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Fungal diversity notes 840–928: micro-fungi associated with Pandanaceae

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Abstract

This paper provides illustrated descriptions of micro-fungi newly found on Pandanaceae in China and Thailand. The fungi are accommodated in 31 families. New taxa described include a new family, seven new genera, 65 new species, 16 previously known species. A new family: Malaysiascaceae (Glomerellales). New genera are *Acremoniisimulans* (Plectosphaerellaceae), *Pandanaceomyces*, *Pseudoachroiostachy* (Nectriaceae*)*, *Pseudohyaloseta* (Niessliaceae), *Pseudoornatispora* (Stachybotriaceae) and *Yunnanomyces* (Sympoventuriaceae). New species are *Acremoniisimulans thailandensis*, *Beltrania krabiensis*, *Beltraniella pandanicola*, *B. thailandicus*, *Canalisporium krabiense*, *C. thailandensis*, *Clonostachys krabiensis*, *Curvularia chonburiensis*, *C. pandanicola*, *C. thailandicum*, *C. xishuangbannaensis*, *Cylindrocladiella xishuangbannaensis*, *Dictyochaeta pandanicola*, *Dictyocheirospora nabanheensis*, *D. pandanicola*, *D. xishuangbannaensis*, *Dictyosporium appendiculatum*, *Di. guttulatum*, *Di. hongkongensis*, *Di. krabiense*, *Di. pandanicola*, *Distoseptispora thailandica*, *D. xishuangbannaensis*, *Helicoma freycinetiae*, *Hermatomyces biconisporus*, *Lasiodiplodia chonburiensis*, *L. pandanicola*, *Lasionectria krabiense*, *Menisporopsis pandanicola*, *Montagnula krabiensis*, *Musicillium pandanicola*, *Neofusicoccum pandanicola*, *Neohelicomyces pandanicola*, *Neooccultibambusa thailandensis*, *Neopestalotiopsis chiangmaiensis*, *N. pandanicola*, *N. phangngaensis*, *Pandanaceomyces krabiensis*, *Paracylindrocarpon nabanheensis*, *P. pandanicola*, *P. xishuangbannaensis*, *Parasarcopodium hongkongensis*, *Pestalotiopsis krabiensis*, *P. pandanicola*, *Polyplosphaeria nabanheensis*, *P. pandanicola*, *P. xishuangbannaensis*, *Pseudoachroiostachys krabiense*, *Pseudoberkleasmium pandanicola*, *Pseudochaetosphaeronema pandanicola*, *Pseudohyaloseta pandanicola*, *Pseudoornatispora krabiense*, *Pseudopithomyces pandanicola*, *Rostriconidium pandanicola*, *Sirastachys phangngaensis*, *Stictis pandanicola*, *Terriera pandanicola*, *Thozetella pandanicola*, *Tubeufia freycinetiae*, *T. parvispora*, *T. pandanicola*, *Vermiculariopsiella hongkongensis*, *Volutella krabiense*, *V. thailandensis* and *Yunnanomyces pandanicola*. Previous studies of micro-fungi on Pandanaceae have not included phylogenetic support. Inspiration for this study came from the book *Fungi Associated with Pandanaceae* by Whitton, McKenzie and Hyde in 2012. Both studies reveal that the micro-fungi on Pandanaceae is particularly rich in hyphomycetes. All data presented herein are based on morphological examination of specimens, coupled with phylogenetic sequence data to better integrate taxa into appropriate taxonomic ranks and infer their evolutionary relationships.

Keywords 65 new taxa · Ascomycota · Dothideomycetes · *Freycinetia* · Lecanoromycetes · Leotiomycetes · *Pandanus* · Saprobic · Sordariomycetes

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Table of contents

The numbers of taxa in this study associated with Pandanaceae are organized as in the "Outline of Ascomycetes" (Wijayawardene et al. 2018).

Phylum Ascomycota Caval.-Sm.
Class Dothideomycetes sensu O.E. Erikss & Winka

For recent treatments of Dothideomycetes we follow Hyde et al. (2013) with updates by Liu et al. (2017) and Wijayawardene et al. (2018).

Subclass Dothideomycetidae P.M. Kirk et al.
Capnodiales Woron.
Mycosphaerellaceae Lindau

840. ***Cercospora capsici*** Heald & F.A. Wolf, Mycologia 3 (1): 15 (1911), ***new host record***

Subclass Pleosporomycetidae C.L. Schoch et al.
Pleosporales Luttrell ex M.E. Barr
Dictyosporiaceae Boonmee & K.D. Hyde

841. ***Dictyocheirospora nabanheensis*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 10 (2018), ***new species***
842. ***Dictyocheirospora pandanicola*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 10 (2018), ***new species***
843. ***Dictyocheirospora xishuangbannaensis*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 14 (2018), ***new species***
844. ***Dictyosporium appendiculatum*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 15 (2018), ***new species***
845. ***Dictyosporium digitatum*** J.L. Chen, C.H. Hwang & Tzean, Mycological Research 95: 1145 (1991)
846. ***Dictyosporium guttulatum*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 17 (2018), ***new species***
847. ***Dictyosporium hongkongensis*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 18 (2018), ***new species***
848. ***Dictyosporium krabiense*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 19 (2018), ***new species***
849. ***Dictyosporium pandanicola*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 20 (2018), ***new species***

Didymosphaeriaceae Munk

850. ***Deniquelata barringtoniae*** Ariyawansa & K.D. Hyde, Phytotaxa 105 (1): 15 (2013), ***new host record***
851. ***Montagnula krabiensis*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 23 (2018), ***new species***
852. ***Pseudopithomyces pandanicola*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 25 (2018), ***new species***

Hermatomycetaceae Locq.

853. ***Hermatomyces biconisporus*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 28 (2018), ***new species***

Melanommataceae G. Winter (= Pseudodidymellaceae A.Hashim. & Kaz. Tanaka)

854. ***Byssosphaeria siamensis*** Boonmee, Q. Tian & K.D. Hyde, Fungal Diversity 74: 283 (2015), ***new host record***

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

855. ***Neooccultibambusa thailandensis*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 31 (2018), ***new species***

Pleosporaceae Nitschke

856. ***Curvularia chonburiensis*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 33 (2018), ***new species***
857. ***Curvularia pandanicola*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 37 (2018), ***new species***
858. ***Curvularia thailandicum*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 38 (2018), ***new species***
859. ***Curvularia xishuangbannaensis*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 39 (2018), ***new species***

Roussoellaceae J.K. Liu et al.

860. ***Roussoella solani*** Crous & M.J. Wingf., Persoonia 36: 341 (2016), ***new host record***

Tetraplosphaeriaceae Kaz. Tanaka & K. Hiray

861. ***Polyplosphaeria nabanheensis*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 42 (2018), ***new species***
862. ***Polyplosphaeria pandanicola*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 42 (2018), ***new species***
863. ***Polyplosphaeria xishuangbannaensis*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 44 (2018), ***new species***

Torulaceae Corda

864. ***Rostriconidium pandanicola*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 45 (2018), ***new species***
865. ***Torula chromolaenae*** J.F. Li, Phook., Mapook & K.D. Hyde, Mycological Progress 16 (4): 454 (2017), ***new host record***
866. ***Torula ficus*** Crous, IMA Fungus 6 (1): 192 (2015), ***new host record***

Pleosporales genera *incertae sedis*

867. ***Pseudoberkleasmium*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 50 (2018), ***new genus***
868. ***Pseudoberkleasmium pandanicola*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 51 (2018), ***new species***
869. ***Pseudochaetosphaeronema pandanicola*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 53 (2018), ***new species***

Dothideomycetes orders *incertae sedis*
Botryosphaeriales C.L. Schoch et al.
Botryosphaeriaceae Theiss. & H. Syd.

870. ***Lasiodiplodia chonburiensis*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 54 (2018), ***new species***

871. ***Lasiodiplodia hyalina*** Zh.P. Dou & Y. Zhang, Mycosphere 8 (2): 1016 (2017), ***new host record***
872. ***Lasiodiplodia pandanicola*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 58 (2018), ***new species***
873. ***Lasiodiplodia pseudotheobromae*** A.J.L. Phillips, A. Alves & Crous, Fungal Diversity 28: 8 (2008), ***new host record***
874. ***Neofusicoccum pandanicola*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 60 (2018), ***new species***

Pseudofusicoccumaceae Yao Tan & Crous
875. ***Pseudofusicoccum adansoniae*** Pavlic, T.I. Burgess & M.J. Wingf., Mycologia 100 (6): 855 (2008), ***new host record***

Tubeufiales Boonmee & K.D. Hyde
Tubeufiaceae M.E. Barr
876. ***Helicoma freycinetiae*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 68 (2018), ***new species***
877. ***Neohelicomyces pandanicola*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 69 (2018), ***new species***
878. ***Tubeufia freycinetiae*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 69 (2018), ***new species***
879. ***Tubeufia inaequalis*** Y.Z Lu, J.C. Kang & K.D. Hyde, Fungal Diversity 92 (2018), ***new host record***
880. ***Tubeufia pandanicola*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 73 (2018), ***new species***
881. ***Tubeufia parvispora*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 74 (2018), ***new species***

Venturiales Y. Zhang ter et al.
Sympoventuriaceae Y. Zhang ter et al.
882. ***Yunnanomyces*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 75 (2018), ***new genus***
883. ***Yunnanomyces pandanicola*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 75 (2018), ***new species***

Class Lecanoromycetes O.E. Erikss. & Winka
Subclass Ostropomycetidae Reeb et al.
Ostropales Nannf.
Stictidaceae Fr.
884. ***Stictis pandanicola*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 78 (2018), ***new species***

Class Leotiomycetes O.E. Erikss. & Winka
Rhytismatales M.E. Barr ex Minter
Rhytismataceae Chevall. (= Hypodermataceae Rehm; = Cryptomycetaceae Höhn. nom. inval. fide Jaklitsch et al. 2016)
885. ***Terriera pandanicola*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 79 (2018), ***new species***

Class Sordariomycetes O.E. Erikss. & Winka
Subclass Diaporthomycetidae Senan. et al.
Diaporthomycetidae families *incertae sedis*
Distoseptisporaceae K.D. Hyde & McKenzie
886. ***Distoseptispora thailandica*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 79 (2018), ***new species***
887. ***Distoseptispora xishuangbannaensis*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 82 (2018), ***new species***

Subclass Hypocreomycetidae O.E. Erikss. & Winka
Glomerellales Chadef. ex Reblová et al.
Glomerellaceae Locq. ex Seifert & W. Gams
888. ***Colletotrichum pandanicola*** Tibpromma & K.D. Hyde, Mycokeys 33: 47 (2018)
889. **Malaysiascaceae** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 88 (2018), ***new family***
890. ***Malaysiasca phaii*** Crous & M.J. Wingf., Persoonia 36: 373 (2016), ***new host record***

Plectosphaerellaceae W. Gams et al.
891. ***Acremoniisimulans*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 88 (2018), ***new genus***
892. ***Acremoniisimulans thailandensis*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 89 (2018), ***new species***
893. ***Musicillium pandanicola*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 91 (2018), ***new species***

Hypocreales Lindau
Bionectriaceae Samuels & Rossman
894. ***Clonostachys krabiensis*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 93 (2018), ***new species***
895. ***Lasionectria krabiense*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 95 (2018), ***new species***
896. ***Paracylindrocarpon nabanheensis*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 102 (2018), ***new species***
897. ***Paracylindrocarpon pandanicola*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 103 (2018), ***new species***
898. ***Paracylindrocarpon xishuangbannaensis*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 104 (2018), ***new species***

Nectriaceae Tul. & C. Tul.
899. ***Cylindrocladiella xishuangbannaensis*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 105 (2018), ***new species***
900. ***Pandanaceomyces*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 107 (2018), ***new genus***
901. ***Pandanaceomyces krabiensis*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 107 (2018), ***new species***
902. ***Pseudoachroiostachys*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 107 (2018), ***new genus***
903. ***Pseudoachroiostachys krabiense*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 108 (2018), ***new species***
904. ***Volutella krabiense*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 110 (2018), ***new species***

905. ***Volutella thailandensis*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 110 (2018), ***new species***

Niessliaceae Kirschst.
906. ***Pseudohyaloseta*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 113 (2018), ***new genus***
907. ***Pseudohyaloseta pandanicola*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 113 (2018), ***new species***

Stachybotryaceae L. Lombard & Crous
908. ***Parasarcopodium hongkongensis*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 114 (2018), ***new species***
909. ***Pseudoornatispora*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 115 (2018), ***new genus***
910. ***Pseudoornatispora krabiense*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 115 (2018), ***new species***
911. ***Sirastachys phangngaensis*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 118 (2018), ***new species***

Microascales Luttr. ex Benny & Kimbr.
Microascaceae Luttr. ex Malloch
912. ***Parascedosporium putredinis*** (Corda) Lackner & de Hoog, IMA Fungus 2 (1): 44 (2011), ***new host record***

Subclass Savoryellomycetidae Hongsanan et al.
Savoryellales Boonyuen et al.
Savoryellaceae Jaklitsch & Réblová
913. ***Canalisporium krabiense*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 122 (2018), ***new species***
914. ***Canalisporium thailandensis*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 122 (2018), ***new species***

Subclass Sordariomycetidae O.E. Erikss & Winka (= Meliolomycetidae P.M. Kirk & K.D. Hyde)
Chaetosphaeriales Huhndorf et al.
Chaetosphaeriaceae Réblová et al.
915. ***Dictyochaeta pandanicola*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 127 (2018), ***new species***
916. ***Dictyochaeta siamensis*** J. Yang, K.D. Hyde & J.K. Liu, Mycological Progress 15 (10): 1159 (2016), ***new host record***
917. ***Menisporopsis pandanicola*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 128 (2018), ***new species***
918. ***Thozetella pandanicola*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 130 (2018), ***new species***

Sordariales Chad. ex D. Hawksw. & O.E. Erikss.
Chaetomiaceae G. Winter
919. ***Chaetomium globosum*** Kunze ex Fr., Systema Mycologicum 3: 255 (1829)

Subclass Xylariomycetidae O.E. Erikss & Winka
Amphisphaeriales D. Hawksw. & O.E. Erikss.
Beltraniaceae Nann.
920. ***Beltrania krabiensis*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 134 (2018), ***new species***
921. ***Beltraniella pandanicola*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 134 (2018), ***new species***
922. ***Beltraniella thailandicus*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 136 (2018), ***new species***

Sporocadaceae Corda.
923. ***Neopestalotiopsis chiangmaiensis*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 139 (2018), ***new species***
924. ***Neopestalotiopsis pandanicola*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 141 (2018), ***new species***
925. ***Neopestalotiopsis phangngaensis*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 142 (2018), ***new species***
926. ***Pestalotiopsis krabiensis*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 143 (2018), ***new species***
927. ***Pestalotiopsis pandanicola*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 145 (2018), ***new species***

Sordariomycetes orders *incertae sedis*
Vermiculariopsiellales Hern.-Restr. et al.
Vermiculariopsiellaceae Hern.-Restr. et al.
928. ***Vermiculariopsiella hongkongensis*** Tibpromma & K.D. Hyde, in Fungal Diversity 92: 146 (2018), ***new species***

Introduction

Pandanaceae is a monocotyledonous family that comprises five genera: *Benstonea*, *Freycinetia*, *Martellidendron*, *Pandanus*, *Sararanga* (Wardah and Setyowati 2009; Callmander et al. 2012). Taxonomy of the Pandanaceae was dealt with by St. John and Stone (1962, 1967, 1968, 1969), however, their identification is relatively difficult because of the lack of literature or absence of flowering parts in the field (Nadaf and Zanan 2012; Whitton et al. 2012). The distribution of Pandanaceae is predominantly tropical, but they are also distributed throughout the Pacific, and New Zealand (Nadaf and Zanan 2012; Whitton et al. 2012).

Micro-fungi on Pandanaceae have long been studied and all taxa described from Pandanaceae were listed by McKenzie and Hyde (1996), while Whitton et al. (2012) listed all fungi recorded on Pandanaceae. McKenzie (1991a, b, c, 1995); McKenzie and Kuthubutheen (1993); Hyde (1994), Hyde and Hawksworth (1997b), McKenzie and Hyde (1996); Dulymamode et al. (1998a, b, c, d, e), Whitton et al. (1998, 1999, 2000a, b, 2001a, b, c, d, 2002a, b, 2003), and Thongkantha et al. (2008) provided a series of papers in which many new species of fungi on Pandanaceae were described. More recently, a few papers on micro-fungi from Pandanaceae have been published (Hosagoudar 2012; Crous et al. 2015a; Lombard et al. 2016; Tibpromma et al. 2016a, b, c, 2017a, b, 2018; Hyde et al. 2017, 2018; Zhang et al. 2017) that include both morphological and phylogenetic analysis. Hawksworth (2000) estimated that there may be 1.5 million species of fungi and later Hawksworth and Lücking (2017) revised the estimate upwards and suggested there were 2.2–3.8 million species. It is a huge challenge to find all of the unknown fungi in the world as currently only 120,000 species have been described (Hawksworth and Lücking 2017). Tropical fungi are a major component of biodiversity and play major roles in ecosystem functioning (Hawksworth 2002) and are very significant for the survival of other organisms in tropical forests (Lodge et al. 1996). Pandanaceae has proven to be a good source of new, interesting and often infrequently collected micro-fungi (Whitton et al. 2012). McKenzie et al. (2002) estimated that less than 40% of fungi on a single member of Pandanaceae are 'unique', but with time it was understood that many can be found on other members of the Pandanaceae, or on other host families.

The objective of this study is to provide a description of recently collected micro-fungi from Pandanaceae, based on both morphology and phylogenetic support to reveal the correct taxonomic placements of these fungi. Thus, information will be compared with previous studies on micro-fungi on Pandanaceae and other hosts. In particular, a comparison will be made with Whitton et al. (2012) who provided a book entitled *Fungi associated with Pandanaceae* in which 114 genera and 226 species of fungi from Pandanaceae based on morphology are listed. The final outcome will be a firm taxonomy and phylogeny that can provide support to researchers who need to identify fungi for their research work.

Materials and methods

Specimens were collected from Thailand and China, especially from southern Thailand and Yunnan Province of China. Each sample was placed into separate zip-lock bags or envelopes together with collection details (host, place and date) and returned to the laboratory for observation following the methods outlined by Tibpromma et al. (2016a, b, c). Single spore isolation was done following the method described in Chomnunti et al. (2014). Germinated spores were observed with a stereo microscope and transferred to malt extract agar (MEA: 33.6 g/l sterile distilled water, Difco malt extract) or potato dextrose agar (PDA: 39 g/l sterile distilled water, Difco potato dextrose) plates and incubated at room temperature for 4 weeks. Hyphomycetes were immediately isolated because conidia are easy to release under dry conditions. Cultures were subcultured and transferred to MEA or PDA containing sterile toothpicks, pine needles (Phookamsak et al. 2015) or Pandanaceae leaves and incubated at room temperature for 3 months to induce the sexual or asexual morph. Herbarium specimens were deposited in Mae Fah Luang University Herbarium (MFLU), Chiang Rai, Thailand and Kunming Institute of Botany Academia Sinica (HKAS). Living cultures were deposited in the Mae Fah Luang University Culture Collection (MFLUCC) and Kunming Institute of Botany Culture Collection (KMUCC). Facesoffungi numbers (FoF) and Index Fungorum (IF) numbers were obtained as explained in Jayasiri et al. (2015) and Index Fungorum (2018). New taxa were established based on recommendations outlined by Jeewon and Hyde (2016).

Morphological classification

The fruiting structures were examined with a Carl Zeiss GmbH (AxioCam ERC 5 S) or JNOEC JSZ4 (ser. No. 030233) stereo microscope. Fruiting bodies were rehydrated in water, 100% lactic acid or 5% KOH. Sections were cut with a razor blade and studied with a Nikon ECLIPSE 80i or Nikon ECLIPSE Ni compound microscope. Photographs were taken with a Canon 550D or Canon 600D digital camera mounted on the microscope. All microscopic structures were measured using Tarosoft® Image Framework program v.0.9.0.7 and images used for figures were processed with Adobe Photoshop CS3 Extended version 10.0 (Adobe Systems, USA).

DNA extraction, PCR amplification and DNA sequencing

Genomic DNA was extracted from pure fungal cultures by using Biospin Fungal Genomic DNA extraction Kit-BSC14S1 (BioFlux, P.R. China). If cultures were unavailable, DNA was extracted directly from fruiting bodies using a Forensic DNA Kit–D3591-01 (OMEGA bio-tek) following the manufacturer's instructions. Polymerase chain reaction (PCR) was used to amplify partial gene regions using primers shown in Table 1. The total volume of PCR mixtures for amplifications were 25 µL containing 8.5 µL ddH$_2$O, 12.5 µL 2× Easy Taq PCR Super Mix (mixture of Easy Taq TM DNA Polymerase, dNTPs, and optimized buffer (Beijing Trans Gen Biotech Co., Chaoyang District, Beijing, PR China), 2 µL of DNA template, 1 µL of each forward and reverse primers (10 pM). The quality of PCR products was checked on 1% agarose gel electrophoresis stained with 4S green nucleic acid (Life Science Products and Services, Cat. No: A616694). Purification and sequencing of PCR products were carried out by Sangon Biotech Co., Shanghai, China.

Phylogenetic analysis

LSU or ITS sequence data generated in this study were subjected to BLAST searches in the nucleotide database of GenBank (www http://blast.ncbi.nlm.nih.gov/) to determine their most probable closely related taxa. Sequence

Table 1 Details of genes/loci with PCR primers and protocols

Family or genus	Gene/loci	PCR primers (forward/reverse)	References for primer
Class Dothideomycetes			
Botryosphaeriaceae	ITS	ITS5/ITS4	White et al. (1990)
	LSU	LROR/LR5	Vilgalys and Hester (1990)
	SSU	NS1/NS4	White et al. (1990)
	RPB2	fRPB2-5f/fRPB2–7cR	Liu et al. (1999)
	TEF1	728F/986R	Carbone and Kohn (1999)
Didymosphaeriaceae, Hermatomycetaceae, Melanommataceae, Occultibambusaceae, Torulaceae, Roussoellaceae, Tetraplosphaeriaceae, Pseudochaetosphaeronema, Tubeufiaceae, Dictyosporiaceae, Mycosphaerellaceae	LSU	LROR/LR5	Vilgalys and Hester 1990)
	ITS	ITS5/ITS4	White et al. (1990)
	SSU	NS1/NS4	White et al. (1990)
	TEF1	983F/2218R	Rehner (2001)
	RPB2	fRPB2-5f/fRPB2–7cR	Liu et al. (1999)
Curvularia	ITS	ITS5/ITS4	White et al. (1990)
	TEF1	983F/2218R	Rehner (2001)
	GPDH	GDF/GDR	Templeton et al. (1992)
Class Lecanoromycetes			
Stictidaceae	LSU	LROR/LR5	Vilgalys and Hester (1990)
	ITS	ITS5/ITS4	White et al. (1990)
	mtSSU	mrSSU1/mrSSU3R	Zoller et al. (1999)
Class Leotiomycetes			
Terriera	LSU	LROR/LR5	Vilgalys and Hester (1990)
Class Sordariomycetes			
Beltraniaceae, Malaysiascaceae, *Canalisporium, Distoseptispora*, Chaetosphaeriaceae, *Chaetomium, Vermiculariopsiella*	LSU	LROR/LR5	Vilgalys and Hester (1990)
	ITS	ITS5/ITS4	White et al. (1990)
	SSU	NS1/NS4	White et al. (1990)
Sporocadaceae	ITS	ITS5/ITS4	White et al. (1990)
	TEF1	526F/1567R	Rehner (2001)
	TUB2	T1/T2	O'Donnell and Cigelnik (1997)
Colletotrichum	ITS	ITS5/ITS4	White et al. (1990)
	GPDH	GDF/GDR	Templeton et al. (1992)
	CHS-1	CHS79F/CHS345R	Carbone and Kohn (1999)
	ACT	ACT512F/ACT783R	Carbone and Kohn (1999)
	TUB2	T1/T2	O'Donnell and Cigelnik (1997)
Plectosphaerellaceae	LSU	LROR/LR5	Vilgalys and Hester (1990)
	ITS	ITS5/ITS4	White et al. (1990)
	SSU	NS1/NS4	White et al. (1990)
	TEF1	983F/2218R	Rehner (2001)
Bionectriaceae, Nectriaceae, Niessliaceae, Stachybotriaceae	LSU	LROR/LR5	Vilgalys and Hester (1990)
	ITS	ITS5/ITS4	White et al. (1990)
	RPB2	fRPB2-5f/fRPB2–7cR	Liu et al. (1999)
	TEF1	983F/2218R	Rehner (2001)
	TUB2	T1/T2	O'Donnell and Cigelnik (1997)

data were retrieved from GenBank based on recent publications. Raw forward and reverse sequences were assembled using Geneious Pro.v4.8.5.

Single gene sequence alignments were made with MAFFT v. 7.215 (Katoh and Standley 2016: http://mafft.cbrc.jp/alignment/server/index.html) and edited manually if necessary in BioEdit v. 7.0 (Hall 2004). The sequence datasets were combined using BioEdit v.7.2.5 (Hall 2004). FASTA alignment formats were exchanged to PHYLIP and NEXUS formats by the website (http://sing.ei.uvigo.es/ALTER/).

Phylogenetic analysis of both individual and combined aligned data were based on maximum likelihood (ML), maximum parsimony (MP) and Bayesian analysis (BYPP). The MP analysis was performed using PAUP v. 4.0b10 (Swofford 2002). MP analysis by bootstrap analysis with 1000 replicates using 10 rounds of heuristic search replicates with random addition of sequences and subsequent TBR branch swapping during each bootstrap replicate. Descriptive tree statistics calculated for parsimony were: tree length (TL), consistency index (CI), retention index (RI), relative consistency index (RC) and homoplasy index (HI). A ML analysis was performed via the CIPRES portal (Miller et al. 2010) using RAxML-HPC BlackBox (8.2.4) (Stamatakis 2006, 2014) with the general time reversible model (GTR) with a discrete gamma distribution as the evolutionary model. Posterior probabilities (PP) (Rannala and Yang 1996) were established by Markov chain Monte Carlo sampling (MCMC) in MrBayes v.3.0b4 (Liu et al. 2012). The model of evolution for the Bayesian analysis was determined by using MrModeltest 2.2 (Nylander 2004). Six simultaneous Markov chains were run for at least 1,000,000 generations, or depending on individual settings for the fungal group, and trees were sampled every 100th or 1,000th generation (Cai et al. 2006). The burn-in was set to 0.25, and the run was automatically stopped when the average standard deviation of split frequencies reached below 0.01 (Maharachchikumbura et al. 2015). The best scoring phylogenetic trees were configured and visualized in FigTree 1.4.2 (Rambaut 2014) with bootstrap values (MP, ML and PP) given at the nodes and edited using Microsoft Office PowerPoint 2007 and Adobe Illustrator CS3 (Adobe Systems, USA). MP/ML bootstrap supports (greater than or equal to 60%) and Bayesian posterior probability (greater than or equal to 0.90) are shown below or above each branch. The resulting phylogenetic trees are presented under each relevant description.

Taxonomy

Phylum Ascomycota Caval.-Sm.

The taxa are arranged as in *Outline of the Ascomycota* – 2017 (Wijayawardene et al. 2018)

Class Dothideomycetes sensu O.E. Erikss & Winka

For the classification of Dothideomycetes we follow Hyde et al. (2013) updates provided by Liu et al. (2017) and Wijayawardene et al. (2018).

Subclass Dothideomycetidae P.M. Kirk et al.
Capnodiales Woron
Mycosphaerellaceae Lindau

Mycosphaerellaceae was erected by Lindau (1897) with the family type *Ramularia* Unger. Members of Mycosphaerellaceae are pathogens, endophytes, saprobes, epiphytes and fungicolous (Ávila et al. 2005; Crous et al. 2006; Arzanlou et al. 2007; Churchill 2010; Hyde et al. 2013; Chang et al. 2016; de Wit 2016). Morphology of the sexual morph was provided by Schoch et al. (2006) and the asexual morphs are coelomycetes and hyphomycetes (Braun et al. 2003; Aptroot 2006; Schoch et al. 2006; Wijayawardene et al. 2017a). Hawksworth et al. (1995) placed Mycosphaerellaceae in Dothideales, while Kirk et al. (2001) assigned the family to the Mycosphaerellales. Kirk et al. (2008) listed Mycosphaerellaceae in Capnodiales. Wijayawardene et al. (2018) accepted 129 genera. We record *Cercospora capsici* from Pandanaceae for the first time.

Cercospora Fresen.

Cercospora was erected by Fresenius with *C. apii* Fresen. as the type species (Fuckel 1863). *Cercospora* contains numerous important plant pathogenic fungi from a diverse range of hosts (Groenewald et al. 2013a, b) with 3178 epithets are listed in Index Fungorum (2018). The unidentified *Cercospora* sp. has been reported from Thailand on *Pandanus amaryllifolius* (Thongkantha et al. 2008).

Cercospora capsici Heald & F.A. Wolf, Mycologia 3 (1): 15 (1911)

Facesoffungi number: FoF04570; Fig. 1

Saprobic on dead leaves of *Pandanus amaryllifolius*. *Mycelium* superficial, rough, branched, septate, light brown to dark brown. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. Caespituli fasciculate to sporodochial, brown to dark brown, thick-walled, predominantly epiphyllous. *Conidiophores* 90–215 × 4–7 µm ($\bar{x}$ = 160 × 5 µm, n = 20), aggregated in dense fascicles, pale brown, cylindrical, up to 6-septate, branched, roughened with scars, straight to curved. *Conidiogenous cells* 20–65 × 4–7 µm ($\bar{x}$ = 45 × 6 µm, n = 20), holoblastic, integrated, cylindrical, pale brown, hyaline at the apex, thick-walled. *Conidia* 85–220 × 4–8 µm ($\bar{x}$ = 151 × 6 µm, n = 20), cylindrical, base truncate with distinctive scar, apex rounded, solitary, hyaline, straight to slightly curved, guttulate, up to 15-septate, not constricted at septa, thick-walled, without a mucilaginous sheath.

Culture characteristics: Conidia germinating on MEA within 12 h. Colonies on MEA, circular, entire edge, smooth, pulvinate, white–grey in middle, white at margin, velvety.

Material examined: THAILAND, Chiang Mai Province, Mae Taeng District, Mushroom Research Foundation, on dead leaf of *Pandanus amaryllifolius* Roxb., 16 December 2017, S. Tibpromma P12 (MFLU 18-0031, HKAS 101799); living culture, MFLUCC 18-0117.

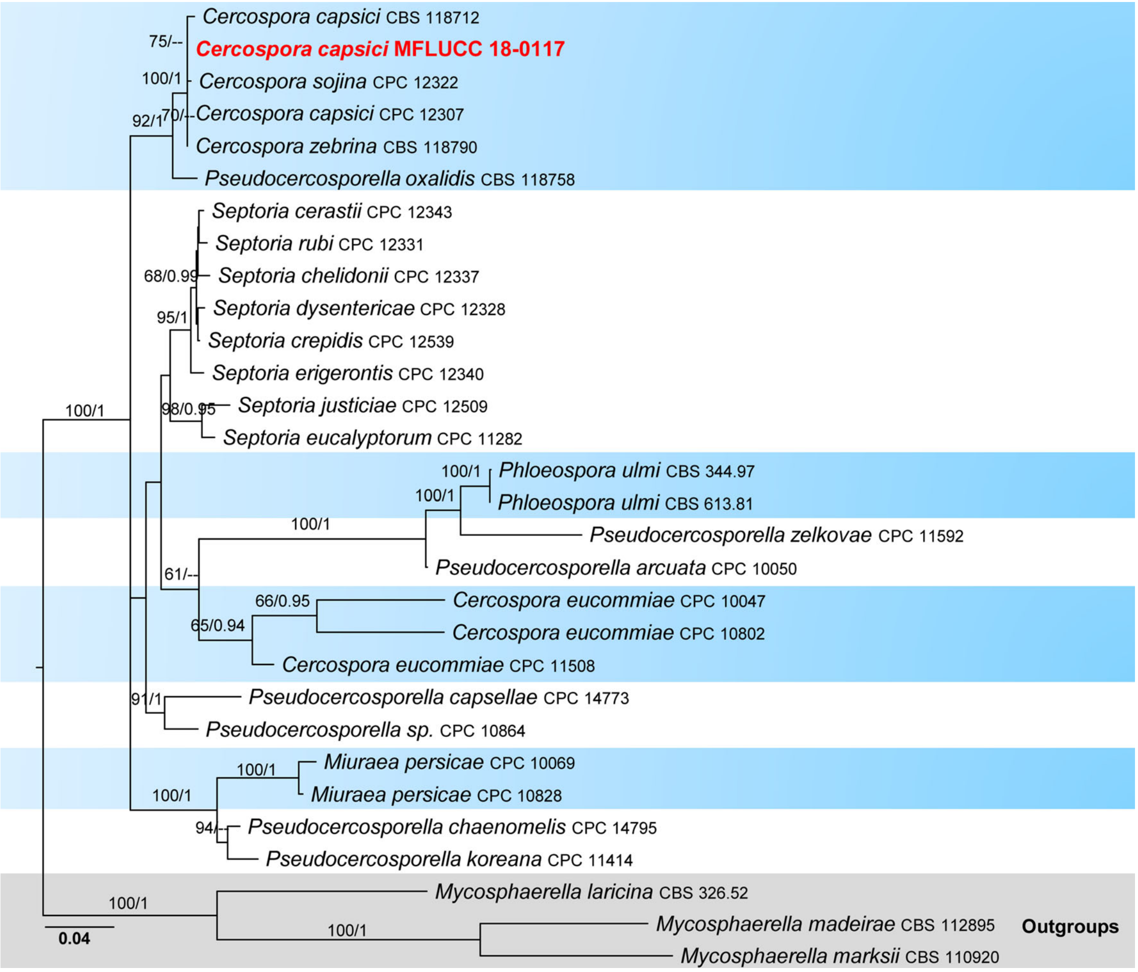


Fig. 1 Phylogram generated from maximum likelihood analysis based on combined LSU, ITS and TEF1 partial sequence data. Thirty strains are included in the sequence analysis, which comprise 1884 characters with gaps. Single gene analysis was carried out and compared with each species, to compare the topology of the tree and clade stability. *Mycosphaerella laricina*, *M. madeirae* and *M. marksii* are used as outgroup taxa. Tree topology of the ML analysis was similar to the BYPP. The best scoring RAxML tree with a final likelihood value of − 8740.769206 is presented. The matrix had 565 distinct alignment patterns, with 12.46% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.237646, C = 0.247630, G = 0.280191, T = 0.234533; substitution rates AC = 1.626221, AG = 2.901339, AT = 1.381886, CG = 1.148995, CT = 6.553424, GT = 1.000000; gamma distribution shape parameter α = 0.460899. Bootstrap support values for ML 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 red

GenBank numbers LSU: MH260285; ITS: MH275053; SSU: MH260331; TEF1: MH412762; RPB2: MH412752; TUB2: MH412741.

Notes: *Cercospora* sp. was recorded from Thailand on *Pandanus amaryllifolius* (Thongkantha et al. 2008). We also collected *Cercospora* from *Pandanus amaryllifolius* in Thailand, but unfortunately cannot compare the morphology with the species in Thongkantha et al. (2008) as it lacked a description. *Cercospora capsici* (MFLUCC 18-0117) grouped with *C. sojina* (CPC 12322) and *C. capsici* (CBS 118712) (Fig. 2). *Cercospora capsici* has acicular conidia, 2–12-septate and subacute at the apex (Groenewald et al. 2013a, b), while *C. sojina* has cylindrical to obclavate or fusiform conidia, with 1–5-septate (Crous et al. 2013). However, when comparing the nucleotide sequences our isolate is almost identical with *Cercospora capsici* (CBS 118712 and CPC 12307) with three ITS base pair (0.59%) differences.

Subclass Pleosporomycetidae C.L. Schoch et al.

Pleosporales Luttrell ex M.E. Barr

Dictyosporiaceae Boonmee & K.D. Hyde

Dictyosporiaceae was informally erected by Liu et al. (2015b) and later it was formally introduced by Boonmee et al. (2016) with *Dictyosporium* Corda. as the type genus based on morphology and multi-gene analysis. Members of Dictyosporiaceae are often saprobes on decaying wood in both terrestrial and freshwater habitats (Boonmee et al. 2016). The sexual morphs of Dictyosporiaceae are

Fig. 2 ***Cercospora capsici*** (MFLU 18-0031). **a** Colonies on dead leaves of *Pandanus amaryllifolius*. **b** Conidiophores, conidiogenous cells and conidia. **c-e** Conidiogenous cells and conidia. **f, g** Conidia. **h, i** Colonies on MEA from above and below. Scale bars: **b** = 100 µm, **c–g** = 20 µm

characterized by immersed to erumpent or superficial, globose to subglobose, dark brown to black ascomata, bitunicate asci with septate, hyaline, sheathed ascospores; the asexual morphs are cheirosporous hyphomycetes (Boonmee et al. 2016). Illustrations were provided by Tanaka et al. (2015). There are twelve genera in the family

(Wijayawardene et al. 2017b, 2018). Asexual morph taxa belonging to *Dictyocheirospora* and *Dictyosporium* were found on Pandanaceae. These are described together with an updated tree for the family.

Dictyocheirospora D'souza et al.

Dictyocheirospora was erected with *D. rotunda* D'souza, Bhat & K.D. Hyde as type species (Boonmee et al. 2016). The genus is characterized by dark sporodochial colonies with aeroaquatic cheiroid dictyospores and members of this genus are saprobes (Boonmee et al. 2016). Index Fungorum lists ten epithets for *Dictyocheirospora* (Index Fungorum 2018). We introduce three new species from Pandanaceae, a genus was not previously found on Pandanaceae.

Dictyocheirospora nabanheensis Tibpromma & K.D. Hyde, ***sp. nov***.

Index Fungorum number: IF554474, *Facesoffungi number*: FoF04483; Fig. 3

Etymology: named after Nabanhe, the place where the fungus was first discovered.

Holotype: HKAS 101807

Saprobic on dead leaves of *Pandanus* sp. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Conidiomata sporodochia* on natural substrate in small groups, scattered, dark brown. *Conidiophores* micronematous, reduced to conidiogenous cell. *Conidiogenous cells* 9–20 × 5–7 µm ($\bar{x}$ = 12 × 5.5 µm, n = 10), holoblastic, cylindrical, wide at the top, sometimes flat at base, dull pale brown, mostly remaining attached to the conidia. *Conidia* 35–40 × 18–21 µm ($\bar{x}$ = 38 × 20 µm, n = 20), solitary, oval to ellipsoid, cheiroid, consisting of 40–48 cells, with a basal connecting cell, pale brown to yellow–brown, smooth-walled, guttulate, individual cells discoid, 27–39 × 5–6 µm, arranged in 6 compact rows, with 6–10 cells per row; with 1–2 rounded to cylindrical appendages, 5–16 × 5–6.5 µm, arising from near middle of conidial rows, hyaline.

Culture characteristics: Conidia germinating on PDA within 12 h. Colonies on PDA, circular, entire edge with white margin and cream to yellow–orange in the central, raised on surface.

Material examined: CHINA, Yunnan Province, Xishuangbanna, Nabanhe, on *Pandanus* sp., 2 August 2016, S. Tibpromma NBH21 (HKAS 101807, **holotype**); ex-type living culture, KUMCC 16-0152 = MFLUCC 17-0562.

GenBank numbers LSU: MH376712; ITS: MH388340; TEF1: MH388375.

Notes: *Dictyocheirospora nabanheensis* is introduced as a new species based on morphology and phylogeny. *Dictyocheirospora nabanheensis* is well-separated in a clade with other members of *Dictyocheirospora* (Fig. 4) and is distinguished by cylindrical conidiogenous cells with wide top, oval to ellipsoid, cheiroid conidia consisting of 40–48 cells, pale brown to yellow–brown, 6–10 cells in each row and 1–2 rounded to cylindrical appendages. In a BLASTn search on NCBI GenBank, the closest matches of ITS sequence of KUMCC 16-0152 is 99% identical with the two strains of *D. rotunda* strain DLUCC 0577 (KY320512) and *D. garethjonesii* strain KUMCC 15-0396 (KY320510), while the closest matches with the TEF1 sequence were with 98% identity with *D. garethjonesii* strain DUCC 0848 (MF953166) and 96% identity *D. rotunda* strain DUCC 0804 (MF953170).

Dictyocheirospora pandanicola Tibpromma & K.D. Hyde, ***sp. nov***.

Index Fungorum number: IF554475, *Facesoffungi number*: FoF04484; Fig. 5

Etymology: named after the host genus, *Pandanus*.

Holotype: MFLU 16-1933

Saprobic on dead leaves of *Pandanus* sp. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Conidiomata sporodochia* on natural substrate, solitary or in small groups, scattered, reddish brown. *Conidiophores* micronematous, reduced to conidiogenous cell. *Conidiogenous cells* 9–15 × 1.5–3 µm ($\bar{x}$ = 12 × 2.5 µm, n = 10), holoblastic, cylindrical, sometimes flat at base, subhyaline, mostly not remaining attached to the conidia. *Conidia* 60–75 × 18.5–35.5 µm ($\bar{x}$ = 65 × 24 µm, n = 30), solitary, oval to ellipsoid, cheiroid, consisting of 95–120 cells, with a basal connecting cell, pale brown, guttulate, individual cells discoid, 53–65 × 6–7.5 µm, arranged in 5–7 compact rows, of which 6 in peripheral positions and one central, each three rows connected to a large basal cell, 13–18 cells per row, smooth-walled, without appendages

Culture characteristics: Conidia germinating on MEA within 24 h. Colonies on MEA, circular, entire edge, yellow brown, velvety, umbonate on media surface.

Material examined: THAILAND, Prachuap Khiri Khan Province, Bang Saphan District, Sai Khu Waterfall, on *Pandanus* sp., 15 July 2015, S. Tibpromma SF15-031 (MFLU 16-1933, **holotype**; HKAS 96282, **isotype**); ex-type living culture, MFLUCC 16-0365.

GenBank numbers LSU: MH376713; ITS: MH388341; SSU: MH388309; TEF1: MH388376.

Notes: In the phylogenetic analysis *Dictyocheirospora pandanicola* clustered with *D. vinaya* D'souza, Bhat & K.D. Hyde. Figure 4, but the two species differ in morphology. *Dictyocheirospora pandanicola* has oval to ellipsoid, cheiroid conidia 60–75 × 18.5–35.5 µm with 13–18 cells in each arm, while *D. vinaya* has cheiroid conidia 58–67 × 15.5–26.5 µm with 9–13 cells in each arm (Boonmee et al. 2016). In a BLASTn search on NCBI

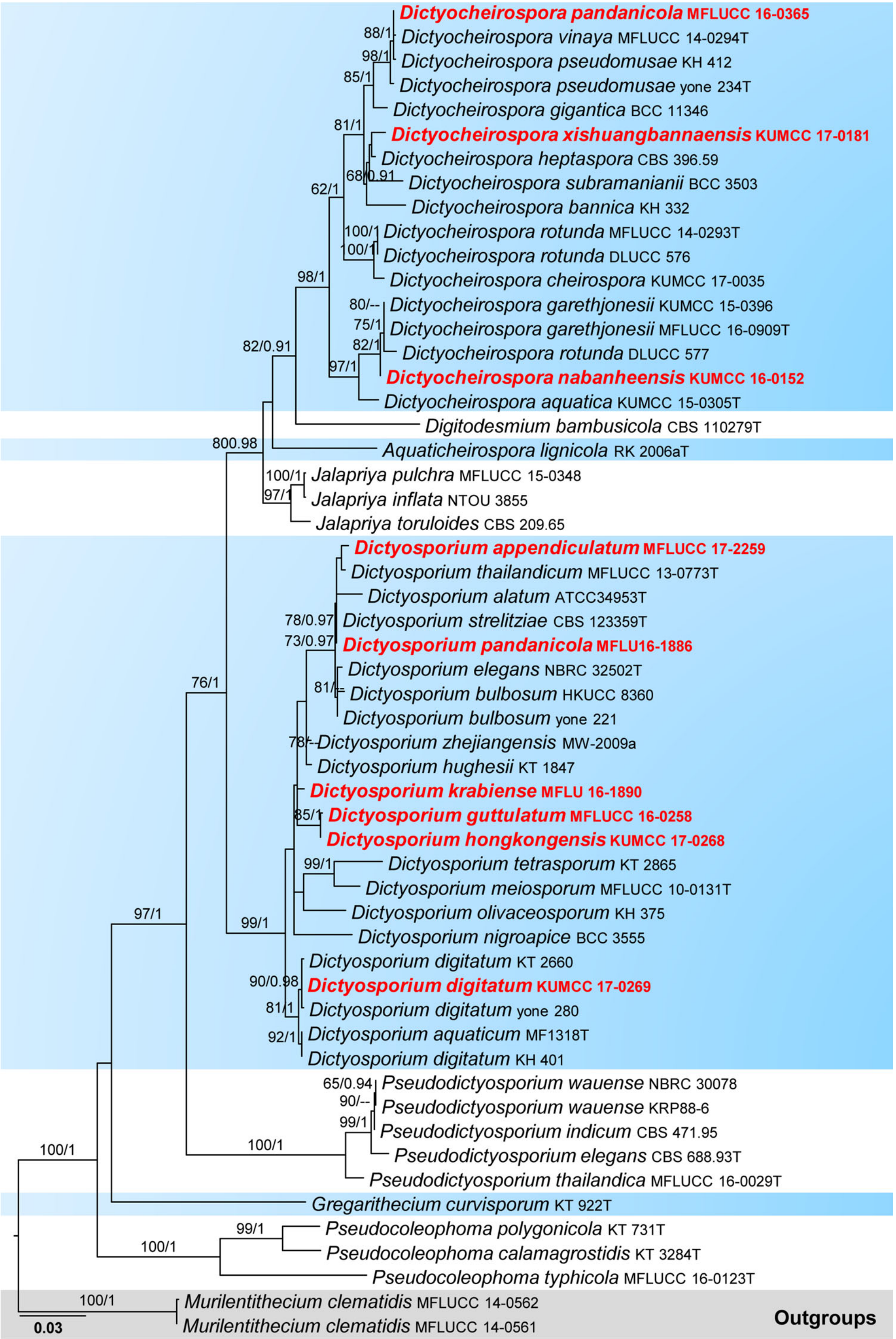


Fig. 3 Phylogram generated from maximum likelihood analysis based on combined LSU and ITS partial sequence data. Fifty-five strains are included in the sequence analysis, which comprise 1460 characters with gaps. Single gene analysis was carried out and compared with each species, to compare the topology of the tree and clade stability. *Murilentithecium clematidis* (Lentitheciaceae) is used as the outgroup taxon. Tree topology of the ML analysis was similar to the BYPP. The best scoring RAxML tree with a final likelihood value of − 7300.219123 is presented. The matrix had 474 distinct alignment patterns, with 19.03% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.240784, C = 0.235601, G = 0.275234, T = 0.248381; substitution rates AC = 1.951883, AG = 3.307241, AT = 2.649573, CG = 0.576092, CT = 8.294481, GT = 1.000000; gamma distribution shape parameter α = 0.744325. Bootstrap support values for ML equal to or greater than 60% and BYPP equal to or greater than 0.90 are given above the nodes. Newly generated sequences are in red

GenBank, the closest matches of ITS sequence of MFLUCC 16-0365 is 100% identical *D. digitatum* strain 30404 (KP714383), while the closest matches with the TEF1 sequence were with 95% identity with *D. pseudomusae* strain EF9a (AB808492).

Fig. 4 ***Dictyocheirospora nabanheensis*** (HKAS 101807, **holotype**). **a** Colonies on dead leaves of *Pandanus* sp. **b–e** Conidiogenous cells and conidia. **f** Crush conidium. **g** One row of conidium. **h** Germinating conidium. Scale bars: **b–g** = 10 µm, **h** = 20 µm

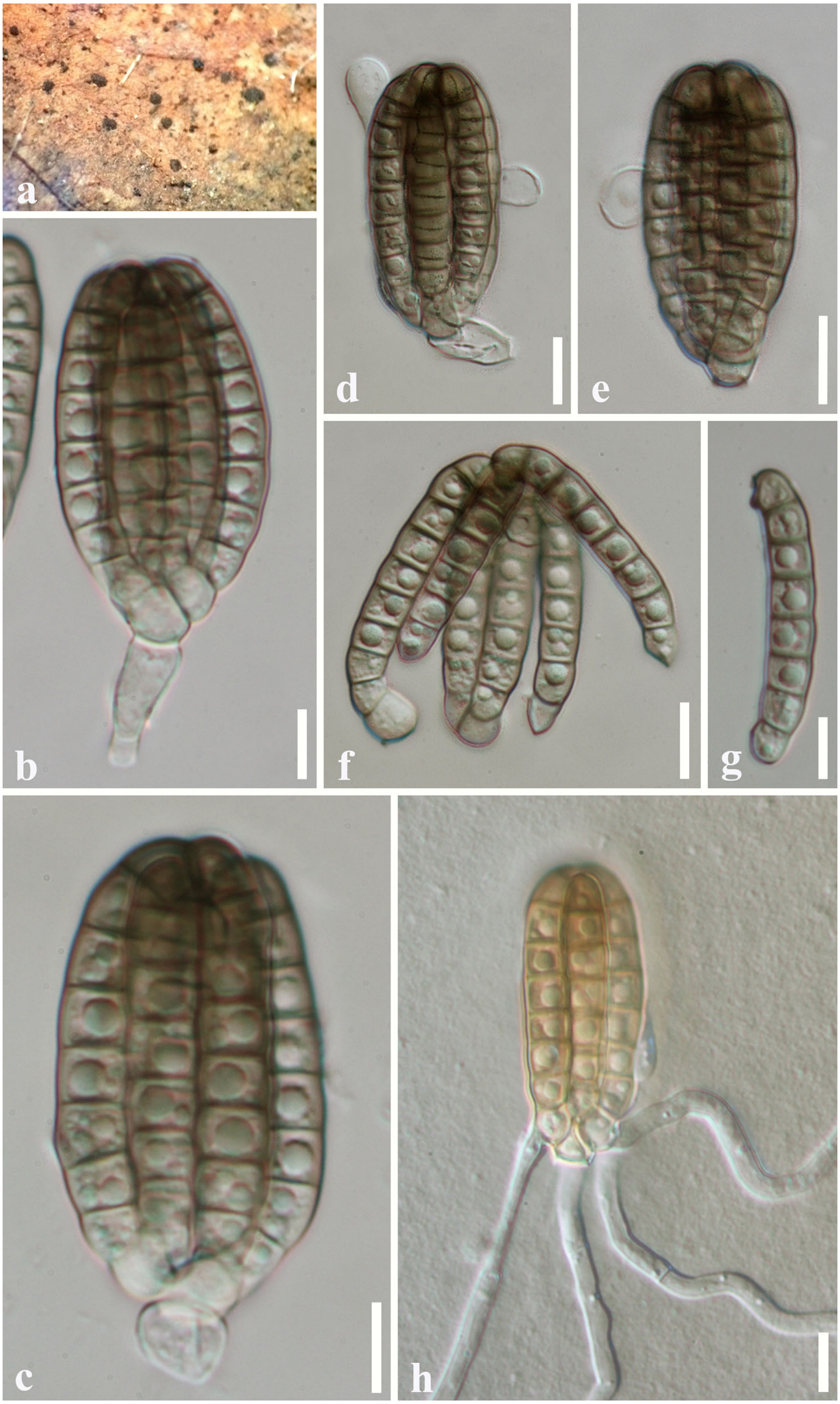
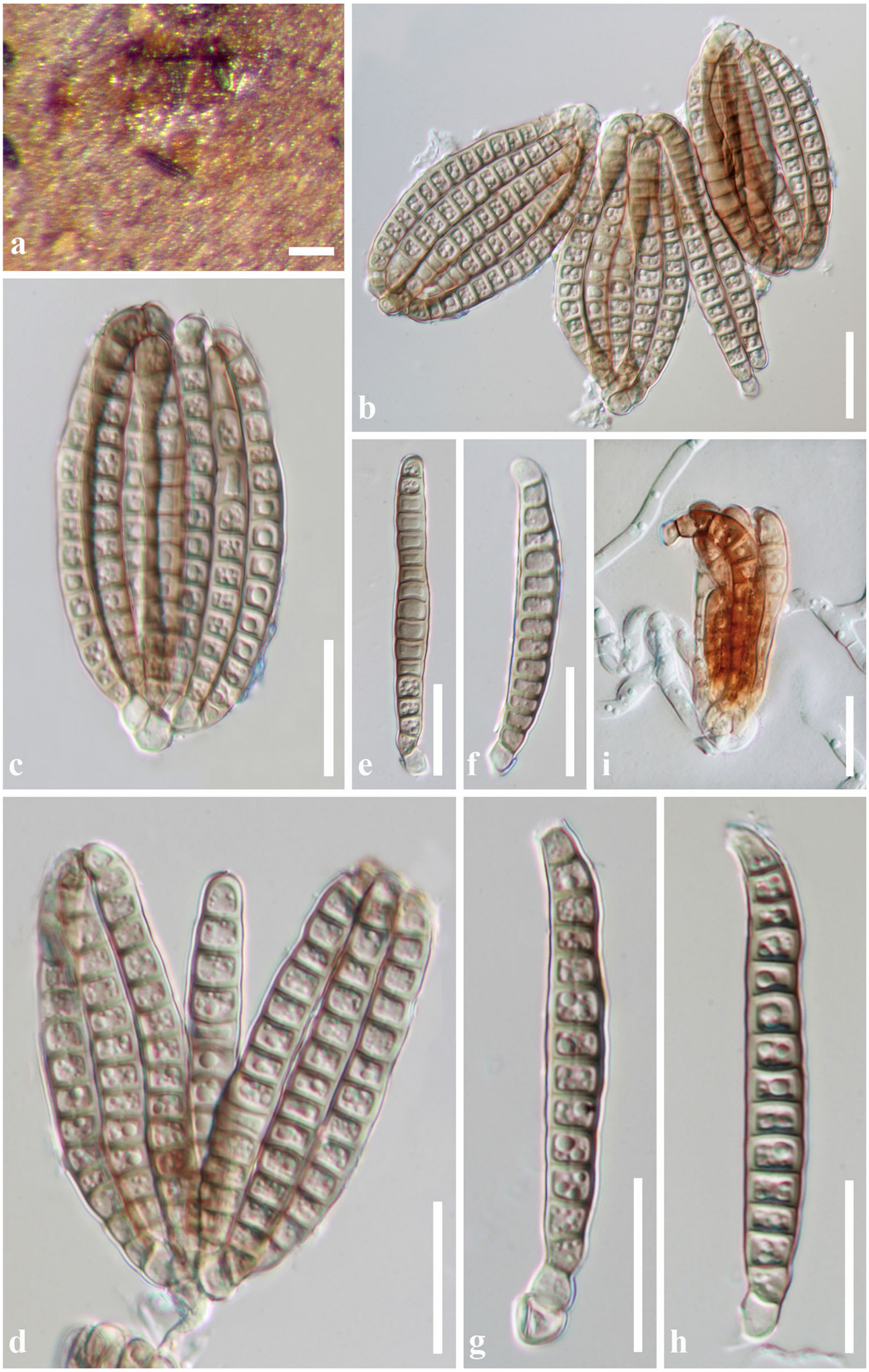


Fig. 5 ***Dictyocheirospora pandanicola*** (MFLU 16-1933, **holotype**). **a** Colonies on dead leaves of *Pandanus* sp. **b-d** Conidiogenous cells and conidia. **e–h** Rows of conidium. **i** Germinating conidium. Scale bars: **a** = 50 µm, **b–i** = 20 µm



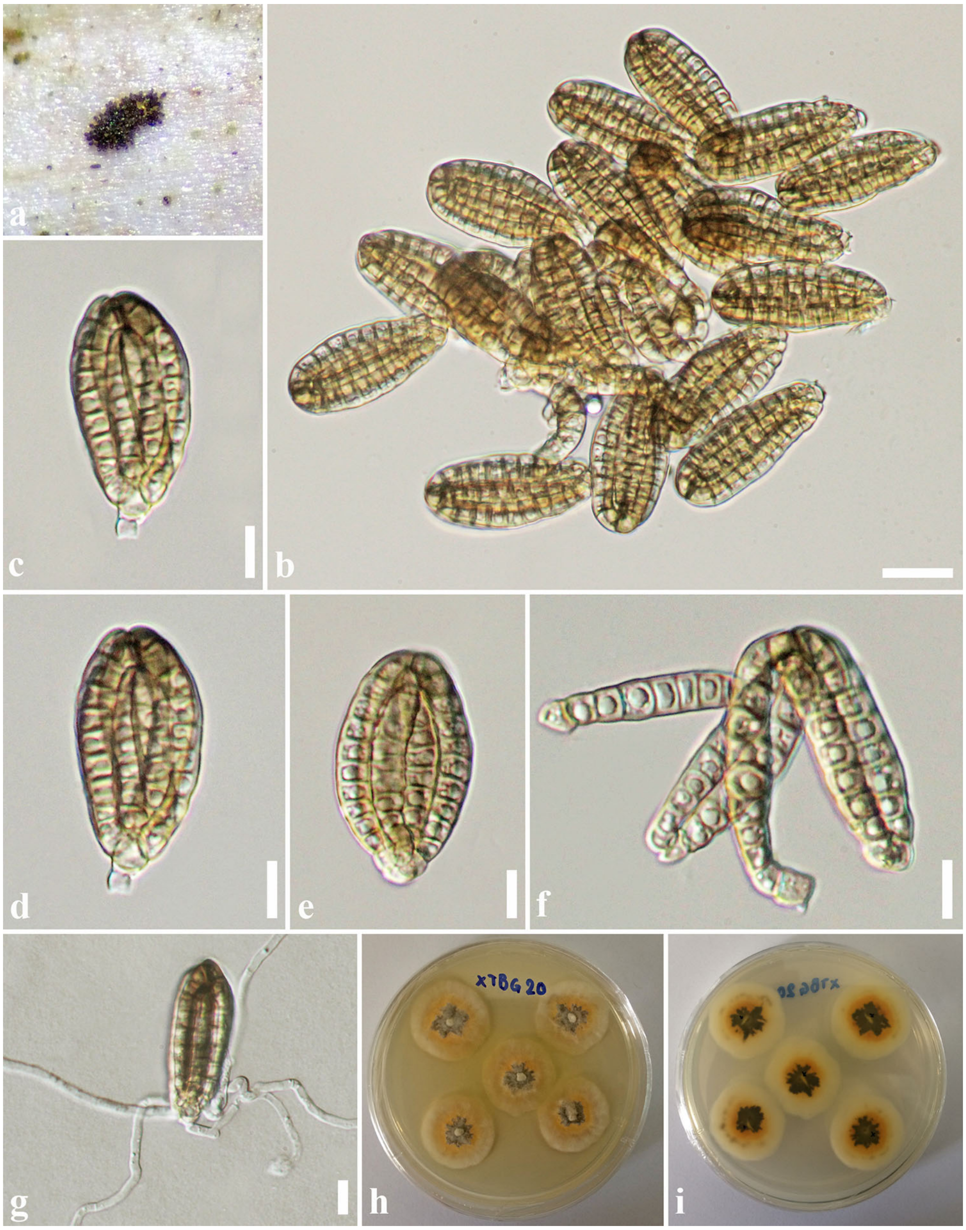


Fig. 6 ***Dictyocheirospora xishuangbannaensis*** (HKAS 99628, **holotype**). **a** Colony on dead leaves of *Pandanus* sp. **b–f** Conidiogenous cells and conidia. **g** Germinating conidium. **h–i** Colonies on MEA from above and below. Scale bars: **b–f** = 10 µm, **g** = 20 µm

Dictyocheirospora xishuangbannaensis Tibpromma & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF554476, *Facesoffungi number*: FoF04485; Fig. 6

Etymology: named after Xishuangbanna, place where fungus was first discovered.

Holotype: HKAS 99628

Saprobic on dead leaves of *Pandanus* sp. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Conidiomata sporodochia* on natural substrate in small groups, dark brown, with base attached on surface of host plant. *Conidiophores* micronematous, reduced to conidiogenous cell. *Conidiogenous cells* 3–7 × 3.5–7 µm ($\bar{x}$ = 5 × 4.5 µm, n = 20), holoblastic, cylindrical, sometimes flat at base, hyaline to pale brown, mostly remaining attached to the conidia. *Conidia* 35–50 × 17–25 µm ($\bar{x}$ = 47 × 21 µm, n = 20), solitary, oval to ellipsoid, cheiroid, consisting of 54–65 cells, with a basal connecting cell, pale brown to green–brown, guttulate, 40–48 × 7–9 µm, arranged in 6 compact rows, of which 6 in peripheral positions connected to large basal cell, with individual cells discoid, 6–12 cells per row, without appendages.

Culture characteristics: Conidia germinating on PDA within 12 h. Colonies on PDA, circular, entire edge with yellowish at the margin and yellow to green in the central, raised on surface media.

Material examined: CHINA, Yunnan Province, Xishuangbanna, on *Pandanus* sp., 27 April 2017, R.

Phookamsak & N.I. de Silva XTBG20 (HKAS 99628, **holotype**); ex-type living culture, KUMCC 17-0181 = MFLUCC 17-2267.

GenBank numbers LSU: MH376714; ITS: MH388342; SSU: MH388310; TEF1: MH388377; RPB2: MH412728.

Notes: *Dictyocheirospora xishuangbannaensis* clustered with *D. heptaspora* (Garov) D'souza, Boonmee & K.D. Hyde in the phylogeny (Fig. 4). There were 22 bp (4.22%) differences in 521 ITS (+5.8S) nucleotides sequences between *D. xishuangbannaensis* and *D. heptaspora*. *Dictyocheirospora xishuangbannaensis* has conidia 35–50 × 17–25 µm, oval to ellipsoid, arranged in 6 compact rows, while *D. heptaspora* has conidia 50–80 × 20–30 µm, cylindrical with 7 compact rows (Goh et al. 1999). In a BLASTn search on NCBI GenBank, the closest matches of ITS sequence of KUMCC 17-0181 is 98% identical *D. heptasporum* strain CBS 396.59 (DQ018090), while the closest matches with the TEF1 sequence were with 96% identity with *D. rotunda* strain DUCC 0804 (MF953170).

Dictyosporium Corda

Dictyosporium was introduced with the single species *Di. elegans* Corda. The members of this genus are saprobes in terrestrial or aquatic environments (Hyde et al. 2011). There are 74 epithets are listed in Index Fungorum (2018). Whitton et al. (2012), provided a key to *Dictyosporium* species and eight species have been described from Pandanaceae. We found five species on Pandanaceae of which only one, *Di. digitatum* had been previously described. This suggests that *Dictyosporium* is very common on Pandanaceae.

Dictyosporium appendiculatum Tibpromma & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF555327, *Facesoffungi number*: FoF04486; Fig. 7

Etymology: name refers to its cylindrical appendages.

Holotype: MFLU 18-0019

Saprobic on dead leaves of *Pandanus* sp. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Conidiomata sporodochia* on natural substrate in small groups, dark brown, with base attached on surface of host plant. *Conidiophores* micronematous, reduced to conidiogenous cell. *Conidiogenous cells* 2–10 × 1–4 µm ($\bar{x}$ = 6 × 2.5 µm, n = 10), holoblastic, cylindrical to obovoid, subhyaline. *Conidia* 30–40 × 12–25 µm ($\bar{x}$ = 34 × 22 µm, n = 30), solitary, oval to ellipsoid, cheiroid, not complanate, yellow–brown, consisting of 30–40 cells arranged in (4–)5 rows, with a basal connecting cell, not easy to separate rows, guttulate, smooth-walled; 1–3-appendages rounded to cylindrical, 18–25 × 4–6 µm, apical on peripheral rows, hyaline, guttulate.

Culture characteristics: Conidia germinating on MEA within 24 h. Colonies on MEA, circular, entire edge with white at the margin and cream to yellow–orange in the central, raised on surface media.

Material examined: THAILAND, Nakhon Si Thammarat Province, Khanom District, on *Pandanus* sp., 22 July 2017, S. Tibpromma SR06 (MFLU 18-0019, **holotype**; HKAS 100846, **isotype**); ex-type living culture, MFLUCC 17-2259 = KUMCC 17-0311.

GenBank numbers LSU: MH376715; ITS: MH388343.

Notes: *Dictyosporium appendiculatum* clusters with *Di. thailandicum* M.J. D'souza, Bhat & K.D. Hyde (Liu et al. 2015b), but morphological comparison showed *Di. appendiculatum* is a distinct species. *Dictyosporium appendiculatum* has conidia 34 × 22 µm, yellow–brown, with 30–40 cells and (4–)5 rows, with 1–3 hyaline appendages, while *Di. thailandicum* has conidia 30.6 × 19 µm, dark brown to black at maturity, with 28–32 cells and 5 rows, with two hyaline appendages (Liu et al. 2015b). Based on morphology *Di. appendiculatum* is similar to *Di. zhejiangense* Wongs., H.K. Wang, K.D. Hyde & F.C. Lin, but the latter has complanate conidia, 25–35 × 17–24 µm and 23–37 cells per conidium (Wongsawas et al. 2009). In a BLASTn search on NCBI GenBank, the closest matches of ITS sequence of MFLUCC 17-2259 is 98% identical *D. strelitziae* strain CBS 123359 (NR_156216).

Dictyosporium digitatum J.L. Chen, C.H. Hwang and Tzean, Mycological Research 95: 1145 (1991)

Facesoffungi number: FoF04487; Fig. 8

Saprobic on dead leaves of *Pandanus* sp. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Conidiomata sporodochia* on natural substrate in small groups, dark brown, with base attached on surface of host plant. *Conidiophores* micronematous, reduced to conidiogenous cell. *Conidiogenous cells* 3–6 × 1–3.5 µm ($\bar{x}$ = 3.5 × 1.5 µm, n = 20), holoblastic, cylindrical, pale brown to yellow–brown. *Conidia* 60–70 × 30–40 µm ($\bar{x}$ = 62.5 × 33.5 µm, n = 20), solitary, oval to ellipsoid, cheiroid, not complanate, consisting of 65–90 cells arranged in 6–8 rows, with a basal connecting cell, not easy to separate, yellow–brown to brown, guttulate, subhyaline at the tip of peripheral rows, smooth-walled.

Culture characteristics: Conidia germinating on MEA within 12 h. Colonies on MEA, circular, entire edge with cream to yellow–orange, raised on surface media, producing yellow–brown pigment in media. Sporulating in culture after 3 months producing conidia similar in shape to those recorded on natural dead leaves.

Material examined: HONG KONG, Lantau Island, Pui O Beach, on *Pandanus* sp., 20 September 2016, S.

