estimated base frequencies were as follows: A = 0.2461, C = 0.2043, G = 0.2006, T = 0.3490; gamma distribution shape parameter = 0.4030. ML Bootstrap values (MLBS) equal or greater than 50% (on the left of '/') and posterior probabilities (BYPP) values equal or greater than 0.50 (on the right of '/') from BA are labeled above or below the nodes. The newly generated sequences are in blue bold. Representative sections and series of the *Marasmius* taxa are marked in the right side

Notes: *Marasmius* sect. *Marasmius* species are unique because they have collariate lamellae (Singer 1976, 1986; Desjardin 1989; Antonín 1991, 2007; Antonín and Noordeloos 2010). Based on nrITS sequences, subsect. *Maramius* is monophyletic while subsect. *Sicciformes* is paraphyletic (Tan et al. 2009; Wannathes et al. 2009). *Marasmius* subsect. *Horriduli* might have a wider range (de Oliveira et al. 2020). *Marasmius jinfoshanensis* is in *Marasmius* sect. *Marasmius* because it has collariate lamellae. ITS and LSU dataset of *M. siccus* were chosen as an outgroup for rooting purposes based on a study by Tan et al. (2009) and Wannathes et al. (2009). Two sequences of *M. jinfoshanensis* constitutes a subclade on a long branch with 100% bootstrap support. *Marasmius jinfoshanensis* is sister to *Marasmius wisteriae* with high support. *Marasmius wisteriae* was described from Korea. It differs from other *Maramius* species by a pale colored pileus with a dark central dot and large, clavate-fusoid, fusoid, narrowly lacrymoid basidiospores (Antonín et al. 2013). Two sequences of *Marasmius rotalis* (KC415765 and JN003837) were likely misidentified. *Marasmius capillaris* is represented on two separate branches in our phylogeny (Fig. 190). Both species were

Fig. 188 ***Marasmius jinfoshanensis*** (HGASMF 01-4344, **holotype**): Basidiomata of on decaying leaves of dicotyledons in the litter in a subtropical-montane forest

collected in two different states in North America. At least one of these species must be misidentified.

Marasmius rotalis differs in having a campanulate to umbilicate, shallowly depressed pileus and distant lamella (8–11). *Marasmius rotula* also differs by having a navel-like central depression in the white pileus. *Marasmius somalomoensis* differs in having a plicate pileus and non-marginate lamellae (Jackie et al. 2017). The distinct pallid zone surrounding a dot in the center of the pileus in *M. jinfoshanensis* is similar to the zone in *M. avellaneus*, *M. vigintifolius* and *M. subvigintifolius*. *Marasmius jinfoshanensis* (Figs. 188 and 189) differs from these species in the colour of the pileus and the size of the basidiospores (7.8–11.5 × 4.5–7, 6.8–10.8 × 3.3–6 µm and 6.6–9 × 3.8–5 µm, respectively) (de Oliveira et al. 2020; Singer 1976). *Marasmius idroboi* has a brown pileus with a white zone around the central dot, but differs in having a pileus with a shallow umbilicus and having much more numerous lamellae (20–23) (Singer 1976). *Marasmius andasibensis* is somewhat similar to *M. jinfoshanensis*. However, the former species differs in having a smaller grey orange pileus and distant lamellae (Antonín and Buyck 2006).

Marasmius subtropicus A.K. Dutta & K. Acharya, ***sp. nov.***

Index Fungorum number: IF557846; *Facesoffungi number*: FoF 07865; Figs. 191, 192

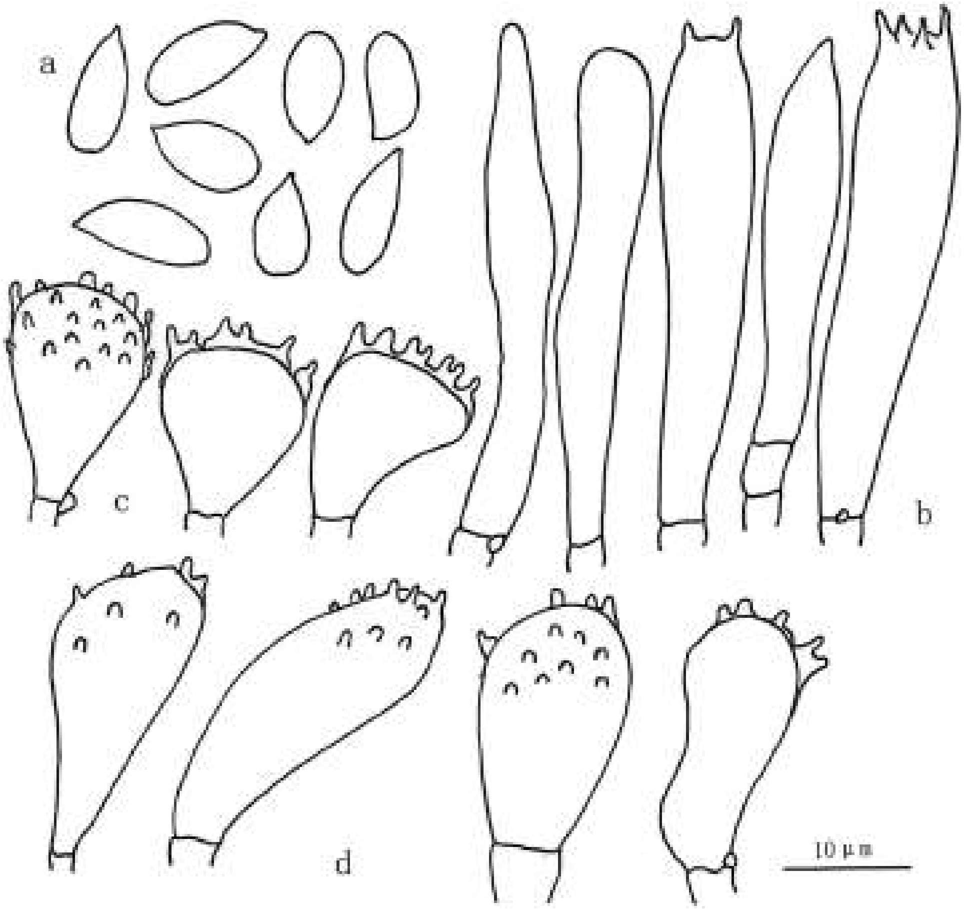


Fig. 189 ***Marasmius jinfoshanensis*** (HGASMF 01-4344, **holotype**): Microscopic structures. **a** Basidiospores. **b** Basidia. **c** Cheilocystidia. **d** Pileipellis. Scale bar: **d** = 10 µm

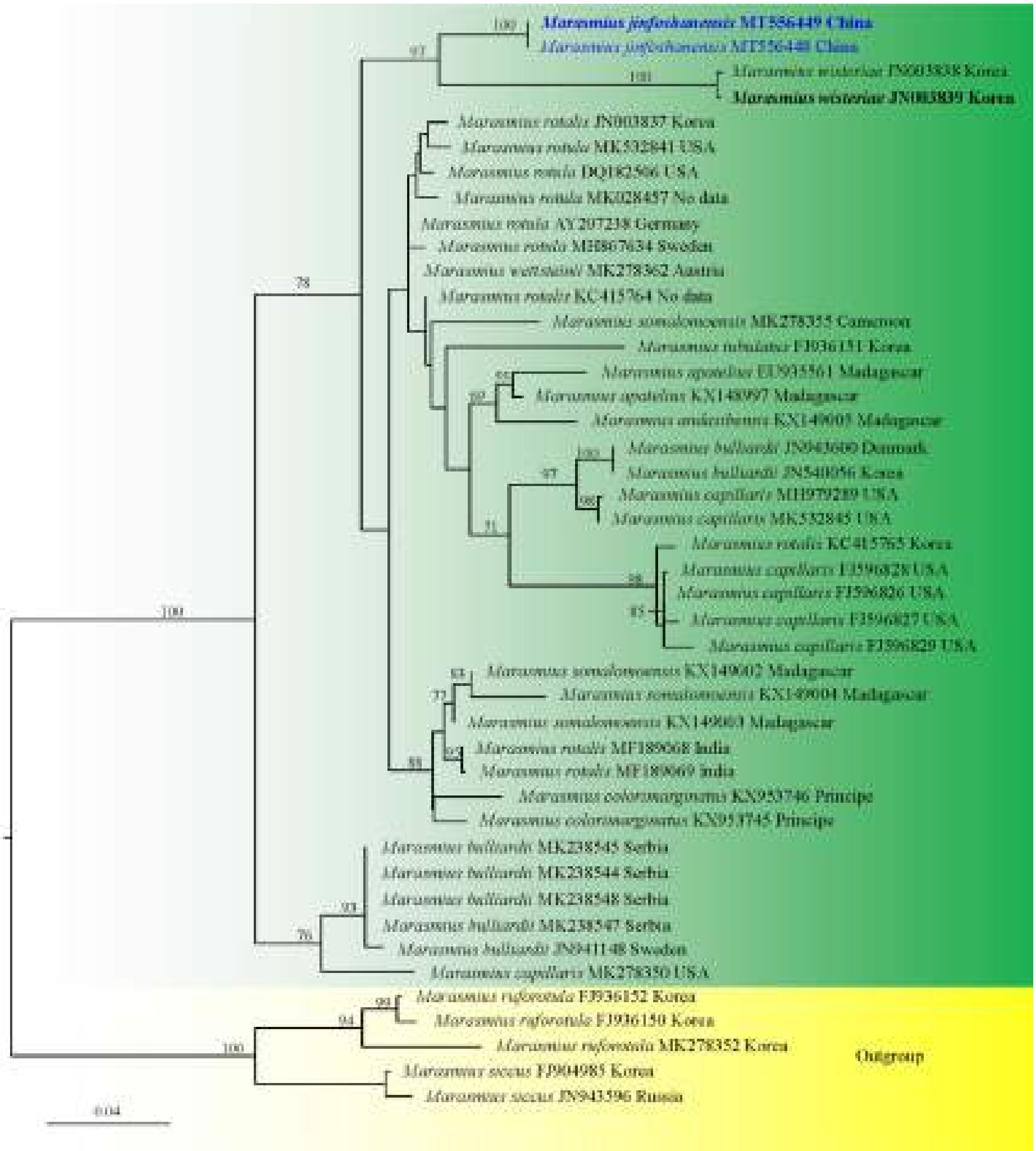


Fig. 190 Maximum likelihood tree inferred from ITS-LSU nrDNA, using RAxML GUI v. 2.0.0 (Edler et al. 2020), showing the placement of *Marasmius jinfoshanensis*. Support values (>50% with 1,000 replicates) are shown above branches. *Marasmius ruforotula* (FJ936150, FJ936152, MK278352) and *M. siccus* (FJ904985, JN943596) were chosen as outgroup. Ex-type strain is in bold and newly generated sequences are in blue

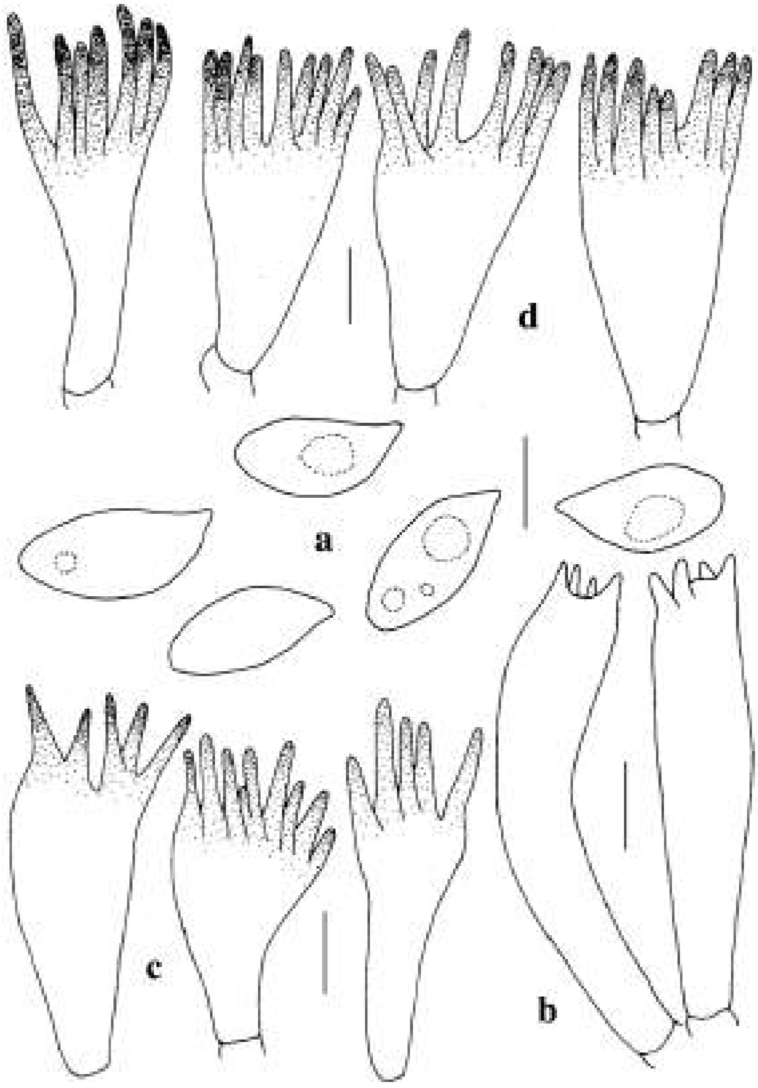
Etymology: '*subtropicus*' refers to the subtropical geographic region from where the taxon was collected.

Holotype: CUH AM226

Pileus 20–58 mm diam., convex when young, becoming broadly convex to plano-convex with a small umbo at maturity, margin often upturned, smooth to minutely pubescent, semi moist to dry, disc light brown (6D6) to brown (6E6-8), slightly rugulose, orange (5A6-7) to brownish yellow (5C7) towards middle, light yellow (1A5) to greyish yellow (1B6-7, 2-3B5, 4B6) towards extreme margin, on drying turns orange (6A7, 6B8) to deep orange (6A8) or brownish orange (6C8) with brown (6E7-8) disc, translucent when young, becoming sulcate to often rimos at maturity, context thin, cream. *Lamellae* 2–3 mm broad, adnexed, distant to subdistant (L = 19–22, l = 4–5), white (1A1) to cream, strongly intervenose, often forked from the middle, concolorous. *Stipe* 25–64 × 2–4 mm, central, cylindrical, noninsititious, equal with slightly broader at base (up to 6 mm),

Fig. 191 Field pictures of the basidiomata. **a**, **b** ***Marasmius subtropicus*** (CUH AM226, **holotype**), habitats of basidiomata and lamellae showing intervenose nature. Scale bars: **a**, **b** = 10 mm

Fig. 192 ***Marasmius subtropicus*** (CUH AM226, **holotype**). **a** Basidiospores. **b** basidia. **c** *Siccus*-type cheilocystidia. **d** *Siccus*-type pileipellis cells. Scale bars: **a**–**d** = 5 µm



often cleft towards middle, brownish yellow (5C7) to orange or deep orange (6A8) with paler to cream towards apex, glabrous, hollow, basal mycelia well developed, orange. *Odour* and *taste* indistinctive. *Basidiospores* (7–)9–10.5(–11.5) × (4–)6–7(–7.2) µm ($\bar{x}$ = 10 × 6.5 µm, n = 30), Q = 1.2–1.7 µm ($\bar{x}$ = 1.5 µm, n = 30), ellipsoid, hyaline, inamyloid, thin-walled. *Basidia* 25–29 × 5–6.5(–7.5) µm, clavate, hyaline, thin-walled, 4-spored, sterigmata 2.5–4 µm long. *Basidioles* (21.5–)28–31(–36) × (5–)6–6.5(–7.5) µm, cylindrical to clavate or fusoid, hyaline, thin-walled. *Pleurocystidia* absent. *Lamellae-edge* sterile, with well-developed cystidia. *Cheilocystidia* common, composed of *Siccus*-type broom cells; main body (10–)11–14(–18) × (3.5–)4.5–6(–8 .5) µm, cylindrical to clavate or irregular in outline, often branched, hyaline, inamyloid, thin- to thick-walled; apical setulae (2.5–)6.5–7.5(–10.5) µm long, cylindrical, hyaline to pale yellow, inamyloid, acute to subacute, thick-walled. *Pileipellis* hymeniform, composed of *Siccus*-type of broom cell; main body (10.5–)14–15(–18) × (5.5–)7–9(–11) µm, cylindrical to clavate, hyaline, inamyloid, thin- to thick-walled; apical setulae (3.5–)6–8(–10.5) µm long, cylindrical, yellowish to light brown, inamyloid, acute to subacute, thick-walled. *Pileus trama* hyphae interwoven, (4–)7–8(–11) µm broad, cylindrical to often inflated, hyaline, dextrinoid, thin-walled, non-gelatinous. *Lamellae trama* hyphae interwoven, 3.5–7(–7.5) µm broad, cylindrical, hyaline, dextrinoid, thin-walled, non-gelatinous. *Stipitipellis* hyphae 3.5–4.5(–5.5) µm broad, parallel to subparallel, cylindrical, thin-walled, pale yellowish in KOH, nongelatinous. *Stipe trama* hyphae 7–8(–9.5) µm broad, parallel, cylindrical, hyaline, dextrinoid, thin- to moderately thick-walled, non-gelatinous. *Caulocystidia* absent. *Clamp-connections* present in all the tissues.

Material examined: INDIA, West Bengal, South-24-Parganas district, Lakshmikantapur, 22°06′35.9″ N 88°19′12.7″ E, 6 msl, among decomposed leaf litter under *Cocos nucifera* tree, 26 June 2015, J. Sarkar (CUH AM226, **holotype**); South-24-Parganas district, Baruipur, 22°21′35.3″ N 88°27′13.6″ E, 9 msl, among decomposed leaf litter, 23 June 2016, A.K. Dutta (CUH AM706).

GenBank numbers: ITS = MF189061, MF189062, LSU = MT254998, MT255000.

Notes: Distinctive feature of the specimen includes a medium to large, convex to plano-convex pileus coloured orange to brownish yellow with light brown to brown towards central small umbo, distant to subdistant, strongly intervenose, white lamellae, a central, non-insititious, glabrous, brownish yellow to orange or deep orange stipe with well-developed basal mycelia coloured orange, ellipsoid basidiospores with a mean of 10 × 6.5 µm (Q mean 1.5), presence of *Siccus*-type cheilocystidia with apical setulae measuring 2.5–10.5 µm, and absence of pleurocystidia and caulocystidia. All these combination features undoubtedly place the present taxon to ser. *Leonini* of the sect. *Sicci* (Desjardin et al. 2000).

Based on the morphological features (Figs. 191 and 192) as well as phylogenetic analysis (Fig. 193), *Marasmius hypochroides* appears to be most close to *M. subtropicus* with 100% MLBS, 1.00 BYPP support. However, *M. hypochroides* primarily differs from *M. subtropicus* by its pileus-coloured brown (Pegler 1986) or brownish orange to yellowish brown (Wannathes et al. 2009), lesser number of lamellae (12–16, Wannathes et al. 2009), and yellowish brown to reddish brown coloured stipe. Among other similar taxa belonging to the same section: *Marasmius cladophyllus*, originally described from Brazil, has smaller pileus (up to 20 mm diam.), adnate, narrow, reticulately interveined or poroid lamellae that possess lamellulae of two lengths, purplish brown stipe, and smaller spores with a mean of 9.2 × 3 µm (Pegler 1983; Singer 1976). *Marasmius submarginatus* Singer primarily differs by brownish orange pileus (Desjardin 1989), lesser number of lamellae (13–15), white coloured basal mycelium and less wide basidiospores (3.5–5 µm, Singer 1989). The Brazilian taxa, *Marasmius asemiformis* has a non-striate pileus, crowded lamellae coloured white, chestnut to brown coloured stipe that is entirely pubescent, less broad basidiospores (8–10 × 3.2–3.7 µm), and presence of caulocystidia (Singer 1989). The Malaysian taxa, *M. angustilamellatus* (Tan et al. 2009), has yellowish brown to light brown pileus with blackish center, much crowded lamellae (24–40) coloured light brown, and basidiospores that is less broad (3.5–4.5 µm broad). *Marasmius hygrocybiformis*, described from China (Deng et al. 2012), has reddish orange to orange red pileus, adnate lamellae with lesser number of lamellulae (L = 12–16, l = 1–2), greyish green coloured stipe, presence of pleurocystidia, pleurosetae, and cheilosetae.

Among previously reported taxa from India: *Marasmius rhizophilus* primarily differs by its much smaller pilei (10–13 mm diam.) coloured cream (Saccardo 1887; Patil 1978). *Marasmius floriceps* reported from Tamil Nadu (Natarajan and Manjula 1982), primarily differs by its brown to light brown pileus surface, rare occurrence of the intervenose lamellae, and smaller pileipellis *Siccus*-type cells measuring 6.6–8.8 × 3.3–6.6 µm.

Mycenaceae Overeem

Notes: *Mycenaceae* belongs to the order *Agaricales*. Members of this family are saprotrophic, distributed worldwide and are found in almost all ecological zones (Cannon and Kirk 2007). Currently, 19 genera and more than 1700 species are included in this family (Kirk et al. 2008; Species Fungorum 2021). We follow the treatment and updated accounts of *Mycenaceae* in Moncalvo et al. (2002) and Matheny et al. (2006). Based on morphological

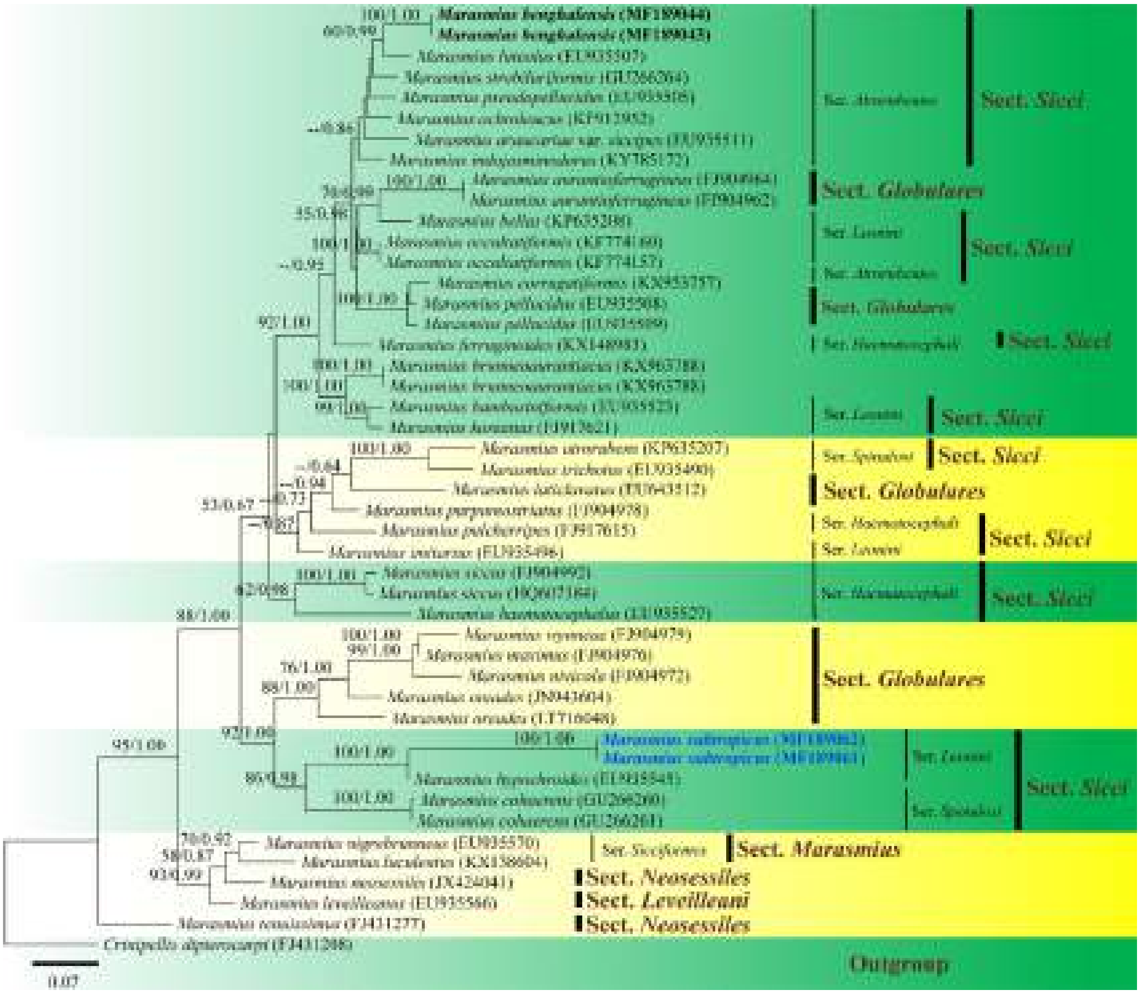


Fig. 193 Phylogram generated from maximum likelihood (ML) analysis based on nrDNA ITS sequence data of *Marasmius* species using best-fit model (HKY + G) with Bayesian Information Criterion (BIC) value of 14371.193718. Related sequences are mostly taken from Wannathes et al. (2009) and Antonín et al. (2012). Thirty-six taxa of *Marasmius* and one outgroup taxon are included in the analyses comprising 742 characters after alignment. *Crinipellis dipterocarpi* is used as the outgroup taxon following Wannathes et al. (2009). Bayesian analysis (BA) reached a standard deviation of split frequencies of 0.004984 after 10^6 generations and produced 11210 credible set of trees after discarding initial 3,792 trees as burnin phase. Tree topology of the ML analysis is similar to the BA. The best RAxML tree with a final likelihood values of 6870.939953 is presented. The matrix had 483 distinct alignment patterns, with 17.46% proportion of gaps and completely undetermined characters. Estimated base frequencies were as follows: A = 0.2461, C = 0.2043, G = 0.2006, T = 0.3490; gamma distribution shape parameter = 0.4030. ML Bootstrap values (MLBS) equal or greater than 50% (on the left of '/') and posterior probabilities (BYPP) values equal or greater than 0.50 (on the right of '/') from BA are labeled above or below the nodes. The newly generated sequences are in blue bold. Representative sections and series of the *Marasmius* taxa are marked in the right side

characteristics and phylogenetic analysis of ITS sequence data, a novel species *Cruentomycena uttarakhandina* is introduced.

Cruentomycena R.H. Petersen, Kovalenko & O.V. Morozova

Notes: *Cruentomycena* is established by Petersen et al. (2008). The genus is characterized by mycenoid or marasminoid basidiomata, viscid blood red pileus, deccurent lamellae, presence of cheilocystidia and elongated basidiospores (Petersen et al. 2008). *Cruentomycena* currently comprises three species namely, *C. kedrovayae*, *C. orientalis* and *C. viscidocruenta* (Petersen et al. 2008; Terashima et al. 2016; Species Fungorum 2021). In this study, a new species *Cruentomycena uttarakhandina* is introduced based on evidence of morphology and phylogenetic placement (Figs. 194 and 195).

Cruentomycena uttarakhandina U. Singh & R.P. Bhatt, ***sp. nov.***

Index Fungorum number: IF557839; *Facesoffungi number*: FoF 07738; Fig. 194

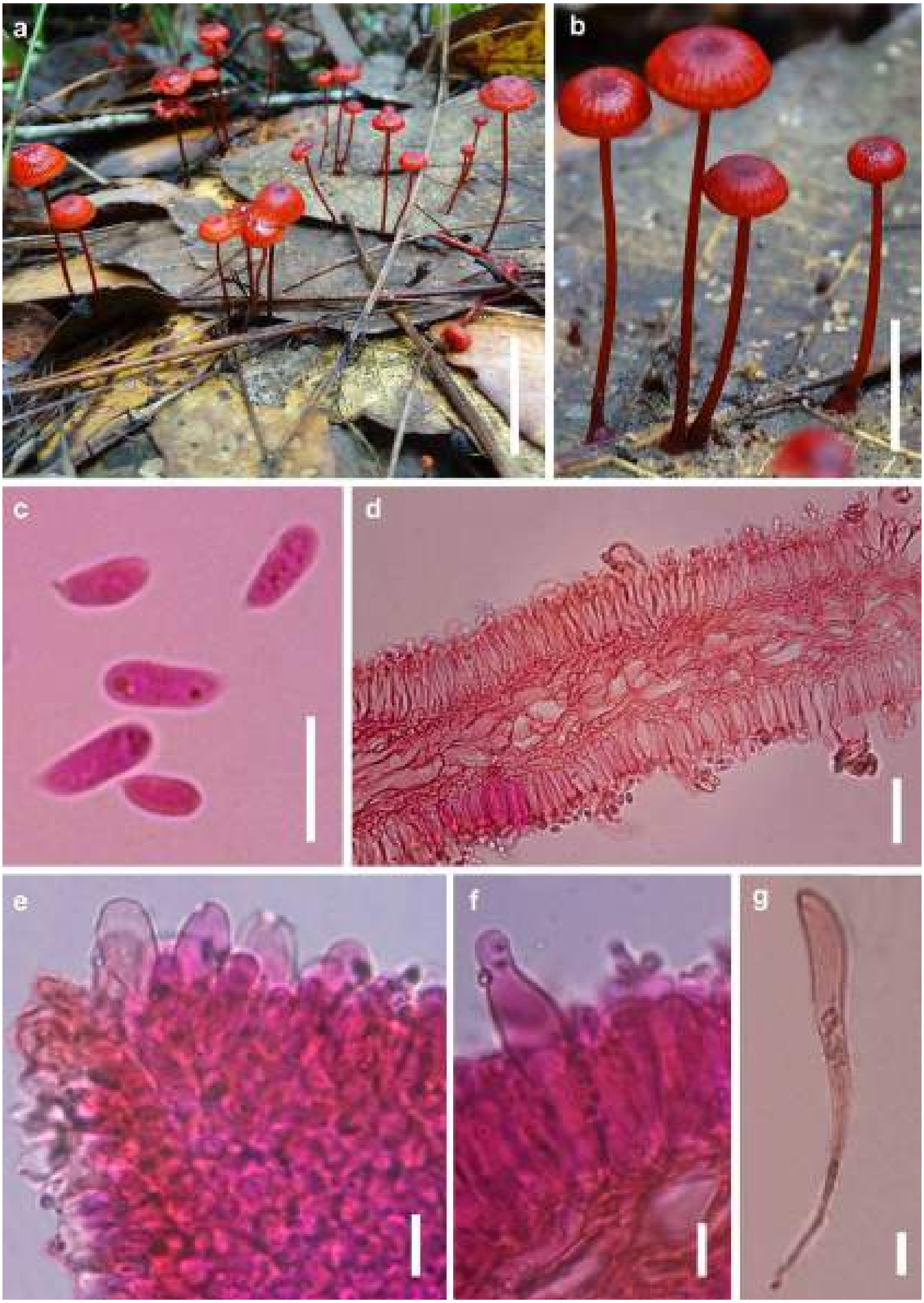


Fig. 194 ***Cruentomycena uttarakhandina*** (US 1510, **holotype**). **a** Habitat. **b** Basidiomata. **c** Basidiospores **d** Transverse section through hymenium showing basidia, pleurocystidia and lamellar trama. **e** Cheilocystidia. **f** Pleurocystidia. **g** Caulocystidia. Scale bars: **a** = 20 mm, **b** = 10 mm, **c**, **e**–**g** = 10 µm, **d** = 25 µm

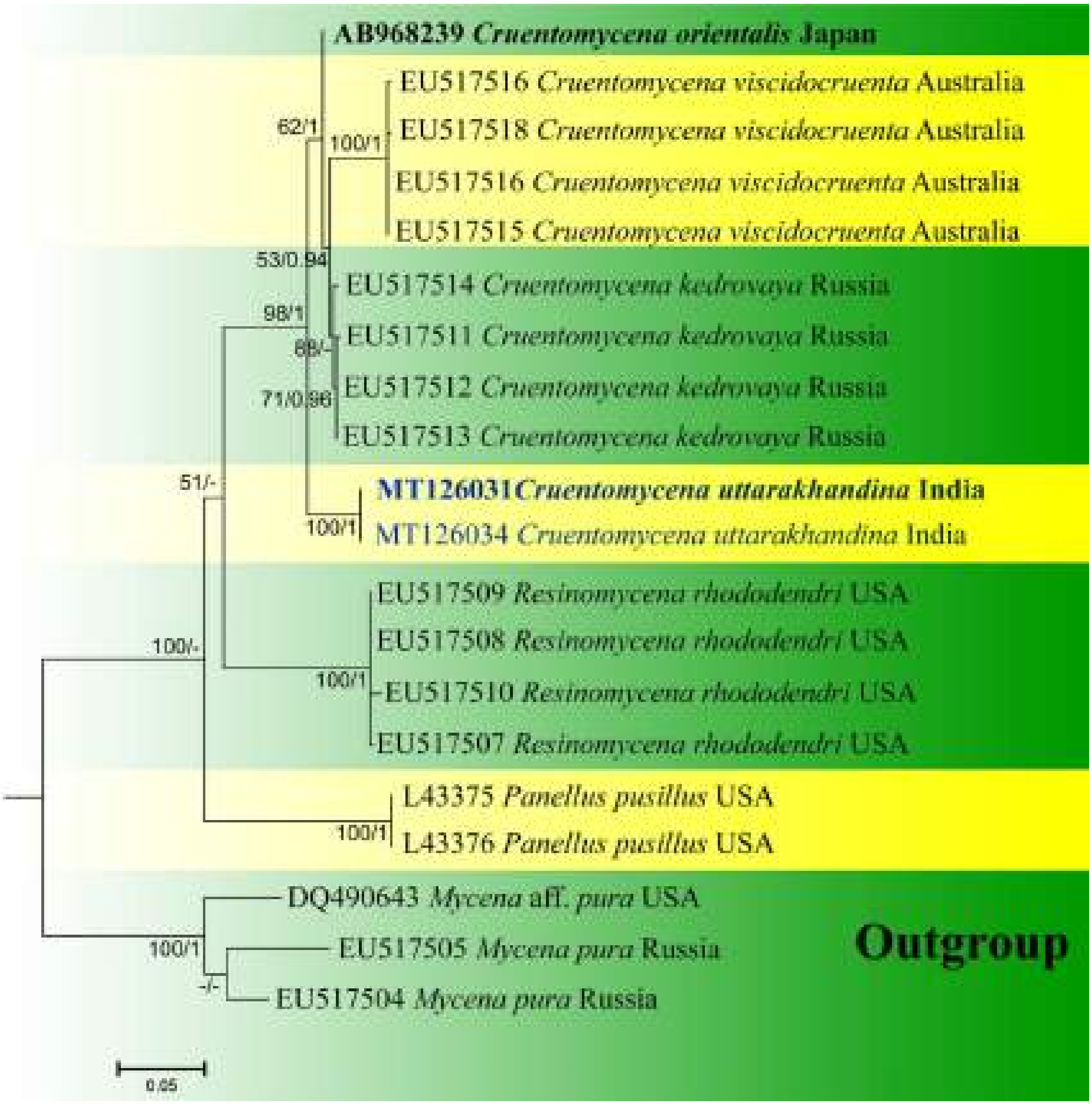


Fig. 195 Phylogenetic analyses were based on data set of nrITS sequences. Reference sequences were selected from relevant literature (Petersen et al. 2008), BLAST searches (Altschul et al. 1997) and data retrieved from GenBank (Clark et al. 2016). Species of *Mycena* are selected as the outgroup taxa (Petersen et al. 2008). Multiple sequence alignment was performed using MAFFT v.7 (Katoh and Standley 2013). Alignments were manually edited in BioEdit v 7.2.5 (Hall 1999). To change the multiple alignment format, Alignment Transformation Environment (ALTER) was used (Glez-Peña et al. 2010). Maximum Likelihood analysis was performed with the programme RAxML GUI 1.5 (Silvestro and Michalak 2012). One thousand bootstrap replicates were analysed to obtain nodal support values. Bayesian inference was computed independently twice in MrBayes v.3.2.2 (Ronquist et al. 2012), under different models. The best-fit substitution model of nucleotide evolution was carried out in MrModeltest 3.7 (Posada and Crandall 1998). Bayesian posterior probabilities (BYPP) were calculated in two simultaneous runs with Markov chain Monte Carlo (MCMC) algorithm (Larget and Simon 1999). Markov chains were run for 10 million generations, saving a tree every 100th generation. Default settings in MrBayes were used for the incremental heating scheme for the chains (3 heated and 1 cold chain), unconstrained branch length [unconstrained: exponential (10.0)] and uniformative topology (uniform) priors. The first 25% of trees was discarded as burnin (Hall 2004). Ex-type strain is in bold and newly generated sequences are in blue

Etymology: Named after Uttarakhand, from where this mushroom was collected.