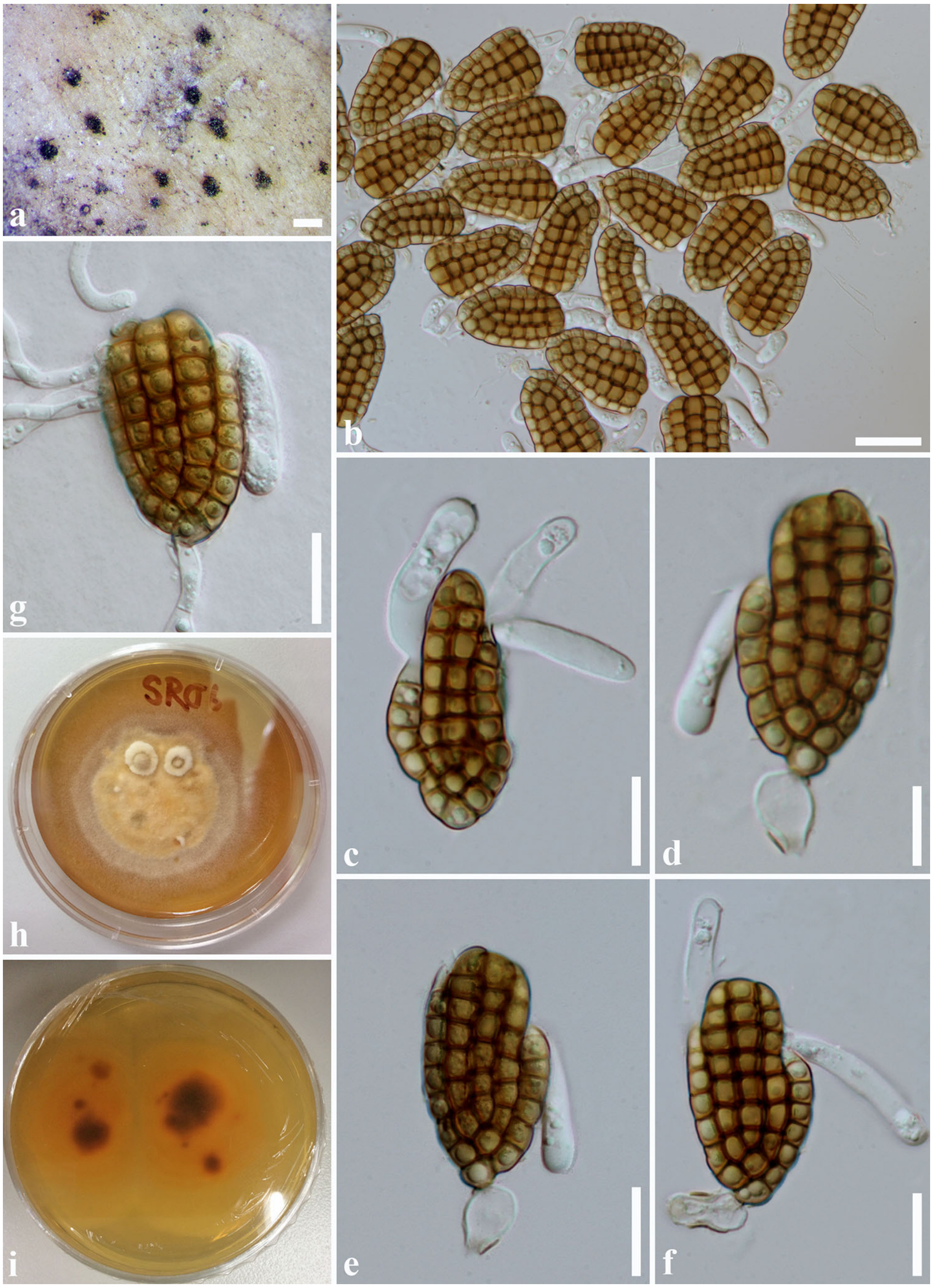


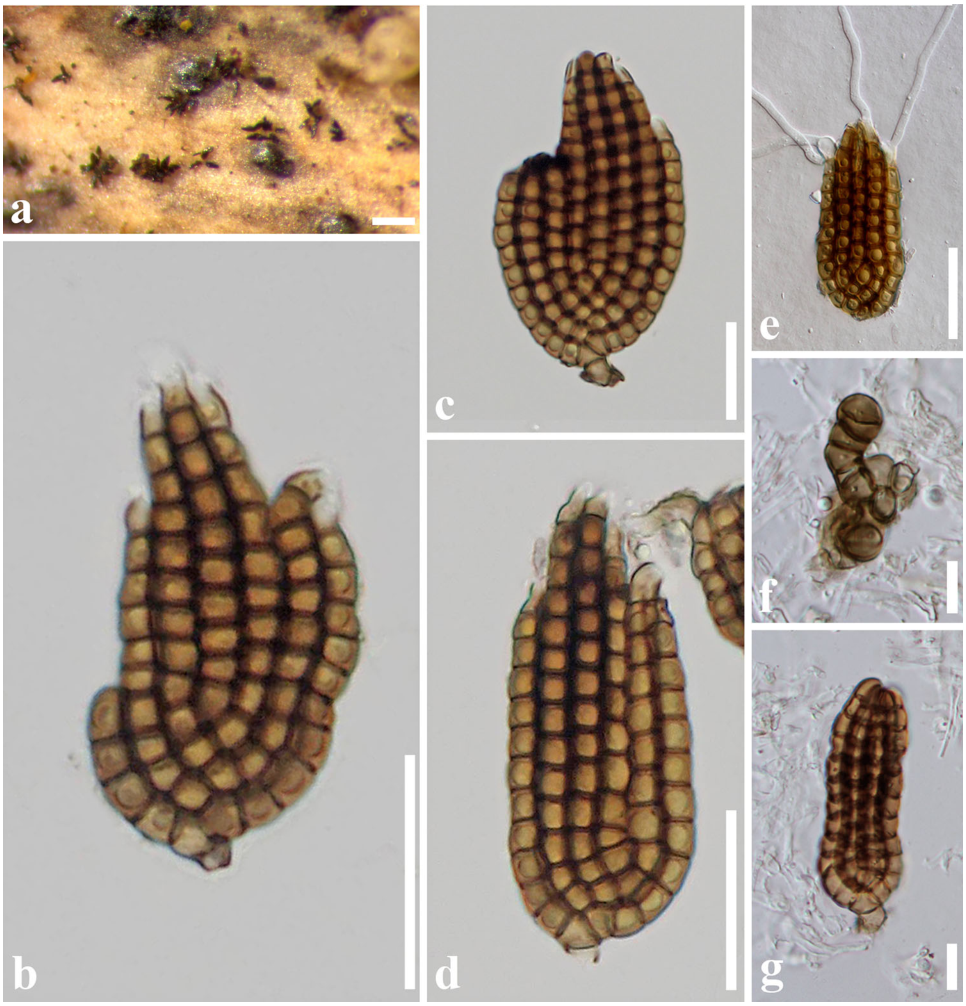
Fig. 7 ***Dictyosporium appendiculatum*** (MFLU 18-0019, **holotype**). **a** Colonies on dead leaves of *Pandanus* sp. **b–f** Conidiogenous cells and conidia with appendages. **g** Germinating conidium. **h, i** Colony on MEA from above and below. Scale bars: **a** = 100 µm, **b** = 20 µm, **c–g** = 10 µm

Tibpromma HK08 (HKAS 100860); living culture, KUMCC 17-0269 = MFLUCC 17-0635.

GenBank numbers LSU: MH376716; ITS: MH388344; SSU: MH388311; TEF1: MH388378.

Notes: *Dictyosporium digitatum* was first described from Taiwan (Chen et al. 1991). Morphologically our isolate is identical to *Di. digitatum* (Chen 1991). *Dictyosporium digitatum* is common on Pandanaceae and has been found on *Pandanus* spp. in Australia, Brunei, Hong Kong, Mauritius, Philippines, Seychelles, Taiwan and Thailand (Whitton et al. 2012) which characterised by thick-walled conidia, often flexuous appendages at the apices of each conidial row. Based on a BLASTn search on NCBI GenBank nucleotide database, the closest matches for the ITS sequence of our isolate is *Di. digitatum* (KT 2660) (identities = 503/503 (100%)).

Fig. 8 ***Dictyosporium digitatum*** (HKAS 100860). **a** Colonies on dead leaves of *Pandanus* sp. **b–d** Conidiogenous cells and conidia. **e** Germinating conidium. **f, g** Conidia formed in culture. Scale bars: **a** = 200 µm, **b–e** = 20 µm, **f, g** = 10 µm



Dictyosporium guttulatum Tibpromma & K.D. Hyde, ***sp. nov***.

Index Fungorum number: IF555328, *Facesoffungi number*: FoF04488; Fig. 9

Etymology: name refers to the guttulate conidia.

Holotype: MFLU 16-1914

Saprobic on dead leaves of *Pandanus* sp. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Conidiomata sporodochia* on natural substrate in small groups, dark, with base attached on surface of host plant. *Conidiophores* micronematous, reduced to conidiogenous cell. *Conidiogenous cells* 4–8.5 × 3–4 µm ($\bar{x}$ = 6 × 3.5 µm, n = 20), holoblastic, cylindrical, pale brown to green–brown. *Conidia* 30–40 × 16–23 µm ($\bar{x}$ = 37 × 20 µm, n = 30), solitary, oval to ellipsoid, cheiroid, not complanate, yellow–brown to brown, consisting of 40–44 cells arranged in (4–)5 rows, with a basal connecting cell, not easy to separate, guttulate, smooth-walled; appendages rounded to cylindrical, 3–11 × 3–5 µm, apical on peripheral rows, hyaline.

Culture characteristics: Conidia germinating on MEA within 24 h. Colonies on MEA, circular, entire edge with white at the margin and cream to yellow–orange in the centre, raised on surface media. Sporulating in culture after 3 months and producing conidia similar in shape to those recorded on dead leaves.

Material examined: THAILAND, Krabi Province, Mueang Krabi District, on *Pandanus* sp., 15 December 2015, S. Tibpromma KB036 (MFLU 16-1914, **holotype**; HKAS 96263, **isotype**); ex-type living culture, MFLUCC 16-0258 = KUMCC 17-0288; Krabi Province, Mueang Krabi District, on *Pandanus* sp., 16 December 2015, S. Tibpromma KB039 (MFLU 16-1917, **paratype**).

GenBank numbers LSU: MH376717; ITS: MH388345; SSU: MH388312; TEF1: MH388379.

Notes: *Dictyosporium guttulatum* clusters with *Di. hongkongensis* but is well-separated with high bootstrap support (85% in ML, 1 in BYPP, Fig. 4). *Dictyosporium guttulatum* and *Di. hongkongensis* are both found on

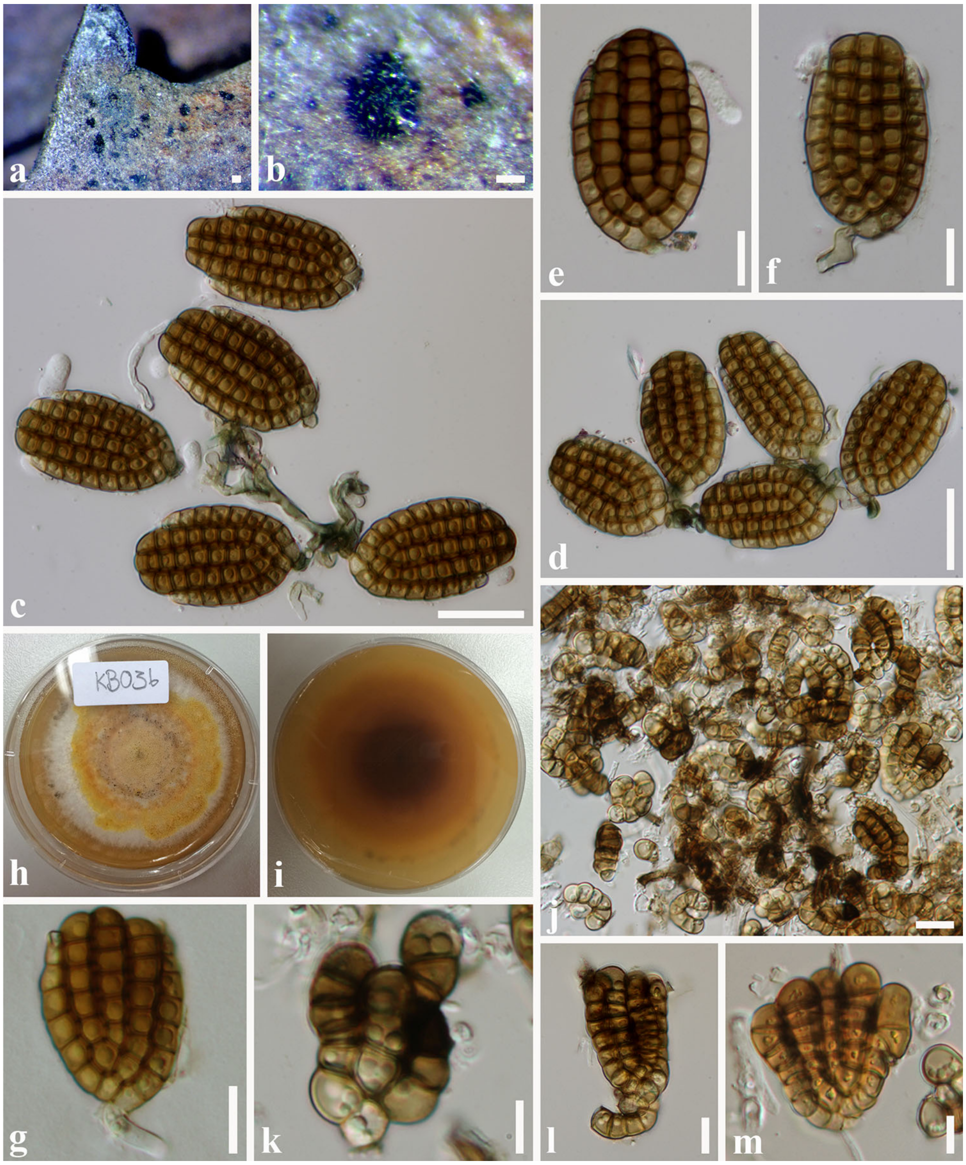


Fig. 9 ***Dictyosporium guttulatum*** (MFLU 16-1914, **holotype**). **a, b** Colonies on dead leaves of *Pandanus* sp. **c–f** Conidiogenous cells with conidiophores and conidia. **g** Germinating conidium. **h, i** Colony on MEA from above and below. **j–m** Conidia formed in culture. Scale bars: **a** = 100 µm, **b** = 50 µm, **c, d, j–m** = 20 µm, **e–g** = 10 µm

Pandanaceae but differ in morphology (Figs. 9, 10). *Dictyosporium guttulatum* has rounded to cylindrical appendages, while *Di. hongkongensis* lacks appendages. In a BLASTn search on NCBI GenBank, the closest matches of ITS sequence of MFLUCC 16-0258 is 96% identical *Di. hughesii* strain KT1847 (LC014548), while the closest matches with the TEF1 sequence were with 97% identity with *Di. digitatum* strain yone 280 (AB808488).

Dictyosporium hongkongensis Tibpromma & K.D. Hyde, ***sp*. *nov*.**

Index Fungorum number: IF554479, *Facesoffungi number*: FoF04489; Fig. 10

Etymology: named after Hong Kong, where the fungus was first discovered.

Holotype: HKAS 100864

Saprobic on dead leaves of *Pandanus* sp. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Conidiomata sporodochia* on natural substrate in small groups, dark brown, with base attached on surface of host plant. *Conidiophores* micronematous, reduced to conidiogenous cell. *Conidiogenous cells* 4.5–8 × 3–5 µm ($\bar{x}$ = 6 × 4 µm, n = 20), holoblastic, cylindrical, sometimes flat at base. *Conidia* 28–41 × 18–26 µm ($\bar{x}$ = 35.4 × 22 µm, n = 20), solitary, oval to ellipsoid, yellow–brown, cheiroid, not complanate, consisting of 16–30 cells arranged in 4–5 rows, 5–7 cells per row with a basal connecting cell, guttulate, without appendages.

Culture characteristics: Conidia germinating on MEA within 24 h. Colonies on MEA, circular, rough, entire edge with yellow–brown to dark–brown, yellow–brown in the

Fig. 10 ***Dictyosporium hongkongensis*** (HKAS 100864, **holotype**). **a** Colony on dead leaves of *Pandanus* sp. **b–e** Conidiogenous cells and conidia. **f** Germinating conidium. Scale bars: **a** = 100 µm, **b** = 10 µm, **c–f** = 5 µm

central, become dark–brown at the margin, raised on surface media.

Material examined: HONG KONG, around Tai Tam Tuk Reservoir Dam, on *Pandanus* sp., 21 September 2016, S. Tibpromma HK03 (HKAS 100864, **holotype**); ex-type living culture, KUMCC 17-0268 = MFLUCC 17-0633.

GenBank numbers LSU: MH376718; ITS: MH388346; SSU: MH388313; TEF1: MH388380.

Notes: There were 23 bp (4.22%) differences of the 545 ITS (+5.8S) nucleotides and 17 bp (1.88%) differences in 900 TEF1 nucleotides between *Di. hongkongensis* and *Di. guttulatum*. Also, *Di. hongkongensis* has similar conidia to *Di. alatum* Emden. *Dictyosporium alatum* has 5 rows of cells, and 4–6 cells per row with appendages (Whitton et al. 2012), while *Di. hongkongensis* has 4–5 rows of cell and 5–7 cells per row but lacks appendages. In a BLASTn search on NCBI GenBank, the closest matches of ITS sequence of KUMCC 17-0268 is 96% identical *Di. zhejiangense* strain MW-2009a (FJ456893), while the closest matches with the TEF1 sequence were with 97% identity with *Di. digitatum* strain yone 280 (AB808488).

Dictyosporium krabiense Tibpromma & K.D. Hyde, ***sp. nov***.

Index Fungorum number: IF554480, *Facesoffungi number*: FoF04490; Fig. 11

Etymology: named after Krabi Province, where the fungus was first discovered.

Holotype: MFLU 16-1890

Colonies on leaf sheath of *Pandanus* sp. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Colonies* black, flat on host surface. *Conidiophores* micronematous, reduced to conidiogenous cell. *Conidiogenous cells* 2–

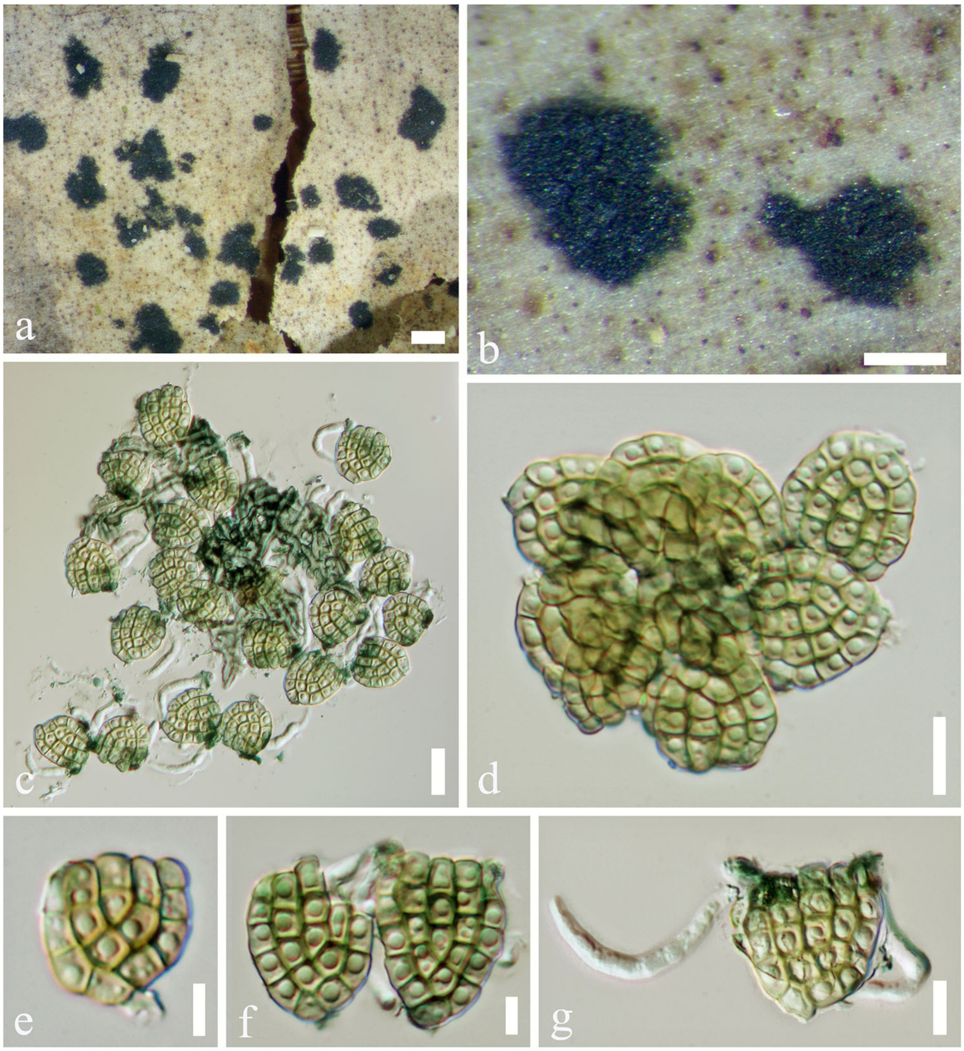


Fig. 11 ***Dictyosporium krabiense*** (MFLU 16-1890, **holotype**). **a, b** Colonies on dead leaf sheath of *Pandanus* sp. **c, d** Conidiogenous cells and conidia. **e–g** Conidia. Scale bars: **a** = 500 µm, **b** = 200 µm, **c, d** = 10 µm, **e–g** = 5 µm

3.5 × 2–3 µm ($\bar{x}$ = 3 × 2.5 µm, n = 20), holoblastic, integrated, terminal, smooth, thin-walled. *Conidia* 14–17 × 15–20 µm ($\bar{x}$ = 16 × 17 µm, n = 40), solitary, yellow green, composed of 4–5 rows, inflated, rows not separating, always in group, each row consisting of 4–6 cell with distinct guttules in each cell; appendages 1–2, cylindrical, conical at apex, hyaline, apical on outside rows.

Material examined: THAILAND, Krabi Province, Mueang Krabi District, on dead leaf sheath *Pandanus* sp., 14 December 2017, S. Tibpromma KB012 (MFLU 16-1890, **holotype**; HKAS 96240, **isotype**).

GenBank numbers LSU: MH376719; SSU: MH388314; TEF1: MH388381.

Notes: *Dictyosporium krabiense* is characterized by 14–17 × 15–20 µm, yellow–green conidia, composed of 4–5 rows, with 1–2 long cylindrical appendages. Based on phylogenetic evidence, *Di. krabiense* is well-separated from other *Dictyosporium* species (Fig. 4). Morphologically *Di. krabiense* has similar conidia to *Di. oblongum* (Fuckel) S. Hughes and *Di. polystichum* (Höhn.) Damon but *Di. oblongum* has conidia 30–50 × 12–30 µm, uniformly medium to dark brown and without appendages (Goh et al. 1999), while *Di. polystichum* has conidia 26–34 × 23–34 µm, uniformly medium to dark brown and without appendages (Goh et al. 1999). In a BLASTn search on NCBI GenBank, the closest matches of TEF1 sequence of MFLU 16-1890 is 98% identical *Di. bulbosum* strain yone 221 (AB808487).

Dictyosporium pandanicola Tibpromma & K.D. Hyde, ***sp. nov***.

Index Fungorum number: IF554481, *Facesoffungi number*: FoF04491; Fig. 12

Etymology: named after the host genus, *Pandanus*.

Holotype: MFLU 16-1886

Saprobic on dead leaves of *Pandanus* sp. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous.

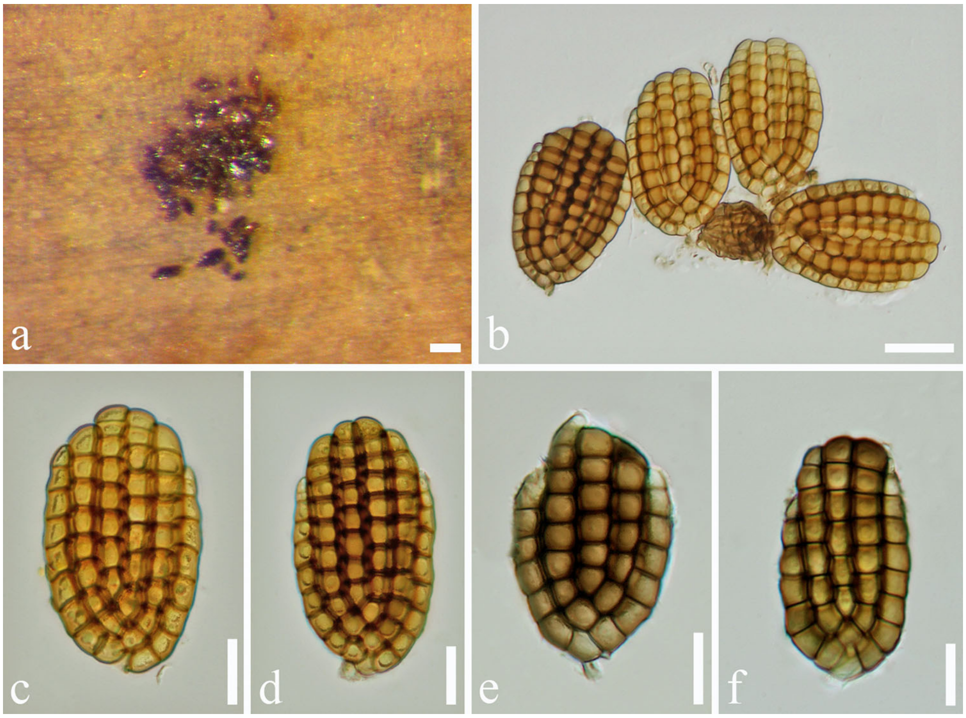


Fig. 12 ***Dictyosporium pandanicola*** (MFLU 16-1886, **holotype**). **a** Colony on dead leaves of *Pandanus* sp. **b** Conidiogenous cells and conidia. **c–f** Conidia. Scale bars: **a** = 50 µm, **b** = 20 µm, **c–f** = 10 µm

Conidiomata sporodochia on natural substrate in small groups, dark brown. *Conidiophores* micronematous, reduced to conidiogenous cell. *Conidiogenous cells* 3.5–8 × 3–3.5 µm ($\bar{x}$ = 5.5 × 3 µm, n = 10), holoblastic, cylindrical sometimes flat at base, hyaline to pale brown. *Conidia* 30–50 × 15–33 µm ($\bar{x}$ = 41 × 23 µm, n = 20), solitary, oval to ellipsoid, cheiroid, not complanate, consisting of 34–62 cells arranged in 5–6 rows, each with 6–8 cells, with a basal connecting cell, yellow–brown to brown with age, without appendages or mucilaginous sheath.

Material examined: THAILAND, Krabi Province, Mueang Krabi District, on *Pandanus* sp., 14 December 2015, S. Tibpromma KB008 (MFLU 16-1886, **holotype**; HKAS 96236, **isotype**).

GenBank numbers LSU: MH376720; ITS: MH388347; TEF1: MH388382.

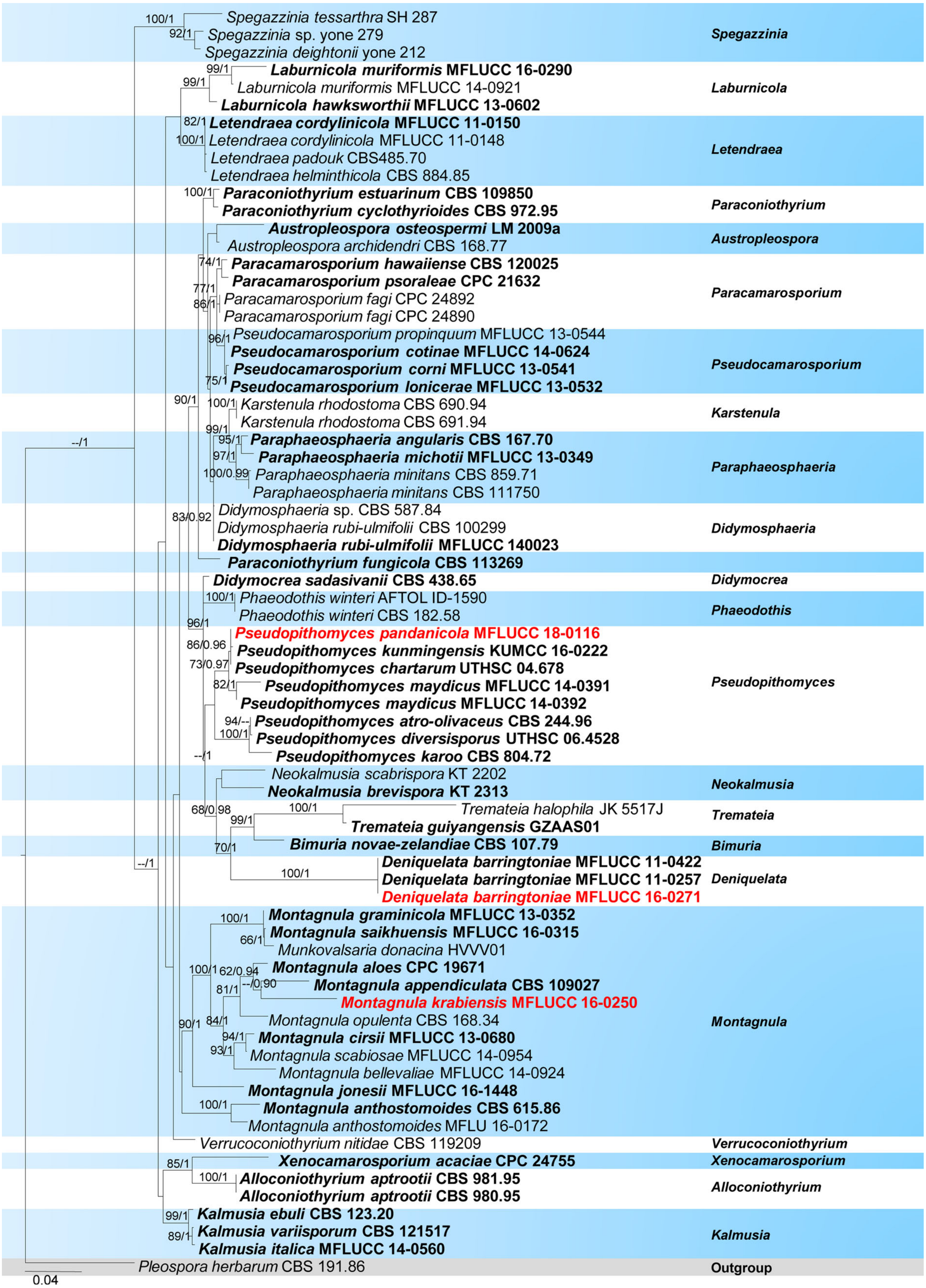
Notes: *Dictyosporium pandanicola* clustered with *Di. strelitziae* Crous & A.R. Wood in the phylogenetic analysis, but conidia of *Di. strelitziae* are arranged in (4–)5(–6) rows with 7–11 cells and with globose, apical appendage (Crous et al. 2009), while conidia of *Di. pandanicola* are arranged in 5–6 rows with 6–8 cells, and lack appendages. *Dictyosporium pandanicola* is also similar to *Di. pandani* but the latter has conidia measuring 22–48 × 14–28 µm with 4–5 rows of cells and 29–49 cells per conidium (Whitton et al. 2012). In a BLASTn search on NCBI GenBank, the closest matches of ITS sequence of MFLU 16-1886 is *Di. strelitziae* with 99% identity to the strain CBS 123359 (NR_156216), while the closest matches with the TEF1 sequence were with 99% identical *Di. bulbosum* strain yone 221 (AB808487).

Didymosphaeriaceae Munk

Didymosphaeriaceae was erected by Munk (1953) with the type genus *Didymosphaeria* Fuckel. and belongs to the order Pleosporales. In previous studies, Didymosphaeriaceae placement was not clear (Barr 1990a; Lumbsch and Huhndorf 2007; Zhang et al. 2012). Wijayawardene et al. (2018) accepted and provided details of 28 genera. We provide an updated tree following Thambugala et al. (2017) and propose a new species of *Pseudopithomyces* and of *Montagnula* from Pandanaceae in Thailand, based on morphology and phylogeny analysis (Fig. 13). We also provide a description of *Deniquelata barringtoniae*, which is newly recorded on Pandanaceae in Thailand.

Deniquelata Ariyaw. & K.D. Hyde

The monotypic genus *Deniquelata* was erected by Ariyawansa et al. (2013) to accommodate *D. barringtoniae* Ariyawansa & K.D. Hyde, which was collected from a leaf of *Barringtonia asiatica* in Chiang Rai, Thailand. We found another collection of *Deniquelata barringtoniae* on dead leaves of *Pandanus* sp. from Prachuap Khiri Khan in Thailand.


Spegazzinia tessarthra SH 287
Spegazzinia sp. yone 279
Spegazzinia deightonii yone 212
Spegazzinia
Laburnicola muriformis MFLUCC 16-0290
Laburnicola muriformis MFLUCC 14-0921
Laburnicola hawksworthii MFLUCC 13-0602
Laburnicola
Letendraea cordylinicola MFLUCC 11-0150
Letendraea cordylinicola MFLUCC 11-0148
Letendraea padouk CBS485.70
Letendraea helminthicola CBS 884.85
Letendraea
Paraconiothyrium estuarinum CBS 109850
Paraconiothyrium cyclothyrioides CBS 972.95
Paraconiothyrium
Austropleospora osteospermi LM 2009a
Austropleospora archidendri CBS 168.77
Austropleospora
Paracamarosporium hawaiiense CBS 120025
Paracamarosporium psoraleae CPC 21632
Paracamarosporium fagi CPC 24892
Paracamarosporium fagi CPC 24890
Paracamarosporium
Pseudocamarosporium propinquum MFLUCC 13-0544
Pseudocamarosporium cotinae MFLUCC 14-0624
Pseudocamarosporium corni MFLUCC 13-0541
Pseudocamarosporium lonicerae MFLUCC 13-0532
Pseudocamarosporium
Karstenula rhodostoma CBS 690.94
Karstenula rhodostoma CBS 691.94
Karstenula
Paraphaeosphaeria angularis CBS 167.70
Paraphaeosphaeria michotii MFLUCC 13-0349
Paraphaeosphaeria minitans CBS 859.71
Paraphaeosphaeria minitans CBS 111750
Paraphaeosphaeria
Didymosphaeria sp. CBS 587.84
Didymosphaeria rubi-ulmifolii CBS 100299
Didymosphaeria rubi-ulmifolii MFLUCC 140023
Didymosphaeria
Paraconiothyrium fungicola CBS 113269
Didymocrea sadasivanii CBS 438.65
Didymocrea
Phaeodothis winteri AFTOL ID-1590
Phaeodothis winteri CBS 182.58
Phaeodothis
Pseudopithomyces pandanicola MFLUCC 18-0116
Pseudopithomyces kunmingensis KUMCC 16-0222
Pseudopithomyces chartarum UTHSC 04.678
Pseudopithomyces maydicus MFLUCC 14-0391
Pseudopithomyces maydicus MFLUCC 14-0392
Pseudopithomyces atro-olivaceus CBS 244.96
Pseudopithomyces diversisporus UTHSC 06.4528
Pseudopithomyces karoo CBS 804.72
Pseudopithomyces
Neokalmusia scabrispora KT 2202
Neokalmusia brevispora KT 2313
Neokalmusia
Trematateia halophila JK 5517J
Trematateia guiyangensis GZAAS01
Tremateia
Bimuria novae-zelandiae CBS 107.79
Bimuria
Deniquelata barringtoniae MFLUCC 11-0422
Deniquelata barringtoniae MFLUCC 11-0257
Deniquelata barringtoniae MFLUCC 16-0271
Deniquelata
Montagnula graminicola MFLUCC 13-0352
Montagnula saikhuensis MFLUCC 16-0315
Munkovalsaria donacina HVVV01
Montagnula aloes CPC 19671
Montagnula appendiculata CBS 109027
Montagnula krabiensis MFLUCC 16-0250
Montagnula opulenta CBS 168.34
Montagnula cirsii MFLUCC 13-0680
Montagnula scabiosae MFLUCC 14-0954
Montagnula bellevaliae MFLUCC 14-0924
Montagnula jonesii MFLUCC 16-1448
Montagnula anthostomoides CBS 615.86
Montagnula anthostomoides MFLU 16-0172
Montagnula
Verrucoconiothyrium nitidae CBS 119209
Verrucoconiothyrium
Xenocamarosporium acaciae CPC 24755
Xenocamarosporium
Alloconiothyrium aptrootii CBS 981.95
Alloconiothyrium aptrootii CBS 980.95
Alloconiothyrium
Kalmusia ebuli CBS 123.20
Kalmusia variisporum CBS 121517
Kalmusia italica MFLUCC 14-0560
Kalmusia
Pleospora herbarum CBS 191.86
Outgroup
0.04

◀**Fig. 13** Phylogram generated from maximum likelihood analysis based on combined LSU, SSU, TEF1 and ITS sequence data. Related sequences were obtained from Tennakoon et al. (2016). Seventy-two strains are included in the combined sequence analysis, which comprise 3168 characters with gaps. *Pleospora herbarum* (CBS 191.86) is used as the outgroup taxon. Tree topology of the ML analysis was similar to the BYPP. The best scoring RAxML tree with a final likelihood value of − 15836.943543 is presented. The matrix had 1031 distinct alignment patterns, with 39.64% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.239912, C = 0.243956, G = 0.276827, T = 0.239305; substitution rates AC = 1.294307, AG = 1.980610, AT = 1.324440, CG = 0.930745, CT = 7.141409, GT = 1.000000; gamma distribution shape parameter α = 0.184270. Bootstrap support values for ML equal to or greater than 60% and BYPP equal to or greater than 0.90 are given above the nodes. Newly generated sequences are in red

Deniquelata barringtoniae Ariyawansa and K.D. Hyde, Phytotaxa 105 (1): 15 (2013)

Facesoffungi number: FoF04492; Fig. 14

Saprobic on dead leaves of *Pandanus* sp. **Sexual morph** *Ascomata* 120–220 × 90–130 µm ($\bar{x}$ = 159.5 × 109 µm, n = 5), scattered to gregarious, immersed, conspicuous on host surface, dark brown, dull, solitary, uniloculate, globose to subglobose, without papilla and ostiole. *Peridium* 22–30 µm wide, composed of several layers of thick-walled, yellow–brown cells of *textura angularis*. *Hamathecium* comprising numerous 2–3 µm wide, filiform, filamentous, unbranched, guttulate, septate pseudoparaphyses. *Asci* 60–130 × 10–25 µm ($\bar{x}$ = 88.5 × 17 µm, n = 20), (6–)8-spored, bitunicate, cylindrical to clavate, with a short furcate pedicel, apically rounded. *Ascospores* 10–20 × 5–10 µm ($\bar{x}$ = 14 × 8 µm, n = 40), overlapping 2–3-seriate, muriform, oblong to narrowly oblong, straight or somewhat curved, pale brown to yellow–brown, with 3 transverse septa and 1−2 longitudinal septa in the middle cells, constricted at septa, verruculose, guttulate, with mucilaginous sheath. **Asexual morph** Undetermined.

Culture characteristics: Ascospores germinating on MEA within 12 h. Colonies on MEA, white–grey on the surface, circular, with entire edge, raised, not yellow–white in reverse, with smooth margin.

Material examined: THAILAND, Prachuap Khiri Khan Province, Bang Saphan District, Sai Khu Waterfall, on *Pandanus* sp., 30 July 2015, S. Tibpromma SF15-035 (MFLU 16-0556); living culture, MFLUCC 16-0271 = KUMCC 16-0161.

GenBank numbers LSU: MH260291; ITS: MH275059; SSU: MH260333; TEF1: MH412766; RPB2: MH412753.

Notes: In the molecular analysis our isolate clustered with *Deniquelata barringtoniae* (CBS 109027) with high bootstrap support (100% in ML, 1 in BYPP, Fig. 13). The morphology of our isolate was similar to that of *D. barringtoniae* described by Ariyawansa et al. (2013), although we note that the ascospores have a mucilaginous sheath. This is the first report of *Deniquelata* from Pandanaceae.

Montagnula Berl.

Montagnula was erected by Berlese (1896) with *M. infernalis* (Niessl) Berl. as type species. The genus is characterized by globose or sphaerical, immersed ascomata with a clypeus, claviform asci, fusoid or ellipsoid ascospores with transverse septa. The members species can be saprobes growing on dead plants, especially dead wood and bark, sometimes on dead leaves (Ariyawansa et al. 2014). Presently, there are 38 epithets are listed in Index Fungorum (2018). We provide an updated tree and introduce a new species from Pandanaceae in Thailand based on morphology and phylogenetic analysis (Fig. 13).

Montagnula krabiensis Tibpromma & K.D. Hyde, ***sp. nov***.

Index Fungorum number: IF554482, *Facesoffungi number*: FoF04493; Fig. 15

Etymology: named after Krabi Province, where the fungus was first discovered.

Holotype: MFLU 16-1891

Saprobic on dead leaves of *Pandanus* sp. **Sexual morph** *Ascomata* 140–160 × 150–170 µm ($\bar{x}$ = 152 × 160 µm, n = 5), immersed, under clypeus, inconspicuous on host surface, solitary or scattered, as small dark brown dots, solitary, uniloculate, globose, without papilla and ostiole. *Peridium* 12–26 µm wide, comprising several layers, composed of dark brown to black cells of *textura angularis*. *Hamathecium* comprising 2–4 µm, numerous filamentous, unbranched, guttulate, septate pseudoparaphyses. *Asci* 70–125 × 15–20 µm ($\bar{x}$ = 94 × 16 µm, n = 10), 8-spored, bitunicate, cylindrical to clavate, long-pedicellate, furcate at base, apically rounded. *Ascospores* 25–32 × 6–7 µm ($\bar{x}$ = 29 × 6.5 µm, n = 20), 1–2-seriate, fusiform, 1-septate, septum median, widest at the centre and tapering towards the narrow ends, constricted at the septa, yellow–brown to brown with age, guttulate, with mucilaginous sheath, thick-walled. **Asexual morph** Undetermined.

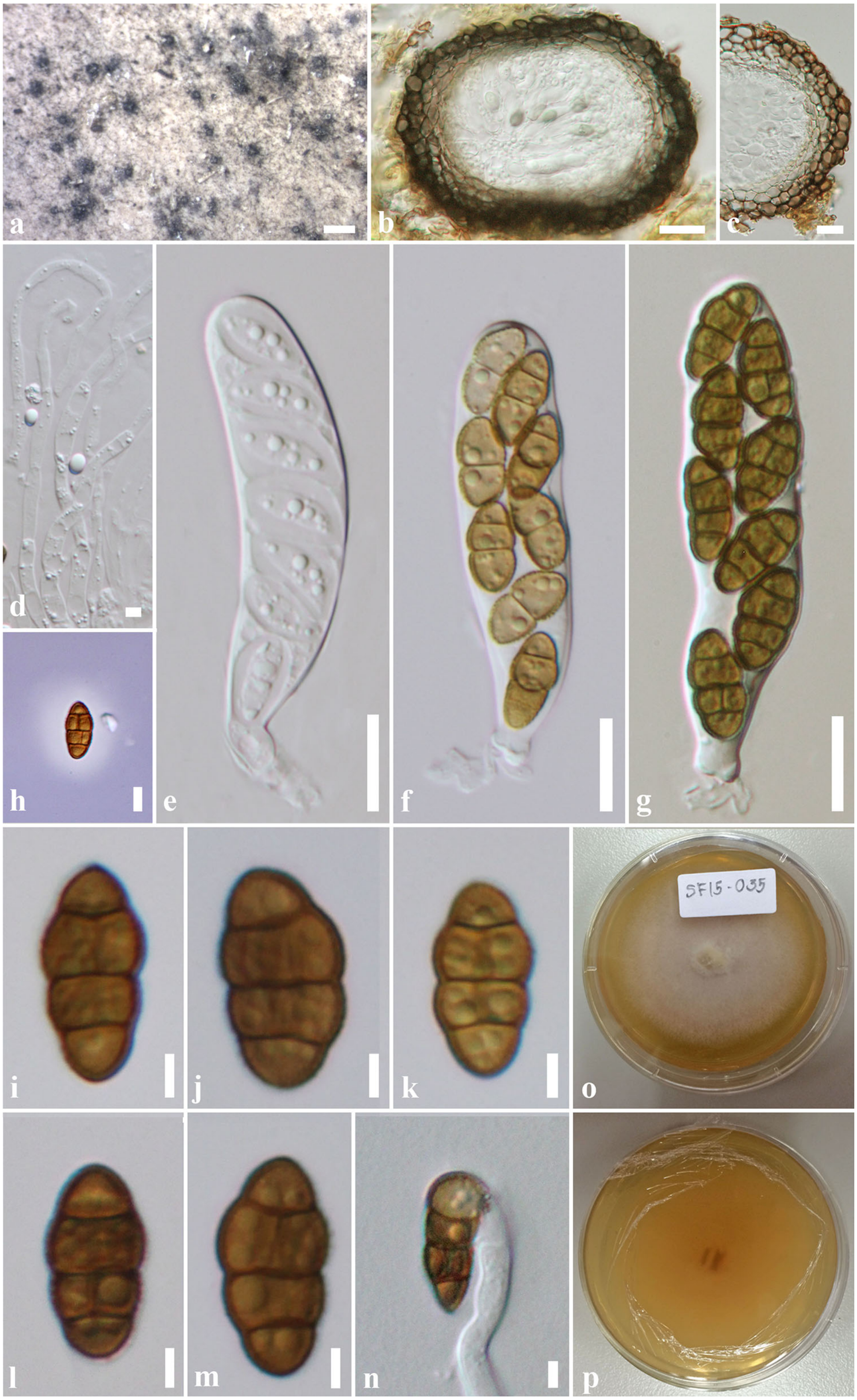
Culture characteristics: Ascospores germinating on MEA within 12 h. Colonies on MEA, reddish brown to brown, circular, with entire edge, raised, dark brown in reverse, with smooth margin.

Material examined: THAILAND, Krabi Province, Mueang Krabi District, on *Pandanus* sp., 14 December 2015, S. Tibpromma KB013 (MFLU 16-1891, **holotype**; HKAS 96241, **isotype**); ex-type living culture, MFLUCC 16-0250 = KUMCC 16-0138.

GenBank numbers LSU: MH260303; ITS: MH275070; SSU: MH260343; TEF1: MH412776.

Notes: *Montagnula krabiensis* has cylindrical to clavate, long-pedicellate asci, and fusiform, narrow 1-septate, yellow brown to brown ascospores, with a rough mucilaginous sheath. Based on phylogenic analysis, *M. krabiensis*

Fig. 14 ***Deniquelata barringtoniae*** (MFLU 16-0556). **a** Appearance of ascomata on host. **b** Section of ascoma. **c** Section of peridium. **d** Pseudoparaphyses. **e–g** Asci and ascospores at different stages of maturity. **h** Ascospore mounted in India ink. **i–m** Ascospores. **n** Germinating ascospore. **o, p** Colony on MEA from above and below. Scale bars: **a** = 500 µm, **b, c** = 50 µm, **d, i–n** = 5 µm, **e–g** = 20 µm, **h** = 10 µm



clusters with *M. appendiculata* (Aptroot) Wanas., E.B.G. Jones & K.D. Hyde (0.90 in BYPP, Fig. 13). However, *M. appendiculata* has reddish brown, broadly fusiform ascospores, with 2–5 greenish oil droplets and two polar hyaline appendages (Aptroot 2004). This is the first report of *Montagnula* species from Pandanaceae. In a BLASTn search on NCBI GenBank, the closest matches of ITS

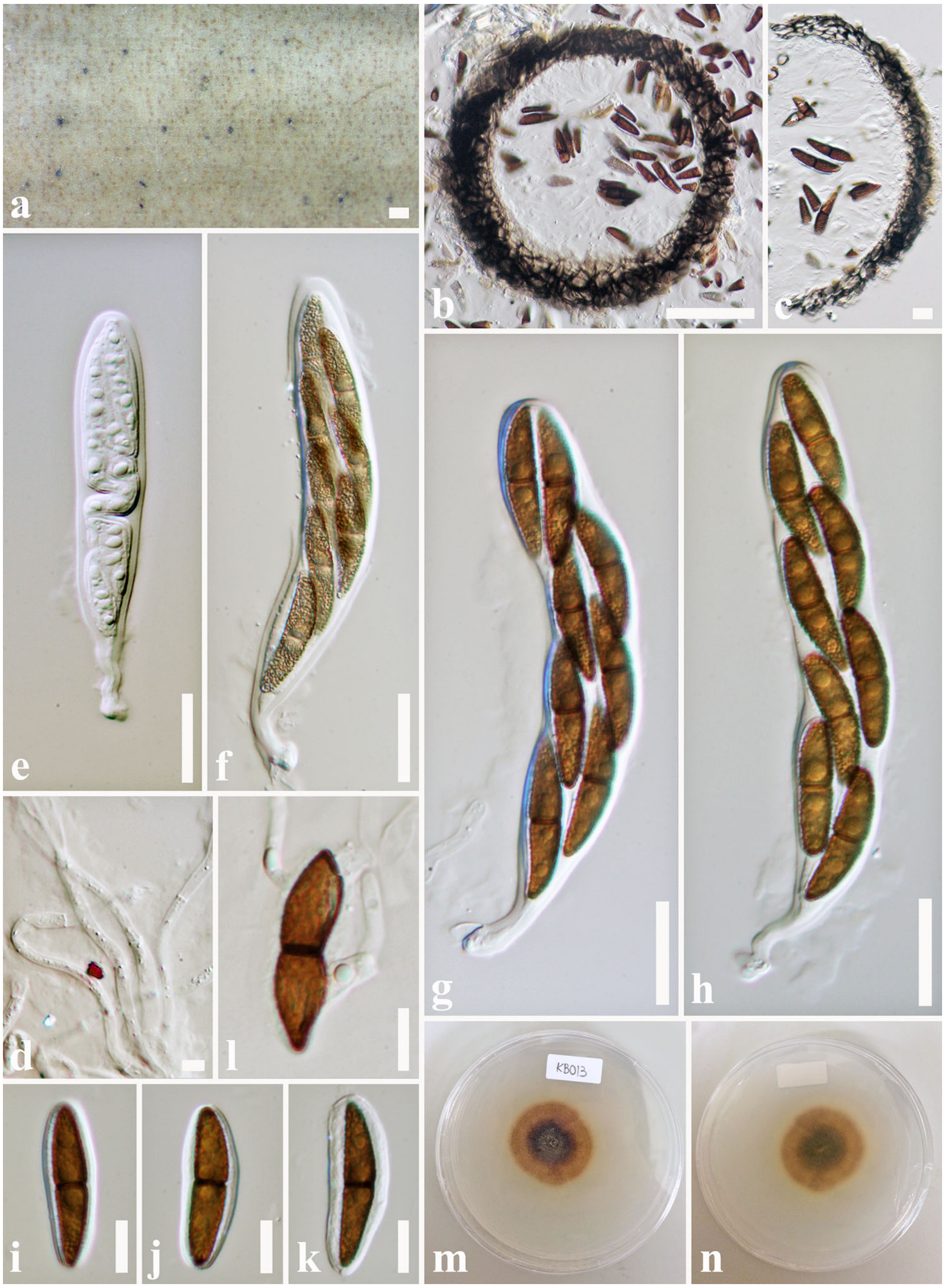


Fig. 15 ***Montagnula krabiensis*** (MFLU 16-1891, **holotype**). **a** Appearance of ascomata on host. **b** Section of ascoma. **c** Section of peridium. **d** Pseudoparaphyses. **e–h** Asci and ascospores at different stages of maturity. **i–k** Ascospores. **l** Germinating ascospore. **m, n** Colony on MEA from above and below. Scale bars: **a** = 200 µm, **b** = 50 µm, **c, i–l** = 10 µm, **d** = 5 µm, **e–h** = 20 µm

sequence of MFLUCC 16-0250 is *M. scabiosae* with 93% identity to the strain MFLUCC 14-0954 (NR_155378).

Pseudopithomyces Ariyaw. & K.D. Hyde

Pseudopithomyces was erected by Ariyawansa et al. (2015b) to accommodate *P. chartarum* (Berk. & M.A. Curtis) J.F. Li, Ariyawansa & K.D. Hyde. The members can be found as saprobes (Ariyawansa et al. 2015b). Nine epithets are listed in Index Fungorum (2018). We introduce a new species of *Pseudopithomyces* based on morphology and phylogeny from Pandanaceae. *Pseudopithomyces* has never been reported from Pandanaceae.

Pseudopithomyces pandanicola Tibpromma & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF554483, *Facesoffungi number*: FoF04494; Fig. 16

Etymology: named after the host genus, *Pandanus*.

Holotype: MFLU 18-0029

Saprobic on dead leaves of *Pandanus amaryllifolius*. *Colonies* effuse, dark brown to black. *Mycelium* mostly superficial or partly immersed on the substrate, composed of septate, branched, smooth, thin-walled, hyaline hyphae. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Conidiophores* micro- to macronematous,

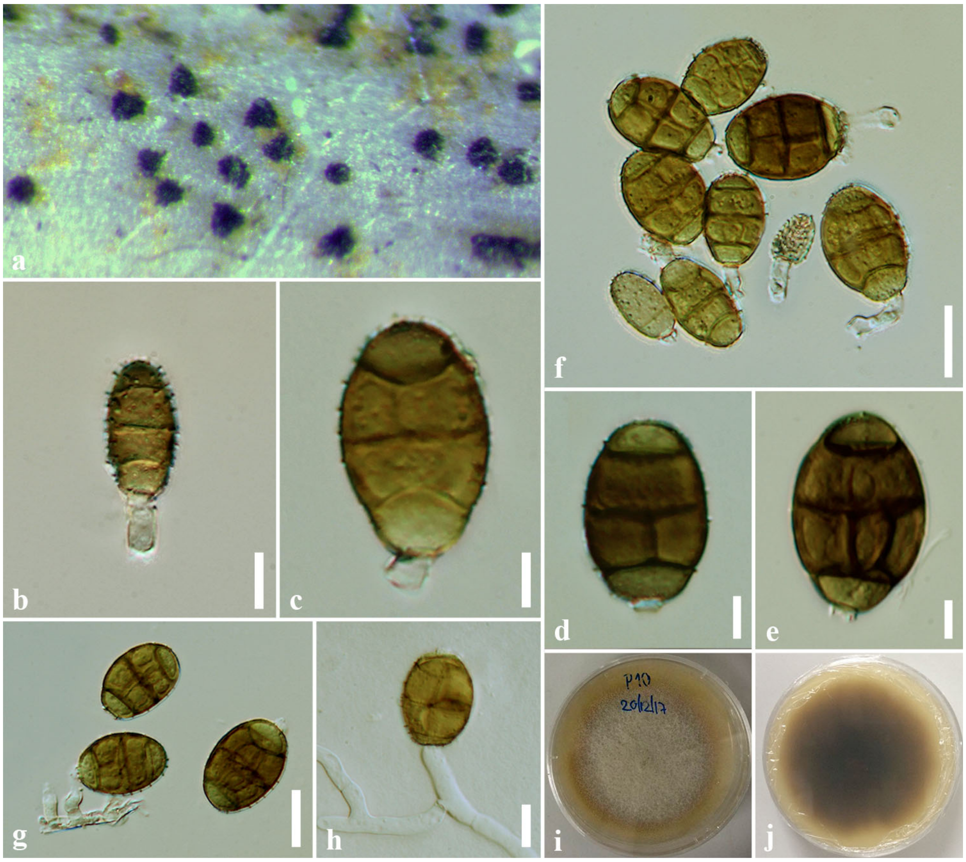


Fig. 16 ***Pseudopithomyces pandanicola*** (MFLU 18-0029, **holotype**). **a** Colonies on dead leaves of *Pandanus amaryllifolius*. **b–g** Conidiogenous cells and conidia. **h** Germinating conidium. **i, j** Colony on MEA from above and below. Scale bars: **a–e, g, h** = 5 µm, **f** = 10 µm

mononematous, hyaline. *Conidiogenous cells* holoblastic, terminal, hyaline, cylindrical. *Conidia* 10–25 × 7–15 µm ($\bar{x}$ = 19 × 11 µm, n = 20), muriform with 2–3 transverse septa and 1–2 longitudinal septa, verruculose to echinulate, amygdaliform or ovoid, yellow to brown, often carrying part of broken conidiogenous cell at base.

Culture characteristics: Conidia germinating on MEA within 12 h. Colonies on MEA, grey on the surface, with dense, circular, with entire edge, raised, dark brown in reverse, with smooth margin.

Material examined: THAILAND, Chiang Rai Province, Mueang District, Mae Fah Luang University, on *Pandanus amaryllifolius* Roxb., 15 December 2017, S. Tibpromma P10 (MFLU 18-0029, **holotype**); ex-type living culture, MFLUCC 18-0116.

GenBank numbers LSU: MH376738; ITS: MH388364; SSU: MH388329; TEF1: MH388399; RPB2: MH412734; TUB2: MH412724.

Notes: *Pseudopithomyces pandanicola* clusters with *P. kunmingnensis* Karun. & K.D. Hyde and *P. chartarum* (Berk. & M.A. Curtis) Jin F. Li, Ariyaw. & K.D. Hyde. However, *P. kunmingnensis* has globose or subglobose conidiogenous cells with verruculose to echinulate and light brown to brown conidia (Hyde et al. 2017), while *P. chartarum* has broadly ellipsoid, mid brown to dark brown conidia (Ariyawansa et al. 2015a, b). In a BLASTn search on NCBI GenBank, the closest matches of ITS sequence of MFLUCC 18-0116 is *P. chartarum* with 100% identity to the strain OA28 (JQ406588), while the closest matches with the RPB2 sequence were with 99% identical *P. chartarum* strain UTHSC 04-678 (LK936414).

Hermatomycetaceae Locq.

Hermatomycetaceae was proposed by Locquin (1984) and formalised by Hashimoto et al. (2017). The type genus, *Hermatomyces* was placed within Ascomycota as 'incertae sedis', in previous studies (Wijayawardene et al. 2012), while Doilom et al. (2017) and Tibpromma et al. (2016b) suggested it belongs in Lophiotremataceae. Five species of *Hermatomyces* have been previously found on Pandanaceae (Tibpromma et al. 2016b, 2017b; Hyde et al. 2017). In addition, we describe a new taxon belonging to *Hermatomyces* which was collected from Pandanaceae in China.

Hermatomyces Speg.

Hermatomyces was introduced as a hyphomycetous genus by Spegazzini (1911) with *H. tucumanensis* Speg. as the type species. The characteristic features of *Hermatomyces* are sporodochial conidiomata with one to two types of conidia (lenticular and cylindrical) (Chang 1995). Sexual morphs have not been found (Hashimoto et al. 2017). There are 23 epithets for *Hermatomyces* listed in Index Fungorum (2018). We provide an updated phylogenetic tree (Fig. 17) for this genus. *Hermatomyces tucumanensis*

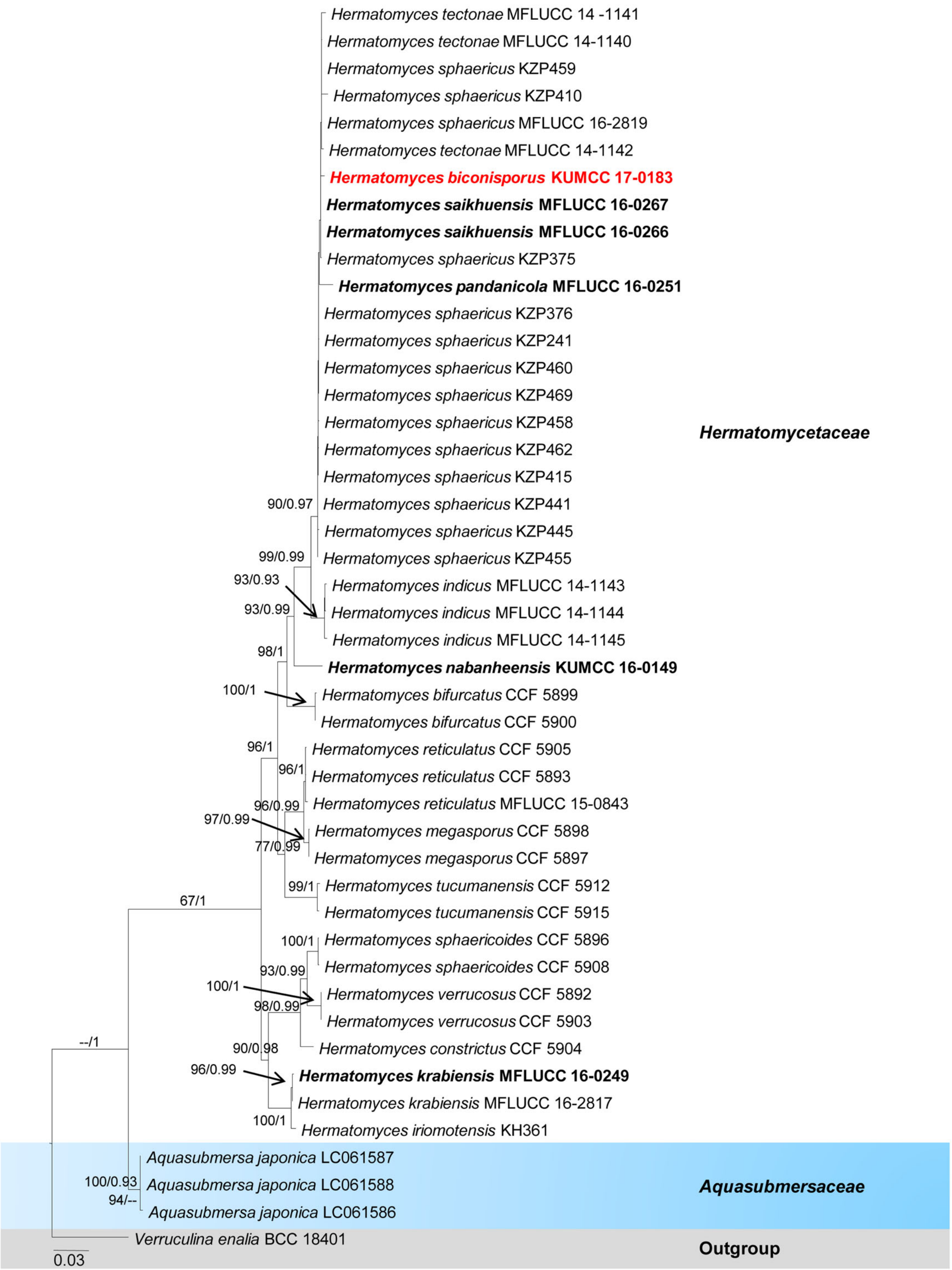


Fig. 17 Phylogram generated from maximum likelihood analysis based on combined LSU, TEF1, RPB2, TUB2 and ITS sequence data. Related sequences were obtained from Tibpromma et al. (2017b) and Koukol et al. (2018). Forty-six strains are included in the combined sequence analysis, which comprise 3835 characters with gaps. *Verruculina enalia* (BCC 18401) is used as the outgroup taxon. Tree topology of the ML analysis was similar to the BYPP. The best scoring RAxML tree with a final likelihood value of − 11360.152489 is presented. The matrix had 793 distinct alignment patterns, with 39.31% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.241274, C = 0.263021, G = 0.260518, T = 0.235186; substitution rates AC = 1.445186, AG = 4.215831, AT = 1.256927, CG = 0.850126, CT = 11.957308, GT = 1.000000; gamma distribution shape parameter α = 0.166181. Bootstrap support values for ML equal to or greater than 60% and BYPP equal to or greater than 0.90 are given above the nodes. Newly generated sequences are in red bold while black bold are previous sequences from *Hermatomyces* species from Pandanaceae

has been found on leaves of *Pandanus* sp., *P. furcatus*, *P. monticola* and *P. tectorius* in Hong Kong (Whitton et al. 2012). Tibpromma et al. (2017b) described four species of *Hermatomyces* on *Pandanus* spp. from Thailand, while Hyde et al. (2017) described *H. nabanheensis* on *Pandanus* sp. from China.

Hermatomyces biconisporus Tibpromma & K.D. Hyde, ***sp. nov*.**

Index Fungorum number: IF554484, *Facesoffungi number*: FoF04495; Fig. 18

Etymology: biconisporus refers to two types of conidia.