Holotype: CAL 1800

Basidiomata small-sized, mycenoid, 16–42 × 2–10 mm. *Pileus* 2–10 mm in diam., convex, centrally depressed, surface viscid to glutinous when moist, maddor red (9A7) to vivid red or cinnabar red (9A8), smooth; margin entire, incurved to decurved, sulcate, concolorous; pileus context concolorous, fleshy. *Lamellae* distant, sub-decurrent, concolorous to pileus, with lamellulae in 4 series of different lengths; lamellar edges slightly lighter than lamellar face, entire. *Stipe* 14–40 × 0.5–1 mm, central, curved, equal to slightly tapered at base, slimy, concolorous to pileus, darker when handling, unchanged after bruising; stipe context concolorous, fibrous, hollow. *Taste* and *odour* indistinct. *Spore print* not obtained. *Basidiospores* 8–9.2–11 × 3–3.4–4 μm (Q = 2.25–2.69–3.14 μm, n = 30), elongated, tapering asymmetrically toward hilar appendage, smooth, hyaline in KOH, weakly amyloid. *Basidia* 20–30 × 5–7 μm, sub-clavate to clavate, thin-walled, 2- to 4- spored; sterigmata up to 5 μm long. *Pleurocystidia* 32–45 × 9–14 μm, clavate to ventricose with rounded to acute apex, emergent up to 22 μm, arising from the trama. *Cheilocystidia* 22–30 × 7–11 μm, clavate to broadly clavate. *Lamellar trama* sub-regular to irregular, of somewhat inflated cells (wide up to 48 μm). *Pileipellis* an ixocutis, composed of repent, cylindrical hyphae (wide up to 4 μm), rarely clamped; terminal hyphae 34–39 × 3–4 μm, cylindrical with rounded apex; *Pileus trama* composed of inflated hyphae up to 34 μm wide, thin-walled. *Stipitipellis* an ixocutis, with parallel hyphae, thin-walled, up to 6 μm wide. *Caulocystidia* 52–79 × 7–10 μm, thin-walled, subcylindrical with tapered base.

Material examined: INDIA, Uttarakhand, Pauri district, Chaurikhal, growing solitary to gregarious, on leaf litters under *Quercus* sp. in mixed forest, 1981 msl, N30°02.389′ E079°03.406′, 1 August 2017, U. Singh, US 1510 (CAL 1800, **holotype**); Phedkhal, 1913 msl, N30°09.697′ E078°51.195′, 24 August 2018, U. Singh, US 1667 (CAL 1801, paratype).

GenBank numbers: ITS = MT126031 (holotype), MT126034 (paratype).

Notes: *Cruentomycena uttarakhandina* can easily be characterized by its small size, red colour basidiomata with viscid to glutinous pileus, distant lamellae with lamellulae in 4 series of different lengths, thin stipe, elongated basidiospores, clavate to sub-clavate basidia, clavate to ventricose pleurocystidia, clavate to broadly clavate cheilocystidia, subregular to irregular lamellar trama, an ixocutis pileipellis without pilocystidia and an ixocutis stipitipellis with subcylindrical caulocystidia (Fig. 194).

Cruentomycena kedrovayae, *C. viscidocruenta* and *C. orientalis* may appear similar to *C. uttarakhandina* in terms of their small-size and red colour basidiomata. However, these three species all show morphological differences from *C. uttarakhandina*. *Cruentomycena kedrovayae* differs from present species by plane to subinfundibuliform pileus, thick (almost fold-like) lamellae, smaller stipe (8–13 × 0.5–0.8 mm), ellipsoid and smaller basidiospores (6–8(–9) × 3.5–4 μm), and absence of pleurocystidia (Petersen et al. 2008). *Cruentomycena viscidocruenta* is distinguished from *C. uttarakhandina* by larger pileus (4–11(–14) mm broad), subdistant lamellae, smaller stipe (6–25 mm long, 0.4–1 mm broad), slightly smaller basidiospores [(6.5–)8–10 × (2.5–)3–4.5 μm] and absence of pleurocystidia (Petersen et al. 2008). *Cruentomycena orientalis* distinctively differs from *C. uttarakhandina* by its smaller pileus (4–8 mm diam.), sub-distant lamellae, smaller stipe (15–35 × 0.7–1 mm), smaller and ellipsoid to oblong-ellipsoid basidiospores [(7.1–)7.9–9(–10.5) × (3.5–)3.8–4.3(–5.1) μm] and absence of pleurocystidia (Terashima et al. 2016).

The ITS dataset consisting of 20 sequences (including our isolates: US 1510, represented by GenBank acc. no. MT126031 and US 1667, represented by GenBank acc. no. MT126034) of *Cruentomycena, Resinomycena, Panellus* and *Mycena* were analysed. Our isolated sequences were recovered as a distinct taxon (marked with blue font) in a strongly supported (98% MLBS, 1.00 BYPP; Fig. 195) clade and clustered with other species of *Cruentomycena*. The combination of morphological features and phylogenetic analysis corroborates the proposed taxon *Cruentomycena uttarakhandina* as a new species being distinct from all the known taxa of *Cruentomycena*.

Nidulariaceae Dumort.

Notes: Species of *Nidulariaceae* are saprobic, growing on decomposing organic matter, on decaying wood and in soils enriched with wood chips or bark mulch; they have a widespread distribution in most ecological regions. Five genera, *Crucibulum*, *Cyathus*, *Mycocalia*, *Nidula* and *Nidularia*. These are distinguished from each other by differences in morphology and peridiole structures. In this study, phylogenetic analysis and comparison of DNA sequences reveal a new species, *Cyathus uniperidiolus* in *Cyathus*, *Nidulariaceae*.

Cyathus Haller

Notes: *Cyathus* was established by von Haller (1768) and is typified by *Cyathus striatus* (Huds.) Willd. The genus is characterized by having deeper or fluted, inverted bell-like fruiting bodies which is covered with shaggy or tomentose hairs on the outside. The inside peridium are filled with a number of small, hard lentil-shaped structures (peridioles) attached with flexible thread-like cords (funiculus). The peridioles bear basidiospores, that are hyaline, smooth or thick-walled and variable in shape and size (Lloyd 1906; Brodie 1975; Miller and Miller 1988).

Cyathus uniperidiolus P.N. Singh & S.K. Singh, ***sp. nov.***

Index Fungorum number: IF556766; *Facesoffungi number*: FoF 06586; Fig. 196

Etymology: specific epithet ‘*uniperidiolus*’ refers to single peridiole in basidiocarp.

Holotype: AMH10196

Colour codes follow: Methuen Handbook of Colour (Kornerup and Wanscher 1978).

Saprobic on dead bamboo grass of *Muhlenbergia* in a terrestrial habitat. **Asexual morph** Undetermined. **Sexual**

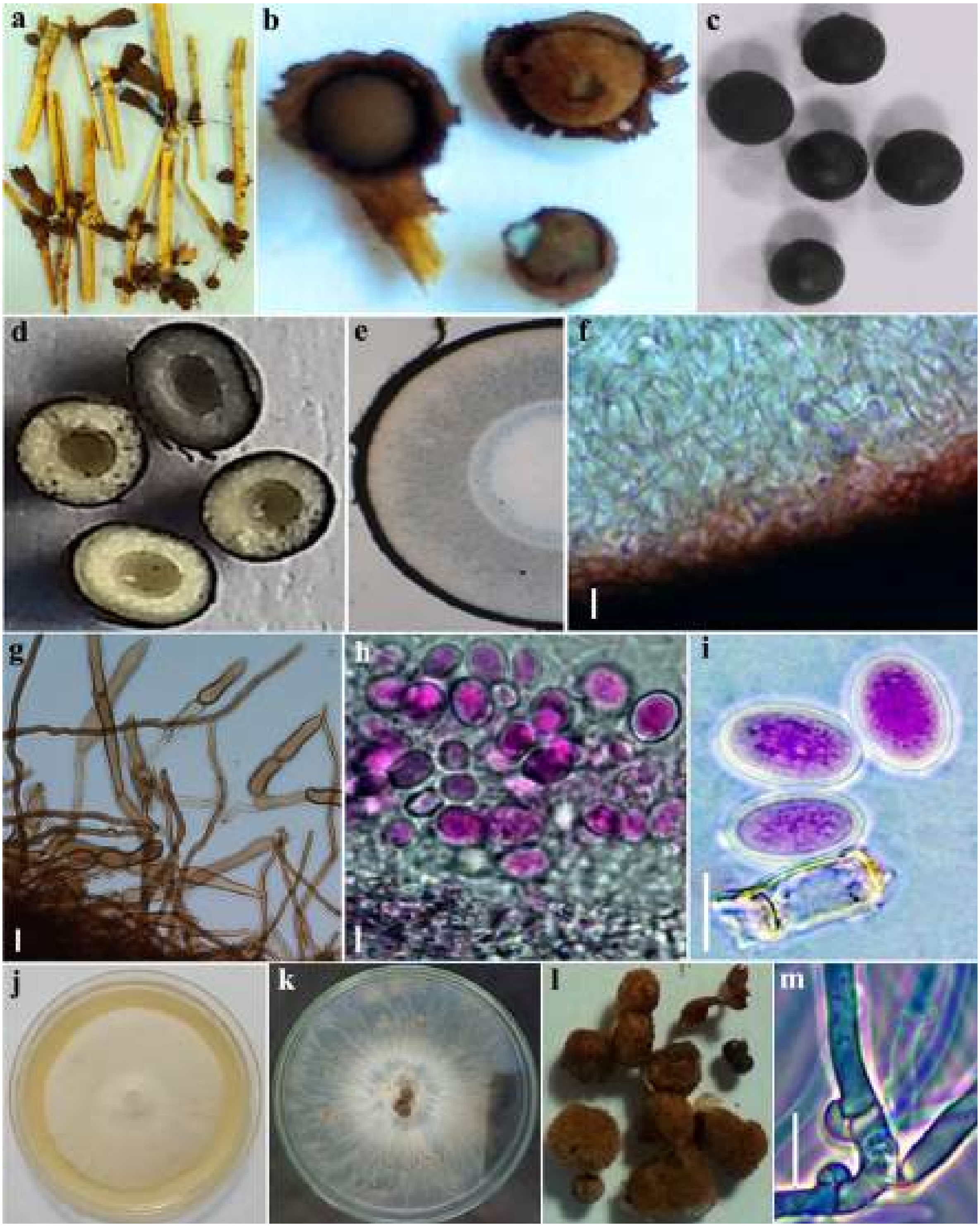


Fig. 196 ***Cyathus uniperidiolus*** (AMH-10196, **holotype**, NFCCI-4697 **ex-type culture**). **a** Substrate (stem of *Muhlenbergia* sp. with attached basidiocarps). **b** Basidiocarps bearing single globose peridiole. **c** Globose peridioles with shiny surfaces. **d** Sections of peridioles showing emptied cavity inside. **e** Transverse section of basidiocarp showing different layers, innermost region showed emptied. **f** Transverse section of peridiole showing layer of cortex and sub-cortex (a part view). **g** Terminal and subterminal thick-walled encrusted loose and interwoven cells of basidiocarp. **h** Hymenial layer with hyphae and basidiospores. **i** Enlarged view of basidiospores. **j** Colony morphology on MEA (front view). **k** Colony with developing basidiocarps. **l** Harvested basidiocarps with velvety surfaces from culture. **m** Hyphae with clamps. Scale bars: **f**–**i**, **m** = 10 µm

morph *Basidiocarp* (peridia) are of two types viz. globose to sub-globose, like small cannon balls, abundant and rarely fluted/deeper, sessile to short stalked, attached to substrate with brownish bulging pad, dark brown 2–12 mm high and 2–3.5 mm wide at mouth with serrate margin. *Exterior wall* of the peridium dark brown (6F8), with slightly velvety surfaces, non-plicate. *Interior wall* of the peridium, dark brown (6F8), nonplicate, smooth walled. *Peridial wall* up to 78 µm thick, made up of terminal and subterminal thick and thin encrusted cells of peridial hairs, 2.7–7.15 µm wide. *Peridioles*, produced singly in each basidiocarp, sessile (funicular cord hard to observe), globose, resembling small cannonballs, hard, smooth, black with shiny surfaces, 2–2.5 mm diam. Transverse section of peridiole showed four layered: cortex, subcortex, hymenium and innermost layer is emptied. *Cortex* thick and black, compact, hard to observe the cells, up to 103.5 µm thick. *Subcortex* layer is made up of compact pseudoparenchymatous cells, light olivaceous to subhyaline, up to 642.7 µm thick. *Hymenium* (fertile layer) up to 275.9 µm thick composed of hyaline hyphae and spore mass, the fourth inner layer is emptied as in coconut. *Basidiopores* broadly ellipsoid to ellipsoid-elongate, rarely oval to sub-globose, thick and smooth walled, hyaline, amyloid, 14.2–28.7 × 11.7–23.7 µm ($\bar{x}$ = 21.8 × 16 µm, n = 30).

Culture characteristics: on MEA (Malt Extract Agar), fast growing, floccose, white (1A1), 61 × 61 µm diam. in 8 days at 25 °C, margin irregular, reverse pale yellow (3A3). Exudates produced in the form of droplets, yellow. *Hyphae* septate, branched, clamped, smooth walled, sub hyaline to light olivaceous, 2.1–7 µm wide. Globose to sub-globose yellowish brown (5E8) basidiocarps produced abundantly which bears single globose black peridiole in each basidiocarp which was entirely covered with thin velvety peridial wall.

Material examined: INDIA, Maharashtra, Pune District, dead stem of *Muhlenbergia* sp (*Poaceae*), 30 August 2017, P.N. Singh (AMH 10196, **holotype**), ex-type living culture (NFCCI 4697), National Fungal Culture Collection of India (WDCM932).

GenBank Numbers: ITS = MN398297, LSU = MN398298.

Notes: The present taxon was isolated in pure cultures from the basidiocarp associated with dead stem of *Muhlenbergia* sp. (Bamboo grass). The macro and micromorphological characters such as basidiocarp and peridioles, multi-layered peridiolar wall, and globose blackish peridioles, broadly ellipsoid to ellipsoid-elongate, hyaline, smooth-walled basidiospores (Fig. 196), place this taxon under *Cyathus* (von Haller 1768; Baseia and Milanez 2001). Present species is distinct from its allied taxa in having unique shape of peridia and peridioles i.e., globose, small cannon ball-like, produced abundantly, deeper or fluted, are rarely produced. These characteristic features clearly separate present taxon from allied *Cythus* spp., viz. *C. albinus*, *C. badius*, *C. renweii*, *C. poeppigii*, *C. thindii* and *C. striatus* (type species) (Table 5) (von Willdenow 1787; Tulasne and Tulasne 1844; Kobayasi 1937; Zhou et al. 2004; Cruz et al. 2014, 2018; Das et al. 2015; Accioly et al. 2018). As such these are the distinct and unique features of the proposed species. The other morphological features are also compared in Table 5. The phylogenetic analysis reveals that *C. uniperidiolus* forms a distinct sister clade with *C. badius* which is statistically supported (Fig. 197). From morphological data and sequence analyses it is evident that *C. uniperidiolus* is distinct from all other species in the genus. Therefore, *Cyathus uniperidiolus* is described and illustrated here as a new species.

Omphalotaceae Bresinsky

Notes: The latest update accounts of *Omphalotaceae* see Haelewaters et al. (2020).

Marasmiellus Murrill

Notes: *Marasmiellus* is widely distributed throughout tropical and subtropical areas (Wilson and Desjardin 2005; Kirk et al. 2008). This genus is saprotrophic and rarely grows on living trees. *Marasmiellus* was previously assigned to *Tricholomataceae* (Singer 1986) but was later transferred to the *Marasmiaceae* (Kirk et al. 2008). However, phylogenetic analysis of ITS and nrLSU showed that it belonged to the *Omphalotaceae* (Moncalvo et al. 2002; Wilson and Desjardin 2005). *Marasmiellus* is characterized by basidiomes that are marasmioid-collybioid, collybioid-mycenoid or sometimes pleurotoid. Basidiomes are mostly whitish or occasionally

Table 5 Morphological comparison of *Cyathus uniperidiolus* with some allied taxa

Morpho-logical features	*C. albinus* Accioly et al. 2018	*C. badius* Kobayasi 1937	*C. renweii* Zhou et al. 2004	*C. poeppigii* Tulasne and Tulasne 1844	*C. thindii* Das et al. 2015	*C. uniperidi-olus* sp. nov., in this study
Basidiocarps	6–8.5 mm high, 5–6.5 mm wide	4.5–9 mm high, 4–6 mm wide	8–10 mm high, 5–6 mm wide	6–8 mm high, 4–6 mm wide	7–9.5 mm high, 5–9 mm wide	2–12 mm high, 2–3.5 mm wide
Peridioles	2.1–2.6 × 1.8 –2.2 mm	2 × 1.5–2 mm	2 mm	2–2.5 mm	1.5–3 mm	2–2.5 mm
Basidiospores	14.8–20 × 10.4–14.3 µm	14–20 × 11–15 µm	21–31 × 10.5–13 µm	25–47 × 15–24 µm	10–16 × 7–10 µm	14 –29 × 11.5–24 µm

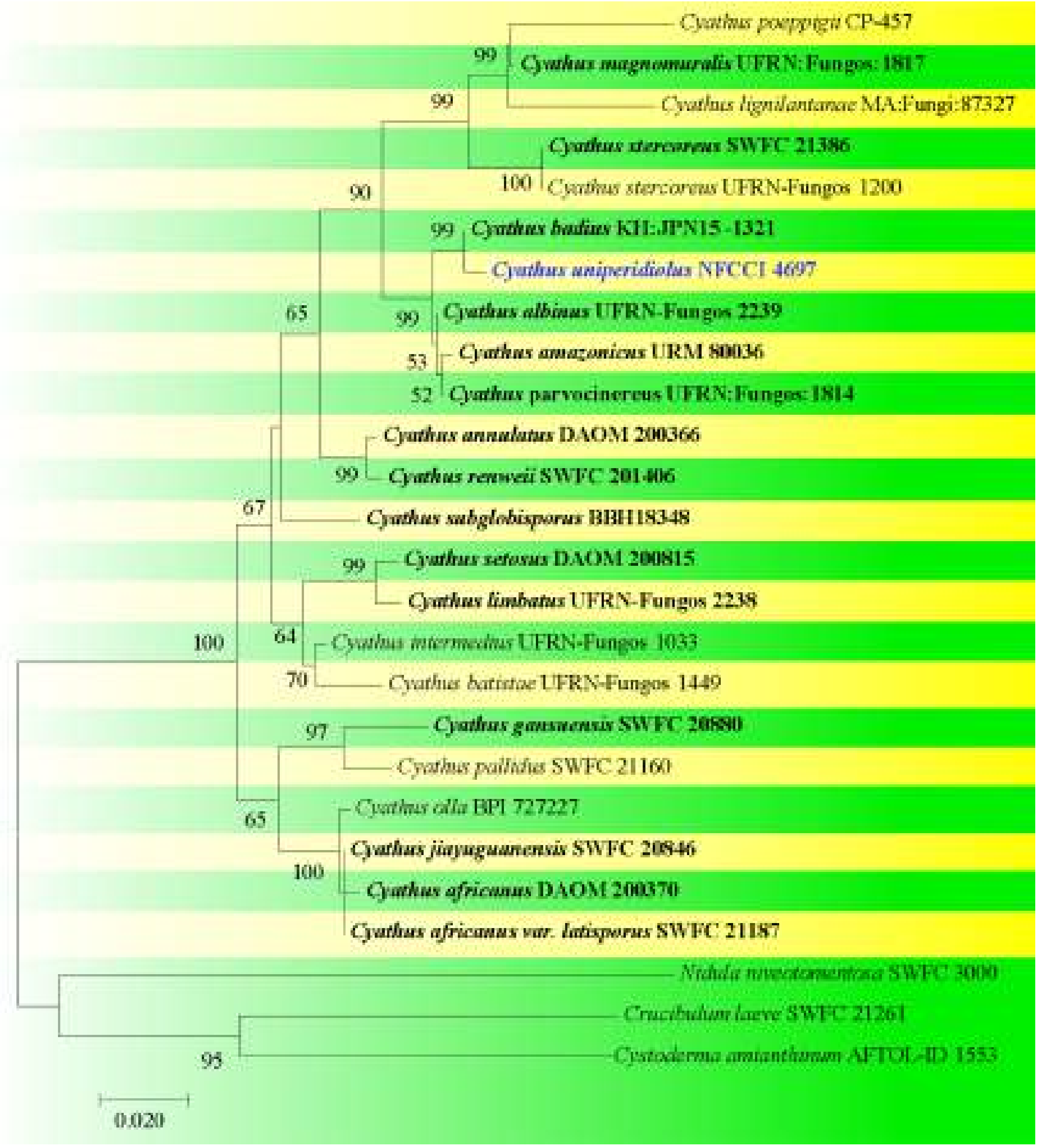


Fig. 197 Phylogram generated from maximum likelihood analysis for *Cyathus uniperidiolus* (NFCCI: 4697) using combined ITS and LSU sequence data based on the General Time Reversible model (Nei and Kumar 2000). A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 0.2814)). Bootstrap support values are indicated at the nodes and values below 50% are not shown. Phylogenetics analyses were conducted in MEGA7 (Kumar et al. 2016). *Nidula niveotomentosa* SWFC 3000, *Crucibulum leave* SWFC 21,261 and *Cystoderma amianthinum* AFTOL-ID 1553 were used as outgroup. Type specimens are in bold and newly sequence is in blue

grayish, reddish brown or dark brown in colour with ellipsoid basidiospores and hyphae having clamp connections (Singer 1973; Moncalvo et al. 2002). There are more than 400 taxa listed in Species Fungorum (2021) for this genus.

Marasmiellus palmivorus (Sharples) Desjardin, Mycologia 97: 670 (2005)

Index Fungorum number: IF613706; *Facesoffungi number*: FoF 09970; Fig. 198

≡ *Marasmius palmivorus* Sharples, Malay. agric. Journal 16(nos 9–10): [1] (1928).

Pileus 10–25 mm in diam., hemispherical to convex, expanding to plano-convex, in age depressed to subumbilicate; margin initially smooth, soon striate to sulcate or

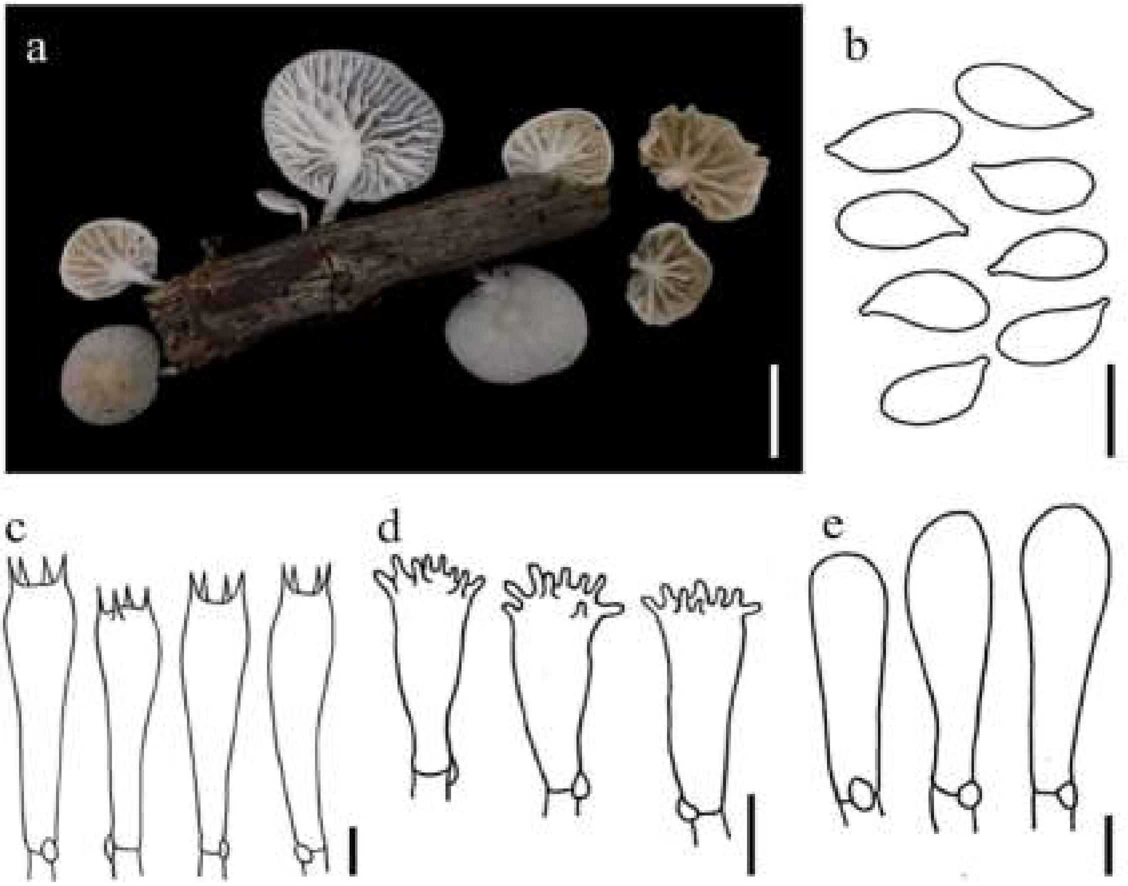


Fig. 198 ***Marasmiellus palmivorus*** (SDBR-CMU-NK076, **new record**). **a** Basidiomata. **b** Basidiospores. **c** Basidia. **d** Cheilocystidia. **e** Caulocystidia. Scale bars: **a** = 1 cm, **b**–**e** = 10 µm

rugulose-striate, sometimes wavy or cleft; surface dull, moist to dry, glabrous to felted or radially appressed-fibrillose, subhygrophanous; when young white (4A1) to pale yellow (4A2) or more commonly orange white (6A2), in age retaining pinkish white (7A2) or light orange (6A4) tones on the disc. *Context* up to 1 mm thick, soft, pliant, white (4A1). Lamellae horizontal, adnate, distant with 1–3 series of lamellulae, often intervenose in age, rarely forked, broad (2–4 mm), white (4A1), sometimes discoloring pinkish white (7A2) or light orange (6A4). *Stipe* 1.5–7 × 1–1.5 mm, central to eccentric, terete, cylindrical, base often enlarged, curved, solid, tough, subinsititious or arising from a pad of appressed white to pale orange mycelium; surface dull, dry, glabrous or minutely silky-pruinose, at first white overall, base darkening in age to greyish red (7B3), reddish orange (7B6–7B7) or reddish brown (8F5); often with fan-like white mycelium over substrate. *Odour* not distinctive. *Basidiospores* 8–12 × 4.5–6 µm, Q = 1.7–2.3, $Q_m = 1.95 \pm 0.1$, ellipsoid, smooth, hyaline, inamyloid, thin-walled. *Basidia* 20–34 × 6–10 µm, clavate, 2 to 4-spored. *Pleurocystidia* absent. *Cheilocystidia* 17.5–24 × 8–12 µm, clavate with numerous apical setulae, hyaline, inamyloid, thin-walled; setulae 1.5–3.5 × 1–3.2 µm, irregularly cylindrical or knob-like, sometimes forked, obtuse to acute, hyaline. *Pileipellis* a cutis of loosely interwoven, repent hyphae, not a hymeniform layer, not a Rameales-structure; hyphae 4–12 µm in diameter, cylindrical, non-diverticulate, smooth or incrusted with annular to helical hyaline or yellow pigments; walls hyaline, inamyloid, non-dextrinoid, non-gelatinous; thin-walled; terminal cells undifferentiated, cylindrical. *Pileus trama* interwoven, lamellar trama regular; hyphae 3–15 µm in diameter, cylindrical or inflated, smooth, hyaline, inamyloid, non-dextrinoid, non-gelatinous, thin-walled or with walls up to 1 µm thick. *Stipe trama* 3–6.5 µm in diameter, cylindrical, parallel, non-diverticulate, smooth, hyaline, inamyloid, non-dextrinoid, non-gelatinous, thin-walled; medullary hyphae similar but many fusoid, up to 20 µm in diameter, some with walls up to 1 µm thick. *Caulocystidia* scattered, 25–30 × 5–8.5 µm, cylindrical to clavate or fusoid, non-diverticulate, hyaline, thin-walled. *Clamp connections* present in all tissue type.

Habitat: scattered on rotten coconut palm wood or fruits, on leaves and stems of banana and *Lagerstroemia* tree, or on undetermined woody debris in coastal coconut groves and banana-cacao groves.

Distribution: Known from Africa (São Tomé), India, Indonesia (Java), Malaysia, Taiwan, Thailand and USA (Hawaiian Islands) (Wilson and Desjardin 2005; Desjardin and Perry 2017; Dutta and Achaya 2018; Pham et al. 2019).

Material examined: THAILAND, Chiang Mai Province, Muang District, Chiang Mai University, 18°48′10″ N 98°57′23″ E, 334 msl, 15 June 2018, on the rotten wood, J. Kumla and N. Suwannarach, SDBR-CMU-NK076 (**new record**).

GenBank numbers: ITS = MW647877, LSU = MW647892.

Notes: *Marasmiellus palmivorus* is characterized by small to moderate-sized basidiomes with white or pink to orange striate, plano-convex pileus that fade to white with age and possess distant, occasionally intervenose white lamellae (Fig. 198). They also have a central to eccentric white stipe that becomes reddish orange to reddish brown at the base, ellipsoid basidiospores, clavate cheilocystidia with apical setulae, a cutis-type pileipellis of non-diverticulate hyphae, clavate and thin-walled caulocystidia. *Marasmiellus palmivorus* is similar to *Collybia purpureogrisea*, which was originally described as *M. purpureogriseus*. However, *C. purpureogrisea* differs by the presence of its non-striate pileus and has a longer stipe (up to 4 cm long). Basidiome is brownish-white, sub-close to crowded lamellae and displays the presence of a rameales structure in the pileipellis (Petch 1947; Manimohan and Leelavathy 1989). Phylogenetic analysis of the combined ITS and LSU regions indicates that our strain of *M. palmivorus* clusters with other strains in a strongly supported subclade (100% MLBS, 1.00 BYPP; Fig. 199).

Psathyrellaceae Vilgalys, Moncalvo & Redhead

Notes: *Psathyrellaceae* was proposed by Redhead et al. (2001) based on molecular phylogenetic studies which circumscribed by *Psathyrella* and *Lacrymaria*, together with related species in the polyphyletic genus *Coprinus* sensu lato, which were transferred to the genera *Coprinellus*, *Coprinopsis* or *Parasola*. Afterwards, several other genera were included in *Psathyrellaceae* and Kirk et al. (2008) consider that this family comprises 12 genera.

Coprinellus P. Karst.

Notes: *Coprinellus*, consists of approximately 85 described species, characterized by independent lineages in *Psathyrellaceae* (Redhead et al. 2001; Walther et al. 2005; Padamsee et al. 2008; Vašutová et al. 2008; Nagy et al. 2011, 2012, 2013; Örstadius et al. 2015; Hussain et al. 2018). Mushrooms belonging to *Coprienllus* are common saprotrophs and are divided into three major sections on the basis of veil anatomy and the presence or absence of pileocystidia. Section Domestici (Singer) D.J. Schaf. is characterized by the veil on the pileus in the form of floccose scales, fusiform or subglobose cells in the form of chains. Section Micacei (Fr.) D.J. Schaf., is represented by presence of veil remnants in the form of scattered, granulose flocks, consisting of globose cells. Section Setulosi (J. Lange) D.J. Schaf., featured by the presence or absence of the veil on pileus, but the pileus and stipe are covered with thin-walled pileocystidia and caulocystidia, respectively (Schafer 2010). However, Nagy et al. (2012) found that these sections were not entirely consistent with the molecular phylogeny, in particular because clades corresponding to sections, Micacei and Domestici, each included some setulosi species.

Coprinellus punjabensis Usman & Khalid ***sp. nov.***

Index Fungorum number: IF557381; *Facesoffungi number*: FoF 07848; Fig. 200

Etymology: Named after Punjab Province, where this fungus was collected.

Holotype: LAH35321

The most important features of *Coprinellus punjabensis*: *Pileus* cylindrical to campanulate, white greyish, plicate from center to margins. *Basidiospores* 7.3–9 × 4.3–5.2 µm ellipsoid to amygdaliform, brown to blackish, germ pore central up to 1.2 µm, with truncate base. *Veil elements* globose to sub globose hyaline cells up to 45 µm. *Macroscopic characters*: *Pileus* 5 – 12 mm diam., cylindrical when young campanulate at maturity, white to light greyish (2.5Y 7/4), surface pruinose, plicate toward margin, edges striate to plicate. *Lamellae* sinuate to uncinate, distant with 1–3 lamellulae, dark greyish-brown. *Stipe* 25 – 40 µm in length, equal, central, light greyish and white near base, hollow, surface pruinose to pulverulent. *Annulus* absent. *Odour* and taste not recorded. *Microscopic characters*: *Basidiospores* (7–)7.3–9(–9.3) × (4–)4.3–5.2(–5.6) µm, ($\bar{x}$ = 8 × 4.8 µm, n = 50), Q = 1.68; in face view, ellipsoid, in side view, amygdaliform, dark brown to blackish (5YR 3/1), in KOH, smooth, thick-walled, apex truncate, germ-pore central, up to 1.2 µm wide. *Basidia* 20 – 30 × 5.8 – 8.4 µm, cylindrical to clavate, hyaline with 2 – 4 strigmata up to 6 µm. *Cheilocystidia* and *pleurocystidia* absent. *Pileipellis* consist of irregular epithelium, arranged by globose to sub-globose cells, 8 – 30 × 10 – 25 µm, hyaline and smooth. *Stipitipellis* 3–10 µm diam., regular, septate and clamp connections not observed. *Veil elements* up to 45 µm, globose to sub-globose, smooth and hyaline.

Habitat and distribution: Solitary to gregarious on moist soil, rich in leaf litter under trees of *Acacia modesta* Wall.