Holotype: HKAS 99630

Saprobic on dead leaves of *Pandanus* sp. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Colonies* on natural blackish brown, velvety, shiny, in small groups, glistening, conidia readily liberated when disturbed. *Mycelium* superficial, composed of a network of branched, septate, hyaline to pale brown, thick-walled hyphae 1.7–3.4 µm wide. *Conidiophores* 2.5–4 × 1.5–2.5 µm, micronematous, straight or flexuous, short, hyaline to pale brown, aseptate, smooth, unbranched, arising from prostrate hyphae at the centre of colony. *Conidiogenous cells* holoblastic, monoblastic, integrated, terminal, cylindrical,

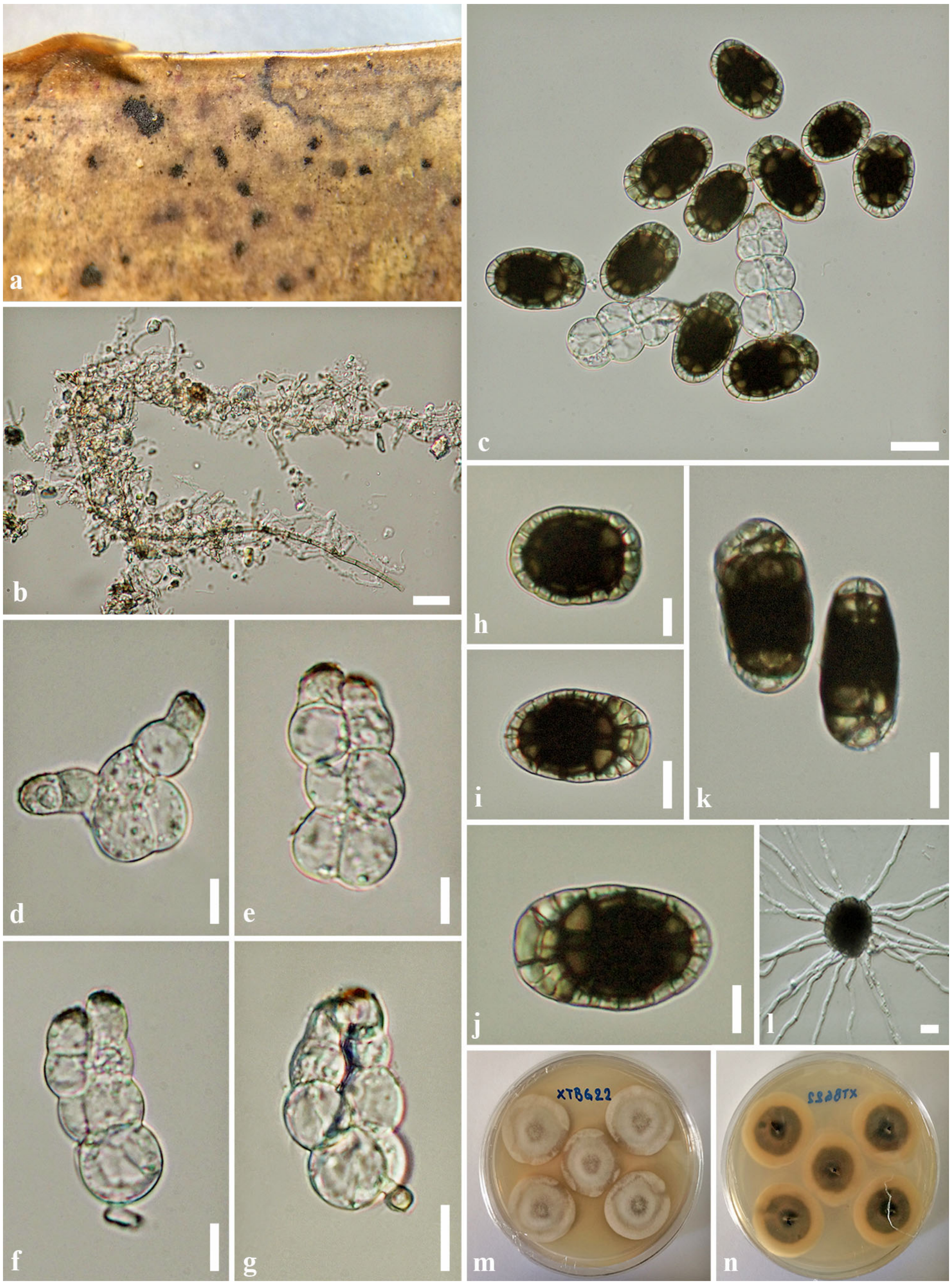


Fig. 18 ***Hermatomyces biconisporus*** (HKAS 99630). **a** Colonies on substrate. **b** Mycelium. **c** Conidia. **d–g** Cylindrical conidia. **h–k** Lenticular conidia. **l** Germinating conidium. **m, n** Colonies on PDA from above and below. Scale bars: **b, c** = 20 µm, **d–l** = 10 µm

hyaline to subhyaline. *Conidia* dimorphic, thick-walled, smooth: *lenticular conidia* 28–34 × 15–25 µm ($\bar{x}$ = 31 × 18 µm, n = 30), numerous, central cells dark brown to black, peripheral cells subhyaline to pale brown, slightly constricted at septa, smooth, in lateral view obovoid, guttulate; *cylindrical conidia* 32–39 × 14.5–26 µm in broadest part of lower cells, ($\bar{x}$ = 36 × 19 µm, n = 20), with 1–2 forked columns of 3–4 cells arising from a common basal cell, each column of rectangular to globose cells, constricted at septa, subhyaline, upper part of terminal cells dark brown, granulate, smooth.

Culture characteristics: Colonies on PDA at room temperature reaching 9 cm in 4 weeks, circular, yellow–white to grey mycelium with white margin, smooth surface, velvety and raised, white to yellow–brown from below.

Material examined: CHINA, Yunnan Province, Xishuangbanna, on dead leaves of *Pandanus* sp., 12 November 2016, T. Aluthwaththa XTBG22 (HKAS 99630, **holotype**); living cultures, KUMCC 17-0183, MFLUCC 17-2267).

GenBank numbers LSU: MH260296; ITS: MH275063; SSU: MH260338; TEF1: MH412771; RPB2: MH412755.

Notes: *Hermatomyces sphaericus* was introduced by Hughes (1953) with a single conidium type (Hughes 1953). Koukol et al. (2018) synonymized several species under *H. sphaericus* (*H. chromolaenae* Jin F. Li, Mapook & K.D. Hyde, *H. saikhuensis* Tibpromma, Bhat & K.D. Hyde and *H. tectonae* Bhat & K.D. Hyde) based on morphological and molecular comparisions. Our isolate of *H. biconisporus* (KUMCC 17-0183) has two conidial types which are similar to *H. tectonae*, but in the phylogenetic analysis, the sequences of our isolate clustered with the *H. sphaericus* clade with a single conidium type. Therefore, we do not agree with Koukol et al. (2018) who synonymized *H. saikhuensis* and *H. tectonae* under *H. sphaericus*. There are important differences in base pairs (bp) even though they clustered together in the phylogenetic analysis. Although the lenticular conidia are similar, we believe that *H. sphaericus* is a species complex comprising several species.

In a BLASTn search in the NCBI GenBank, the closest match to the ITS sequence of *H. biconisporus* KUMCC 17-0183 is *H. sphaericus* strain PMA:116081 (LS398283) with 99% similarity, while the closest match to the TEF1 sequence is *H. sphaericus* strain PRC 4100 (LS398429) with 99% similarity. The closest match to the RPB2 sequence is *H. tectonae* strain KH 409 (LC194456) with 99% similarity and the closest match to the RPB2 sequence is *H. tectonae* strain KH 409 (LC194332) with 99% similarity.

There is evidence that our strain is a new species based on the recommendations of Jeewon and Hyde (2016). Thus, we introduce our collection as a new species based on morphological differences and difference in nucleotide base pairs. *Hermatomyces chromolaenae*, *H. saikhuensis* and *H. tectonae* clustered with the *H. sphaericus* clade, but these taxa lack TUB2 gene sequence data which is needed when introducing new species of *Hermatomyces*. We also maintain these names as distinct species until further research proves otherwise.

Melanommataceae G. Winter (= Pseudodidymellaceae A. Hashim. & Kaz. Tanaka)

Melanommataceae was established by Winter (1885a, b) with *Melanomma* Nitschke ex Fuckel as type genus. The family is characterized by globose or depressed perithecial ascomata, bitunicate and fissitunicate asci and pigmented and phragmosporous ascospores (Sivanesan 1984; Barr 1990a; Zhang et al. 2012; Hyde et al. 2013). A key to genera of Melanommataceae is provided in Tian et al. (2015). There are twenty-four genera in the family (Wijayawardene et al. 2017b, 2018). We collected *Byssosphaeria siamensis* on decaying dead leaves of *Pandanus* sp.; it has superficial ascomata, surrounded by brown to dark brown setae.

Byssosphaeria Cooke

Byssosphaeria was erected by Cooke and Plowright (1879) with *B. keithii* (Berk. & Broome) Cooke as type species. There are 25 epithets are listed in Index Fungorum (2018) which are commonly are found as saprobes (Lumbsch and Huhndorf 2010; Wijayawardene et al. 2017a, b). Tian et al. (2015) provided an update to *Byssosphaeria* based on morphology and phylogeny with new species and records have been introduced by Hyde et al. (2018). We found *Byssosphaeria siamensis* on Pandanaceae in Thailand. This species was originally described from decaying wood in Thailand.

Byssosphaeria siamensis Boonmee, Q. Tian and K.D. Hyde, Fungal Diversity 74: 283 (2015)

Facesoffungi number: FoF04499; Fig. 19

Saprobic on dead leaves of *Pandanus* sp. **Sexual morph** *Ascomata* 290–405 × 335–465 µm ($\bar{x}$ = 352 × 378.5 µm, n = 5), superficial, with flat base, conspicuous at the surface, globose to subglobose, uni-loculate, black, hairy, ostiole at central, with pore-like opening, surrounded by orange to yellow disc. *Peridium* 50–65 µm wide, outer layer comprising 4–6 layers of flattened, brown cells, arranged in a *textura angularis*, inner layer comprising 3–5 layers, hyaline cells, arranged in *textura angularis* to *textura prismatica*. *Hamathecium* comprising numerous, dense, 1–2.5 µm wide, filiform, filamentous, branched, guttulate, septate pseudoparaphyses. *Asci* 85–170 × 9–16 µm ($\bar{x}$ = 129 × 14 µm, n = 20), 8-spored, bitunicate, fissitunicate, clavate, long-pedicellate with knob-like pedicel, apically rounded. *Ascospores* 30–40 × 5.5–7.5 µm ($\bar{x}$ = 34 × 7 µm, n = 20), overlapping 1–2-seriate, fusiform, conical at each end, hyaline to pale brown with age, 1-septate, constricted at the septum, smooth-walled,

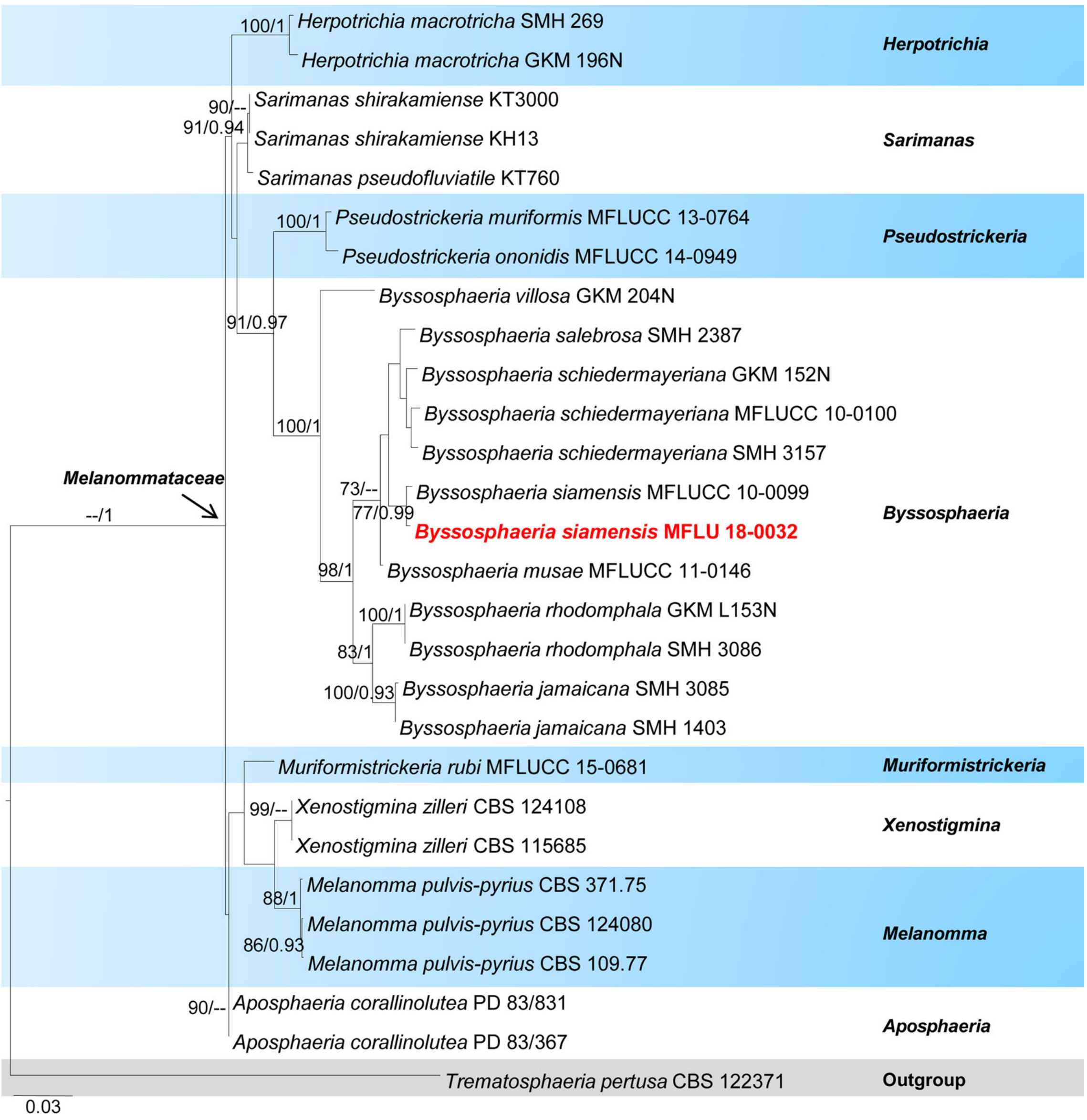


Fig. 19 Phylogram generated from maximum likelihood analysis based on combined LSU, SSU, TEF1 and RPB2 sequence data. Related sequences were obtained from Tian et al. (2015). Twenty-eight strains are included in the combined sequence analysis, which comprise 4229 characters with gaps. *Trematosphaeria pertusa* (CBS 122371) is used as the outgroup taxon. Tree topology of the ML analysis was similar to the BYPP. The best scoring RAxML tree with a final likelihood value of − 4630.742815 is presented. The matrix had 366 distinct alignment patterns, with 20.38% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.247303, C = 0.233841, G = 0.315115, T = 0.203741; substitution rates AC = 0.959786, AG = 2.362319, AT = 1.107025, CG = 1.419953, CT = 9.165549, GT = 1.000000; gamma distribution shape parameter α = 0.321701. Bootstrap support values for ML 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 red

guttulate, with mucilaginous sheath. **Asexual morph** Undetermined.

Material examined: THAILAND, Phang Nga Province, Thap Put District, on *Pandanus* sp., 20 December 2017, N. Chaiwan P13 (MFLU 18-0032 = HKAS 101800).

GenBank numbers LSU: MH376706; ITS: MH388334; SSU: MH388303; TEF1: MH388370; TUB2: 18-0032.

Notes: Our new strain of *Byssosphaeria siamensis* has the same characteristics as that reported on decaying wood in Thailand (MFLUCC 10-0099) (Tian et al. 2015). They both have superficial, globose to subglobose ascomata, with orange to yellow disc around the pore, clavate asci with long and knob-like pedicel and fusiform ascospores with conical ends and a mucilaginous sheath. Phylogenetic analyses

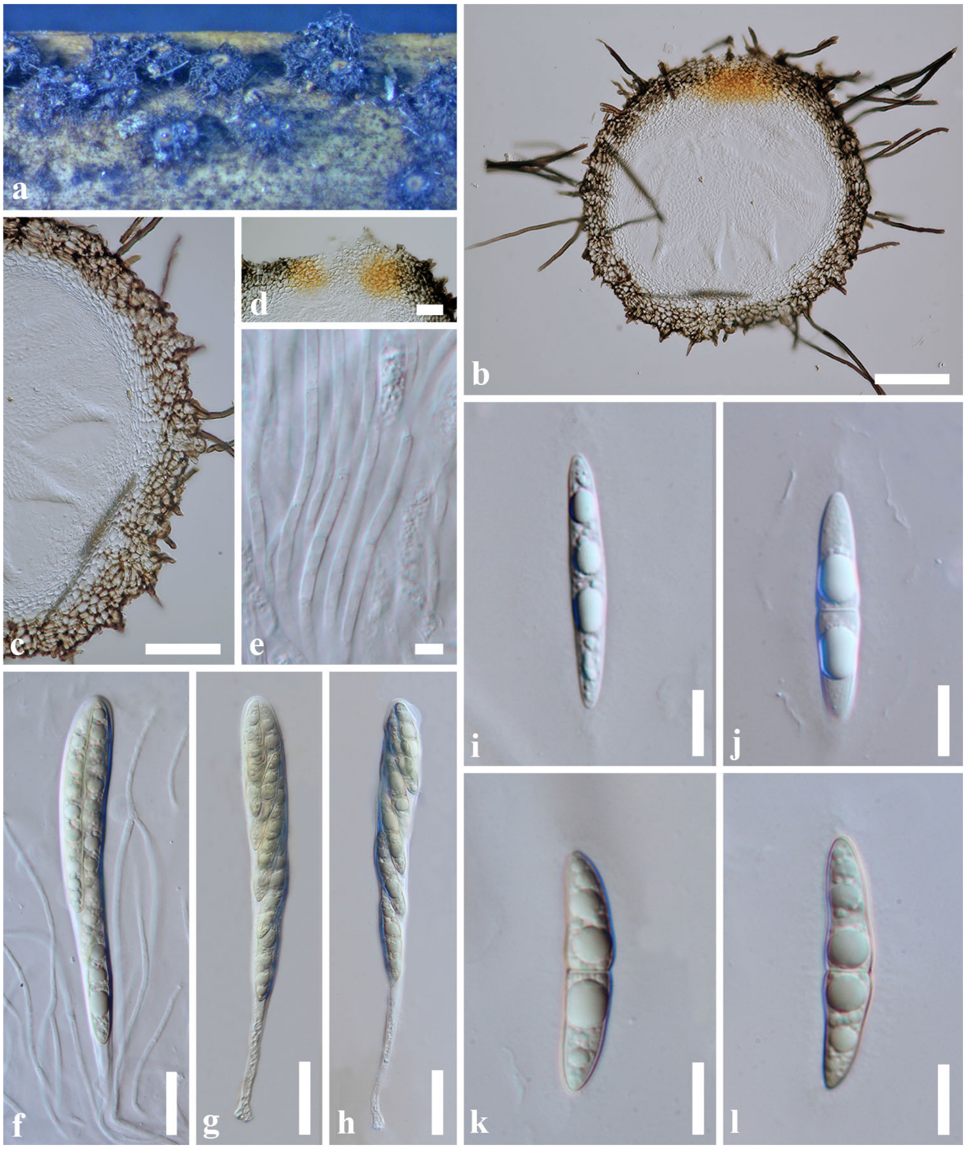


Fig. 20 ***Byssosphaeria siamensis*** (MFLU 18-0032). **a** Appearance of ascomata on host. **b** Section of ascoma. **c** Section of peridium. **d** Section of ostiole. **e** Pseudoparaphyses. **f–h** Asci. **i–l** Ascospores. Scale bars: **b** = 100 µm, **c, d, f–h** = 20 µm, **e** = 5 µm, **i–l** = 10 µm

using combined LSU, SSU, TEF1 and RPB2 sequence data demonstrate that our strain is *B. siamensis* (Fig. 20). The ascospores of this fungus failed to germinate and grow in culture and we extracted DNA directly from fruiting bodies. This is the first record of *B. siamensis* on Pandanaceae.

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

Occultibambusaceae was erected by Dai et al. (2017) with *Occultibambusa* as the type genus. Members of the family Occultibambusaceae are usually found on monocotyledons hosts, but can also be found on hardwood trees (Dai et al. 2017). The characteristic features of asci and ascospores of Occultibambusaceae are similar to *Bambusicola* (Bambusicolaceae), *Lophiostoma* (Lophiostomataceae) and *Massarina* (Massarinaceae) (Zhang et al. 2009; Dai et al. 2012, 2015). There are four genera in the family (Wijayawardene et al. 2018). *Neooccultibambusa pandanicola* (asexual morph), which belongs in Occultibambusaceae, has been reported on Pandanaceae (Hyde et al. 2018). We introduce a new species of *Neooccultibambusa*.

Neooccultibambusa Doilom & K.D. Hyde

Neooccultibambusa was erected by Doilom et al. (2017) to accommodate *N. chiangraiensis* Doilom & K.D. Hyde, which is provided with both sexual and asexual morphs. *Neooccultibambusa* shares similar morphology with *Occultibambusa* (Doilom et al. 2017). There are three species for *Neooccultibambusa* are listed in Index Fungorum (2018).

Neooccultibambusa thailandensis Tibpromma & K.D. Hyde, ***sp. nov*.**

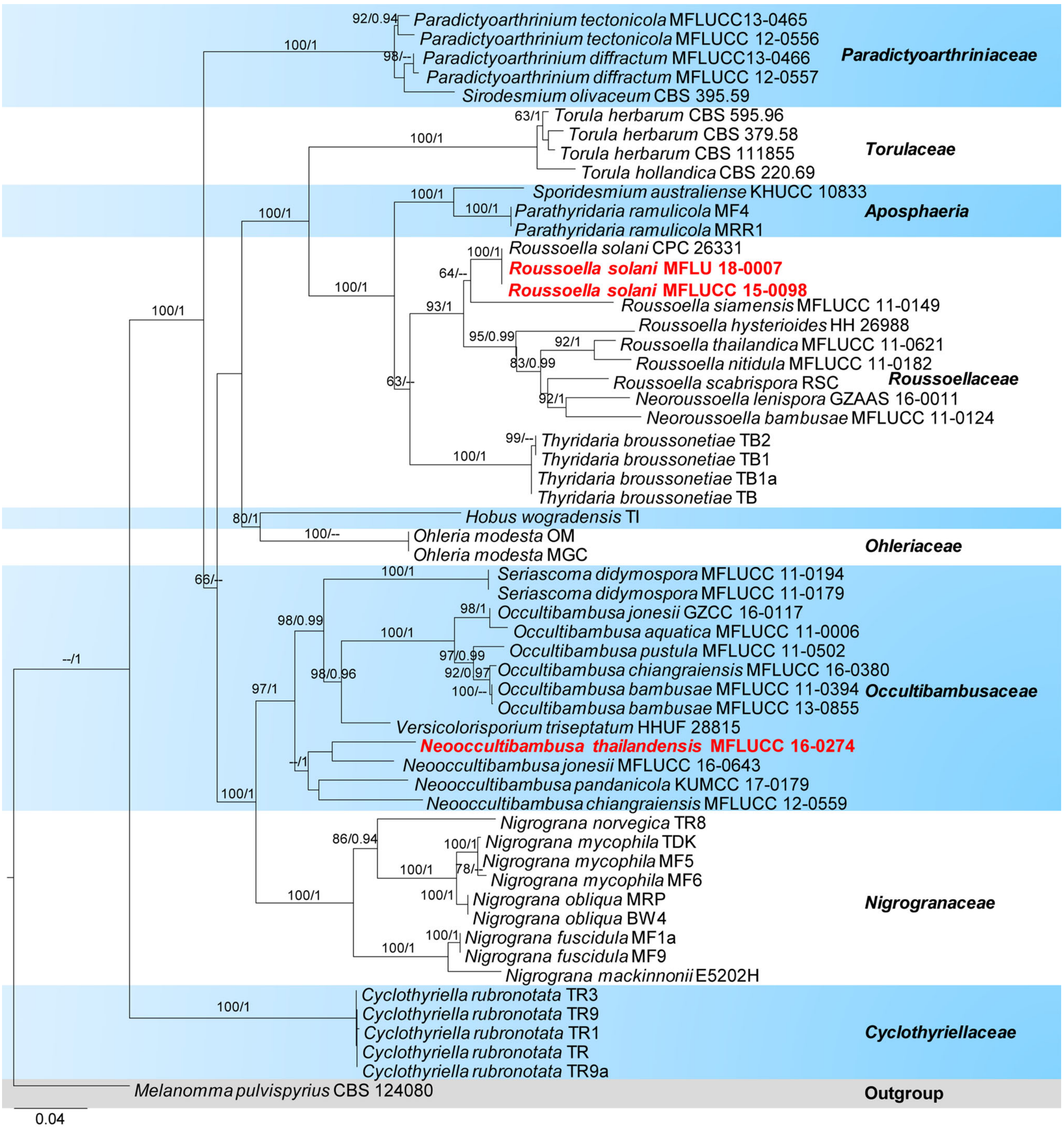


Fig. 21 Phylogram generated from maximum likelihood analysis based on combined LSU, RPB2, SSU and ITS sequence data. Related sequences were obtained from Zhang et al. (2016). Fifty-five strains are included in the combined sequence analysis, which comprise 3605 characters with gaps. *Melanomma pulvispyrius* (CBS 124080) is used as the outgroup taxon. Tree topology of the ML analysis was similar to the BYPP. The best scoring RAxML tree with a final likelihood value of − 4630.742815 is presented. The matrix had 366 distinct alignment patterns, with 20.38% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.247303, C = 0.233841, G = 0.315115, T = 0.203741; substitution rates AC = 0.959786, AG = 2.362319, AT = 1.107025, CG = 1.419953, CT = 9.165549, GT = 1.000000; gamma distribution shape parameter α = 0.463512. Bootstrap support values for ML equal to or greater than 60% and BYPP equal to or greater than 0.90 are given above the nodes. Newly generated sequences are in red

Index Fungorum number: IF554488, *Facesoffungi number*: FoF04500; Fig. 21

Etymology: named after Thailand, where the fungus was first discovered.

Holotype: MFLU 18-0017

Saprobic on dead leaf of *Pandanus* sp. **Sexual morph** *Ascomata* 65–80 × 44–61 µm ($\bar{x}$ = 72 × 51 µm, n = 5), superficial, globose to subglobose, flat at the base, solitary, papillate, ostiole central, black, smooth-walled. *Peridium* 5.6–14 µm wide, composed several layers of dark brown to black cells of *textura angularis. Hamathecium* comprising 0.7–1.7 µm wide, aseptate pseudoparaphyses. *Asci* 34–51 × 5–8 µm (= 45 × 6 µm, n = 20), (6–)8-spored, bitunicate, fissitunicate, cylindrical to cylindric-clavate, short-pedicellate, apically rounded with an ocular chamber. *Ascospores* 6–11 × 2–3.5 µm ($\bar{x}$ = 9 × 2.6 µm, n = 40), overlapping uni- to bi-seriate, yellow–brown, fusiform, 1-septate, constricted at the septum, conical at each end, guttulate, smooth-walled, without appendages or mucilaginous sheath. **Asexual morph** Undetermined.

Culture characteristics: Ascospores germinating on MEA within 24 h. Colonies on MEA circular, convex, aerial in the center, edge entire, rough, dark brown to black mycelium.

Material examined: THAILAND, Prachuap Khiri Khan Province, Bang Saphan District, Sai Khu Waterfall, on dead leaf of *Pandanus* sp., 30 July 2015, S. Tibpromma & K.D Hyde SF15-044 (MFLU 18-0017, **holotype**; HKAS 100843, **isotype**); ex-type living culture, MFLUCC 16-0274 = KUMCC 17-0309.

GenBank numbers LSU: MH260308; ITS: MH275074; SSU: MH260348; TEF1: MH412780; RPB2: MH412758.

Notes: Based on phylogeny this species group with *Neooccultibambusa* (Fig. 22). The previous species was reported with an asexual morph and we compare morphological characteristics of *N. thailandensis* (sexual morph) is distinct. *Neooccultibambusa thailandensis* and differs from *N. chiangraiensis* Doilom & K.D. Hyde which has 1–3 transverse septate ascospores surrounded by a mucilaginous sheath, while *N. thailandensis* has 1-septate ascospores and without a mucilaginous sheath. Lacking asexual morph is also a factor to distinguish two species. In a BLASTn search on NCBI GenBank, the closest matches of ITS sequence of MFLUCC 16-0274 is *Neokalmusia didymospora* with 97% identity to the strain MFLUCC 11-0613 (KP091433), while the closest matches with the TEF1 sequence were with 95% identical *Occultibambusa maolanensis* strain GZCC 16-0116 (KY814757).

Pleosporaceae Nitschke

Pleosporaceae was erected by Nitschke (1869) with *Pleospora* Rabenh. ex Ces. & De Not. as the type genus, based on structure of ascomata and pseudoparaphyses and was assigned to the order Sphaeriales. The placement of Pleosporaceae was not clear (Theissen and Sydow 1917) and later Lumbsch and Huhndorf (2010), Zhang et al. (2012), Hyde et al. (2013), Ariyawansa et al. (2015a) and Thambugala et al. (2017) used multi-gene phylogenetic analyses to establish the placement of this family. Pathogens or saprobes on wood, dead herbaceous stems or leaves can be found in Pleosporaceae (Hyde et al. 2013). *Curvularia* (Pleosporaceae) comprises species associated with plants (saprobes and pathogens), living organisms including humans, fresh-water and soils worldwide (Sivanesan 1987; Manamgoda et al. 2011, 2012a, b; da Cunha et al. 2013; de Aldana et al. 2013; Rangaswamy et al. 2013; Verma et al. 2013; Hyde et al. 2014). Seven species of *Curvularia* are known from Pandanaceae (Whitton et al. 2012). We introduce four new species of saprobic *Curvularia* from Pandanaceae based on both morphology and phylogeny.

Curvularia Boedijn

Curvularia was erected by Boedijn (1933) with *C. lunata* (Wakker) Boedijn as the type species and characterised by long, dark coloured, polytretic conidiophores, and conidia that are usually curved, often versicoloured and multi-septate (Ellis 1971, 1976). More than 150 epithets are listed in Index Fungorum (2018). Whitton et al. (2012) reported seven species of *Curvularia* as known from Pandanaceae. An updated phylogenetic tree for *Curvularia* is presented (Fig. 23).

Curvularia chonburiensis Tibpromma & K.D. Hyde, ***sp. nov***.

Index Fungorum number: IF554492, *Facesoffungi number*: FoF04501; Fig. 24

Etymology: named after Chonburi Province, where the fungus was first discovered.

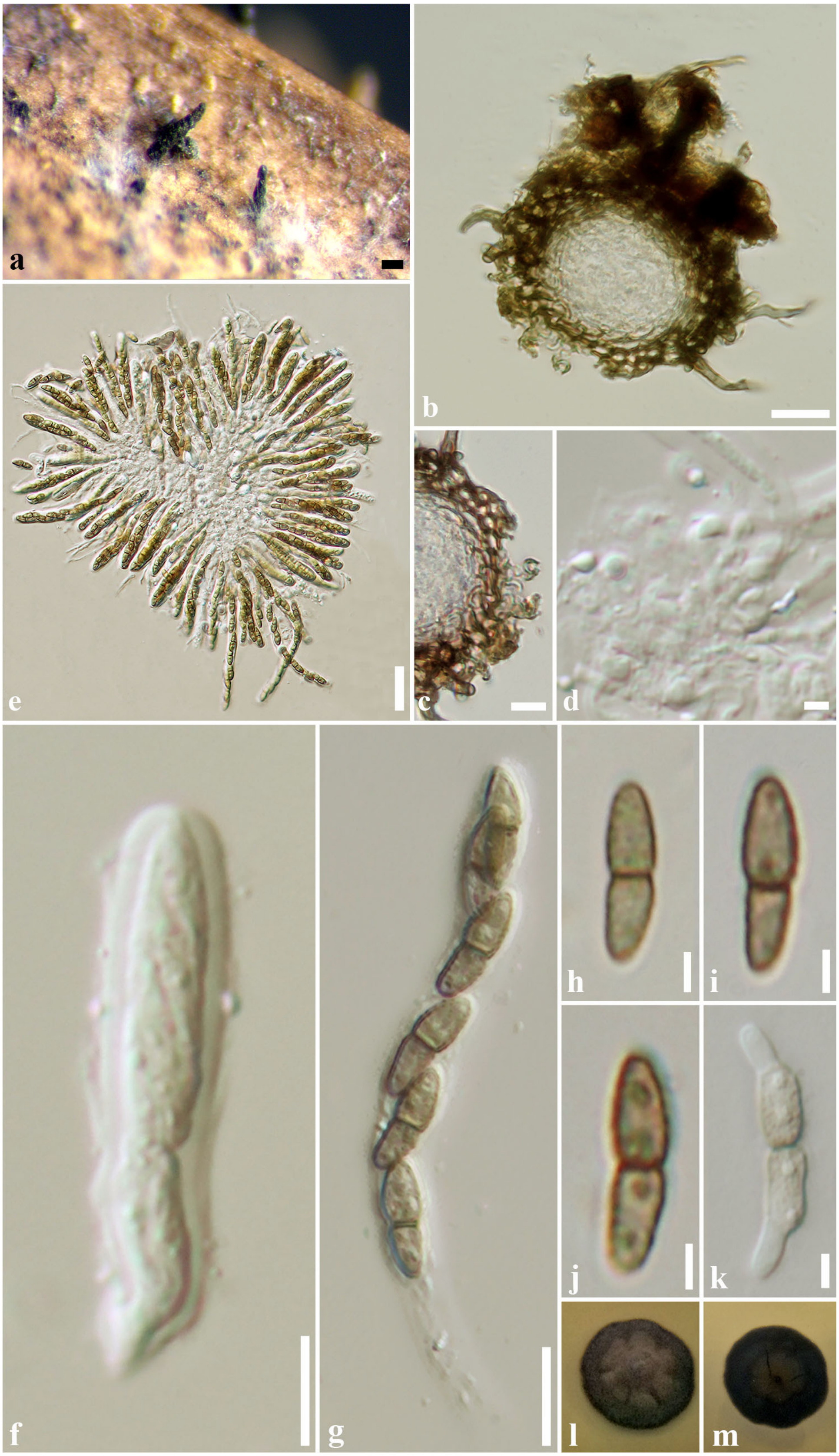
Holotype: MFLU 16-1876

Saprobic on dead leaf of *Pandanus* sp. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Mycelium* composed of septate, branched, smooth, subhyaline hyphae. *Conidiophores* 70–200 × 4–7 µm ($\bar{x}$ = 116 × 6 µm, n = 10), unbranched, septate, flexuous, geniculate, pale brown. *Conidiogenous cells* polytretic, sympodial, integrated, smooth, swollen, brown. *Conidia* 17–28 × 7–15 µm ($\bar{x}$ = 23 × 11 µm, n = 40), ovoid to obclavate, narrowing towards rounded ends, (2–)3-distoseptate, with a dark brown band at septa, with end cells hyaline to pale brown, with 2 middle cells dark brown, third cell from base often larger, with a scar (hilum) at base.

Culture characteristics: Colonies on MEA attaining 9 cm diam., within 1 week at room temperature, beginning white and become black with age, circular, entire edge with curled, raised on media surface, smooth, velvety.

Material examined: THAILAND, Chonburi Province, Bang Lamung District, on dead leaf of *Pandanus* sp., 18 July 2016, W. Jaidee PTY01 (MFLU 16-1876, **holotype**);

Fig. 22 ***Neooccultibambusa thailandensis*** (MFLU 18-0017, **holotype**). **a** Colonies on dead leaves of *Pandanus* sp. **b** Section of ascoma. **c** Peridium. **d** Hamathecium. **e–g** Asci. **h-j** Ascospores. **k** Germinating ascospore. **l, m** Colony on PDA from above and below. Scale bars **a** = 100 µm, **b** = 10 µm, **c, f, g** = 5 µm, **d, f, h–k** = 2 µm, **e** = 20 µm



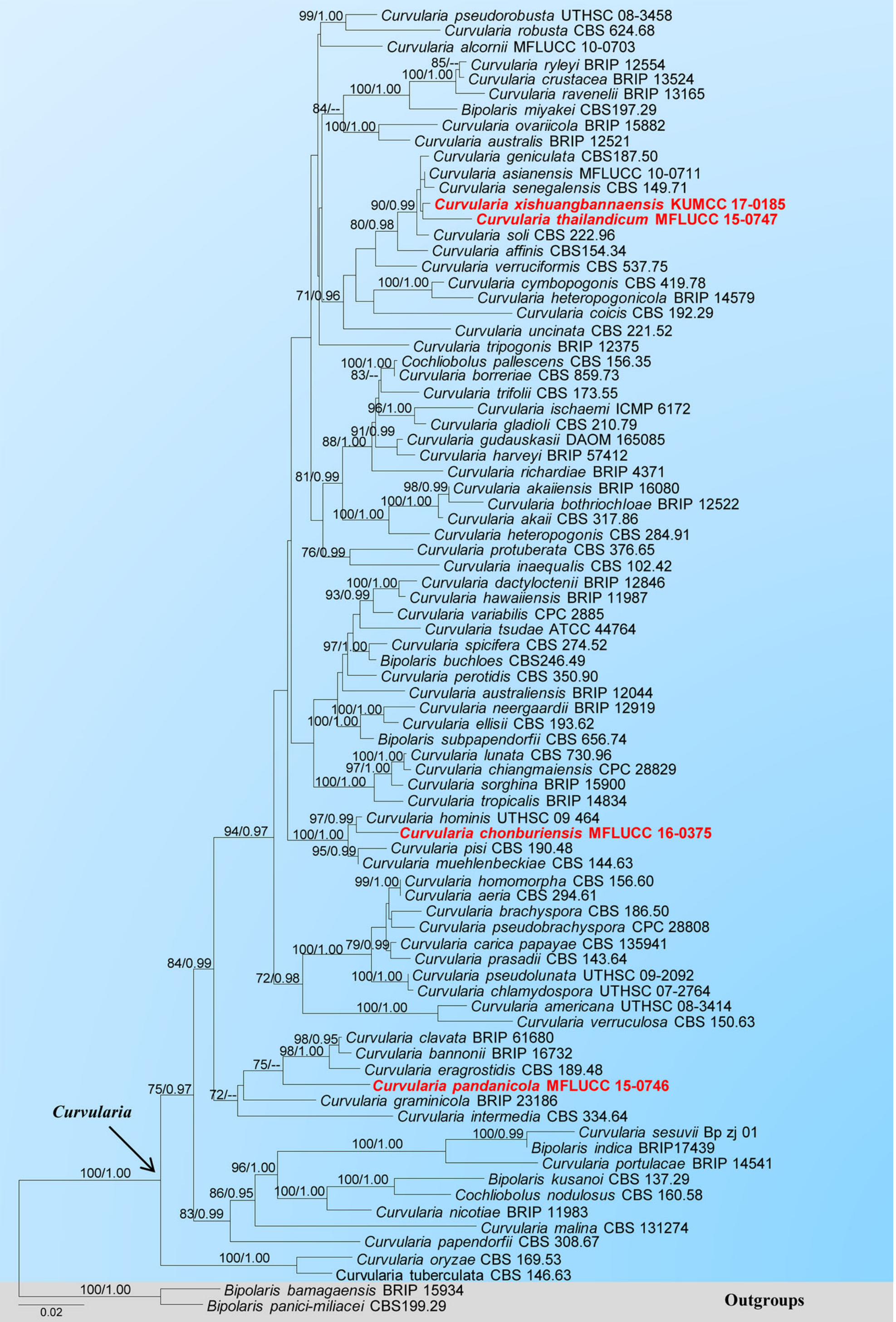


Fig. 23 Phylogram generated from maximum likelihood analysis based on combined ITS, GPDH and TEF1 sequence data of *Curvularia*. Related sequences were obtained from Marin-Felix et al. (2017) and Hyde et al. (2017). Eighty-three strains are included in the combined sequence analysis, which comprise 2221 characters with gaps. *Bipolaris bamagaensis* (BRIP 15934) and *Bipolaris panici-miliacei* (CBS199.29) are used as the outgroup taxa. Tree topology of the ML analysis was similar to the BYPP. The best scoring RAxML tree with a final likelihood value of − 15729.11775 is presented. The matrix had 897 distinct alignment patterns, with 23.55% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.232486, C = 0.300291, G = 0.241124, T = 0.226099; substitution rates AC = 0.833112, AG = 2.362707, AT = 1.030919, CG = 1.030374, CT = 5.190668, GT = 1.000000; gamma distribution shape parameter α = 0.737704. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. Newly generated sequences are in red

Fig. 24 ***Curvularia chonburiensis*** (MFLU 16-1876, **holotype**). **a** Colonies on dead leaf of *Pandanus* sp. **b** Conidiophores and conidia. **c–h** Conidia. **i** Germinating conidium. **j, k** Colonies on MEA from above and below. Scale bars: **a** = 100 µm, **b** = 10 µm, **c–i** = 5 µm

HKAS 96270, **isotype;** ex-type living culture, MFLUCC 16-0375 = KUMCC 17-0298.

GenBank numbers LSU: MH260287; ITS: MH275055; GPDH: MH412747.

Notes: Based on multi-gene analysis (ITS, GPDH and TEF1), our collection clustered with *Curvularia hominis* K.C. Cunha, Madrid, Gené & Cano with 97% in ML, 0.99 in BYPP (Fig. 23). *Curvularia hominis* is characterized by versicoloured conidia that are 18–30 × 7–14 µm, slightly curved, and 4–5-distoseptate (Madrid et al. 2014). *Curvularia chonburiensis* has larger conidia (17–28 × 7–15 µm) that are ovoid to obclavate, and 2–3-distoseptate. Thus, based on both morphological and molecular characteristics we introduce the new species, *C. chonburiensis.* In a

BLASTn search on NCBI GenBank, the closest matches of GPDH sequence of MFLUCC 16-0375 is *C.lunata* with 95% identity (X58718), while the closest matches with the TEF1 sequence were with 99% identical *C. hominis* strain MFLUCC 12-0178 (KM196591) and ITS sequence were with 100% identical *C. platzii* strain BRIP27703 (MH414906).

Curvularia pandanicola Tibpromma & K.D. Hyde, ***sp. nov***.

Index Fungorum number: IF554491, *Facesoffungi number*: FoF04502; Fig. 25

Etymology: named after the host genus, *Pandanus*.

Holotype: MFLU 18-0009

Saprobic on dead leaf of *Pandanus* sp. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Mycelium* composed of septate, branched, smooth, subhyaline hyphae. *Conidiophores* 100–180 × 1.5–5 µm ($\bar{x}$ = 140 × 3 µm, n = 10), arising in groups, unbranched, septate, flexuous, nodose, pale brown. *Conidiogenous cells* polytretic, sympodial, integrated, smooth, swollen, brown. *Conidia* 9–17 × 4–8 µm ($\bar{x}$ = 12 × 6 µm, n = 10), ovoid to obclavate, narrowing towards rounded ends, 3(–4)-distoseptate, with middle septum appearing as a thick black

Fig. 25 ***Curvularia pandanicola*** (MFLU 18-0009, **holotype**). **a, b** Colonies on dead leaves of *Pandanus* sp. **c–f** Conidiophores and conidia. **g–k** Conidia. **l** Germinating conidium. **m, n** Colony on MEA from above and below. Scale bars: **a** = 100 µm, **b** = 10 µm, **c–f** = 5 µm

band, pale brown at end cells, dark brown in 2 middle cells, slightly curved, with a scar (hilum) at base.

Culture characteristics: Colonies on MEA attaining 9 cm diam., within 1 week at room temperature, yellow–brown to brown, circular, entire edge with raised on media surface, smooth.

Material examined: THAILAND, Krabi Province, Mueang Krabi District, on dead leaf of *Pandanus* sp., 8 December 2014, S. Tibpromma & K.D Hyde SF14-042 (MFLU 18-0009, **holotype**; HKAS 100833, **isotype**); ex-type living cultures, MFLUCC 15-0746 = KUMCC 16-0156.

GenBank numbers LSU: MH260288; ITS: MH275056; TEF1: MH412763; ACT: MH412737; GPDH: MH412748.

Notes: *Curvularia pandanicola* has similar conidia to *C. eragrostidis* (Henn.) J.A. Mey. However, the conidia of *C. eragrostidis* are 20 × 12 µm, ellipsoidal or barrel shaped, and 3-distoseptate (Su et al. 2015). Multi-gene phylogenetic analysis (Fig. 23) showed that *C. pandanicola* is distinct from *C. eragrostidis* and other *Curvularia*. In a BLASTn search on NCBI GenBank, the closest matches of GPDH sequence of MFLUCC 15-0746 is *C.lunata* with 94% identity (X58718), while the closest matches with the TEF1 sequence were with 99% identical *Curvularia* sp. strain 5854 (KT012577) and ITS sequence were with 100% identical *C. eragrostidis* strain CBS 189.48 (HG778986).

Curvularia thailandicum Tibpromma & K.D. Hyde, ***sp. nov***.

Index Fungorum number: IF554493, *Facesoffungi number*: FoF04503; Fig. 26

Etymology: named after Thailand, where the fungus was first discovered.

Holotype: MFLU 18-0010

Saprobic on dead leaf of *Pandanus* sp. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Conidiophores* 63–95 × 2.5–4 µm ($\bar{x}$ = 78 × 3 µm, n = 10), arising in groups, unbranched, septate, flexuous, geniculate, pale brown to brown, guttulate, thick-walled. *Conidiogenous cells* polytretic, sympodial, integrated, smooth, swollen, brown. *Conidia* 8–15 × 5–8 µm ($\bar{x}$ = 10.5 × 6 µm, n = 40), ovoid to obclavate, tapering towards rounded ends, subhyaline to yellow–brown or brown with age,

Fig. 26 ***Curvularia thailandicum*** (MFLU 18-0010, **holotype**). **a** Colonies on dead leaf of *Pandanus* sp. **b–d** Conidiophores and conidia. **e–g** Conidia. **h** Germinating conidium. Scale bars: **a** = 200 µm, **b–d** = 10 µm, **e–h** = 5 µm

basal cell subhyaline, smooth-walled, 3(–4)-distoseptate, with dark brown septa, guttulate, with a scar (hilum) at base.

Culture characteristics: Colonies on MEA attaining 9 cm diam., within 1 week at room temperature, white in the beginning and brown to black with age, circular, entire edge with raised on media surface, smooth, velvety.

Material examined: THAILAND, Phang Nga Province, Mueang Phang Nga District, on fallen dead and decaying leaves of *Pandanus* sp., 6 December 2014, S. Tibpromma SF14-046 (MFLU 18-0010, **holotype**; HKAS 100835, **isotype**); ex-type living culture, MFLUCC 15-0747 = KUMCC 17-0302.

GenBank numbers LSU: MH260289; ITS: MH275057; TEF1: MH412764; ACT: MH412738; GPDH: MH412749.

Notes: The verruculose, curved, 3–4(–5)-distoseptate conidia with middle cells unequally enlarged, reniform, pale brown to brown, apical and basal cells paler than middle cells being subhyaline to pale brown are characteristic features of *Curvularia soli*, while our new species showed ovoid to obclavate, subhyaline to yellow–brown or brown, 3–4-distoseptate conidia with basal cell always subhyaline. *Curvularia thailandicum* is introduced here as a new saprobic fungus on *Pandanus* sp. In a BLASTn search on NCBI GenBank, the closest matches of GPDH sequence of MFLUCC 15-0746 is *C. lunata* with 96% identity (X58718), while the closest matches with the TEF1 sequence were with 99% identical *C. soli* strain CBS 222.96 (KY905698) and ITS sequence were with 99% identical *C. geniculata* strain JUF0011 (MH371471).

Curvularia xishuangbannaensis Tibpromma & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF554494, *Facesoffungi number*: FoF04504; Fig. 27

Etymology: named after Xishuangbanna, where the fungus was first discovered.

Holotype: HKAS 99632

Saprobic on dead leaf of *Pandanus amaryllifollus*. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Conidiophores* 100–400 × 6–10 µm ($\bar{x}$ = 197 × 7 µm, n = 10), arising in groups, branched, septate, flexuous, geniculate, yellow–brown to brown, guttulate, thick-walled. *Conidiogenous cell* polytretic, sympodial, integrated, smooth, swollen, brown. *Conidia* 32–46 × 13–20 µm ($\bar{x}$ = 38 × 16 µm, n = 30), ovoid to obclavate, tapering towards rounded ends, yellow–green to dark brown, 3–5-distoseptate with thick dark brown septa, guttulate, with a dark scar (hilum) at base.

Culture characteristics: Colonies on MEA attaining 9 cm diam., within 1 week at room temperature, white in the beginning and brown to black with age, circular, entire edge with raised on media surface, smooth, velvety.

Material examined: CHINA, Yunnan Province, Xishuangbanna, on fallen dead and decaying leaves of *Pandanus amaryllifollus* Roxb., 15 November 2016, T. Aluthwaththa XTBG24 (HKAS 99632, **holotype**); ex-type living culture, KUMCC 17-0185 = MFLUCC 17-2271.

GenBank numbers LSU: MH260290; ITS: MH275058; TEF1: MH412765; ACT: MH412739; GPDH: MH412750.

Notes: *Curvularia xishuangbannaensis* is characterized by ovoid to obclavate conidia that are yellow-green to dark brown, 3–5-distoseptate, thick dark brown septa and rough. In the phylogenetic analysis, this species clustered with *C. thailandicum*, which has also been collected from Pandanaceae. *Curvularia thailandicum* differs from *C. xishuangbannaensis* by having subhyaline to yellow–brown or brown, 3(–4)-distoseptate conidia with basal cell always subhyaline. In a comparison of the 528 ITS (+5.8S) nucleotides of these two strains reveals 18 (3.40%) nucleotide differences with *C. thailandicum* and *C. xishuangbannaensis*. In a BLASTn search on NCBI GenBank, the closest matches of GPDH sequence of KUMCC 17-0185 is *C. senegalensis* with 98% identity to the strain CBS 431.75 (LT715832), while the closest matches with the TEF1 sequence were with 100% identical *C. soli* strain CBS 222.96 (KY905698) and ITS sequence were with 99% identical *C. affinis* strain CMRP2493 (MF154614).

Roussoellaceae J.K. Liu et al.

Roussoellaceae was erected by Liu et al. (2014) with *Roussoella* Sacc. as the type genus, based on both morphology and phylogenetic analyses. Members of Roussoellaceae are known from bamboo and palms (Hyde et al. 2013). Jaklitsch and Voglmayr (2016) treated Roussoellaceae as a synonym of Thyridariaceae, but Tibpromma et al. (2017b) recommended to retain Roussoellaceae based on phylogenetic analysis and also the two families have distinct morphological characteristics. Six genera are listed in Wijayawardene et al. (2018). We describe *Roussoella solani* on Pandanaceae from Thailand based on both morphology and phylogeny (Fig. 22).

Roussoella Sacc.

Roussoella was introduced with *R. nitidula* Sacc. & Paol. 1888 as type species. The species are commonly found as saprobes (Liu et al. 2014). There are 42 epithets are listed in Index Fungorum (2018). We describe another species from Pandanaceae, the first report of *Roussoella* from Pandanaceae.

Fig. 27 ***Curvularia xishuangbannaensis*** (HKAS 99632, **holotype**). **a** Colonies on dead leaf of *Pandanus amaryllifollus*. **b, c** Conidiophores and conidia. **d–h** Conidia. **i** Germinating conidium. **j, k** Colonies on PDA from above and below. Scale bars: **b** = 40 μm, **c, i** = 20 μm, **d–h** = 5 μm

Roussoella solani Crous & M.J. Wingf., Persoonia 36: 341 (2016)

Facesoffungi number: FoF04505; Fig. 28

Saprobic on dead root of *Pandanus* sp. **Sexual morph** Undetermined. **Asexual morph** *Conidiomata* pycnidial, 160–170 × 77–105 µm ($\bar{x}$ = 166 × 94 µm, n = 5), immersed to erumpent, under clypeus, visible as black, ovoid or obpyriform, solitary, scattered or gregarious, ostiolate, with an ostiole. *Pycnidial wall* 13–23 µm, composed of thin layers of cells of *textura angularis*, hyaline to pale brown. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 4–6 × 3–4 µm ($\bar{x}$ = 5 × 3.5 µm, n = 10), enteroblastic, phialidic, integrated, ovoid to obpyriform, hyaline to pale brown, smooth. *Conidia* 2–5 × 1.5–4 µm ($\bar{x}$ = 4 × 2.5 µm, n = 40), oval to ellipsoidal, initially hyaline, becoming pale brown, aseptate with one or two guttules, thick-walled, smooth-walled.

Culture characteristics: Conidia germinating on MEA within 12 h. Colonies on MEA, brown on the surface, with dense, circular, with entire edge, convex with floosy and velvety, dark brown in reverse, with smooth margin.

Material examination: THAILAND, Phang Nga Province, Mueang Phang Nga District, on dead root of *Pandanus* sp., 6 December 2014, S. Tibpromma & K.D. Hyde SF14-004 (MFLU 18-0007; HKAS 100827); living culture, MFLUCC 15-0098.

GenBank numbers MFLUCC 15-0098 LSU: MH260309; ITS: MH275075; SSU: MH260349. MFLUCC 18-0007 LSU: MH260310; ITS: MH275076; SSU: MH260350.

Notes: In molecular phylogenetic analysis our isolates clustered with *Roussoella solani* Crous & M.J. Wingf (Fig. 22). We compared our isolates with *R. solani* (CPC 26331) and both have similar conidiogenous cells and conidia. *Roussoella solani* (CPC 26331) has hyaline, ampulliform to doliiform, 4–6 × 3–4 µm conidiogenous cells and (4–)4.5–5(–7) × 2(–3) µm, aseptate, pale brown, subcylindrical conidia (Crous et al. 2016a), while our isolate has 4–6 × 3–4 µm, hyaline to pale brown, ovoid to obpyriform conidiogenous cells and 2–5 × 1.5–4 µm, oval to ellipsoidal, aseptate conidia, initially hyaline, becoming pale brown. This is the first record of *Roussoella* on *Pandanus* sp.

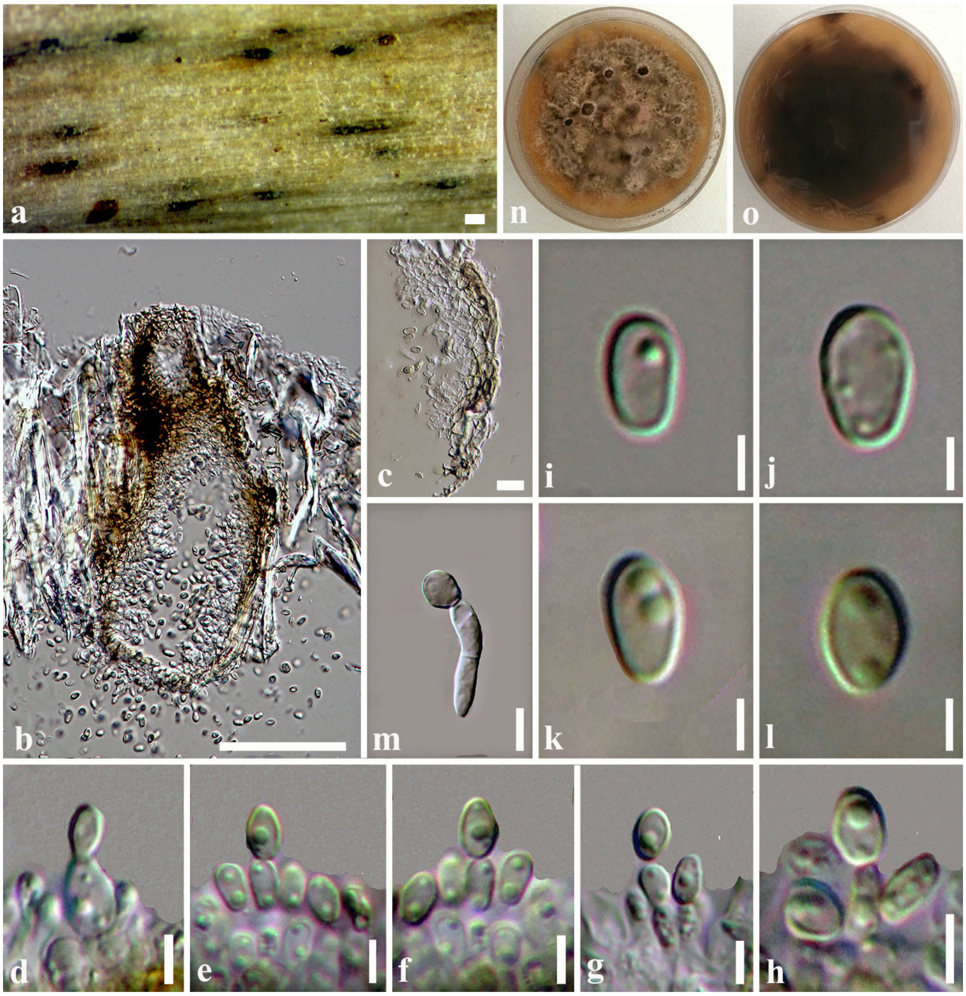


Fig. 28 ***Roussoella solani*** (MFLU 18-0007). **a** Conidiomata on host substrate. **b** Section through conidioma. **c** Section of pycnidial wall. **d–h** Conidiogenous cells and conidia. **i–l** Conidia. **m** Germinating conidium. **n, o** Colony on MEA from above and below. Scale bars: **a** = 500 µm, **b, c** = 200 µm, **d–h** = 50 µm, **i–m** = 2 µm

Tetraplosphaeriaceae Kaz. Tanaka & K. Hiray

Tetraplosphaeriaceae was introduced with *Tetraplosphaeria* as the type genus (Tanaka et al. 2009). The morphology of Tetraplosphaeriaceae are *Massarina*-like sexual morph with hyaline 1(–3)-septate ascospores and/or *Tetraploa*-like asexual morph with several setose appendages (Tanaka et al. 2009). There are five genera accepted in Wijayawardene et al. (2018). We describe three new species of *Polyplosphaeria* on Pandanaceae from China.

Polyplosphaeria Kaz. Tanaka & K. Hiray

Polyplosphaeria is typified by *P. fusca* Kaz. Tanaka & K. Hirayama. The members are saprobes and characteristics including globose ascomata surrounded by numerous brown hyphae and *Piricauda*-like conidia (e.g. *P. cochinensis* and *P. longispora*) (Tanaka et al. 2009). Two epithets are listed in Index Fungorum (2018). This is the first report of *Polyplosphaeria* from Pandanaceae, and we provide an updated synopsis of *Polyplosphaeria* species (Table 2).

Polyplosphaeria nabanheensis Tibpromma & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF554496, *Facesoffungi number*: FoF04506; Fig. 29

Etymology: named after Nabanhe, where the fungus was first discovered.

Holotype: HKAS 96219

Saprobic on dead leaves of *Pandanus* sp. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Colonies* on natural substrate, scattered or gregarious, blackish, dull, easy to remove. *Mycelium* superficial. *Conidiophores* micronematous, reduced to conidiogenous cell. *Conidiogenous cells* monoblastic, forming directly on creeping hyphae holoblastic, determinate, with guttules, hyaline. *Conidia* 110–150 × 75–88 µm ($\bar{x}$ = 143 × 82 µm, n = 10), oval to ellipsoid, made up of cells, 2–3 celled, dark brown, verrucose and dark at base, with setose appendages on surface, rough-walled; appendages unbranched, smooth, brown to black, of two types, long appendages 60–125 × 4–6 µm ($\bar{x}$ = 86 × 5 µm, n = 10), 3–9-septate, arising from apical part of conidia; short appendages 35–40 × 3.5–6 µm ($\bar{x}$ = 38 × 4.5 µm, n = 10), wide at the base, 0–2-septate and arising eccentrically from conidial base.

Culture characteristics: Conidia germinating on PDA within 12 h. Colonies on PDA, circular, undulate with dark brown mycelium. Mycelium superficial, velvety, flossy.

Material examined: CHINA, Yunnan Province, Xishuangbanna, Nabanhe, on fallen dead and decaying leaves of *Pandanus* sp., 2 August 2016, S. Tibpromma NBH19 (HKAS 96219, **holotype**); ex-type living culture, KUMCC 16-0151.

GenBank numbers LSU: MH260312; ITS: MH275078; SSU: MH260352; TUB2: MH412745.

Notes: In the phylogenetic analysis, *Polyplosphaeria nabanheensis* is in a distinct lineage, and basal to *Polyplosphaeria* (Fig. 30). *Polyplosphaeria nabanheensis* has oval to ellipsoid conidia while other *Polyplosphaeria* spp. are with globose, subglobose, obovoid, pyriform or ellipsoidal conidia (Tanaka et al. 2009). In a BLASTn search on NCBI GenBank, the closest matches of ITS sequence of KUMCC 16-0151 is *Quadricrura meridionalis* with 94% identity to the accession number NR_119401, while the closest matches with the TUB2 sequence were with 91% identical *P. fusca* strain KT 2124 (AB524853).

Polyplosphaeria pandanicola Tibpromma & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF554497, *Facesoffungi number*: FoF04507; Fig. 31

Etymology: named after the host genus, *Pandanus*.

Holotype: HKAS 99627

Saprobic on dead leaves of *Pandanus* sp. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Colonies* on natural substrate scattered or gregarious, blackish, dull. *Mycelium* partly superficial. *Conidiophores* micronematous, reduced to conidiogenous cell. *Conidiogenous cells* monoblastic, forming directly on creeping hyphae, holoblastic, integrated, terminal, determinate, incomplete globose connected to base of conidia, with guttules, hyaline. *Conidia* 35–70 × 40–75 µm ($\bar{x}$ = 41.4 × 44.6 µm, n = 20), globose to subglobose, solitary, brown to dark brown, verrucose at base, with setose appendages on surface; appendages of two forms, unbranched, smooth,

Table 2 Synopsis of *Polyplosphaeria* species and new isolates from this study is indicated in bold

Species	Conidia			References
	Size (µm)	Shape	Colour	
P. fusca	43–100(–125)	Globose to subglobose	Brown	Tanaka et al. (2009)
P. nabanheensis	**110–150 × 75–88**	**Oval to ellipsoid**	**Dark brown**	**This study**
P. pandanicola	**36–70 × 40–75**	**Globose to subglobose**	**Brown to dark brown**	**This study**
P. thailandica	20.5–43 × 17.5–54	Globose, obovoid, pyriform, ellipsoidal	Grey to brown	Li and Hou (2016)
P. xishuangbannaensis	**53–115 × 45–105**	**Subglobose**	**Black**	**This study**

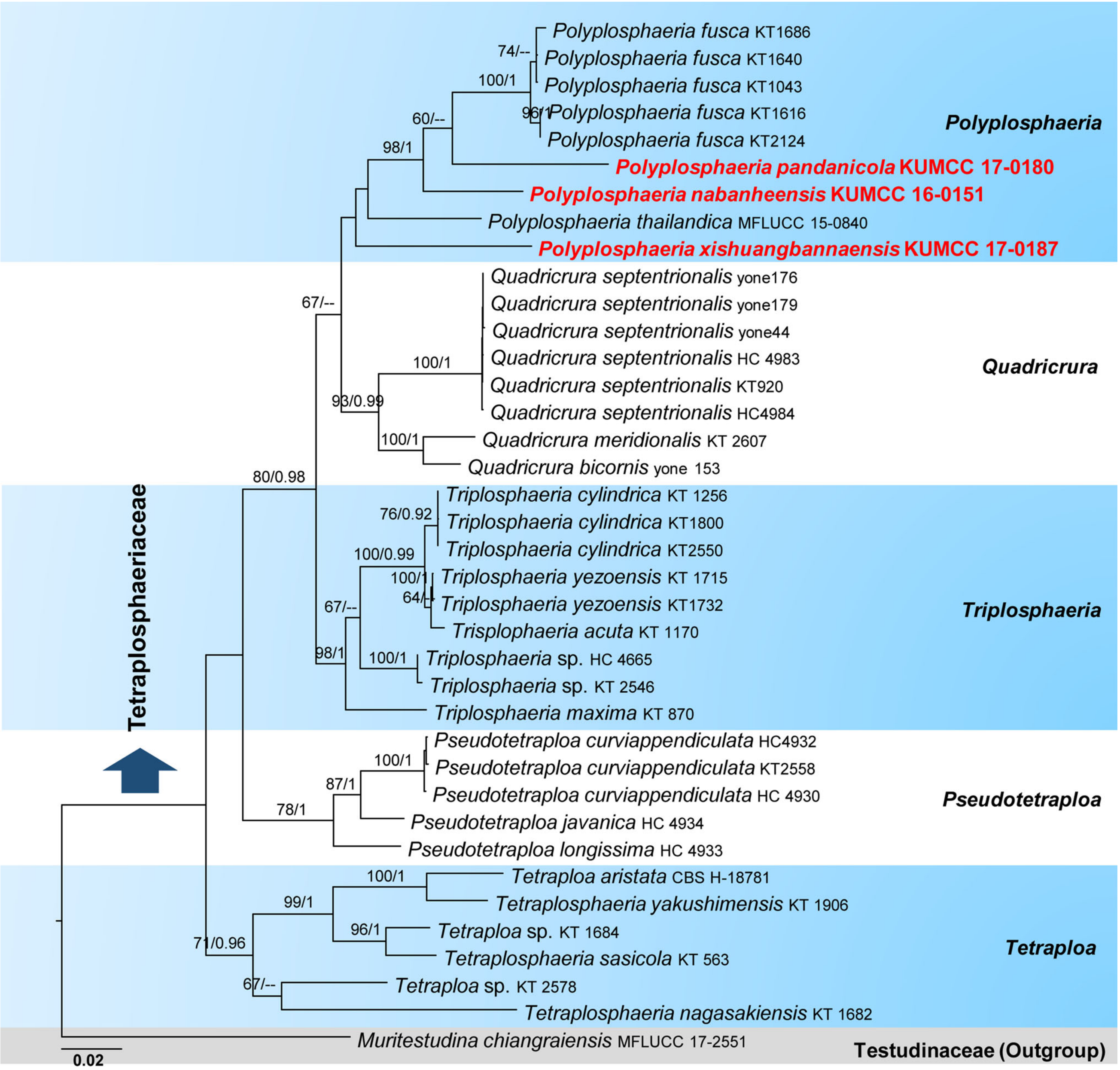


Fig. 29 Phylogram generated from maximum likelihood analysis based on combined LSU, SSU, ITS, TUB2 and TEF1 partial sequence data. Thirty-eight strains are included in the sequence analysis, which comprise 4198 characters with gaps. Single gene analysis was carried out and compared with each species, to compare the topology of the tree and clade stability. *Muritestudina chiangraiensis* (Testudinaceae) is used as the outgroup taxon. Tree topology of the ML analysis was similar to the BYPP. The best scoring RAxML tree with a final likelihood value of − 16498.013303 is presented. The matrix had 940 distinct alignment patterns, with 17.89% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.243803, C = 0.246513, G = 0.272484, T = 0.237200; substitution rates AC = 2.655152, AG = 4.461936, AT = 2.147661, CG = 1.746218, CT = 11.186368, GT = 1.000000; gamma distribution shape parameter α = 0.751821. Bootstrap support values for ML equal to or greater than 60% and BYPP equal to or greater than 0.90 are given above the nodes. Newly generated sequences are in red

brown at base and almost hyaline at apex, long appendages 60–105 × 3–5 µm ($\bar{x}$ = 81 × 4 µm, n = 10), wide at the apex, 4–6-septate, arising from apical part of conidia; short appendages 20–35 × 3.5–5 µm ($\bar{x}$ = 26.4 × 4 µm, n = 10), wide at the base, 0–2-septate, arising eccentrically from conidial base.

Culture characteristics: Conidia germinating on PDA within 24 h. Colonies on PDA, circular, undulate with dark brown in the middle and grey at the margin, smooth and raised on surface media. Mycelium superficial, velvety, flossy.