Material examined: PAKISTAN, Punjab, Pabbi Forest Park, (32°49′52.94″ N 73°50′12.04″ E,) 286 msl, 11 August 2016, M. Usman and A.N. Khalid, MU30 (LAH35321, **holotype**). PAKISTAN, Punjab, Pabbi Forest Park, (32°49′51.30″

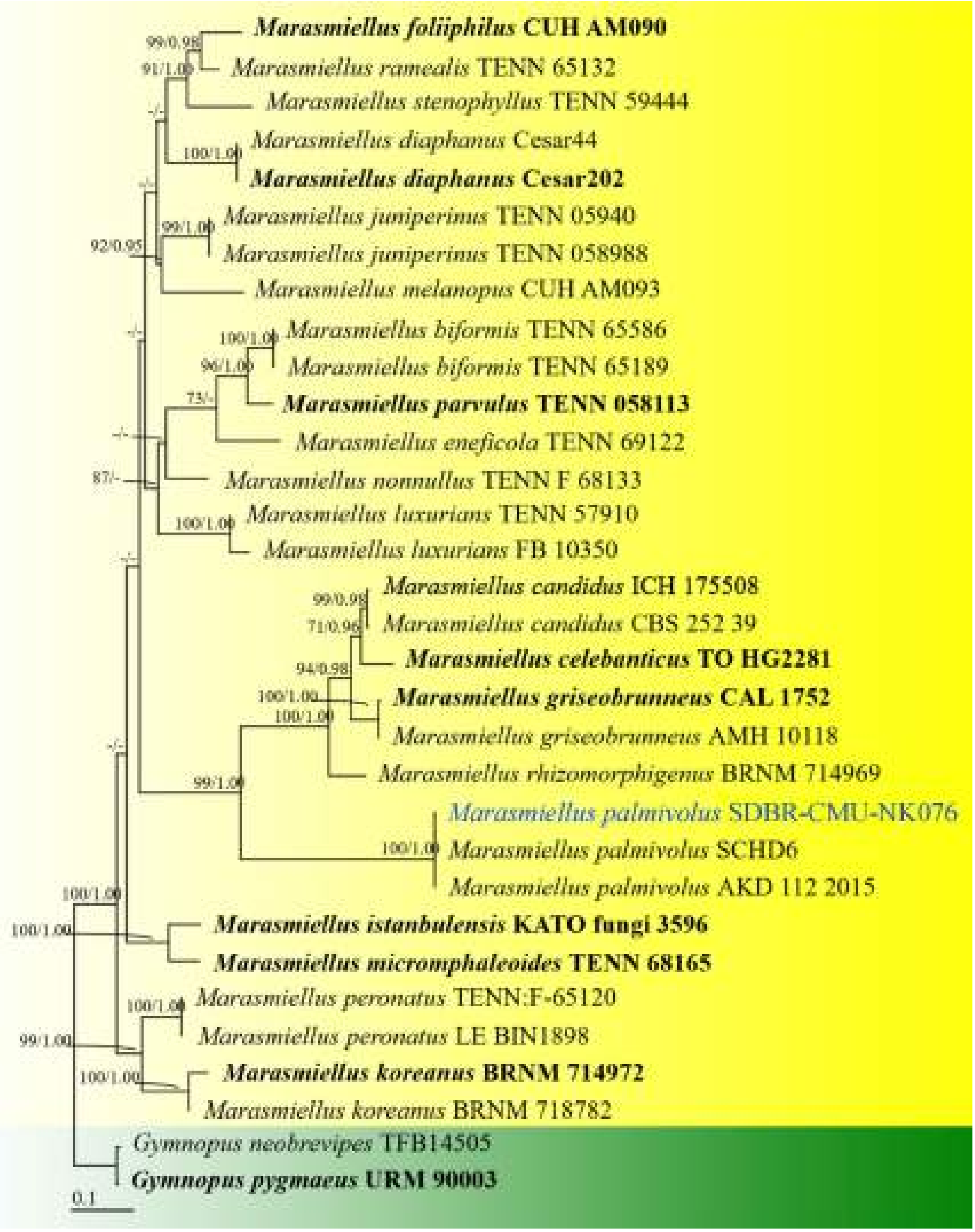


Fig. 199 Phylogenetic tree derived from maximum likelihood analysis of a combined ITS, and LSU genes of 22 sequences and the aligned dataset was comprised of 2070 characters including gaps (ITS: 1–1120 and LSU: 1121–2070). The average standard deviation of the split frequencies of the BI analysis was 0.00731. A best scoring RAxML tree was established with a final ML optimization likelihood value of − 10104.6944. The matrix had 806 distinct alignment patterns with 56.72% undetermined characters or gaps. Estimated base frequencies were found to be: A = 0.2519, C = 0.1827, G = 0.2462, T = 0.3193; substitution rates AC = 1.0427, AG = 3.9637, AT = 1.7229, CG = 0.7530, CT = 4.8493, GT = 1.0000; proportion of invariable sites = 0.0510 and gamma distribution = 0.4750. *Gymnopus nebrevipes* TFB14505 and *Gynnopus pygmaeus* URM90003 were used as outgroup. Numbers above branches are the bootstrap statistics percentages equal to or greater than 70% (MLBS, left) and Bayesian posterior probabilities equal to or greater than 0.95 (BYPP, right). Ex-type strains are in bold and newly generated sequence is in blue

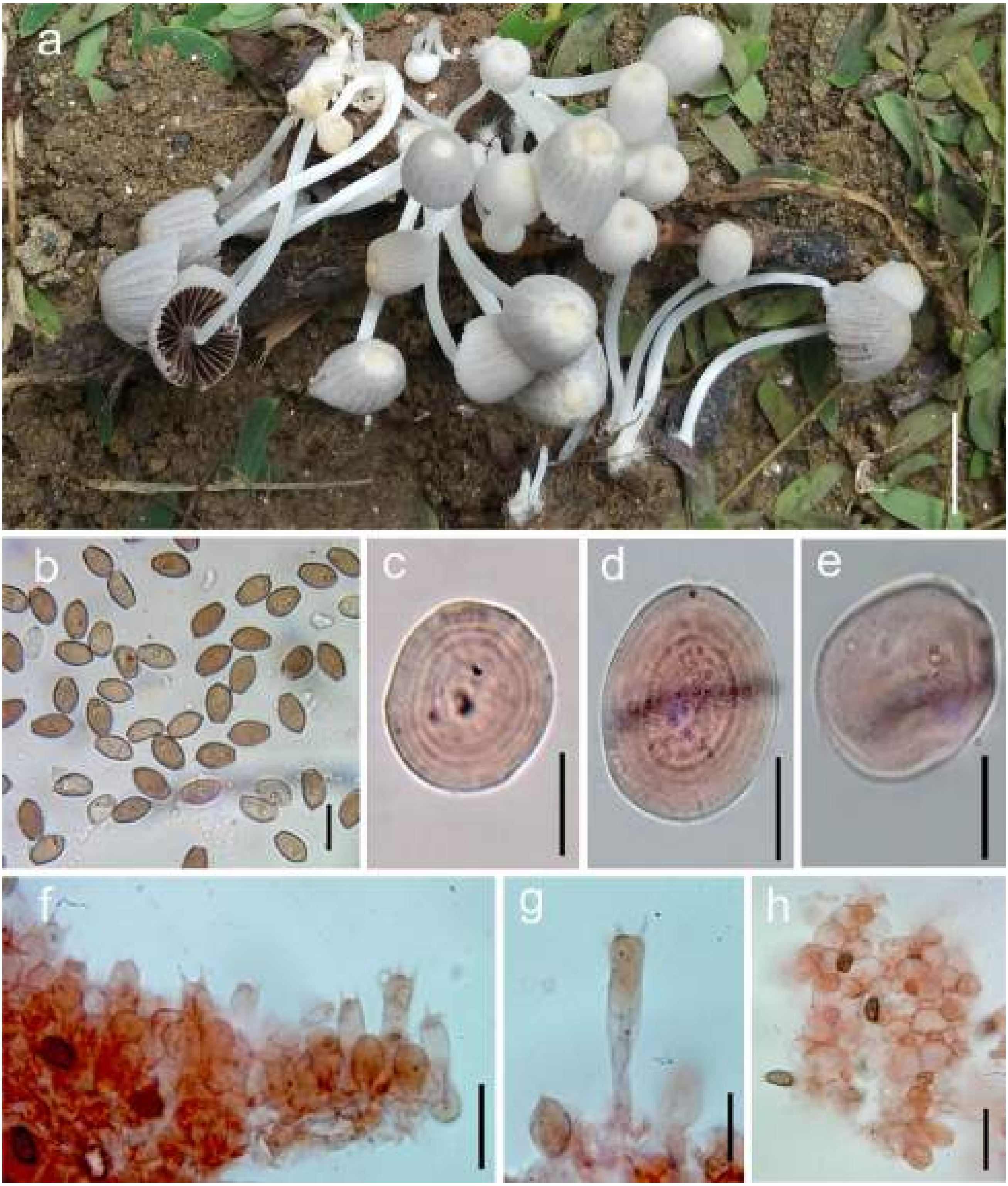


Fig. 200 ***Coprinellus punjabensis*** (LAH35321, **holotype**). **a** Fresh basidiomata. **b** Basidiospores. **c–e** Veil elements. **f** Hymenium having immature and mature basidia. **g** A mature basidium with sharp strigmata. **h** Pileipellis. Microscopic structures were captured after stain with Congo red. Scale bars: **a** = 10 mm, **b = 10** µm, **c**–**g** = 20 µm, **h** = 15 µm

N 73°50′16.24″ E,) 288 msl, 26 July 2017, M. Usman and A. Hameed, MU58 (LAH36392).

GenBank numbers: ITS = MT180990, MT180991.

Notes: Closely related species, including *Coprinellus disseminatisimilis* Hussain mostly resemble *C. punjabensis* (Fig. 200) in having cylindrical to campanulate pileus, length of cylindrical stipe 20–40 µm, absence of annulus, ellipsoid to amygdamliform dark brownish basidiospores and hyaline cylindrical to clavate basidia (Hussain et al. 2018). *Coprinellus disseminatus* also resemble with our taxon in having whitish grey cylindrical stipe, lamellulae 0–3, globose to subglobose veil elements up to 40 µm (Uljé 2005). However, *C. punjabensis* differs from *C. disseminatisimilis* in smaller size of white greyish pileus up to 12 mm diam., lamellulae 0–3, pileipellis irregular epithelium, veil elements hyaline globose to sub-globose up to 45 µm while *C. disseminatisimilis* has larger greyish-brown to greyish-yellowish-brown pileus (15–20 µm diam.), lamellulae 0–2, pileipellis light brown to hyaline loosely euhymenoderm, veil elements greyish brown up to 40 µm (Hussian et al. 2018). *Coprinellus disseminates* also differs from *C. punjabensis* in having larger pale-brown to yellow–brown, sometime almost white conical to convex pileus (up to 20 µm diam.), ovoid to obconical red dark brown basidiospores (Uljé 2005). Furthermore, phylogenetic analyses indicate that *C. punjabensis* forms a basal lineage in the clade with 100% MLBS support (Fig. 201). To provide the recommendation to justify our new species, we follow Hussain et al. (2018). Comparison of 625 nucleotides of the ITS sequences between *C. punjabensis* (MT180990) and *C. disseminatisimilis* (MH753670) reveals 32 substitutions and 6 deletions in our taxon (6.08% nucleotide difference) while comparison of 643 nucleotides of ITS sequences between *C. punjabensis* (MT180990) and *C. disseminates* (JN159560) reveals 23 substitutions and 27 deletions in our taxon (7.77% nucleotide differences), which we believe should be sufficient to delineate our new species.

Geastrales K. Hosaka & Castellano

Notes: The latest update accounts of *Geastrales* see Wijayawardene et al. (2020).

Geastraceae Corda

Notes: *Geastraceae* [as *Geastrideae*] was proposed by Corda (1842) with *Geastrum* Pers. [as *Geaster* P. Micheli] as the generic type. Currently two genera are accepted in *Geastraceae*: *Geastrum* and *Myriostoma*. Traditionally, these genera have been considered close to puffballs (e.g., *Bovista*, *Calvatia* and *Lycoperdon*) in the obsolete class Gasteromycetes in the obsolete order *Lycoperdales*. Hibbett et al. (1997) based on molecular analyses, placed puffballs in the euagaric groups; while *Geastrum* is phylogenetically far in the gomphoid-phalloid clade, together with *Sphaerobolus*. Later, Hosaka et al. (2006) proposed the new order *Geastrales* (Phallomycetidae) to include four families: *Geastraceae*, *Pyrenogastraceae*, *Sphaerobolaceae* and *Sclerogastraceae*. Jeppson et al. (2013) followed this treatment in their systematic approach for European *Geastraceae*.

The family is characterized by globose to subglobose unexpanded basidiomata, with a multi-layer exoperidium, and an endoperidium enclosing the mature gleba. At maturity, the exoperidium splits in a stellate manner, revealing the globose endoperidium, which may have one or multiple ostioles; the endoperidium can be sessile, or with one or multiple pseudostipes. The mature spores are globose to subglobose and ornamented (verrucose to irregularly baculate or with crests).

Geastrum Pers.

Notes: *Geastrum* was described by Persoon (1794) to accommodate three species *G. multifidum*, *G. quadrifidium* and *G. rufescens*. Later, Persoon (1801) expanded the genus to include *G. coliforme*, *G. coronatum*, *G. pectinatum*, *G. quadrifidum*, *G. rufescens* and *G. hygrometricum*. Currently, two of these species are included in two different genera: *Geastrum coliforme* in *Myriostoma* and *G. hygrometricum* in *Astraeus*.

Clements and Shear (1931) made the first typification of *Geastrum* selecting *G. pectinatum* as the type of the genus; however, Demoulin (1984) selected *G. multifidum* as the generic type, and later, Zamora (2014) proposed that the generic name *Geastrum* should be conserved with *G. coronatum* as the conserved type. Currently, Index Fungorum (2021) and Mycobank (Robert et al. 2005) databases, both accessed on November 2019, maintain *G. pectinatum* as the generic type.

Geastrum comprises ca. 100–120 widely distributed species (Zamora et al. 2014), although this number is increasing every year. In the last five years, according to the databases mentioned above, 24 new species have been described. The main morphological characters to delimitate the *Geastrum* species or ‘earthstar’ fungi are the exoperidium, hygroscopic or not; the endoperidium persistent or sometimes evanescent, sessile or pseudostipitate, with a unique ostiole that can be delimitated or not, mammiform or broadly conical forming a peristome, fibrillose or sulcate (Calonge 1998; Douanla-Meli et al. 2005; Trierveiler-Pereira et al. 2011). The size and ornamentation of the spores, verrucose to irregularly baculate, are important characters to identify species; also, as indicated in Zamora et al. (2013), the presence and shapes of calcium oxalate crystals in the rhizomorphs are also good characters to delimitate species in *Geastrum*.

In this study, we introduce two new species, *Geastrum gorgonicum* and *G. hansagiense* based on morphology and molecular phylogenetic analyses (Figs. 202, 203, 204 and 205).

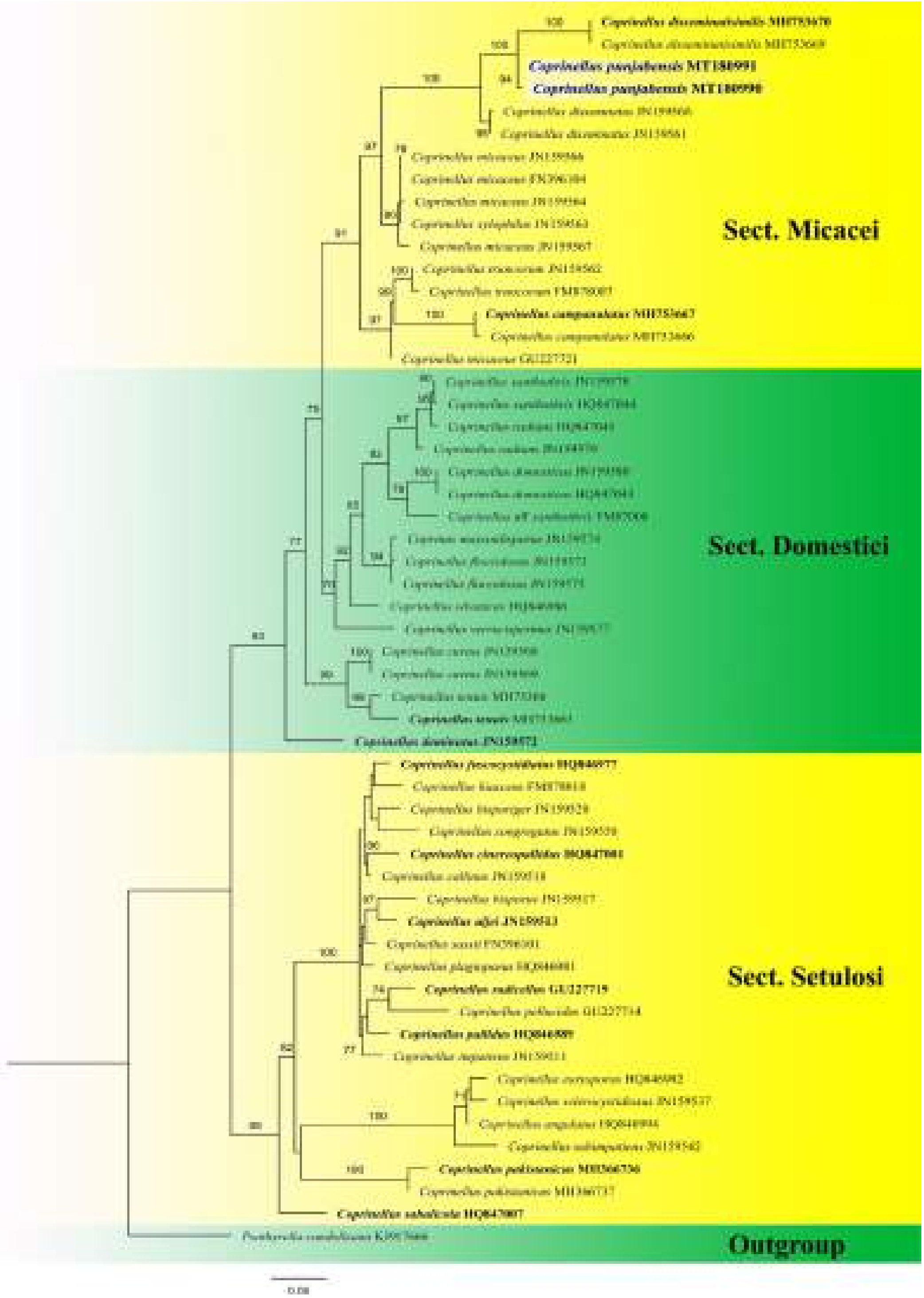


Fig. 201 Phylogram generated from maximum likelihood analysis based on ITS sequence data representing *Coprinellus punjabensis* (MT180990) and related species. Related sequences are taken from Hussain et al. (2018). Fifty-five sequences are included in the analysis which comprise 708 characters after alignement. *Psathyrella candolleana* (KJ917666) is used as the outgroup taxon. The best RAxML tree with a final likelihood values of − 4869.810366 is presented. The matrix had 351 distinct alignment patterns, with 15.82% undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.233377, C = 0.241159, G = 0.233394, T = 0.292070; substitution rates AC = 1.849754, AG = 2.784571, AT = 1.813146, CG = 1.135142, CT = 1.135142, GT = 1.000000; gamma distribution shape parameter α = 0.294349. Bootstrap values for maximum likelihood (MLBS) equal to or greater than 75%. The newly generated sequence is in blue bold

Geastrum gorgonicum M.P. Martín, M. Dueñas & Telleria, ***sp. nov.***

Mycobank number: MB834616; *Facesoffungi number*: FoF 09203; Fig. 202

Etymology: Named after Gorgades, an ancient name for the Cape Verde Islands, Atlantic Ocean.

Holotype: MA-Fungi 92118

Colour code follow: XXX Code Universal des couleurs (Séguy 1936).

Unexpanded basidiomata 11–12 mm high, 7–11 mm diam., rounded with an umbo, and attached to the ground by a basal mycelium tuft, with many rhizomorphs. *Peridium* smooth to felt-like, pale brown (702); when the surface is damaged the fibrous layer appears dirty white (680). *Expanded basidiomata* 10–11 mm high × 11–23 mm diam. *Exoperidium* splitting in 8–10 more or less equal rays, not hygroscopic; the rays are often recurved under the exoperidial disk. *Mycelial layer* brownish (702) to dirty white (680), when peeling off. *Fibrous layer* dirty white (680),

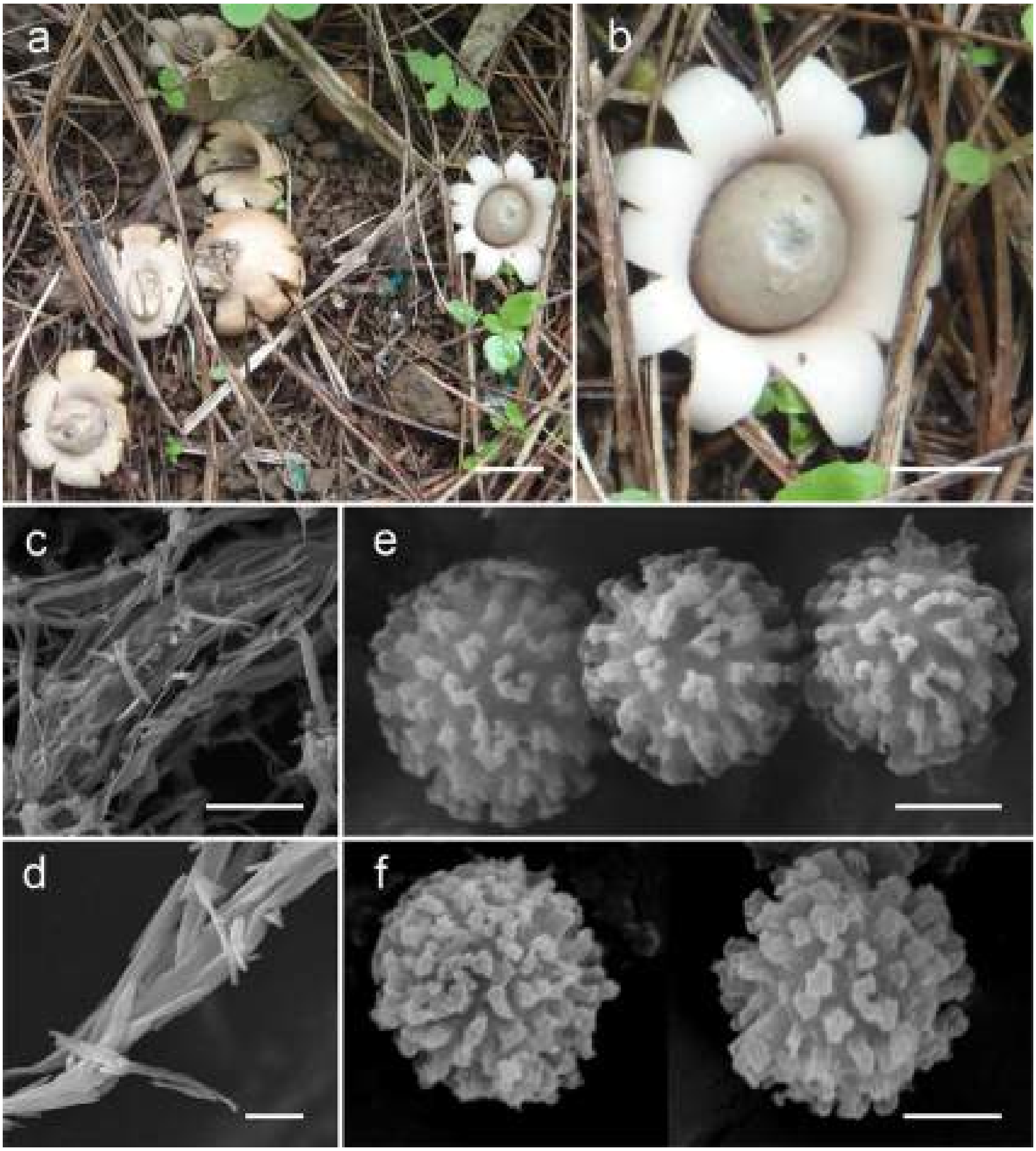


Fig. 202 ***Geastrum gorgonicum*** (MA-Fungi 92118, **holotype**). **a**, **b** Fresh basidiomata in field. **c**, **d** Rhizomorphs with acicular crystals. **e**, **f** Basidiospores. Scale bars: **a** = 1 cm, **b** = 5 mm, **c** = **10** µm, **d**–**f** = 2 µm

papery when dry. *Pseudoparenchymatous layer* pale brown (190), peeling off when dry. *Endoperidium* globose, 7–11 mm diam., sessile, brown (702), without crystals. *Peristome* finely fibrillose, well delimited, conical, colour similar to the mycelial layer (190). *Mature gleba* brown (697, 702). *Mycelial* layer with the outer part formed by 2–3 µm diam., brownish, unbranched, aseptate hyphae, with walls < 0.2 µm wide; and inner part with 1.5–2 µm diam., hyaline, unbranched, aseptate hyphae, with some clamps, and with very thin walls (< 0.1 µm wide). *Fibrous* layer 1.5–3 µm diam., hyaline, thick-walled hyphae with narrow lumen. *Pseudoparenchymatous layer* with thin-walled, hyaline cells, variable in shape and size, about 18–58 µm diam. *Endoperidial layer* with 2.5–4 µm diam., hyaline hyphae, some with thin walls (< 0.2 µm wide) and others thick-walled with narrow lumen. *Peristome* with 2–3 µm diam., yellowish, aseptate hyphae, thick-walled with narrow lumen and without clamps. *Capillitium* formed by 1.5–3 µm diam., brown, aseptate hyphae with walls < 0.2 µm wide. *Basidia* not seen. *Basidiospores* globose to subglobose, brownish to yellowish brown, with an oil drop; basidiospores 4.5–5 µm diam. including the baculate ornamentation (0.3–0.5 µm high).

Material examined: CAPE VERDE, Santiago, Parque Natural da Serra da Malagueta, Concejo de Sta. Catarina, 15°10′28″ N 28°40′37″ W, 914 msl, in a slope under *Pinus* sp., 20 November 2010, J. Cardoso, L.M. Caterino, L.M. Catarino, M. Dueñas, M.P. Martín, I. Melo, I. Salcedo and M.T. Telleria, 3242MPM (MA-Fungi 92118, **holotype**); idem, 3243MPM (MA-Fungi 92116); idem, 3244MPM (MA-Fungi 92114); idem, 13248MD (MA-Fungi 92112).

GenBank numbers: MA-Fungi 92118: ITS = MN754045, LSU = MN754083; MA-Fungi 92116: ITS = MN754046, LSU = MN754084; MA-Fungi 92114: ITS = MN754047, LSU = MN754085.

Notes: Based on ITS and LSU analyses (Fig. 203), *Geastrum gorgonicum* clustered in sect. *Corollina* J.C. Zamora in its own well-supported clade (100% MPBS, 95% MLBS, 1.00 BYPP) close to two collections under *Geastrum* aff. *saccatum* 1 in Zamora et al. (2014), one from Argentina

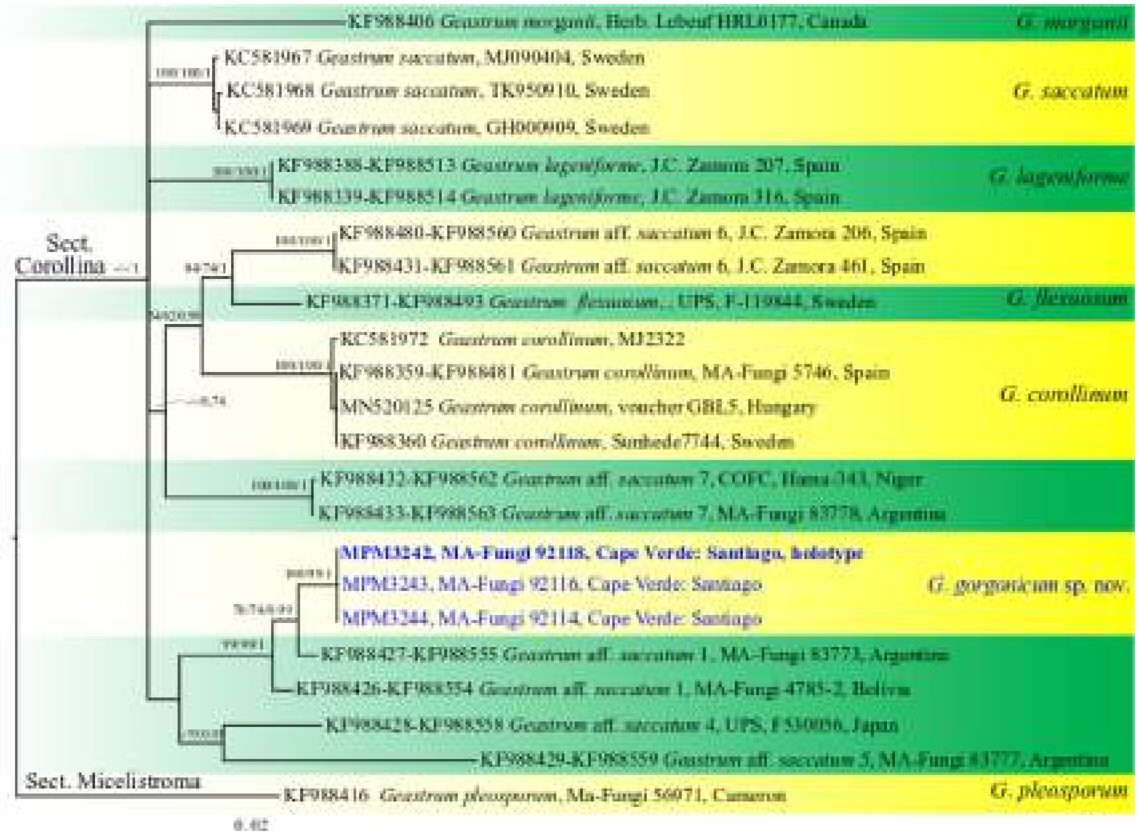


Fig. 203 Phylogram generated from Bayesian analysis based on ITS and LSU nrDNA sequence data representing *Geastrum* from *Section Corollina*, with *G. pleosporum* from *Sect Micelistroma* as outgroup. Related sequences are mainly taken from Zamora et al. (2014). Twenty-three sequences are included in the combined analyses, which comprise 1561 characters. Maximum parsimony (MP) and maximum likelihood (ML) analyses were undertaken; MP and ML tree topologies (not shown) were similar to the Bayesian one. Bootstrap values for MP and ML equal to or greater than 50%, and clade credibility values greater than 0.90 (the rounding of values to 2 decimal places) from Bayesian-inference analysis are labeled on the nodes. The newly generated sequences are in blue bold

(MA-Fungi 83775), and the other from Bolivia (MA-Fungi 47185-2). On the other hand, the *G. gorgonicum* clade grouped separately from other species of section *Corollina*: *Geastrum corollinum*, *G. flexuosum*, *G. lageniforme*, *G. morganii* and *G. saccatum*, as well as from *Geastrum* aff. *saccatum* 4, 5, 6 and 7 from Zamora et al. (2014).

Geastrum gorgonicum can be separated from *G. saccatum* by a number of characters (Fig. 202). The expanded basidiomata of *G. saccatum* are larger (10–40 mm diam.) with an endoperidium of 10–20 mm diam., beige to greyish brown; whereas in *G. gorgonicum* the endoperidium is brown, and the two types of hyphae (thin and thick-walled) are not wider than 11 µm diam. The capillitium in *G. saccatum* is formed by hyphae up to 10 µm wide, but in *G. gorgonicum* these hyphae are not wider than 3 µm. In general, in *G. gorgonicum* all the hyphae are narrower than those mentioned by Sunhede (1989) for *G. saccatum*.

Geastrum gorgonicum can be separated easily from *G. lageniforme* by the kind of rhizomorph crystals: acicular in *G. gorgonicum* (Fig. 202), and horn-like in *G. lageniforme*; as well as by the basidiospores that, according to Jeppson et al. (2013), are smaller (2.5–3.5 µm) in *G lageniforme*. *Geastrum morganii* has larger fully expanded basidiomata (30–60 mm diam.) and an irregularly folded peristome; whereas in *G. gorgonicum* the basidiomata are not larger than 23 mm diam., and the peristome is fibrillose.

Geastrum hansagiense Bóna, Merényi, Boros, Stielow & Bratek, ***sp. nov.***

MycoBank number: MB834968; *Facesoffungi number*: FoF 08141; Fig. 204

Etymology: The name refers to a Hungarian area (Hanság), where the type specimen was collected.

Holotype: BP110893

Basidiomata epigeous at maturity. *Unexpanded basidiomata* subglobose, depressed, 6.6(4–10) mm high, the minimal width 10.4(6–16) mm, the maximal 12(8–19) mm. *Expanded basidiomata* subglobose, 9.3(5.5–12) mm high, the minimal width 24.5(11–37), the maximal 27.5(20–38) mm, including rays. The outer surface of exoperidium smooth, light brown, silvery shining, vinaceous buff (31) with shade of smoke grey (34), the inner surface of exoperidium darker, date brown (24) under dry condition (Colour Identification Chart of Royal Botanic Garden, Edinburgh (RBGE) 1969). *Exoperidium* strongly hygroscopic, splitting into 7–9(6–12) triangular rays. *Endoperidial body* subglobose, saccate, flatted, sessile, distinctly pruinose, 13.2(9.5–19) high and 15.2(11–23) mm wide, light brownish, vinaceous buff (31), clay buff (32), drab (33) (RBGE 1969). *Mycelial layer* not always visible or intact, white to pale yellow, encrusted with some debris, formed hyaline to quite pale yellow, sinuous hyphae, 4.8(3–9.1) µm diam., thin–walled (< 1 µm), lumen evident. *Fibrous layer* papery, compact, persistent, yellowish to brownish, formed yellowish, sinuous hyphae, 4.4(3–6.5) µm diam., thin–walled (< 1 µm), lumen evident. *Pseudoparenchymatous layer* persistent, yellowish, with irregular subglobose to ellipsoid hyphal cells, in various shapes and size, 21.2(12.5–37.1) µm long and 14.4(8–26.7) µm wide, with 1.5(0.5–2.5) µm wall. *Stalk* absent. *Apophysis* absent. *Peristome* undelimited, almost flat to slightly elevated, mammiform, tenderly fibrillose, closed or opened with age, with irregularly shaped pores, similar or lighter than the endoperidium, milky coffee (28) or fawn (29) (RBGE 1969), but seems too darker because of the effused basidiospores. *Columella* central, pyramid shape, often imperceptible, light brown, clay buff (32) (RBGE 1969). *Mature gleba* forcibly dark brown to blackish, fuscous black (36) (RBGE 1969). *Basidiospores* globose, brownish or dark brown in 5% KOH, 5.7(4.9–7.1) µm diam. with verrucose ornamentation. *Basidia* not seen. *Eucapillitium* sinuous, 5.9(3.5–8) µm diam., rarely verrucosed, unbranched, thin–walled (≤ 1 µm), lumen evident.

Habit and habitat: Hundreds of specimens were found in a small, few m^2 area. The habitat of *G. hansagiense* is a ruderal nitrogen–rich grassland (dominant plant species *Galium aparine*, *Conium maculatum*, *Urtica dioica*) with nutritious soils.

Distribution: Specimens were found near to Mosonmagyaróvár (47°50′22.3″ N 17°14′30.1″ E), Hanság–area, Hungary. The formerly drained sweetwater turf marshland, Hanság–area is situated in the Little Hungarian Plain and closely connected with the westernmost Salt Lake of Eurasia, Lake Neusiedl. Until now the known distribution is restricted to the *locus classicus*.

Material examined: HUNGARY, Hanság–area, Mosonmagyaróvár, 47°50′22.3″ N 17°14′30.1″ E, on a ruderal nitrogen–rich grassland, 17 October 2015, L. Boros (BP110893, **holotype**).

GenBank numbers: ITS = MN582753, MN582754, LSU = MN582739.

Notes: Macromorphological descriptions based on ca. 30 fruitbodies in different developmental stages. *Geastrum hansagiense* is recognized by depressed, flatted, subglobose, usually wider than higher basidiomata, distinctly pruinose, sessile endoperidial body, tenderly fibrillose, mammiform, undelimited peristome, hygroscopic exoperidium, lacking of the stalk and apophysis and almost black gleba with globose, verrucose basidiospores (Fig. 204). One species with nearly identical characters is *G. floriforme*. *Geastrum hansagiense* is differentiated from *G. floriforme* by the size of the basidiomata, since the unexpanded *G. floriforme* basidiomata is 8.5 mm wide, the expanded basidiomata 21.5 mm wide and the endoperidial body 8.8 mm wide on average, based on our own mesurements and data from the literature (Hollós 1903; Jeppson et al. 2013; Sousa et al. 2014). Similarly, hygroscopic and sessile species are in genus *Geastrum*, *G. kotlabae, G. corollinum* and *G. hungaricum,* but their peristomes

Fig. 204 ***Geastrum hansagiense*** (BP110893, **holotype**). **a** Habitat of *G. hansagiense*. **b** Basidiomata. **c** Columella. **d** Peristome. **e** Basidiospore under SEM **f** Basidiospores and eucapillitium under LM. Scale bars: **e** = 1 μm, **f** = 6 μm

are totally different. *Geastrum hansagiense* is presumably a pseudocryptic species in the absence of remarkable morphological differences from *G. floriforme*. However, *G. hansagiense* differs from *G. floriforme* in some unique fixed alleles of the ITS locus, based on the alignments of sequences (Fig. 205). *Geastrum hansagiense*'s unique fixed alleles are: 14(T), 16(A), 17(G), 18(A), 19(T), 21(A), 22(G), 23(A), 26(G), 41(C), 43(gap), 46–48(gap), 62(T), 72(C), 111–112(A), 119(T), 125(C), 127–128(T), 152(A), 155–156(gap), 158(gap), 159(G), 160(T), 176–178(A), 179(T), 180(A), 184(T), 348(C), 362–363(T), 370(A), 375(G), 382(C), 387(A), 394(C), 395(G), 405(G), 411(C), 432(C), 463(gap), 468(T), 478(T), 492(A), 493(T), 505(C), 510(gap), 513–514(gap), 522(T), 534(G).