Material examined: CHINA, Yunnan Province, Xishuangbanna, on fallen dead and decaying leaves of

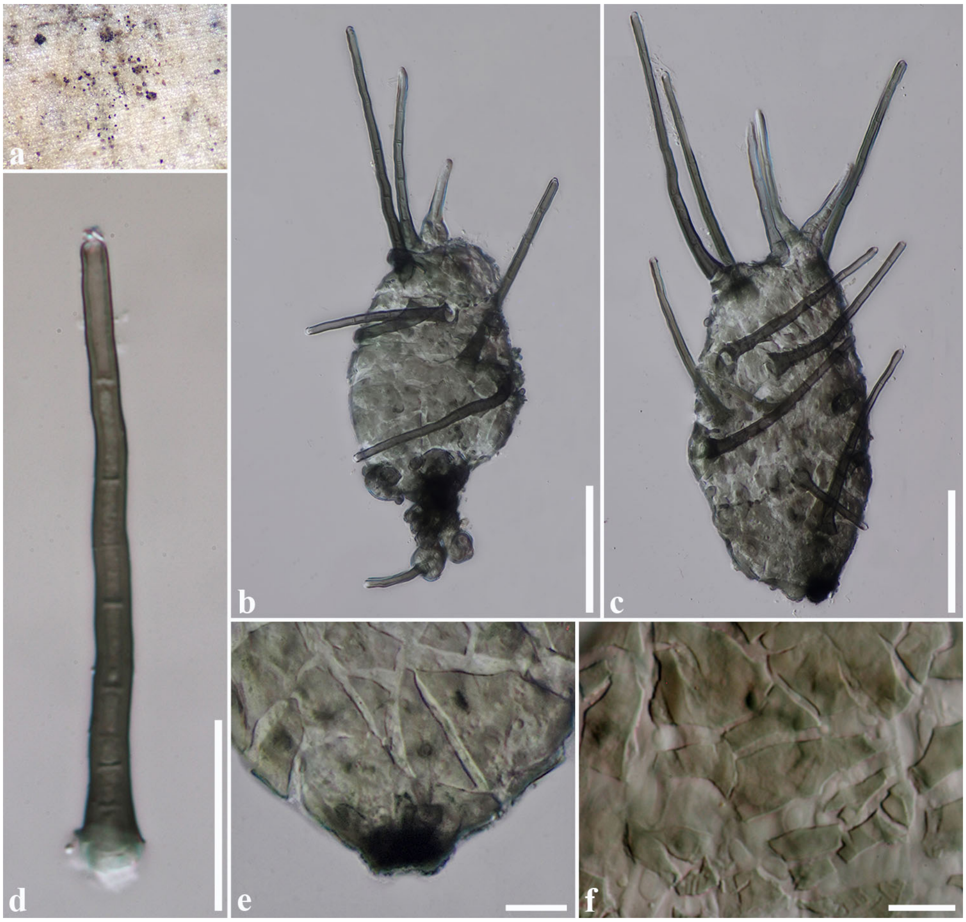


Fig. 30 ***Polyplosphaeria nabanheensis*** (HKAS 96219, **holotype**). **a** Colonies on dead leaf of *Pandanus* sp. **b, c** Conidia. **d** Appendages. **e** Base of conidium. **f** Conidial body with peel-like wall. Scale bars: **b, c** = 50 µm, **d, f** = 20 µm, **e** = 10 µm

Pandanus sp., 28 April 2017, R. Phookamsak & N.I. de Silva XTBG19 (HKAS 99627, **holotype**); ex-type living culture, KUMCC 17-0180 = MFLUCC 17-2266.

GenBank numbers LSU: MH260313; ITS: MH275079; SSU: MH260353.

Notes: *Polyplosphaeria pandanicola* shares common features with other *Polyplosphaeria* spp., but it differs by size of conidia (Table 2). According to our phylogenetic analysis, based on combined multi-gene sequence data, *P. pandanicola* formed a distinct lineage with 60% in ML bootstrap support (Fig. 30) compared with other known species in *Polyplosphaeria*. In a BLASTn search on NCBI GenBank, the closest matches of ITS sequence of KUMCC 17-0180 is *P. fusca* with 90% identity to the strain KT 1640 (AB524790).

Polyplosphaeria xishuangbannaensis Tibpromma & K.D. Hyde, ***sp. nov***.

Index Fungorum number: IF554498, *Facesoffungi number*: FoF04508; Fig. 32

Etymology: named after Xishuangbanna, where the fungus was first discovered.

Holotype: HKAS 101810

Saprobic on dead leaves of *Pandanus* sp. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Colonies* on natural substrate scattered or gregarious, blackish, shining. *Mycelium* superficial. *Conidiophores* micronematous, reduced to conidiogenous cell. *Conidiogenous cells* monoblastic, forming directly on creeping hyphae, holoblastic, integrated, terminal, determinate, incomplete globose connected to base of conidia, with guttules, hyaline. *Conidia* 53–115 × 45–105 µm ($\bar{x}$ = 76 × 69 µm, n = 10), subglobose, solitary, black, verrucose at base, with setose appendages on surface; appendages of two forms, unbranched, smooth, brown at base and almost hyaline at apex, long appendages 75–132 × 4–7 µm ($\bar{x}$ = 105 × 5 µm, n = 20), wide at the apex, 4–7-septate, arising from apical part of conidia; short appendages 20–40 × 2–4.5 µm ($\bar{x}$ = 31 × 4 µm, n = 20), wide at the base, 1–3-septate, arising eccentrically from conidial base.

Culture characteristics: Conidia germinating on PDA within 24 h. Colonies on PDA, circular, undulate with dark-grey, smooth and raised on surface media. Mycelium superficial, velvety, flossy.

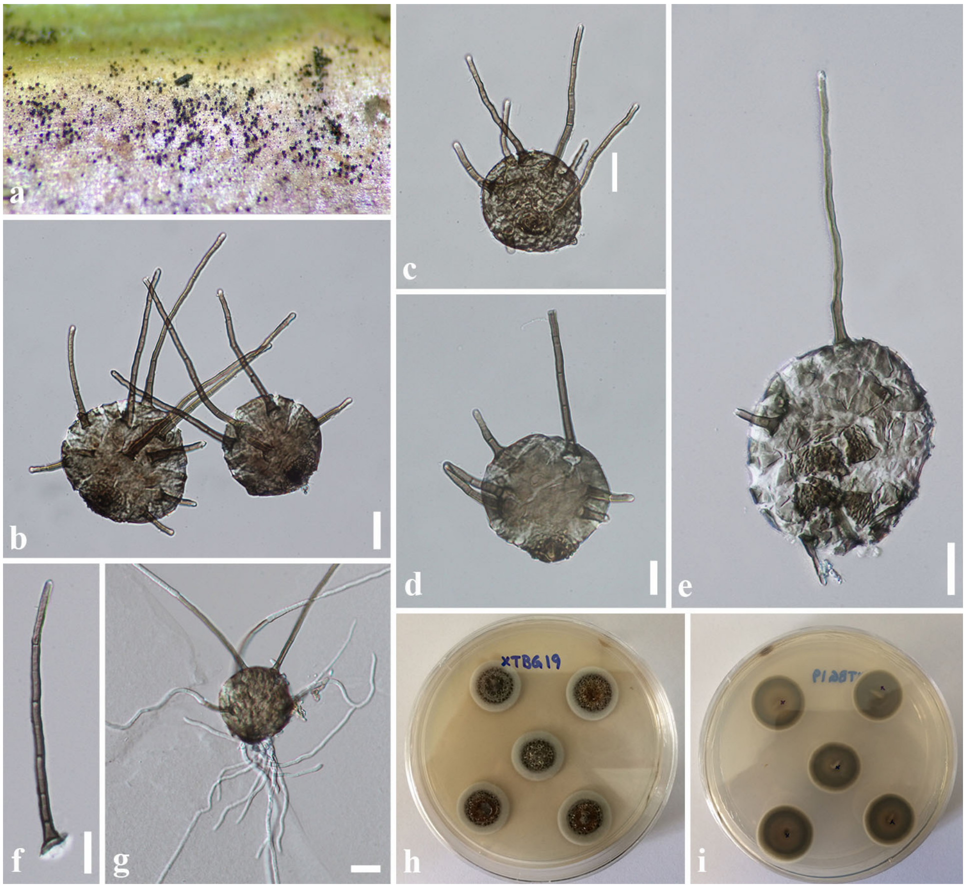


Fig. 31 ***Polyplosphaeria pandanicola*** (HKAS 99627, **holotype**). **a** Colonies on leaf of *Pandanus* sp. **b–d** Conidia. **e** Conidial body with peel-like wall. **f** Appendages. **g** Germinating conidium. **h, i** Colonies on PDA from above and below. Scale bars: **b–g** = 20 μm

Material examined: CHINA, Yunnan Province, Xishuangbanna, on fallen dead and decaying leaves of *Pandanus* sp., 28 April 2017, R. Phookamsak & N.I. de Silva XTBG27 (HKAS 101810, **holotype**); ex-type living culture, KUMCC 17-0187.

GenBank numbers LSU: MH260314; ITS: MH275080; SSU: MH260354.

Notes: *Polyplosphaeria xishuangbannaensis* was collected from a dead leaf of *Pandanus* sp. Phylogenetic analysis placed our collection in Tetraplosphaeriaceae and grouped within *Polyplosphaeria* (Fig. 30). *Polyplosphaeria xishuangbannaensis* is distinct by black, subglobose conidia, while other *Polyplosphaeria* spp. have brown, dark brown or grey conidia (Table 2). Therefore, we refer our new isolates to a new species. In a BLASTn search on NCBI GenBank, the closest matches of ITS sequence of KUMCC 17-0187 is *Triplosphaeria* sp. with 98% identity to the accession number KY315599.

Torulaceae Corda

Torulaceae was erected by Corda (1829) with *Torula* Pers. as type genus. Crous et al. (2015b) provided molecular data for Torulaceae. There are four genera in the family (Wijayawardene et al. 2018). We describe two known species of *Torula* and a new species of *Rostriconidium* collected on Pandanaceae from Thailand and China.

Rostriconidium Z.L. Luo et al.

Rostriconidium was erected by Su et al. (2018) as a monotypic genus for *R. aquaticum* Z.L. Luo, K.D. Hyde & H.Y. Su, from decaying wood in a river in China. *Rostriconidium* is characterized by long conidiophores with monotretic or polytretic conidiogenous cells. The conidia are rostrate with a sheath at the apex, multi-septate with a subhyaline apex and a distinctive, dark basal hilum with a pale coloured cell immediately above. We describe a new species of *Rostriconidium.* This is the first report of *Rostriconidium* on Pandanaceae.

Rostriconidium pandanicola Tibpromma & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF554490, *Facesoffungi number*: FoF04571; Fig. 33

Etymology: named after the host genus, *Pandanus*.

Holotype: HKAS 99620

Saprobic on dead leaves of *Pandanus* sp. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Colonies* on natural substrate consisting of long, dark, flexuous conidiophores. *Mycelium* immersed in the substrate, composed of septate, branched, brown hyphae. *Conidiophores*

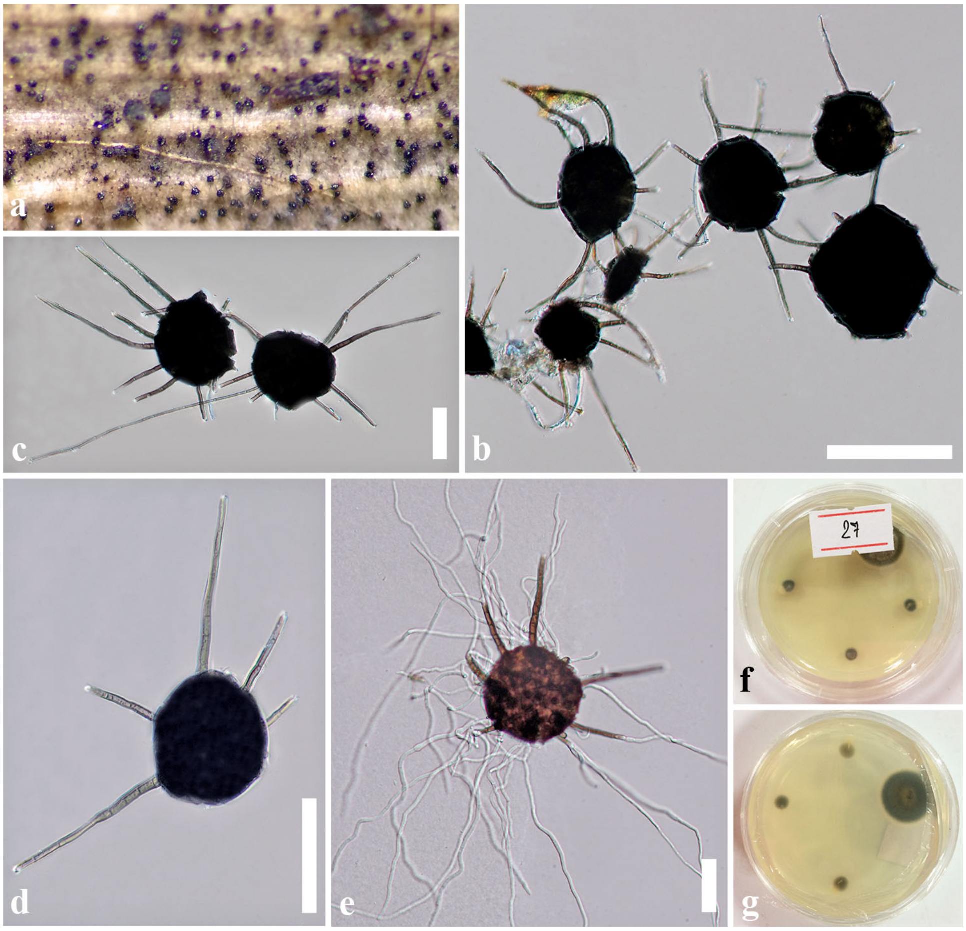


Fig. 32 ***Polyplosphaeria xishuangbannaensis*** (HKAS 101810, **holotype**). **a** Colonies on dead leaf of *Pandanus* sp. **b–d** Conidia. **e** Germinating conidium. **f, g** Colonies on PDA from above and below. Scale bars: **b** = 100 µm, **c** = 20 µm, **d, e** = 50 µm

360–485 × 11–13 µm ($\bar{x}$ = 423 × 12.5 µm, n = 10), macronematous, mononematous, scattered, dark brown to black, rough-walled, septate, unbranched, straight or slightly flexuous. *Conidiogenous cells* 15–30 × 8.5–12 µm ($\bar{x}$ = 21.6 × 10.6 µm, n = 20), polyblastic, sympodial, integrated, terminal, later becoming intercalary, cylindrical, dark brown, smooth, with black conidiogenous scars. *Conidia* 55–110 × 18–26 µm ($\bar{x}$ = 69.5 × 21 µm, n = 20), solitary, pale brown to dark brown, rostrate, 4–7-septate, with dark bands at the septa, slightly constricted at septa, with truncate, thick scar at base, narrower at base, flattened and paler towards the apex, short apex when young, long rostrate apex when mature, with hyaline thin sheath at the apex, granulate, smooth-walled.

Culture characteristics: Conidia germinating on PDA within 24 h. and germ tubes produced at the apex. Colonies on PDA reaching 9 cm diam., in 2 weeks at room temperature, circular, undulate with white to cream, raised on surface media with flossy with velvety. Mycelium superficial, branched, septate, hyaline to pale yellow, smooth.

Material examined: CHINA, Yunnan Province, Xishuangbanna, on fallen dead and decaying leaves of *Pandanus* sp., 30 April 2017, R. Phookamsak & N.I. de Silva XTBG12 (HKAS 99620, **holotype**); ex-type living culture, KUMCC 17-0176 = MFLUCC 17-2262; Yunnan Province, Xishuangbanna, on fallen dead of *Pandanus* sp., 28 April 2017, R. Phookamsak XTBG28 (HKAS 99626, **paratype**).

GenBank numbers LSU: MH260318; ITS: MH275084; SSU: MH260358; TEF1: MH412781; RPB2: MH412759.

Notes: The conidia of *Rostriconidium aquaticum* Z.L. Luo, K.D. Hyde & H.Y. Su are larger conidia (134–180 × 22–26 um) and have more septa (8–9) (Su et al. 2018) than those of *R. pandanicola*. Maximum likelihood of combined sequence data indicated that *Rostriconidium pandanicola* and *R. aquaticum* form a well-supported clade in Torulaceae (Fig. 34). In a BLASTn search on NCBI GenBank, the closest matches of ITS sequence of KUMCC 17-0176 is *R. aquaticum* with 95% identity to the strain MFLUCC 16-1113 (MG208164), while the closest matches with the TEF1 sequence were with 98% identical *R. aquaticum* strain KUMCC 15-0297 (MG207995) and RPB2 sequence were with 96% identical *R. aquaticum* strain KUMCC 15-0297 (MG207975).

Torula Pers.

Torula was erected by Persoon (1795) to accommodate *T. monilis* Pers. The genus is characterized by dark or subhyaline moniliform conidia (Persoon 1795). Crous et al.

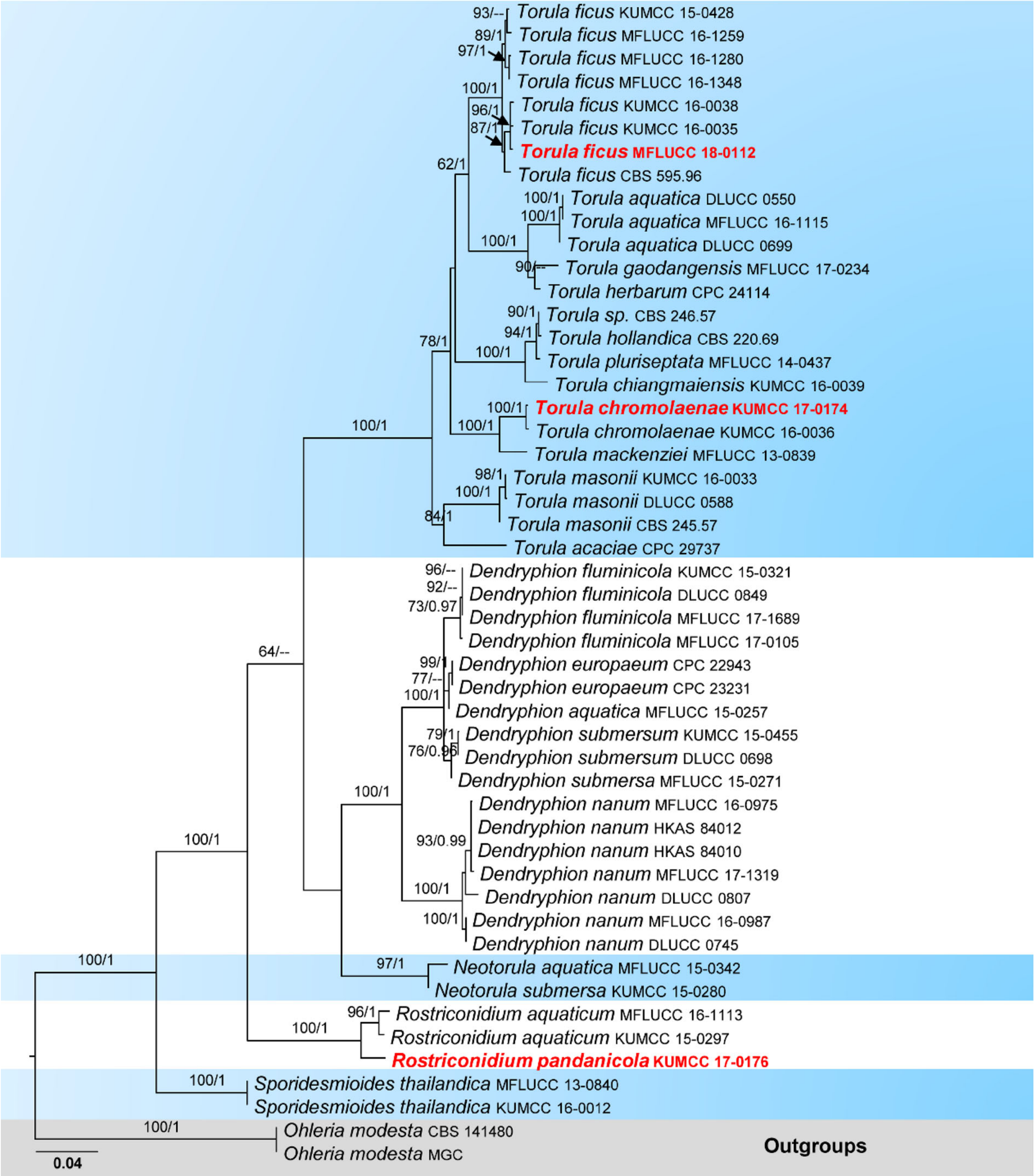


Fig. 33 Phylogram generated from maximum likelihood analysis based on combined LSU, ITS, RPB2 and TEF1 partial sequence data. Fifty strains are included in the sequence analysis, which comprise 3015 characters with gaps. Single gene analysis was carried out and compared with each species, to compare the topology of the tree and clade stability. *Ohleria modesta* (Ohleriaceae) is used as the outgroup taxon. Tree topology of the ML analysis was similar to the BYPP. The best scoring RAxML tree with a final likelihood value of − 13481.727487 is presented. The matrix had 946 distinct alignment patterns, with 26.17% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.242018, C = 0.268530, G = 0.274306, T = 0.215146; substitution rates AC = 2.017469, AG = 4.885145, AT = 2.212961, CG = 1.112797, CT = 12.027062, GT = 1.000000; gamma distribution shape parameter α = 0.614798. Bootstrap support values for ML equal to or greater than 60% and BYPP equal to or greater than 0.90 are given above the nodes. Newly generated sequences are in red

Fig. 34 ***Rostriconidium pandanicola*** (HKAS 99620, **holotype**). **a** Colonies on dead leaf of *Pandanus* sp. **b, c** Conidiophores, conidiogenous cells and conidia. **d, e** Conidiogenous cells and conidia. **f, g** Conidia. **h** Germinating conidium. **i, j** Colonies on PDA from above and below. Scale bars: **b, c** = 100 μm, **d–h** = 10 μm

(2015b) accepted *Torula* in Torulaceae (Pleosporales). More than 500 epithets are listed in Index Fungorum (2018). We collected *T. chromolaenae* and *T. ficus* from Pandanaceae.

Torula chromolaenae J.F. Li, Phook., Mapook & K.D. Hyde, Mycological Progress 16 (4): 454 (2017)

Facesoffungi number: FoF04572; Fig. 35

Saprobic on dead leaf of *Pandanus tectorius*. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Colonies* on natural substrate effuse, black, powdery. *Conidiophores* up 40 μm long, micronematous, reduced to conidiogenous cells, with hyaline to pale brown supporting cell. *Mycelium* immersed or superficial, composed of 2–4 μm, hyaline, branched, septate, hyphae. *Conidiogenous cells* 10–35 × 3–5 μm ($\bar{x}$ = 17 × 4 μm, n = 10), macronematous, solitary, cylindrical, hyaline to pale brown, verruculose at apex, mono- to polyblastic. *Conidia* 13–30 × 6–10 μm ($\bar{x}$ = 23 × 8 μm, n = 50), phragmosporous, in short branched chains, 1 − 3-septate, with dark bands at septa, acrogenous, pale brown when young, brown when mature, pale brown at apex, constricted at septa, verrucose, fragmenting into segments.

Culture characteristics: Colonies on PDA attaining 9 cm diam., within 2 weeks at room temperature, brown to yellow–brown, irregular with undulate edge raised on media surface, smooth, velvety.

Material examined: CHINA, Yunnan Province, Xishuangbanna, on fallen dead and decaying leaves of

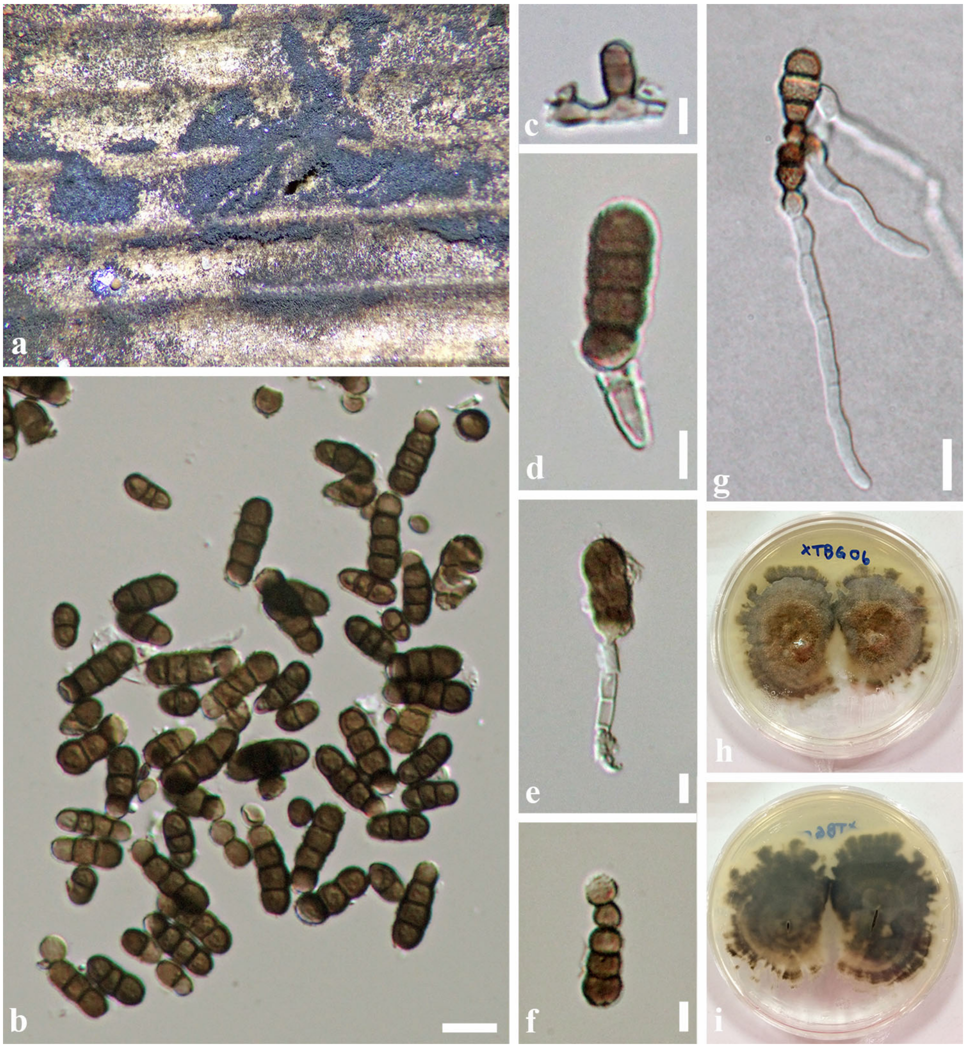


Fig. 35 ***Torula chromolaenae*** (HKAS 99614). **a** Colony on natural substratum. **b** Conidia in chains **c–e** Conidiophores, conidiogenous cells and conidia. **f** Conidia. **g** Germinating conidia. **h, i** Colonies on PDA from above and below. Scale bars: **b, g** = 10 μm, **c–f** = 5 μm

Pandanus tectorius Parkinson ex Du Roi., 15 October 2016, T. Aluthwaththa XTBG06 (HKAS 99614); living culture, KUMCC 17-0174.

GenBank numbers LSU: MH260321; ITS: MH275087; TEF1: MH412784; RPB2: MH412760.

Notes: *Torula chromolaenae* was described from *Chromolaena odorata* (Asteraceae) in Thailand (Li et al. 2017). In pair-wise comparison of DNA sequences of RPB2 and TEF1 regions of *Torula chromolaenae* (KUMCC 17-0174) and *T. chromolaenae* (KMUCC 16-0035) (type stain), they are almost identical (Fig. 34). Morphologically our isolate is identical to *Torula chromolaenae.*

Torula ficus Crous, IMA Fungus 6 (1): 192 (2015)

Facesoffungi number: FoF 04609; Fig. 36

Saprobic on dead leaf of *Pandanus* sp. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Colonies* on natural substrate effuse, black, powdery. *Mycelium* immersed or superficial, composed of 1–2.5 μm, hyaline, branched, septate hyphae. *Conidiophores* up to 25 μm, micronematous, reduced to conidiogenous cells, with hyaline to pale brown supporting cell. *Conidiogenous cells* 3–5 × 2–3 μm ($\bar{x}$ = 4 × 2.5 μm, n = 10), solitary on mycelium, cylindrical, hyaline to pale brown, verruculose at apex, mono- to polyblastic. *Conidia* 10–23 × 4–7 μm ($\bar{x}$ = 15 × 5 μm, n = 20), phragmosporous, in long branched chains, 1–3-septate, with dark bands at the septa, acrogenous, pale brown when young, brown when mature, pale brown at apex, constricted at septa, verrucose, fragmenting into segments.

Culture characteristics: Colonies on MEA attaining 9 cm diam., within 2 weeks at room temperature, circular with entire edge, raised on media surface, white at the middle with velvety, pale brown at the margin with flat mycelium.

Material examined: THAILAND, Chiang Mai Province, Mae Taeng District, Mushroom Research Foundation, on dead leaf of *Pandanus* sp., 16 December 2017, S. Tibpromma P06 (MFLU 18-0025, HKAS 101794); living culture, MFLUCC 18-0112.

GenBank numbers LSU: MH260322; ITS: MH275088; TEF1: MH412785.

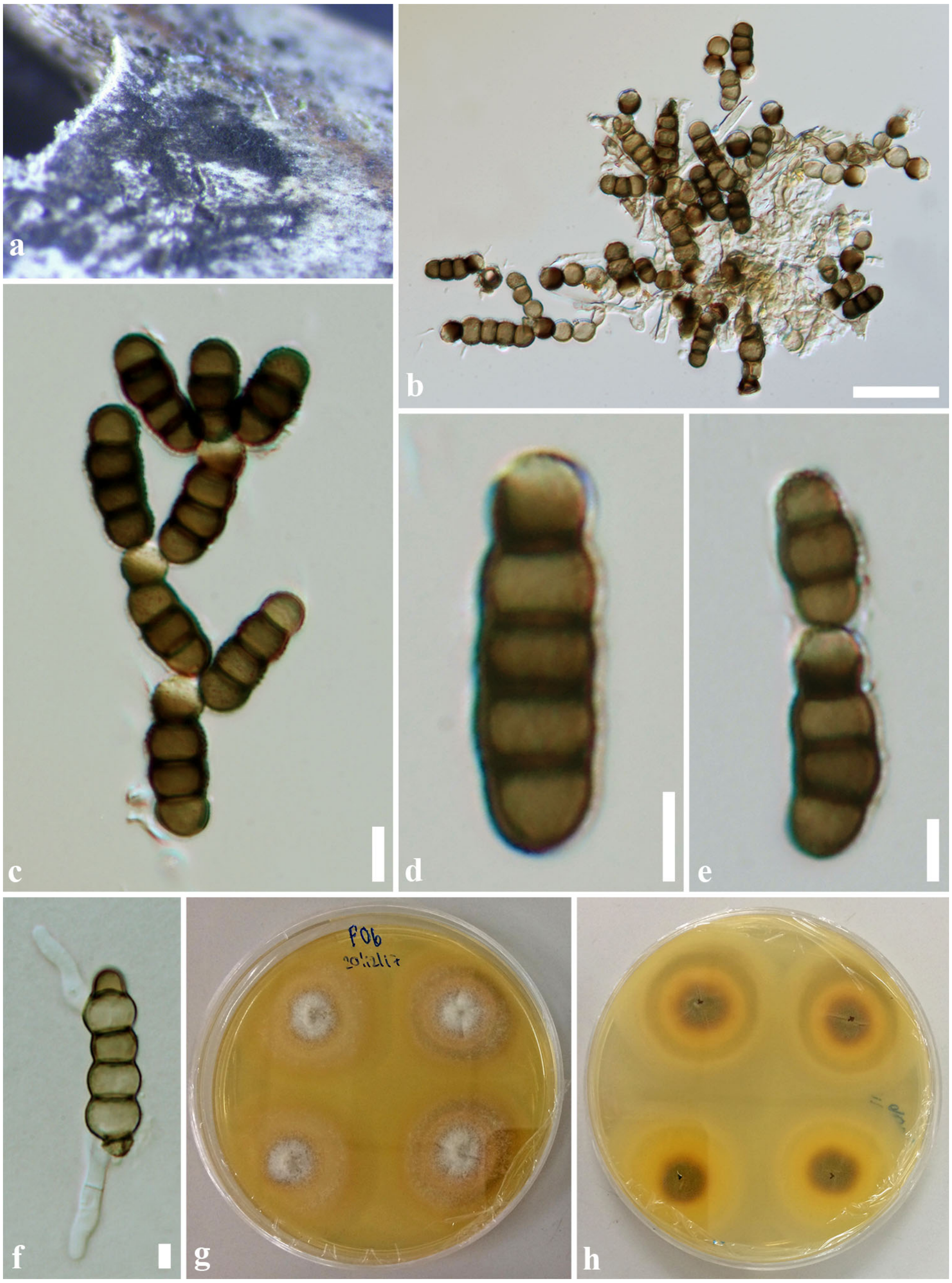


Fig. 36 ***Torula ficus*** (MFLU 18-0025). **a** Colony on natural substratum. **b** Conidiophore, conidiogenous cell and attached. **c** Conidia in chain. **d, f** Conidia. **f** Germinating conidium. **g, h** Colonies on MEA from above and below. Scale bars: **b** = 20 µm, **c–f** = 5 µm

Notes: *Torula ficus* was originally collected from *Ficus* in Europe (Crous et al. 2015b) and later found on submerged decaying wood of *Chromolaena odorata* in Thailand (Li et al. 2017). We provide sequence data (Fig. 34) for an isolate collected from *Pandanus* sp. (Pandanaceae) in Thailand. The morphology our isolate is identical with *T. ficus.*

Pleosporales genera *incertae sedis*

Pseudoberkleasmium Tibpromma & K.D. Hyde, ***gen. nov.***

Index Fungorum number: IF555331, *FacesofFungi number*: FoF04509

Etymology: name refers to its characteristic features of *Berkleasmium.*

Type species: *Pseudoberkleasmium pandanicola* Tibpromma & K.D. Hyde

Saprobic on dead or decaying leaves and wood in terrestrial habitats. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Colonies* on natural substrate, in small groups, blackish to brown, velvety, glistening, with conidia readily liberated when disturbed. *Mycelium* immersed in the substrate, composed of branched, septate, smooth, hyaline to subhyaline hyphae. *Conidiophores* micronematous, mononematous, fasciculate, septate, hyaline or subhyaline. *Conidiogenous cells* holoblastic, monoblastic, integrated, terminal, determinate, globose, with or without guttules, hyaline to subhyaline. *Conidia* acrogenous, solitary, broadly ellipsoidal to obovoid, flattened, one-cell thick, muriform, brown olivaceous green, with or without guttules.

Notes: *Pseudoberkleasmium* is established with *Ps. pandanicola* as the type species based on morphology and phylogenetic analyses. In a BLASTn search on NCBI GenBank, the closest matches for LSU sequence of KUMCC 17-0178 was *Hermatomyces chiangmaiensis* strain MFLUCC 16-2819 (KY559394) with 96% similarity, while the closest matches for the ITS sequence of KUMCC 17-0178 was *H. krabiensis* strain MFLUCC 16-0249 (KX525750) with 92% similarity. Multi-gene (LSU, SSU, TEF1 and ITS genes) analyses of *Pseudoberkleasmium* indicated that it separates from the family of Hermatomycetaceae with 62% in ML, 0.99 in BYPP support (Fig. 37) and the morphology totally differs from *Hermatomyces* by having lenticular and cylindrical conidia (one to two types of conidia) (Chang 1995).

The genus has similar morphology to *Bahugada* K.A. Reddy & V. Rao and *Berkleasmium* Zobel. *Pseudoberkleasmium* has funnel/globose shaped conidiogenous cells and brown to olivaceous green conidia, usually with a globose attached conidiogenous cell, while *Bahugada* has sympodial and denticulate conidiogenous cells and dark brown conidia (Reddy and Rao 1984). *Berkleasmium* is polyphyletic, as many species clustered in different clades and even in different families in the phylogenetic analysis (Fig. 37). Moreover, the type species of the genus (*Berkleasmium concinnum*) has been moved to Tubeufiaceae (Tubeufiales) (Tanney and Miller 2017; Lu et al. 2018). *Berkleasmium concinnum* has obovoid conidia with a scar (hilum) at base and cylindrical conidiogenous cells with a dark apex (Ellis 1971; Bussaban et al. 2001; Seifert et al. 2011; Tanney and Miller 2017). This genus needs to be revised based on both morphology and phylogenetic analysis. Therefore, based on different nature of both morphological and phylogenetic evidence from *B. concinnum*, we introduce a new genus here to accommodate our collection.

Pseudoberkleasmium pandanicola Tibpromma & K.D. Hyde, ***sp. nov***.

Index Fungorum number: IF555332, *Facesoffungi number*: FoF04510; Fig. 38

Etymology: named after the host genus, *Pandanus*.

Holotype: HKAS 99622

Saprobic on dead leaf sheath of *Pandanus* sp. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Colonies* on natural substrate, in small groups, blackish brown, velvety, glistening, with conidia readily liberated when disturbed. *Mycelium* immersed in the substrate, composed of branched, septate, smooth, hyaline hyphae. *Conidiophores* micronematous, mononematous, fasciculate, hyaline, smooth. *Conidiogenous cells* 5–11 × 9–12 µm ($\bar{x}$ = 8.5 × 10 µm, n = 20), holoblastic, monoblastic, integrated, terminal, determinate, subglobose, connected at the base of conidia, with guttules, hyaline. *Conidia* 26–31 × 15–19 µm ($\bar{x}$ = 29 × 17 µm, n = 30), acrogenous, solitary, broadly ellipsoidal to obovoid, flattened, one-cell thick, muriform, smooth, brown to olivaceous green, guttulate, usually with conidiogenous cell attached.

Culture characteristics: Conidia germinating on PDA within 24 h. Colonies on PDA, circular, undulate with dark grey mycelium and raised on surface media. Mycelium superficial, velvety.

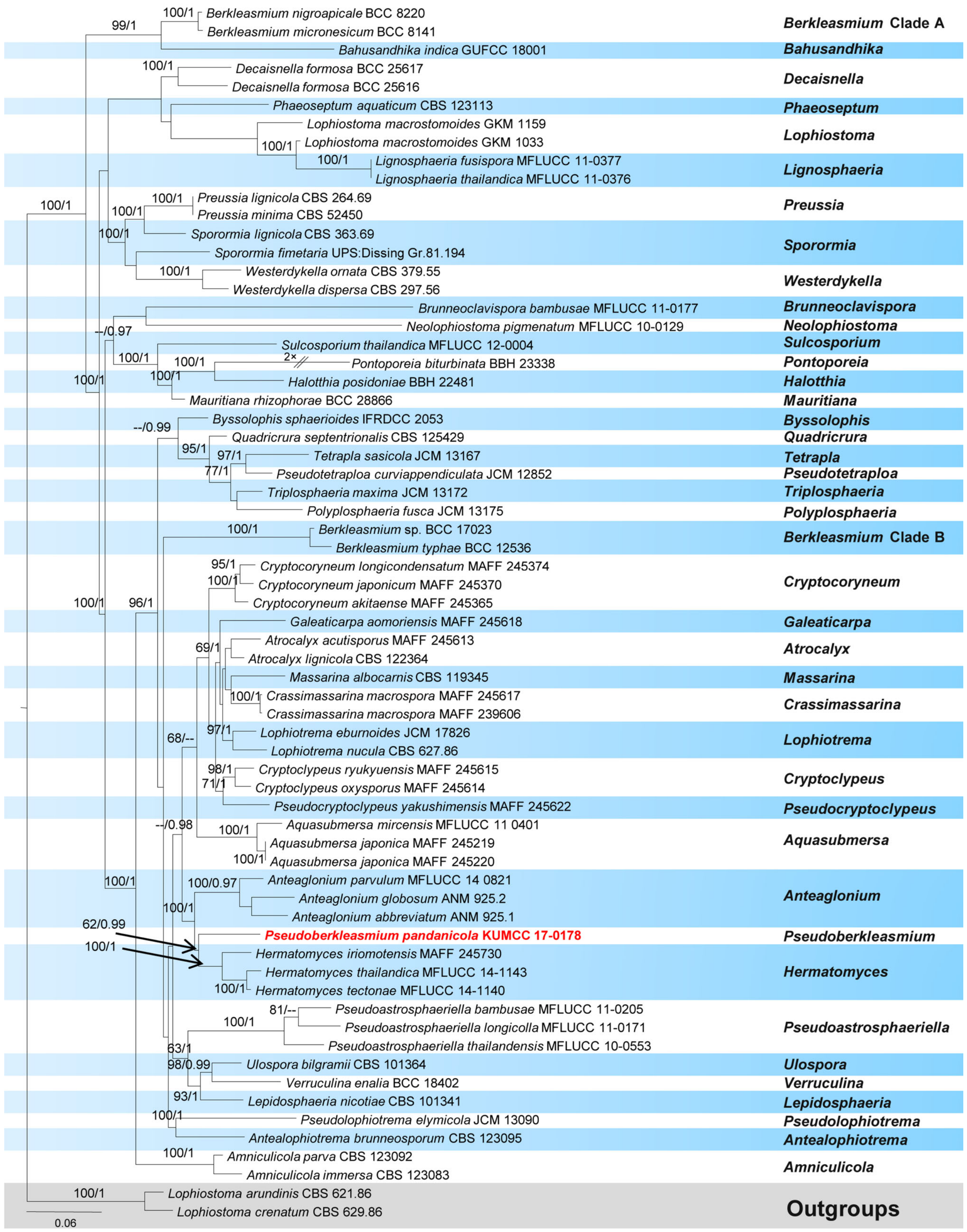
Material examined: CHINA, Yunnan Province, Xishuangbanna, on fallen dead and decaying leaf sheath of *Pandanus* sp., 28 April 2017, R. Phookamsak & N.I. de Silva XTBG14 (HKAS 99622, **holotype**); ex-type living culture, KUMCC 17-0178 = MFLUCC 17-2264.

GenBank numbers LSU: MH260304; ITS: MH275071; SSU: MH260344.

Notes: *Pseudoberkleasmium pandanicola* is the type species of the genus *Pseudoberkleasmium*, which can be distinguished morphologically. In the phylogenetic tree the strain formed a separate branch from other species based on combined LSU, SSU, ITS and TEF1 data, thus it is considered as a new genus and species (Fig. 37).

Pseudochaetosphaeronema Punith.

Pseudochaetosphaeronema was erected by Punithalingam (1979) with *P. larense* (Borelli and R. Zamora) Punith. as the type species. *Pseudochaetosphaeronema* was placed in Macrodiplodiopsidaceae by Crous et al. (2015b), while Wijayawardene et al. (2017a) placed in Pleosporales genera *incertae sedis*. Members can found as saprobic in terrestrial or aquatic habitats but some also can be human pathogens (Zhang et al. 2012; Ahmed et al. 2015a). Morphological characteristics of asexual morph of this genus are black obpyriform pycnidia with a long neck, hyaline and phialidic conidiophores and unicellular subspherical to ellipsoidal conidia (Zhang et al. 2016). The sexual morph is undetermined (Ahmed et al. 2014). Two epithets are listed in Index Fungorum (2018). We introduce a new species in *Pseudochaetosphaeronema* based on molecular and morphological characteristics; this is the fully described and illustrated study using morphological and phylogenetic evidences for this genus.


100/1 Berkleasmium nigroapicale BCC 8220
99/1 Berkleasmium micronesicum BCC 8141
Berkleasmium Clade A
Bahusandhika indica GUFCC 18001
Bahusandhika
100/1 Decaisnella formosa BCC 25617
Decaisnella formosa BCC 25616
Decaisnella
Phaeoseptum aquaticum CBS 123113
Phaeoseptum
Lophiostoma macrostomoides GKM 1159
100/1 Lophiostoma macrostomoides GKM 1033
Lophiostoma
100/1 Lignosphaeria fusispora MFLUCC 11-0377
Lignosphaeria thailandica MFLUCC 11-0376
Lignosphaeria
100/1
100/1 Preussia lignicola CBS 264.69
100/1 Preussia minima CBS 52450
Preussia
100/1 Sporormia lignicola CBS 363.69
Sporormia fimetaria UPS:Dissing Gr.81.194
Sporormia
100/1 Westerdykella ornata CBS 379.55
Westerdykella dispersa CBS 297.56
Westerdykella
Brunneoclavispora bambusae MFLUCC 11-0177
Brunneoclavispora
--/0.97 Neolophiostoma pigmenatum MFLUCC 10-0129
Neolophiostoma
Sulcosporium thailandia MFLUCC 12-0004
Sulcosporium
100/1 100/1 2× Pontoporeia biturbinata BBH 23338
Pontoporeia
100/1 100/1 Halotthia posidoniae BBH 22481
Halotthia
Mauritiana rhizophorae BCC 28866
Mauritiana
--/0.99 Byssolophis sphaerioides IFRDCC 2053
Byssolophis
Quadricrura septentrionalis CBS 125429
Quadricrura
95/1 97/1 Tetrapla sasicola JCM 13167
Tetrapla
77/1 Pseudotetraploa curviappendiculata JCM 12852
Pseudotetraploa
Triplosphaeria maxima JCM 13172
Triplosphaeria
Polyplosphaeria fusca JCM 13175
Polyplosphaeria
100/1 Berkleasmium sp. BCC 17023
Berkleasmium typhae BCC 12536
Berkleasmium Clade B
95/1 Cryptocoryneum longicondensatum MAFF 245374
100/1 Cryptocoryneum japonicum MAFF 245370
Cryptocoryneum akitaense MAFF 245365
Cryptocoryneum
100/1 96/1
Galeaticarpa aomoriensis MAFF 245618
Galeaticarpa
69/1 Atrocalyx acutisporus MAFF 245613
Atrocalyx lignicola CBS 122364
Atrocalyx
Massarina albocarnis CBS 119345
Massarina
100/1 Crassimassarina macrospora MAFF 245617
Crassimassarina macrospora MAFF 239606
Crassimassarina
68/-- 97/1 Lophiotrema eburnoides JCM 17826
Lophiotrema nucula CBS 627.86
Lophiotrema
98/1 Cryptoclypeus ryukyuensis MAFF 245615
71/1 Cryptoclypeus oxysporus MAFF 245614
Cryptoclypeus
Pseudocryptoclypeus yakushimensis MAFF 245622
Pseudocryptoclypeus
--/0.98 100/1 Aquasubmersa mircensis MFLUCC 11 0401
Aquasubmersa japonica MAFF 245219
100/1 Aquasubmersa japonica MAFF 245220
Aquasubmersa
100/1 100/0.97 Anteaglonium parvulum MFLUCC 14 0821
100/1 Anteaglonium globosum ANM 925.2
Anteaglonium abbreviatum ANM 925.1
Anteaglonium
62/0.99
Pseudoberkleasmium pandanicola KUMCC 17-0178
Pseudoberkleasmium
100/1
Hermatomyces iriomotensis MAFF 245730
Hermatomyces thailandica MFLUCC 14-1143
100/1 Hermatomyces tectonae MFLUCC 14-1140
Hermatomyces
81/-- Pseudoastrosphaeriella bambusae MFLUCC 11-0205
100/1 Pseudoastrosphaeriella longicolla MFLUCC 11-0171
Pseudoastrosphaeriella thailandensis MFLUCC 10-0553
Pseudoastrosphaeriella
63/1
98/0.99 Ulospora bilgramii CBS 101364
Ulospora
Verruculina enalia BCC 18402
Verruculina
93/1 Lepidosphaeria nicotiae CBS 101341
Lepidosphaeria
100/1 Pseudolophiotrema elymicola JCM 13090
Pseudolophiotrema
Antealophiotrema brunneosporum CBS 123095
Antealophiotrema
100/1 Amniculicola parva CBS 123092
Amniculicola immersa CBS 123083
Amniculicola
100/1 Lophiostoma arundinis CBS 621.86
Lophiostoma crenatum CBS 629.86
Outgroups
0.06

◀**Fig. 37** Phylogram generated from maximum likelihood analysis based on combined LSU, SSU, ITS and TEF1 partial sequence data. Sixty-six strains are included in the sequence analysis, which comprise 3307 characters with gaps. Single gene analysis was carried out and compared with each species, to compare the topology of the tree and clade stability. *Lophiostoma arundinis* (CBS 621.86) and *Lophiostoma crenatum* (CBS 629.86) were used as outgroups taxa. Tree topology of the ML analysis was similar to the BYPP. The best scoring RAxML tree with a final likelihood value of − 26522.759094 is presented. The matrix had 1375 distinct alignment patterns, with 27.73% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.241919, C = 0.250696, G = 0 0.273797, T = 0.233589; substitution rates AC = 1.515500, AG = 2.699099, AT = 1.528593, CG = 1.081356, CT = 7.828217, GT = 1.000000; gamma distribution shape parameter α = 0.209065. Bootstrap support values for ML equal to or greater than 60% and BYPP equal to or greater than 0.90 are given above the nodes. Newly generated sequences is in red

Pseudochaetosphaeronema pandanicola Tibpromma & K.D. Hyde, ***sp. nov***.

Index Fungorum number: IF554501, *Facesoffungi number*: FoF04511; Fig. 39

Etymology: named after the host genus, *Pandanus*.

Holotype: MFLU 18-0016

Saprobic on dead leaves of *Pandanus* sp. **Sexual morph** Undetermined. **Asexual morph** *Conidiomata* 100–110 × 156–167 µm ($\bar{x}$ = 107 × 161 µm, n = 5), scattered to gregarious, superficial, flat on the base, conspicuous on host surface, dark brown, shiny, solitary, uniloculate, globose to subglobose, without papilla and ostiole. *Pycnidial wall* 11–18 µm, composed of several layers of thick-walled, dark brown cells of *textura prismatica*. *Conidiogenous cells* 8–17 × 1–3 µm ($\bar{x}$ = 11 × 2 µm, n = 20), monophialidic, cylindrical, thick-walled, smooth, each with a small collarette at the tip. *Conidia* 2–5 × 1.5–3 µm ($\bar{x}$ = 3 × 2 µm, n = 30), subglobose to oval, aseptate, hyaline to subhyaline, guttulate without mucilaginous sheath.

Culture characteristics: Conidia germinating on MEA within 12 h. Colonies on MEA, grey on the surface, with dense, circular, with entire edge, raised, velvety, brown in reverse, with smooth margin. Sporulating in MEA after 3 months.

Material examined: THAILAND, Prachuap Khiri Khan Province, Bang Saphan District, Sai Khu Waterfall, on *Pandanus* sp., 30 July 2015, S. Tibpromma SF15-040 (MFLU 18-0016, **holotype**; HKAS 100842, **isotype**); ex-type living culture, MFLUCC 16-0272 = KUMCC 17-0308.

GenBank numbers LSU: MH260316; ITS: MH275082; SSU: MH260356.

Notes: In the phylogenetic analysis, *Pseudochaetosphaeronema pandanicola* clustered with *P. martinelli* S.A. Ahmed, Desbois, Miossec, Atoche, Bonifaz, & de Hoog. but was well-separated with high bootstrap support of 99% in ML and 1 in BYPP (Fig. 40). *Pseudochaetosphaeronema martinelli* is a human pathogen and hyphae are present in culture (Ahmed et al. 2015a). According to Ahmed et al. (2015a) some *Pseudochaetosphaeronema* species can produce coelomycetous fruit bodies after extended incubation. Our taxon produced conidia in culture. Based on molecular phylogeny, *P. pandanicola* is described here as a new species. In a BLASTn search on NCBI GenBank, the closest matches of ITS sequence of MFLUCC 16-0272 is *P. martinelli* with 96% identity to the strain JP105B-2X (MG649295).

Dothideomycetes orders *incertae sedis*

Botryosphaeriales C.L. Schoch et al.

Botryosphaeriaceae Theiss. & H. Syd.

Botryosphaeriaceae was erected by Theissen and Sydow (1918) with *Botryosphaeria* Ces. & De Not. as type genus. Members of this family are saprobes, endophytes and opportunistic pathogens and many of them cause disease on ecologically and economically important plants in forestry and agriculture (Schoch et al. 2006; Slippers and Wingfield 2007; Mehl et al. 2014). They are widespread in all climatic regions worldwide, but apparently absent from polar regions (Hyde et al. 2013, 2014; Phillips et al. 2013; Slippers et al. 2013; Dissanayake et al. 2016). Phillips et al. (2013) accepted 17 genera based on morphology and multigene analysis, while Wijayawardene et al. (2018) accepted and provided details of 28 genera. This family has been well circumscribed by several authors (Crous et al. 2006; Phillips et al. 2008, 2013; Slippers et al. 2013; Hyde et al. 2014; Dissanayake et al. 2017). New isolates and specimens collected on Pandanaceae in Thailand and China are described.

Lasiodiplodia Ellis & Everh.

Lasiodiplodia was formally erected by Ellis & Everh. (Clendenin 1896), and typified by *L. theobromae* (Phillips et al. 2013). Members of this genus, which can cause cankers, die-back, fruit or root rot, branch blight or discoloration on a wide range of woody hosts, are mostly distributed in tropical and subtropical regions (Punithalingam 1980; Ismail et al. 2012; Phillips et al. 2013). There are 52 epithets for *Lasiodiplodia* are listed in Index Fungorum (2018). *Lasiodiplodia abnormis* Traverso &

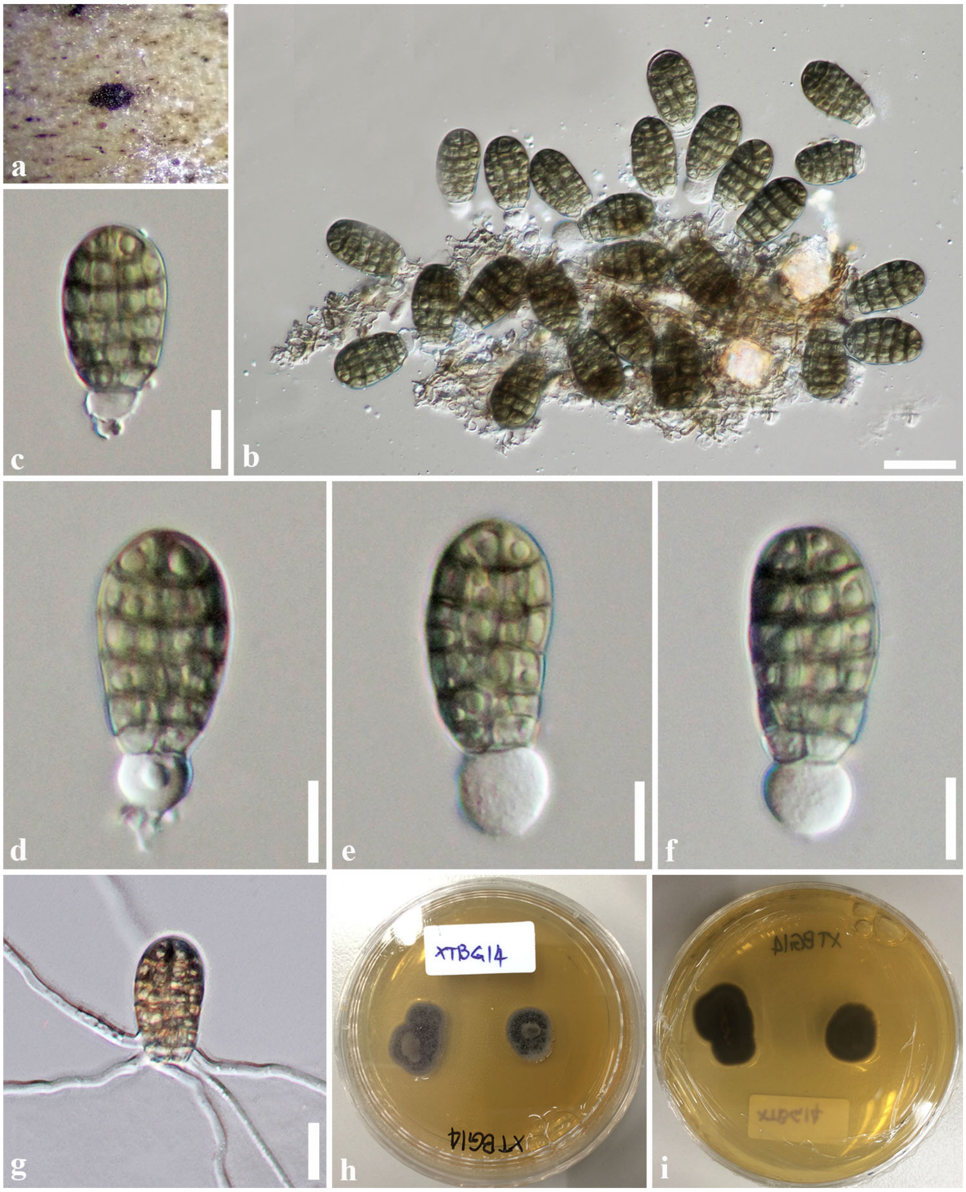


Fig. 38 ***Pseudoberkleasmium pandanicola*** (HKAS 99622, **holotype**). **a** Colony on dead leaf sheath of *Pandanus* sp. **b–f** Conidia attached with conidiogenous cells. **g** Germinating conidium. **h, i** Colonies on PDA from above and below. Scale bars: **b** = 20 µm, **c–g** = 10 µm

Spessa and *L. theobromae* (Pat.) Griffon & Maubl. are known from Pandanaceae (Whitton et al. 2012).

Lasiodiplodia chonburiensis Tibpromma & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF554472, *Facesoffungi number*: FoF04564; Fig. 41

Etymology: named after Chonburi Province, where the fungus was first discovered.

Holotype: MFLU 16-1877

Saprobic on dead leaves of *Pandanus* sp. **Sexual morph** Undetermined. **Asexual morph** *Conidiomata* 210–250 × 270–300 µm ($\bar{x}$ = 236 × 287 µm, n = 5), scattered to gregarious, immersed, conspicuous on host surface, dark

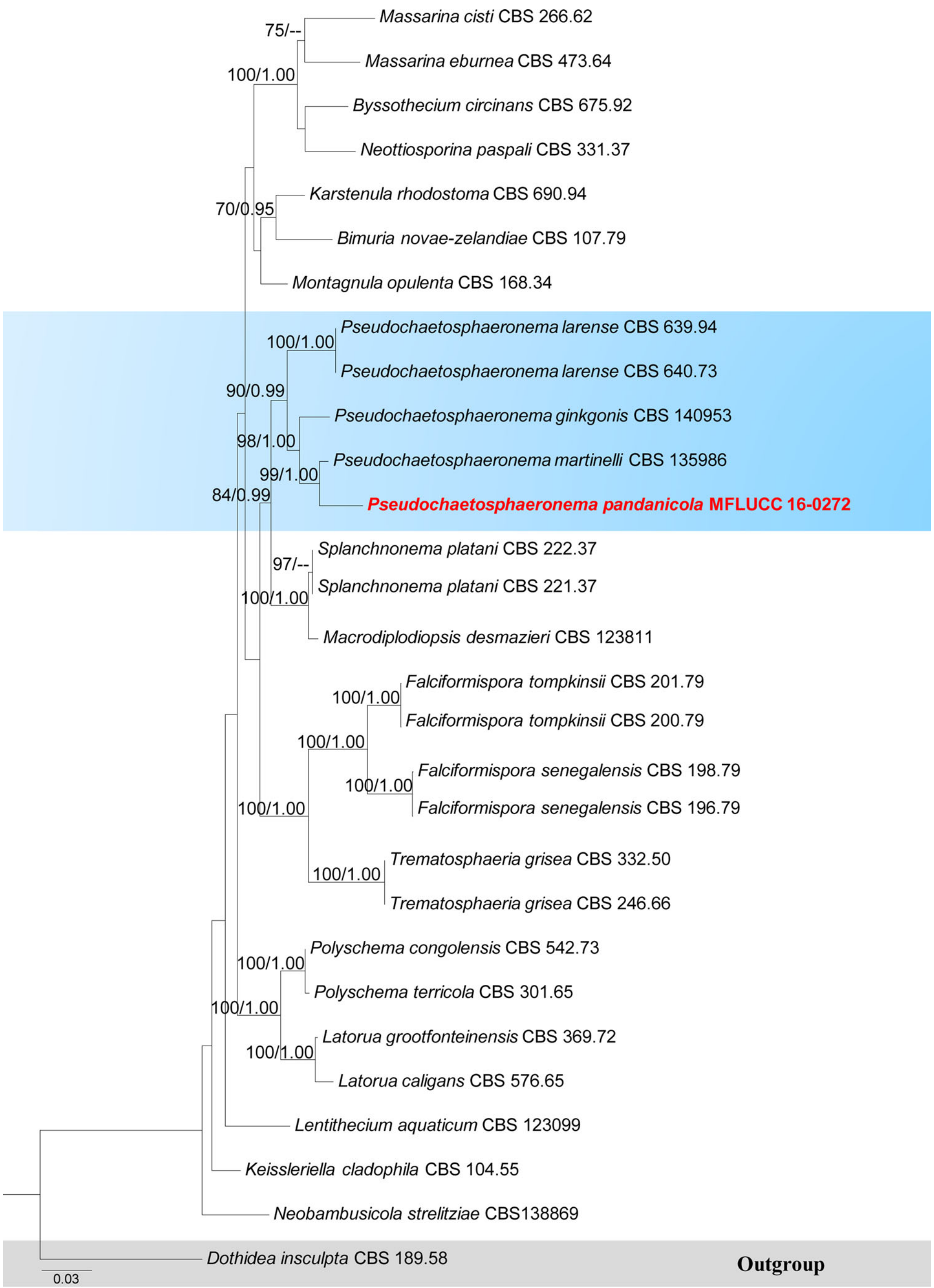


Fig. 39 Phylogram generated from maximum likelihood analysis based on combined LSU, SSU, ITS and TEF1 sequence data. Related sequences were obtained from Zhang et al. (2016). Twenty-nine strains are included in the combined sequence analysis, which comprise 4502 characters with gaps. *Dothidea insculpta* (CBS 189.58) is used as the outgroup taxon. Tree topology of the ML analysis was similar to the PP. The best scoring RAxML tree with a final likelihood value of − 16777.220849 is presented. The matrix had 1151 distinct alignment patterns, with 37.92% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.244562, C = 0.237859, G = 0.273035, T = 0.244544; substitution rates AC = 0.994384, AG = 2.031393, AT = 1.306799, CG = 0.988463, CT = 5.904665, GT = 1.000000; gamma distribution shape parameter α = 0.463512. Bootstrap support values for ML equal to or greater than 70% and BYPP equal to or greater than 0.90 are given above the nodes. The newly generated sequence is in red

brown, solitary, uniloculate, globose to subglobose, ostiole without papilla. *Pycnidial wall* 20–51 µm, composed of several layers of thick-walled, hyaline to dark brown cells of *textura angularis*. *Conidiogenous cells* 9–13 × 3–5 µm ($\bar{x}$ = 11 × 4 µm, n = 20), annellidic, cylindrical, thick-walled, smooth. *Conidia* 15–30 × 10–15 µm ($\bar{x}$ = 23 × 12 µm, n = 30), subglobose to oval, aseptate, hyaline to subhyaline with age, guttulate, without longitudinal striations and mucilaginous sheath.

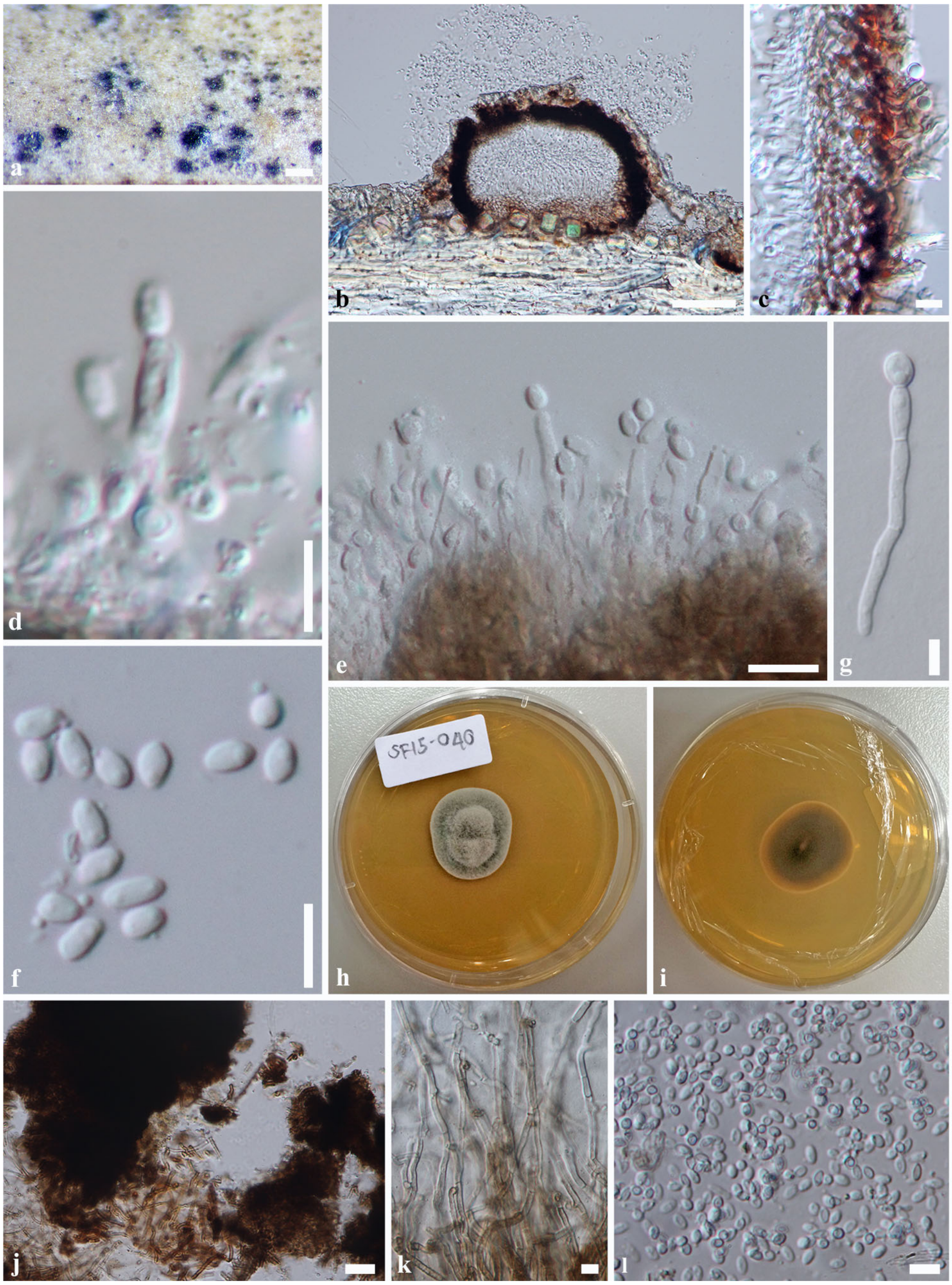


Fig. 40 ***Pseudochaetosphaeronema pandanicola*** (MFLU 18-0016, **holotype**). **a** Appearance of ascomata on host substrate. **b** Section of conidioma. **c** Section of pycnidial wall. **d, e** Conidiogenous cell producing conidia. **f** Conidia. **g** Germinating conidium. **h, i** Colony on MEA from above and below. **j, k** Mycelium formed in culture. **l** Conidia formed in culture. Scale bars: **a** = 200 μm, **b** = 50 μm, **c**, **d–g, j** = 5 μm, **k**, **l** = 20 μm

Culture characteristics: Conidia germinating on MEA within 12 h. Colonies on MEA, white at first, becoming black with age, circular, with entire edge, raised, velvety, black in reverse, with smooth margin.

Material examined: THAILAND, Chonburi Province, Bang Lamung District, on dead leaf of *Pandanus* sp., 18 July 2016, W. Jaidee PTY02 (MFLU 16-1877, **holotype;** HKAS 96271, **isotype**); ex-type living culture, MFLUCC 16-0376 = KUMCC 17-0299.

GenBank numbers LSU: MH260299; ITS: MH275066; TEF1: MH412773; TUB2: MH412742.