Schizoporaceae Jülich

Notes: Jülich (1981) proposed *Schizoporaceae* with *Schizopora* Velen. as the generic type. It is one of the most

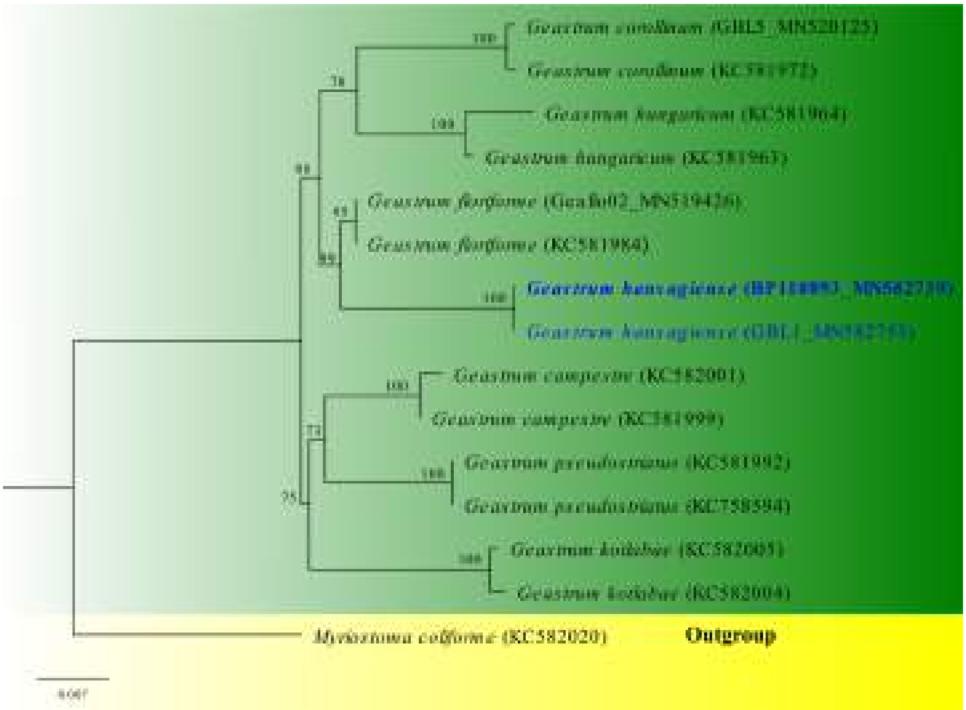


Fig. 205 Maximum likelihood (ML) phylogenetic tree of *Geastrum* species derived from concatenated internal transcribed spacer (ITS) and 28S rRNA (LSU) regions. Analysis was performed by RAxML under GTR + GAMMA model. *Myriostoma coliforme* (KC582020) is selected as the outgroup taxon. ML bootstrap values were obtained from 1000 replicates and values greater than 70% were indicated. The scale bar represents 0.007 expected nucleotide changes per site. The novel species are in blue, holotype specimen is in bold, herbarium numbers and NCBI Accession Numbers in brackets

widespread and diverse families in *Hymenochaetales*. It includes species characterized by basidiomata with corticioid, hydnoid to poroid hymenophore, a monomitic or dimitic hyphal system, skeletal hyphae often poorly developed, generative hyphae bearing clamp connections, cystida usually capitate with encrustions; basidiospores ellipsoid, colorless, thin-walled, negative in Melzer's reagent and cyanophilous in Cotton Blue (Jülich 1981).

Hyphodontia J. Erikss.

Notes: This genus is one of the largest genera in *Schizoporaceae* and was proposed by Eriksson (1958) with *Hyphodontia pallidula* (Bres.) J. Erikss as the type species. Species in this widespread genus commonly occur in temperate to tropical areas causing white rot. *Hyphodontia* are characterized by a monomitic hyphal system with clamped generative hyphae, broadly-ellipsoid basidiospores (Eriksson 1958). In addition, the various shapes of cystidia elements are also important morphological characteristics for the identification in the genus.

Hyphodontia yunnanensis C.L. Zhao & Y.C. Dai, ***sp. nov.***

Index Fungorum number: IF558551, *Facesoffungi number*: FoF 09971; Figs. 206, 207

Etymology: "*yunnanensis*" refers to collecting site.

Holotype: SWFC 00006804

Basidiomata: Annual, resupinate, adnate, without odour or taste when fresh, becoming fragile to slightly rigid upon drying, up to 12 cm long, 3 cm wide, 1.5 mm thick. Hymenial surface odontioid, vinaceous to brownish vinaceous when fresh, becoming pale brown upon drying, aculei conical, 2–4 per mm, up to 1 mm long. Subiculum very thin to lacking, 50–100 µm thick. Margin pale brown, usually determinate and thinning out. *Hyphal structure*, hyphal system monomitic; generative hyphae bearing clamp connections, colorless, slightly thick-walled, frequently branched, IKI–, CB +; tissues unchanged in KOH. *Hymenium*: *Cystidia* numerous, obviously projecting, cylindrical or tubular, colorless, encrusted, 26–37.5 × 2.5–4.5 µm; basidia clavate, 13.5–20.5 × 2.5–4.5 µm, four-spored and with a basal clamp connection; basidioles dominant, in shape similar to basidia, but slightly smaller. *Basidiospores* broadly ellipsoid to subglobose, colorless, thin-walled, IKI–, CB–, with a distinct apiculus, some bearing a guttule, (3.3–)3.5–4.5(–4.8) × (2.7–)3–3.6(–3.9) µm, L = 4.04 µm, W = 3.26 µm, Q = 1.23–1.25 (n = 90/3).

Material examined: CHINA, Yunnan Province, Chuxiong, Zixishan National Forestry Park, on angiosperm trunk, 30 June 2018, C.L. Zhao, CL Zhao 6804 (SWFC 00006804, **holotype**); Puer, Jingdong County, Huilianghe Village, on fallen branch of angiosperm, 5 January 2019, C.L. Zhao, CL Zhao 9570 (SWFC 00009570, paratype); Yuxi, Xinping County, Mopanshan National Forestry Park, on angiosperm trunk, 18 January 2018, C.L. Zhao, CL Zhao 6397 (SWFC 00006397, paratype).

GenBank numbers: ITS = MW020702, MW020701, MW020700.

Notes: Phylogenetically, *Hyphodontia yunnanensis* is sister to *H. mollis* Sheng H. Wu with 97% MLBS, 100%

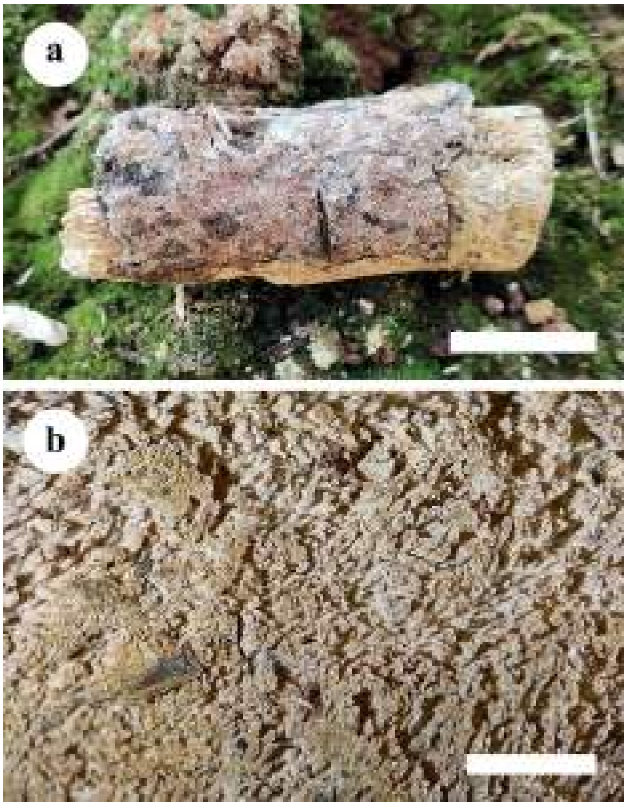


Fig. 206 ***Hyphodontia yunnanensis*** (CL Zhao 6804, **holotype**). **a**, **b** Basidiomata. Scale bars: **a** = 2 cm, **b** = 3 mm

MPBS, 1.00 BYPP support (Fig. 208). However, *H. mollis* differs from *H. yunnanensis* (Figs. 206 and 207) in having the ochraceous, distinctly hydnoid hymenophore with a pink tint and larger basidiospores (4–5.5 × 3–4 µm, Wu 1990). In addition, the two species share less than 96% in common based on the ITS.

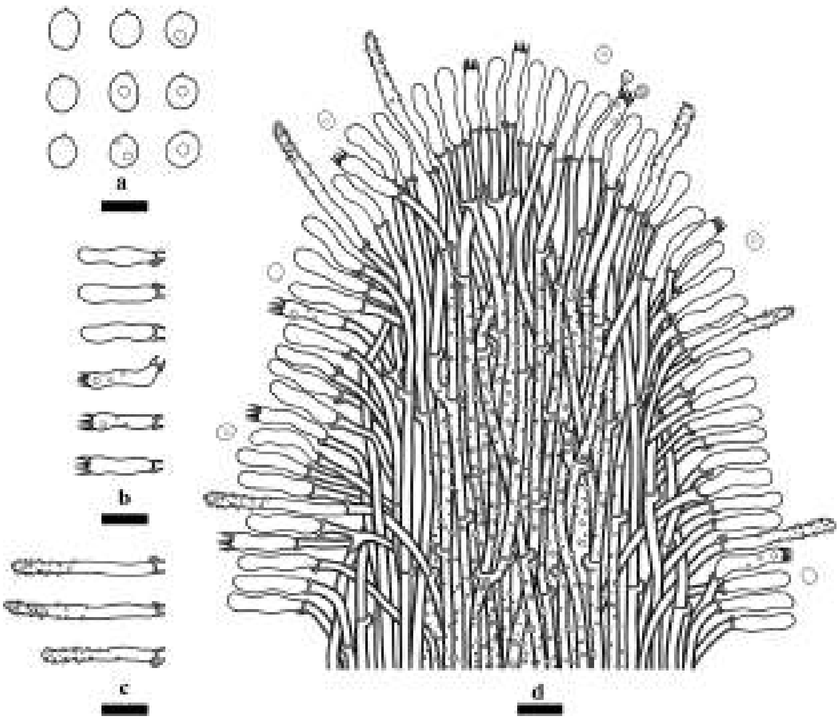
Thelephoraceae Chevall.

Notes: *Thelephoraceae* was built up by Chevallier (1826) based on the type genus *Thelephora*, and is composed of 34 genera. Most of the species of *Thelephoraceae* belong to ectomycorrhizal fungi which play an extremely important role in maintaining the balance of a terrestrial ecosystems by receiving energy from their host plants and, in return, transporting nutrients to them (Deckmyn et al. 2014).

Odontia Pers.

Notes: *Odontia* was introduced by Persoon (1794) with the type species *O. ferruginea* Pers. *Odontia* had been considered to be a synonym of *Tomentella*. However, recent phylogenetic analyses revealed that *Odontia* was in a monophyletic position close to *Tomentella*, and the species were generally collected in old forests possessing a saprotrophic lifestyle compared with an ectomycorrhizal one (Gorjón and Greslebin 2012; Tedersoo et al. 2014). The general characteristics of the genus are: resupinate and arachnoid basidiomata which are separable from the substrate, smooth to granulose or hydnoid hymenophoral surface, a dimitic hyphal system in the rhizomorphs, a monomitic or dimitic hyphal system in the

Fig. 207 ***Hyphodontia yunnanensis*** (drawn from the holotype), microscopic structures. **a** Basidiospores. **b** Basidia and basidioles. **c** Cystidia. **d** A section of aculei trama. Scale bars: **a**–**d** = 10 µm



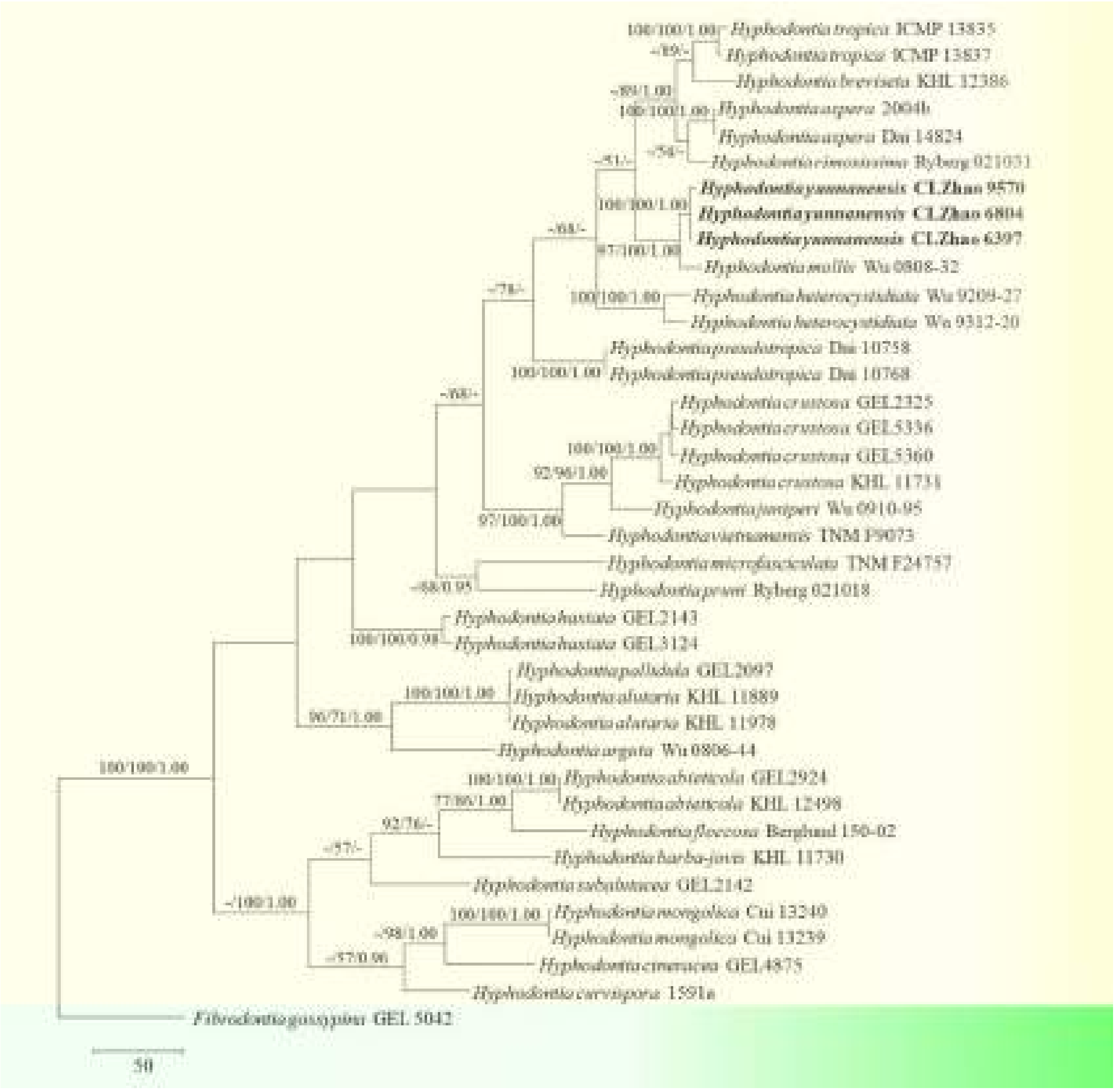


Fig. 208 Maximum parsimony strict consensus tree of *Hyphodontia yunnanensis* and related species in *Hyphodontia* based on ITS sequences. The ITS dataset included sequences from 38 fungal specimens representing 24 taxa. *Fibrodontia gossypina* (GEL 5042) was selected as an outgroup for phylogenetic analyses of ITS phylogenetic trees (Zhao et al. 2014). The PCR procedure and editing the DNA sequences and approaches to phylogenetic analysis from maximum parsimony, maximum Likelihood (ML) and Bayesian inference (BI) followed previous studies (Dai 2012; Zhao and Wu 2017; Cui et al. 2019).The dataset had an aligned length of 755 characters in the dataset, of which 307 characters are constant, 92 are variable and parsimony-uninformative, and 356 are parsimony-informative. Maximum parsimony analysis yielded 1 equally parsimonious tree (TL = 1954, CI 0.4417, HI = 0.5583, RI = 0.6329, RC = 0.2795). Best model for ITS estimated and applied in the Bayesian analysis: GTR + I + G, lset nst = 6, rates = invgamma; prset statefreqpr = dirichlet (1,1,1,1). Bayesian analysis resulted in the similar topology with an average standard deviation of split frequencies = 0.009980 (BI). The ITS region was amplified with primer pairs ITS5 and ITS4 (White et al. 1990). Branches are labeled with maximum likelihood bootstrap values greater than 70% (MLBS), parsimony bootstrap values higher than 50% (MPBS) and Bayesian posterior probabilities greater than 0.95 (BYPP), respectively

subiculum, clavate basidia and irregular ellipsoid to globose verruculose basidiospores (Kõljalg 1996; Yuan et al. 2018). The species of *Odontia* were reported to be spread over temperate Eurasia, North America, Africa, France, Australia, New Zealand, China and Turkey (Rodway 1897; Larsen 1974; Kõljalg 1996; Kõljalg and Larsson 1998; Gorjón and Greslebin 2012; Tedersoo et al. 2014; Yuan et al. 2018).

Odontia huanrenensis Y.H. Mu, H.S. Yuan & Y.C. Dai, ***sp. nov.***

MycoBank number: MB840455; *Facesoffungi number*: FoF 09972; Figs. 209, 210, 211

Etymology: The specific epithet "*huanrenensis*" refers to the Huanren County, where the specimen is found.

Holotype: Yuan 10663

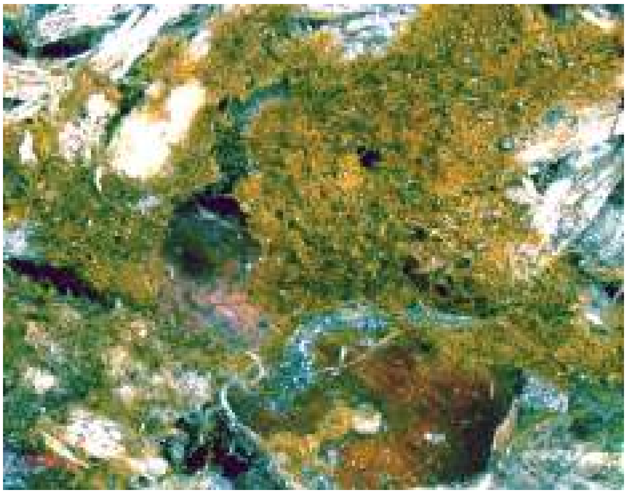


Fig. 209 ***Odontia huanrenensis*** (Yuan 10663, **holotype**): Basidiomata

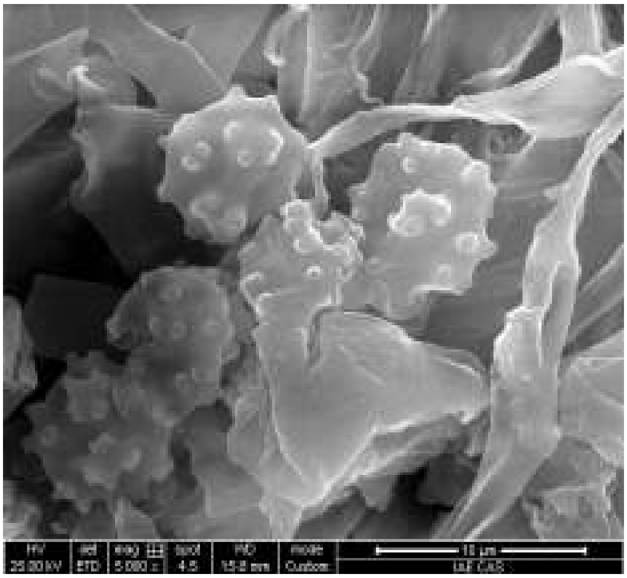


Fig. 210 ***Odontia huanrenensis*** (Yuan 10663, **holotype**): SEM of basidiospores

Basidiomata annual, resupinate, easily separable from the substrate, arachnoid, continuous, without odour or taste when fresh, becoming cottony upon drying, up to 0.25 mm thick. *Hymenophoral surface* light brown to brown (6D7–6E8) when dry, hydnoid; spines conical, up to 0.4 mm long, 0.1–0.2 mm wide at the base, evenly distributed, 2–4 per mm, turning darker or concolorous with subiculum. Subiculum mostly brown. Sterile margin determinate, byssoid, concolorous with hymenophore. Rhizomorphs present in subiculum and margins, 10–50 µm diam.; rhizomorph surface rather smooth; hyphal structure in rhizomorphs dimitic, differentiated, of type C (according to Agerer 1987–2008), compactly arranged; generative hyphae in center of rhizomorph simple-septate, thick-walled, 3–5 µm diam., colorless in KOH; skeletal hyphae at outer part of rhizomorph thick-walled, 1–2 µm diam., grayish yellow in KOH, cyanophilous, inamyloid. *Hyphal structure* subicular hyphae monomitic, generative hyphae with clamp connections, thin- to slightly thick-walled, 2.5–4 µm diam., occasionally collapsed, without encrustation, grayish yellow in KOH, acyanophilous, inamyloid. *Subhymenial hyphae* with clamp connections, thin-walled, 3–4 µm diam.; hyphal cells more or less uniform, colorless in KOH, acyanophilous, inamyloid. *Spine tramal hyphae* monomitic, generative hyphae with clamp connections, slightly thick-walled, 2.5–4(–5) µm diam., grayish yellow in KOH, cyanophilous, inamyloid.

Hymenium cystidia and cystidioles absent. *Basidia* 18–33 µm long and 5–9 µm diam. at apex, 3–4 µm at base, with a clamp connection at base, clavate, stalked, sinuous, without transverse septa, grayish yellow in KOH and in distilled water, bearing 4 sterigmata; sterigmata up to 3 µm long, 1–2 µm diam. at base. *Basidiospores* (7–)7.1–9.4(–9.9) × (6–)6.1–8.3(–9) µm in lateral and frontal face, L = 8.48 µm, W = 7.6 µm, Q = 1.12–1.13 (n = 60/2), irregular globose frontal and ellipsoid lateral face, oildrops absent, verruculose, light brown in KOH and in distilled water, acyanophilous, inamyloid; warts usually grouped in 2 or more, bi- to trifurcate alike, 1–1.6 µm long. *Chlamydospores* absent.

Material examined: CHINA, Liaoning Province, Huanren County, Laotudingzi Nature Reserve, on fallen angiosperm trunk, 20 October 2015, H.S. Yuan (Yuan 10663, **holotype**); Qingyuan County, ecological observatory station, on fallen angiosperm trunk, 23 October 2015, H.S. Yuan (Yuan 10741).

GenBank numbers: Yuan 10663: ITS = MW033326; Yuan 10741: ITS = MW033327.

Notes: *Odontia huanrenensis* is closely related to *O. aculeata* and *O. ferruginea* in phylogeny (Fig. 215). *Odontia huanrenensis* is similar to *O. aculeata* in having resupinate, arachnoid, continuous basidiomata separable from the substrate, hydnoid hymenophoral surface, determinate and byssoid sterile margin, a dimitic hyphal system in the rhizomorphs, monomitic and clamped subicular hyphae, the absence of cystidia and irregular globose to ellipsoid and verruculose basidiospores (Figs. 209, 210 and 211). However, *O. aculeata* differs from *O. huanrenensis* in having thinner basidiomata (up to 0.15 mm vs. up to 0.25 mm in *O. huanrenensis*), longer spines (up to 1 mm vs. up to 0.4 mm in *O. huanrenensis*), clamped and thin-walled generative hyphae in the center of rhizomorph, thin-walled spinal tramal hyphae and shorter basidia (12–15 µm vs. 18–33 µm in *O. huanrenensis*) (Yuan et al. 2018). *Odontia huanrenensis* shares features with *O. ferruginea* including hydnoid basidiomata, a dimitic hyphal system in the rhizomorphs, clamped

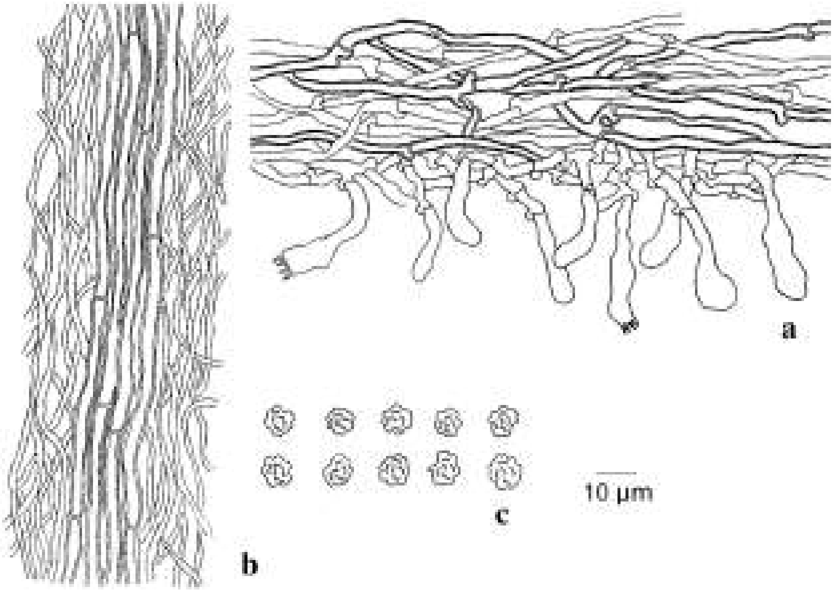


Fig. 211 ***Odontia huanrenensis*** (drawn from the holotype), microscopic structures. **a** Section through basidiomata. **b** Section through rhizomorph. **c** Basidiospores in frontal and lateral view

subicular hyphae and verruculose basidiospores of similar shape. However, *O. ferruginea* differs from *O. huanrenensis* in having longer spines (up to 1.75 mm vs. up to 0.4 mm in *O. huanrenensis*), the presence of simple-septate and pseudoskeletal hyphae in spine trama and clamped generative hyphae in rhizomorphs (Larsen 1967; Kõljalg 1996).

Odontia parvispina Y.H. Mu, H.S. Yuan & Y.C. Dai, ***sp. nov.***

MycoBank number: MB840456; *Facesoffungi number*: FoF 09973; Figs. 212, 213, 214

Etymology: The specific epithet "*parvispina*" refers to hymenophoral surface with very small spines.

Holotype: Yuan 10652

Basidiomata annual, resupinate, easily separable from the substrate, arachnoid, continuous, without odour or taste when fresh, becoming cottony upon drying, up to 0.25 mm thick. *Hymenophoral surface* yellowish brown to brown (5D8–6E8) when dry, smooth or hydnoid to the naked eye; spines conical, up to 0.06 mm long, 0.02–0.03 mm wide at the base, evenly distributed, 4–6 per mm, turning darker than subiculum. Subiculum mostly brown. Sterile margin determinate, byssoid, paler than hymenophore, brown. Rhizomorphs present in subiculum and margins, 10–60 µm diam.; rhizomorph surface rather smooth; hyphal structure in rhizomorphs dimitic, differentiated, of type C (according to Agerer 1987–2008), compactly arranged; generative hyphae in center of rhizomorph simple-septate, slightly thick-walled, 3–4 µm diam., colorless in KOH; skeletal hyphae at outer part of rhizomorph thick-walled, 1–2 µm diam., grayish yellow in KOH, cyanophilous, inamyloid.

Hyphal structure subicular hyphae monomitic, generative hyphae simple-septate, thin- to slightly thick-walled, 3–4 µm diam., occasionally collapsed, without encrustation, grayish yellow in KOH, acyanophilous, inamyloid. *Subhymenial hyphae* simple-septate, thin-walled, 2–3 µm diam.; hyphal cells more or less uniform, colorless in KOH, acyanophilous, inamyloid. *Spine tramal hyphae* monomitic, generative hyphae with clamp connections, thick-walled, 3–5(–6) µm diam., grayish yellow in KOH, cyanophilous, inamyloid (Fig. 215).

Hymenium cystidia and cystidioles absent. *Basidia* 15–44 µm long and 3–8 µm diam. at apex, 2–4 µm at base, simple-septate at base, clavate, stalked, sinuous, with transverse septa, grayish yellow in KOH and in distilled water, bearing 4 sterigmata; sterigmata up to 5 µm long, 1–3 µm diam at base. *Basidiospores* (5.5–)6–7(–8) × (4–)5–6.4(–7) µm in lateral and frontal face, L = 6.39 µm, W = 5.68 µm, Q = 1.13–1.15 (n = 60/2), irregular subglobose frontal and ellipsoid lateral face, oil drops absent, verruculose, light brown in KOH and in distilled water, acyanophilous, inamyloid; warts usually grouped in 2 or more, bi- to trifurcate alike, 1–2 µm long. *Chlamydospores* absent.

Material examined: CHINA, Liaoning Province, Huanren County, Laotudingzi Nature Reserve, on fallen angiosperm trunk, 20 October 2015, H.S. Yuan (Yuan 10652, **holotype**); Kuandian County, Baishilazi Nature Reserve, on fallen angiosperm branch, 22 October 2015, H.S. Yuan (Yuan 10716).

GenBank numbers: Yuan 10652: ITS = MW033328, Yuan 10716: ITS = MW033329.

Notes: *Odontia parvispina* is closely related to *O. fibrosa* in the phylogenetic tree (Fig. 215) and share similar morphological and anatomical characteristics: annual, resupinate, arachnoid basidiomata, smooth or hydnoid hymenophoral surface, brown subiculum, the presence of rhizomorphs with

Fig. 212 ***Odontia parvispina*** (Yuan 10652, **holotype**): Basidiomata

dimitic hyphal system, thin- to slightly thick-walled and simple-septate generative hyphae in the subiculum and clavate basidia of similar size (Figs. 212, 213 and 214). However, *O. fibrosa* can be differentiated by thicker basidiomata (up to 0.4 mm vs. up to 0.25 mm in *O. parvispina*), dark brown and granulose hymenophoral surface when dry, longer spines (up to 1 mm vs. up to 0.06 mm in *O. parvispina*), simple-septate and wider hyphae (5–7 µm vs. 3–5 µm in *O. parvispina*) in spine trama and larger basidiospores (7.1–9 × 6.1–8 µm vs. 6–7 × 5–6.4 in *O. parvispina*). *Odontia sparsa* resembles *O. parvispina* in having resupinate and arachnoid basidiomata, a dimitic system in the rhizomorphs with simple-septate and slightly thick-walled generative hyphae and thick-walled skeletal hyphae and verruculose basidiospores. However, the former species differs by thin and clamped generative hyphae, the presence of skeletal hyphae in the subicular and reddish brown basidiospores in KOH with shorter warts (0.3–0.8 µm vs. 1–2 µm in *O. parvispina*) (Yuan et al. 2018).

Bartheletiomycetes Thines

Polyporales Gäum.

Notes: The latest treatments and updated accounts of *Polyporales* in Phookamsak et al. (2019) and Wijayawardene et al (2020).

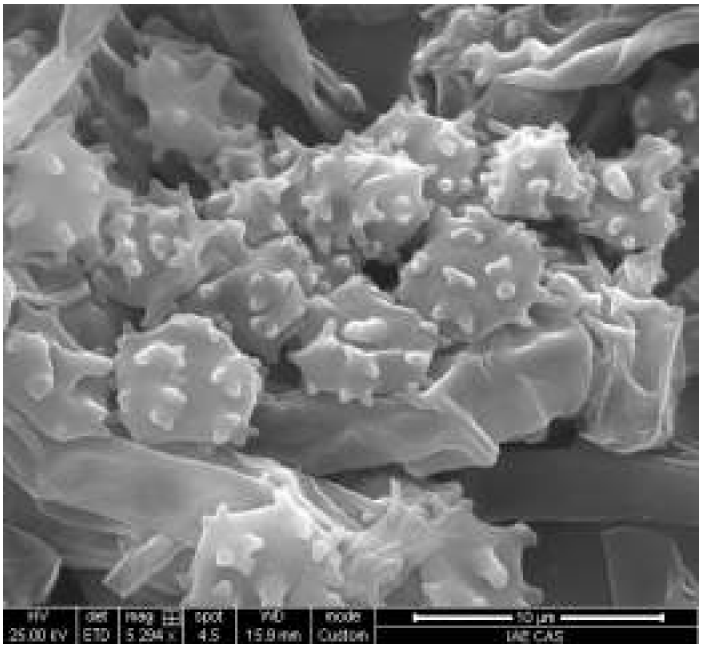
Hyphodermataceae Jülich

Notes: Jülich (1981) described *Hyphodermataceae* with *Hyphoderma* as the generic type, also including the genera *Athelidium*, *Atheloderma*, *Basidioradulum*, *Bulbillomyces*, *Conohypha*, *Granulobasidium*, *Hyphoderma*, *Hyphodermella*, *Hypochnicium*, *Intextomyces* and *Metulodontia*. Currently, according to the phylogenetic study of *Polyporales* at the family-level carried out by Justo et al. (2017), only *Hyphoderma* is considered in this family which includes corticioid species with monomitic hyphal systems, hyphae with clamp-connections; cystidia present in most species; spores thin-walled, smooth, and hyaline.

Hyphoderma Wallr.

Notes: *Hyphoderma* is one of the largest genera of corticioid fungi, with 105 recognized species (Index Fungorum 2021). All species of *Hyphoderma* produce white rot and their main habitat is decaying wood of deciduous and coniferous trees. From a morphological point of view, the species included in this genus are characterized by their basidioma, resupinate and

Fig. 213 ***Odontia parvispina*** (Yuan 10652, **holotype**): SEM of basidiospores



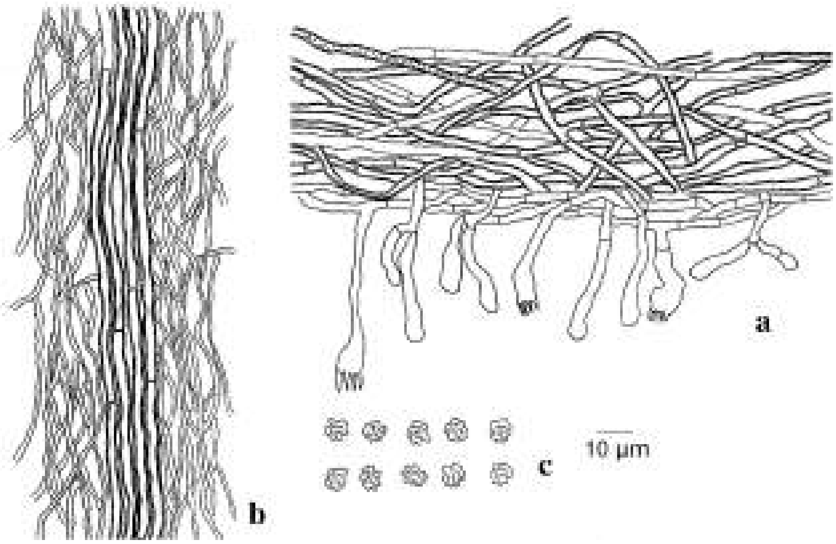


Fig. 214 ***Odontia parvispina*** (drawn from the holotype), microscopic structures. **a** Section through basidiomata. **b** Section through rhizomorph. **c** Basidiospores in frontal and lateral view

effused, with hymenophore smooth, tuberculate or hydnoid; a monomitic hyphal system and the hyphae with clamps; cystidia are frequent; basidia are suburniform to subcylindrical, with two or four sterigmata and basal clamps; spores are subglobose, ellipsoid, cylindrical to allantoid, thin-walled, smooth, with oily contents, and non-amyloid (Larsson 2007).

Hyphoderma was described by Wallroth (1833) to accommodate eight species namely *Hyphoderma aspera*, *H. fibrillosa*, *H. granulosa*, *H. lintaceum*, *H. spiculosum*, *H. sulphurea* and *H. terrestre*. Long time neglected, this genus was recovered and emended by Donk (1949, 1957) who designated *H. spiculosum* Wallr. [= *Hyphoderma setigerum* (Fr.) Donk] as the generic type. Parmasto (1968) divided it into three sections i.e., *Hyphoderma* sect. *Hyphoderma*, *Hyphoderma* sect. *Stephanocystis*, and *Hyphoderma* sect. *Mutatoderma*, and, several years after, Eriksson and Ryvarden (1975) recognized twelve groups: *Hyphoderma albocremeum*-group, *H. argillaceum*-group, *H. capitatum*-group, *H. cremeoalbum*-group, *H. guttuliferum*-group, *H. mutatum*-group, *H. orphanellum*-group, *H. praetermissum*-group, *H. puberum*-group, *H. radula*-group, *H. roseocremeum*-group and *H. setigerum*-group.

Hyphoderma setigerum-group was characterized by its cystidia, which are multi-septate, clamped and more or less encrusted (Eriksson and Ryvarden 1975) and was represented by only one species, *H. setigerum*, widely distributed with great variation in both macro and microscopic characters. Based on molecular, morphological and crossing test analyses, Nilsson et al. (2003) concluded that *H. setigerum* is a species complex and nine taxa exist inside it. Moreover, a succession of studies (Gilbertson and Blackwell 1988; Wu 1997; Boidin and Gilles 2003; Yurchenko and Wu 2014) described four more species with this type of cystidia: *Hyphoderma nudicephalum* from Louisiana, USA, *Hyphoderma subsetigerum* from Taiwan, *Hyphoderma bisetigerum* from Madagascar, and *Hyphoderma pinicola* from China.

Hyphoderma australosetigerum M. Dueñas, Telleria & M.P. Martín, ***sp. nov.***

MycoBank number: MB834614; *Facesoffungi number*: FoF 09204; Fig. 216

Etymology: From Latin "*australis*" which means southern and "*setigerum*" refers to morphological similarity of this species with *Hyphoderma setigerum* (Fr.) Donk.

Holotype: 13970MD, MA-Fungi 92235

Colour codes follow: ISCC-NBS Centroid Colour Charts (Kelly and Judd 1976)

Basidiomata resupinate, orbicular to confluent, porose-reticulate under the lens, adnate; hymenophore smooth, under the lens pilose by the projecting cystidia; white (92. Y White) to greyish (264. L Gray). *Margin* thin, fimbriate, not differentiated. *Hyphal system* monomitic. *Hyphae* thin- to thick-walled, 3–4 µm wide, with clamps, loosely interwoven in the subiculum and more densely interwoven in the subhymenium. *Cystidia* cylindrical, multi-septate, with clamps, thick-walled except for the apical cell, at first naked then encrusted, apex obtuse, 108–160 × 10–11 µm. *Basidia* subclaviform to claviform, four sterigmata, 18–30 × 5–6 µm, with basal clamp. *Spores* narrowly ellipsoid to cylindrical, 9–11(–12) × 4.5–5(–5.5) µm, ($\bar{x}$ = 10 × 5 µm), hyaline, thin-walled, smooth, with oil drops in the protoplasm, Q (L/W) = 2.

Habitat and distribution: Frequent in the Chilean Patagonian region, both on typical species of the Valdivian temperate rainforest such as *Lophosoria quadripinnata, Eucryphia cordifolia,* and in plantations of *Eucalyptus globulus* or *Pinus radiata.*

Material examined: CHILE, Los Lagos, Palena, Hornopirén, comuna Hualaihué, Huinay Biological Reserve,

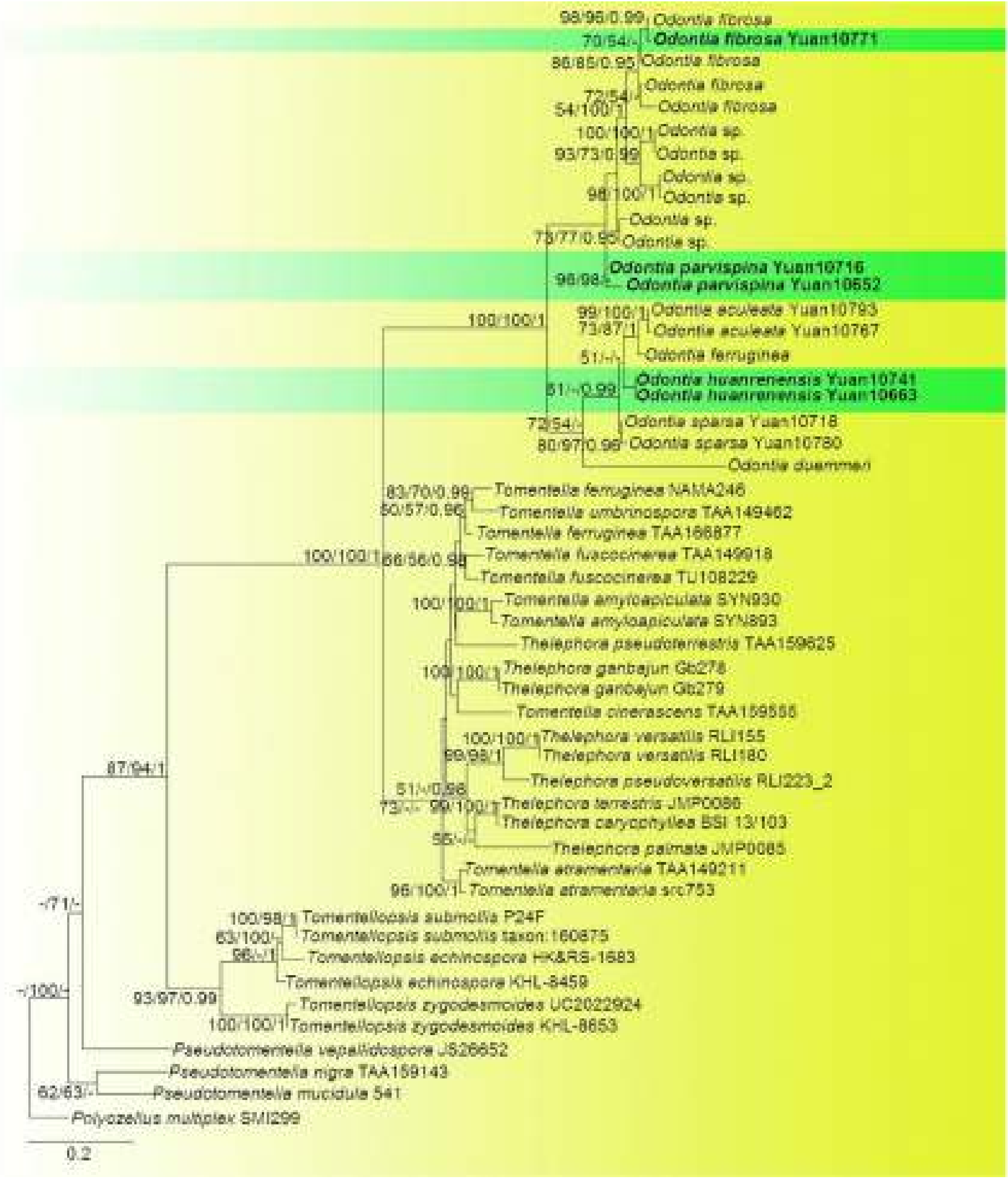


Fig. 215 Maximum likelihood tree illustrating the phylogeny of *Odontia huanrenensis, O. parvispina* and related taxa based on ITS sequence dataset. Fifty sequences are included in the analyses. *Polyzellus multiplex* SMI299 was selected as the outgroup taxa. Branches are labeled with maximum likelihood bootstrap support greater than 50% (MLBS), parsimony bootstrap proportions greater than 50% (MPBS) and Bayesian posterior probabilities greater than 0.95 (BYPP). The new species and new record are in bold

path to Cerro del Tambor, 42°22′50.9″ S 72°24′54.7″ W, 34 msl, on *Eucryphia cordifolia,* 25 April 2012, M. Dueñas, M.P. Martín and M.T. Telleria, 13970MD (MA-Fungi 92235, **holotype**); 13995MD (MA-Fungi 92240); on fallen branches, 13983MD (MA-Fungi 92234). Los Lagos, Palena, Hornopirén, comuna Hualaihué, Huinay Biological Reserve, path to Cerro del Tambor, 42°22′50.6″ S 72°24′50.6″ W, 202 msl, on *Lophosoria quadripinnata*, 7 May 2013, M. Dueñas, M.P. Martín and M.T. Telleria, 20070Tell. (MA-Fungi 92236); on unidentified wood, 20089Tell. (MA-Fungi 92233). Los Lagos, Palena, Hornopirén, comuna Hualaihué, Huinay Biological Reserve, path to Cerro del Tambor, behind the hydroelectric power station, 42°22′54.2″ S 72°24′53.5″ W, 202 msl, on *Lophosoria quadripinnata*,

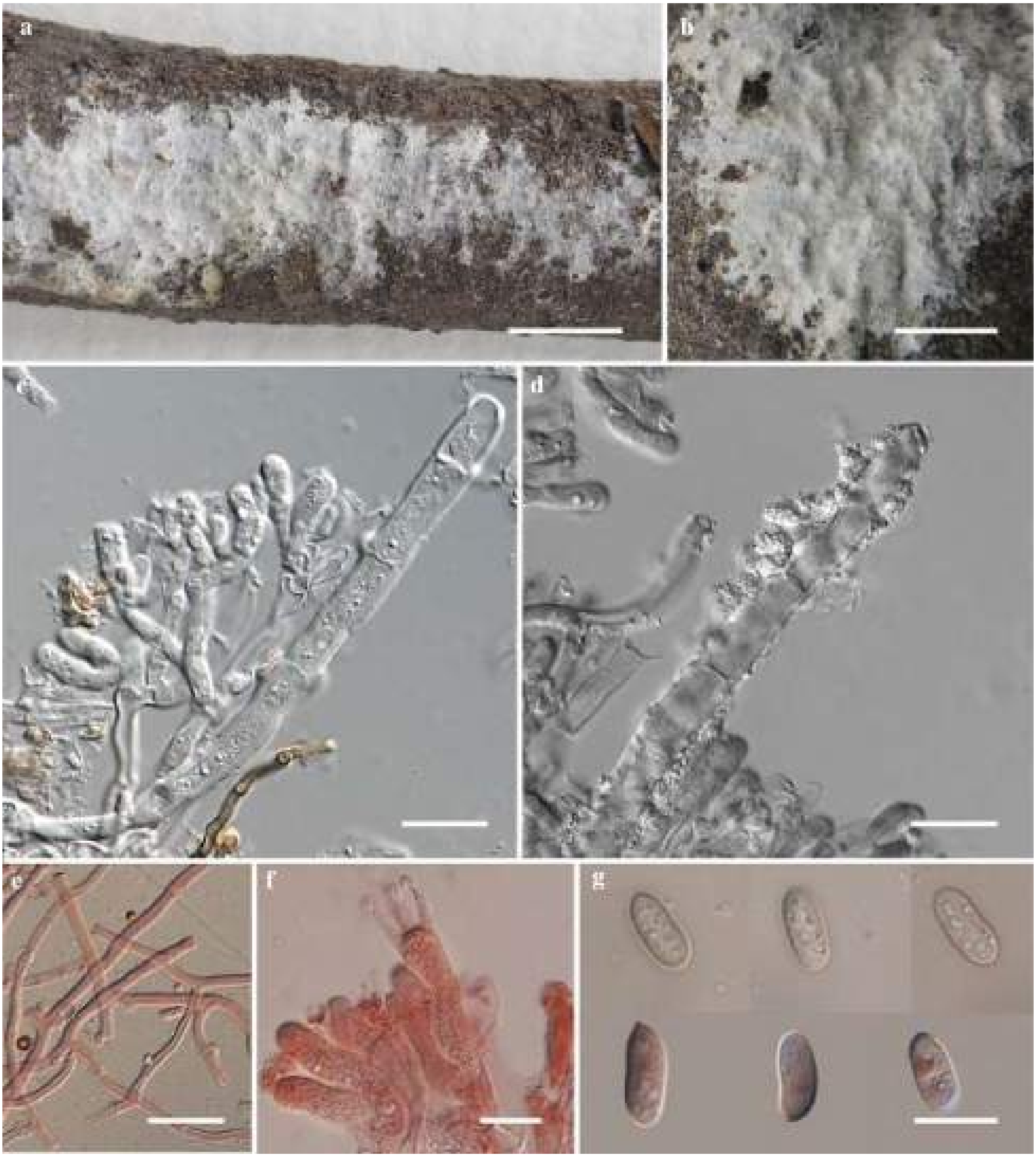


Fig. 216 ***Hyphoderma australosetigerum*** (13970MD, MA-Fungi 92235, **holotype**). **a** Basidiomata dry specimen. **b** Hymenophore. **c** Septate cystidium. **d** Septate and encrusted cystidium. **e** Basal hyphae thick-walled, with clamps. **f** Basidium and probasidia. **g** Spores. Scale bars: **a**, **b** = 5 mm, **c**–**e** = 20 µm, **f**–**g** = 10 µm

8 May 2013, M. Dueñas, M.P. Martín and M.T. Telleria, 14580MD (MA-Fungi 92239). Los Lagos, Palena, Hornopirén, comuna Hualaihué, Huinay Biological Reserve, "Cementerio de los Alerces" experimental plot, 42°22′01.5″ S 72°24′57.8″ W, 50 msl, on unidentified wood, 10 May 2013, M. Dueñas, M.P. Martín and M.T. Telleria, 3636MPM (MA-Fungi 92241). Los Ríos, Ranco, comuna de La Unión, T-80 road, km 27.500, 40°15′53.9″ S 73°18′45.0″ W, 188

msl, on *Pinus radiata*, 6 November 2017, M. Dueñas, J. Fernández López, M.P. Martín, S. Nogal-Prata and M.T. Telleria, 15624MD (MA-Fungi 92238). Los Ríos, Ranco, comuna de La Unión, T-80 road, km 18, Putraro detour, 40°18′12.0″ S 73°14′15.0″ W, 82 msl, on *Eucalyptus globulus*, 6 November 2017, M. Dueñas, J. Fernández López, M.P. Martín, S. Nogal-Prata and M.T. Telleria, 508JFL (MA-Fungi 92237).

GenBank numbers: 13970MD, MA-Fungi 92235 (holotype): ITS = MN963764; 13995MD, MA-Fungi 92240: ITS = MN963760; 13983MD, MA-Fungi 92234: ITS = MN963763; 20070Tell., MA-Fungi 92236: ITS = MN963765; 20089Tell., MA-Fungi 92233: ITS = MN963762; 14580MD, MA-Fungi 92239: ITS = MN963759; 3636MPM, MA-Fungi 92241: ITS = MN96376; 15624MD, MA-Fungi 92238: ITS = MN963758; 508JFL, MA-Fungi 92237: ITS = MN963757.

Notes: Based on ITS analysis (Fig. 217), 11 sequences of *Hyphoderma australosetigerum* clustered together in their own clade (68% MPBS, 88% MLBS, 1.00 BYPP); nine obtained from our Chilean specimens and two from GenBank sequences from Argentina. Two sequences from GenBank under *H. setigerum* from South Africa are quite close to those of the new species. *Hyphoderma australosetigerum* grouped close to different clades from Nilsson et al. (2003) under *H. setigerum*: 1A (Germany, Norway, Romania and Russia), 1B (Greenland), 2 (Canada), 3A (Canada), 3B (USA), 4 (Norway, UK), and 6 (Canada). As well as with two sequences from GenBank under *H. setigerum* from the USA, and clade 5 (Nilsson et al. 2003) from China and Japan under *H. nudicephalum*. On the other hand, *H. setigerum* s.str and *H. subsetigerum* (clades 7A and 7B) from Nilsson et al. (2003) grouped close to *H. pinicola* described from China by Yurchenko and Wu (2014).

From a morphological point of view, *H. australosetigerum* (Fig. 216) differs from *H. bisetigerum* and *H. pinicola* in that they have bisporic basidia; from *H. nudicephalum* by the cystidia with swollen apex, characteristic of this species; from *H. subsetigerum* by the size of spores, 6–8 × 2.8–3.2 µm in *H. substigerum*, while *H. australosetigerum* has spores 9–11(–12) × 4.5–5(–5.5) µm. This species is difficult to separate from *H. setigerum* s. str.; molecular characters and their geographic origin are useful for its identification. *Hyphoderma australosetigerum* is frequent in Patagonia region, where it probably has been confused with *H. setigerum* reported by Gorjón and Hallenberg (2013) from Chile and by Greslebin and Rajchenberg (2003) from Argentina.

Irpicaceae Spirin & Zmitr.

Notes: *Irpicaceae* (*Polyporales*) was described by Spirin and Zmitovich in Spirin (2003), with *Irpex* as the generic type, to accommodate *Antrodiella*, *Fabisporus*, and *Phyllotopsis*. Currently, according to Justo et al. (2017), the family includes the following genera *Byssomerulius*, *Ceriporia*, *Cytidiella*, *Efibula*, *Emmia*, *Flavodon*, *Gloeoporus*, *Hydnopolyporus*, *Leptoporus*, *Meruliopsis* and *Trametopsis*, as well as several more additional species. These taxa include a great assortment of basidiomata and hymenophore types; microscopically, they are characterized by a hyphal system that is monomitic, rarely dimitic, and most hyphae are without clamps; cystidia are usually absent and spores thin-walled, smooth and hyaline. All species are saprobes, growing on decayed wood, and most of them are associated with white rot.

Efibula Sheng H. Wu

Notes: *Efibula* was described by Wu (1990) to accommodate species previously included in *Phlebia* (*Ph. deflectens*) and *Phanerochaete* (*Ph. avellanea* and *Ph. pallidovirens*, in addition, two new species *Efibula lutea* and *Efibula tropica* were also described and proposing *E. tropica* as the generic type. Two more species were accommodated in the genus by Kotiranka and Saarenoska (1993) i.e., *Efibula rosea* and *E. verruculosa*. Zmitrovich et al. (2006) enlarged the genus with eight more species, *E. aurata*, *E. bubalina*, *E. cordylines*, *E. corymbata*, *E. ginnsii*, *E. subodontoidea*, *E. subquercina* and *E. tuberculata*. Subsequent phylogenetic analysis (Wu et al. 2010) showed that *Efibula* sensu Zmitrovich et al. (2006) was polyphyletic and, according to Floudas and Hibbett (2015), only five species were accepted in the genus namely *E. americana*, *E. clarki*, *E. gracilis*, *E. tropica* and *E. tuberculata*.

From a morphological point of view, the species included in this genus are characterized by their basidiomata resupinate, effused, subceraceous to ceraceous; smooth hymenophore; compact subiculum, with hyphae densely interwoven; monomitic hyphal system, hyphae mostly without clamps; cystidia absent; basidia with four sterigmata; spores ellipsoid to broadly ellipsoid, thin-walled, smooth and hyaline, Melzer (–), and acyanophilous (Wu 1990; Floudas and Hibbett 2015).

Efibula rodriguezarmasiae Telleria, M. Dueñas, Beltrán-Tej., Melo, Salcedo & M.P. Martín, ***sp. nov.***

MycoBank number: MB834615; *Facesoffungi number*: FoF 09205; Fig. 218

Etymology: Named after the Canary mycologist J. Laura Rodríguez-Armas, "Susi", colleague and friend.

Holotype: 17681Tell., MA-Fungi 86635

Colour codes follow: ISCC-NBS Centroid Colour Charts (Kelly and Judd 1976)

Basidiomata resupinate, effuse, ceraceous, when dry specimens pale to dark orange yellow or light yellowish brown (73. p. OY—72. d. OY, 76. L. y Br); *hymenophore*

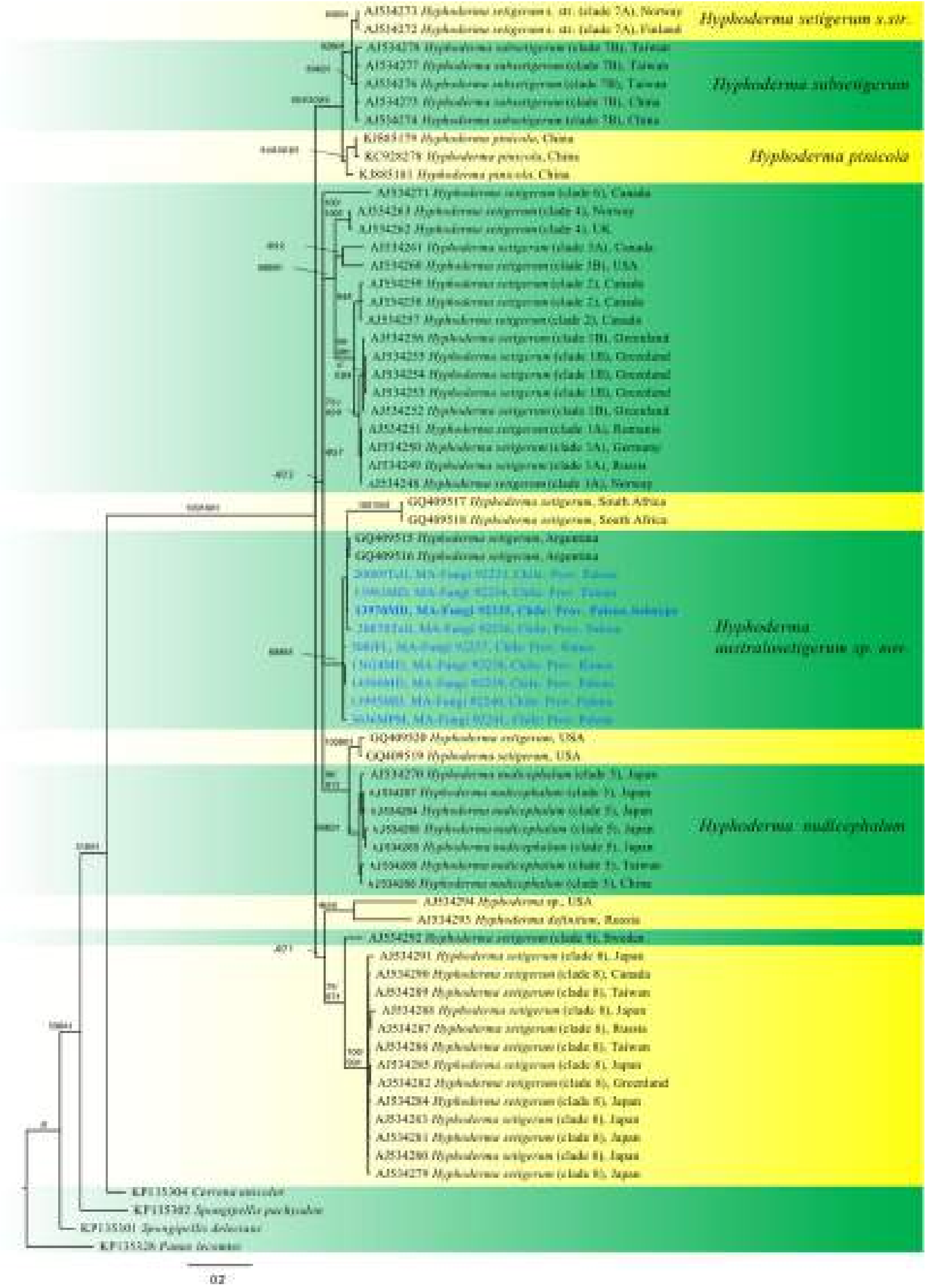


Fig. 217 Phylogram generated from Bayesian analysis based on newly-generated ITS sequence data and including sequences mainly from Nilsson et al. (2003) and Yurchenko and Wu (2014); *Cerrena unicolor, Panus lecomtei, Spongipellis delectans* and *S. pachyodon* are included as outgroup. The alignment comprises 701 characters. Maximum parsimony (MP) and maximum likelihood (ML) analyses were also performed; the tree topologies were similar to the Bayesian one. Bootstrap values for MP and ML analyses equal to or greater than 50%, and posterior probabilities of the Bayesian analysis are labeled on the nodes. The newly generated sequence is in blue bold

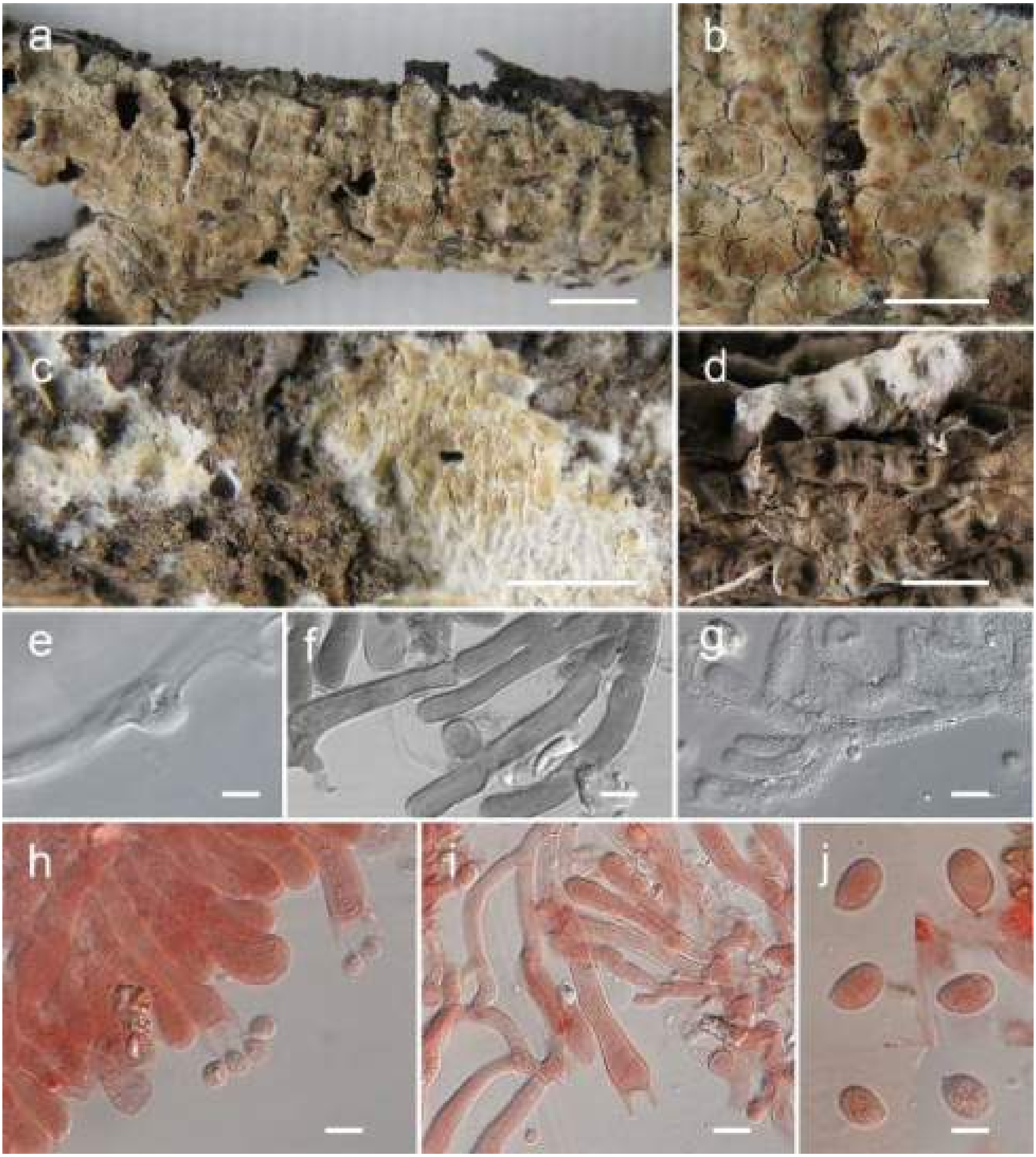


Fig. 218 ***Efibula rodriguezarmasiae*** (17681Tell., MA-Fungi 86635, **holotype**). **a** Basidiomata dry specimen. **b** Hymenophore. **c**, **d** Basidiomata young and dry specimen. **e** Basal hyphae with clamp. **f** Hyphae with a vesicle. **g** Basidia, probasidia and subhymenial hyphae with thin crystals. **h**, **i** Basidia. **j** Spores. ***Efibula rodriguezarmasiae*** (18761Tell., MA-Fungi 86652). **d** Basidiomata with little strands. Scale bars: **a**–**d** = 5 mm, **e**–**j** = 5 µm

smooth to tuberculate, sometimes cracked; *margin* indistinct, little strands present in some specimens. *Hyphal system* monomitic, subicular hyphae 4–6 µm wide, thin walled, with occasional clamps, and small vesicles; subhymenial hyphae 4 µm wide, without clamps, short celled, sometimes with very thin crystals scattered on the hyphae. *Cystidia* absent. *Basidia* claviform, 35–48 × 6–8 µm, with four sterigmata, basal clamp absent. *Spores* ellipsoid, 6–7 × 4–5 µm (L/W = 1.4), thin-walled, smooth, colorless.

Habitat and distribution: This species is distributed throughout the Macaronesian region: Canary Archipelago and West coast of Morocco, growing on debris and decayed wood of *Pericallis murrayi, Euphorbia regis-jubae, Euphorbia balsamifera, Euphorbia officinarum* and *Kleinia neriifolia,* among others.

Material examined: SPAIN, Canary Islands: El Hierro, Frontera, Sabinar de la Dehesa, 27°44′43.97″ N 18°07′2.01″ W, 610 msl, 26 January 2007, on *Pericallis murrayi*, E. Beltrán-Tejera, J. Cardoso, M. Dueñas, J. Leal, I. Melo, J.L. Rodríguez-Armas and M.T. Telleria, 11400MD (MA-Fungi 86626). Gran Canaria, Aldea de San Nicolás, barranco de Tasarte, 672 msl, on *Euphorbia regis-jubae*, 6 December 2007, E. Beltrán-Tejera, M. Dueñas, J.L. Rodríguez-Armas and M.T. Telleria, 17681Tell. (MA-Fungi 86635, **holotype**). Lanzarote, Haría, Órzola, 29°12′54.50″ N 13°27′3.92″ W, 30 msl, 2 December 2007, on *Nicotiana glauca*, E. Beltrán-Tejera, M. Dueñas, J.L. Rodríguez-Armas and M.T. Telleria, 12233MD (MA-Fungi 86638). Lanzarote, Teguise, Arrieta, 30 msl, on *Euphorbia balsamifera*, 2 December 2007, E. Beltrán-Tejera, M. Dueñas, J.L. Rodríguez-Armas and M.T. Telleria, 17629Tell. (MA-Fungi 86633); on *Kleinia neriifolia*, 2 December 2007, 17633Tell. (MA-Fungi 86632). Lanzarote, Parque Nacional de Timanfaya, Yaiza, El Mojón, 29°02′38.86″ N 13°45′08.66″ W, 150 msl, 3 December 2007, on *Euphorbia balsamifera*, E. Beltrán-Tejera, M. Dueñas, J.L. Rodríguez-Armas and M.T. Telleria, 12238MD (MA-Fungi 86637). Lanzarote, Parque Nacional de Timanfaya, Yaiza, Tinajo, next to Montaña Bermeja, 114 msl, on *Nicotiana glauca*, 3 December 2007, E. Beltrán-Tejera, M. Dueñas, J.L. Rodríguez-Armas and M.T. Telleria, 17657Tell. (MA-Fungi 86631). Fuerteventura, Betancuria, 357 msl, on *Pinus* sp., 4 December 2007, E. Beltrán-Tejera, M. Dueñas, J.L. Rodríguez-Armas and M.T. Telleria, 17665Tell. (MA-Fungi 86634). MOROCCO, Souss-Massa-Daraa, road Tiznit to Anglou Plage, 29°45′29.3″ N 09°46′42.2″ W, 158 msl, on *Euphorbia* sp., 20 April 2010, J. Cardoso, M. Dueñas, I. Melo, M.P. Martín, I. Salcedo and M.T. Telleria, 18699Tell. (MA-Fungi 86648). Souss-Massa-Daraa, road N1, Agadir to Essaouira, next to Tamri, 30°37′36.9″ N 09°50′57.4″ W, 23 msl, on *Euphorbia officinarum*, 21 April 2010, J. Cardoso, M. Dueñas, I. Melo, M.P. Martín, I. Salcedo and M.T. Telleria, 18761Tell. (MA-Fungi 86652). Souss-Massa-Daraa, road R104, Tiznit to Mirleft, 29°37′21.7″ N 09°53′05.3″ W, 278 msl, on *Euphorbia* sp., 21 April 2010, J. Cardoso, M. Dueñas, I. Melo, M.P. Martín, I. Salcedo and M.T. Telleria, 18704Tell. (MA-Fungi 86650); 18743Tell., MA-Fungi 86651. Souss-Massa-Daraa, road R104, Mirleft to Sidi Ifni, 29°32′15.4″ N 10°03′24.1″ W, 50 msl, on *Euphorbia* sp., 20 April 2010, J. Cardoso, M. Dueñas, I. Melo, M.P. Martín, I. Salcedo and M.T. Telleria, 18701Tell. (MA-Fungi 86649).

Other material examined: *Phanerochaete* sp.: SPAIN, Canary Islands, Lanzarote, Haría, Órzola, 29°12′54.50″ N 13°27′3.92″ W, 30 msl, on *Nicotiana glauca*, 2 December 2007, E. Beltrán-Tejera, M. Dueñas, J.L. Rodríguez-Armas and M.T. Telleria, 12234MD (MA-Fungi 86625). *Efibula tuberculata*: SPAIN, Canary Islands, La Palma, Santa Cruz de La Palma, Parque Natural de Las Nieves, road to Roque de los Muchachos, next to César Manrique monument, 28°45′05.36″ N 17°50′06.70″ W, 2,137 msl, 20 January 2007, on *Adenocarpus viscosus* subsp. *spartioides* E. Beltrán-Tejera, J. Cardoso, J. Leal, J.L. Rodríguez-Armas and M.T. Telleria, 16871Tell. (MA-Fungi 86621). *Corticium tuberculatum* P. Karst. [≡ *Efibula tuberculata*]: FINLAND, Etelä – Maine (EH/Ta). Temmela, Mustiala, in populo, 7 October 1895, P.A. Karsten 1503 (H6003416, lectotype). *Phanerochaete xerophila* Burdsall: USA, Arizona, Cochise County, San Pedro River Rd., between Redington and Benson, on *Prosopis velutina*, 26 February 1971, R.L. Gilbertson, RLG-10082 (CFMR, holotype); idem (MA-Fungi 63223, isotype).

GenBank numbers: *Efibula rodriguezarmasiae*, 11400MD, MA-Fungi 86626: ITS = KF483015, LSU = KF528106; 17657Tell., MA-Fungi 86631: ITS = KF483020, LSU = KF528111; 17633Tell., MA-Fungi 86632: ITS = KF483021, LSU = KF528112; 17629Tell., MA-Fungi 86633: ITS = KF483022, LSU = KF528113; 17665Tell., MA-Fungi 86634: ITS = KF483023, LSU = KF528114; 17681Tell., MA-Fungi 86,635 (**holotype**): ITS = KF483024, LSU = KF528115; 12238MD, MA-Fungi 86,637: ITS = KF483026, LSU = KF528117; 12233MD, MA-Fungi 86,638: ITS = KF483027, LSU = KF528118; 18699Tell., MA-Fungi 86648: ITS = KF483041, LSU = KF528132; 18701Tell., MA-Fungi 86649: ITS = KF483039, LSU = KF528130; 18704Tell., MA-Fungi 86650: ITS = KF483040, LSU = KF528131; 18743Tell., MA-Fungi 86651: ITS = KF483042, LSU = KF528133; 18761Tell., MA-Fungi 86652: ITS = KF483038, LSU = KF528129. *Efibula tuberculata*, 16871Tell., MA-Fungi 86621: ITS = KF483011, LSU = KF528102. *Phanerochaete* sp, 12234MD, MA-Fungi 86625: ITS = KF483014, LSU = KF528105. *Phanerochaete xerophila* (isotype), MA-Fungi 63223: ITS = KF483056, LSU = KF528147.