Notes: *Lasiodiplodia chonburiensis* clusters with *L. caatinguensis* I.B.L. Cout., F.C. Freire, C.S. Lima & J.E. Cardoso in phylogenetic analyses (86% in ML, 0.99 in BYPP, Fig. 42). *Lasiodiplodia caatinguensis* has ovoid to ellipsoids conidia 18.15 × 11.78 μm (Coutinho et al. 2017), while *L. chonburiensis* has subglobose to oval conidia 23 × 12 μm. Therefore, *L. chonburiensis* is introduced as a new species based on morphology and phylogeny. In a BLASTn search on NCBI GenBank, the closest matches of ITS sequence of MFLUCC 16-0376 is *Lasiodiplodia* sp. with 96% identity to the strain CMW40968 (KP872323), while the closest matches with

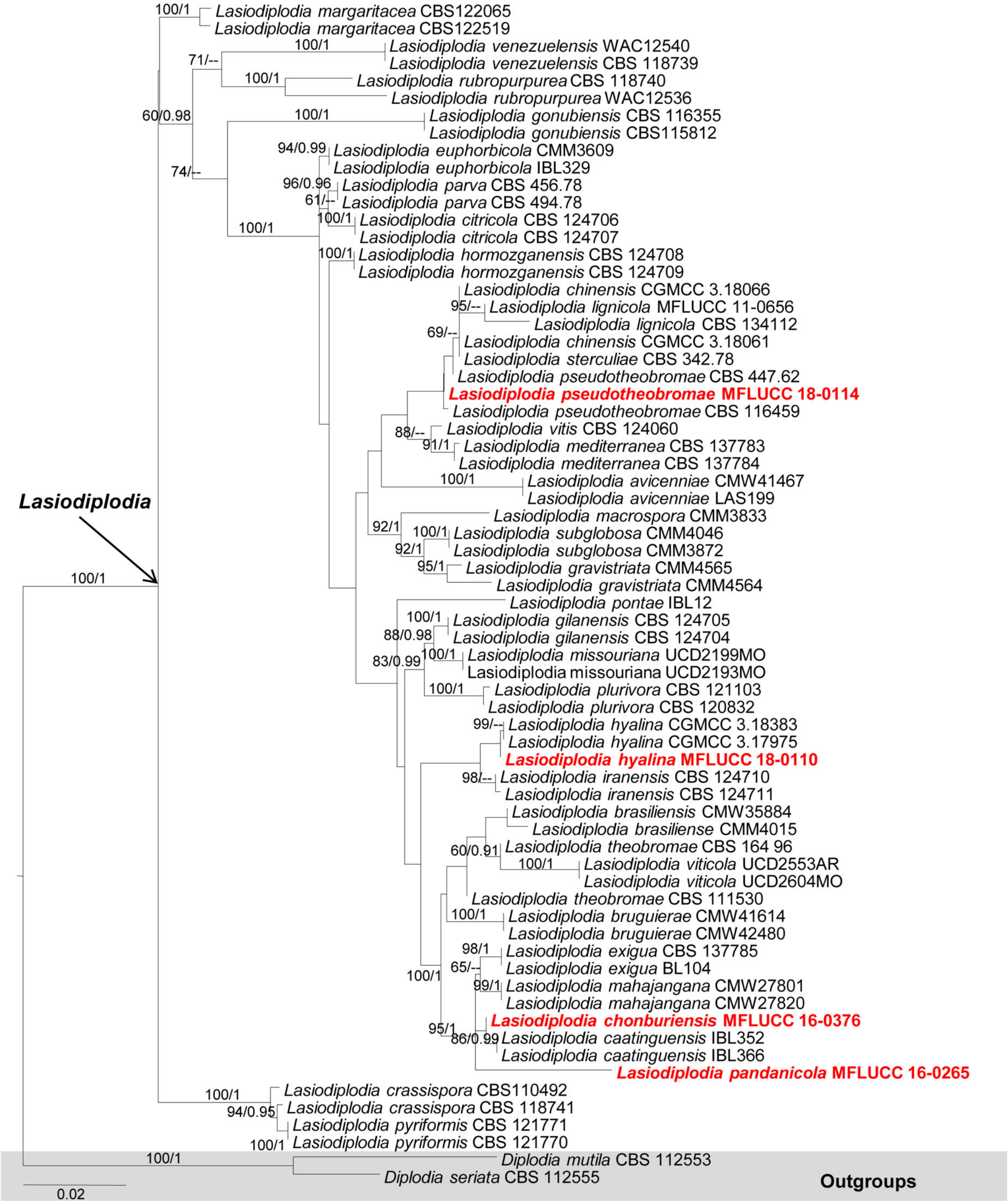


Fig. 41 Phylogram generated from maximum likelihood analysis based on combined ITS, TUB2 and TEF1 sequence data. Related sequences were obtained from Dissanayake et al. (2016). Sixty-eight strains are included in the combined sequence analysis, which comprise 1384 characters with gaps. *Diplodia mutila* (CBS112553) and *Diplodia seriata* (CBS 112555) are used as the outgroup taxa. Tree topology of the ML analysis was similar to the BYPP. The best scoring RAxML tree with a final likelihood value of − 5260.567452 is presented. The matrix had 439 distinct alignment patterns, with 19.02% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.209713, C = 0.304662, G = 0.257279, T = 0.257279; substitution rates AC = 1.066215, AG = 3.169642, AT = 1.471415, CG = 0.952504, CT = 4.325945, GT = 1.000000; gamma distribution shape parameter α = 0.141773. Bootstrap support values for ML equal to or greater than 60% and BYPP equal to or greater than 0.90 are given above the nodes. Newly generated sequences are in red

the TEF1 sequence were with 100% identical *L. theobromae* strain CBS190.73 (EF622048) and closest matches with the TUB2 sequence were with 99% identical *L. theobromae* strain L10 (KR260829).

Lasiodiplodia hyalina Zh.P. Dou & Y. Zhang, Mycosphere 8 (2): 1016 (2017)

Facesoffungi number: FoF04565; Fig. 43

Saprobic on dead leaves of *Pandanus* sp. **Sexual morph** Undetermined. **Asexual morph** *Conidiomata* 197–244 × 134–156 µm ($\bar{x}$ = 222.6 × 148.5 µm, n = 5), scattered to gregarious, immersed, conspicuous on host surface, dark brown, solitary, uniloculate, obpyriform, ostiole central, without papilla, always sporulating on host surface. *Pycnidial wall* 22–55 µm, composed of several layers of thick-walled, pale brown to dark brown cells of *textura angularis*. *Conidiogenous cells* 5–10 × 4–7 µm ($\bar{x}$ = 7 × 5.5 µm, n = 10), holoblastic, phialidic, ovoid, thick-walled, smooth. *Conidia* 20–30 × 10–15 µm ($\bar{x}$ = 23 × 12 µm, n = 30), oval, becoming 1-septate with age, with a dark band at septum, not constricted at septum, initially hyaline to yellow–brown or brown with age, rounded at both ends, guttulate, with longitudinal surface striations from apex to base, without mucilaginous sheath.

Culture characteristics: Conidia germinating on MEA within 12 h. Colonies on MEA, white at first, becoming black with age, circular, with entire edge, raised, velvety, black in reverse, with smooth margin.

Material examined: THAILAND, Chiang Mai Province, Mae Taeng District, Mushroom Research Foundation, on dead leaf of *Pandanus* sp., 16 December 2017, S. Tibpromma P04 (MFLU 18-0023 = HKAS 101792); living culture, MFLUCC 18-0110.

GenBank numbers LSU: MH260300; ITS: MH275067; SSU: MH260341; TUB2: MH412743.

Notes: Our isolate similar with *Lasiodiplodia hyalina* Z.P. Dou & Ying Zhang which found from cankered stems of *Acacia confuse* and unidentified woody plant (Dou et al. 2017). *Lasiodiplodia hyalina* has cylindrical to ampulliform conidiogenous cells and ellipsoid to ovoid, 24 × 13.6 µm conidia (Dou et al. 2017) and similar to our isolate. *Lasiodiplodia hyalina* (MFLUCC 18-0110) is supported by our molecular data (Fig. 42) and this is the first record of *L. hyalina* on dead leaves of *Pandanus* sp.

Lasiodiplodia pandanicola Tibpromma & K.D. Hyde, ***sp. nov***.

Index Fungorum number: IF554473, *Facesoffungi number*: FoF04566; Fig. 44

Etymology: named after the host genus, *Pandanus*.

Holotype: MFLU 18-0011

Saprobic on dead root of *Pandanus* sp. **Sexual morph** Undetermined. **Asexual morph** *Conidiomata* 185–210 × 187–240 µm ($\bar{x}$ = 198 × 211 µm, n = 5), immersed to erumpent through host, visible as black, subglobose to ovoid, solitary, scattered or gregarious, ostiole. *Pycnidial wall* 20–42 µm, composed of several layers of *textura angularis*, dark brown. *Conidiophores* micronematous, reduced to conidiogenous cell. *Conidiogenous cells* 4–6.5 × 5–7 µm ($\bar{x}$ = 5 × 6 µm, n = 5), phialidic, integrated, cylindrical or cylindric-clavate or irregular swollen cell, hyaline, smooth. *Conidia* 14–38 × 9–22 µm ($\bar{x}$ = 27 × 14 µm, n = 30), ellipsoidal to obovate, initially hyaline and aseptate, later becoming brown and 1-septate, thick and rough-walled, guttulate, with longitudinal striations.

Culture characteristics Conidia germinating on MEA within 12 h. Colonies on MEA, initially white–grey and later become black, with dense mycelium, circular, with entire edge, raised, velvety, black in reverse, with smooth margin. Sporulating in culture after 2 months, producing conidia similar in shape to those recorded on natural dead leaves.

Material examined: THAILAND, Phatthalung Province, Mueang Phatthalung District, on dead leaves of *Pandanus* sp., 14 June 2015, B. Thongbai SF15-009 (MFLU 18-0011, **holotype**); ex-type living culture, MFLUCC 16-0265 = KUMCC 16-0158.

GenBank numbers LSU: MH260301; ITS: MH275068; TEF1: MH412774; TUB2: MH412744.

Notes: Phylogenetic analyses indicated *Lasiodiplodia pandanicola* is well-separated with other *Lasiodiplodia* spp. (95% in ML, 1 in BYPP, Fig. 42). *Lasiodiplodia parva* A.J.L. Phillips, A. Alves & Crous share similar conidia to *L. pandanicola*. However, *L. parva* has conidia 16–23.5 × 10.5–13 µm, ovoid (Alves et al. 2008), while *L. pandanicola* has conidia 14–38 × 9–22 µm and ellipsoidal to obovate. Therefore, we propose *L. pandanicola* as a new species. In a BLASTn search on NCBI GenBank, the closest matches of ITS sequence of MFLUCC 16-0265 is *L. theobromae* with 100% identity to the strain Lt-A2 (KX270362), while the closest matches with the TEF1 sequence were with 100% identical *L. theobromae* strain IRNHM-KB64-2 (KU737511) and closest matches with the TUB2 sequence were with 95% identical *Botryosphaeria quercuum* strain CBS177.89 (DQ026404).

Lasiodiplodia pseudotheobromae A.J.L. Phillips, A. Alves & Crous

Facesoffungi number: FoF04567; Fig. 45

Saprobic on dead leaves of *Pandanus* sp. **Sexual morph** Undetermined. **Asexual morph** *Conidiomata* 165–240 × 140–215 µm ($\bar{x}$ = 193.6 × 180 µm, n = 5), scattered to gregarious, immersed, conspicuous on host surface, dark brown, solitary, uniloculate, obpyriform, ostiole

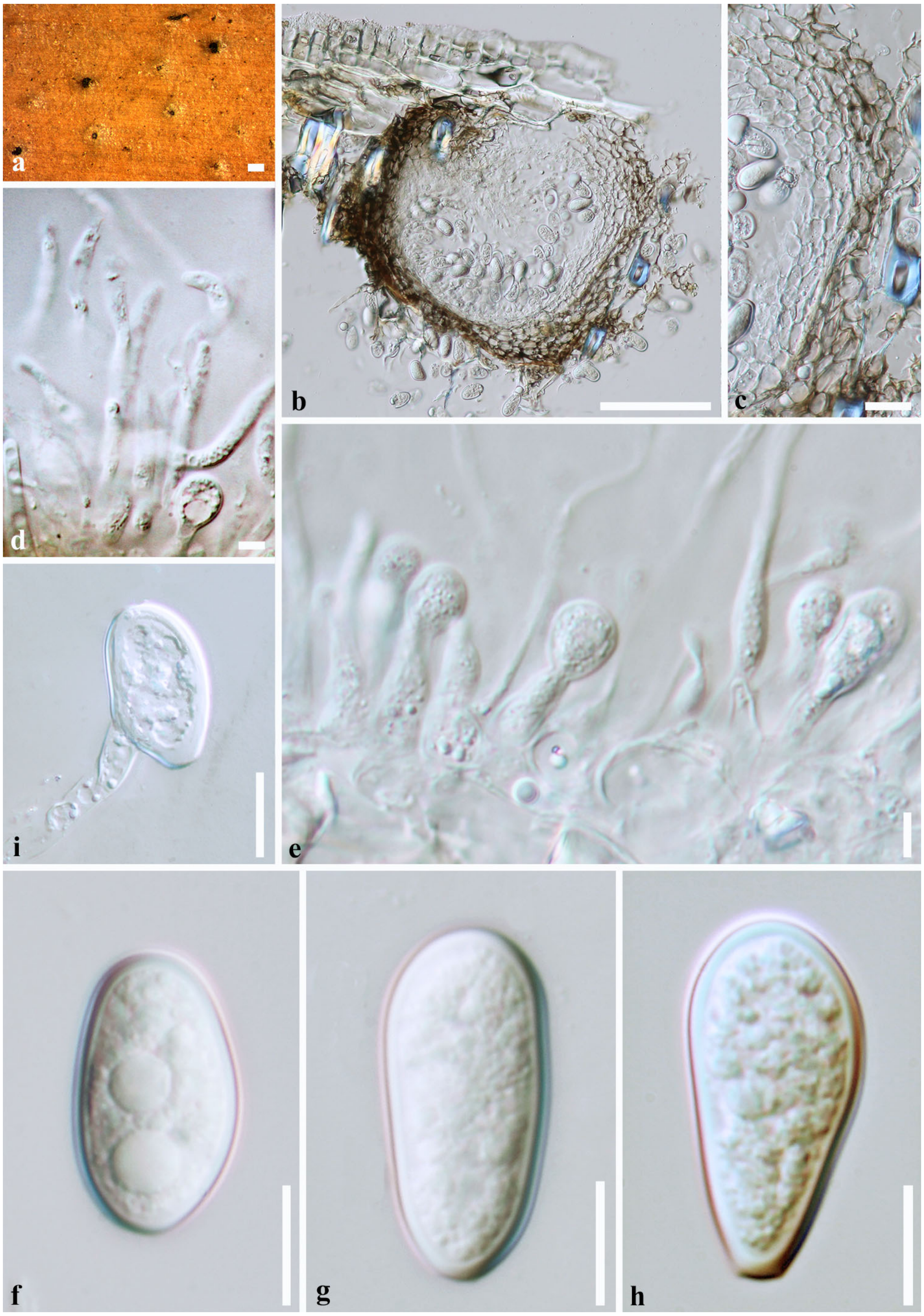


Fig. 42 ***Lasiodiplodia chonburiensis*** (MFLU 16-1877, **holotype**). **a** Appearance of conidiomata on host substrate. **b** Section of conidioma. **c** Section of pycnidial wall. **d, e** Conidiogenous cell producing conidia. **f–h** Conidia. **i** Germinating conidium. Scale bars: **a** = 200 µm, **b** = 100 µm, **c** = 20 µm, **d, e** = 5 µm, **f–i** = 10 µm

in the central, without papilla, always sporulate on host surface. *Pycnidial wall* 10–35 µm, composed of several layers, thick-walled, pale brown to dark brown cells of *textura angularis*. *Conidiogenous cell* 4.5–8 × 2.5–8 µm ($\bar{x}$ = 6 × 5 µm, n = 10), holoblastic, cylindrical, flat at the base, thick-walled, smooth. *Conidia* 20–30 × 10–15 µm ($\bar{x}$ = 24 × 12.4 µm, n = 30), oval to ellipsoid, 1-septate with age, dark band at the septum, not constricted at septum, initially hyaline becoming yellow–brown or brown with age, rounded at apex, guttulate, longitudinal striations from apex to base, without mucilaginous sheath.

Culture characteristics: Conidia germinating on MEA within 12 h. Colonies on MEA, white at first and becoming black with age, circular, with entire edge, raised, velvety, black in reverse, with smooth margin.

Material examined: THAILAND, Chiang Rai Province, Muang District, Mae Fah Luang university, on dead leaf of *Pandanus* sp., 15 December 2017, S. Tibpromma P08

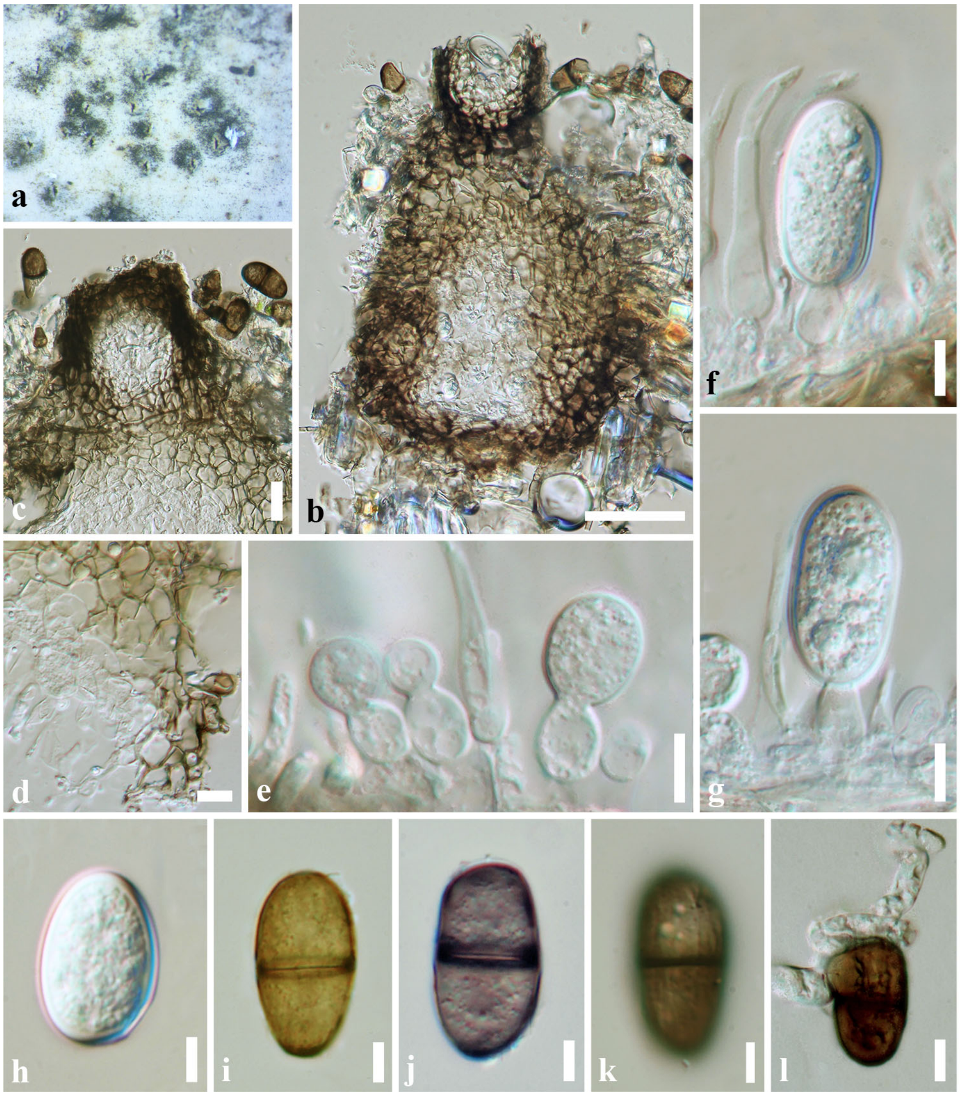


Fig. 43 ***Lasiodiplodia hyalina*** (MFLU 18-0023). **a** Appearance of conidiomata on host substrate. **b** Section of conidioma. **c** Section through ostiole. **d** Pycnidial wall. **e–g** Conidiogenous cell producing conidia. **h–j** Conidia. **k** Conidium with dark longitudinal striations. **l** Germinating conidium. Scale bars: **b** = 50 μm, **c** = 20 μm, **d** = 10 μm, **e–l** = 5 μm

(MFLU 18-0027, HKAS 101796); living culture, MFLUCC 18-0114.

GenBank numbers LSU: MH376724; ITS: MH388351; SSU: MH388318; TEF1: MH388386; TUB2: MH412719.

Notes: In the phylogeny our collection clusters between *Lasiodiplodia pseudotheobromae* (CBS 447.62) and *L. pseudotheobromae* (CBS 116459), first reported on grapevine in Brazil as a trunk pathogen (Correia et al. 2013). Conidial dimensions of our collection are similar to the values given by Alves et al. (2008). This is the first record of *L. pseudotheobromae* on dead leaves of *Pandanus* sp.

Neofusicoccum Crous et al.

Neofusicoccum was erected by Crous et al. (2006) with *N. parvum* (Pennycook & Samuels) Crous, Slippers & A.J.L. Phillips, as the type species. Morphologically the genus is Fusicoccum-like, but it forms a Dichomera-like synanamorph with brown, globose to pyriform conidia (Crous et al. 2006). There are 44 epithets for *Neofusicoccum* are listed in Index Fungorum (2018). *Neofusicoccum* has never been reported on Pandanaceae.

Neofusicoccum pandanicola Tibpromma & K.D. Hyde, ***sp. nov.***

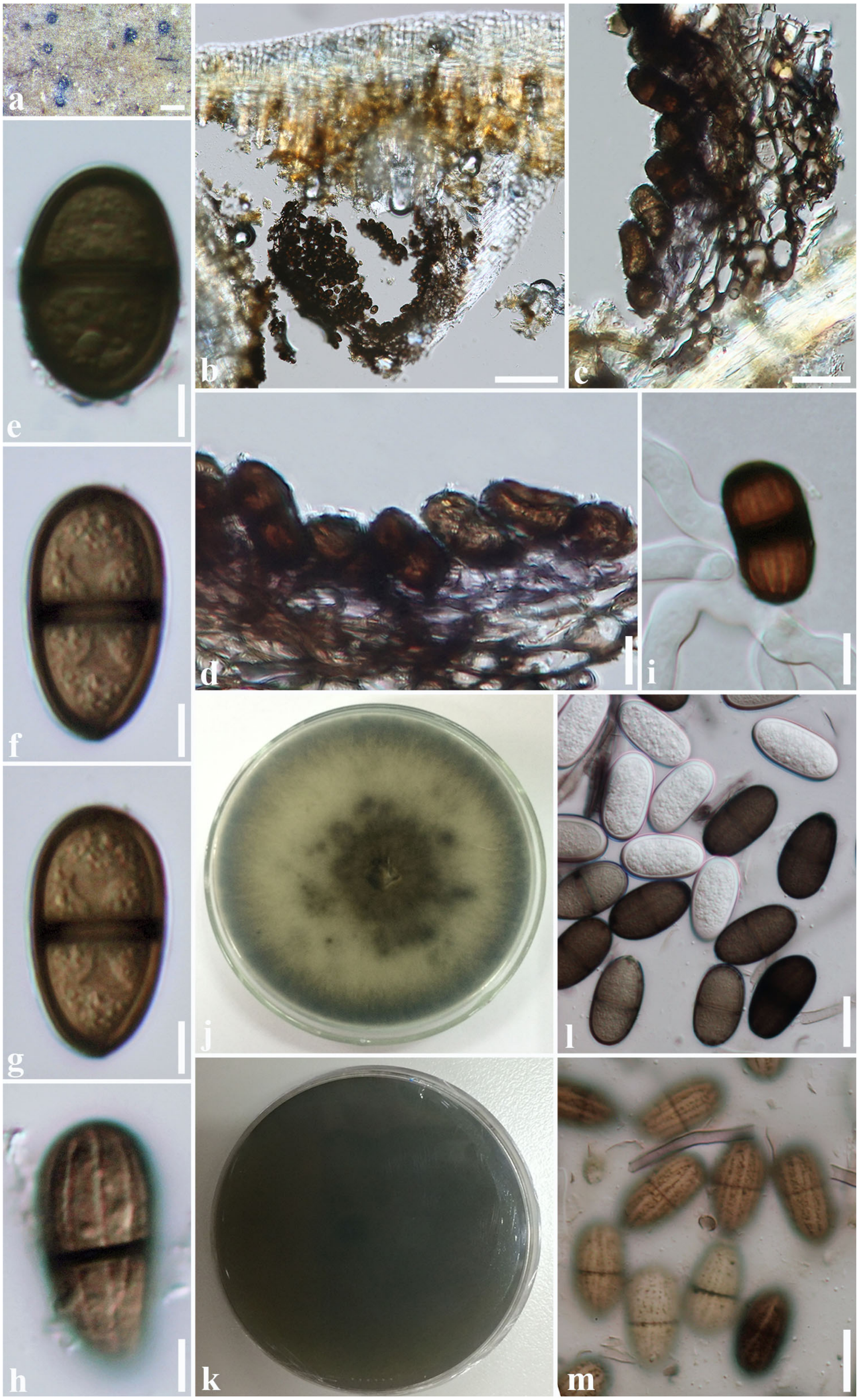
Index Fungorum number: IF554752, *Facesoffungi number*: FoF04568; Fig. 46

Etymology: named after the host genus, *Pandanus*.

Holotype: HKAS 99631

Saprobic on dead leaves of *Pandanus* sp. **Sexual morph** Undetermined. **Asexual morph** *Conidiomata* 180–250 × 280–295 μm ($\bar{x}$ = 225 × 289 μm, n = 5), immersed in the host, solitary or gregarious, brown to dark brown, globose to subglobose, uniloculate, ostiolate. *Pycnidial wall* 33–81 μm, thick-walled, composed of dark brown to pale brown cells of *textura angularis*. *Conidiophores* micronematous, reduced to conidiogenous cell. *Conidiogenous cells* 10–17 × 4–8 μm ($\bar{x}$ = 15 × 5.4 μm, n = 10), monoblastic, holoblastic, integrated, hyaline, smooth. *Conidia* 15–26 × 8–12 μm ($\bar{x}$ = 22 × 10 μm,

Fig. 44 ***Lasiodiplodia pandanicola*** (MFLU 18-0011, **holotype**). **a** Appearance of conidiomata on host substrate. **b** Section of conidioma. **c** Section of pycnidial wall. **d** Conidiogenous cell producing conidia. **e–g** Conidia. **h** Conidium with longitudinal striations. **i** Germinating conidium. **j, k** Colony on MEA from above and below. **l, m** Conidia formed in culture. Scale bars: **a** = 200 µm, **b** = 100 µm, **c, d, l, m** = 20 µm, **e–i** = 5 µm



n = 20), ovoid to ellipsoid, thin-walled, rounded at apex, hyaline, aseptate, rough, without a mucilaginous sheath.

Culture characteristics: Colonies on PDA covering the entire plate after 7 days at room temperature, mycelium velvety and moderately fluffy with an irregular margin, surface initially white and later becoming dark from the middle of the colony and dark in reverse.

Fig. 45 ***Lasiodiplodia pseudotheobromae*** (MFLU 18-0027). **a, b** Appearance of conidiomata on host substrate. **c** Section of conidioma. **d** Section of pycnidial wall. **e–g** Conidiogenous cell producing conidia. **h–j** Conidia. **k** Germinating conidium. **l, m** Colony on MEA from above and below. Scale bars: **c** = 50 µm, **d–k** = 5 µm

Material examined: CHINA, Yunnan Province, Xishuangbanna, on fallen dead and decaying leaves of *Pandanus* sp., 12 November 2016, T. Aluthwaththa XTBG23 (HKAS 99631 **holotype**); ex-type living culture, KUMCC 17-0184 = MFLUCC 17-2270.

GenBank numbers LSU: MH260306; ITS: MH275072; SSU: MH260346; TEF1: MH412778; ACT: MH412740; GPDH: MH412751; CHS-1: MH412746.

Notes: *Neofusicoccum pandanicola* was recovered from fallen dead and decaying leaves of *Pandanus* sp. in China. *Neofusicoccum pandanicola* shares a close phylogenetic affinity to *N. algeriense* Berraf-Tebbal & A.J.L. Phillips (CBS 137504) (Fig. 47). However, *N. algeriense* has fusiform conidia with a subtruncate to bluntly rounded base and 17.6 × 5.6 µm (Berraf-Tebbal et al. 2014), while *N. pandanicola* has ovoid to ellipsoid conidia rounded at both ends and 22 × 10 µm. In a BLASTn search on NCBI

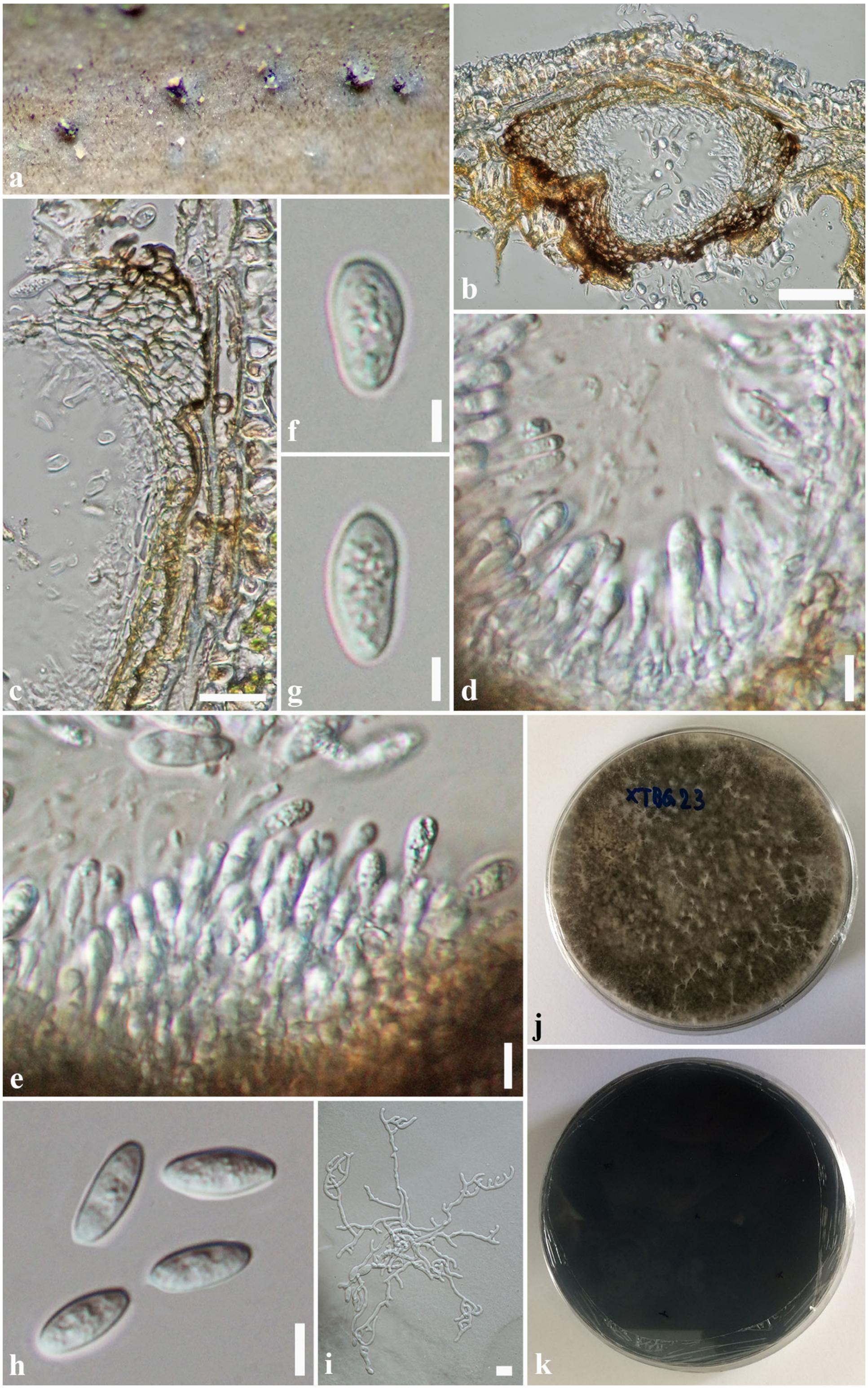


Fig. 46 ***Neofusicoccum pandanicola*** (HKAS 99631, **holotype**). **a** Conidiomata on dead leaves of *Pandanus* sp. **b** Cross section of the conidioma. **c** Conidiomatal wall. **d**, **e** Conidia attached to conidiogenous cell. **f–h** Conidia. **i** Germinating conidium. **j, k** Colony on MEA from above and below. Scale bars **b** = 50 µm, **c, i** = 20 µm, **d, e, h** = 10 µm, **f, g** = 5 µm

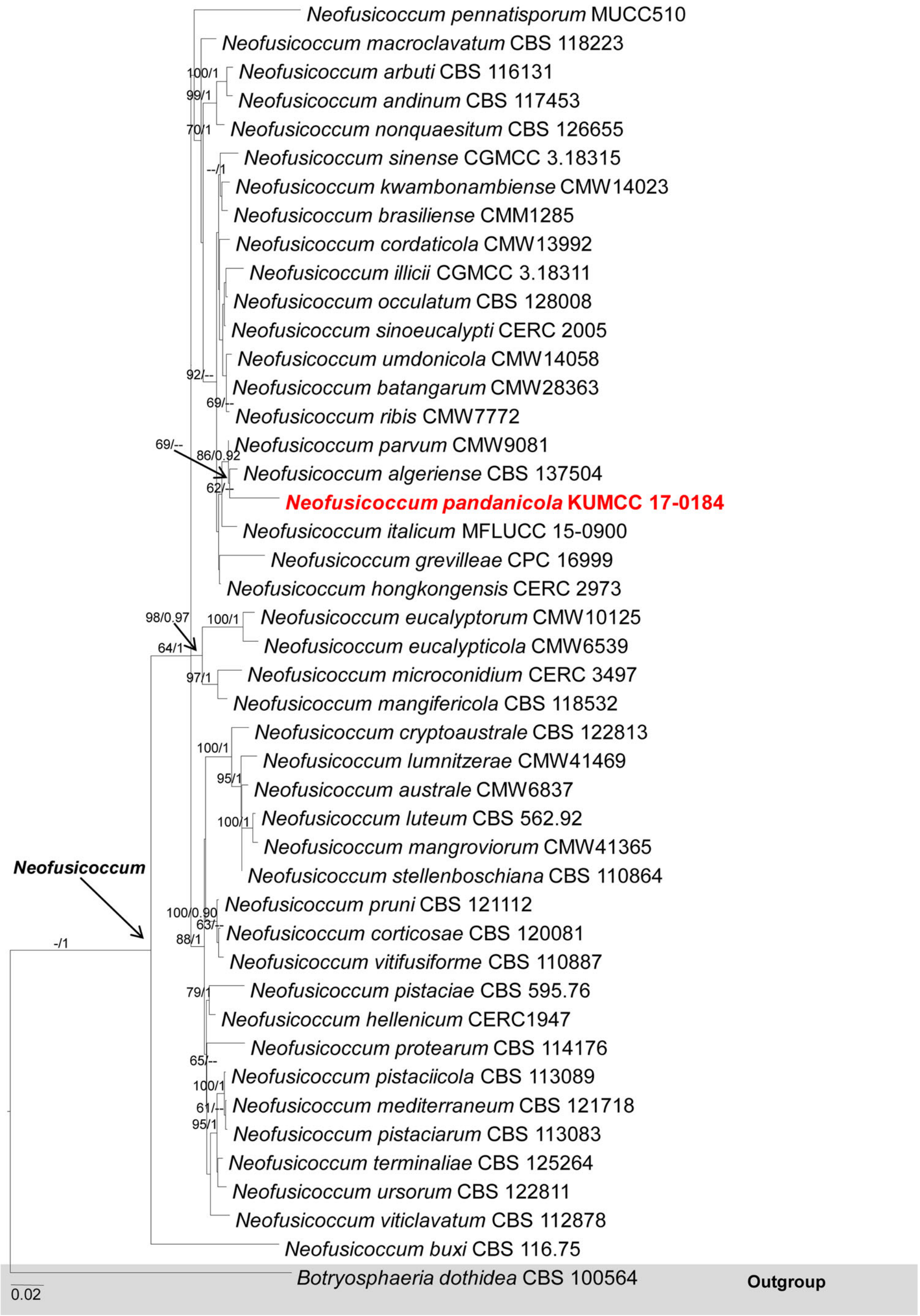


Fig. 47 Phylogram generated from maximum likelihood analysis based on combined ITS, RBP2, TUB2 and TEF1 sequence data. Related sequences were obtained from Dissanayake et al. (2016). Forty-five strains are included in the combined sequence analysis, which comprise 1929 characters with gaps. *Botryosphaeria dothidea* (CBS 100564) is used as the outgroup taxon. Tree topology of the ML analysis was similar to the BYPP. The best scoring RAxML tree with a final likelihood value of − 7606.259934 is presented. The matrix had 592 distinct alignment patterns, with 22.67% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.217869, C = 0.290809, G = 0.275107, T = 0.216215; substitution rates AC = 1.027099, AG = 4.400483, AT = 0.842514, CG = 1.163706, CT = 9.026961, GT = 1.000000; gamma distribution shape parameter α = 0.248719. Bootstrap support values for ML 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 red

GenBank, the closest matches of ITS sequence of KUMCC 17-0184 is *N. parvum* with 100% identity to the strain OMNP10 (KY657475), while the closest matches with the TEF1 sequence were with 94% identical *N. parvum* strain JTTL3 (KP183195).

Pseudofusicoccumaceae Yao Tan & Crous

Pseudofusicoccumaceae was erected by Tao Yang & Crous which is typified by *Pseudofusicoccum* Mohali, Slippers & M.J. Wingf. (Yang et al. 2017). The morphology this family is similar to *Fusicoccum* by differ in conidia tend to be more cylindrical in shape and are encased in a persistent mucoid sheath (Yang et al. 2017).

Pseudofusicoccum Mohali

Pseudofusicoccum was erected by Crous et al. (2006) with *P. stromaticum* (Mohali, Slippers & M.J. Wingf.) Mohali, Slippers & M.J. Wingf. as the type species. *Pseudofusicoccum* resembles *Fusicoccum*, but is distinct in conidia encased in a persistent mucous sheath (Crous et al.

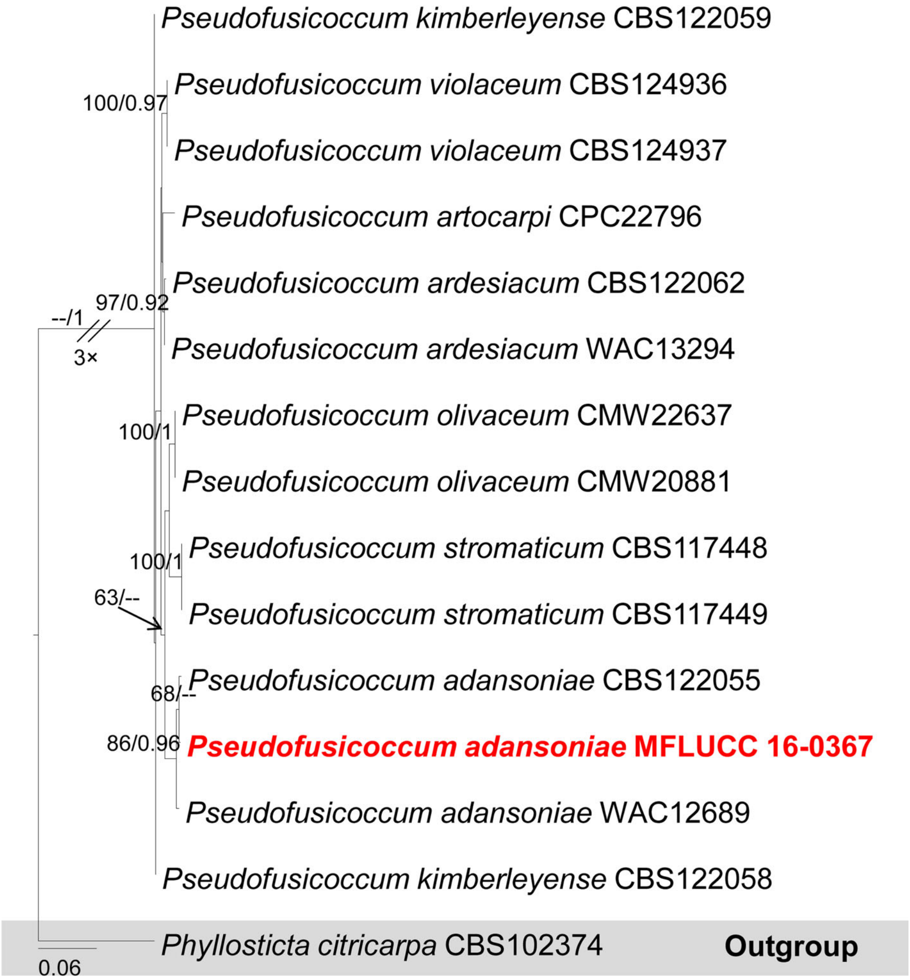


Fig. 48 Phylogram generated from maximum likelihood analysis based on combined ITS and TEF1 sequence data. Related sequences were obtained from Dissanayake et al. (2016). Fifteen strains are included in the combined sequence analysis, which comprise 850 characters with gaps. *Phyllosticta citricarpa* (CBS102374) is used as the outgroup taxon. Tree topology of the ML analysis was similar to the BYPP. The best scoring RAxML tree with a final likelihood value of − 2202.181718 is presented. The matrix had 98 distinct alignment patterns, with 3.38% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.199529, C = 0.289959, G = 0.268934, T = 0.241578; substitution rates AC = 0.835955, AG = 4.035372, AT = 0.562345, CG = 0.351128, CT = 6.074342, GT = 1.000000; gamma distribution shape parameter α = 0.228580. Bootstrap support values for ML 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 red

2006). *Pseudofusicoccum* contains seven epithets are listed in Index Fungorum (2018). *Pseudofusicoccum adansoniae* is the first report of *Pseudofusicoccum* from Pandanaceae.

Pseudofusicoccum adansoniae Pavlic, T.I. Burgess & M.J. Wingf., Mycologia 100 (6): 855 (2008)

Facesoffungi number: FoF04569; Fig. 48

Saprobic on dead fruit of *Pandanus* sp. **Sexual morph** Undetermined. **Asexual morph** *Conidiomata* 75–125 × 108–170 µm ($\bar{x}$ = 92.5 × 134 µm, n = 5), scattered to gregarious, immersed, conspicuous on host surface, dark brown, shiny, solitary, uniloculate, globose to subglobose, ostiolate, without a papilla. *Pycnidial wall* 12–25 µm, composed of several layers, thick-walled, with hyaline to pale brown cells of *textura angularis*. *Conidiogenous cells* 6–13 × 1–3 µm ($\bar{x}$ = 9 × 2.5 µm, n = 20), annellidic, cylindrical, thick-walled, smooth. *Conidia* 12–15 × 6.5–9 µm ($\bar{x}$ = 14 × 8 µm, n = 20), cylindrical to ellipsoid, aseptate, hyaline to subhyaline, rounded at the ends, granular, without a mucilaginous sheath.

Culture characteristics: Conidia germinating on MEA within 12 h. Colonies on MEA, initially white, becoming black with age, dense, circular, with raised entire edge, velvety, black in reverse, with smooth margin.

Material examined: THAILAND, Prachuap Khiri Khan Province, Bang Saphan District, on dead fruit of *Pandanus* sp., 30 July 2015, S. Tibpromma SF15-013 (MFLU 16-0551, HKAS 96275); living culture, MFLUCC 16-0367.

GenBank numbers LSU: MH260317; ITS: MH275083; SSU: MH260357.

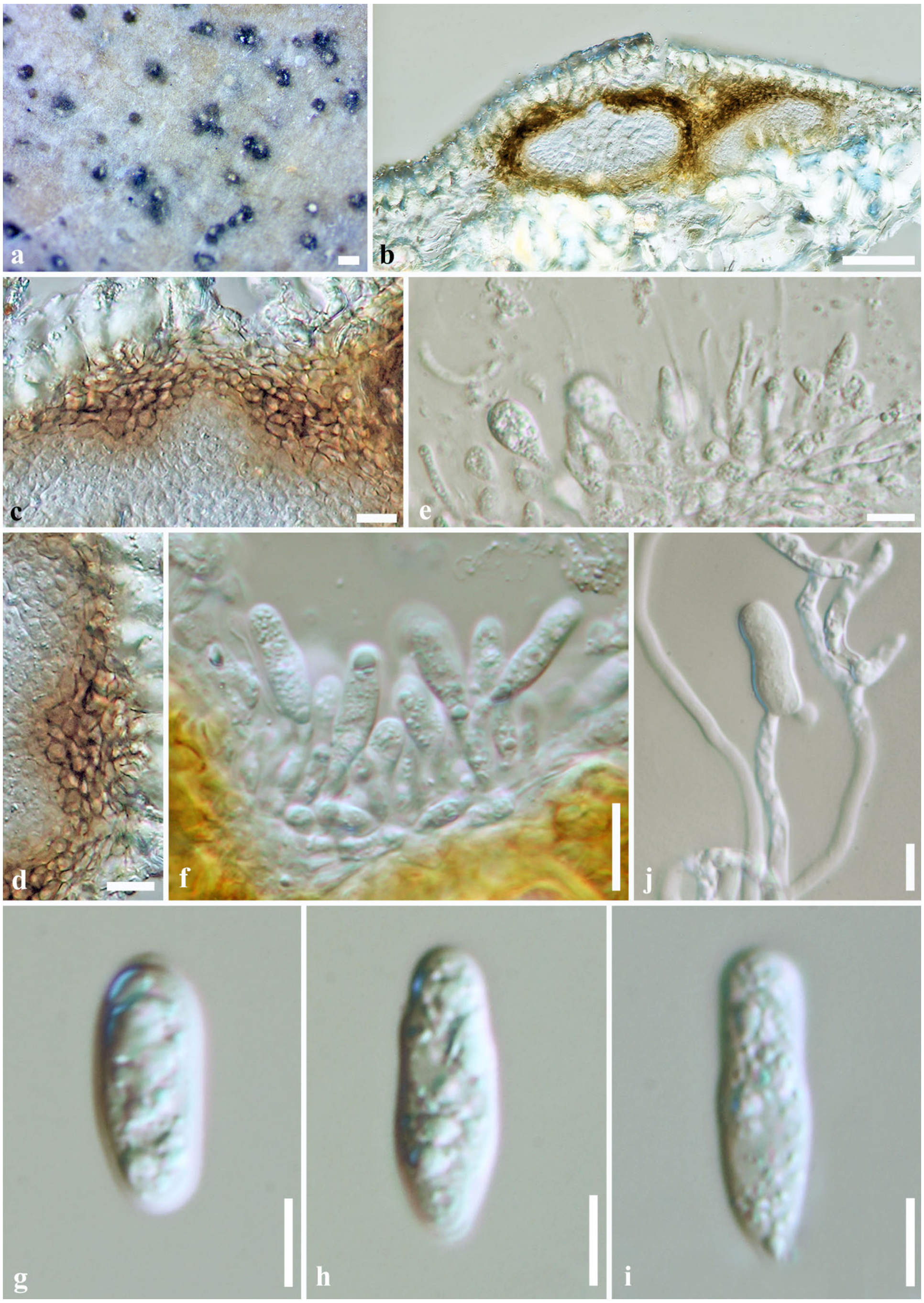


Fig. 49 ***Pseudofusicoccum adansoniae*** (MFLU 16-0551). **a** Appearance of conidiomata on host substrate. **b** Section of conidioma. **c** Section through ostiole. **d** Section of pycnidial wall. **e, f** Conidiogenous cells producing conidia. **g–i** Conidia. **j** Germinating conidium. Scale bars: **a** = 200 µm, **b** = 50 µm, **c–f** = 10 µm, **g–j** = 5 µm

Notes: *Pseudofusicoccum adansoniae* is known from *Acacia synchronica*, *Adansonia gibbosa*, *Eucalyptu*s sp., and *Ficus opposite* (Pavlic et al. 2008) but has never been reported from Pandanaceae. Our isolate (MFLUCC 16-0367) clustered with two *P. adansoniae* isolates from *Adansonia gibbosa* (Fig. 49). The morphology of these isolates is similar with our isolate by having ellipsoid conidia, rounded, smooth with granular, hyaline (Pavlic et al. 2008). In a BLASTn search on NCBI GenBank, the closest matches of ITS sequence of MFLUCC 16-0367 is *P. ardesiacum isolate* with 99% identity to the strain CFE-11 (MH168331), while the closest matches with the TEF1 sequence were with 99% identical *P. adansoniae* strain B0341 (KM006477).

Tubeufiales Boonmee & K.D. Hyde

Tubeufiaceae M.E. Barr.

Tubeufiales was introduced by Boonmee et al. (2014) to accommodate the type family, Tubeufiaceae M.E. Barr. Tubeufiaceae was established in Pleosporales by Barr (1979) with *Tubeufia* as the type genus. The characteristic features of this family are uniloculate, superficial, pigmented ascomata

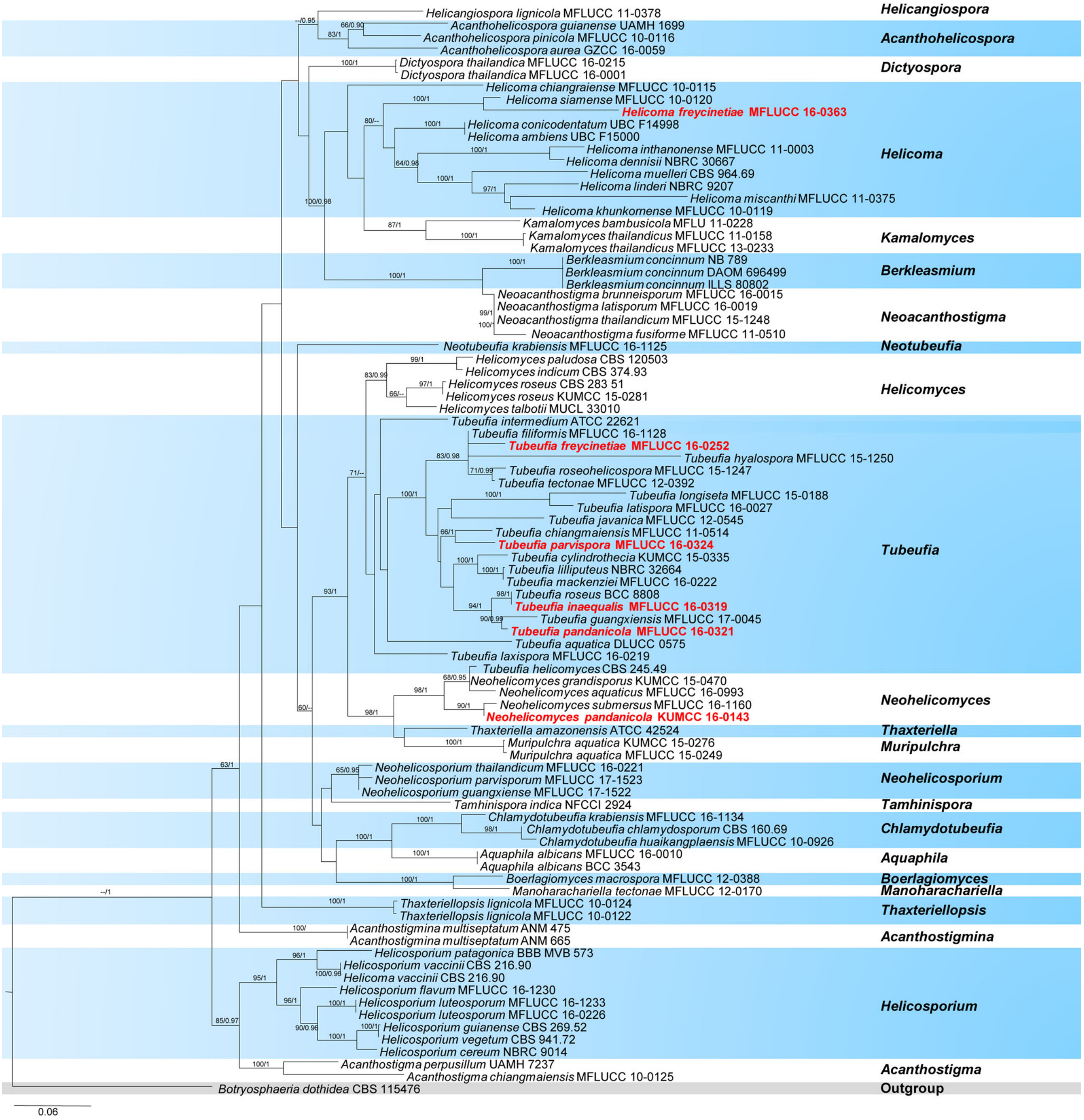
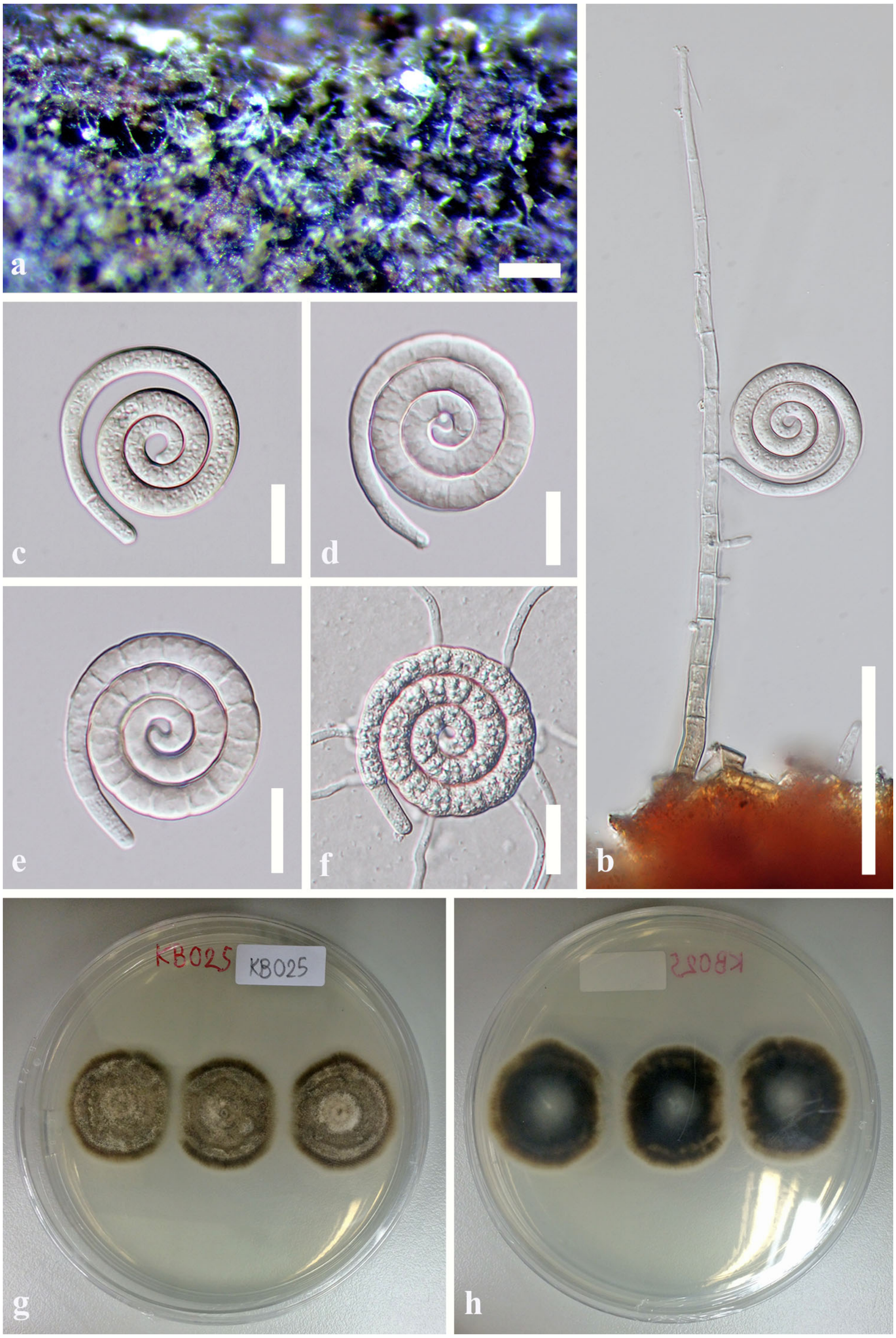


Fig. 50 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU and TEF1 sequence data. Related sequences were obtained from Chaiwan et al. (2017). Eighty-eight strains are included in the combined sequence analysis, which comprise 2216 characters with gaps. *Botryosphaeria dothidea* (CBS 115476) is used as the outgroup taxon. Tree topology of the ML analysis was similar to the BYPP. The best scoring RAxML tree with a final likelihood value of − 21765.784174 is presented. The matrix had 1068 distinct alignment patterns, with 44.44% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.239982, C = 0.242120, G = 0.269480, T = 0.248419; substitution rates AC = 0.754032, AG = 3.061196, AT = 2.077623, CG = 0.823599, CT = 6.542463, GT = 1.000000; gamma distribution shape parameter α = 0.463512. Bootstrap support values for ML equal to or greater than 60% and BYPP equal to or greater than 0.90 are given above the nodes. Newly generated sequences are in red

with hyaline ascospores (sexual morph) and producing helicosporous conidia (asexual morph) (Tsui et al. 2006; Boonmee et al. 2011, 2014). There are 25 genera in the family (Wijayawardene et al. 2018). An updated phylogenetic analysis of Tubeufiaceae is presented (Fig. 50). Recenlty, Lu et al. (2018) provided an update of this family. Five new species and one known species collected on Pandanaceae are described based on morphology and phylogeny support.

Fig. 51 ***Helicoma freycinetiae*** (MFLU 16-1903, **holotype**). **a** Colonies on dead root of *Freycinetia javanica*. **b** Conidiophore, conidiogenous cell and conidia. **c–e** Conidia. **f** Germinating conidium. **g, h** Colonies on MEA from above and below. Scale bars: **a** = 200 µm, **b** = 50 µm, **c–f** = 20 µm



Helicoma Corda

Helicoma was established by Corda with the type species *H. muelleri* Corda. *Helicoma* has relatively short, erect, dark brown, holoblastic conidiogenous cells and helicoid, hyaline, brown to dark brown conidia and is a saprobe (Boonmee et al. 2011, 2014). There are 81 epithets are listed in Index Fungorum (2018). This is the first record of *Helicoma* from Pandanaceae.

Helicoma freycinetiae Tibpromma & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF554502, *Facesoffungi number*: FoF04517; Fig. 51

Etymology: named after the host genus, *Freycinetiae*.

Holotype: MFLU 16-1903

Saprobic on dead root of *Freycinetia javanica*. *Colonies* on natural substratum effuse, subhyaline. *Mycelium* partly immersed in leaf substratum and partly superficial;

composed of branched, septate, subhyaline, smooth, thin-walled hyphae. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Conidiophores* 160–250 × 6–12 µm, subhyaline, light brown at base, macronematous, septate, erect, conical at apex, smooth-walled. *Conidiogenous cells* monoblastic, holoblastic, integrated, denticulate. *Conidia* 44–57 µm, conidial filament 4–9 µm ($\bar{x}$ = 52.5 × 7 µm, n = 20), 205–276 µm long, tightly coiled 3½ times, rounded at apex, solitary, up to 31-euseptate, slightly constricted at septa, subhyaline, smooth-walled, guttulate, without mucilaginous sheath.

Culture characteristics: Conidia germinating on MEA within 12 h. Colonies on MEA, circular, surface rough, edge entire, yellow–brown to dark brown in MEA medium, yellow–brown in the middle, become dark brown at the margin. Mycelium superficial and partially immersed, raised.

Material examined: THAILAND, Phang Nga Province, Thap Put District, on *Freycinetia javanica* Blume, 17 December 2015, S. Tibpromma KB025 (MFLU 16-1903, **holotype**; HKAS 96252, **isotype**); ex-type living culture, MFLUCC 16-0363.

GenBank numbers LSU: MH260295; ITS: MH275062; SSU: MH260337; TEF1: MH412770.

Notes: *Helicoma freycinetiae* is introduced as a new species based on phylogenetic analysis (Fig. 50). It clustered with *H. siamense* Boonmee & K.D. Hyde (MFLUCC 10-0120) but is well-separated with high bootstrap support (100% in ML, 1 in BYPP, Fig. 50). *Helicoma siamense* has partly heavily pigmented conidia, with filaments 7–10 µm wide, coiled 2–3 times and darkened at septa (Boonmee et al. 2014), while *H. freycinetiae* has subhyaline conidia, filaments 4–9 µm wide and coiled 3½ times. In a BLASTn search on NCBI GenBank, the closest matches of ITS sequence of MFLUCC 16-0363 is *H. siamense*with 99% identity to the strain MFLUCC 10-0120 (JN865204), while the closest matches with the RPB2 sequence were with 85% identical *Acanthohelicospora aurea* strain GZCC 16-0060 (MF589911).

Neohelicomyces Z.L. Luo et al.

Neohelicomyces was erected by Luo et al. (2017) with *N. aquaticus* Z.L. Luo, Bhat & K.D. Hyde as type species. Its characteristics are similar to *Helicomyces*. There are three species for *Neohelicomyces* are listed in Index Fungorum (2018). This is the first report of *Neohelicomyces* from Pandanaceae.

Neohelicomyces pandanicola Tibpromma & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF554503, *Facesoffungi number*: FoF04512; Fig. 52

Etymology: named after the host genus, *Pandanus*.

Holotype: HKAS 96202

Saprobic on dead roots of *Pandanus* sp. *Colonies* on substratum superficial, effuse, gregarious, subhyaline to pinkish. *Mycelium* partly immersed in leaf substratum and partly superficial, consisting of branched, septate, subhyaline, smooth, thin-walled hyphae. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Conidiophores* 110–220 × 3–6 µm, subhyaline to pale brown, macronematous, straight, simple or branched, septate, smooth-walled. *Conidiogenous cells* monoblastic, holoblastic, integrated, denticulate. *Conidia* 28–44 µm diam., conidial filament 60–123 µm long, 2–3 µm wide ($\bar{x}$ = 106 × 2.5 µm, n = 20), filament coiled 2½-3½ times when tightly coiled, rounded at both ends, becoming loosely coiled in water, solitary, up to 10-euseptate, not constricted at septa, hyaline, smooth-walled, with numerous guttules, without mucilaginous sheath.

Culture characteristics: Conidia germinating on PDA within 24 h. Colonies on PDA, irregular, surface rough, pale brown to yellow–brown in PDA medium. Mycelium superficial and partially immersed raised.

Material examined: CHINA, Yunnan Province, Xishuangbanna, Nabanhe, on *Pandanus* sp., 27 July 2016, S. Tibpromma NBH02 (HKAS 96202, **holotype**); ex-type living culture, KUMCC 16-0143; Yunnan Province, Xishuangbanna, Nabanhe, on *Pandanus* sp., 2 August 2016, S. Tibpromma NBH07 (HKAS 96207, **paratype**).

GenBank numbers LSU: MH260307; ITS: MH275073; SSU: MH260347; TEF1: MH412779.

Notes: *Neohelicomyces pandanicola* was collected in China on *Pandanus* sp. In the phylogenetic analysis it clustered with *N. submersus* Z.L. Luo, Hong Y. Su & K.D. Hyde, collected on decaying wood from China, but well-separated as a distinct species with high bootstrap support (90% in ML, 1 in BYPP) (Fig. 50). *Neohelicomyces submersus* has hyaline to pale brown colonies with 142.5–207.5 µm long, pale brown conidia and filament coiled 3–3½ times (Luo et al. 2017), while *N. pandanicola* has subhyaline to pinkish colonies conidia 106 × 2.5 µm long, hyaline and filament coiled 2–3½ times. In a BLASTn search on NCBI GenBank, the closest matches of ITS sequence of KUMCC 16-0143 is *N. grandisporus* with 94% identity to the strain KUMCC 15-0470 (KX454173).

Tubeufia Penz. & Sacc.

Tubeufia was erected by Penzig and Saccardo (1898) with *T. javanica* Penz. & Sacc. as the type species, which was described from *Bambusa emarcidis*. There are 60 epithets are listed in Index Fungorum (2018). Only one species, *Tubeufia helicoma* has been reported previously on Pandanaceae (*Freycinetia banksii*) from New Zealand (Hughes 1978).

Tubeufia freycinetiae Tibpromma & K.D. Hyde, ***sp. nov.***

Fig. 52 ***Neohelicomyces pandanicola*** (HKAS 96202, **holotype**). **a, b** Colonies on dead leaf of *Pandanus* sp. **c, d** Conidiogenous cell and conidia. **e–g** Conidia. **h** Germinating conidium. **i, j** Colonies on MEA from above and below. Scale bars: **c, d** = 20 µm, **e–h** = 10 µm

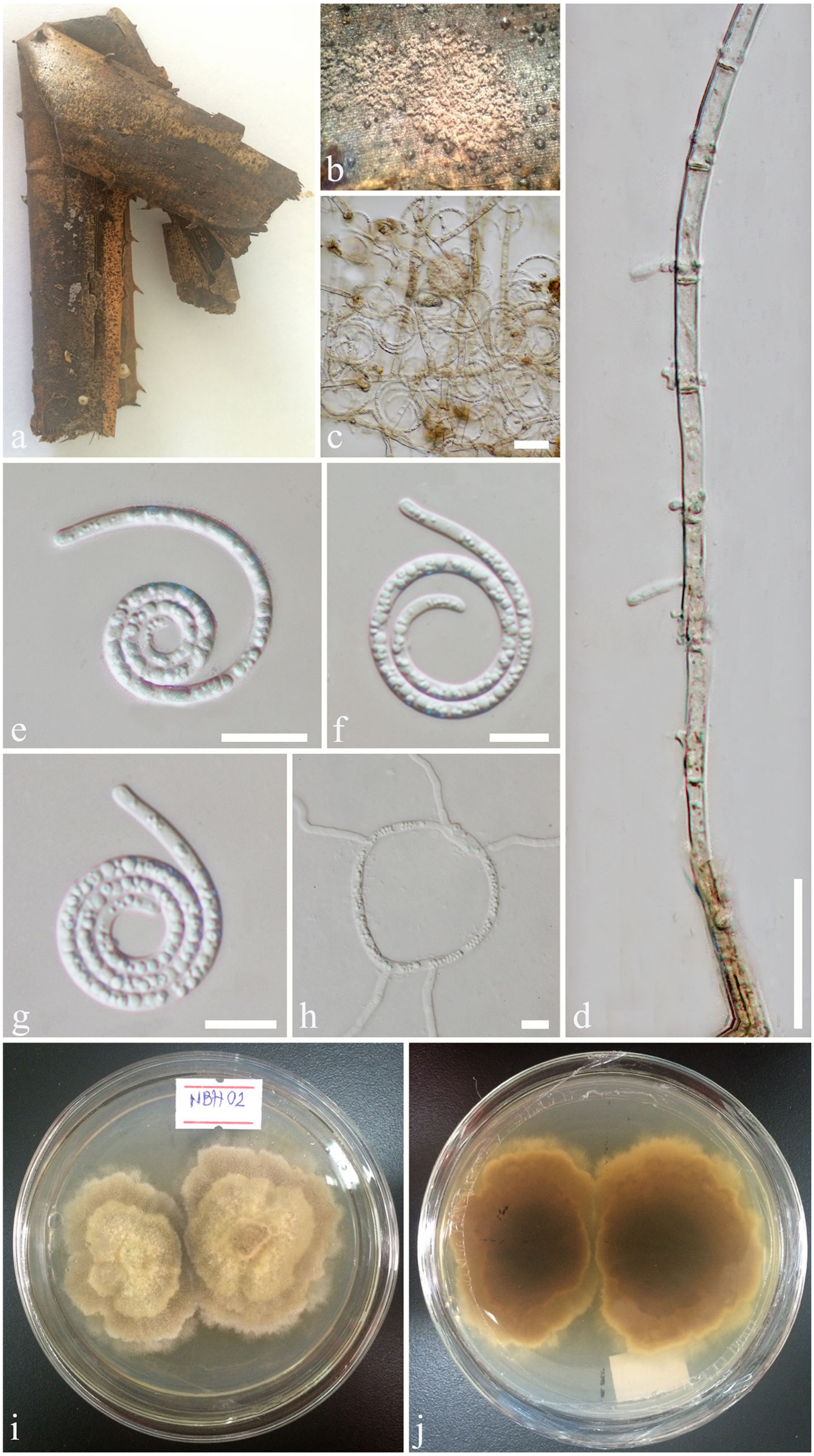


Fig. 53 ***Tubeufia freycinetiae*** (MFLU 16-1897, **holotype**). **a** Colonies on dead roots of *Freycinetia javanica*. **b** Conidiogenous cells and conidium. **c, d** Conidia. **e** Conidium stained with cotton blue reagent. **f** Germinating conidium. **g, h** Colonies on MEA from above and below. Scale bars: **a** = 50 μm, **b–f** = 10 μm

Index Fungorum number: IF554504, *Facesoffungi number*: FoF04513; Fig. 53

Etymology: named after the host genus, *Freycinetiae*.