Notes: Based on ITS and LSU analysis (Fig. 219), 13 sequences of *Efibula rodriguezarmasiae* clustered together in its own clade (93% MPBS, 73% MLBS, 1.00 BYPP) and appear as sister species of a clade formed by nine sequences of *Efibula americana* (85% MPBS, 84% MLBS, 1.00 BYPP). From a morphological point of view, these species can be separated by the shape and size of basidia and spores (Fig. 218). *Efibula americana* has cylindrical to clavate

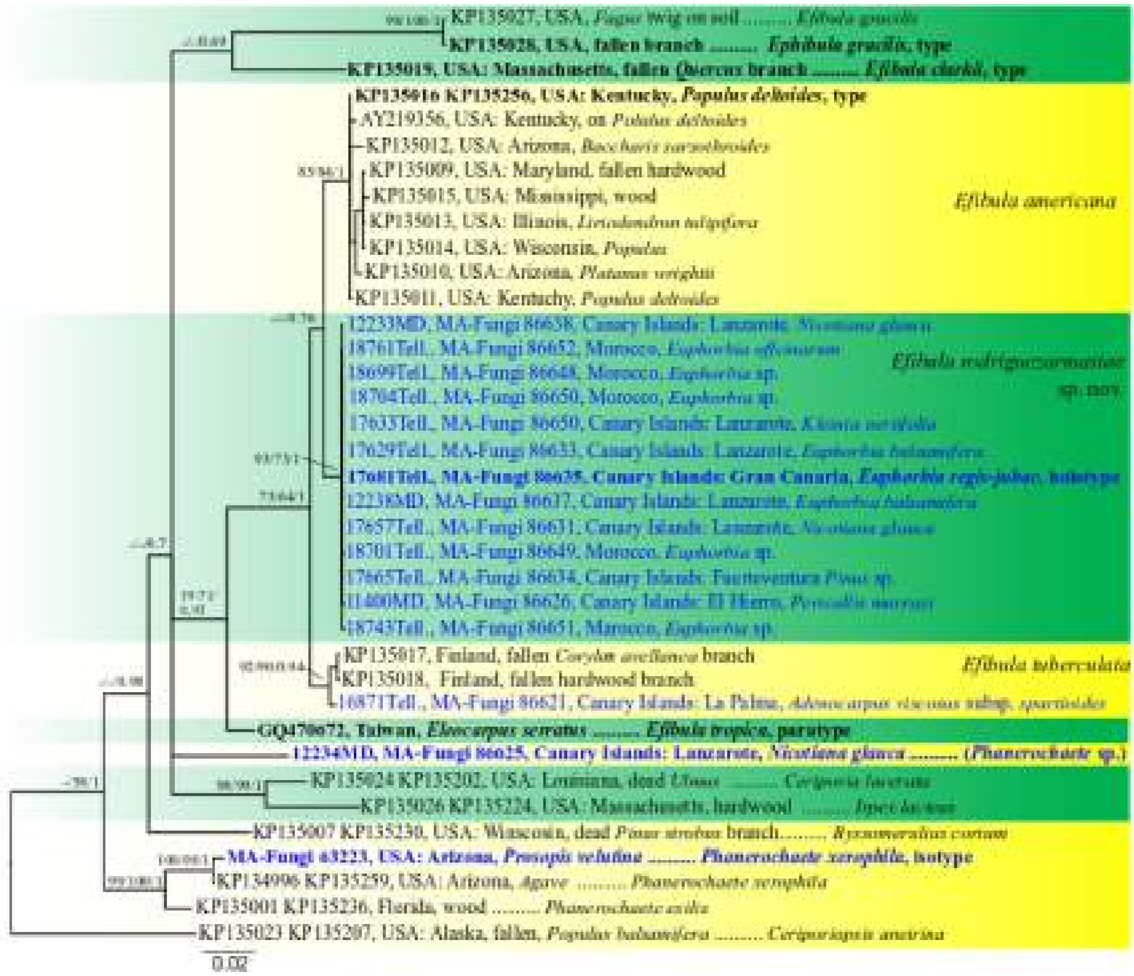


Fig. 219 Phylogram generated from Bayesian analysis based on new generated ITS + LSU sequences data and including sequences from clades 5 (*Phanerochaete* s.l.) and 6 (*Efibula*) in Floudas and Hibbett (2015). The sequence of *Efibula tropica* (paratype) is included (Floudas and Hibbett 2015: Fig. S5B, 1) and *Ceriporiopsis aneirina* as outgroup. The alignment comprises 2061 characters. Maximum parsimony (MP) and maximum likelihood (ML) analyses were also performed; the tree topologies were similar to the Bayesian one. Bootstrap values for MP and ML analyses equal to or greater than 50%, and posterior probabilities to the Bayesian analysis are labeled on the nodes. The newly generated sequences are in blue bold

basidia, 20–32 × 5–8 µm, and ellipsoid to cylindrical spores, (4.5–)5.3–6.5(–7.3) × (2.3–)3–3.8(–4.5) µm, L/W = 1.71 (Floudas and Hibbett 2015), while *E. rodriguezarmasiae* has clavate and longer basidia, 35–48 × 6–8 µm, and ellipsoid and wider spores, 6–7 × 4–5 µm, L/W = 1.4. Furthermore, the phylogenetic analysis indicated that these two species grouped with three sequences of *Efibula tuberculata* (73% MPBS, 64% MLBS, 1.00 BYPP) that, according to Floudas and Hibbett (2015), can be confused with *E. americana* without characters to easily separate one from the other. The thirteen collections of the new species have been reported from arid, semiarid or dry zones of the Canary Islands and Morocco where it is frequent and, probably, has been confused with *Phanerochaete xerophila* (Beltrán-Tejera and Rodríguez-Armas 1999; Beltrán-Tejera et al. 2013).

Phanerochaetaceae Jülich

Notes: *Phanerochaetaceae* is one of the three largest subclades of the phleboid clade of *Polyporales*, Basidiomycota (Miettinen et al. 2016; Justo et al. 2017). The family includes about 17 known genera, most of which are corticioid fungi with *Phanerochaete*, *Phlebiopsis* and *Rhizochaete*. as the three largest genera in the family (Floudas and Hibbett 2015; Miettinen et al. 2016; Nakasone et al. 2017). Although several new genera were described recently by different mycologists (Miettinen et al. 2016; Yuan et al. 2017; Chen et al. 2018; Ma and Zhao 2019), the phylogeny of the family still needs further study. All species in the family are saprobes and cause a white rot on many kinds of substrates.

Phanerochaete P. Karst.

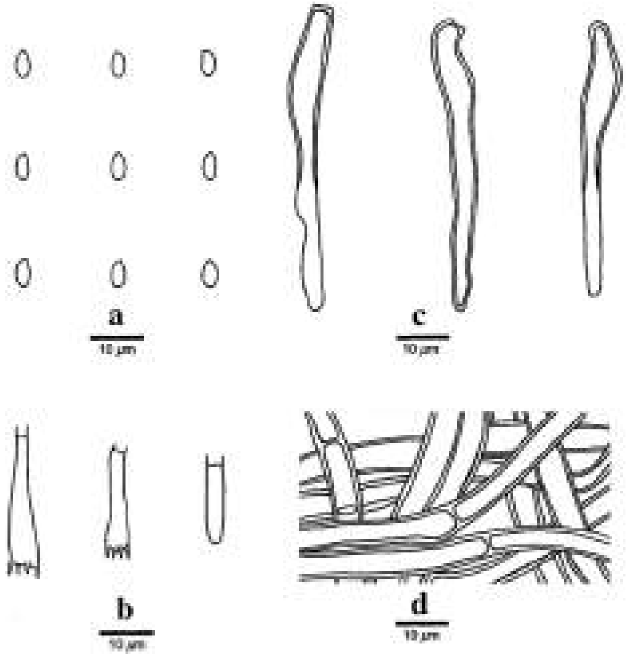


Fig. 220 ***Phanerochaete hainanensis*** (BJFC 022063, **holotype**). **a** Basidiospores. **b** Basidia and basidiole. **c** Cystidia. **d** Hyphae from subiculum

Notes: Recent molecular studies demonstrate that *Phanerochaete* s.l. is polyphyletic and distributed across several lineages in the phlebioid clade of the *Polyporales* and also the *Hymenochaetales* (De Koker et al. 2003; Greslebin et al. 2004; Wu et al. 2010; Floudas and Hibbett 2015; Miettinen et al. 2016; Justo et al. 2017; Chen et al. 2018). In several studies, *Phanerochaete* s.s. which includes the type, *P. alnea* (Fr.) P. Karst., formed a strongly supported clade in *Phanerochaetaceae* (Floudas and Hibbett 2015; Miettinen et al. 2016; Spirin et al. 2017). Many new species were described in *Phanerochaete* s.s. based on both morphological and molecular evidence in recent years (Ghobad-Nejhad et al. 2015; Volobuev et al. 2015; Liu and He 2016; Sádlíková and Kout 2017; Spirin et al. 2017; Wu et al. 2018a, b; Phookamsak et al. 2019; Xu et al. 2020).

Phanerochaete hainanensis S.H. He & Y.C. Dai, ***sp. nov.***

MycoBank number: MB837508; *Facesoffungi number*: FoF 09974; Fig. 220

Etymology: The specific epithet “*hainanensis*” refers to the Hainan Province, southern tropical China where the type was collected.

Holotype: BJFC 022063

Fruiting body: *Basidiomata* annual, resupinate, broadly effused, closely adnate, inseparable from substrate, coriaceous to soft corky, first as small patches, later confluent up to 20 µm long, 8 cm wide. *Hymenophore* smooth, pale orange (5A3), light orange [5A (4–5)] to greyish orange [5B (3–6)], darkening in KOH, uncracked; *margin* thinning out, distinct, lighter than hymenophore surface, white (5A1) to orange white [5A2], up to 0.2 cm wide. Context greyish orange, up to 500 µm thick.

Microscopic structures—Hyphal system monomitic; all hyphae without clamp connections. Subiculum thin; hyphae colorless, distinctly thick-walled with a wide lumen, smooth, rarely branched, moderately septate, interwoven, 4–9 µm in diam. Subhymenium thickening; hyphae colorless, thin-walled, smooth, vertically arranged, more or less agglutinated, 3–7 µm in diam. *Cystidia* subulate to subcylindrical, slight tapered toward the apex, sometimes with one or two secondary simple septa, colorless, slightly thick-walled or thin-walled at the tip part, smooth, projecting above the hymenium, with a basal simple septum, 35–70 × 3–7 µm. *Basidia* clavate, colorless, thin-walled, with a basal simple septum and four sterigmata, 16–25 × 4–5.5 µm; basidioles numerous, similar to basidia but smaller. *Basidiospores* ellipsoid, colorless, thin-walled, smooth, neither dextrinoid nor amyloid in Melzer’s agent, acyanophilous in cotton blue, (4.3–) 4.5–5 (–5.3) × 2.2–2.8 (–3) µm, L = 4.9 µm, W = 2.5 µm, Q = 1.96 (n = 30/1).

Material examined: CHINA, Hainan Province, Lingshui County, Diaoluoshan Nature Reserve, on fallen angiosperm trunk, 17 March 2016, He 3562 (BJFC 022063, **holotype**). Guangxi Autonomous Region, Shangsi County, Shiwandashan Forest Park, on fallen angiosperm trunk, 26 July 2012, He20120726-1 (BJFC 014522), BJM (isotype).

GenBank numbers: ITS = MT235692, LSU = MT248179.

Notes: *Phanerochaete hainanensis* is characterized by the large basidiomata with pale orange hymenophore, thickened subhymenium with a compact texture, smooth leptocystida and small basidiospores (Fig. 220). The new species is similar to *P. argillacea* in that it shares the compact texture and similar size of leptocystidia and basidiospores but differs in having lighter hymenophore darkening in KOH (Wu 1998). *Phanerochaete hainanensis* is somewhat similar to *P. metuloidea* and *P. sordida* in that they share the thick and tough basidiomata, which, however, differs in having encrusted cystidia and a well-developed subiculum (Burdsall 1985; Xu et al. 2020). In the phylogenetic tree, *P. hainanensis* forms a distinct lineage and is not closely related to other species of *Phanerochaete* s.s. (Fig. 221).

Polyporaceae Fr. ex Corda

Notes: *Polyporaceae* [as 'Polyporei'] belongs to polyporoid fungi, which was established by Corda (1839). The fruit bodies may be soft or tough having fertile layer with vertical pores on the underside of the elongated pores which constitute a corky labyrinth. They form brackets with a small or definite stipe.

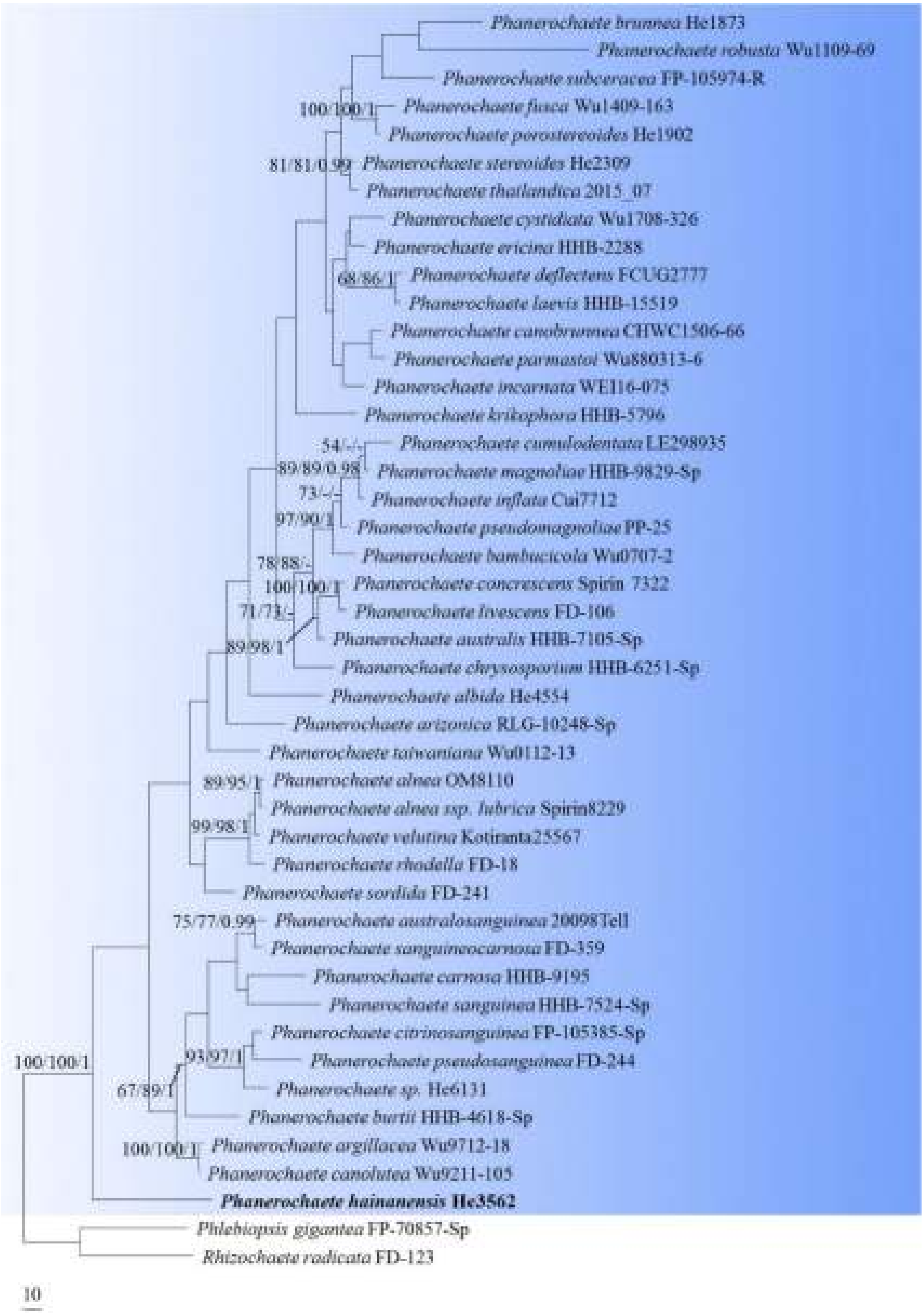


Fig. 221 Phylogenetic tree obtained from maximum parsimony analysis of a concatenated ITS and nrLSU sequence data of *Phanerochaete s.s.* Branches are labelled with parsimony bootstrap values equal to or greater than 50% (front), likelihood bootstrap values equal to or greater than 50% (middle) and Bayesian posterior probabilities equal to or greater than 0.95 (back). The new species is in bold

Favolus Fr.

Notes: *Favolus* was established by Fries (1828) with the type species, *F. brasiliensis*. Species of this genus are considered as wood decaying fungi. The basidiocarps of *Favolus* species are fleshy with radially arranged pores on the underside of the cap that are angular and deeply pitted, somewhat resembling a honeycomb. Earlier, *Favolus* was treated as a synonym of *Polyporus* (Nunez and Ryvarden 1995). Sotome et al. (2013) proposed new genus, *Favolus* based on morphological and molecular phylogenetic analysis.

Favolus septatus J.L. Zhou & B.K. Cui, Mycologia 109(5): 773 (2017)

Index Fungorum number: IF817942; *Faces of fungi number*: FoF 08019; Fig. 222

Colour codes follow: Methuen Handbook of Colour (Kornerup and Wanscher 1978)

Fruit bodies associated with dead wood of *Dalbergia melanoxylon* Guill. & Perr. (*Fabaceae*). *Basidiocarps* solitary or 1–2 in group, tough or leathery and flexible when fresh, fragile when dry, persistently attached with dead branches in the form of brackets, stipitate. *Stipe* short, up to 5 mm long and 7 mm diam. *Pileus* circular to flabellate, sometimes notched, fibrillose with flattened, radially striate, azonate, from base to tip up to 5.5 cm long × 3.5 cm wide. *Pilial surface* wet, buff to yellowish, smooth-walled. *Pores* surface buff when fresh, buff brown when dry, pores hexangular, radially elongated, 4–5 mm long, 1–2 mm wide near stipe to 1 per mm at margin. *Context* (internal tissue of the fruit body) has a tough and fleshy to leathery texture when fresh, buff brown, corky, brittle when dry, buff brown, up to 4 mm thick. *Tube* continuous with the context, up to 5–6 mm thick. *Spore* prints white. *Hyphal system* dimitic. *Generative hyphae* without clamp connection, hyaline in KOH, thin and smooth-walled, 1.8–5 µm. *Skeletal-binding hyphae* thick walled, aseptate, highly branched, hyaline, 2.5–6.5 µm. *Cystidial* cells absent. *Basidia* persistant, clavate, sometimes bulged, constricted near septa, septate, pigmented, 11.5–11.8 × 5.9–6.3 µm. *Sterigmata* persistent, straight to incurved, tip sub-obtuse, 2–4 in numbers per basidium, 1–2.4 µm ($\bar{x}$ = 14.3 × 6 µm, n = 6). *Basidiospores*, cylindric to oblong, pigmented, smooth and thin walled, hyaline, 6.5–9.5 × 3.3–4.3 µm.

Culture characteristics: Colonies on PDA (Potato Dextrose Agar), center pale yellow (4A3), periphery white (1A1), floccose, 7.5 cm diam. in 24 days. Margin irregular, reverse pale yellow (4A3). *Hyphae* septate, unbranched to branched, smooth and thin walled, subhyaline to light olivacous, sometimes coroloid, rope like, twisted, forming loose and compact parallel bundles of hyphae, pigmented or granulated. *Chlamydospores* produced from superficial hyphae, terminal to lateral, solitary, bulbus, stalked, up to 8.9 × 8.6 µm wide. Clamp connections in hyphae absent.

Material examined: INDIA, Maharashtra, Pune District, on dead wood of *Dalbergia melanoxylon* (*Fabaceae*), 17 July 2019, D.K. Maurya (AMH 10219, **new record**), living culture (NFCCI 4776).

GenBank numbers: ITS = MT372798, LSU = MT372843.

Notes: Phylogenetic analysis based on a combined ITS and LSU sequence dataset of 35 taxa shows that the Indian taxon (NFCCI 4776) clusters with type of *Favolus septatus*. A Megablast search of the ITS sequence shows 99.48% similarity (569/572) with *Favolus septatus* (Zhou 287, Type) (Fig. 223). In our observation, the morphological features, especially length and width of basidiocarps is somewhat larger in the present collection than originally described in *Favolus septatus* (Fig. 222). The pilial surface is buff to yellowish in the present collection, while it is pinkish buff to yellowish in the original description of *F. septatus*. However, based on similarity regarding other morphological characteristics, and phylogenetic analysis, similarity of the present collection is confirmed as *Favolus septatus* (Zhou and Cui 2017). As per our understanding, this is the first report of *Favolus septatus* being reported from India. Therefore, described and illustrated here.

Russulales Kreisel ex P.M. Kirk, P.F. Cannon & J.C. David

Notes: We follow the latest treatment of *Russulales* (He et al. 2019).

Russulaceae Losty

Notes: *Russulaceae* was introduced to accommodate three genera *Lactarius*, *Russula* and *Russulina* with *Russula* as the type genus (Donk 1971). The family is characterized by convex to funnel-shaped pileus, stipes without annulus and volva, granular fragile context, spiny basidiospores, and sphaerocytes intermixed in filamentous hyphae. Currently, seven genera, *Boidinia*, *Gloeopeniophorella*, *Lactarius*, *Lactifluus*, *Multifurca*, *Pseudoxenasma* and *Russula* are known as members of *Russulaceae*. Approximately 1,900 known species are included in this family (He et al. 2019; Species Fungorum 2021). We follow the latest treatment of the genera in *Russulaceae* (He et al. 2019). Two new species *Lactarius pallidozonarius* and *Russula paravioleipes* are introduced with support from morphological and phylogenetic analyses.

Lactarius Pers.

Notes: *Lactarius* currently contains roughly 450 agaricoid and gasteroid species. Despite the establishments of *Lactifluus* and *Multifurca*, it is still one of the major groups in family *Russulaceae* based on morphological characters and phylogenic topology (Buyck et al. 2010; Verbeken et al. 2011, 2012; Stubbe 2012). In this study, one new species *Lactarius pallidozonarius* is introduced new to science. The morphology and phylogenetic placement of this new species are provided below (Figs. 224 and 225).

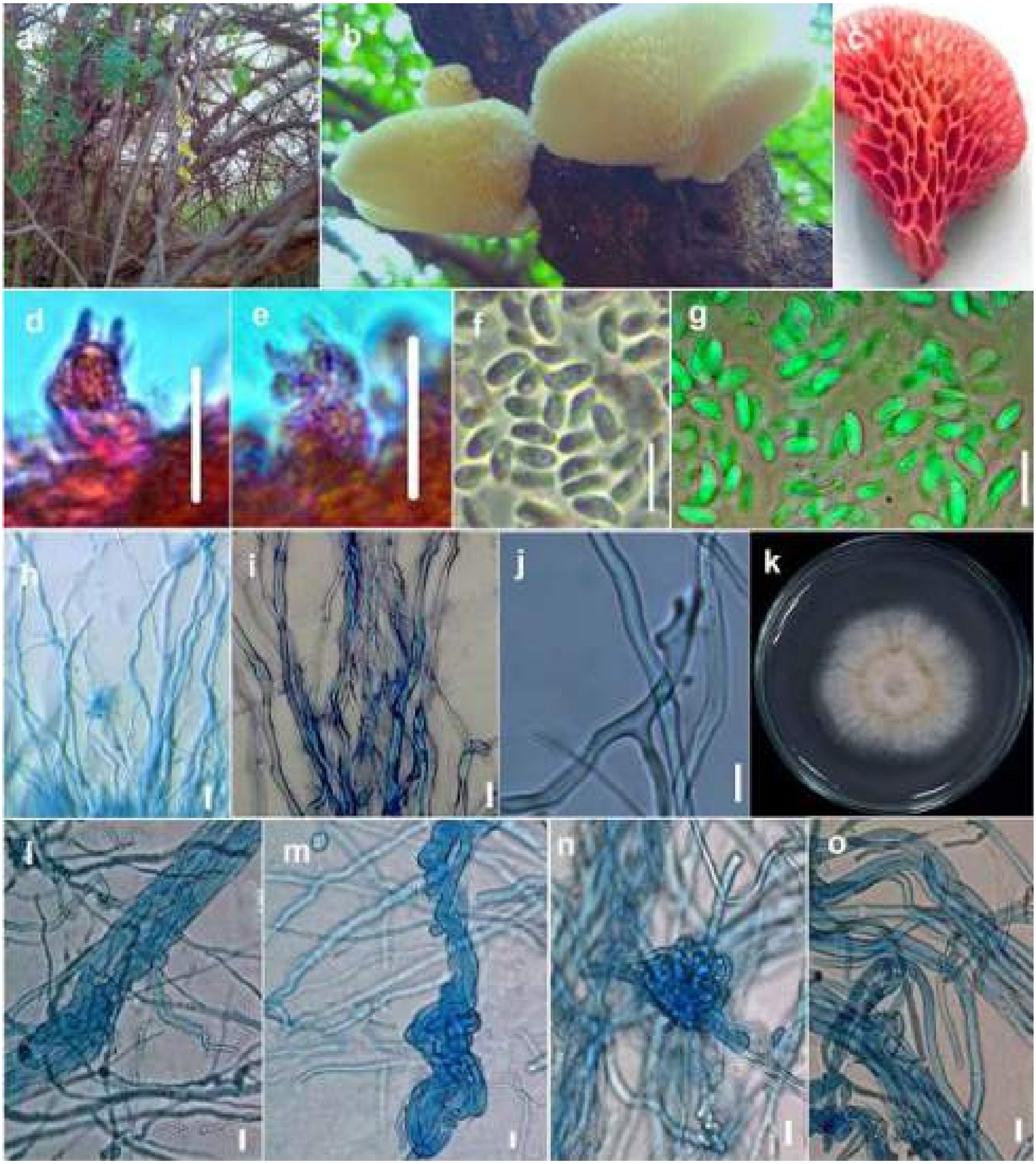


Fig. 222 ***Favolus septatus*** (AMH 10219, **new record**). **a** Habitat. **b** Basidiomata growing on substrate. **c** Basidioma showing hexagonal pores on lower surfaces. **d**, **e** Basidia with sterigmata. **f**, **g** Basidiospores. **h, i** Generative hyphae. **j** Skeletal binding hyphae. **k** Culture on PDA after 24 days (surface view). **l** Simple and compact hyphal bundle. **m**, **n** Simple and rope like twisted hyphae. **o** Parallel loose bundles of hyphae. Scale bars: **d**–**o** = 10 µm

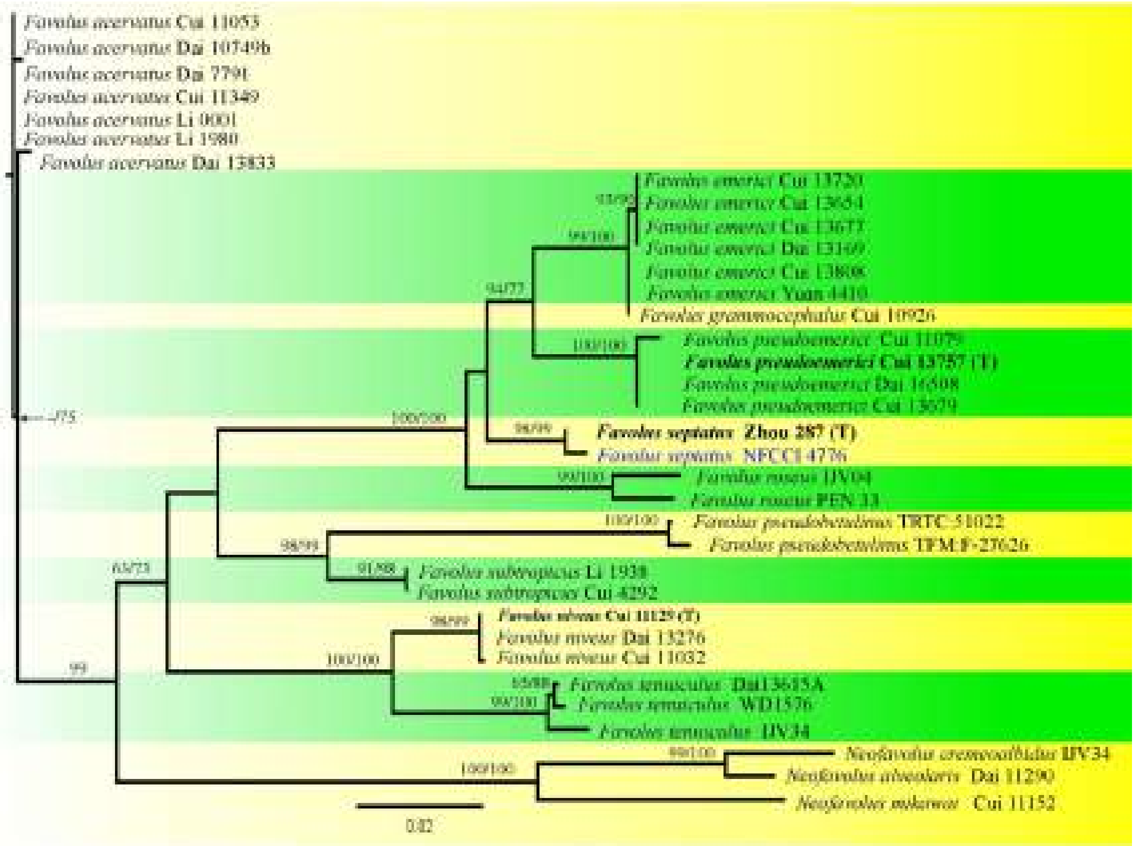


Fig. 223 The phylogenetic tree has been generated using maximum likelihood analysis based on LSU and ITS sequence data. Thirty-five strains are included in the LSU and ITS combined analyses comprising 1532 sites of which 1202 were the conserved and 320 were the variable sites, and 264 parsimony-informative sites. *Neofavolus* species are used as the outgroup taxa. The optimal tree with a final likelihood value of − 5057.256 is presented. Estimated base frequencies were as follows: A = 0.250, C = 0.250, G = 0.250, T = 0.250; substitution rates AC = 1.00000, AG = 4.63563, AT = 1.00000, CG = 1.00000, CT = 8.90564, GT = 1.00000; gamma distribution shape parameter α = 0.961. Bootstrap values for maximum likelihood (ML) equal to or greater than 50% are labeled on the nodes. Type sequences are in bold and newly generated sequence of *Favolus septatus* NFCCI 4776 is in blue bold

Lactarius pallidozonarius G.J. Li & W.F. Lin, ***sp. nov.***

Index Fungorum number: IF55864; *Facesoffungi number*: FoF 09206; Fig. 224

Etymology: Refers to the pale zonary pileus.

Holotype: HBAU 15004

Basidiomata medium sized. *Pileus* 42–58 mm in diam., convex to hemispheric when young, then applanate to shallow funneled, depressed at center when old, a pale erythrinus tinge of army brown (XL13‴i), vinaceous fawn (XL13‴b), fawn colour (XL13‴) to light vinaceous-fawn (XL13‴d) at center, fade to vinaceous buff (XL17‴d), avellaneous (XL17‴b) to pale vinaceous-fawn (XL13‴f) towards the margin, densely zonate, dull, smooth, not viscid when wet; margin decurved first, expanded to partly curled upwards when mature, even, not striate, rarely cracked. *Lamellae* adnate to slightly decurrent, dense, 16–20 pieces per centimeter in the edge, interveined, rarely forked near stipe, 4–5 mm in height, white (LIII), turning a pale brownish tinge of yellow ocher (XV17′) to buckthorn brown (XV17′i) when injured, lamellulae numerous. *Stipes* 25–34 × 12–17 mm, central, cylindrical, tapered towards the base, white (LIII), turning a brownish tinge of tawny-olive (XXXIX17″i) to isabella colour (XXX19″i) when bruised, dull, smooth, not viscid when wet, first stuffed, partly cavernous when mature, annulus absent. *Context* 3–5 mm thick at the pileus center, White (LIII), same colour changes as the lamellae, taste mild, smell indistinct. *Latex* watery white, unchanging. *Spore print* cream to pale ocher.

Basidiospores [200/4/4] (6.2)6.5–8.1(–8.4) × 4.8–6.0(–6.3) µm, Q = 1.01–1.30(1.34) µm, Q = 1.17 ± 0.08 µm), hyaline, subglobose to broad ellipsoid, rarely globose and ellipsoid, ornamentations amyloid, up to 1 µm in height, composed of incompletely to completely reticulated long ridges, isolated warts and short crests also exist, suprahilar area plage distinct and amyloid. *Basidia* 40–58 × 10–12 µm, hyaline, subcylindrical to clavate, four-spored, projecting 15–30 µm beyond hymenium, sterigmata 5–6 µm long. *Hymenial cystidia* not observed. *Marginal cells*

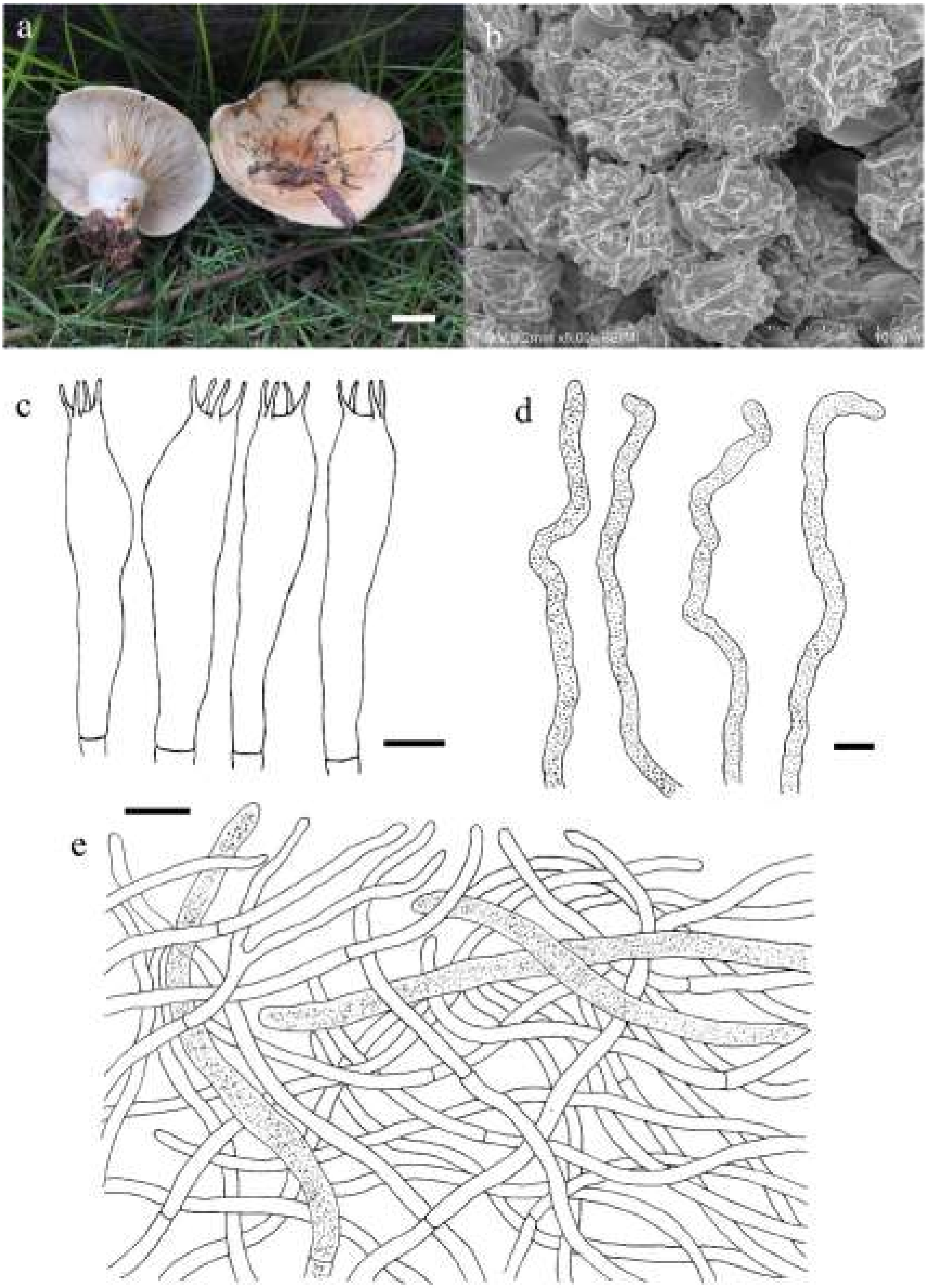


Fig. 224 ***Lactarius pallidozonarius*** (HBAU 15004, **holotype**). **a** Appearance of basidiomata on ground. **b** SEM photo of basidiospores. **c** Basidia. **d** Pseudocystidia. **e** Pileipellis. Scale bars: a = 10 mm, **c**–**e** = 10 μm

22–33 × 8–11 µm, subclavate to clavate, hyaline. *Pseudocystidia* abundant, aseptate, mostly embedded in subhymenium, rarely emergent, not brached, content granular; apex obtuse. *Pileipellis* a cutis, 100–300 µm thick, hyphae densely interwoven, rarely shriveled, 3–5 µm wide, hyaline, apex obtuse, rarely attenuated. *Stipipellis* an ixocutis, composed of interwoven, pale yellowish hyphae 3–5 µm wide.

Habit and habitat: scattered in broad-leaved forest of *Salix* spp. and *Cinnamomum camphora*.

Material examined: CHINA, Zhejiang Province, Hangzhou City, Xihu District, Zhejiang University, Zijingang Campus, on ground, 28 June 2019, W.F. Lin, 20190016 (HBAU 15004, **holotype**); *ibid*, 20190701 (HBAU 15006); *ibid*, 26 June 2019, 20190005 (HBAU 15005); *ibid*, 20190753 (HBAU 15007).

GenBank numbers: ITS = MN658520, MN658521, MN658522, MN658523.

Notes: A new species, *Lactarius pallidozonarius* (Figs. 224 and 225) resembles *L. inquinatus* for their pale reddish brownish tinge near pileus center, lamellae turning reddish brown when injured, and watery white latex. *Lactarius inquinatus* however, has larger basidiospores 7.8–11 × 6.5–8.2 µm with lower ornamentations up to 0.5 µm in height, absence of hymenial pleurocystidia, and a habitat of forest dominated by *Quercus* (Lee et al. 2019). The other two closely related European species, *L. evosmus* and *L. zonarius* can be differentiated as following: *L. evosmus* has basidiocarps of fruity smell, and lower and less reticulated basidiospore ornamentations; *L. zonarius* has pale yellowish tinged pileus and subreticulate basidiospores (Heilmann-Clausen et al. 1998).

Russula Pers.

Notes: *Russula* consists of ca. 800 agaricoid and gasteroid species which contain the most members of species in *Russulaceae* based on evidence of morphology and molecular data. In this study, one new species *Russula paravioleipes* is described based on morphological evidence and phylogenetic placement (Figs. 226 and 227).

Russula paravioleipes G.J. Li & W.F. Lin, ***sp. nov.***

Index Fungorum number: IF558649; *Facesoffungi number*: FoF 09207; Fig. 226

Etymology: Named after the close phylogenetic relationship with *R. violeipes*.

Holotype: HBAU 15001

Basidiomata small to medium sized. *Pileus* 28–46 mm diam., first hemisphere, then convex, applanate when mature, a tinge of brightly purplish red, daphne red (XXXVIII69″), spinal red (XXVI71′), to eosine pink (I1d), sometimes faded to a paler orange reddish tinge of peach red (I5b) to strawberry pink (I5d), smooth, glabrous, slightly viscid when wet; margin not striate, rarely cracked, peeling 1/3–1/2 from the edge, rose colour (XII71b) to spinal pink (XXVI71′b). *Lamellae* adnate, 3–4 mm in height, 13–16 pieces per centimeter at edge, not forked, interveined, white (LIII), unchanging when bruised, lamellulae not observed. *Stipes* 29–48 × 10–13 mm, central to subcentral, cylindrical, rugulose longitudinally, White (LIII), unchanging when injured, smooth, dull, not viscid when wet, slightly attenuate downward the base, first stuffed, hollow when old, annulus absent. *Context* 2–3 mm thick at pileus center, White (LIII), unchanging, taste mild, smell indistinct. *Spore print* pale cream (Romagnesi IIa–IIb).

Basidiospores [150/3/3] 5.5–7.1(–7.4) × 5.5–7.2 µm, Q = 1.02–1.27(1.31) µm, Q = 1.17 ± 0.07) µm, hyaline, subglobose to broad ellipsoid, rarely globose and ellipsoid, ornamentations amyloid, up to 0.7 µm in height, composed of long ridges interconnected as incomplete reticulum, isolated warts and short crests rare, suprahilar area plage distinct but inamyloid. *Basidia* 35–45 × 8–12 µm, cylindrical, subcylindrical to subclavate, rarely clavate four-spored, projecting 10–20 µm beyond hymenium, sterigmata 4–6 µm long. *Hymenial cystidia* 91–110 × 8–10 µm, hyaline, fusiform to subulate, sometimes clavate, unchanging in sulfovanillin (SV), apex acute. *Pileipellis* two layered; epipellis pseudoparenchymatous, ca. 150–200 µm deep, not clearly delimited from the spherocytes in context, terminal cells hyaline, subulate to bayonet-shaped, 57–85 × 5–8 µm, subapical cells 7–11 µm wide, pileocystidia absent; subpellis composed of somewhat gelatinized, densely interlaced, rarely branched and septate, hyaline hypha 3–6 µm wide. *Stipitipellis* a cutis, composed of parallel hyaline hypha 3–5 µm wide.

Habit and habitat: scattered in broad-leaved forest of *Salix* spp. and *Cinnamomum camphora*.

Material examined: CHINA, Zhejiang Province, Hangzhou City, Xihu District, Zhejiang University, Zijingang Campus, 26 June 2019, W.F. Lin, 20190001 (HBAU 15001, **holotype**); *ibid*, 20190688 (HBAU 15002); *ibid*, 20190699 (HBAU 15003).

GenBank numbers: ITS = MN658517, MN658518, MN658519.

Notes: *Russula paravioleipes* is a member of subsection *Amoeninae* Buyck, subgenus *Heterophyllidia* Romagn., section *Heterophyllae* Fr. because of its absence of pileocystidia, long and subulate terminal hyphal cells of pileipellis, and empty hymenial cystidia not turning grey or black in Sulfovanillin (Sarnari 1998). The reddish tinged pileus is the remnants of "*R. violeipes* Quél." in Park et al. (2013). The Korean "*R. violeipes*" can be differentiated from this new species for its areolate pileus surfaces and flushed stipes. However, the ITS phylogenetic analyses of this study cannot distinguish them (Fig. 227). Whether or not these Chinese and Korean specimens are of the same species still needs further analysis. The other members of subsection

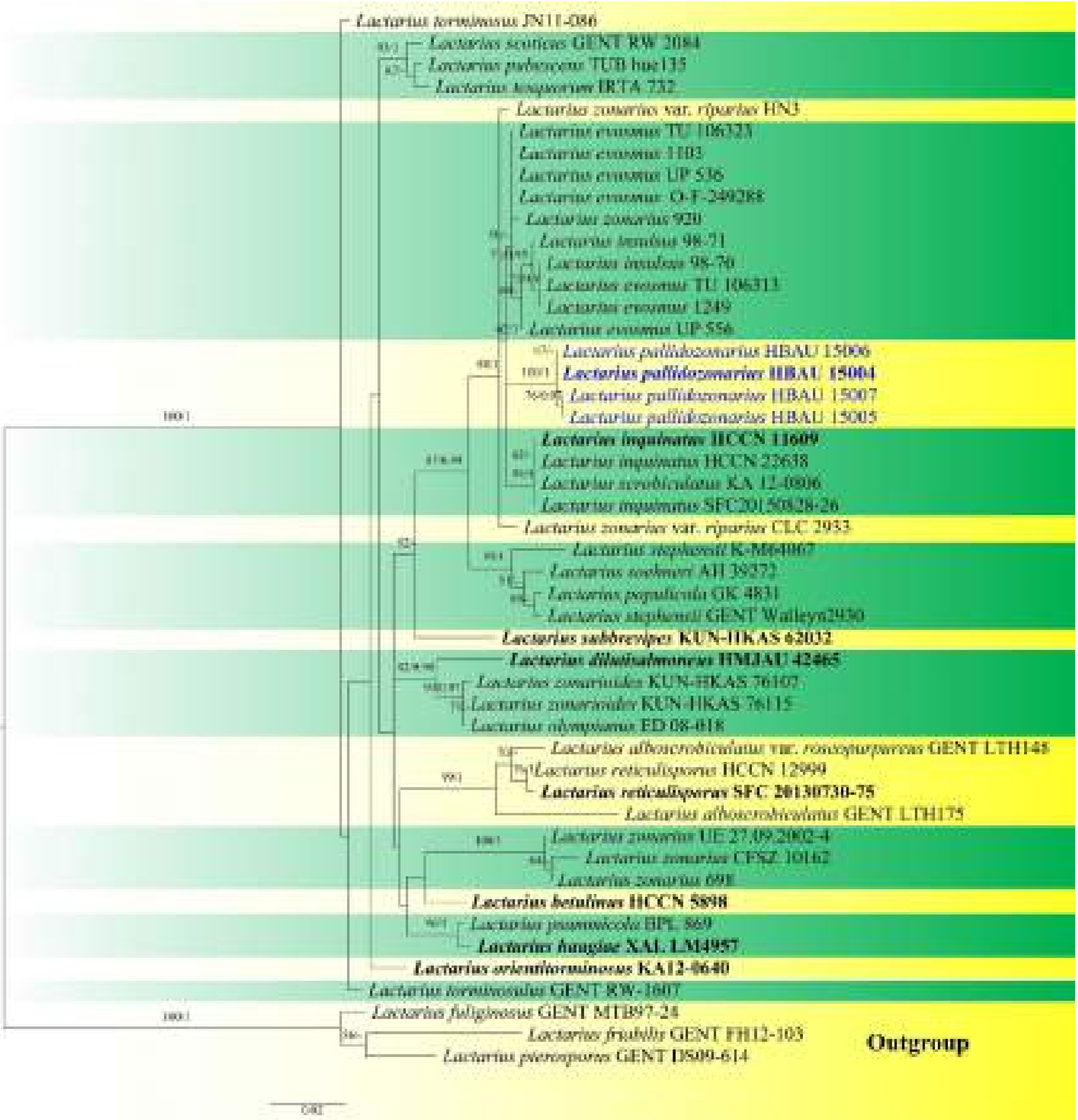


Fig. 225 Phylogram generated from maximum likelihood analysis based and ITS sequence data representing *Lactarius pallidozonarius* and closely related species. Related sequences are taken from Lee et al. (2019), UNITE and GenBank databases. Forty-nine sequences are included in the combined analysis which comprises 2505 characters 546 characters for ITS after alignment. *Lactarius friabilis* (GENT FH12-103), *L. fuliginosus* (GENT MTB97-24) and *L. pterosporus* (GENT DS09-614) in subg. *Plinthogalus* are used as the outgroup taxa. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RAxML tree with a final likelihood values of − 2161.573832 is presented. The matrix had 158 distinct alignment patterns, with 0.71% undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.229615, C = 0.259476, G = 0.226053, T = 0.284855; substitution rates AC = 0.965485, AG = 9.458565, AT = 0.865989, CG = 0.392267, CT = 8.367348, GT = 1.000000; gamma distribution shape parameter α = 0.217720. Bootstrap values for maximum likelihood (ML) greater than 50% and posterior probability values greater than 0.90 (the rounding of values to 2 decimal proportions) from Bayesian-inference analysis are shown above the nodes. Sequences of type specimens are presented in bold and newly generated sequences are in blue

Amoeninae can be distinguished from *R. paravioleipes* (Fig. 226) by the following morphological characteristics: *R. violeipes* in Europe differs in its violaceous pileus and conspicuous hymenial cystidia 10–20 μm wide; *R. amoenicolor* Romagn. has purple, green, or variegated pileus, dark cream basidiospore print (IIc–IId), and a habitat of *Quercus* forest; *R. amoena* can be differentiated by its violaceous purple to olive greenish tinged pileus, and longer basidia 60–70 × 9–12 μm (Sarnari 1998); *R. mariae* differs in its soft pruinose pileus surface, and wider hymenial cystidia up to 12.5 μm (Adamčík et al. 2018).

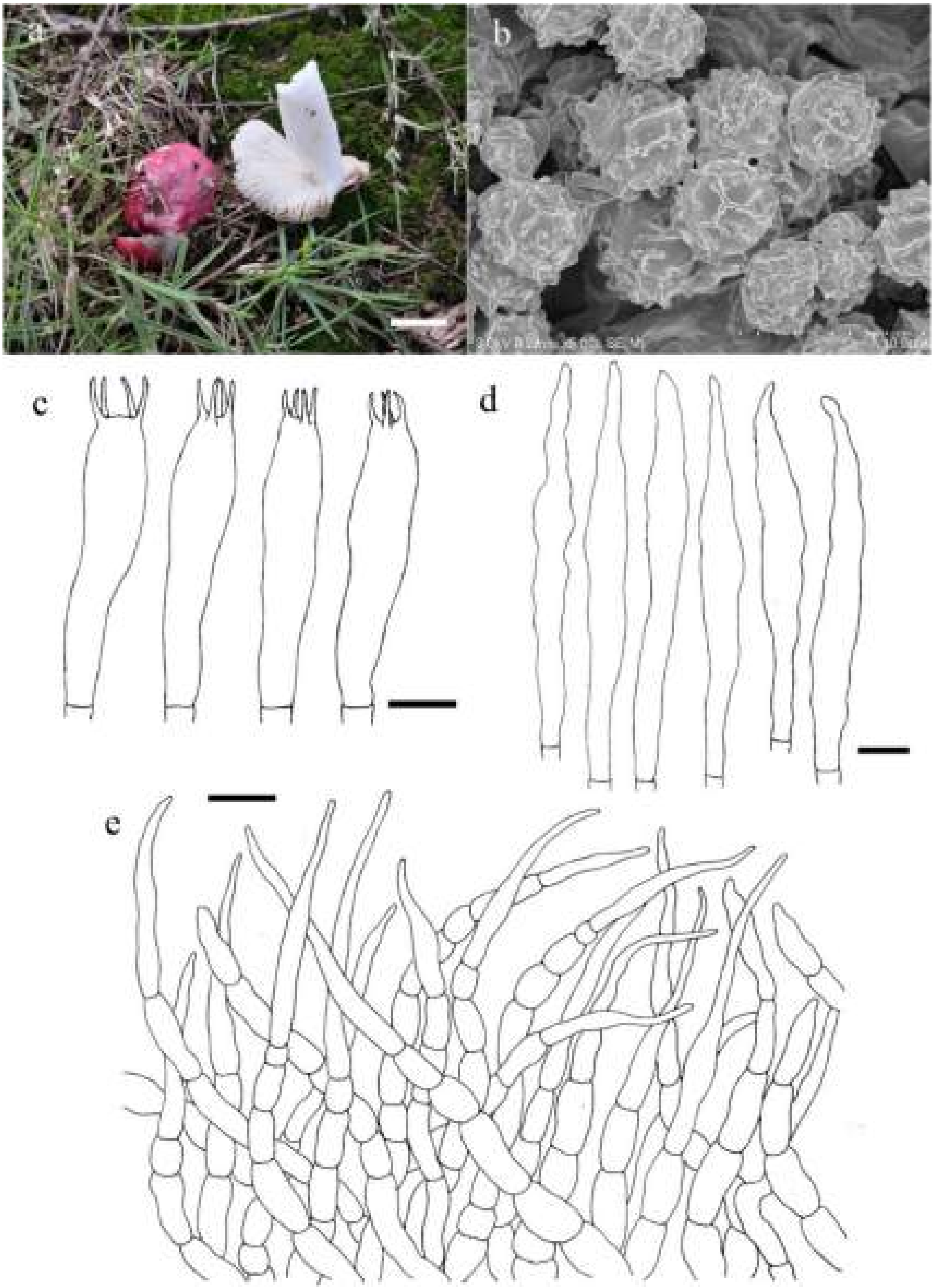


Fig. 226 ***Russula paravioleipes*** (HBAU 15001, **holotype**). **a** Appearance of basidiomata on ground. **b** SEM photo of basidiospores. **c** Basidia. **d** Pseudocystidia. **e** Pileipellis. Scale bars: **a** = 10 mm, **c**–**e** = 10 µm

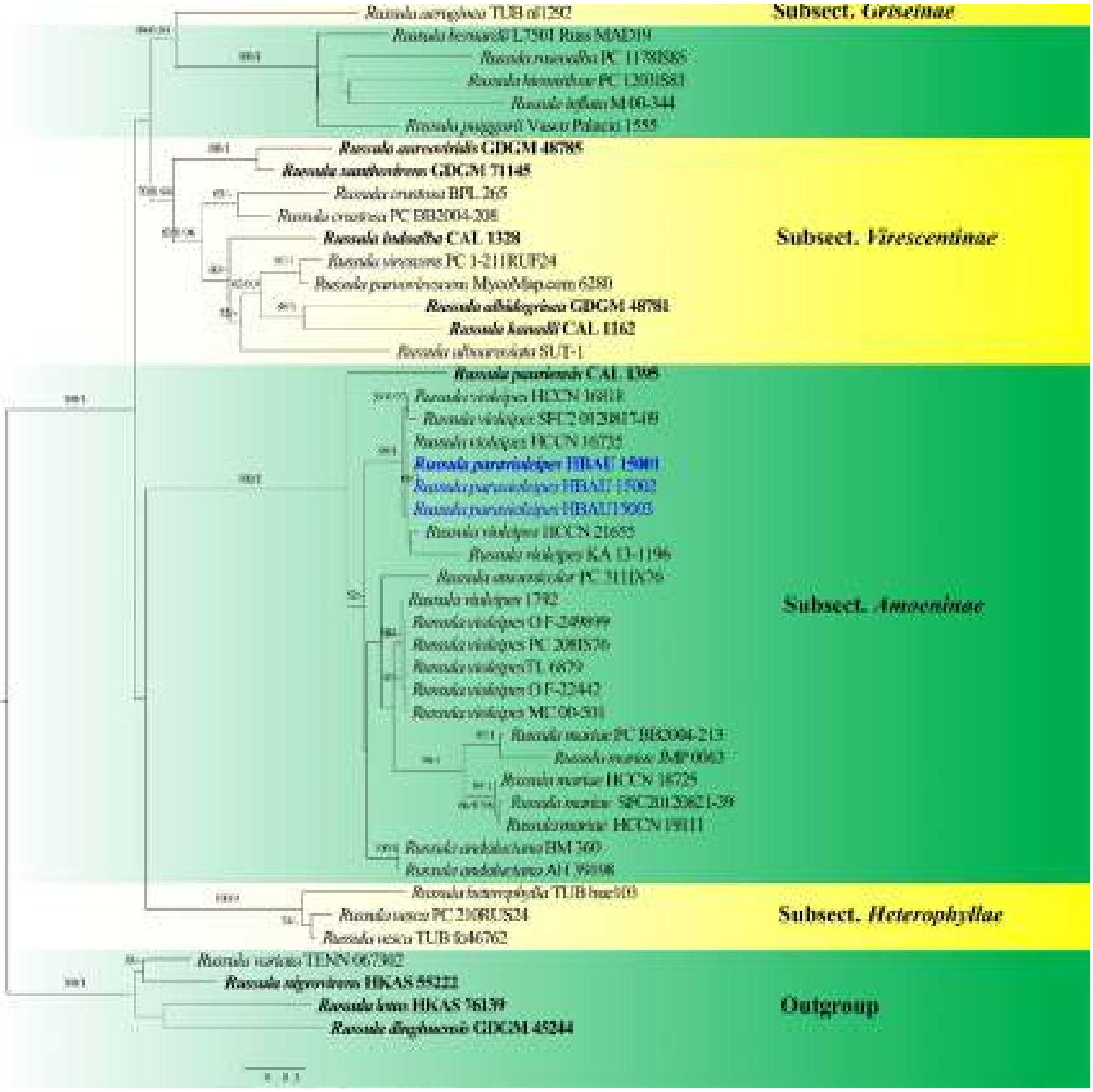


Fig. 227 Phylogram generated from maximum likelihood analysis based and ITS sequence data representing *Russula paravioleipe* and related species in Sect. *Heterophyllae*. Related sequences are retrieved from GenBank and UNITE databases. Forty-seven ITS sequences are included in the analysis comprises 546 characters after alignments. *Russula dinghuensis* (GDGM 45244), *R. lotus* (HKAS 76139), *R. nigrovirens* (HKAS 55222) and *R. variata* (TENN 067302) in Sect. *Cyanoxanthinae* (Subg. *Heterophyllidia*) are used as the outgroup taxa. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RAxML tree with a final likelihood values of − 4326.910274 is presented. The matrix had 281 distinct alignment patterns, with 2.78% undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.217569, C = 0.256487, G = 0.225771, T = 0.300173; substitution rates AC = 1.359519, AG = 4.554062, AT = 0.588669, CG = 0.728567, CT = 5.548012, GT = 1.000000; gamma distribution shape parameter α = 0.379017. Bootstrap values for maximum likelihood (ML) greater than 50% and posterior probability values greater than 0.90 (the rounding of values to 2 decimal proportions) from Bayesian-inference analysis are shown above the nodes. Type and ex-type are indicated in bold and the newly generated sequences are indicated in blue

Microbotryomycetes R. Bauer et al.

Notes: The classification of the orders in Microbotryomycetes follows Begerow and McTaggart (2018).

Microbotryales R. Bauer & Oberw

Notes: There are two families in this order: *Microbotryaceae* and *Ustilentylomataceae* (Vánky 2013; He et al. 2019).

Microbotryaceae R.T. Moore

Notes: *Microbotryaceae* was introduced by Moore (1996). Five genera are currently recognized in this family (He et al. 2019; Denchev et al. 2020).

Microbotryum Lév.

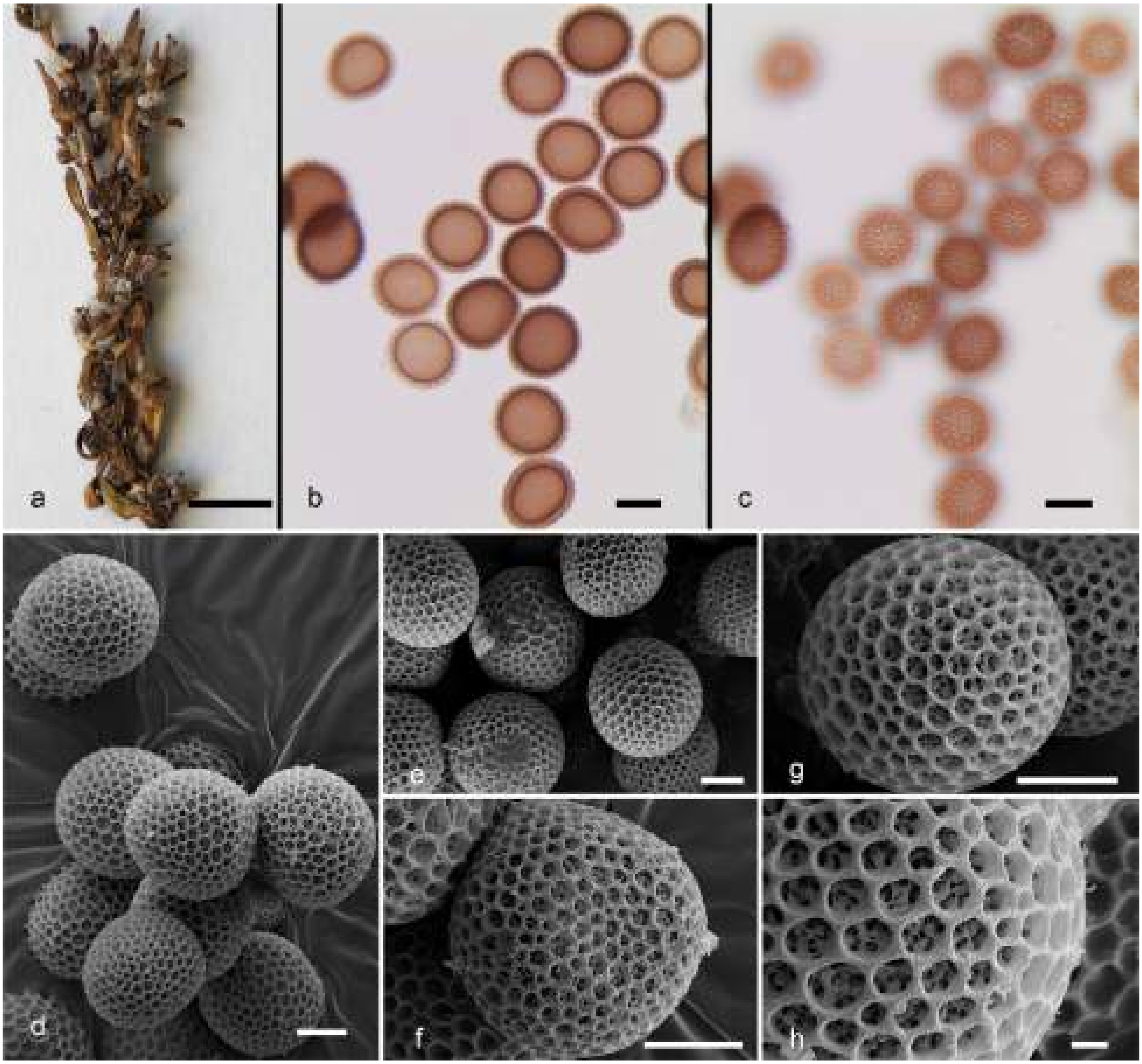


Fig. 228 ***Microbotryum polycnemoides*** (SOMF 30200, **holotype**). **a** Habit. **b**, **c** Spores in LM (in median and surface view, respectively). **d**–**h** Spores in SEM. Scale bars: **a** = 0.5 cm, **b**, **c** = 10 µm, **d**–**g** = 5 µm, **h** = 1 µm

Notes: In its broad circumscription, *Microbotryum* comprises 99 species (Denchev and Denchev 2011; Vánky 2011; Piątek et al. 2012, 2013; Denchev et al. 2019; Ziegler et al. 2018; Kemler et al. 2020). During an examination of *Polygonum* specimens in the herbarium of the Meise Botanic Garden, Belgium (BR), a smut fungus belonging to *Microbotryum* was found on a specimen of *Polygonum polycnemoides* (BR, s.n.) from Turkey. Based on distinct morphology (Table 6; Fig. 228) and phylogenetic evidence (Fig. 229), this fungus is introduced here as a novel species.

Microbotryum polycnemoides T. Denchev, Denchev, Kemler & Begerow, ***sp. nov.***

Index Fungorum number: IF557222; *Facesoffungi number*: FoF 07517; Fig. 228

Etymology: The specific epithet refers to the host species.

Holotype: SOMF 30200

Parasitic on *Polygonum polycnemoides*. *Infection* systemic, all flowers of an inflorescence affected. *Sori* in perianth tube, hypanthium, and filaments of each flower, and in achenes, swelling considerably the affected organs and filling them with pulverulent, blackish brown spore mass. Ovaries, anthers, and perianth lobes remain intact. *Spores* subglobose, broadly ellipsoidal, ovoid, globose, slightly irregular or sometimes ellipsoidal, (14–)15–19(–21) × (12.5–)13.5–17(–18.5) (16.6 ± 1.1 × 15.2 ± 0.9) µm (n = 300), medium reddish brown; wall reticulate, (1.7–)2–2.7(–3) µm thick (including reticulum), meshes (8–)9–12(–13) per spore diameter, 0.4–2.5(–3.5) µm wide, muri 1–1.9(–2.3) µm high. In SEM meshes mostly rounded, interspaces often perforate with up to 4(–6) holes per interspace, sometimes with 2(–4) warts.

Material examined: TURKEY, the Anti-Taurus Mts (Aladağlar), Niğde Province, near Çamardı, Mt. Küçük Denizli, alt. 2300–2500 mls, on *Polygonum polycnemoides* Jaub. & Spach (*Polygonaceae*), 11 August 1992, V. Vašák s.n. (SOMF 30200, **holotype**).

GenBank numbers: ITS = MN989380, LSU = MN989381.

Additional material examined: *Microbotryum aviculare* (Liro) Vánky—SWEDEN, Uppland, near Uppsala, on *Polygonum aviculare* L., 10 August 1978, Sz., T. & K. Vánky (as '*Ustilago avicularis*', H.U.V. 7439, kept at BRIP); *M. shastense* (Zundel) Vánky—USA, California, Siskiyou Co., Mt. Shasta, 41°22′N 122°12′W, ca 2700 msl, on *Polygonum shastense* W.H. Brewer, 8 August 1988, F. Oberwinkler et al., 3207 (Vánky, Ustilag. 717, in SOMF 19825; topotype).

Notes: *Polygonum polycnemoides* is an Irano-Turanian species, distributed in Armenia, Nakhichevan, Turkey, Syria, Lebanon, Israel, North Iraq, Iran, the Central Asian Republics, Xinjiang, Mongolia, Afghanistan, and West Himalaya (Davis 1967; Li et al. 2003; Uotila 2017). *Microbotryum polycnemoides* is known only from the type collection.

Microbotryum contains species that parasitize plants from many different lineages of euasterids, with host-specificity of individual parasite species in general being exceptionally high (Kemler et al. 2020). On hosts in *Polygonum*, only two species of *Microbotryum* have been previously known: *M. aviculare* on *Polygonum aviculare*, *P. norvegicum* and *P. oxyspermum* subsp. *raii* (from Europe, Asia, and North America), and *M. shastense* on *Polygonum shastense* (from North America) (Vánky 2011). *Microbotryum polycnemoides* (Fig. 228) can be easily distinguished from *M. aviculare* and *M. shastense* in having a different colour of the spore mass, larger spores, higher number of meshes per spore diameter, and higher spore wall muri (Table 6).

Microbotryum polycnemoides is closely related to *M. parlatorei* (97% MLBS support) and does not form a monophylum with *M. shastense*. The topology of our phylogenetic tree additionally indicates that *M. polycnemoides* is not closely related to *M. shastense*, but there is no statistical support for this relationship. Further analyses are warranted to understand the relationship between the clade of *M. polycnemoides*/*M. parlatorei* and *M. shastense* (Fig. 229).

Mortierellomycota Tedersoo, Sanchez-Ramirez, Kõljalg, Bahram, M. Döring, Schigel, T.W. May, M. Ryberg & Abarenkov

Mortierellomycetes Doweld

Mortierellales Caval.-Sm.

Notes: We follow the latest treatments and updated accounts of *Mortierellales* in Wagner et al. (2013) and Spatafora et al. (2016).

Mortierellaceae A. Fisch.

Notes: We follow the updated concept of *Mortierellaceae* as presented in Wagner et al. (2013).

Mortierella Coem.

Notes: *Mortierella* (phylum Mortierellomycota) was described by Coemans (1863) based on the type *M. polycephala*. *Mortierella* is widespread in the temperate zone, where it is almost cosmopolitan and occurs in a wide range of habitats; *Mortierella* sp. have been reported from bat dung (Degawa and Gams 2004), anthropods (Hyde et al. 2017), freshwaters (Nguyen et al. 2019), and from the recently deglaciated barren ground in glacier forefields (Kuhnert et al. 2012; Dresch et al. 2019). Numerous pure culture isolates of *Mortierella* spp. were obtained during a study focusing on the seasonal dynamics of soil fungi in a glacier forefield, among them also *Mortierella gamsii*. Moreover, an undescribed species was repeatedly isolated. Micromorphological studies elucidated clear distinctive

Table 6 Diagnostic morphological characters of the smut fungi of *Microbotryum* on *Polygonum*

Character	*M. aviculare*	*M. polycnemoides*	*M. shastense*
Spore mass (colour)	Cinnamon	Blackish brown	Dark reddish brown
Spore length (µm)	(9.5–)10.5–14.5(–16)	(14–)15–19(–21)	(7–)7.5–10(–11)
Spore mean length (µm)	12.4 ± 0.9	16.6 ± 1.1	8.8 ± 0.6
Meshes per spore diameter (number)	(4–)5–8(–9)	(8–)9–12(–13)	6–9
Muri (height, µm)	0.6–1.1(–1.4)	1–1.9(–2.3)	0.5–0.8

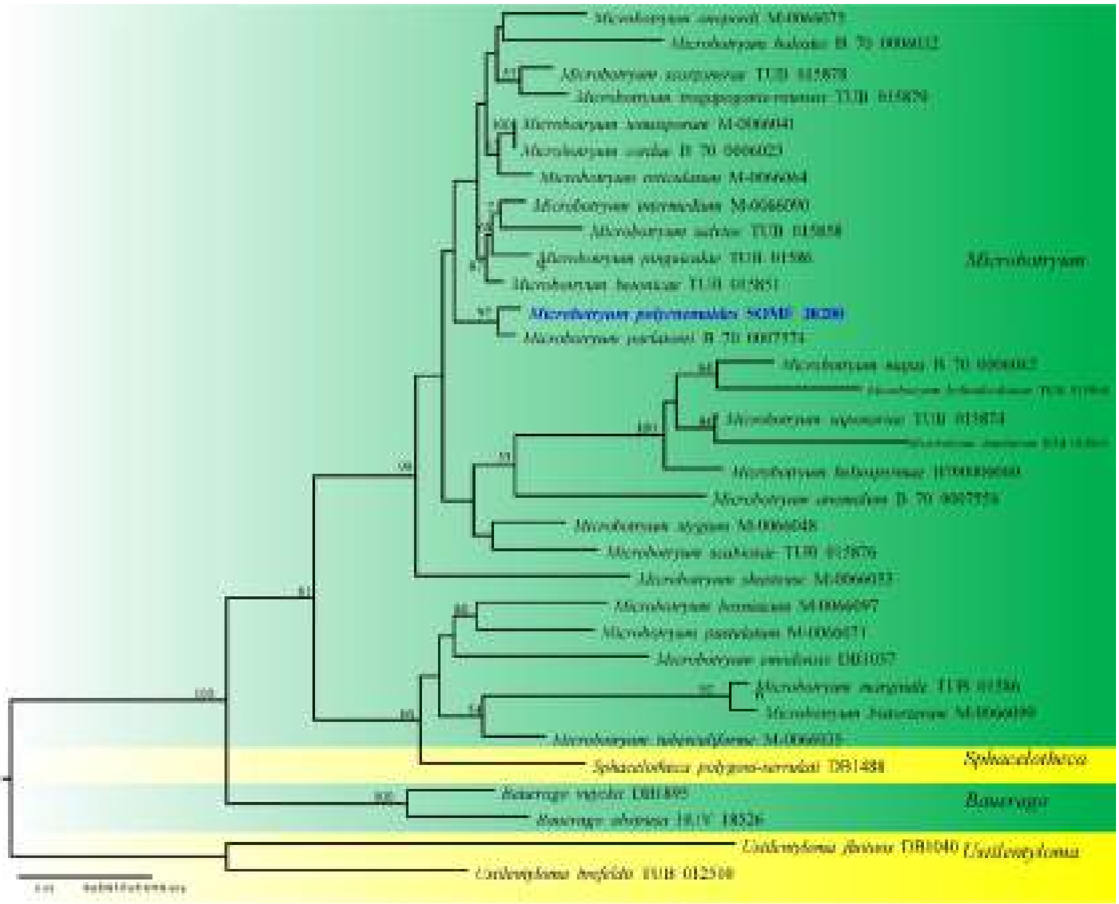


Fig. 229 Most likely tree inferred by maximum likelihood analysis via RAxML version 8.2.11 (Stamatakis 2014) based on concatenated MAFFT v7.450 (Katoh and Standley 2013) alignments of ITS and LSU dataset for *Microbotryum* species and several closely related genera in *Microbotryales*. The tree is based on the same dataset as in Kemler et al. (2009), but was pruned to only show one specimen per fungal species. Values at nodes indicate bootstrap values inferred by 100 replicates; only values greater than 50% are shown. The newly generated sequence is in blue bold

morphological characters. Together with phylogenetic analyses of ITS and LSU sequence data, a novel species *Mortierella solitaria* is introduced (Figs. 230, 231, 232, 233 and 234).

Mortierella solitaria Telagathoti, M. Probst & Peintner ***sp. nov.***

Index Fungorum number: IF557446; *Facesoffungi number*: FoF 09208; Figs. 230, 231, 232

Etymology: Latin solitaria means solitary, living / acting on its own. This refers to i) the unbranched sporangiophores, which usually appear solitary or in small groups on the mycelium. ii) The phylogenetic position without a clear sister–group. iii) The solitary status of people in quarantine during the COVID 19 pandemic.