Holotype: MFLU 16-1897

Saprobic on dead roots of *Freycinetia javanica*. *Colonies* on natural substratum effuse, subhyaline. *Mycelium* partly

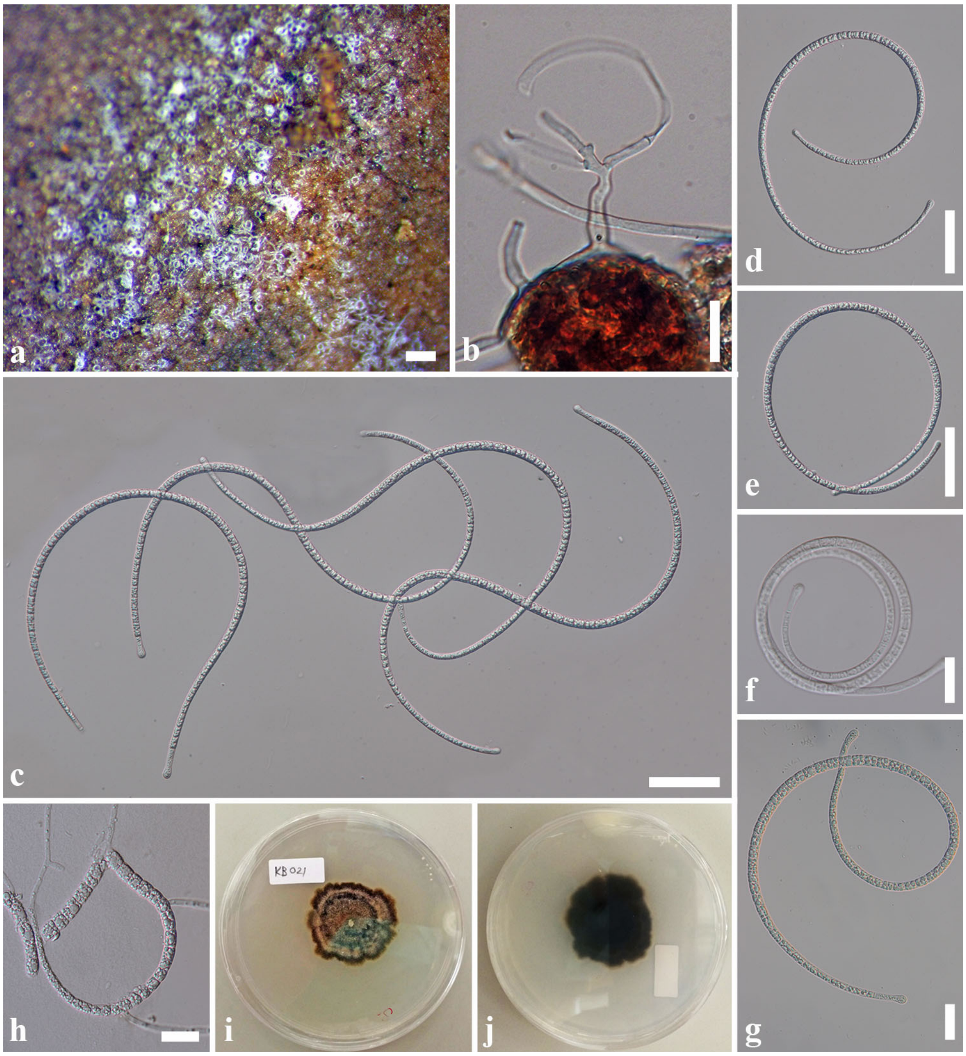


Fig. 54 ***Tubeufia inaequalis*** (MFLU 16-1899). **a** Colonies on dead leaves of *Pandanus* sp. **b** Conidiophores, Conidiogenous cells and conidium. **c–g** Conidia. **h** Germinating conidium. **i, j** Colony on MEA from above and below. Scale bars: **a** = 200 µm, **b–h** = 20 µm

immersed in leaf substratum and partly superficial, consisting of branched, aseptate, subhyaline, smooth, thin-walled hyphae. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Conidiophores* 6–36 × 1.5–5 µm, subhyaline, macronematous, slightly curved, unbranched, smooth. *Conidiogenous cells* monoblastic, integrated, each with single conidium. *Conidia* 24–46 µm diam., conidial filament 105–155 µm long, 3.5–7.5 µm wide ($\bar{x}$ = 35.4 × 6 µm, n = 20), tightly coiled 1½–2½ times, with rounded apical end, up to 33-euseptate, slightly constricted at septa, hyaline, smooth-walled, with guttules, without mucilaginous sheath.

Culture characteristics: Conidia germinating on MEA within 12 h. Colonies on MEA, irregular, surface rough, edge undulate, brown to dark brown in MEA medium. Mycelium superficial and partially immersed raised.

Material examined: THAILAND, Phang Nga Province, Thap Put District, on *Freycinetia javanica* Blume., 17 December 2015, S. Tibpromma KB019 (MFLU 16-1897, **holotype**; HKAS 96246, **isotype**); ex-type living culture, MFLUCC 16-0252.

GenBank numbers LSU: MH260323; ITS: MH275089; SSU: MH260361; TEF1: MH412786.

Notes: *Tubeufia helicoma* have been reported from Pandanaceae (Hughes 1978). *Tubeufia freycinetiae* has hyaline, 105–155 µm long conidiophores with conidia 1½–2½ times coiled and up to 33–euseptate. In the phylogenetic tree, *Tubeufia freycinetiae* formed a clade between *T. hyalospora* Y.Z. Lu, Boonmee & K.D. Hyde. and *T. filiformis* Y.Z. Lu, Boonmee & K.D. Hyde. *Tubeufia freycinetiae* differs from *T. hyalospora* by having 16–33 µm diam conidia with conidial filament 110–225 µm long and 1½–3½ times coiled. Morphologically *Tubeufia freycinetiae* is similar to *T. filiformis* but the latter has pale brown conidiophores and conidia that are 110–225 µm long, tightly coiled 2½–3½ times and multi-septate (Hyde et al. 2016). In a BLASTn search on NCBI GenBank, the closest matches of ITS sequence of MFLUCC 16-0252 is *T. roseohelicospora* with 94% identity to the strain MFLUCC 15-1247 (KX454177), while the closest matches with the TEF1 sequence were

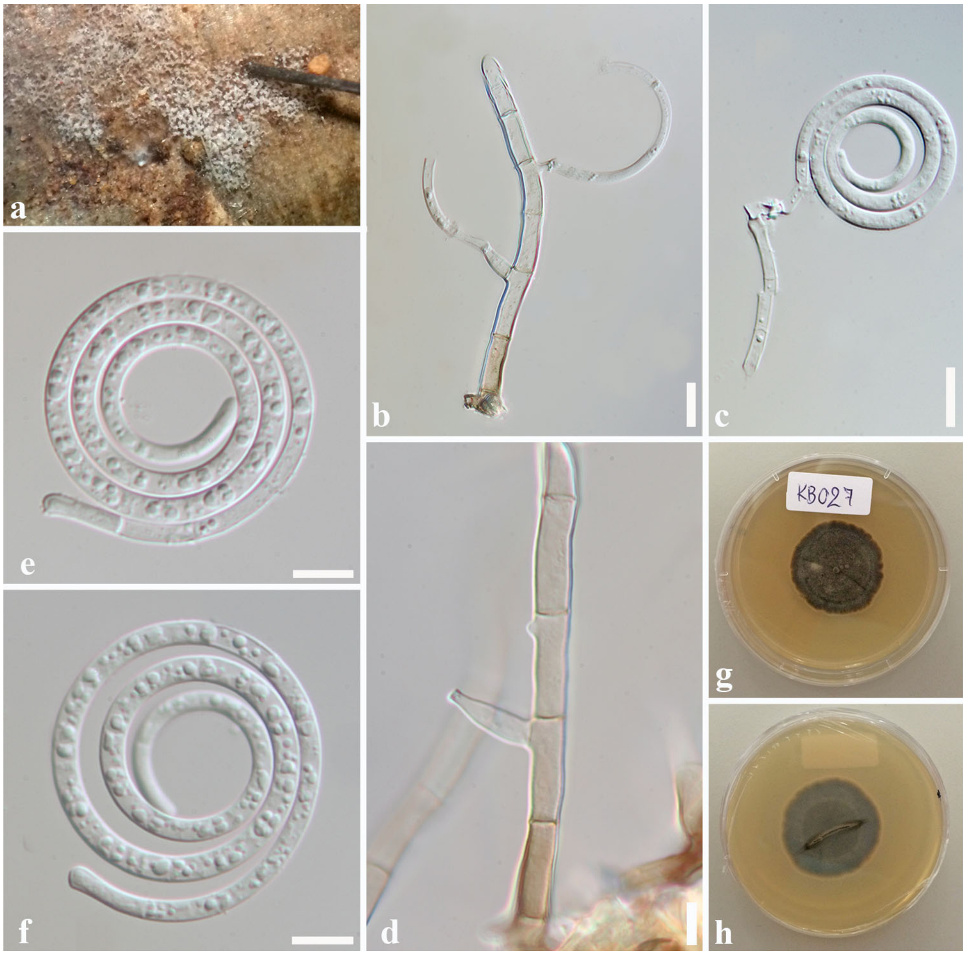


Fig. 55 ***Tubeufia pandanicola*** (MFLU 16-1905, **holotype**). **a** Colonies on dead leaves of *Pandanus* sp. **b** Conidiophores, conidiogenous cells and conidia. **c** Conidiogenous cells with conidium. **d** Conidiophores and conidiogenous cells. **e, f** Conidia. **g, h** Colony on MEA from above and below. Scale bars: **b–d** = 20 μm, **e, f** = 10 μm

with 95% identical *T. filiformis* strain MFLUCC 16-1135 (KY117032).

Tubeufia inaequalis Y.Z. Lu, J.C. Kang & K.D. Hyde, Fungal Diversity 92: (2018)

Facesoffungi number: FoF04516; Fig. 54

Saprobic on dead leaves of *Pandanus* sp. *Colonies* on natural substratum effuse, subhyaline. *Mycelium* partly immersed in leaf substratum and partly superficial, consisting of branched, septate, subhyaline, smooth, thin-walled hyphae. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Conidiophores* 18–39 × 4–6 μm, hyaline, macronematous, slightly curved, simple or branched, smooth. *Conidiogenous cells* monoblastic, holoblastic, integrated, denticulate. *Conidia* 350–550 × 2.5–8 μm ($\bar{x}$ = 478 × 6 μm, n = 20), coiled 2–2½ times, becoming uncoiled in water, rounded at both ends, solitary, up to 50-euseptate, not constricted at septa, hyaline, smooth-walled, with numerous guttules, without mucilaginous sheath.

Culture characteristics: Conidia germinating on MEA within 12 h. Colonies on MEA, irregular, surface rough, edge curled, grey in the middle with switch yellow–white and dark brown, in MEA medium. Mycelium superficial and partially immersed raised.

Material examined: THAILAND, Krabi Province, Tha Pom Klong Song Num, on *Pandanus* sp., 16 December 2015, S. Tibpromma KB021 (MFLU 16-1899; HKAS 96248); living culture, MFLUCC 16-0319.

GenBank numbers LSU: MH260326; SSU: MH260364.

Notes: *Tubeufia inaequalis* was previously known from on submerged decaying wood in a freshwater stream (Lu et al. 2018). The phylogenetic analysis showed that our isolate groups with *T. inaequalis* MFLUCC 17-0053 (98% in ML, 1 in BYPP, Fig. 50). The morphology of our isolate is similar to that of *T. inaequalis* (MFLUCC 17-0053). This is first report *T. inaequalis* from Pandanaceae.

Tubeufia pandanicola Tibpromma & K.D. Hyde, ***sp. nov***.

Index Fungorum number: IF554506, *Facesoffungi number*: FoF04515; Fig. 55

Etymology: named after the host genus, *Pandanus*.

Holotype: MFLU 16-1905

Saprobic on dead leaves of *Pandanus* sp. *Colonies* on natural substratum effuse, subhyaline. *Mycelium* partly immersed in leaf substratum and partly superficial,

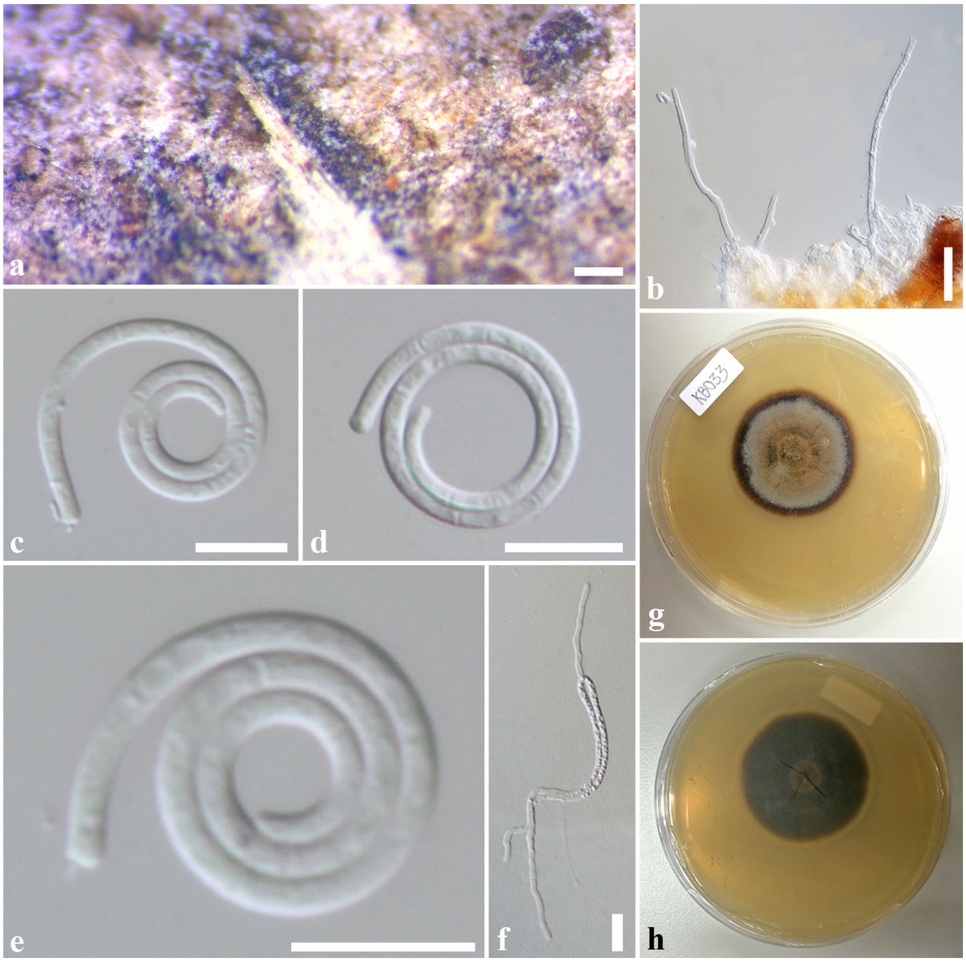


Fig. 56 ***Tubeufia parvispora*** (MFLU 16-1911, **holotype**). **a** Colonies on dead leaves of *Pandanus* sp. **b** Conidiogenous cells with conidiophores. **c–e** Conidia. **f** Germinating conidium. **g, h** Colony on MEA from above and below. Scale bars: **a** = 200 µm, **b, f** = 10 µm, **c–e** = 5 µm

consisting of branched, septate, subhyaline, smooth, thin-walled hyphae. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Conidiophores* 90–145 × 5–6.5 µm, subhyaline at the tip, pale brown at base, macronematous, septate, erect, rounded at apex, smooth. *Conidiogenous cells* 4–15 × 2–5.5 µm ($\bar{x}$ = 9 × 4 µm, n = 10), monoblastic, holoblastic, obclavate, hyaline. *Conidia* 30–45 µm diam., conidial filament 220–300 µm long, 3–4.5 µm wide ($\bar{x}$ = 240 × 4 µm, n = 20), tightly coiled 3–3½ times, rounded at apex, solitary, up to 5-euseptate, not constricted at septa, hyaline, smooth-walled, guttulate, without mucilaginous sheath.

Culture characteristics: Conidia germinating on MEA within 12 h. Colonies on MEA, circular, surface rough, edge entire, yellow–brown to dark brown in MEA medium, yellow–brown in the middle, become dark brown at the margin. Mycelium superficial and partially immersed raised.

Material examined: THAILAND, Krabi Province, Mueang Krabi District, on *Pandanus* sp., 14 December 2015, S. Tibpromma KB027 (MFLU 16-1905, **holotype**; HKAS 96254, **isotype**); ex-type living culture, MFLUCC 16-0321.

GenBank numbers LSU: MH260325; ITS: MH275091; SSU: MH260363.

Notes: *Tubeufia pandanicola* has conidiophores that are subhyaline at the apex and pale brown at the base, obclavate conidiogenous cells and up to 5-septate conidia that are 3–3½ times tightly coiled. In phylogeny, *T. pandanicola* clustered with *T. guangxiensis* Chaiwan, Boonmee, Y.Z. Lu & K.D. Hyde with 90% support in ML, and 0.99 in BYPP. However, *T. guangxiensis* has short, pale brown cylindrical conidiophores, with conidia that are 1½–2½ times coiled and up to 50-septate (Chaiwan et al. 2017). In a BLASTn search on NCBI GenBank, the closest matches of ITS sequence of MFLUCC 16-0321 is *T. roseohelicospora* with 86% identity to the strain MFLUCC 15-1247 (KX454177).

Tubeufia parvispora Tibpromma & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF555292, *Facesoffungi number*: FoF04514; Fig. 56

Etymology: "parvispora" referring to smaller-sized conidia compared to the other species of *Tubeufia* genus.

Holotype: MFLU 16-1911

Saprobic on dead leaves of *Pandanus* sp. *Colonies* on natural substratum effuse, subhyaline. *Mycelium* partly immersed in leaf substratum and partly superficial, consisting of branched, septate, subhyaline, smooth, thin-walled hyphae. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Conidiophores* 44–58 × 1–2.5 µm, hyaline, macronematous, straight or slightly curved, unbranched, smooth. *Conidiogenous cells* monoblastic, holoblastic, integrated, denticulate. *Conidia* 11–15 µm, conidial filament 60–66 µm long, 1–2 µm wide ($\bar{x}$ = 63 × 1.5 µm, n = 20), tightly coiled 2–3 times, rounded at both ends, becoming loosely coiled in water, solitary, up to 15-euseptate, not constricted at septa, hyaline, smooth-walled, without guttules and mucilaginous sheath.

Culture characteristics: Conidia germinating on MEA within 12 h. Colonies on MEA, circular, surface rough with wrinkled, edge entire, grey to dark brown in MEA medium. Mycelium superficial and partially immersed raised.

Material examined: THAILAND, Krabi Province, Mueang Krabi District, on *Pandanus* sp., 16 December 2015, S. Tibpromma KB033 (MFLU 16-1911, **holotype**; HKAS 96260, **isotype**); ex-type living culture, MFLUCC 16-0324.

GenBank numbers LSU: MH260324; ITS: MH275090; SSU: MH260362; TEF1: MH412787; RPB2: MH412761.

Notes: In our phylogenetic analysis *Tubeufia parvispora* clustered with *T. chiangmaiensis* Boonmee & K.D. Hyde with high support (66% in ML, 1 in BYPP). Sexual morph is known only for *T. chiangmaiensis* (Boonmee et al. 2014). When we compare nucleotides, there are 44 bp (8.81%) differences in 499 ITS (+5.8S) nucleotides and 34 bp (3.86%) differences in 879 TEF1 nucleotides between *T. chiangmaiensis* and *T. parvispora*. In a BLASTn search on NCBI GenBank, the closest matches of ITS sequence of MFLU 16-1911 is *Helicoma* sp. with 93% identity to the strain BCC 3512 (AY916484), while the closest matches with the TEF1 sequence were with 97% identical *T. mackenziei* strain MFLUCC 16-0222 (KY117031) and the closest matches with the RPB2 sequence were with 90% identical *T. guangxiensis* strain GZCC 16-0041 (MG012016).

Venturiales Y. Zhang ter et al.

Sympoventuriaceae Y Zhang ter et al.

Sympoventuriaceae was erected by Zhang et al. (2011) with *Sympoventuria* Crous & Seifert as the type genus. The family contains the asexual genus as hyphomycetes (Wijayawardene et al. 2017a). More details have been provided by Hyde et al. (2013). There are four genera in the family (Wijayawardene et al. 2018). We introduce the new genus, *Yunnanomyces* collected on Pandanaceae from China.

Yunnanomyces Tibpromma & K.D. Hyde, ***gen. nov.***

Index Fungorum number: IF555334, *Facesoffungi number*: FoF04518

Etymology: named after Yunnan Province, where the fungus was first discovered.

Type species: *Yunnanomyces pandanicola* Tibpromma & K.D. Hyde

Saprobic on decaying leaves or wood in terrestrial habitats. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Colonies* on natural substrate, group together in small groups, blackish to brown, velvety, glistening, conidia readily liberated when disturbed. *Mycelium* immersed in the substrate, composed of branched, septate, hyaline to subhyaline hyphae. *Conidiophores* mononematous, fasciculate, septate, hyaline to subhyaline, branched or unbranched. *Conidiogenous cells* holoblastic, monoblastic, integrated, terminal, determinate, cylindrical, hyaline to subhyaline. *Conidia* acrogenous, globose to broadly oval, flattened, one-cell thick, muriform, yellow–brown to brown.

Notes: *Yunnanomyces* is introduced to accommodate *Y. pandanicola* an asexual fungus with globose to broadly oval, yellow–brown, muriform conidia which was collected from Yunnan Province, China. It is morphologically similar to *Pseudocoleodictyospora*, reported from teak (Doilom et al. 2017), but in the phylogenic analysis *Yunnanomyces* does not cluster with Pseudocoleodictyosporaceae. It differs from *Fusicladium* and *Verruconis* by the presence of conidiophores and conidia (Fig. 57).

Yunnanomyces pandanicola Tibpromma & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF555335, *Facesoffungi number*: FoF04519; Fig. 58

Etymology: named after the host genus, *Pandanus*.

Holotype: HKAS 96206

Saprobic on dead leaves of *Pandanus amaryllifolius*. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Colonies* on natural substrate, in small groups, blackish brown, velvety, glistening, conidia readily liberated when disturbed. *Mycelium* immersed in the substrate, composed of branched, septate, smooth, hyaline hyphae. *Conidiophores* mononematous, fasciculate, septate, hyaline, smooth, unbranched. *Conidiogenous cells* 2.5–5 × 1.5–5 µm ($\bar{x}$ = 4 × 3.4 µm, n = 10), holoblastic, monoblastic, integrated, terminal, determinate, cylindrical, hyaline. *Conidia* 20–25 × 13–18 µm ($\bar{x}$ = 22 × 15 µm, n = 20), acrogenous, solitary, globose to broadly oval, flattened, one-cell thick, thick-walled, muriform, consisting of 9–30 cells, yellow–brown.

Culture characteristics: Conidia germinating on PDA within 24 h. Colonies on PDA, circular, undulate with brown, velvety, floosy.

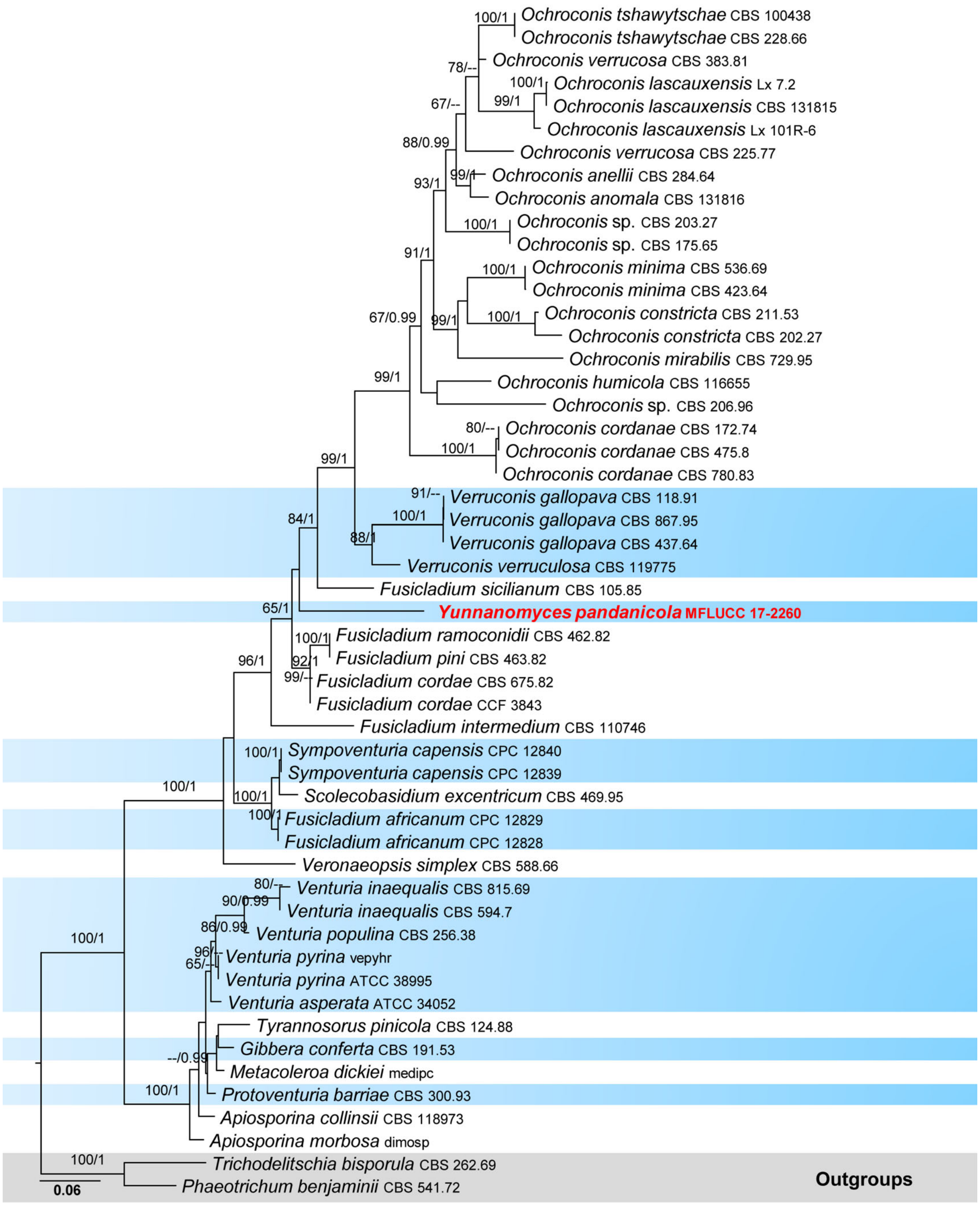


Fig. 57 Phylogram generated from maximum likelihood analysis based on combined LSU, SSU and RPB2 partial sequence data. Fifty-two strains are included in the sequence analysis, which comprise 3001 characters with gaps. Single gene analysis was carried out and compared with each species, to compare the topology of the tree and clade stability. *Phaeotrichum benjaminii* and *Trichodelitschia bisporula* are used as outgroup taxa. Tree topology of the ML analysis was similar to the BYPP. The best scoring RAxML tree with a final likelihood value of − 13481.727487 is presented. The matrix had 1173 distinct alignment patterns, with 45.44% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.255891, C = 0.225681, G = 0.291461, T = 0.226966; substitution rates AC = 1.415398, AG = 3.201141, AT = 1.396732, CG = 1.092537, CT = 7.699345, GT = 1.000000; gamma distribution shape parameter α = 0.487049. Bootstrap support values for ML 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 red

Fig. 58 ***Yunnanomyces pandanicola*** (HKAS 99611, **holotype**). **a** Colonies on dead leaf of *Pandanus amaryllifolius*. **b–e** Conidiogenous cells with conidiophores and conidia. **f** Germinating conidium. **g, h** Colony on MEA from above and below. Scale bars: **b** = 20 µm, **c–f** = 10 µm

Material examined: CHINA, Yunnan Procince, Xishuangbanna, on fallen dead and decaying leaves of *Pandanus amaryllifolius* Roxb., 15 November 2016, T. Aluthwaththa XTBG03 (HKAS 99611, **holotype**); ex-type living culture, MFLUCC 17-2260.

GenBank numbers LSU: MH376743; ITS: MH388369; SSU: MH388333; RPB2: MH412736.

Notes: Based on the multi-gene sequence analyses, isolate MFLUCC 17-2260 clusters between *Fusicladium sicilianum* Koukol. (CBS 105.85) and *F. ramoconidii* Crous & de Hoog (CBS 462.82). However, *Fusicladium* morphologically differs from *Yunnanomyces pandanicola* by forming small sporodochial conidiomata with conidia amero- to phragmosporous (Seifert et al. 2011). In a BLASTn search on NCBI GenBank, the closest matches of LSU sequence of MFLUCC 17-2260 is *Fusicladium ramoconidii* with 95% identity to the strain CBS 462.82 (EU035439), while the closest matches with the ITS sequence were with 90% identical *Fusicladium rhodense* strain CPC 13156 (EU035440).

Class Lecanoromycetes O.E. Erikss. & Winka
Subclass Ostropomycetidae Reeb et al.
Ostropales Nannf.
Stictidaceae Fr.

Stictidaceae was erected by Fries (1849) with *Stictis* Pers. as type genus. Members of this family occur as saprobic discomycetes, but also as lichens, parasites, and endophytes (Gilenstam 1969; Fernández-Brime et al. 2011; Baloch et al. 2013; Aptroot et al. 2014; Jahn et al. 2017). Stictidaceae are characterised by deeply immersed apothecia, long, cylindrical asci and filiform, cylindrical or fusoid, septate ascospores sometimes fragmenting at maturity (Hawksworth et al. 1995). Stictidaceae is still very limited, and contains a small group of generally drought tolerant fungi, which are easily overlooked and rarely collected (Fernández-Brime et al. 2018). There are 25 genera in the family (Wijayawardene et al. 2018). We collected a *Stictis* species from Pandanaceae. Three species of *Stictis* are known on Pandanaceae (Whitton et al. 2012).

Stictis Pers.

Stictis was erected by Persoon (1780) with *S. radiata* (L.) Pers. as type species. The members can be found on many substrates, including decaying leaves, wood, bark, herbaceous stems, grass culms, fern rachises and many other hosts (Sherwood 1977; Johnston 1983; Kirk et al. 2008). *Stictis* contains 345 epithets (Index Fungorum 2018). *Stictis* can also be found on Pandanaceae hosts (*S. carnea*, *S. pandani* and *S. subiculata*) (Whitton et al. 2012).

Stictis pandanicola Tibpromma & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF554510, *Facesoffungi number*: FoF04520; Fig. 59

Etymology: named after the host genus, *Pandanus*.

Holotype: HKAS 96206

Saprobic on dead leaf of *Pandanus* sp. with immersed apothecia, later opening by a pore, with margin white-pruinose on host surface. **Sexual morph** *Ascomata* 350–410 × 520–650 μm ($\bar{x}$ = 386 × 593 μm, n = 5), immersed, globose to subglobose, solitary, without papilla and ostiole, black. *Peridium* 27–46 μm wide, composed several layers of hyaline or colourless cells of *textura epidermoidea*. *Hamathecium* comprising 0.8–1.1 μm, numerous, filiform, hyaline, aseptate paraphyses. *Asci* 160–240 × 7.5–23 μm ($\bar{x}$ = 212 × 17 μm, n = 20), unitunicate, (2–)8-spored, cylindrical to cylindric-clavate, with a short pedicel, apically thick and rounded. *Ascospores* 190–265 × 4–5 μm ($\bar{x}$ = 241 × 4.4 μm, n = 10), overlapping uni- to bi-seriate, hyaline, fusiform, up to 40-septa, constricted at the central septum, smooth-walled, not surrounded by a mucilaginous sheath. **Asexual morph** Undetermined.

Material examined: CHINA, Yunnan Province, Xishuangbanna, Nabanhe, on *Pandanus* sp., 28 July 2016, S. Tibpromma NBH06 (HKAS 96206, **holotype**).

GenBank numbers LSU: MH260319; ITS: MH275085; mt-SSU: MH260359; TEF1: MH412782.

Notes: *Stictis pandanicola* has colonies on host very similar to those of *S. carnea* Seaver & Waterston. However, *S. pandanicola* has biger asci than *S. carnea* (*S. pandanicola* 160–240 × 7.5–23 vs.

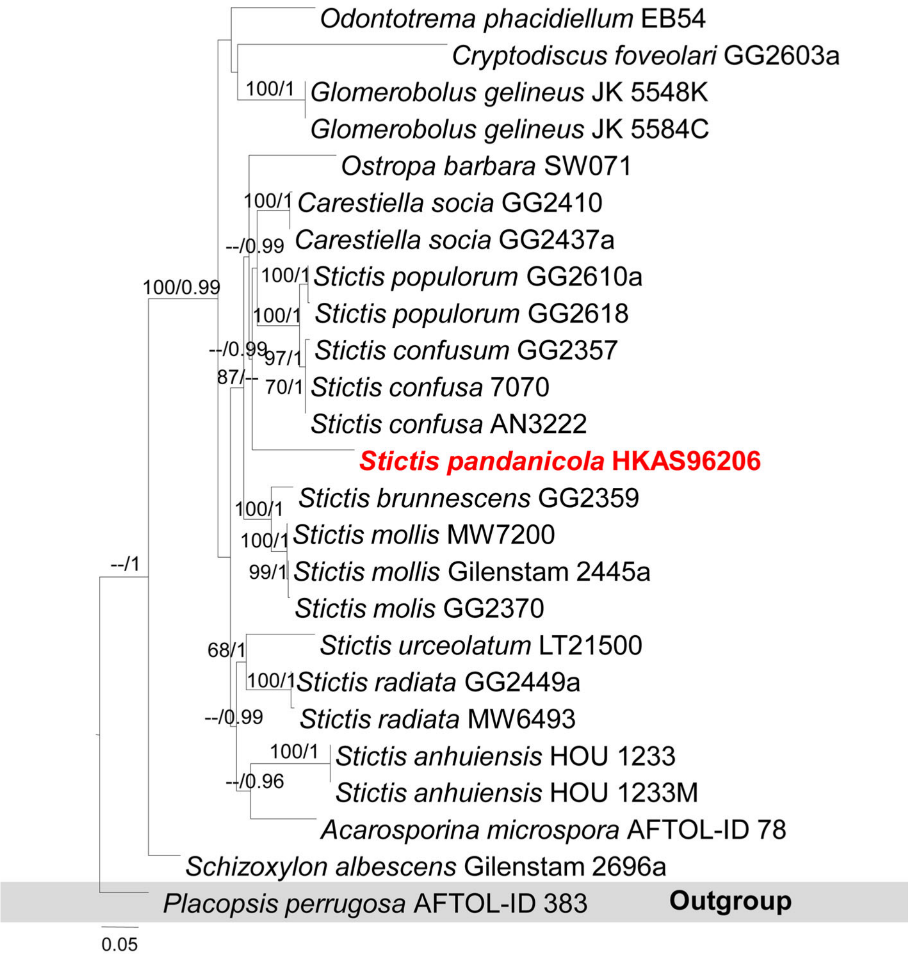


Fig. 59 Phylogram generated from maximum likelihood analysis based on combined LSU, mt-SSU and ITS sequence data. Related sequences were obtained from Li and Hou (2016) and Fernández-Brime et al. (2018). Twenty-five strains are included in the combined sequence analysis, which comprise 2933 characters with gaps. Placopsis perrugosa (AFTOL-ID 383) is used as the outgroup taxon. Tree topology of theML analysis was similar to the BYPP. The best scoring RAxML tree with a final likelihood value of -14421.897248 is presented. The matrix had 1067 distinct alignment patterns, with 30.70% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.287575, C = 0.206010, G = 0.260355, T = 0.246059; substitution rates AC = 1.331310, AG = 2.504484, AT = 1.875317, CG = 1.124721, CT = 5.842916, GT = 1.000000; gamma distribution shape parameter a = 0.267597. Bootstrap support values for ML equal to or greater than 60% and BYPP equal to or greater than 0.95 are given above the nodes. The newly generated sequence is in red

118–165 × 4–5.6 µm *S. carnea*) (Seaver and Waterston 1941). Based on multi-gene phylogenetic analysis, *S. pandanicola* is distinct from other species of *Stictis* (0.99 in BYPP, Fig. 60). The placement of this genus requires resolving through additional collections and phylogenetic data. In a BLASTn search on NCBI GenBank, the closest matches of mt-SSU sequence of HKAS 96206 is *S. confusum* swith 88% identity to accession number DQ401141.

Class Leotiomycetes O.E. Erikss. & Winka

Rhytismatales M.E. Barr ex Minter

Rhytismataceae Chevall. (= Hypodermataceae Rehm; = Cryptomycetaceae Höhn. nom. inval. fide Jaklitsch et al. 2016)

Rhytismataceae was established by Chevallier (1826) with *Rhytisma* Fr. as the type genus and it is the largest family in order Rhytismatales (Johnston 2001). Forty-four genera have been are listed in Rhytismataceae by Lumbsch and Huhndorf (2010), while Wijayawardene et al. (2018) provided 50 genera in Rhytismataceae. *Lophodermium* is the largest genus with more than 100 species accepted (Lantz et al. 2011). A new species of *Terriera*, is introduced here and this is the first record of Rhytismataceae from Pandanaceae.

Terriera B. Erikss.

Eriksson (1970) introduced *Terriera* based on *T. cladophila* (Lév.) B. Erikss. (≡ *Hysterium cladophilum* Lév.). A modern description of *T. cladophila* was provided by Minter (1996). *Terriera* contains 37 epithets (Index Fungorum 2018), but only five species have sequences in GenBank. *Terriera* never have been recorded from Pandanaceae.

Terriera pandanicola Tibpromma & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF554511, *Facesoffungi number*: FoF04521; Fig. 61

Etymology: named after the host genus, *Pandanus*.

Holotype: MFLU 16-1931

Saprobic on dead leaf of *Pandanus* sp. **Sexual morph** *Ascomata* hysterothecial in the surface view, 160–220 × 230–290 µm ($\bar{x}$ = 190 × 264 µm, n = 5), elliptical, conspicuous at the surface, dull, with rounded to subacute ends, the central part of the ascomata strongly raising the surface of the substrate at maturity, opening by a longitudinal split that extends almost whole length of ascoma, rough. *Peridium* 15–37 µm wide, carbonaceous, hyaline cells of *textura globulosa*. *Hamathecium* composed of dense 1–2.6 µm, hyaline, aseptate, cylindrical, long, anastomosing paraphysate hyphae among asci. *Asci* 50–66 × 4–5 µm ($\bar{x}$ = 57 × 4.5 µm, n = 20), 8-spored, unitunicate, cylindrical, apex obtuse to truncate, short-pedicellate, with a J-, apical ring. *Ascospores* 55–78 × 1–2 µm ($\bar{x}$ = 66 × 1.6 µm, n = 10), overlapping bi-seriate, arranged in a fascicle, hyaline, filiform, tapering slightly towards each end, aseptate, guttulate, without a gelatinous sheath or appendages. **Asexual morph** Undetermined.

Material examined: THAILAND, Prachuap Khiri Khan Province, Bang Saphan District, Sai Khu Waterfall, on dead leaf of *Pandanus* sp., 30 July 2015, S. Tibpromma & K.D Hyde SF15-025 (MFLU 16-1931, **holotype**).

GenBank numbers LSU: MH260320; ITS: MH275086; SSU: MH260360; TEF1: MH412783.

Notes: *Terriera pandanicola* is similar to *T. aequabilis* Qing Li & Y.R. Lin. *Terriera. aequabilis* has asci 75–105 × 4.5–5.5 µm, 8-spored, with ascospores 55–78 × 0.8–1 µm and covered by a 0.3–0.5 µm gelatinous sheath (Li et al. 2015), while *T. pandanicola* has asci 50–66 × 4–5 µm with ascospores 55–78 × 1–2 µm and, without a gelatinous sheath or appendages. Based on phylogenetic analysis, *T. pandanicola* is well-separated from other *Terriera* spp. (Fig. 62). *Terriera* has not been previously reported on Pandanaceae. In a BLASTn search on NCBI GenBank, the closest matches of LSU sequence of MFLU 16-1931 is *T. minor* with 98% identity to the strain ICMP 13974 (HM140571).

Class Sordariomycetes O.E. Erikss. & Winka

Subclass Diaporthomycetidae Senan. et al.

Diaporthomycetidae families *incertae sedis*

Distoseptisporaceae K.D. Hyde & McKenzie

Distoseptisporaceae was introduces by Su et al. (2016) with *Distoseptispora* K.D. Hyde, McKenzie & Maharachch as the type genus. Morphologically, members of this family are sporidesmium-like taxa, a grouping that has been shown to be polyphyletic in the class Dothideomycetes (Shenoy et al. 2006; Su et al. 2016), with one family Distoseptisporaceae in Sordariomycetes. No sexual morph is known for this family. We follow Su et al. (2016) and Hyde et al. (2017) and introduce two new species in *Distoseptispora* from Pandanaceae and provide an updated tree for the family (Fig. 63).

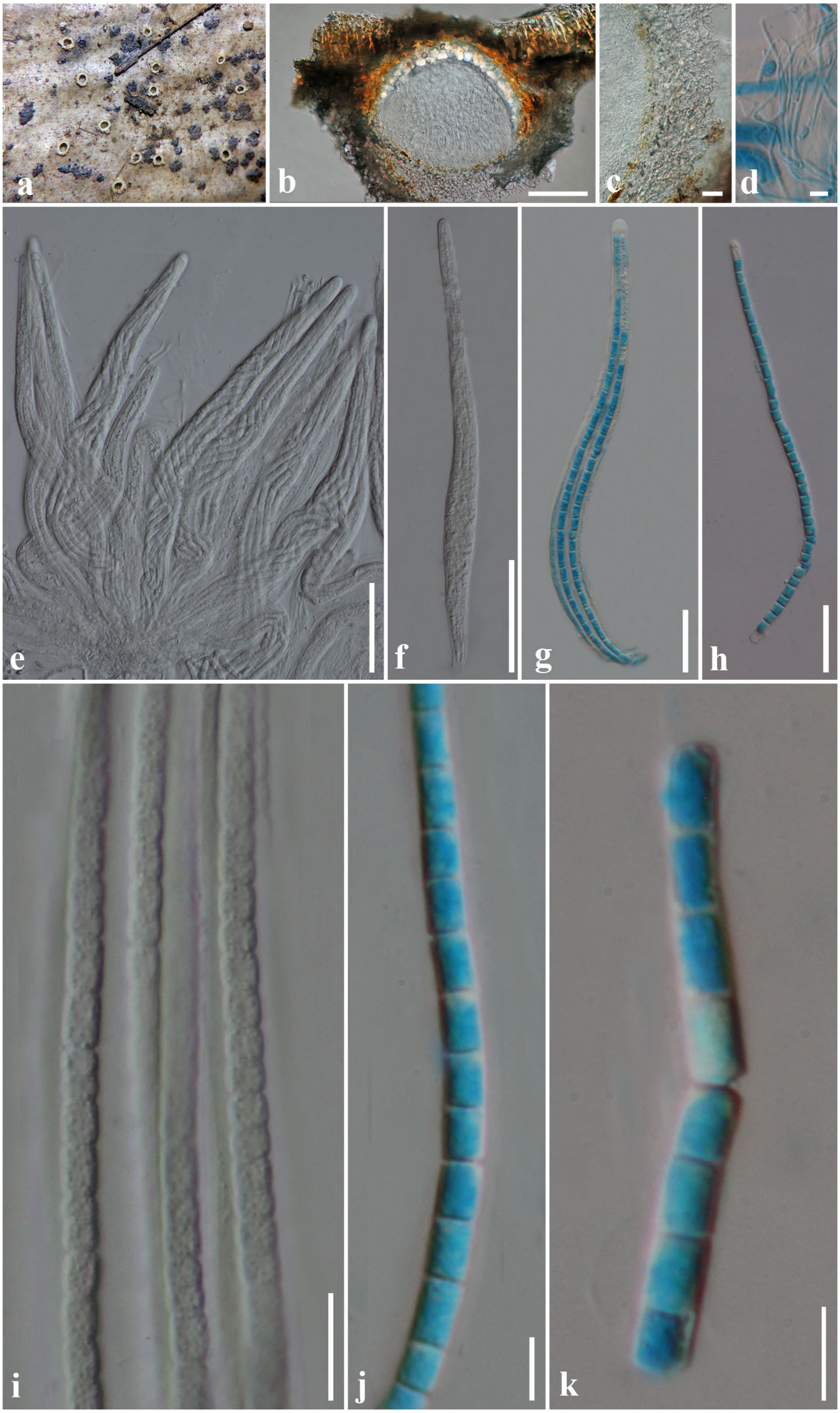
Distoseptispora K.D. Hyde et al.

Distoseptispora was introduced by Su et al. (2016) with *D. aquatica* Z.L. Luo, Hong Y. Su & K.D. Hyde as type species. Members of this genus have dark conidia with a slightly paler, rounded apex, and distinct basal cells. The conidia are of indeterminate length, while the conidiophores are relatively short. No sexual morph has been reported in this genus. *Distoseptispora* contains 13 epithets are listed in Index Fungorum (2018). We introduce two new species of *Distoseptispora* from Pandanaceae.

Distoseptispora thailandica Tibpromma & K.D. Hyde, ***sp. nov***.

Index Fungorum number: IF554553, *Facesoffungi number*: FoF04562; Fig. 64

Fig. 60 ***Stictis pandanicola*** (HKAS 96206, **holotype**). **a** Colonies on dead leaves of *Pandanus* sp. **b** Section of ascoma. **c** Peridium. **d** Hamathecium. **f, g** Asci. **h–i** Ascospores. **j, k** Ascospores stained with cotton blue reagent. Scale bars **b** = 100 µm, **c, f, g** = 20 µm, **d, i–k** = 5 µm, **e** = 50 µm, **h** = 10 µm



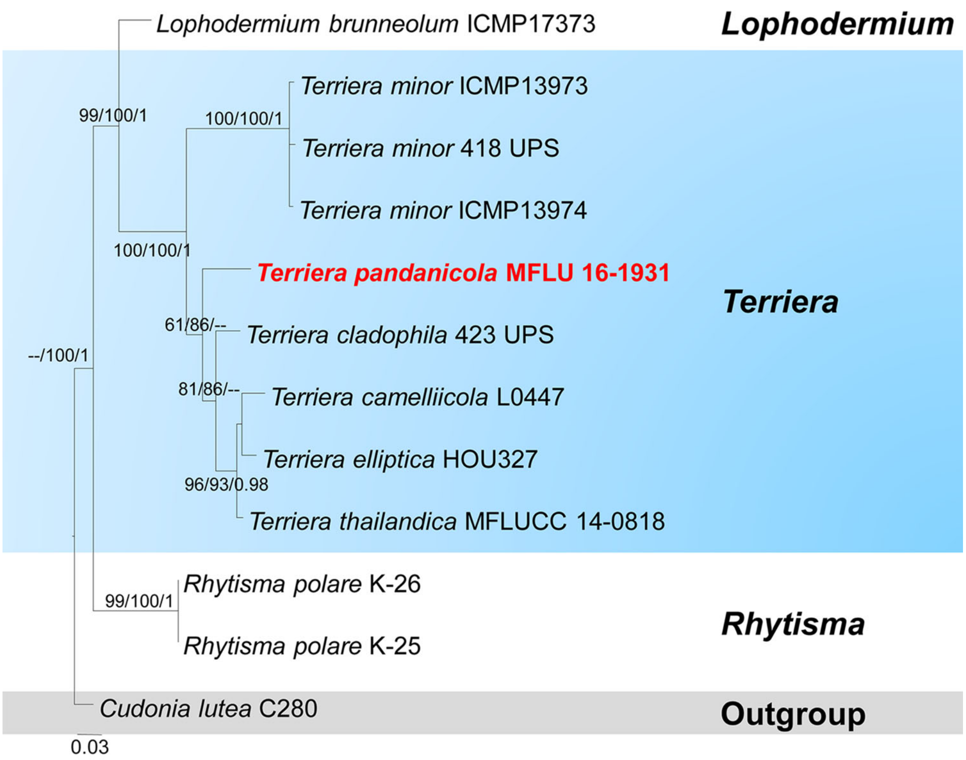


Fig. 61 Phylogram generated from maximum likelihood analysis based on LSU sequence data. Related sequences were obtained from Hyde et al. (2016). Twelve strains are included in the combined sequence analysis, which comprise 1206 characters with gaps. *Cudonia lutea* (C280) is used as the outgroup taxon. Tree topology of the ML analysis was similar to MP and BI. The best scoring RAxML tree with a final likelihood value of − 4022.180007 is presented. The matrix had 289 distinct alignment patterns, with 13.76% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.249070, C = 0.218694, G = 0.310904, T = 0.221332; substitution rates AC = 2.159879, AG = 3.488602, AT = 1.289966, CG = 1.444688, CT = 6.586959, GT = 1.000000; gamma distribution shape parameter α = 0.194634. Bootstrap support values for MP, ML equal to or greater than 60% and BYPP equal to or greater than 0.95 are given above the nodes. The newly generated sequence is in red

Etymology: named after Thailand,where the fungus was first discovered.

Holotype: MFLU 16-0555

Saprobic on dead leaves of *Pandanus* sp. Colonies on the substratum superficial, effuse, hairy or velvety, black. *Mycelium* mostly immersed, branched, septate, smooth, pale brown. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Conidiophores* 15–26 × 3–6 µm, macronematous, mononematous, septate, unbranched, single or in groups, erect, straight or flexuous, smooth, brown to red-brown, cylindrical, thickened at the base. *Conidiogenous cells* monoblastic, integrated, determinate, terminal, red-brown, cylindrical. *Conidia* 130–230 × 13.5–17 µm ($\bar{x}$ = 195 × 14.5 µm, n = 20), acrogenous, solitary, dry, oblong, obclavate, cylindrical or rostrate, straight or curved, truncate at the base, rounded at the apex, 35–52-distoseptate, reddish brown to brown, pale brown towards the apex, thick-walled. *Conidial secession* schizolytic.

Culture characteristics: Conidia germinating on MEA within 12 h. Colonies on MEA, dark grey on the surface, dense, circular, with entire edge, velvety, raised, dark brown from below, with smooth margin.

Material examined: THAILAND, Prachuap Khiri Khan Province, Bang Saphan District, on *Pandanus* sp., 30 July 2015, S. Tibpromma SF15-033 (MFLU 16-0555, **holotype**; HKAS 100838, **isotype**); ex-type living culture, MFLUCC 16-0270 = KUMCC 17-0306.

GenBank numbers LSU: MH260292; ITS: MH275060; SSU: MH260334; TEF1: MH412767.

Notes: *Distoseptispora thailandica* clusters with *D. phangngaensis* J. Yang, Maharachch. & K.D. Hyde but is separated as a distinct species with high bootstrap support (96% in ML, 0.97 in BYPP). Both species were collected in Thailand. *Distoseptispora thailandica* has reddish brown to brown conidia, remain pale brown towards the apex, measuring 130–230 × 13.5–17 µm, while *D. phangngaensis* has dark olivaceous to mid or dark brown conidia, with a subcylindrical basal cell and measuring 165–350 × 14–19 µm (Yang et al. 2018). In a BLASTn search on NCBI GenBank, the closest matches of ITS sequence of MFLUCC 16-0270 is *D. phangngaensis* with 99% identity to the strain MFLU 17-0855 (MF077545), while the closest matches with the TEF1 sequence were with 99% identical *D. phangngaensis* strain MFLUCC 16-0857 (MF135653).

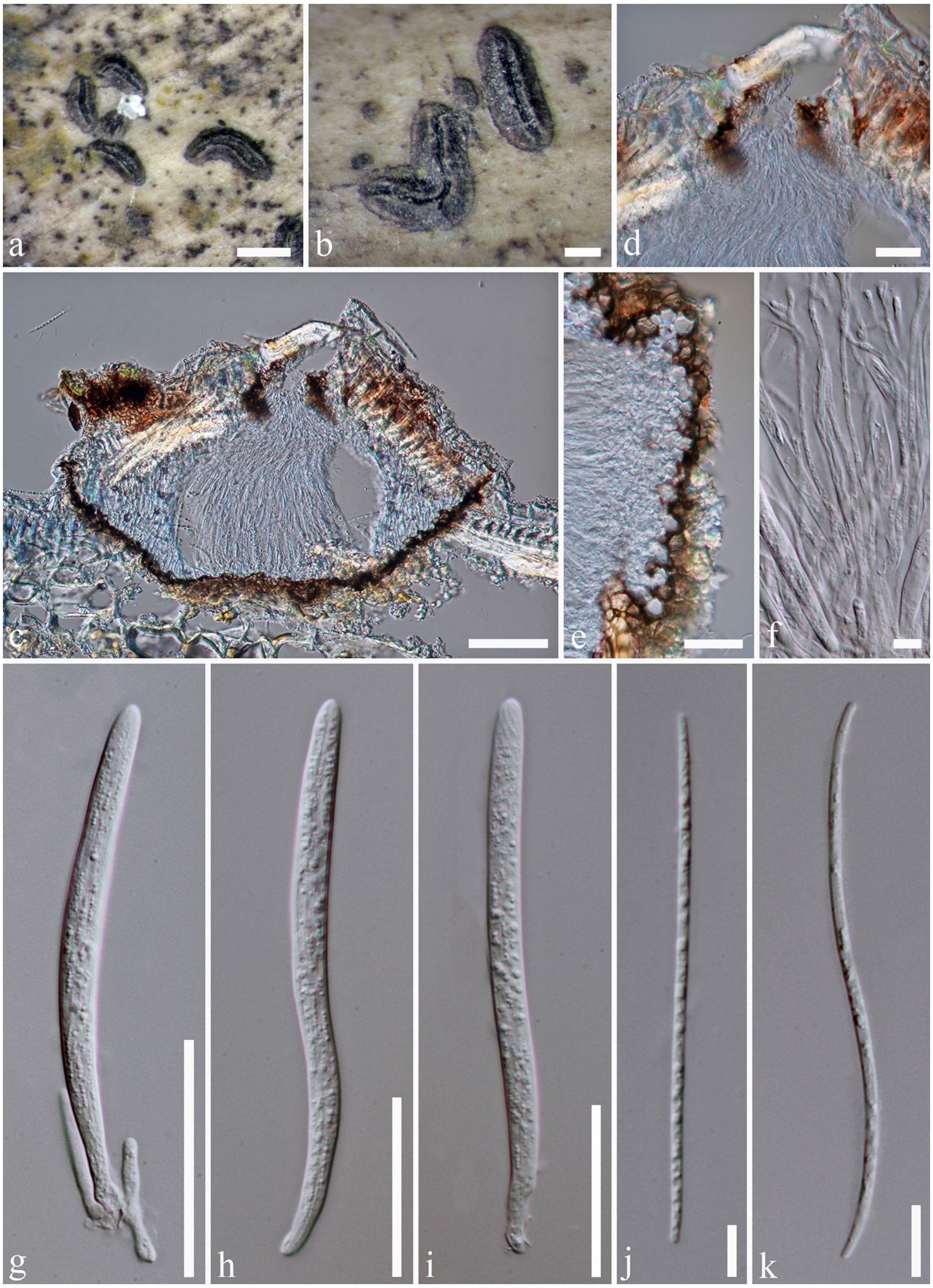


Fig. 62 ***Terriera pandanicola*** (MFLU 16-1931, **holotype**). **a, b** Colonies on dead leaves of *Pandanus* sp. **c, d** Hand section of hysterothecia. **e** Peridium. **f** Hamathecium. **g–i** Asci. **j, k** Ascospores. Scale bars **a** = 500 µm, **b** = 200 µm, **c** = 50 µm, **d, e, g–i** = 20 µm, **f, j, k** = 5 µm

Distoseptispora xishuangbannaensis Tibpromma & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF554554, *Facesoffungi number*: FoF04563; Fig. 65

Etymology: named after the location Xishuangbanna, the fungus was first discovered.

Holotype: HKAS 101809

Saprobic on dead leaf sheaths of *Pandanus utilis*. *Colonies* effuse, dark brown, hairy or velvety. *Mycelium* mostly immersed, composed of branched, septate, smooth, hyaline to pale brown hyphae. **Asexual morph** Hyphomycetous. *Conidiophores* 12–17 × 2–5 µm ($\bar{x}$ = 14.4 × 4 µm, n = 10), macronematous, mononematous, solitary, 2–3-septate, straight or slightly flexuous, erect, slightly tapering distally, truncate at the apex. *Conidiogenous cells* holoblastic, monoblastic, integrated, terminal, brown, determinate, cylindrical. *Conidia* 160–305 × 8–15 µm ($\bar{x}$ = 244 × 11.5 µm, n = 10), acrogenous, solitary, cylindric-obclavate, up to 40-distoseptate, tapering towards apex, green–brown to brown, elongate, straight or slightly curved, rounded at apex, obconically truncate at base, thick-walled, smooth. *Conidial secession* schizolytic (Fig. 66).

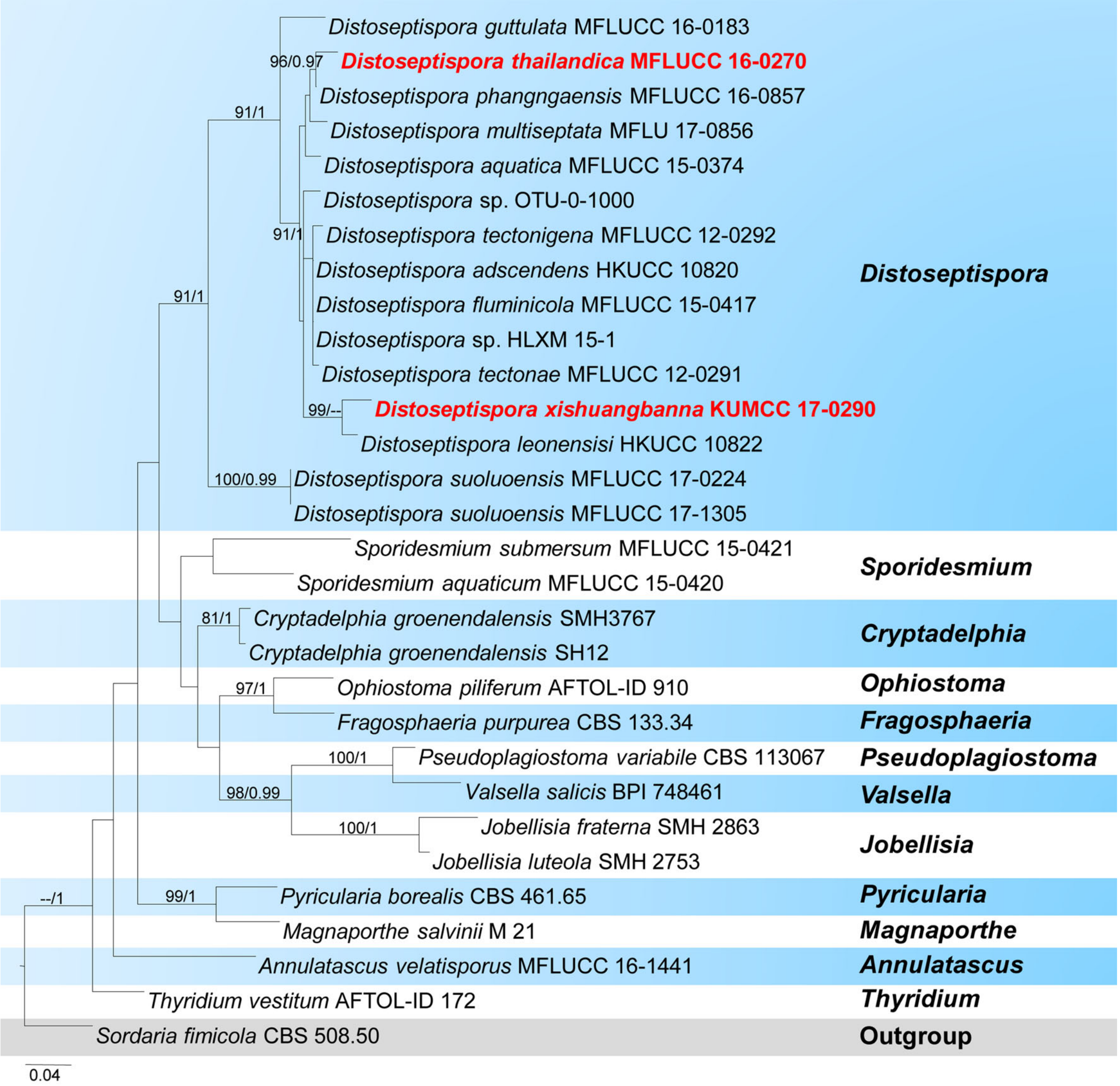


Fig. 63 Phylogram generated from maximum likelihood analysis based on combined ITS and LSU sequenced data. Related sequences were obtained from Su et al. (2016). Thirty strains are included in the combined sequence analysis, which comprise 1507 characters with gaps. *Sordaria fimicola* (CBS 508.50) is used as the outgroup taxon. Tree topology of the ML analysis was similar to the BYPP. The best scoring RAxML tree with a final likelihood value of − 7839.454976 is presented. The matrix had 649 distinct alignment patterns, with 39.30% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.243435, C = 0.245581, G = 0.299666, T = 0.211318; substitution rates AC = 1.626130, AG = 2.358078, AT = 1.438741, CG = 1.405567, CT = 7.750979, GT = 1.000000; gamma distribution shape parameter α = 0.334834. Bootstrap support values for ML equal to or greater than 60% and BYPP equal to or greater than 0.95 are given above the nodes. Newly generated sequences are in red

Culture characteristics: Conidia germinating on PDA within 12 h. Germ tubes produced from both ends. Colonies on PDA reaching 9 cm diam., after 2 weeks at room temperature, white to cream, circular with undulate edge, velvety, dense, dark brown in reverse.

Material examined: CHINA, Yunnan Province, Xishuangbanna, on fallen dead and decaying leaves of *Pandanus utilis* Bory., 28 April 2017, R. Phookamsak XTBG26 (HKAS 101809, **holotype**); ex-type living culture, KUMCC 17-0290; Chiang Mai Province, Mae Taeng District, Mushroom Research Foundation, on *Pandanus* sp., 16 December 2017, S. Tibpromma P03 (MFLU 18-0022, **paratype**).

GenBank numbers LSU: MH260293; ITS: MH275061; SSU: MH260335; TEF1: MH412768; RPB2: MH412754.

Notes: The morphology of *Distoseptispora xishuangbannaensis* is very similar to *Distoseptispora*, *Ellisembia* and *Sporidesmium* (Shenoy et al. 2007; Su et al. 2016). However, based on DNA sequence analysis this strain belongs to *Distoseptispora*. *Distoseptispora xishuangbannaensis* clusters with *D. leonensisi* but is well-separated (99% in ML). There are more than 50 bp (> 4.42%)

Fig. 64 ***Distoseptispora thailandica*** (MFLU 16-0555, **holotype**). **a** Colony on dead leaves of *Pandanus* sp. **b–d** Conidiophores, conidiogenous cells and conidium. **e** Conidiogenous cells with conidiophores. **f** Apex of conidia. **g** Germinating conidium. **h, i** Colony on MEA from above and below. Scale bars: **a–c** = 50 μm, **d, g** = 20 μm, **e, f** = 10 μm

differences in 1130 RPB2 nucleotides between the two species. In a BLASTn search on NCBI GenBank, the closest matches of ITS sequence of KUMCC 17-0290 is *D. fluminicola* with 94% identity to the strain MFLUCC 15-0417 (NR_154041), while the closest matches with the TEF1 sequence were with 97% identical *D. tectonae* strain MFLUCC 12-0291 (KX751710) and the closest matches

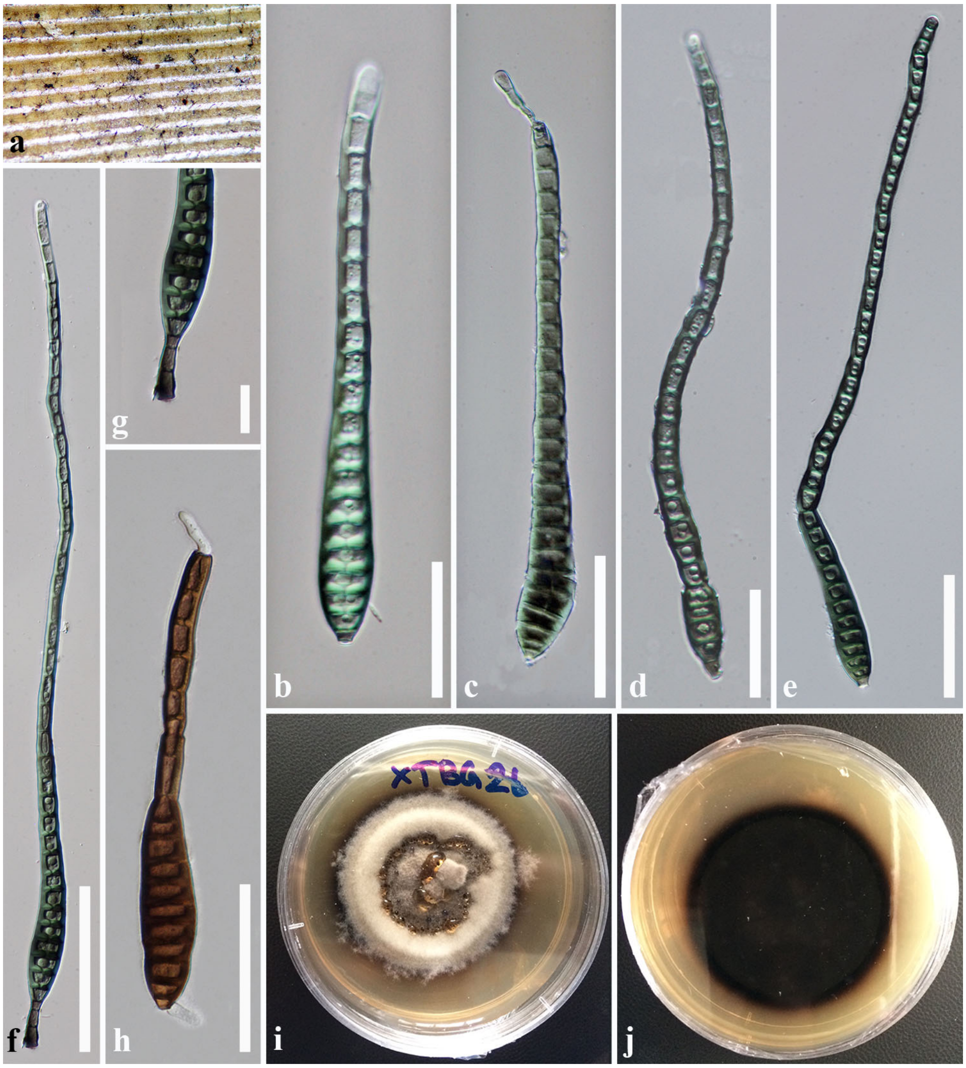


Fig. 65 ***Distoseptispora xishuangbanna*** (HKAS 101809, **holotype**). **a** Colonies on dead leaf of *Pandanus* sp. **b–e** Conidia. **f** Conidiophores, conidiogenous cells and conidium. **g** Conidiophores and conidiogenous cells. **h** Germinating conidium. **i, j** Colony on MEA from above and below. Scale bars **a** = 100 μm, **b–f, h** = 50 μm, **g** = 10

with the RPB2 sequence were with 94% identical *D. multiseptata* strain MFLUCC 16-1044 (MF135644).

Subclass Hypocreomycetidae O.E. Erikss. & Winka

Glomerellales Chadef. ex Réblová et al.

Glomerellaceae Locq. ex Seifert & W. Gams

Glomerellaceae was informally erected by Locquin (1984) as *Glomerella* Spauld. & H. Schrenk as type genus. Uecker (1994) showed that *Colletotrichum* does not belong in the same order as *Phyllachora* based on preliminary sequence-based studies. Thus, Kirk et al. (2001) placed Glomerellaceae in an uncertain position in Sordariomycetidae. Zhang et al. (2006) validated the family Glomerellaceae with a Latin description placing this family in Hypocreomycetidae. Subsequently, Kirk et al. (2008) placed the family in an uncertain position in subclass Hypocreomycetidae. Réblová et al. (2011) validated the order Glomerellales with two new families (Australiascaceae and Reticulascaceae) based on analysis of combined sequence data (ITS, LSU, SSU and RPB2). Jayawardena et al. (2016b) provided a list of accepted species of *Colletotrichum*.

Colletotrichum Corda

Colletotrichum was erected by Corda (1831), for *C. lineola* Corda (Hyde et al. 2009) and comprises endophytes, pathogens and saprobes (Guo et al. 2001; Than et al. 2008; Hyde et al. 2009; Yang et al. 2011). Five species have been recorded on Pandanaceae: *Colletotrichum dematium* (Pers.) Grove, *C. fructicola* Prihast., L. Cai & K.D. Hyde, *C. gloeosporioides* (Penz.) Penz. & Sacc., *C. pandani* Syd. & P. Syd. and *C. pandanicola* Tibpromma S & Hyde KD (Whitton et al. 2012; Tibpromma et al. 2018). There are 869 epithets listed in Index Fungorum (2018).

Colletotrichum pandanicola Tibpromma & K.D. Hyde, Mycokeys 33: 47 (2018)

Facesoffungi number: FoF04534; Fig. 67

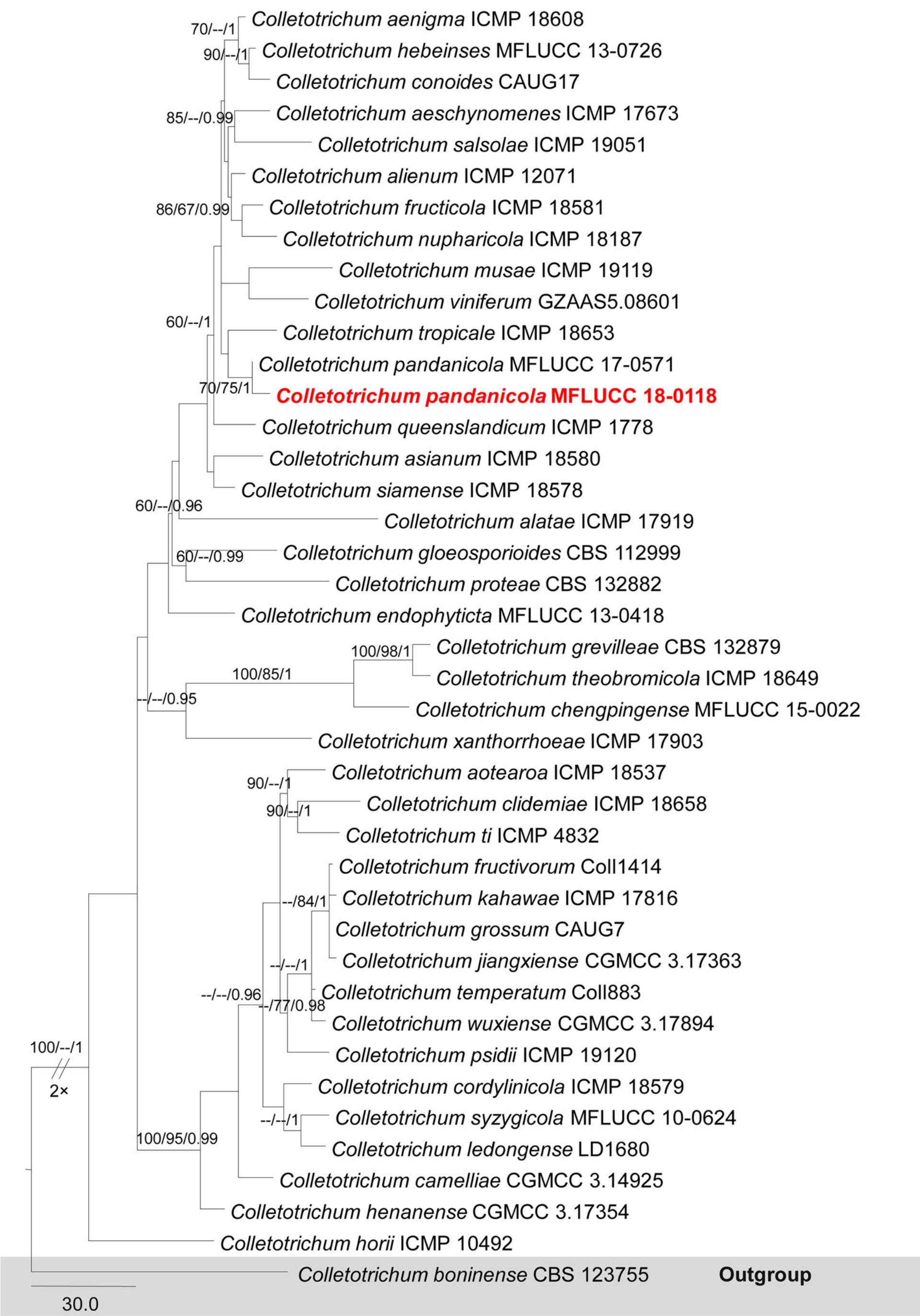


Fig. 66 One of the 10 most parsimonious trees obtained from a heuristic search of combined ITS, GPDH, CHS-1, HIS3, ACT and TUB2 sequence data of taxa from the gloeosporioides species complex. Fourty strains are included in the combined sequence analysis. *Colletotrichum boninense* (MAFF 305972) is used as the outgroup taxon. Tree topology of the MP analysis was similar to the ML and BYPP. The maximum parsimonious dataset consisted of 1840 characters, which 1280 were constant, 251 parsimony-informative and 306 parsimony uninformative. The parsimony analysis of the data matrix resulted in the maximum of 10 equally most parsimonious trees with a length of 961 steps (CI = 0.710, RI = 0.751, RC = 0.533, HI = 0.290) in the first tree. Bootstrap support values for MP, ML equal to or greater than 60%, BYPP equal to or greater than 0.95 are given above or below the nodes. The newly generated sequence is in red

Saprobic on dead leaves of *Pandanus* sp. **Sexual morph** Undetermined. **Asexual morph** *Conidiomata* acervular, without setae, yellow to orange. *Conidiophores* hyaline to subhyaline, smooth-walled, aseptate. *Conidiogenous cells* 7–24.5 × 2–4 µm ($\bar{x}$ = 13 × 3 µm, n = 20), hyaline to subhyaline, smooth-walled, phialidic, cylindrical, with distinct collarette, often extending to form new conidiogenous loci. *Conidia* 13–19 × 4.5–6 µm ($\bar{x}$ = 15.5 × 5.4 µm, n = 40), oblong to cylindrical, hyaline to subhyaline, smooth-walled, aseptate, guttulate.

Culture characteristics: Conidia germinating on MEA within 12 h. Colonies on MEA, circular with entire edge, grey in the central and white at the margin and become black with age, velvety.

Material examined: THAILAND, Phang Nga Province, Thap Put District, on *Pandanus* sp., 20 December 2017, S. Tibpromma P17 (MFLU 18-0036; HKAS 101802); living culture, MFLUCC 18-0118.

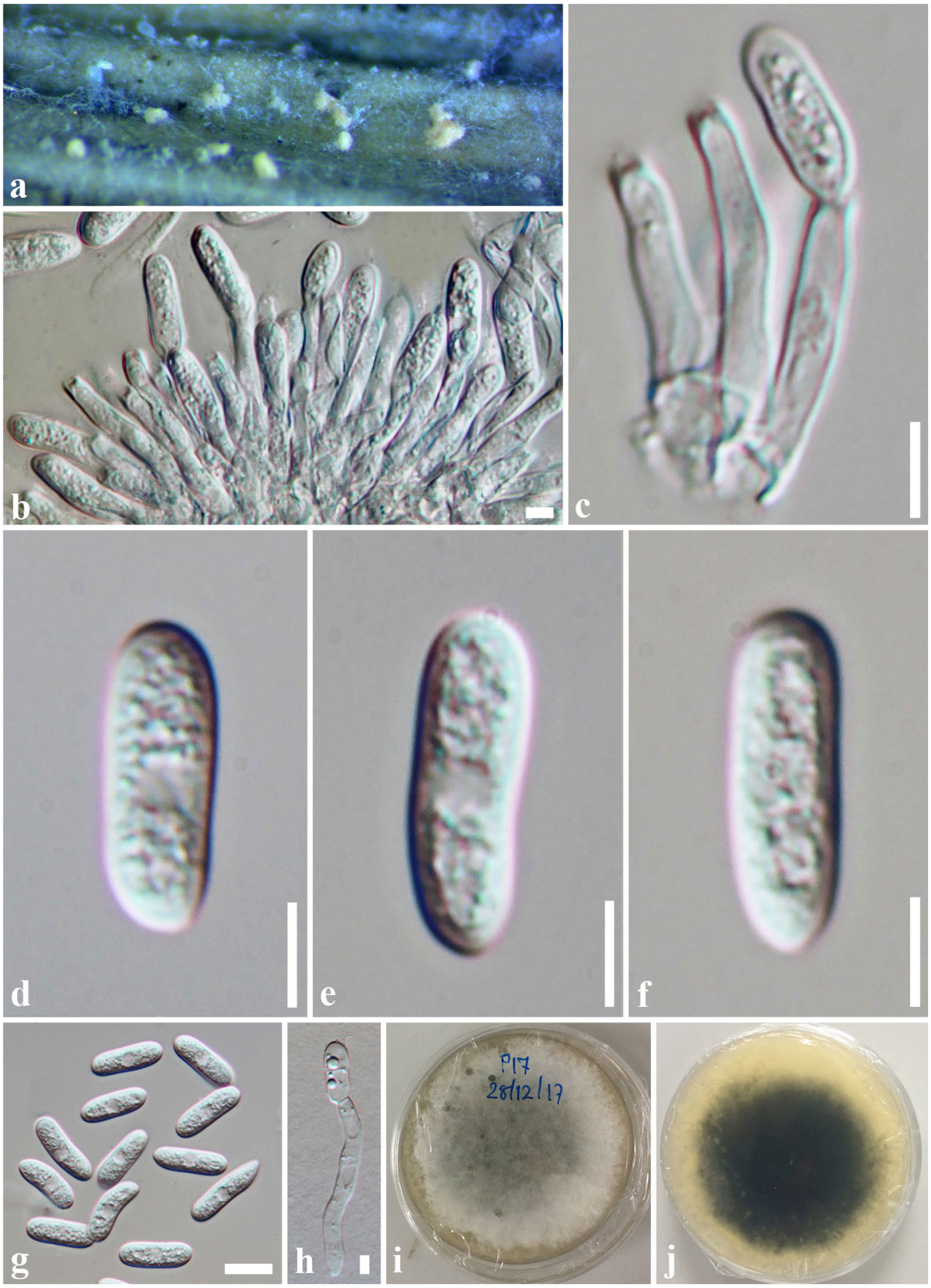


Fig. 67 ***Colletotrichum pandanicola*** (MFLU 18-0036). **a** Colonies on dead leaf of *Pandanus* sp. **b, c** Conidiogenous cells with conidiophores and conidia. **d–g** Conidia. **h** Germinating conidium. **i, j** Colony on MEA from above and below. Scale bars: **b–f, h** = 5 µm, **g** = 10 µm

GenBank numbers LSU: MH376708; ITS: MH388336; SSU: MH388305; TEF1: MH388371; ACT: MH412714; TUB2: MH412718; GPDH: MH412726.

Notes: The gloeosporioides species complex are mainly known as plant pathogens although some can be found as endophytes (Weir et al. 2012; Liu et al. 2015a, b). We followed Jayawardena et al. (2016a, b) and identified our collection as *C. pandanicola. Colletotrichum pandanicola* is known as endophytic fungi which have been isolated from healthy leaves of *Pandanus* sp. in Thailand (Tibpromma et al. 2018). Our isolate is from the same host and from country, differing only in lifestyle. This fact supports the hypothesis that endophytes can change their life styles accordingly (Petrini 1991; Ghimire and Hyde 2004; Photita et al. 2004; Hyde et al. 2006).

Even though there is a short branch length difference in the phylogenetic tree, we were unable to find a reasonable base pair differences between our isolate and *C. pandanicola* type strain. The morphology of the two isolates also appear to be much more similar. Therefore, we prefer to keep this as *C. pandanicola* instead of describing it as a new species.

Malaysiascaceae Tibpromma & K.D. Hyde, ***fam*. *nov*.**

Index Fungorum number: IF554753, *Facesoffungi number*: FoF 04611

Saprobic on dead or decaying leaves, wood in terrestrial habitats. **Sexual morph** Undetermined. **Asexual morph** *Conidiophores* subcylindrical, unbranched, macronematous, erect, flexuous, thick-walled, rounded at apex, guttulate, multi-septate, pale brown to bark brown, pale brown towards slightly tapered apex, smooth-walled. *Conidiogenous cells* enteroblastic, phialidic, subcylindrical, subhyaline, terminal, integrated. *Conidia* solitary, cylindric-ellipsoid, rounded at apex, aseptate, hyaline, smooth-walled, guttulate, with dry in mass.

Type genus: *Malaysiasca* Crous & M.J. Wingf., Persoonia 36: 373 (2016)

Notes: Malaysiascaceae is introduced to accommodate the holomorphic genus *Malaysiasca*. Based on Bayesian analysis of LSU gene data, *Malaysiasca* is related to members of the order Glomerellales genera, *incertae sedis*, Sordariomycetes (Crous et al. 2016a). In the present phylogenetic analysis, *Malaysiasca* forms a well-supported clade (88% in ML, 1 in BYPP, Fig. 68) sister to Australiascaceae and Glomerellaceae. Morphologically Malaysiascaceae is similar to Australiascaceae; the asexual morph of the latter has phialidic conidiogenesis, with hyaline 0(–3)-septate conidia, aggregated in slime or in chains (Réblová et al. 2011). Malaysiascaceae is monotypic comprising only *Malaysiasca phaii*, which was found on leaves of *Phaius reflexipetalus* (Crous et al. 2016a) and now on *Freycinetia javanica*.

Malaysiasca Crous & M.J. Wingf.

Malaysiasca was erected by Crous et al. (2016a) to accommodate *M. phaii* Crous & M.J. Wingf. which first collected from Malaysia. The characteristics of this genus are perithecial ascomata, ellipsoid to oblong asci, hyaline, 1-septate ascospores, while the asexual morph forms a fascicle of long conidiophores, cylindrical phialides producing ellipsoidal to cylindrical-ellipsoid to somewhat clavate conidia in a slimy mass (Crous et al. 2016a).

Malaysiasca phaii Crous & M.J. Wingf., Persoonia 36: 373 (2016)

Facesoffungi number: FoF04538; Fig. 69

Saprobic on dead leaves of *Freycinetia javanica*. *Colonies* on natural substratum effuse, brown to dark brown. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Conidiophores* 160–240 × 4–5 µm, subcylindrical, unbranched, macronematous, erect, flexuous, thick-walled, round at the apex, guttulate, 5–7-septate, pale brown to dark brown, becoming somewhat pale brown towards slightly tapered apex, smooth-walled. *Conidiogenous cells* 50–100 × 4–7 µm ($\bar{x}$ = 69.5 × 5 µm, n = 20), terminal, enteroblastic, phialidic, subcylindrical, subhyaline. *Conidia* 7–24 × 6–10 µm ($\bar{x}$ = 14 × 8 µm, n = 20), solitary, cylindric-ellipsoid, rounded at apex, aseptate, hyaline, smooth-walled, guttulate, produced in a slimy mass.

Culture characteristics: Conidia germinating on MEA within 12 h. Colonies on MEA, irregular, edge undulate, grey to dark grey in MEA medium. Mycelium superficial, flossy and raised.

Material examined: THAILAND, Krabi Province, Khlong Thom District, on dead leaves of *Freycinetia javanica* Blume., 15 December 2015, S. Tibpromma KB032 (MFLU 16-1910, HKAS 96259); living culture, MFLUCC 16-0256 = KUMCC 17-0285.

GenBank numbers LSU: MH260302; ITS: MH275069; SSU: MH260342; TEF1: MH412775.

Notes: In our phylogenetic tree, the Thai strain (MFLUCC 16-0256) clusters with *Malaysiasca phaii* Crous & M.J. Wingf. (CPC 27548). The new strain from *Freycinetia javanica* has 69.5 × 5 µm conidiogenous cells with 14 × 8 µm, cylindrical-ellipsoid, hyaline conidia, without a mucilaginous sheath. The type strain of *M. phaii* has conidiogenous cells 55–80 × 6 µm, which are similar to our strain but the conidia are slightly larger (16–)18–20(–24) × (8–)9–10(–11) µm (Crous et al. 2016a). This is the first record of *Malaysiasca* from Pandanaceae.

Plectosphaerellaceae W. Gams et al.

Plectosphaerellaceae was erected by Zare et al. (2007), with *Plectosphaerella* as the type genus. Hyde et al. (2017) updated phylogeny of this family and eleven genera are recognized in Plectosphaerellaceae. We introduce a new monotypic genus, *Acremoniisimulans* in Plectosphaerellaceae, and a new species of *Musicillium* on Pandanaceae (Fig. 70).

Acremoniisimulans Tibpromma & K.D. Hyde, ***gen*. *nov*.**

Index Fungorum number: IF555329, *Facesoffungi number*: FoF04535

Etymology: refers to the morphology similar to *Acremonium*.

Type species: *Acremoniisimulans thailandensis* Tibpromma & K.D. Hyde

Saprobic on dead or decaying leaves, wood in terrestrial habitats. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Colonies* on natural substrate, erect, straight or slightly flexuous, simple, blackish to brown. *Mycelium* immersed on the substrate, composed of septate, branched or unbranched, pale brown. *Conidiophores* macronematous, mononematous, scattered, brown with pale brown to hyaline apex, smooth, thick-walled, multi-septate, branched or unbranched, straight or slightly flexuous. *Conidiogenous cells* monophialidic, hyaline to subhyaline, cylindrical, slightly. *Conidia* solitary, hyaline or

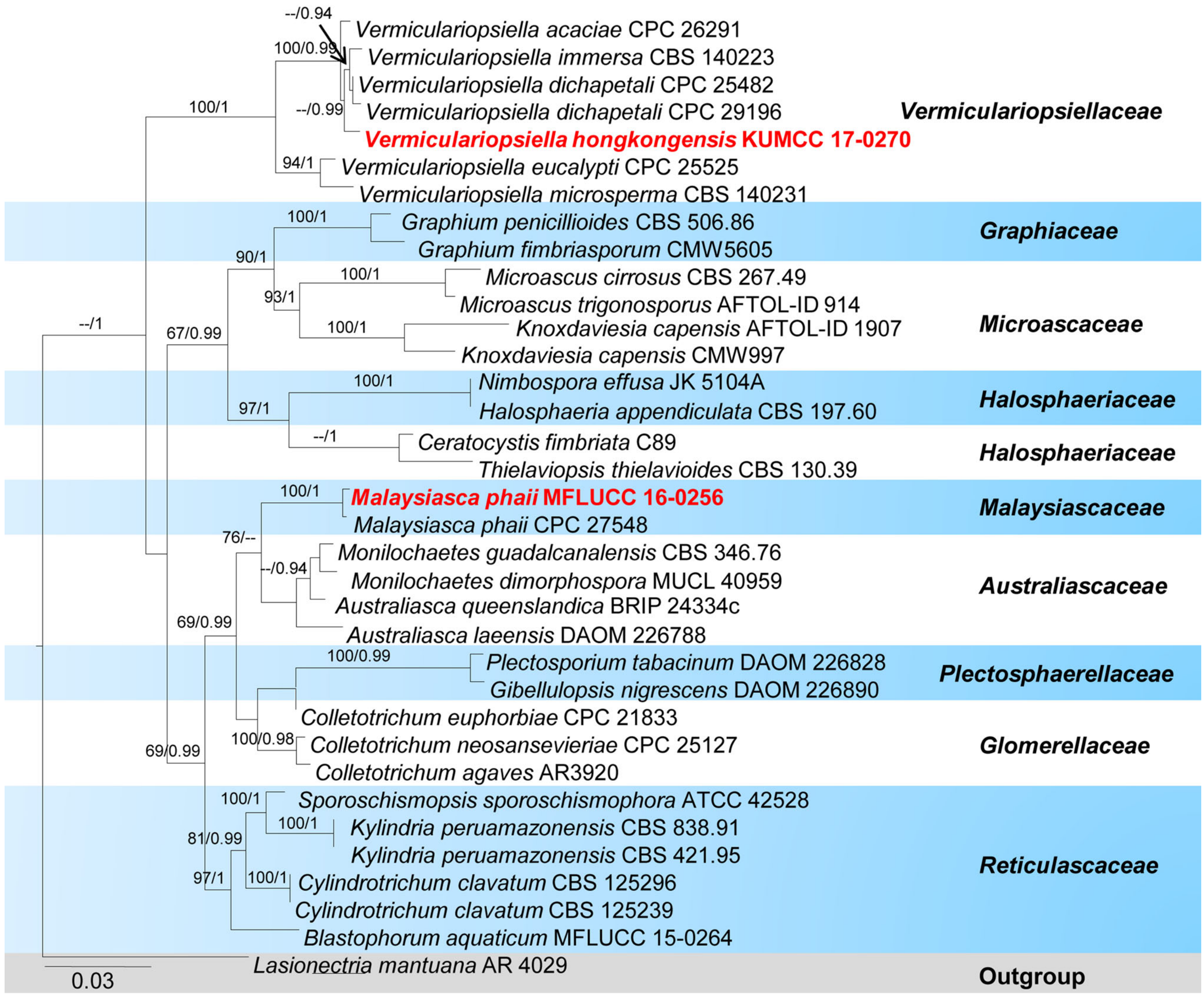


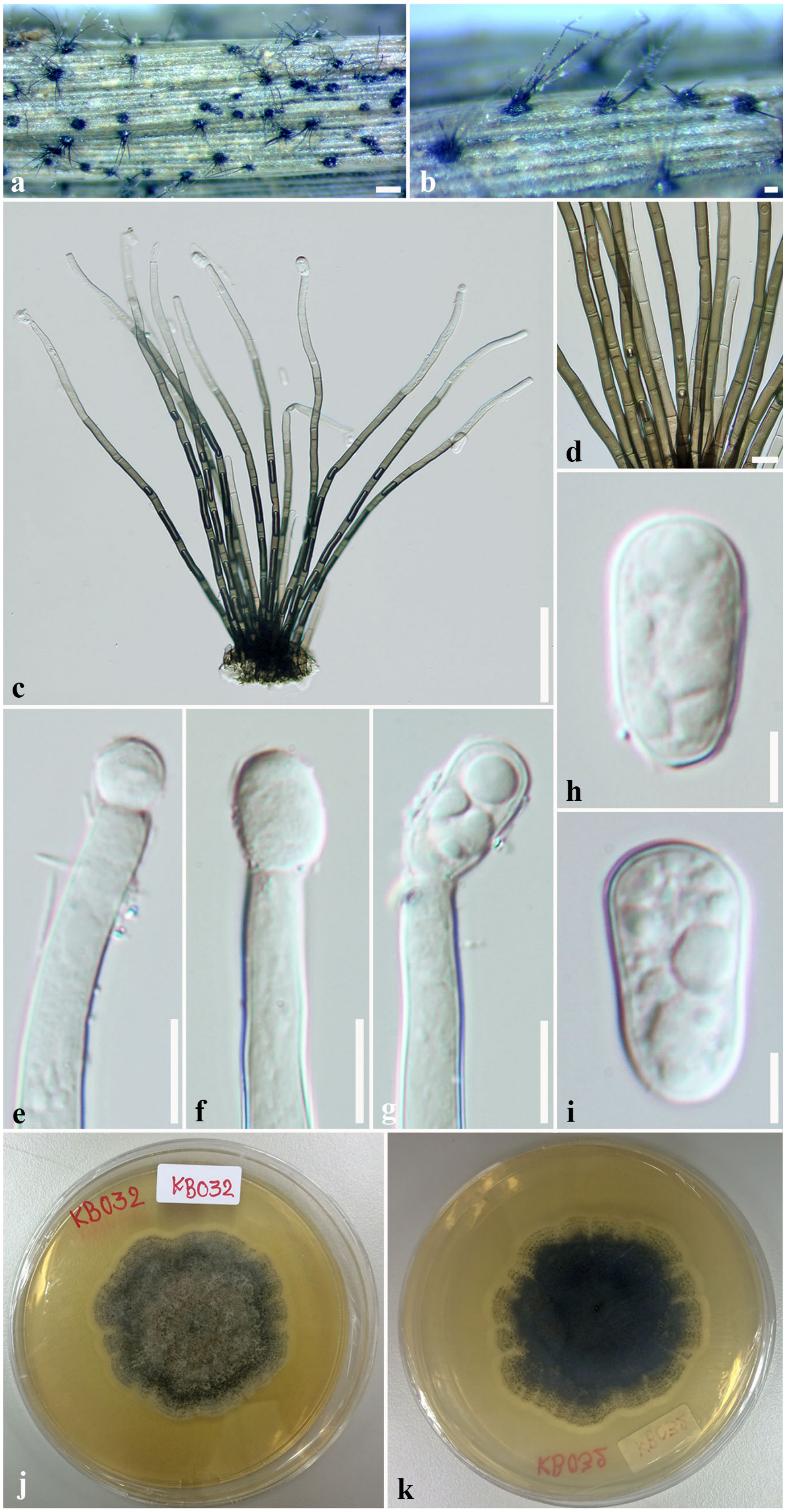
Fig. 68 Phylogram generated from maximum likelihood analysis based on combined LSU, SSU and ITS sequence data. Related sequences were obtained from Crous et al. (2016a). Thirty-five strains are included in the combined sequence analysis, which comprise 2366 characters with gaps. *Lasionectria mantuana* (AR 4029) is used as the outgroup taxon. Tree topology of the ML analysis was similar to the BYPP. The best scoring RAxML tree with a final likelihood value of − 12724.747933 is presented. The matrix had 941 distinct alignment patterns, with 41.31% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.250455, C = 0.232927, G = 0.281835, T = 0.234784; substitution rates AC = 1.410406, AG = 2.256966, AT = 2.157471, CG = 1.313307, CT = 6.866289, GT = 1.000000; gamma distribution shape parameter α = 0.214370. Bootstrap support values for ML equal to or greater than 60% and BYPP equal to or greater than 0.90 are given above the nodes. Newly generated sequences are in red

subhyaline to pale brown, oval, aseptate, rounded at end, slimy, with or without mucilaginous sheath.

Notes: We introduced a new genus, *Acremoniisimulans* having similar morphology with *Acremonium*, for a fungus isolated from dead leaves of Pandanaceae. *Acremoniisimulans* has similar conidia to *Acremonium.* The closest hits using a BLASTn search on NCBI GenBank of the LSU DNA sequence data are 99% similar to *Stachylidium bicolor* (GenBank GU180651), *Wallrothiella gmelinae* strain CBS 142520 (KY979808) and *Acremonium hyalinulum* strain CBS 652.96 (LN810512). The phylogenetic analysis of the combined LSU, SSU, ITS and TEF1 data set revealed that our novel taxon clusters independently in Plectosphaerellaceae. Our novel taxon includes different morphological characters from other members of Plectosphaerellaceae, in has brown with pale brown to hyaline at apex, septate, unbranched conidiophores with solitary, pale brown to brown, oval, aseptate conidia. However, *Acremonium* and *Acremoniisimulans* are phylogenetically distinct genera, well-segregated with high support (78% in ML and 0.95 in BYPP, Fig. 70) in our phylogeny.

Acremoniisimulans thailandensis Tibpromma & K.D. Hyde, ***sp***. ***nov***.

Fig. 69 ***Malaysiasca phaii*** (MFLU 16-1910). **a, b** Colonies on dead leaf of *Freycinetia* sp. **c** Conidiophores, conidiogenous cells and conidia. **d** Conidiophores. **e–g** Conidiogenous cells and conidium. **h, i** Conidia. **j, k** Colony on MEA from above and below. Scale bars: **a** = 200 µm, **b, c** = 50 µm, **d, e–g** = 10 µm, **h, i** = 5 µm



Index Fungorum number: IF555330, *Facesoffungi number*: FoF04536; Fig. 71

Etymology: named after Thailand, where the fungus was first discovered.

Holotype: MFLU 18-0012

Saprobic on dead leaves of *Pandanus* sp. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Colonies* on natural substrate consisting of erect conidiophores. *Mycelium* immersed in the substrate, composed of septate, branched, brown hyphae. *Conidiophores* 106–112 × 3–4.5 µm ($\bar{x}$ = 109 × 4 µm, n = 10), macronematous, mononematous, scattered, brown, pale brown to subhyaline at apex, smooth, thick-walled, 3–4-septate, unbranched, straight or slightly flexuous. *Conidiogenous cells* 28.5–44 × 3–4.5 µm ($\bar{x}$ = 37 × 3.5 µm, n = 20), monophialidic, subhyaline, cylindrical. *Conidia* 5.5–8 × 3–4 µm ($\bar{x}$ = 6.5 × 3.5 µm, n = 30), solitary, pale brown to brown, oval, aseptate, rounded at each end, smooth-walled, slimy, without mucilaginous sheath.

Culture characteristics: Conidia germinating on PDA within 12 h. Colonies on PDA reaching 9 cm in 2 weeks at room temperature, circular, undulate with white to cream, raised on surface media, velvety.

Material examined: THAILAND, Prachuap Khiri Khan Province, Bang Saphan District, Sai Khu Waterfall, on *Pandanus* sp., 30 July 2015, S. Tibpromma SF15-028 (MFLU 18-0012, **holotype**); ex-type living culture, MFLUCC 16-0372 = KUMCC 16-0159.

GenBank numbers LSU: MH260315; ITS: MH275081; SSU: MH260355.

Notes: *Acremoniisimulans thailandensis* is described as a unique new species based on our phylogenetic analysis where it formed a well-separated clade from other genera with high support. It has pale brown to brown, oval, aseptate conidia.

Musicillium Zare & W Gams

Musicillium is a monotypic genus which was erected by Zare et al. (2007) with *M. theobromae* (Turconi) Zare & W. Gams as the type species. This genus is a verticillium-like hyphomycete. We collected a new species of *Musicillium* from Pandanaceae in Thailand.

Musicillium pandanicola Tibpromma & K.D. Hyde, ***sp. nov***.

Index Fungorum number: IF555295, *Facesoffungi number*: FoF04537; Fig. 72

Etymology: named after the host genus, *Pandanus*.

Holotype: MFLU 18-0124

Saprobic on dead leaves of *Pandanus* sp. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Colonies* consisting of erect conidiophores. *Mycelium* immersed in the substrate, composed of septate, branched, brown hyphae. *Conidiophores* 500–578 × 6–9 µm ($\bar{x}$ = 547 × 7 µm, n = 5), macronematous, mononematous, scattered, brown, pale brown at apex, smooth, thick-walled, multi-septate, branched, straight or slightly flexuous. *Conidiogenous cells* 15–23 × 1–5 µm ($\bar{x}$ = 18 × 4.5 µm, n = 20), monophialidic, subhyaline, cylindrical or flask-shaped, slightly tapering. *Conidia* 4–5 × 1–3 µm ($\bar{x}$ = 4.6 × 2.4 µm, n = 30), hyaline to subhyaline, oval, aseptate, rounded at both ends, smooth-walled, without slime.

Culture characteristics: Conidia germinating on PDA within 12 h. Colonies on PDA reaching 9 cm diam., in 2 weeks at room temperature, circular, entire edge with black-grey in the middle and white at the margin, raised on surface media, velvety.

Material examined: THAILAND, Chiang Mai Province, Mae Taeng District, Mushroom Research Foundation (MRF), on *Pandanus* sp., 16 December 2017, S. Tibpromma P02 (MFLU 18-0124, **holotype**; HKAS 101790, **isotype**); ex-type living culture, MFLUCC 18-0109.

GenBank numbers LSU: MH260305; SSU: MH260345; TEF1: MH412777; RPB2: MH412757.

Notes: *Musicillium* was described from several hosts (*Theobroma*, *Cacao* and *Musa*). Phylogenetic analysis and a morphological comparison revealed that our new strain is closely related to *M. theobromae* (Turconi) Zare & W. Gams (CBS 548.51), but *M. theobromae* has conidiophores which are clearly distinct from the vegetative hyphae, brown 3–6 (rarely solitary), subhyaline, 17–35 × 1.5–2.7 µm phialides, and hyaline, cylindrical, symmetrically rounded, 4–6.5(− 9) × 1.0–1.7(− 2) µm conidia, adhering in slimy heads (Zare et al. 2007). In a BLASTn search on NCBI GenBank, the closest matches of ITS sequence of MFLUCC 18-0109 is *M. theobromae* with 98% identity to the strain NZD-mf44 (AJ292422).

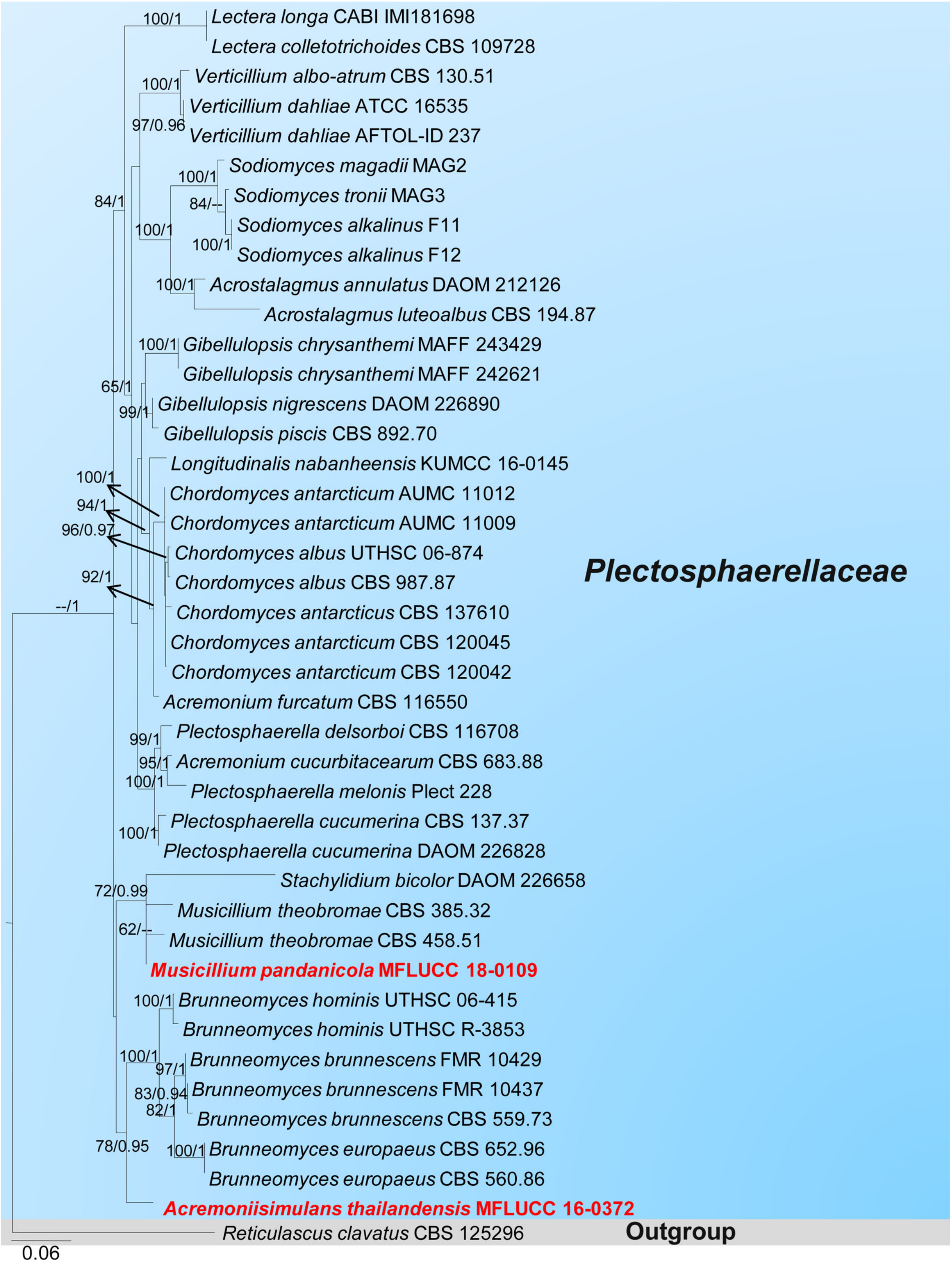
Hypocreales Lindau

Bionectriaceae Samuels & Rossman

Bionectriaceae was erected by Rossman et al. (1999) with *Bionectria* Speg. as the type genus. This family is characterized by uniloculate perithecia or rarely cleistothecial ascomata lacking a stroma, and superficial or immersed in the substratum (Rossman et al. 1999). Rossman et al. (2001) included many genera and related asexual morph taxa and confirmed that Bionectriaceae is monophyletic within Hypocreales based on phylogenetic analysis. Thirty-nine genera are accepted in Bionectriaceae and we follow Wijayawardene et al. (2018) for the genera and provide an updated tree for members of Bionectriaceae collected from Pandanaceae.

Clonostachys Corda

Clonostachys was introduced with *C. araucaria* (Corda 1839). *Clonostachys* is an older, although asexual name for *Bionectria*. Thus, Rossman et al. (2013) synonymized


100/1
Lectera longa CABI IMI181698
Lectera colletotrichoides CBS 109728
100/1
Verticillium albo-atrum CBS 130.51
Verticillium dahliae ATCC 16535
97/0.96
Verticillium dahliae AFTOL-ID 237
Sodiomyces magadii MAG2
100/1
Sodiomyces tronii MAG3
84/1
84/--
Sodiomyces alkalinus F11
100/1
100/1
Sodiomyces alkalinus F12
100/1
Acrostalagmus annulatus DAOM 212126
Acrostalagmus luteoalbus CBS 194.87
100/1
Gibellulopsis chrysanthemi MAFF 243429
Gibellulopsis chrysanthemi MAFF 242621
65/1
Gibellulopsis nigrescens DAOM 226890
99/1
Gibellulopsis piscis CBS 892.70
Longitudinalis nabanheensis KUMCC 16-0145
100/1
Chordomyces antarcticum AUMC 11012
94/1
Chordomyces antarcticum AUMC 11009
96/0.97
Chordomyces albus UTHSC 06-874
Chordomyces albus CBS 987.87
92/1
Plectosphaerellaceae
--/1
Chordomyces antarcticus CBS 137610
Chordomyces antarcticum CBS 120045
Chordomyces antarcticum CBS 120042
Acremonium furcatum CBS 116550
Plectosphaerella delsorboi CBS 116708
99/1
95/1
Acremonium cucurbitacearum CBS 683.88
100/1
Plectosphaerella melonis Plect 228
Plectosphaerella cucumerina CBS 137.37
100/1
Plectosphaerella cucumerina DAOM 226828
Stachylidium bicolor DAOM 226658
72/0.99
Musicillium theobromae CBS 385.32
62/--
Musicillium theobromae CBS 458.51
Musicillium pandanicola MFLUCC 18-0109
100/1
Brunneomyces hominis UTHSC 06-415
Brunneomyces hominis UTHSC R-3853
100/1
Brunneomyces brunnescens FMR 10429
97/1
83/0.94
Brunneomyces brunnescens FMR 10437
82/1
Brunneomyces brunnescens CBS 559.73
78/0.95
100/1
Brunneomyces europaeus CBS 652.96
Brunneomyces europaeus CBS 560.86
Acremoniisimulans thailandensis MFLUCC 16-0372
Reticulascus clavatus CBS 125296
Outgroup
0.06

◀**Fig. 70** Phylogram generated from maximum likelihood analysis based on combined LSU, SSU, TEF1 and ITS sequence data. Related sequences were obtained from Hyde et al. (2017). Forty-two strains are included in the combined sequence analysis, which comprise 3439 characters with gaps. *Reticulascus clavatus* (CBS 125296) is used as the outgroup taxon. Tree topology of the ML analysis was similar to the BYPP. The best scoring RAxML tree with a final likelihood value of − 13281.808204 is presented. The matrix had 852 distinct alignment patterns, with 50.50% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.229967, C = 0.276753, G = 0.279862, T = 0.213418; substitution rates AC = 0.717151, AG = 1.411613, AT = 1.372652, CG = 0.561709, CT = 4.777886, GT = 1.000000; gamma distribution shape parameter α = 0.463512. Bootstrap support values for ML equal to or greater than 60% and BYPP equal to or greater than 0.95 are given above the nodes. Newly generated sequences are in red

Bionectria under *Clonostachys.* An update for *Clonostachys* was provided by Maharachchikumbura et al. (2015). The asexual morph of *Clonostachys* is characterized by penicillate, frequently sporodochial and, in many cases, dimorphic conidiophores (Schroers 2001). There are 83 epithets are listed in Index Fungorum (2018). *Clonostachys compactiuscula* (Sacc.) D. Hawksw. & W. Gams has been reported from Pandanaceae (Hawksworth and Punithalingam 1975; Dulymamode et al. 2001). We introduce a new species isolated from *Pandanus* in Thailand.

Clonostachys krabiensis Tibpromma & K.D. Hyde, ***sp. nov***.

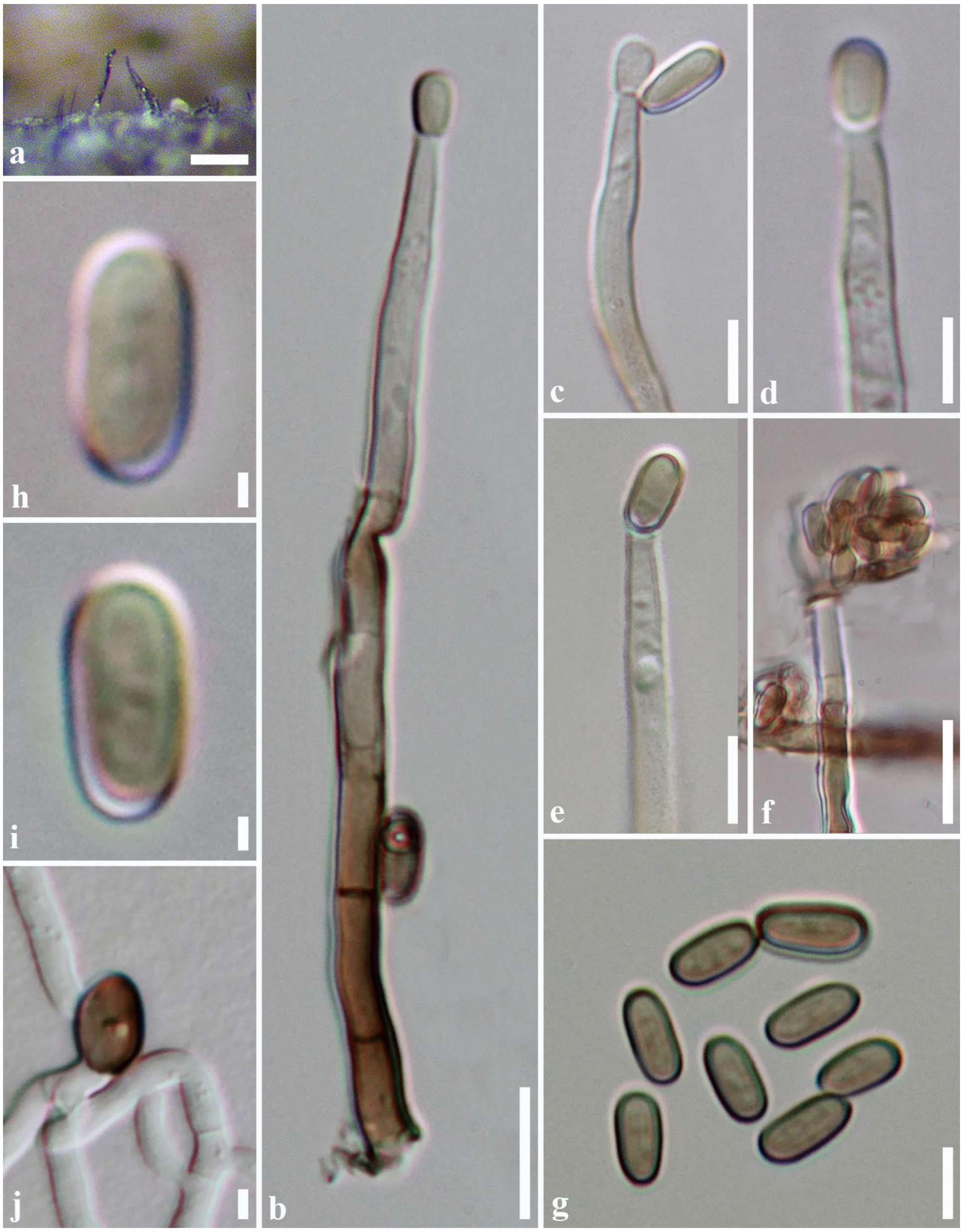
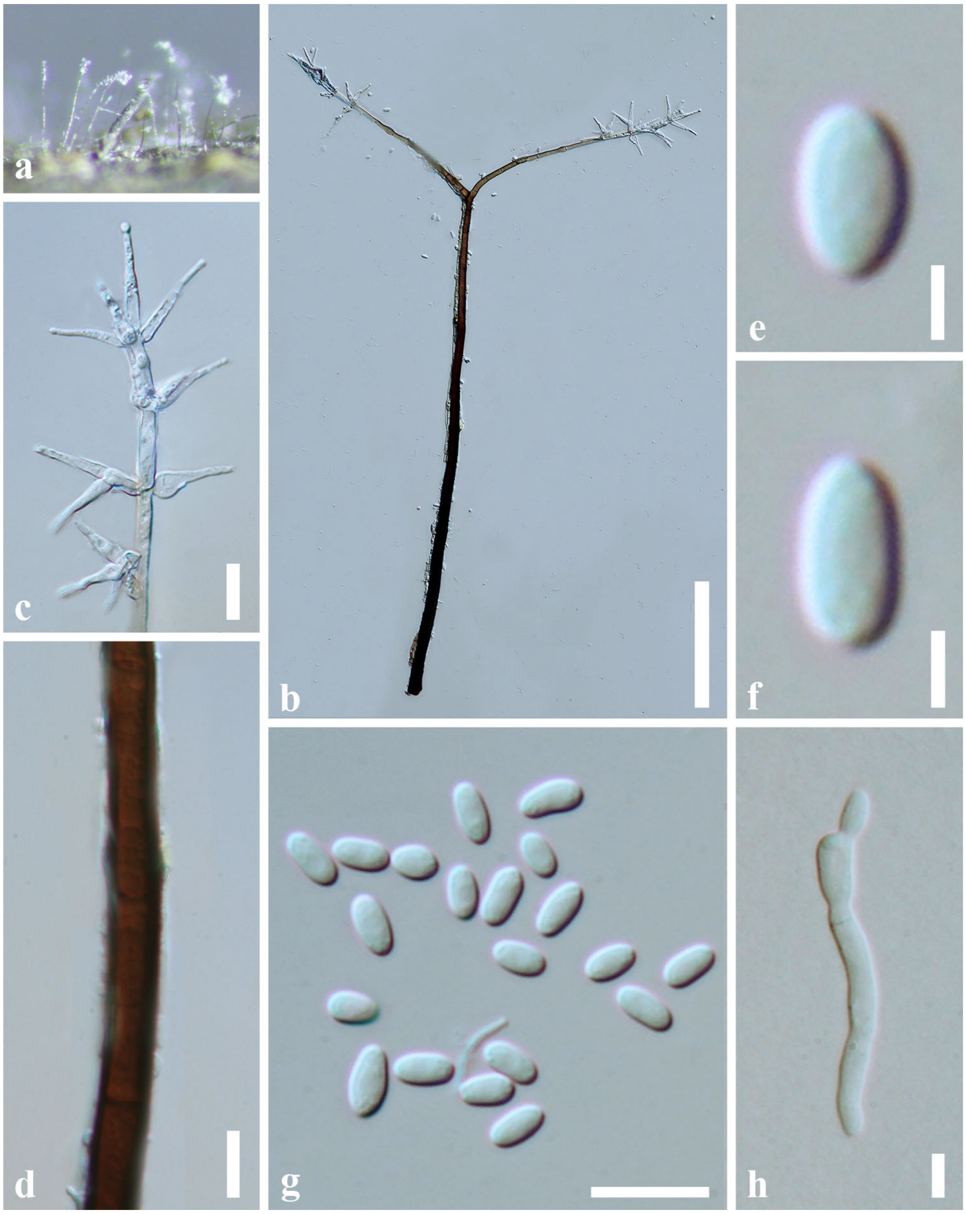


Fig. 71 ***Acremoniisimulans thailandensis*** (MFLU 18-0012, **holotype**). **a** Colonies on dead leaf of *Pandanus* sp. **b** Conidiophores, conidiogenous cells and conidia. **c–f** Conidiogenous cells and conidia. **g–i** Conidia. **j** Germinating conidium. Scale bars: **a** = 100 µm, **b** = 10 µm, **e–g** = 5 µm, **h–j** = 2 µm

Fig. 72 ***Musicillium pandanicola*** (MFLU 18-0124, **holotype**). **a** Colonies on dead leaf of *Pandanus* sp. **b** Conidiophore, conidiogenous cells and conidia. **c** Conidiogenous cells and conidia. **d** Conidiophores. **e–g** Conidia. **h** Germinating conidium. Scale bars: **b** = 100 µm, **c, d, g** = 10 µm, **e, f** = 2 µm, **h** = 5 µm



Index Fungorum number: IF554527, *Facesoffungi number*: FoF04539; Fig. 73

Etymology: named after Krabi Province, where the fungus was first discovered.

Holotype: MFLU 16-1907

Saprobic on dead leaves of *Pandanus* sp. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Setae* 173–375 × 2–4 µm ($\bar{x}$ = 252 × 3 µm, n = 20), hyaline, aseptate, cylindrical with conical apex. *Conidiophores* aggregated into sporodochia, with hyaline setae around the margin. *Conidiogenous cells* 10–13 × 1.5–2.5 µm ($\bar{x}$ = 11.5 × 2 µm, n = 20), monophialidic, hyaline, subulate. *Conidia* 5–7 × 1–2 µm ($\bar{x}$ = 6 × 1.6 µm, n = 40), slimy, solitary, aseptate, hyaline, cylindrical to oblong, smooth-walled.

Culture characteristics: Conidia germinating on MEA within 12 h. Colonies on MEA, irregular, undulate edge with whorls, yellow–white, flat on media surface.

Material examined: THAILAND, Krabi Province, Mueang Krabi District, on *Pandanus* sp., 14 December 2015, S. Tibpromma KB029 (MFLU 16-1907, **holotype**; HKAS 96256, **isotype**); ex-type living culture, MFLUCC 16-0254.

GenBank numbers LSU: MH376707; ITS: MH388335; SSU: MH388304.

Notes: Based on phylogeny *Clonostachys kraviensis* clusters with *C. byssicola* Schroers (95% in ML, Fig. 74). However, *C. byssicola* has shorter conidia (frequently less than 5 µm long) with slightly curved, and a laterally displaced hilum (Schroers 2001). We also compared our

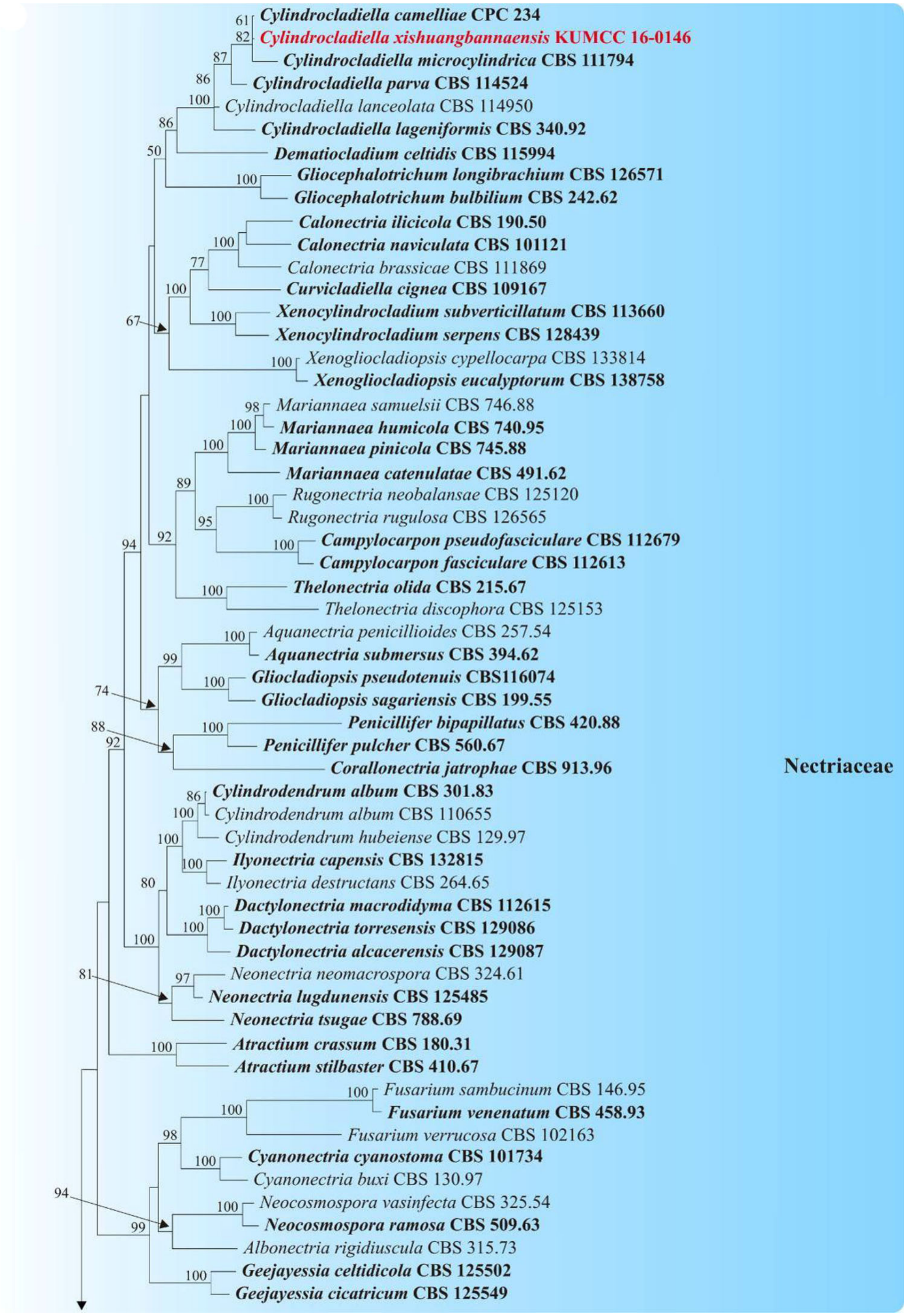


Fig. 73 Phylogram generated from maximum likelihood analysis based on combined LSU, ITS, cmdA, RPB2, TEF1 and TUB2 sequence data. Two hundred and eighty five strains are included in the combined sequence analysis, which comprise 4417 characters with gaps. *Gelasinospora tetrasperma* (AFTOL-ID 1287), *Neurospora crassa* (ICMP 6360) and *Sordaria fimicola* (AFTOL-ID 216) are used as the outgroup taxa. Tree topology of the ML analysis was similar to the BYPP. The best scoring RAxML tree with a final likelihood value of − 146671.299056 is presented. The matrix had 2852 distinct alignment patterns, with 46.08% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.239937, C = 0.264170, G = 0.277202, T = 0.21869; substitution rates AC = 1.466937, AG = 3.219738, AT = 1.533143, CG = 0.996922, CT = 6.732220, GT = 1.000000; gamma distribution shape parameter α = 0.371105. Bootstrap support values for ML equal to or greater than 50% and BYPP equal to or greater than 0.95 are given above the nodes. Newly generated sequences are in red

fungus with *Clonostachys compactiuscula* but it has conidia produced in long chains up to 150 µm long (Hawksworth and Punithalingam 1975). In a BLASTn search on NCBI GenBank, the closest matches of ITS sequence of MFLUCC 16-0254 is *C. rosea* with 99% identity to the strain FIS26 (KY378958), while the closest matches with the SSU sequence were with 99% identical *C. rosea* strain WY-1 (MH031706).

Lasionectria (Sacc.) Cooke

Lasionectria was erected by Cooke (1884) to accommodate *L. mantuana* (Sacc.) Cooke. *Lasionectria* occurs as saprobes in terrestrial and temperate habitats (Lumbsch and Huhndorf 2010). *Lasionectria* has 36 epithets are listed in Index Fungorum (2018). *Lasionectria mantuana* (Sacc.) Cooke and *L. sylvana* (Mouton) Rossman & Samuels have been reported from Pandanaceae (Whitton et al. 2012).