Holotype: OAS3

Saprobic barren or poorly vegetated ground in alpine areas. **Asexual morph** *Colonies* rapidly forming characteristic concentrically zonate pattern consisting of broad lobes is produced on LCA media, whereas this pattern is inconspicuous under the thick cottony layer of mycelium, which readily appears on PDA from day 1. A pronounced smell of garlic at 10 °C changes to a faded slightly fruity odour when incubated at the higher temperatures. Colonies exhibiting faster growth rates at temperatures > 10 °C, forming thick mycelial layers, but no or very few sporangia. *Sporangia* hyaline, many–spored, globose with a smooth-walled surface. They are 15–22 µm diam. with a deliquescent wall. A conspicuous collarette is left after spore liberation. *Sporangiophores* arise from both the aerial and substrate mycelium. They are simple and unbranched, 50–200 µm (–500 µm) tall, non–septate. Sporangiophores are tapering from 4–9 µm at the base to 3–4 µm near the tip. One of the isolates (OAS4) formed part of the sporangiophores with a swollen base similar to those formed by *M. alpina*. Sporangiophores typically awl–like, sometimes slightly widening to an inconspicuous 6–8 µm wide apophysis–like inflation. The columella is slightly bulged, but without spinose outgrowing typical for *M. gamsii*. *Sporangiospores* are subglobose

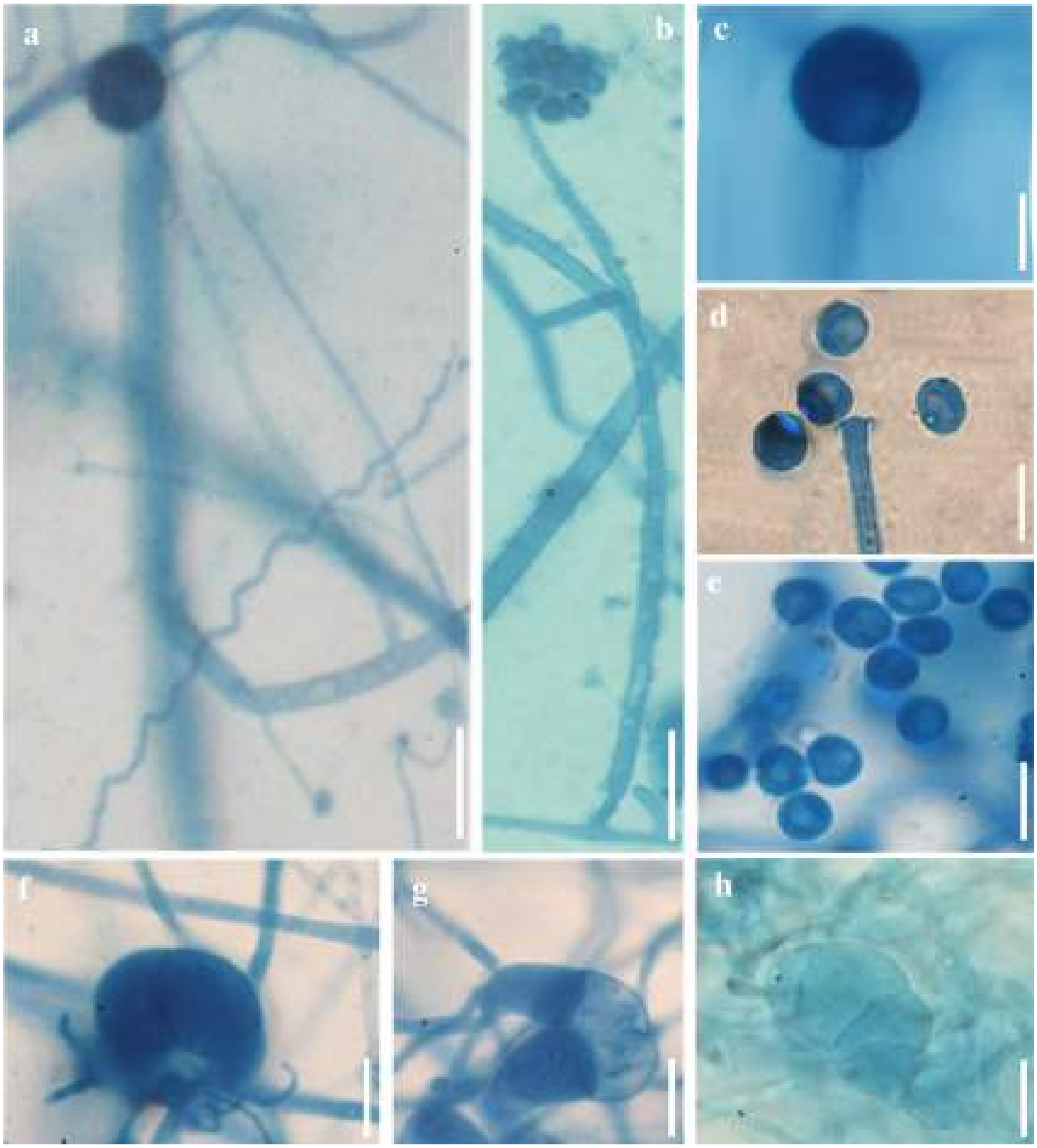


Fig. 230 ***Mortierella solitaria*** (OAS3, **holotype**). **a**, **b** Sporangiophores formed on aerial or basal hyphae. **c** Sphaerical sporangial head with intact smooth peridium and small apophysis-like widening of the sporangiophore. **d** Tip of a sporangiophore with collarette and spores. **e** Sporangiospores released from the sporangium. **f**–**h** Initial stages of gametangiogamy with empty, aborted zygospore. Scale bars: **a**, **b** = 20 µm, **c**–**h** = 10 µm

to cylindrical–ovoid, smooth-walled, (6–) 7–8 (–10) µm × (5.5–)6–8 µm ($\bar{x}$ = 7.8 × 6.9 µm, n = 30), often with an oil drop. *Gemme* with 5.3–5.7 µm diam., appears macroscopically as white-spotted clusters. They were observed in the substrate mycelium on Hempseed agar at 25 °C. Chlamydospores and stylospores undetermined. **Sexual morph** Undetermined. The formation of zygospores is initiated, but aborted on PDA and SNA at 20 °C: suspensor cells and the progametangia are formed but do not further develop: empty hyphal compartment remained after plasmogamy.

Culture characteristics: Colonies rapidly growing, white, and filling the agar plate (8 cm) within 5–10 d of incubation (Fig. 231).

Material examined: AUSTRIA, Obergurgl, Rotmoos glacier forefield 2300 msl., barren ground with scattered *Saxifraga aizoides* and *Persicaria vivipara,* 10 September 2016, A. Telagathoti, J. Falbesoner P. Dresch (OAS3, **holotype**), ex–type living culture JMRC: SF013920; OAS4 (JMRC: SF013921) and OAS5 (JMRC: SF013922) are from the same origin, but different sampling sites.

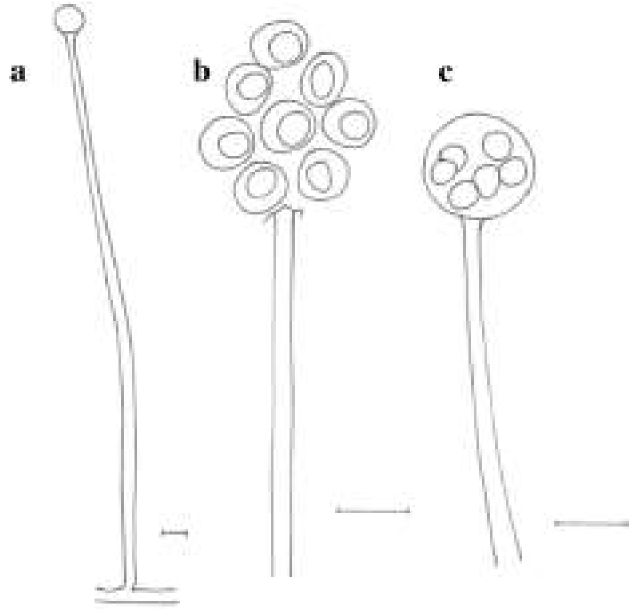


Fig. 231 Sporangia of ***Mortierella solitaria***. **a** Length of the sporangia (–500 µm tall). **b** Sporangiophore tips showing collarette and the spores. **c** Details of the peridial wall of the sporangia. Scale bars: **a**–**c** = 10 µm

GenBank numbers: ITS = MT279272, MT279273, MT279274, LSU = MT279275, MT279276.

Notes: The rDNA ITS sequences generated from our *Mortierella solitaria* isolates showed < 95% sequence similarity to the sequences generated from the type materials of *M. gamsii* and of *M. fluviae*. The phylogenetic analysis (maximum likelihood, parsimony bootstrap analysis, and Bayesian inference analysis; Fig. 233) indicates that *M. solitaria* could belong to *M. gamsii* species complex. However, *M. solitaria* lineage is clearly distinct from *M. gamsii, M. fluviae, M. exigua, M. elongata, M. alpina, M. schmuckeri, M. cogitans* and *M. sclerotiella* (Fig. 232). An analysis of the concatenated ITS and LSU sequences confirmed that *M. solitaria* constitutes a distinct lineage of *Mortierella* (Fig. 234), but relationships have not yet been further resolved.

Mortierella solitaria differs in several morphological features from similar species. Based on the classical concepts (Linnemann 1941), *M. solitaria* species could either be placed in *M. simplex* or *M. alpina* morpho-groups. However, species in *M. simplex* group usually have sporangiophores longer than 200 µm, and typical representative species of *M. alpina* morpho-group have sporangiophores with a typically widening base. All currently described species of *M. alpina* group differ due to e.g., presence of chlamydospores or different spore morphology. According to our studies, only one (OAS4) of the three isolates occasionally forms sporangiophores with a swollen base. However, the sporangiophore base is only slightly widened. In *M. simplex* group, *M. rostafinskii* could be similar, but it differs by larger sporangiophores and smaller spores 5–6.5 × 3–5 µm. Sequences of these species (including sequences from type strains) are available in public databases, further confirming that *M. solitaria* is a morphologically and phylogenetically distinct species.

Mortierella solitaria is clearly distinct from all species in *M. gamsii* complex: *M. gamsii* differs by its branched sporangiophores (Figs. 230 and 231). *Mortierella fluviae* differs clearly by branched sporangiophores with a bell-shaped apophysis, *M. humilis* differs by warted sporangiophores and *M. exigua* has pronounced acrotonous branching of larger sporangiophores and has amoeba-like chlamydospores. Two of *M. solitaria* isolates (MT279272 and MT279274) were found to be associated with endohyphal bacteria of *Burkholderiaceae*. The isolates were cured with antibiotics before performing the experiments in this current study.

Mucoromycota Doweld

Mucoromycetes Doweld

Mucorales Dumort

Notes: We follow the latest treatments and updated accounts of *Mucorales* in Phookamsak et al. (2019) and Wanasinghe et al. (2018).

Mucoraceae Fr.

Notes: We follow the latest treatments and updated accounts of *Mucoraceae* in Spatafora et al. (2016), Wanasinghe et al. (2018), and Phookamsak et al. (2019).

Mucor Fresen.

Notes: *Mucor* was described by Fresenius (1850), and contains the largest number of species within the *Mucorales* (Benny et al. 2014; Walther et al. 2013). Species of *Mucor* are characterized by the formation of sporangia, equally and unequally shaped suspensors, as well as the presence of apophysis, rhizoids, and sporangiola (Walther et al. 2013; Wagner et al. 2019). *Mucor* species are known to be saprobes that are usually isolated from dung, soil, water, food products, other plant debris, or human clinical specimens (Benny 2008; Álvarez et al. 2011; Walther et al. 2013; Wanasinghe et al. 2018). Some species have positive or negative impacts on human activities. Several species of *Mucor* have important biotechnological applications and are used in Asia for the production of fermented foods and beverages (Batra and Millner 1974; Nout and Aidoo 2010). *Mucor* belongs to the main genera causing mucormycoses (Jeong et al. 2019). To date, 12 species are known to be involved in infections (Wagner et al. 2019). *Mucor* contains 76 accepted species (Walther et al. 2019).

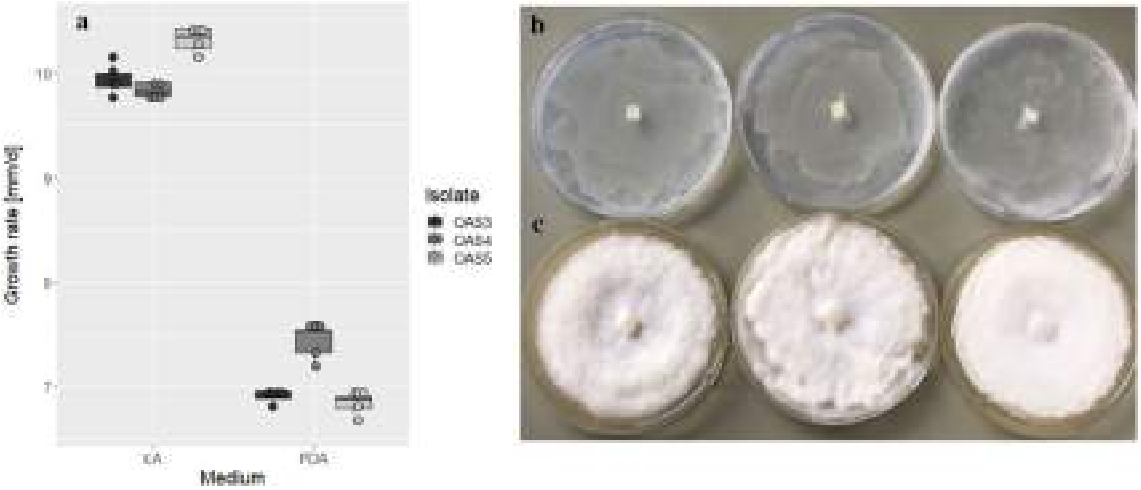


Fig. 232 **Growth rates of *Mortierella solitaria*** as boxplots. **a** Boxplot displaying the mean 25th and 75th percentiles as box and outside values as dots. **b**, **c** Seven days old culture of the isolates on LcA and PDA

During an investigation of fungi of the order *Mucorales* from insects in the Jeonnam Province, Korea, a new species *Mucor harpali* was isolated from the head of a bombardier beetle (*Harpalus* sp.). The new species is described and illustrated herein based on morphological characters and molecular phylogenetic analyses (Figs. 235, 236 and 237).

Mucor harpali Hyang B. Lee, P.M. Kirk & T.T.T. Nguyen ***sp. nov.***

Index Fungorum number: IF557325; *Facesoffungi number*: FoF 09209; Fig. 235

Etymology: Referring to the name of a bombardier beetle, *Harpalus* sp.

Holotype: CNUFC HT18012

Colonies on MEA at 25 °C in darkness moderate reddish-brown (8.1R/3.1), the central part with mature sporangia and the margin with immature sporangia, reaching 72−75 mm diam. after 4 days incubation; reverse vivid yellow (1.3Y/7.3). *Sporangiophores* arising directly from the hyphae immersed in the substrate, tall, 8–19.5 µm diam., usually unbranched or with few secondary branches, septate or coenocytic; one or two septa may be formed below the columella; branches commonly bearing a sterile sporangium. *Sporangia* non-apophysate, hyaline to yellow when young, becoming reddish-brown, globose, subglobose, 36.5–103.5 × 35–100.5 µm, wall deliquescent. *Columellae* often globose to subglobose, but also obovoid with truncate base, 27.5–55.5 × 26.5–52.5 µm, with distinct colar; a few reniform columellae also found. *Sporangiospores* mostly ellipsoidal, subglobose, reniform, or some irregular, 5.5–11.5 × 3–5.5 µm, smooth-walled. *Oidia* often observed. *Zygospores* not observed. Substrate mycelium branched, containing inflated regions terminating in thin rhizoid-like filaments and yellow droplets.

Culture characteristics: The isolate grew over a wide range of temperatures with varying growth rates on SMA (synthetic mucor agar), PDA (potato dextrose agar) and MEA (malt extract agar) of 13 mm, 15 mm, and 18.5 mm per 24 h, respectively. Optimal growth was observed around 25 °C, and slow growth was observed at below 10 °C. Maximum growth temperature was 35 °C. The fungus did not grow at 36 °C.

Material examined: REPUBLIC OF KOREA, Jeonnam Province, garden of the Chonnam National University located in Gwangju (35°10′20.3″ N 126°53′56.9″ E), from head of a bombardier beetle (*Harpalus* sp.), 30 July 2018, collected by H.B. Lee (CNUFC HT18012, **holotype**), ex-type living culture (CNUFC ICT18001).

GenBank numbers: ITS = MT192528, MT192529, LSU = MT192532, MT192533.

Notes: Phylogenetic analyses (Figs. 236 and 237) clearly placed *Mucor harpali* among other *Mucor* species within the *Mucor racemosus* group previously suggested by Walther et al. (2013). *Mucor harpali* and *Mucor* sp. CBS 608.78 (former: *M. circinelloides* f. *griseocyanus*) are the phylogenetically nearest species in the ITS tree (Fig. 236). *Mucor harpali* (Fig. 235) shared some similarities with *M. circinelloides* f. *griseocyanus* (current name: *Mucor griseocyanus*) such as ellipsoidal sporangiospores, and maximum temperature growth (Schipper 1978; Wagner et al. 2019). However, sporangia (up to 60 µm) and collumella (38 × 35 µm) of *M. griseocyanus* reported in the literature (Schipper 1978; Wagner et al. 2019) were smaller than those of *M. harpali*. *Mucor harpali* can be distinguished from the other species in this

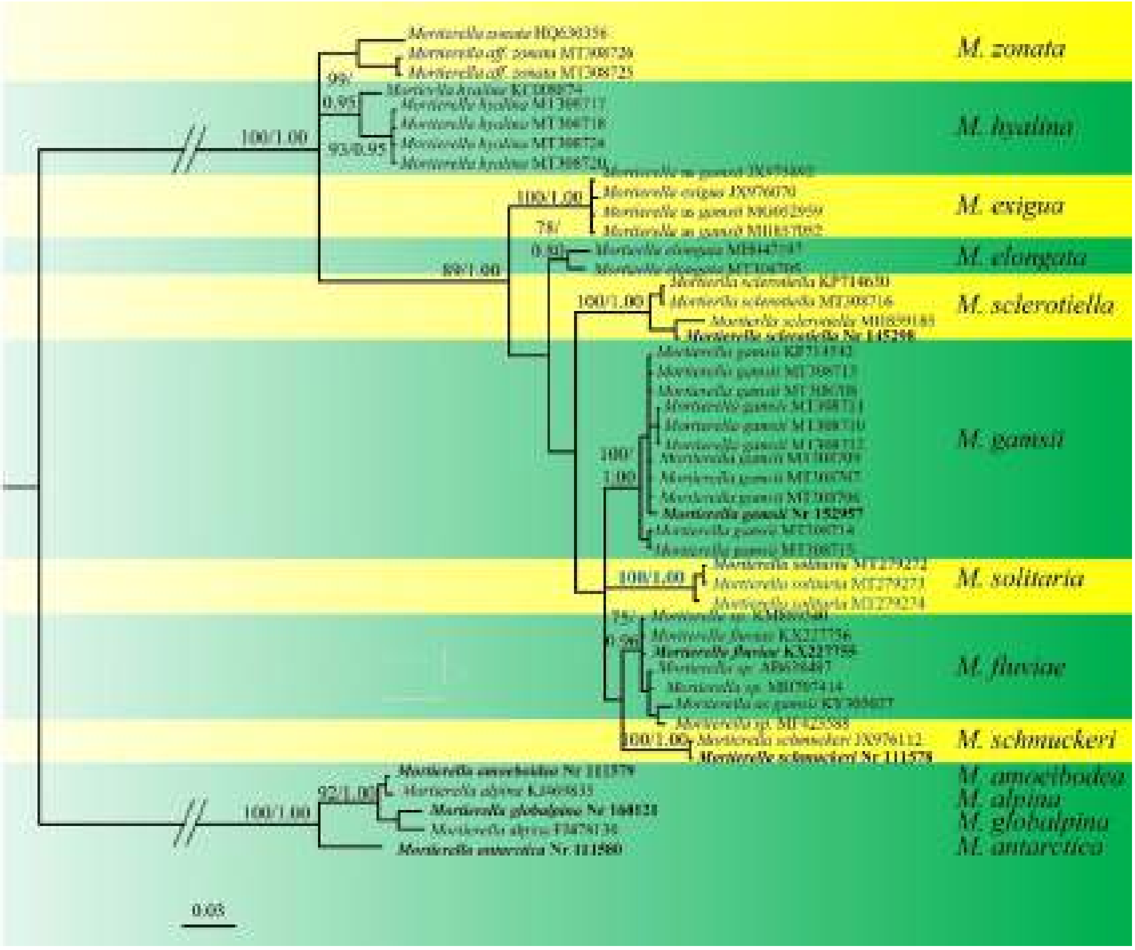


Fig. 233 Phylogenetic relationship of *Mortierella solitaria* with related taxa based on the nucleotide sequences of the ITS. The maximum likelihood (ML) tree (-ln likelihood = 1899.6675) was constructed in MEGA X (Kumar et al. 2018). Five representatives of *Mortierella alpina* complex are used as the outgroup taxa. The dataset includes 494 total characters. Phylogenetic trees obtained from ML and Bayesian inference posterior probabilities (BYPP) were similar in topology. Bootstrap support on the nodes represents MPBS/BYPP. The new species *M. solitaria* is highlighted in blue in the yellow box

group, including *M. racemosus*, *M. plumbeus*, *M. racemosus* f. *sphaerosporus*, *M. brunneogriseus*, and *M. mousanensis*. Schipper (1978) has mentioned that *M. plumbeus* produces columellae usually with apical projections, whereas in *M. harpali* apical projections are absent. *Mucor racemosus* f. *sphaerosporus* produces mainly subglobose sporangiospores (Schipper 1978), while *M. harpali* produces variable in shape, mostly ellipsoidal. *Mucor mousanensis* produces columellae applanate elongated conical (up to 70 × 50 µm) (Schipper 1978), while *M. harpali* does not produce this structure. Based on the phylogenetic analyses and morphological comparison with similar species of *Mucor*, *M. harpali* is a distinct species.

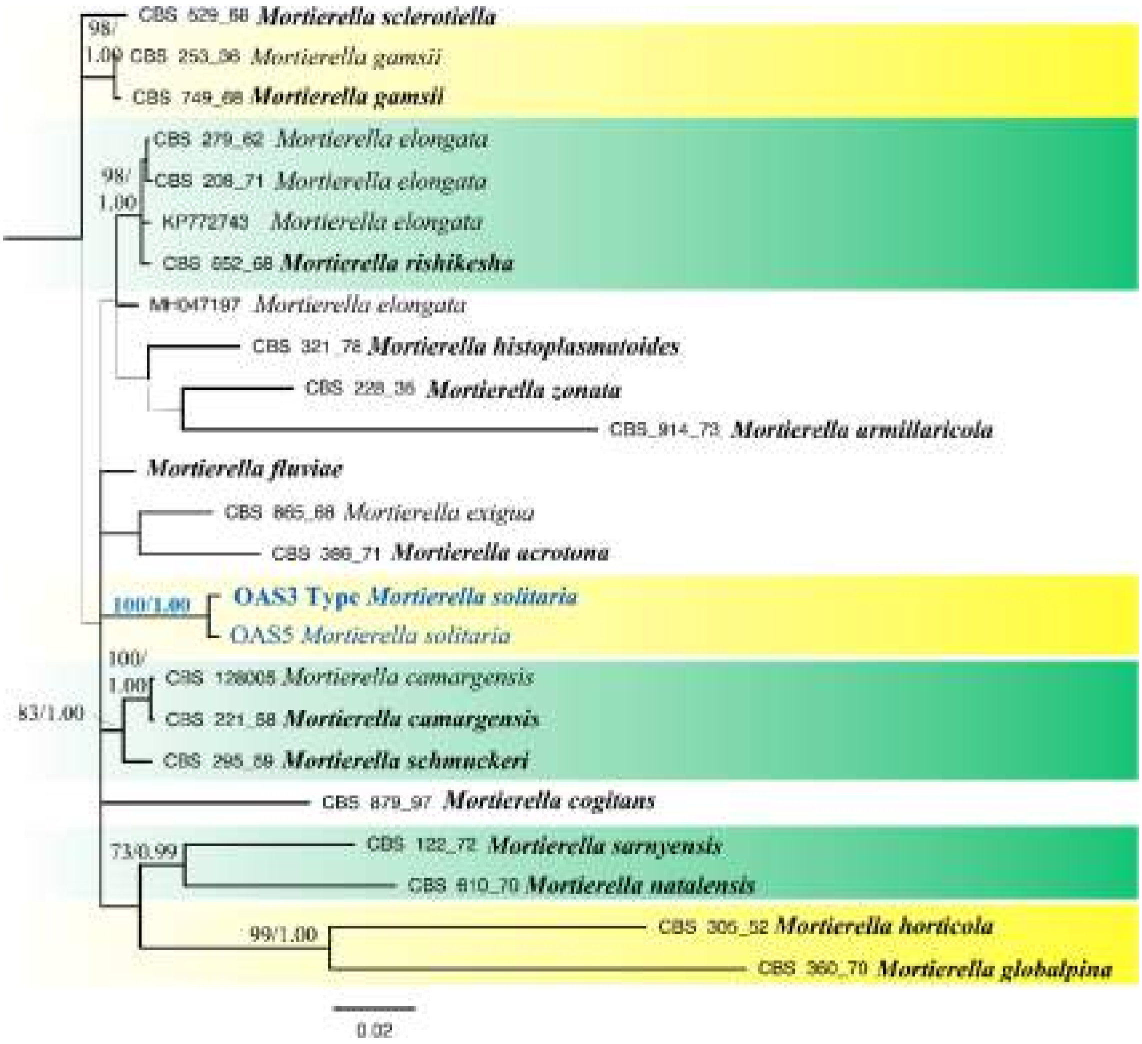


Fig. 234 Phylogenetic relationship of *Mortierella solitaria* with related taxa based on the concatenated nucleotide sequences of the ITS and LSU. The maximum likelihood (ML) tree (-ln likelihood = 5141.7516) was constructed in MEGA X (Kumar et al. 2018). *Mortierella horticola* and *M. globalpina* are used as the outgroup taxa. The dataset includes 1439 total characters. Phylogenetic trees obtained from ML, and Bayesian inference posterior probabilities (BYPP) were similar in topology. Bootstrap support on the nodes represents MPBS/BYPP. The new species *Mortierella solitaria* is highlighted in blue in the yellow box

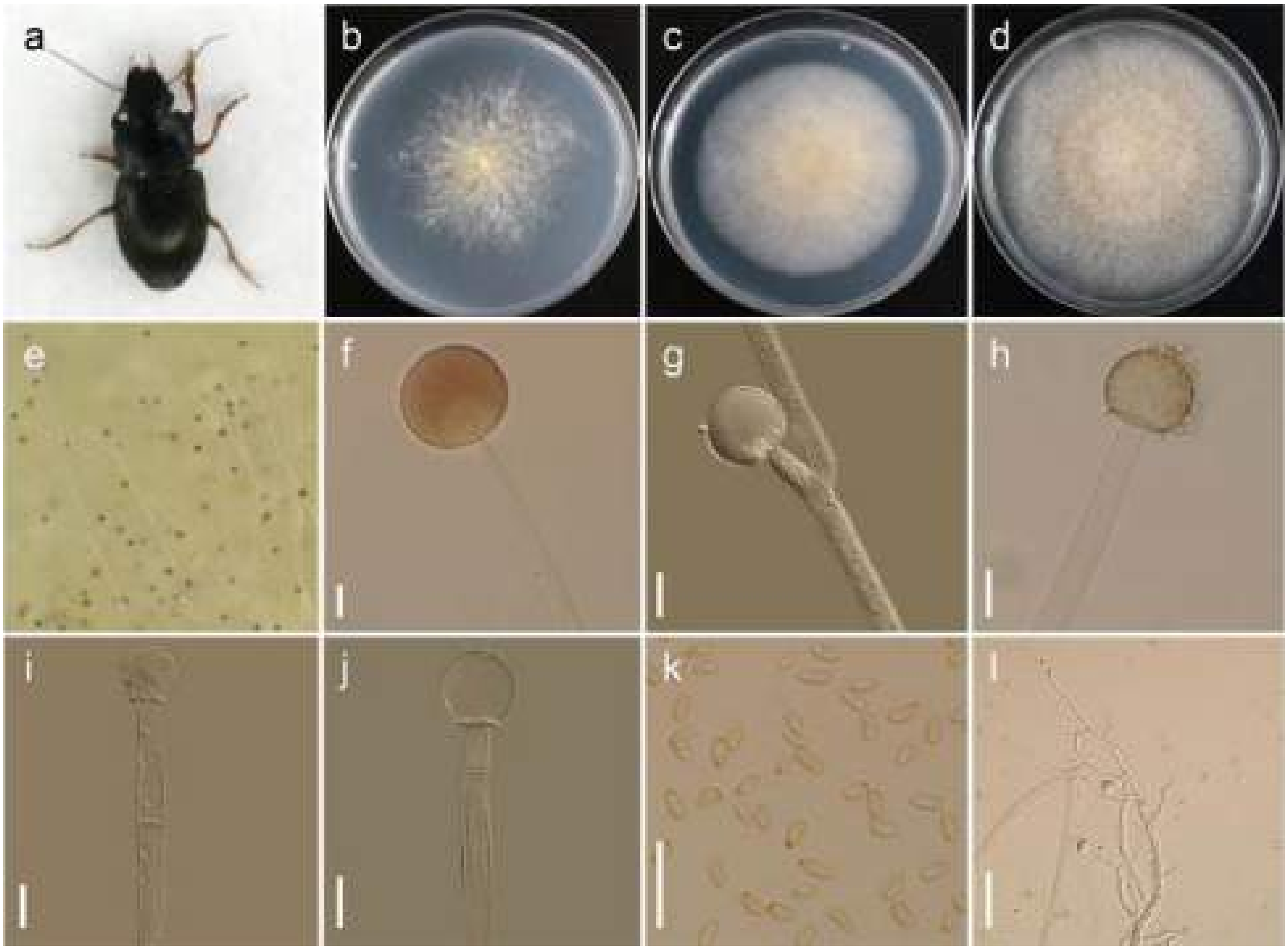


Fig. 235 ***Mucor harpali*** (CNUFC ICT18001, **ex-type living culture**). **a** A bombardier beetle of *Harpalus* sp. belonging to Coleoptera. **b** Colony on synthetic mucor agar (SMA). **c** Colony on potato dextrose agar (PDA). **d** Colony on malt extract agar (MEA). **e**, **f** Sporangiophores and sporangia. **g** Sterile sporangium. **h**–**j** Typical columellae. **k** Sporangiospores. **l** Rhizoids (Fig. e: observed under a stereomicroscope; Figs. f–l: light microscope). Scale bars: **f**–**l** = 20 μm

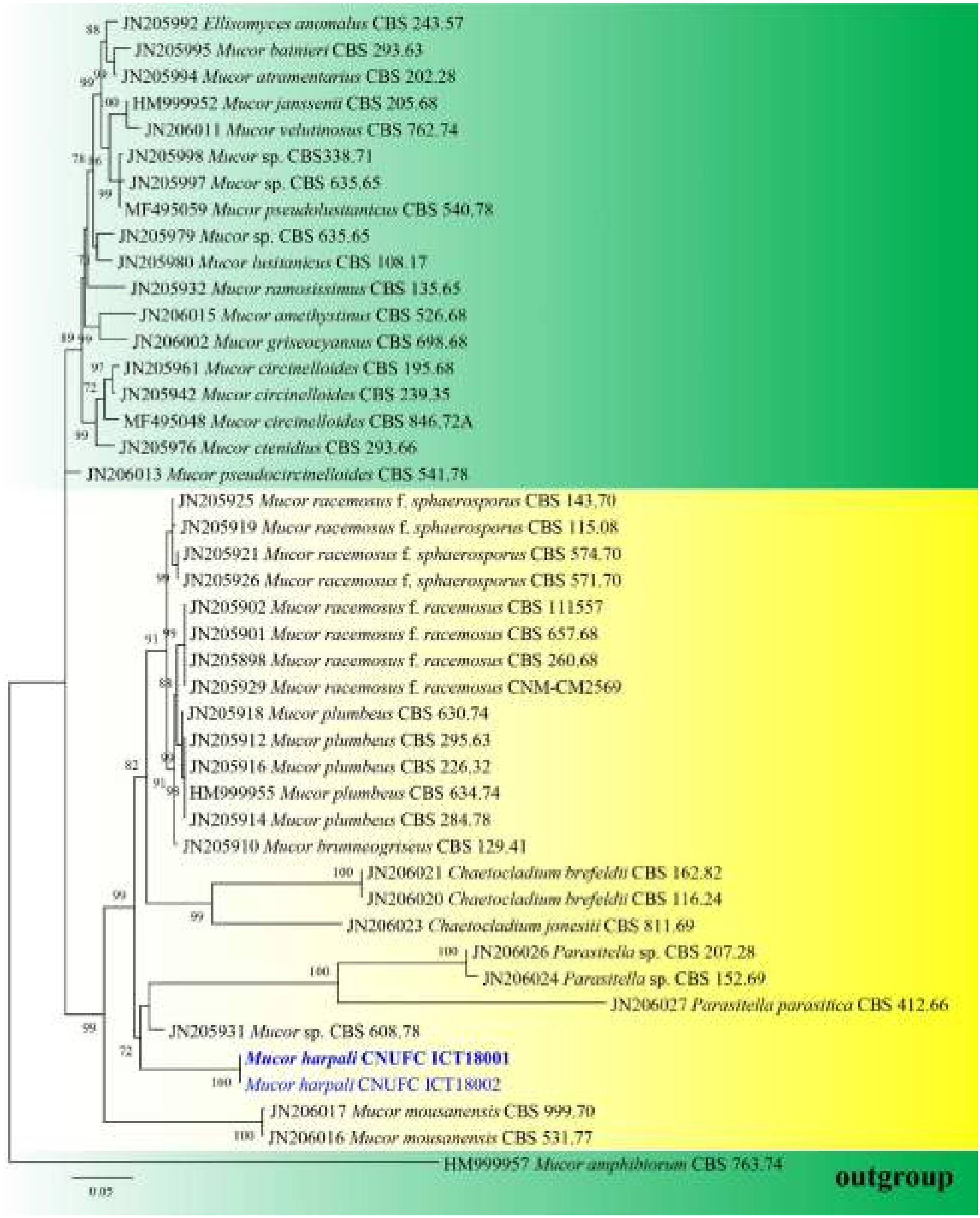


Fig. 236 Phylogram generated from maximum likelihood analysis based on ITS sequence data for the species of *Mucor*. Bootstrap values equal to or greater than 70% for ML analyses is presented at the nodes. *Mucor amphibiorum* is used as the outgroup taxon. Type strains are in bold and newly generated sequences are in blue

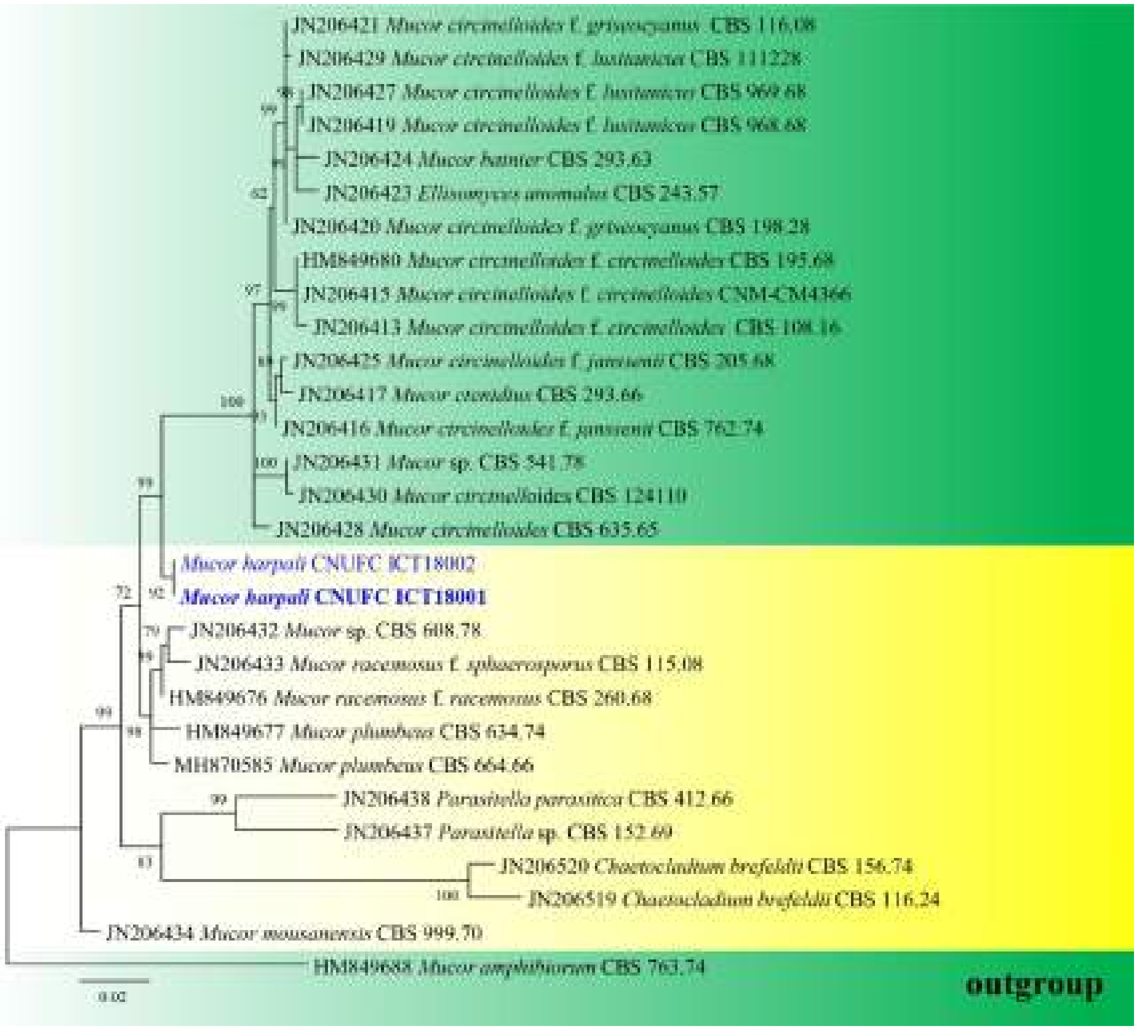


Fig. 237 Phylogram generated from maximum likelihood analysis based on LSU sequence data for the species of *Mucor*. Bootstrap values equal to or greater than 70% for ML analyses is presented at the nodes. *Mucor amphibiorum* is used as the outgroup taxon. Type strains are in bold and newly generated sequences are in blue

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Declarations

Conflict of interest The authors declare that they have no conflict of interest.

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