Lasionectria krabiense Tibpromma & K.D. Hyde, ***sp. nov.***

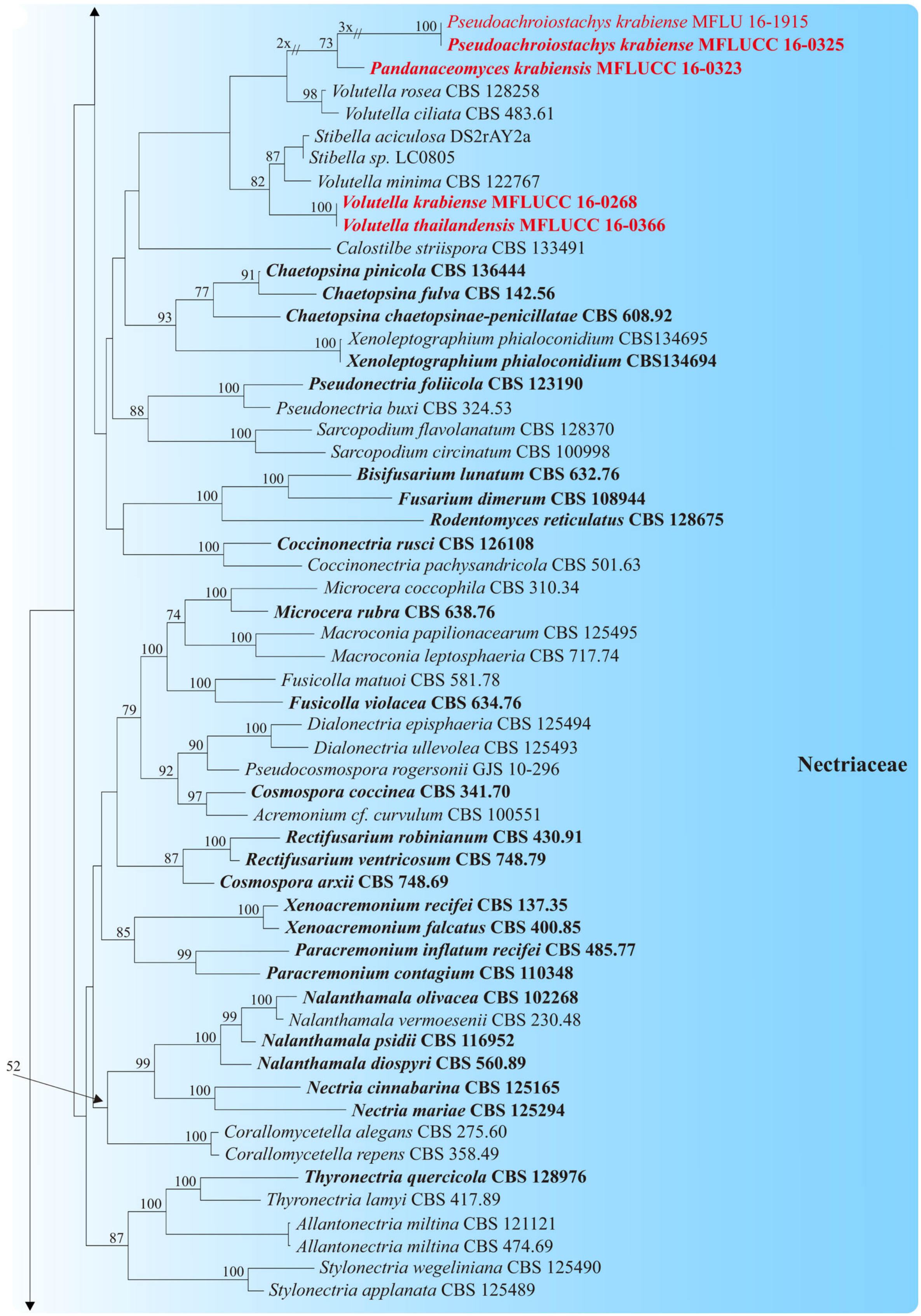


Fig. 73 continued

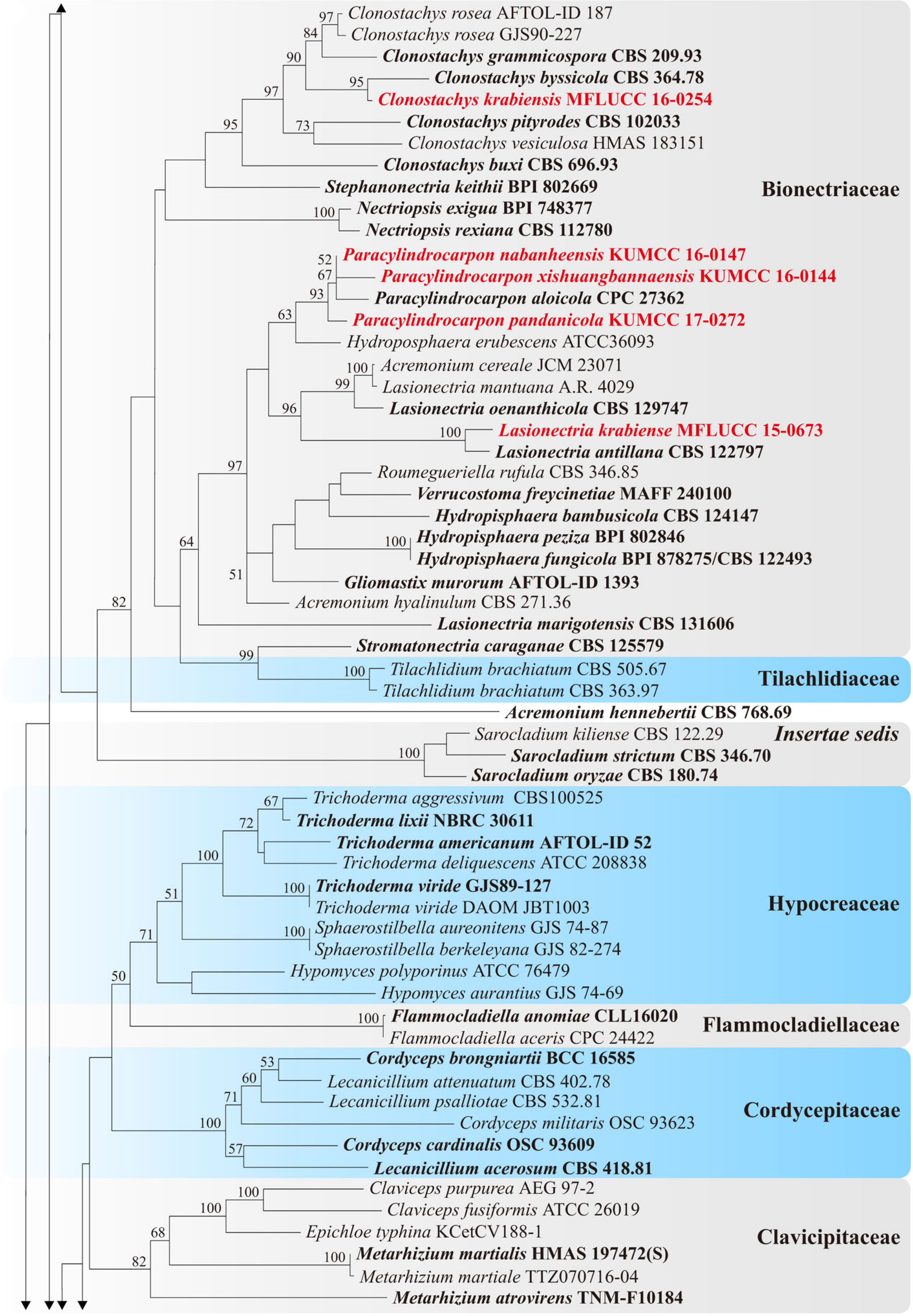


Fig. 73 continued

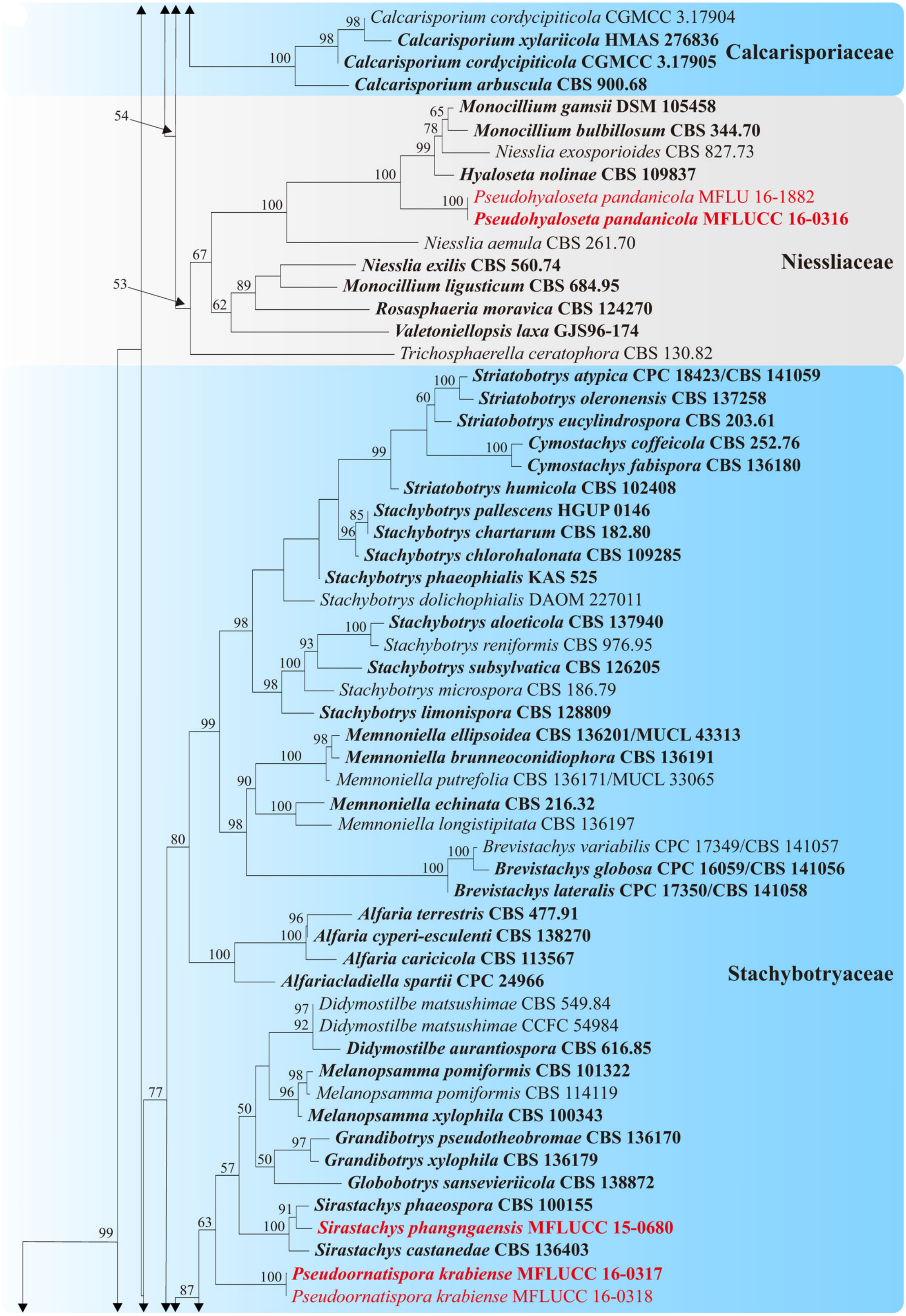


Fig. 73 continued

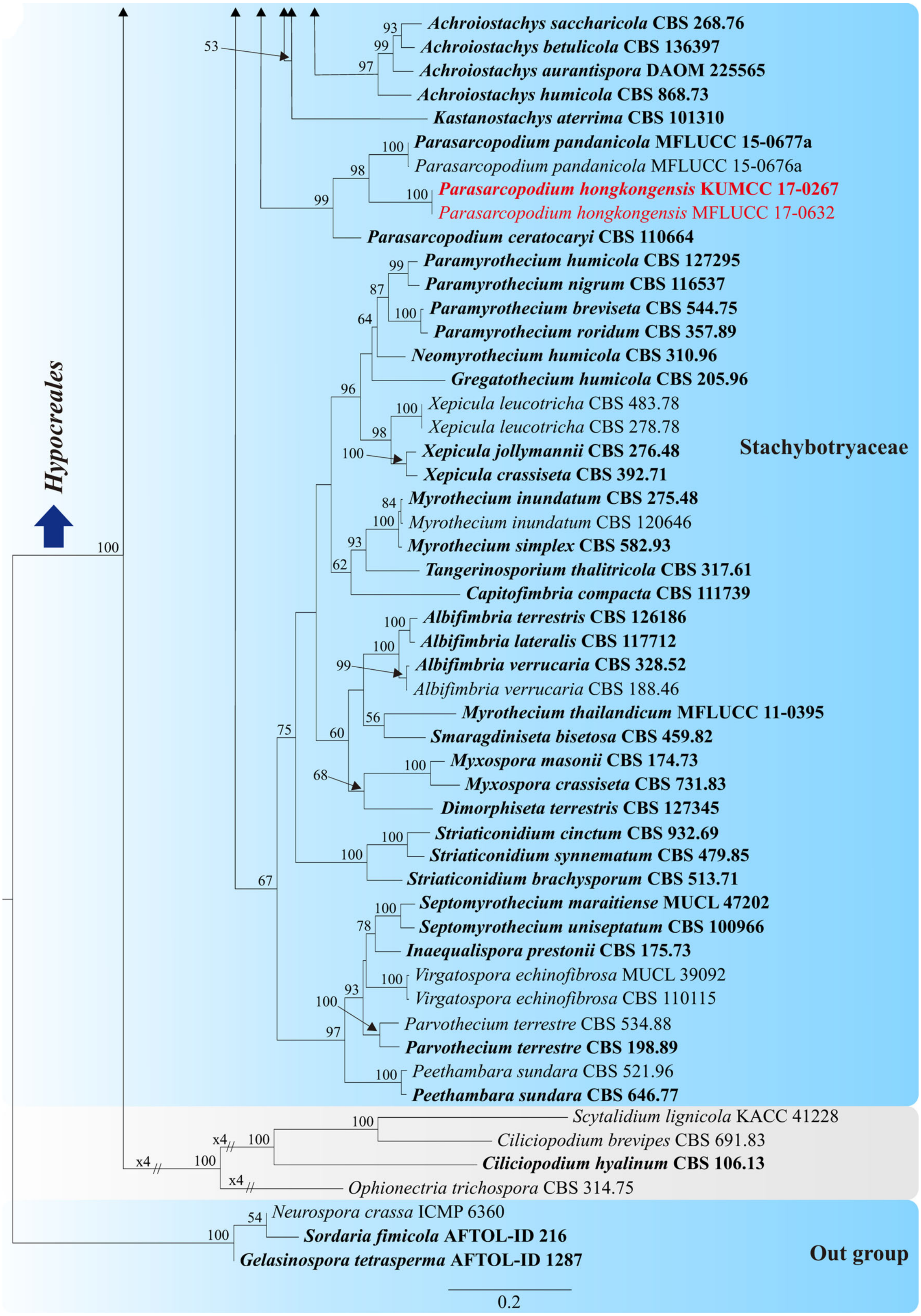


Fig. 73 continued

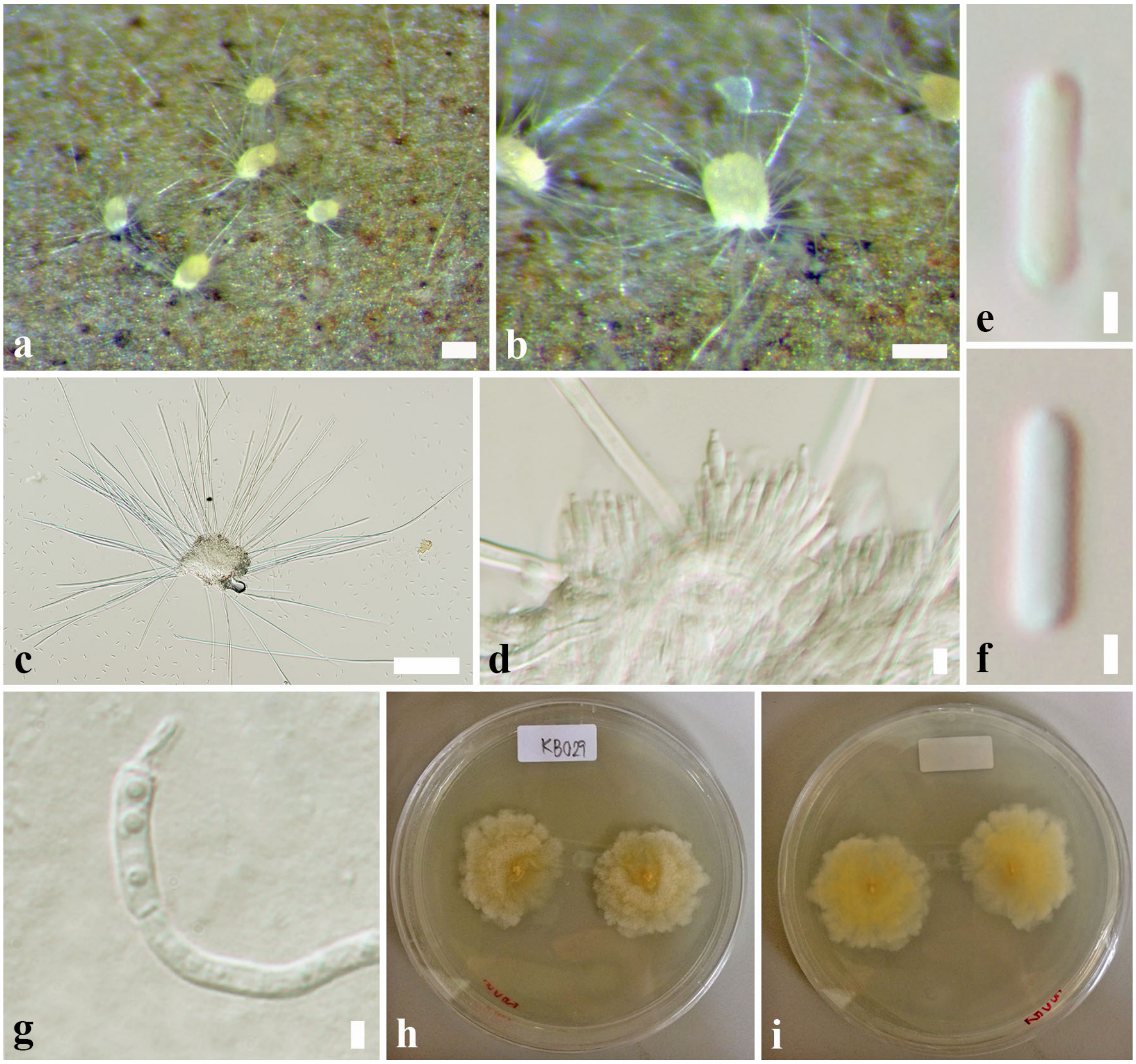


Fig. 74 ***Clonostachys krabiensis*** (MFLU 16-1907, **holotype**). **a–c** Sporodochial conidiomata on dead leaves of *Pandanus* sp. **d** Conidiophores, conidiogenous cells and conidia. **e, f** Conidia. **g** Germinating conidium. **h, i** Colonies on MEA from above and below. Scale bars: **a–c** = 100 µm, **d, g** = 5 µm, **e, f** = 2 µm

Index Fungorum number: IF554528, *Facesoffungi number*: FoF04540; Fig. 75

Etymology: named after Krabi Province, where the fungus was first discovered.

Holotype: MFLU 16-0540

Saprobic on dead leaf of *Pandanus* sp. **Sexual morph** *Ascomata* 140–200 × 220–260 µm ($\bar{x}$ = 168 × 236 µm, n = 5), solitary, superficial, globose to subglobose, with apex flattened with a minute papilla, orange to brownish orange, collapsing and becoming cupulate when dry, without ostiole. *Peridium* 15–30 µm wide, composed of hyaline to orange, hypha-like cells of *textura prismatica*. *Hamathecium* 1.5–3 µm wide, comprising numerous, dense, filiform, filamentous, branched, guttulate, septate paraphyses. *Asci* 30–55 × 8–11 µm ($\bar{x}$ = 43 × 9 µm, n = 20), 6–8-spored, unitunicate, cylindrical to cylindric-clavate, short-pedicellate, apically rounded. *Ascospores* 15–20 × 3–5 µm ($\bar{x}$ = 17 × 4 µm, n = 20), overlapping bi-seriate, fusoid-ellipsoidal, hyaline to subhyaline, 1-septate in the middle, rough, with longitudinal striations, granulate, not surrounded by a mucilaginous sheath. **Asexual morph** Undetermined.

Culture characteristics: Ascospore germinating on MEA within 12 h. Colonies on MEA, circular to irregular, undulate with white to yellow–white, flat on media, rough with wrinkles edge.

Material examined: THAILAND, Krabi Province, Mueang Krabi District, on *Pandanus* sp., 14 December 2014, S. Tibpromma SF14-022 (MFLU 16-0540 **holotype**; HKAS 100829, **isotype**); living culture, MFLUCC 15-0673; CHINA, Yunnan Province, Xishuangbanna,

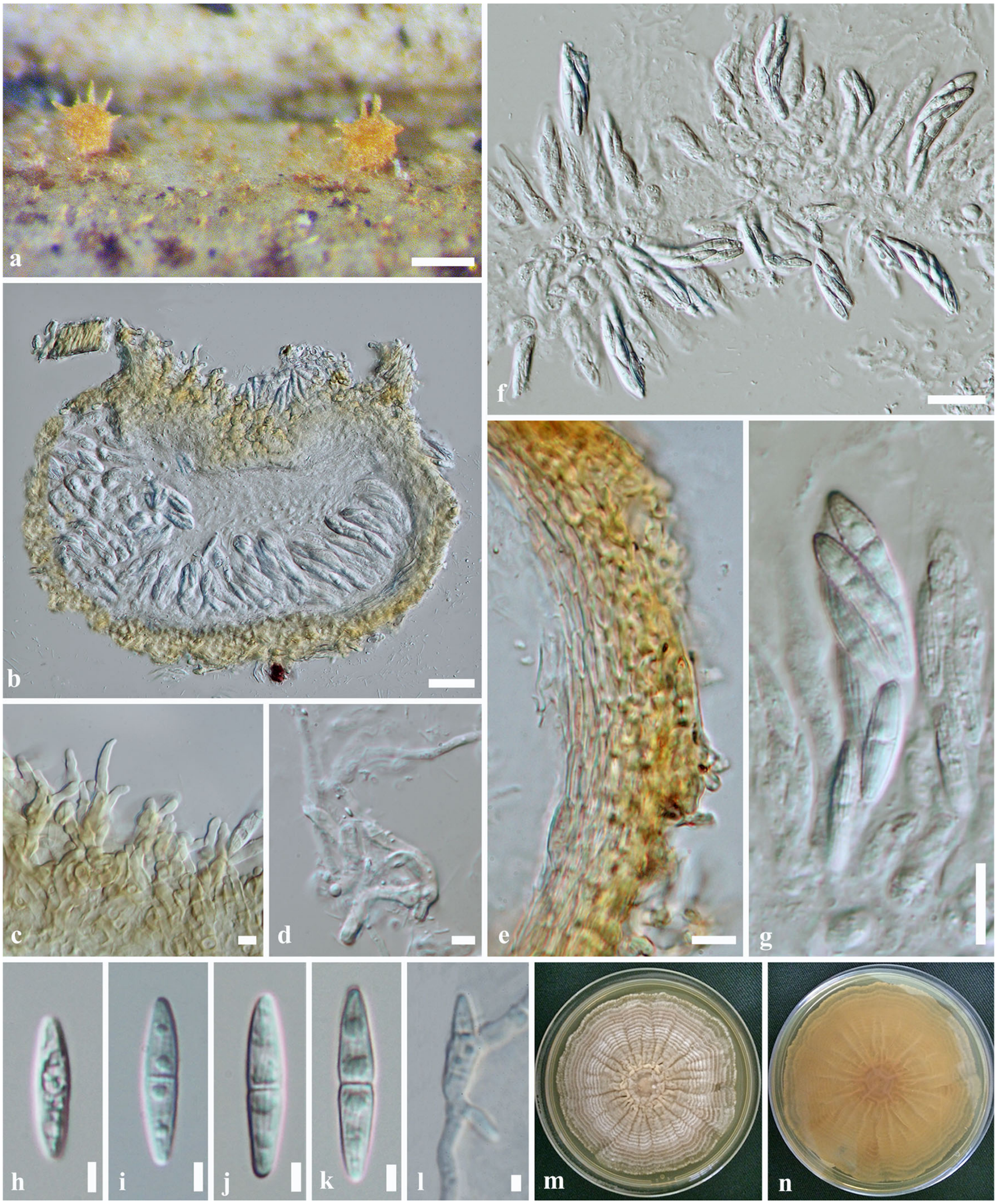


Fig. 75 ***Lasionectria krabiense*** (MFLU 16-0540 **holotype**). **a** Colonies on dead leaf of *Pandanus* sp. **b** Section of ascoma. **c** Papilla. **d** Paraphyses. **e** Peridium. **f, g** Asci. **h–k** Ascospores. **l** Germinating ascospore. **m, n** Colony on MEA from above and below. Scale bars: **a** = 200 µm, **b, f** = 20 µm, **c–e** = 5 µm, **g** = 10 µm, **h–l** = 2 µm

Nabanhe, on *Pandanus* sp., 27 July 2016, PE Mortimer NBH13 (HKAS 96213, **paratype**).

GenBank numbers LSU: MH376725; ITS: MH388352; SSU: MH388319; TEF1: MH388387.

Notes: On combined gene analysis, *Lasionectria krabiense* clusters with *L. antillana* (Lechat & Courtec.) Schroers, Ashrafi & W. Maier with strong bootstrap support (100% in ML, Fig. 74). The ascomata and ascospore morphology of both species is very similar, but *L. antillana* has 12.7 × 3.2 µm ascospores without longitudinal striations (Lechat and Courtecuisse 2010). There are more than 34 bp (6.77%) differences in the 502 ITS (+5.8S) nucleotides of *L. antillana* and *L. krabiense* which indicates they are distinct species. In a BLASTn search on

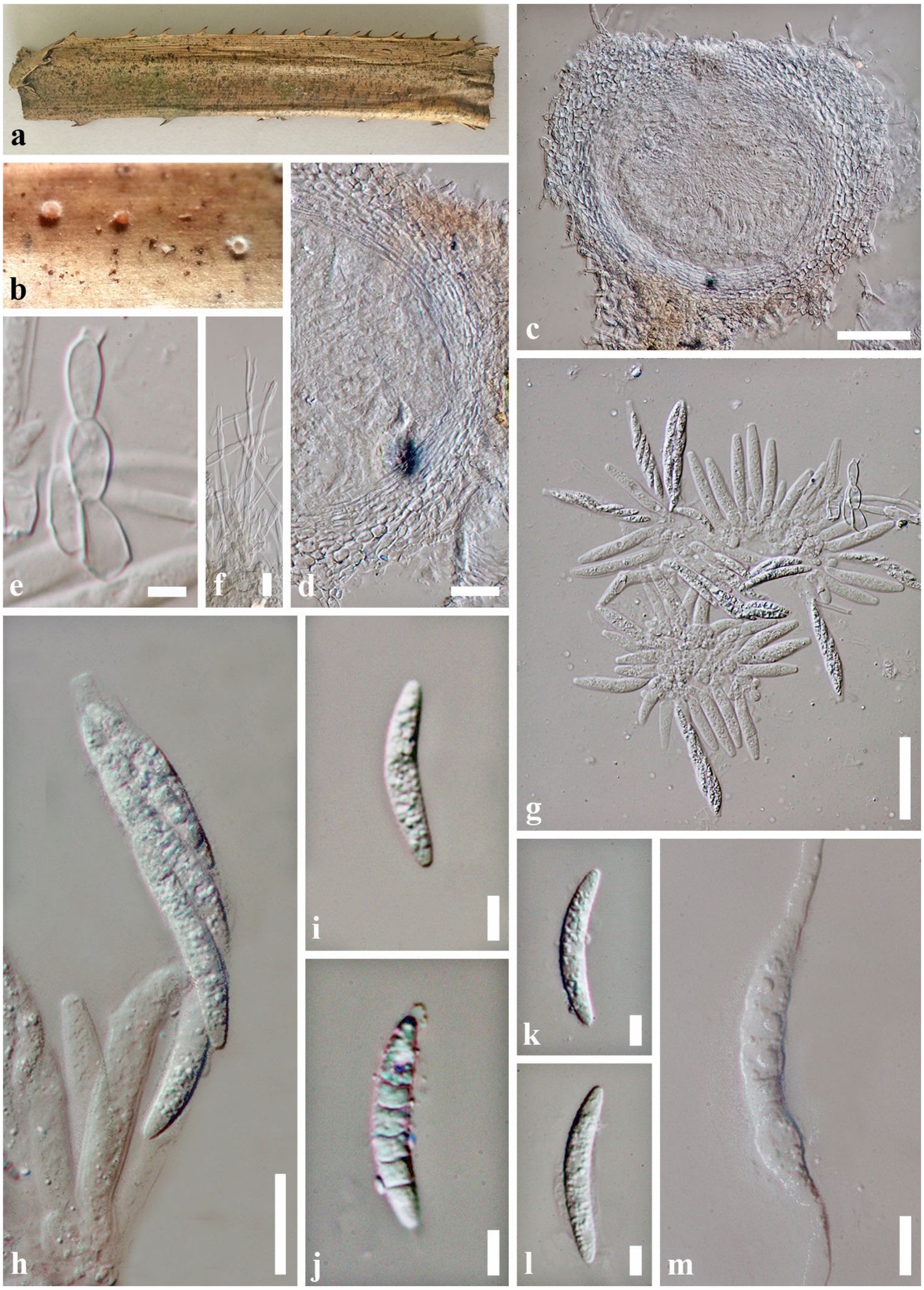


Fig. 76 ***Paracylindrocarpon nabanheensis*** (HKAS 96210, **holotype**). **a, b** Appearance of ascomata on host substrate. **c** Section of ascoma. **d** Section of peridium. **e** Hamathecium. **f** Hyaline papilla. **g, h** Asci. **i–l** Ascospores. **m** Germinating ascospore. Scale bars: **c, g** = 50 µm, **d** = 20 µm, **e, f, i–m** = 5 µm, **h** = 10 µm

NCBI GenBank, the closest matches of ITS sequence of MFLUCC 15-0673 is *L. antillana* with 94% identity to the strain CBS 122797 (KY607537).

Paracylindrocarpon Crous et al.

Paracylindrocarpon was erected by Crous et al. (2016a) to accommodate *P. aloicola* Crous, Roets & L. Lombard. *Paracylindrocarpon* has morphological similarities to *Cylindrocarpon* with both having hyaline, smooth, conidiophores with hyaline granular, cylindrical, (0–)3-septate, conidia with obtuse apex and truncate base (Crous et al. 2016a). We describe three species of *Paracylindrocarpon*; this is the first report of *Paracylindrocarpon* from Pandanaceae.

Paracylindrocarpon nabanheensis Tibpromma & K.D. Hyde, ***sp***. ***nov***.

Index Fungorum number: IF554529, *Facesoffungi number*: FoF04541; Fig. 76

Etymology: named after Nabanhe, where the fungus was first discovered.

Holotype: HKAS 96210

Saprobic on dead leaves of *Pandanus* sp. **Sexual morph** *Ascomata* 214.5–346 × 320–367 µm ($\bar{x}$ = 276.4 × 342.4 µm, n = 5), scattered to gregarious, globose to subglobose, superficial, flat at the base, conspicuous on host surface, easy to remove, orange, solitary, uniloculate, covered with hyaline papilla, with ostiole at the centre. *Peridium* 43–79 µm wide, composed of several layers, thick-walled hyaline to subhyaline cells of *textura prismatica. Hamathecium* comprising 7–9 µm wide, ellipsoid, cellular, unbranched, guttulate, septate paraphyses. *Asci* 58–81 × 9–14 µm ($\bar{x}$ = 64.4 × 10.5 µm, n = 10), (6–)8-spored, unitunicate, cylindrical to cylindrical-clavate, with furcate pedicel, with J- apical ring. *Ascospores* 37–47 × 6–7.5 µm ($\bar{x}$ = 40 × 6.5 µm, n = 10), fusiform, conical at both ends, 6-septate when mature, not constricted at the septa, hyaline to subhyaline, guttulate, without mucilaginous sheath, smooth-walled. **Asexual morph** Undetermined.

Culture characteristics: Ascospores germinating on MEA within 12 h. Colonies on MEA, purple at the central and pink at the margin, with irregular, curled, with raised on media surface, dark-purple at the central with white at the margin in reverse.

Material examined: CHINA, Yunnan Province, Xishuangbanna, Nabanhe, on *Pandanus* sp., 27 July 2016, PE Mortimer NBH10 (HKAS 96210, **holotype**); ex-type living culture, KUMCC 16-0147.

GenBank numbers LSU: MH376730; ITS: MH388356; SSU: MH388324; TEF1: MH388392.

Notes: Based on morphology *Paracylindrocarpon nabanheensis* is similar to *P. xishuangbannaensis*, which was collected from the same host and same location. Both species are known from only the sexual morph. In a comparison of the 506 ITS (+5.8S) nucleotides of *P. nabanheensis* and *P. xishuangbannaensis* reveals 20 (3.95%) nucleotide differences which justifies these two isolates as two distinct taxa and we also comparison ITS nucleotides of *Paracylindrocarpon* species (Table 3). In a BLASTn search on NCBI GenBank, the closest matches of ITS sequence of KUMCC 16-0147 is *P. aloicola* with 97% identity to the strain CPC 27362 (KX228277).

Paracylindrocarpon pandanicola Tibpromma & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF554530, *Facesoffungi number*: FoF04542; Fig. 77

Etymology: named after the host genus, *Pandanus*.

Holotype: HKAS 100863

Saprobic on dead leaves of *Pandanus* sp. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Mycelium* consisting of hyaline, smooth, branched, septate. *Conidiophores* sporodochial, solitary, hyaline, smooth, erect, straight to geniculate-sinuous, arising from superficial hyphae, unbranched or branched. *Conidiogenous cells* 26–38 × 2–3 µm ($\bar{x}$ = 32.5 × 2 µm, n = 10), phialidic, hyaline, smooth, subcylindrical with slight apical taper, straight to slightly irregularly curved, terminal or lateral on conidiophores, apex with minute periclinal thickening. *Conidia* 15–22 × 2–4 µm ($\bar{x}$ = 18 × 3 µm, n = 50), hyaline, smooth, granular, cylindrical, 2–3-septate, hyaline, filiform, slightly constricted at septa, slightly curved, thick-walled, distinctly guttulate, without appendages or mucilaginous sheath.

Culture characteristics: Conidia germinating on MEA within 12 h. Colonies on MEA reaching 9 cm diam., after 7 days at room temperature, circular, edge entire, white to yellow.

Material examined: HONG KONG, Tai Tam Tuk Reservoir, on *Pandanus* sp., 21 September 2016, S. Tibpromma HK21 (HKAS 100863, **holotype**); ex-type living culture, KUMCC 17-0272 = MFLUCC 17-0639.

GenBank numbers LSU: MH376731; ITS: MH388357; SSU: MH388325; TEF1: MH388393.

Notes: Based on multi-gene analyses, *Paracylindrocarpon pandanicola* clusters with other *Paracylindrocarpon* spp. with strong bootstrap support (Fig. 74). *Paracylindrocarpon pandanicola* differs from *P. aloicola* Crous, Roets & L. Lombard has cylindrical conidia that have an obtuse apex, a truncate base and (0–)3-septa (Crous et al. 2016a). In a BLASTn search on NCBI GenBank, the closest matches of ITS sequence of KUMCC 16-0147 is *P. aloicola* with 94% identity to the strain CPC 27362 (KX228277).

Table 3 Polymorphic nucleotides from the ITS sequence data of *Paracylindrocarpon* species

Species	Position												
	164	165	166	167	168	169	170	224	373	374	544	545	546
P. aloicola CPC 27362	T	A	T	A	G	G	A	C	T	T	T	G	C
P. hongkongensis KUMCC 17-026	G	T	G	G	C	A	T	T	C	C	C	G	C
P. nabanheensis KUMCC 16-0147	T	T	G	A	G	A	A	C	C	T	T	G	C
P. xishuangbannaensis KUMCC 16-0144	A	T	T	G	A	G	A	C	C	T	G	T	G

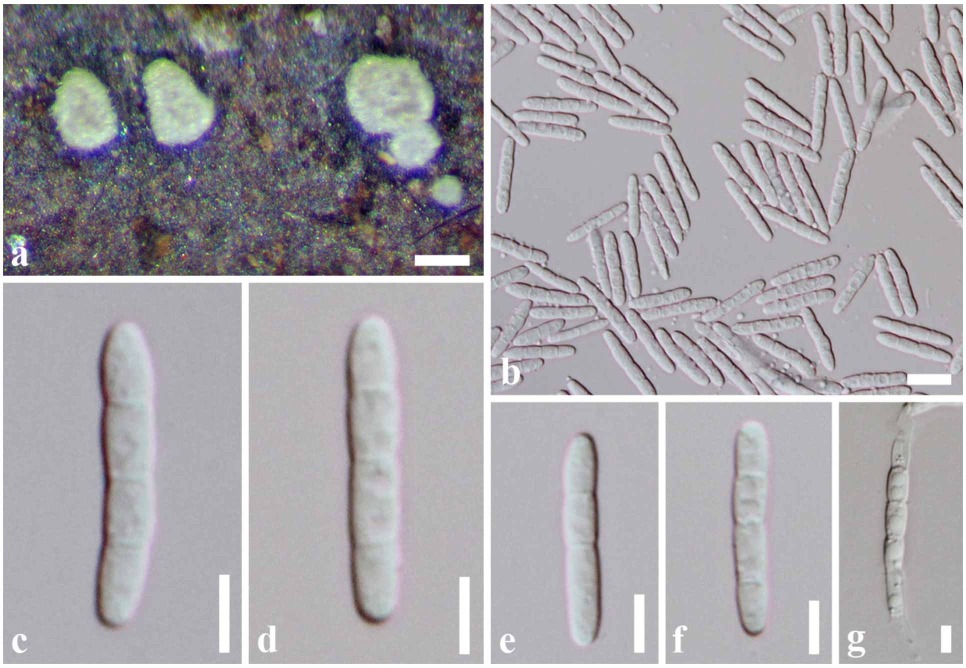


Fig. 77 ***Paracylindrocarpon pandanicola*** (HKAS 100863, **holotype**). **a** Colonies on dead leaves of *Pandanus* sp. **b–f** Conidia. **g** Germinating conidium. Scale bars: **a** = 500 µm. **b** = 10 µm. **c–g** = 5 µm

Paracylindrocarpon xishuangbannaensis Tibpromma & K.D. Hyde, ***sp***. ***nov***.

Index Fungorum number: IF554535, *Facesoffungi number*: FoF04543; Fig. 78

Etymology: named after Xishuangbanna, where the fungus was first discovered.

Holotype: HKAS 96204

Saprobic on dead leaves of *Pandanus* sp. **Sexual morph** *Ascomata* 225–300 × 277.5–295 µm ($\bar{x}$ = 259 × 288.5 µm, n = 5), scattered to gregarious, globose to subglobose, superficial, flat at the base, conspicuous on the host surface, easy to remove, orange, dull, solitary, uniloculate, with pale brown papilla, with central ostiole. *Peridium* 33–70.5 µm wide, composed of several layers of thick-walled, hyaline to pale brown cells of *textura angularis*. *Hamathecium* comprising 2.2–4 µm wide, cylindrical, filamentous, unbranched, guttulate, septate paraphyses. *Asci* 67–95 × 10–17 µm ($\bar{x}$ = 72 × 12 µm, n = 20), 8-spored, unitunicate, cylindrical-clavate, with short pedicel, with J- apical ring. *Ascospores* 27–41 × 3–8 µm ($\bar{x}$ = 34.5 × 5.6 µm, n = 20), fusiform, conical towards both ends, 3–5-septate, not constricted at septa, hyaline, guttulate without mucilaginous sheath, smooth-walled. **Asexual morph** Undetermined.

Culture characteristics: Ascospores germinating on PDA within 12 h. Colonies on PDA, yellow–white, with irregular whorls, raised and rough on media surface, yellow–brown in reverse.

Material examined: CHINA, Yunnan Province, Xishuangbanna, Nabanhe, on *Pandanus* sp., 27 July 2016, PE Mortimer NBH04 (HKAS 96204, **holotype**); ex-type living culture, KUMCC 16-0144 = MFLUCC 17-0557.

GenBank numbers LSU: MH376732; ITS: MH388358; SSU: MH388326.

Notes: Here we provide first record sexual morphs of *Paracylindrocarpon.* Based on morphology *P. xishuangbannaensis* and *P. nabanheensis* both have fusiform, 3–5-septate, hyaline ascospores, that are not constricted at septa, while *P. xishuangbannaensis* has 72 × 12 µm, 8-spored asci, with 34.5 × 5.6 µm ascospores, but *P. nabanheensis* has smaller (6–)8-spored, 64.4 × 10.5 µm asci, with larger ascospores (41 × 6.5 µm). In a BLASTn search on NCBI GenBank, the closest matches of ITS sequence of KUMCC 16-0144 is *Hyaloseta nolinae* with 90% identity to the strain CBS 109837 (NR_156291).

Nectriaceae Tul. & C. Tul.

Nectriaceae was erected by Tulasne and Tulasne (1865) with *Nectria* (Fr.) Fr. as the type genus. Nectriaceae is characterized by uniloculate, pigmented ascomata and phialidic amerosporous to phragmosporous conidia (Rossman et al. 1999; Rossman 2000; Lombard et al. 2015). Members of this family can be found as pathogens, saprobes, or are fungicolous or insecticolous (Rossman et al. 1999; Rossman 2000; Chaverri et al. 2011; Schroers et al. 2011; Hyde et al. 2014). In previous studies, the placement of Nectriaceae was not stable and it was placed in different orders such as Hypocreales (Seaver 1909a, b, 1910a, b, 1911) and Sphaeriales (Munk 1957; Dennis 1960). Petch (1938) accepted Nectriaceae as a separate family in Hypocreales and later, Miller (1949), Bessy (1950), Luttrell (1951), Dingley (1951a, b, 1952a, b, 1953, 1954, 1956), von Arx and

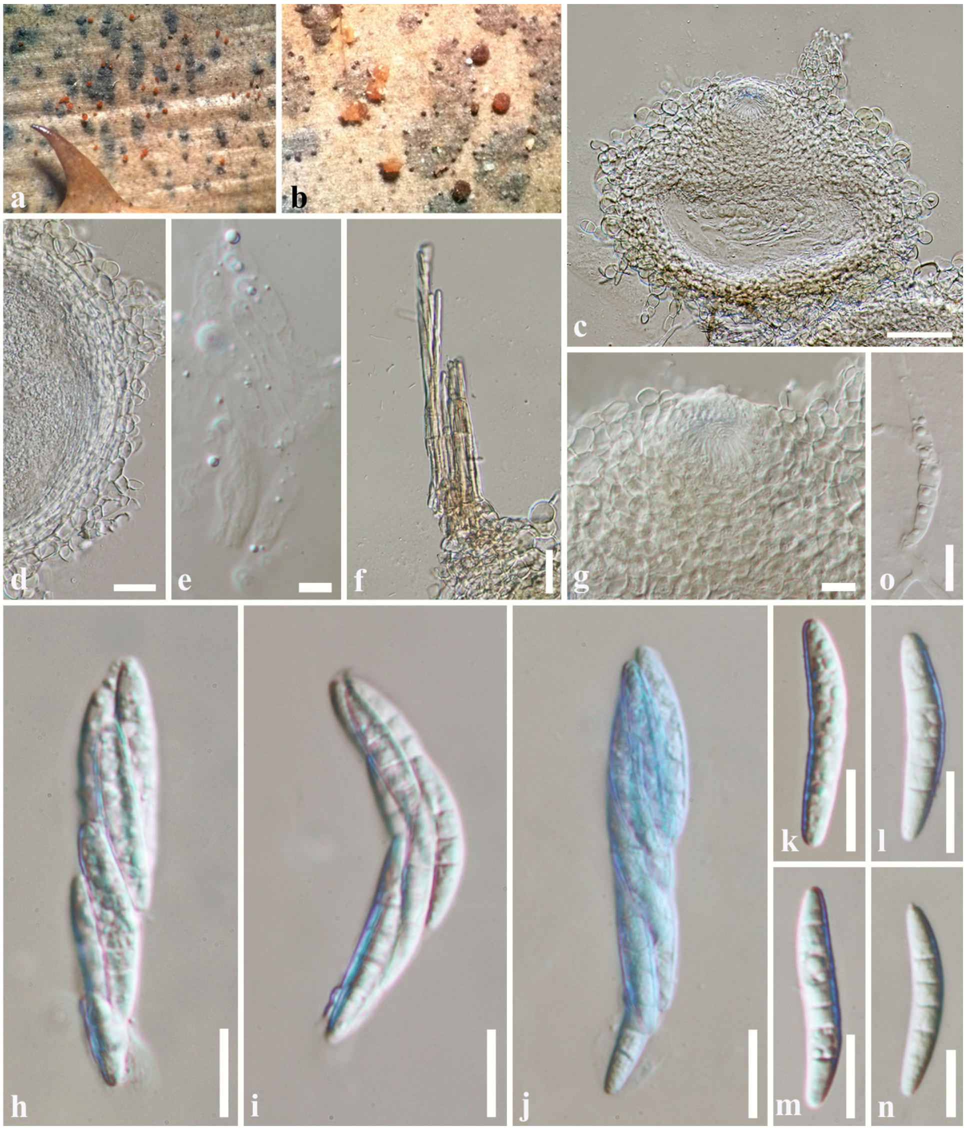


Fig. 78 ***Paracylindrocarpon xishuangbannaensis*** (HKAS 96204, **holotype**). **a, b** Appearance of ascomata on host substrate. **c** Section of ascoma. **d** Section of peridium. **e** Hamathecium. **f** Papilla. **g** Ostiole. **h, i** Asci. **j** Ascus strained with cotton blue reagent. **k–n** Ascospores. **o** Germinating ascospore. Scale bars: **c** = 40 µm, **d, f** = 20 µm, **e** = 5 µm, **g–o** = 10 µm

Müller (1954), Müller and von Arx (1962), Gäumann (1964), Rogerson (1970), and Barr (1990b) placed Nectriaceae synonyms under Hypocreaceae as one family. The family was later resolved by Lumbsch and Huhndorf (2010), Maharachchikumbura et al. (2015) and Lombard et al. (2015). There are 66 genera in the family (Wijayawardene et al. 2018). In this paper, we introduce new taxa to Nectriaceae based on phylogenetic evidence and morphology.

Cylindrocladiella Boesew.

Cylindrocladiella was erected by Boesewinkel (1982) to accommodate *C. parva* (P.J. Anderson) Boesew. Members of *Cylindrocladiella* spp. are found as soil-borne fungi, pathogens and/or saprobes of various plant hosts and substrates in temperate, sub-tropical and tropical regions. *Cylindrocladiella* has 43 epithets are listed in Index Fungorum (2018). We describe a new species from China.

Cylindrocladiella xishuangbannaensis Tibpromma & K.D. Hyde, ***sp. nov***.

Index Fungorum number: IF554536, *Facesoffungi number*: FoF04546; Fig. 79

Etymology: named after Xishuangbanna, where the fungus was first discovered.

Holotype: HKAS 96209

Saprobic on dead leaves of *Pandanus* sp. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Conidiophores* dimorphic, penicillate and subverticillate, mononematous, hyaline, penicillate, 456–476 × 6–7 µm ($\bar{x}$ = 469 × 6.4 µm, n = 5), conidiophores comprising a stipe, a penicillate arrangement of fertile branches, a stipe extension and a terminal vesicle; stipe septate, hyaline, smooth; stipe extension aseptate, straight, thick-walled with one basal septum, terminating in a thin-walled,

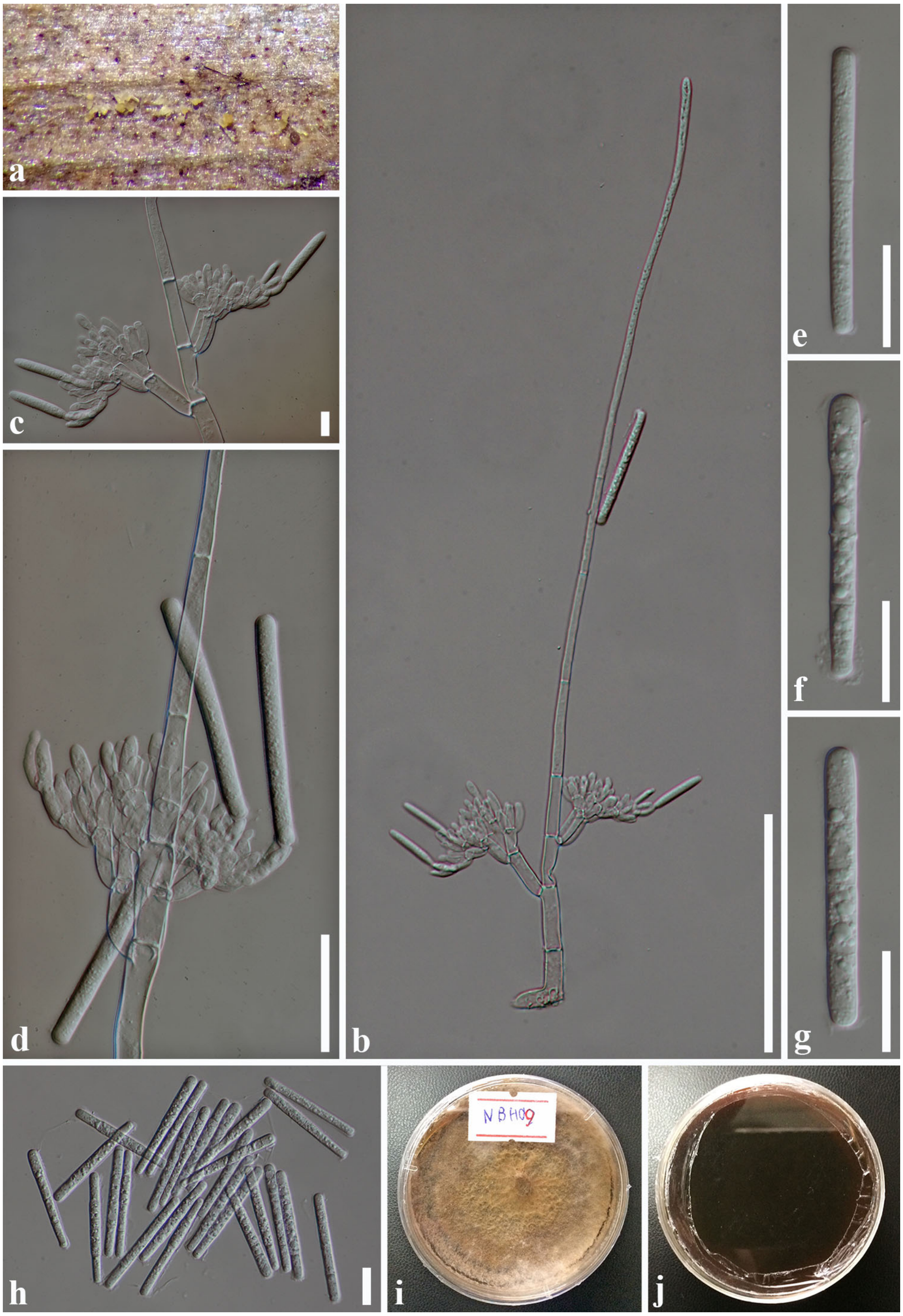


Fig. 79 ***Cylindrocladiella xishuangbannaensis*** (HKAS 96209, **holotype**). **a** Colonies on dead leaves of *Pandanus* sp. **b** Penicillate conidiophores. **c, d** Conidiophore branches, conidiogenous apparatus and phialides. **e–h** Conidia. **i, j** Colony on PDA from above and below. Scale bars: **b** = 100 µm, **c–h** = 20 µm

cylindrical vesicle. *Penicillate conidiogenous apparatus* 18–47.5 × 2.5–4 µm ($\bar{x}$ = 30 × 3.6 µm, n = 10), with primary branches aseptate, secondary branches aseptate, each terminal branch producing 2–4 phialides; phialides doliiform to cymbiform, hyaline, aseptate, apex with minute periclinal thickening and collarette. *Subverticillate* 6–12 × 2–4 µm ($\bar{x}$ = 9 × 3 µm, n = 20), conidiophores in moderate numbers, comprising a septate stipe, primary and secondary branches terminating in 1–3 phialides; primary branches straight, hyaline, 0–1-septate. *Conidia* 52.5–60.5 × 3–6 µm ($\bar{x}$ = 57 × 5 µm, n = 40), cylindrical, rounded at both ends, straight, 1-septate, frequently slightly flattened at the base, held in asymmetrical clusters by colourless slime.

Culture characteristics: Conidia germinating on PDA within 12 h. Colonies on PDA, circular, entire edge with cinnamon, raised on surface media, produce pigment on the media.

Material examined: CHINA, Yunnan Province, Xishuangbanna, Nabanhe, on *Pandanus* sp., 28 July 2016, S. Tibpromma NBH09 (HKAS 96209, **holotype**); ex-type living culture, KUMCC 16-0146 = MFLUCC 17-0559.

GenBank numbers LSU: MH376709; ITS: MH388337; SSU: MH388306; RPB2: MH412727.

Notes: This species morphologically fits within the generic concepts of *Cylindrocladiella*. Based on the multi-gene sequence analyses, *C. xishuangbannaensis* clusters with *C. camelliae* (Venkataram. & C.S.V. Ram) Boesew. (Fig. 74). We compare the morphology with *C. camelliae*, but they differ. *Cylindrocladiella camelliae* has a slight difference in terminal vesicle shape with conidia size 15–26 × 2–3.5 µm (Boesewinkel 1982). In a BLASTn search on NCBI GenBank, the closest matches of ITS sequence of KUMCC 16-0146 is *C. solicola* with 99% identity to the strain CMW47198 (MH017021), while the closest matches with the RPB2 sequence were with 99% identical *C. camelliae* strain CPC 234 (KM232304).

Pandanaceomyces Tibpromma & K.D. Hyde, ***gen. nov.***

Index Fungorum number: IF554537, *Facesoffungi number*: FoF04544

Etymology: named after the host family, Pandanaceae.

Type species: *Pandanaceomyces krabiensis* Tibpromma & K.D. Hyde

Saprobic on dead or decaying leaves and wood in terrestrial habitats. **Sexual morph** *Ascomata* scattered to gregarious, superficial or semi-immersed with flat on the base, conspicuous on host surface, pigments, solitary, uniloculate, oval, papillate with ostiole. *Peridium* composed of several layers, thin-walled of *textura prismatica*. *Hamathecium* cellular, comprising branched or unbranched, guttulate, septate paraphyses. *Asci* 6–8-spored, unitunicate, cylindrical to cylindrical-clavate, with furcated pedicel, apically with J- or J + apical ring. *Ascospores* fusiform, curved towards both ends, 1-septate, not constricted at septa, hyaline to subhyaline, with or without guttulate and mucilaginous sheath. **Asexual morph** Undetermined.

Notes: *Pandanaceomyces* bears a close morphological similarity with *Nectria* which has light to bright coloured, soft-textured, superficial, uniloculate ascomata and unitunicate asci (Hirooka et al. 2012). A new genus *Pandanaceomyces*, is therefore introduced to accommodate the present collection. However, *Pandanaceomyces* based on DNA data it can be distinguished from other genera (Fig. 74) and no high similarity (> 99%) hits were obtained when the LSU gene sequences were blasted against NCBI GenBank nucleotide database.

Pandanaceomyces krabiensis Tibpromma & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF554538, *Facesoffungi number*: FoF04545; Fig. 80

Etymology: named after Krabi Province, where the fungus was first discovered.

Holotype: MFLU 16-1909

Saprobic on dead leaves of *Pandanus* sp. **Sexual morph** *Ascomata* 115–133 × 100–120 µm ($\bar{x}$ = 125 × 109 µm, n = 5), scattered to gregarious, superficial to erumpent, with flat base, conspicuous on the host surface, easy to remove, yellow–orange, dull, solitary, uniloculate, oval, with hyaline papilla, with ostiole at centre. *Peridium* 7–10 µm wide, composed of several layers of thin-walled, yellow cells of *textura prismatica. Hamathecium* 8.5–11 µm wide, oval to ellipsoid, composed of cellular, unbranched, guttulate, septate paraphyses. *Asci* 37.5–48 × 6–11 µm ($\bar{x}$ = 43 × 7.5 µm, n = 20), (6–)8-spored, unitunicate, cylindrical to cylindrical-clavate, with short, furcate pedicel, with J- apical ring. *Ascospores* 11–16 × 2–3 µm ($\bar{x}$ = 13 × 2.5 µm, n = 20), fusiform, curved towards both ends, 1-septate, not constricted at the septum, hyaline to subhyaline, guttulate, without mucilaginous sheath, smooth-walled. **Asexual morph** Undetermined.

Culture characteristics: Ascospore germinating on MEA within 12 h. Colonies on MEA, purple at the central and pink at the margin, with irregular whorls, raised on media surface, dark-purple at the central with white at the margin from below.

Material examined: THAILAND, Krabi Province, Mueang Krabi District, on *Pandanus* sp., 14 December 2015, S. Tibpromma KB031 (MFLU 16-1909, **holotype**; HKAS 96258, **isotype**); ex-type living culture, MFLUCC 16-0323.

GenBank numbers LSU: MH376729; ITS: MH388355; SSU: MH388323; TEF1: MH388391.

Notes: Phylogenetic analysis of combined sequence data indicated that *Pandanaceomyces krabiensis* clusters in a separate clade from other members of Nectriaceae with 73% ML bootstrap support (Fig. 74). *Pandanaceomyces krabiensis* has fusiform, 1-septate, not constricted at septa, hyaline to subhyaline ascospores curved towards both ends.

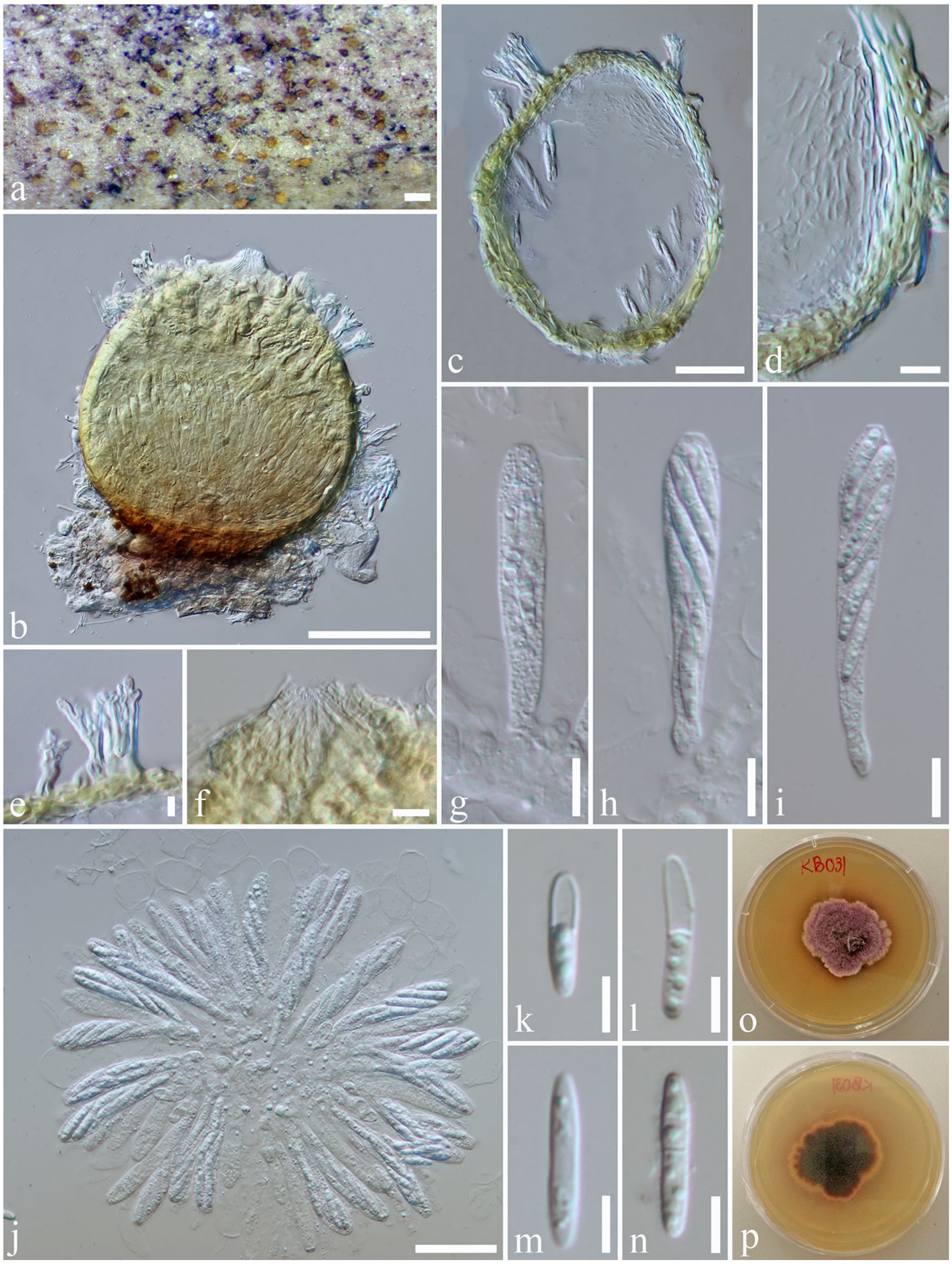
Pseudoachroiostachys Tibpromma & K.D. Hyde, ***gen. nov.***

Index Fungorum number: IF554547, *Facesoffungi number*: FoF04554

Etymology: name refers to the morphology being similar to *Achroiostachys*.

Type species: *Pseudoachroiostachys krabiense* Tibpromma & K.D. Hyde

Fig. 80 ***Pandanaceomyces pandanicola*** (MFLU 16-1909, **holotype**). **a** Appearance of ascomata on host substrate. **b** Ascoma. **c** Section of ascoma. **d** Section of peridium. **e** Papilla. **f** Ostiole. **g–j** Asci. **k-n** Ascospores. **o, p** Colony on MEA from above and below. Scale bars: **a** = 200 µm, **b** = 50 µm, **c, j** = 20 µm, **d, e, k–n** = 5 µm, **f–i** = 10 µm



Saprobic on dead or decaying leaves, wood in terrestrial habitats. *Mycelium* superficial, hyaline, rough, unbranched, septate, pale orange. **Sexual morph** Undetermined. **Asexual morph** *Conidiophores* macronematous, mononematous, unbranched, erect, straight, multi-septate, slightly thick-walled towards the base, hyaline and glassy, bearing a whorl of 5–6 conidiogenous cells. *Conidiogenous cells* terminal, phialidic, cylindrical, hyaline, smooth, narrowing to a short neck. *Conidia* ovoid, aseptate, sometimes flattened on one side, smooth, hyaline to subhyaline, rounded apex, in slimy masses, with or without mucilaginous sheath.

Notes: Combined rDNA gene sequence data revealed that *Pseudoachroiostachys* belongs to the family Stachybotryaceae and is closely related to *Pandanaceomyces* (Fig. 74). *Pseudoachroiostachys* is also similar to *Achroiostachys*, but the conidia of *Achroiostachys* are ellipsoidal, limoniform, globose to subglobose and contain 1–2 large or several small guttules (Lombard et al. 2016), while *Pseudoachroiostachys* has ovoid slimy conidia.

Pseudoachroiostachys krabiense Tibpromma & K.D. Hyde, ***sp. nov***.

Index Fungorum number: IF554548, *Facesoffungi number*: FoF04555; Fig. 81

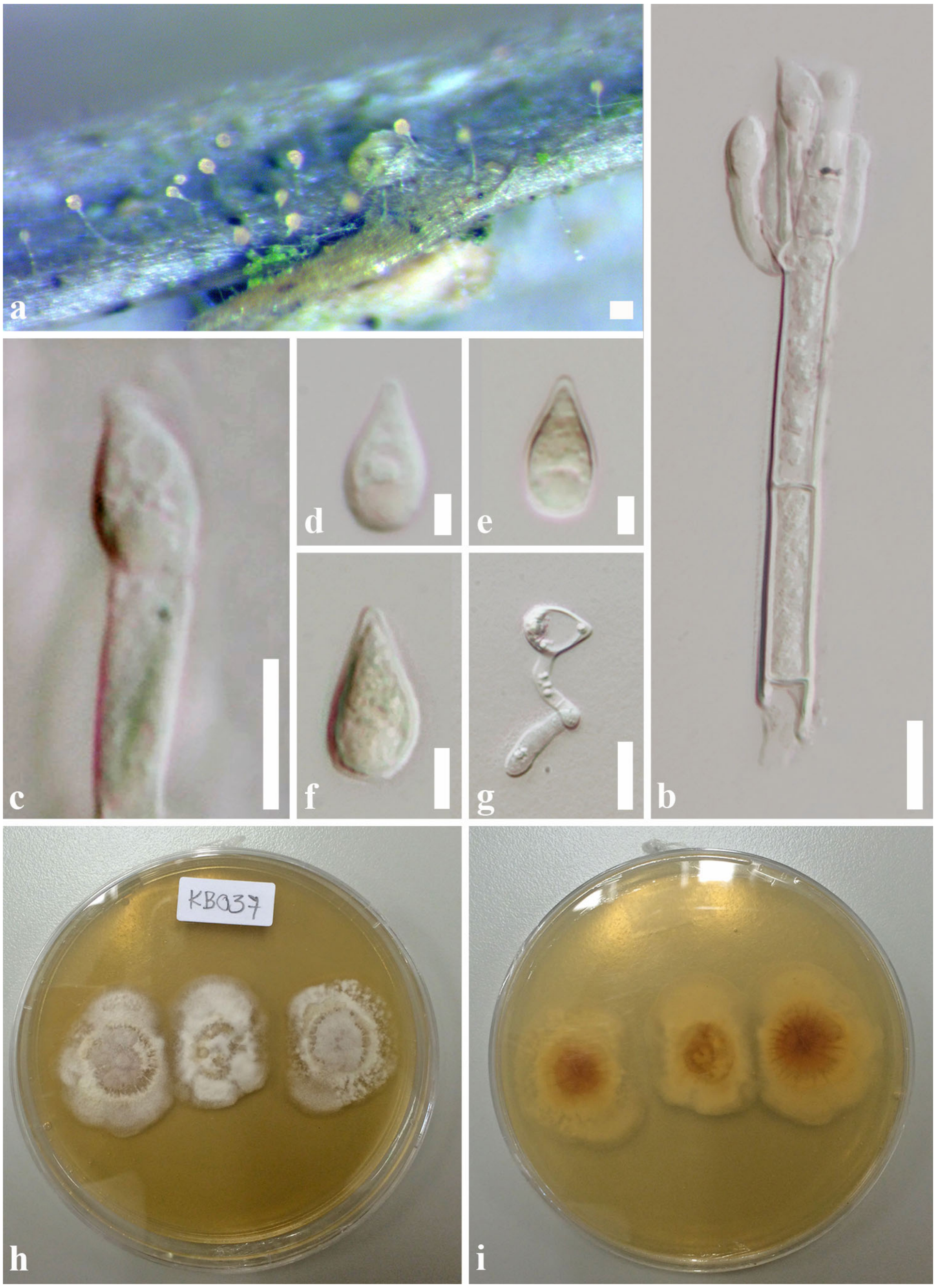


Fig. 81 ***Pseudoachroiostachy krabiense*** (MFLU 16-1915, **holotype**). **a** Colonies on dead leaf of *Pandanus* sp. **b** Conidiophores, conidiogenous cells and conidia. **c** Conidiogenous cells and conidia. **d–f** Conidia. **g** Germinating conidium. **h, i** Colonies on MEA from above and below. Scale bars: **a** = 50 μm, **b, c, g** = 5 μm, **d–f** = 2 μm

Etymology: named after Krabi Province, where the fungus was first discovered.

Holotype: MFLU 16-1915

Saprobic on dead leaves of *Pandanus* sp. *Mycelium* superficial, hyaline, rough, unbranched, septate, aggregated in dense fascicles, pale orange. **Sexual morph** Undetermined. **Asexual morph** *Conidiophores* 40–50 × 3.5–4.5 μm ($\bar{x}$ = 46 × 4 μm, n = 20), macronematous, mononematous, single, unbranched, erect, straight, 1–3-septate, slightly thick-walled towards the base, smooth, hyaline and glassy, bearing a whorl of 5–6 conidiogenous cells. *Conidiogenous cells* 6–8 × 1–2.5 μm ($\bar{x}$ = 7 × 2 μm, n = 20), terminal, phialidic, discrete, cylindrical, hyaline, smooth, 10–13 × 3.5–4.5 μm, narrowing to a short neck about 1 μm. *Conidia* 5–9 × 3–4 μm ($\bar{x}$ = 7 × 3.5 μm, n = 40), ovoid, in a group, aseptate, sometimes flattened on one side, smooth, hyaline, with rounded apex, slimy in mass, without mucilaginous sheath.

Culture characteristics: Conidia germinating on MEA within 12 h. Colonies on MEA, circular with whorls, undulate, white, smooth and raised on surface media, velvety.

Material examined: THAILAND, Krabi Province, Mueang Krabi District, on *Pandanus* sp., 15 December 2015, S. Tibpromma KB037 (MFLU 16-1915, **holotype**; HKAS 96264, **isotype**); ex-type living culture, MFLUCC 16-0325.

GenBank numbers LSU: MH376736; ITS: MH388362; SSU: MH388328; TEF1: MH388397.

Notes: *Achroiostachys aurantispora* L. Lombard & Crous has similar morphology with *Pseudoachroiostachys krabiense* in having similar colonies on host plant and conidiophores. *Achroiostachys aurantispora* has elongate ampulliform to ventricose or clavate conidiogenous cells and ellipsoidal conidia (Lombard et al. 2016) while *Pseudoachroiostachys krabiense* has cylindrical conidiogenous cells and ovoid conidia.

Volutella Fr.

Volutella was erected by Fries (1832) to accommodate *V. ciliata* (Alb. & Schwein.) Fr. *Volutella* is characterised by discoid sporodochia with marginal setae, simple to verticillate conidiophores, compact and phialidic conidiogenous cells, and 1-celled, ovoid to oblong conidia (Gräfenhan et al. 2011; Luo and Zhuang 2012; Lombard et al. 2015). There are 144 epithets are listed in Index Fungorum (2018), but only eight species have available sequences in GenBank. *Volutella mellea* J.F. Clark and *Volutella* sp. have been reported from Pandanaceae (Dingley et al. 1981; Thongkantha et al. 2008).

Volutella krabiense Tibpromma & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF554539, *Facesoffungi number*: FoF04547; Fig. 82

Etymology: named after Krabi Province, where the fungus was first discovered.

Holotype: MFLU 16-1932

Saprobic on dead leaves of *Pandanus* sp. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Setae* 60–113 × 2–4 µm ($\bar{x}$ = 92 × 3 µm, n = 10), hyaline, aseptate, cylindrical with conical apex. *Conidiophores* aggregated into sporodochia, with hyaline, stiff setae around the margin of conidiomata. *Conidiogenous cells* 2–4 × 2–3.5 µm ($\bar{x}$ = 3 × 2.5 µm, n = 20), monophialidic, hyaline, subulate. *Conidia* 3–4 × 1–2 µm ($\bar{x}$ = 3.4 × 1.5 µm, n = 30), slimy, aseptate, hyaline, oblong, guttulate, without mucilaginous sheath.

Culture characteristics: Conidia germinating on MEA within 12 h. Colonies on MEA, irregular, undulate edge with curled, white, flat on media surface.

Material examined: THAILAND, Krabi Province, Mueang Krabi District, on *Pandanus* sp., 14 December 2015, S. Tibpromma SF15-030 (MFLU 16-1932, **holotype**; HKAS 96281, **isotype**); ex-type living culture, MFLUCC 16-0268 = KUMCC 17-0305.

GenBank numbers LSU: MH376741; ITS: MH388367; SSU: MH388331; TEF1: MH388401.

Notes: *Volutella krabiense* has a close phylogenetic affinity to *V. thailandensis* in multi-gene phylogenetic analysis (Fig. 74). *Volutella krabiense* has smaller conidia than *V. thailandensis* (4 × 1.3 vs. 5 × 2 µm) and conidiomata of *V. thailandensis* lack setae. In a BLASTn search on NCBI GenBank, the closest matches of SSU sequence of MFLUCC 16-0268 is *V. aeria* with 99% identity to the strain CGMCC 3.17945 (KY883302).

Volutella thailandensis Tibpromma & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF554540, *Facesoffungi number*: FoF04548; Fig. 83

Etymology: named after Thailand, where the fungus was first discovered.

Holotype: MFLU 18-0014

Saprobic on dead leaves of *Pandanus* sp. **Sexual morph** *Ascomata* 115–140 × 100–130 µm ($\bar{x}$ = 128 × 114 µm, n = 5), scattered to gregarious, superficial, flat at the base, conspicuous on host surface, easy to remove, black, dull, solitary, uniloculate, black with conspicuous setae, without ostiole. *Peridium* composed of several layers of thin-walled subhyaline to pale brown cells of *textura prismatica. Hamathecium* composed of 2–9.4 µm wide, cylindrical, cellular, unbranched, guttulate, septate paraphyses. *Asci* 25–40 × 6–9 µm ($\bar{x}$ = 36 × 7.4 µm, n = 20), (6–)8-spored, unitunicate, cylindrical to cylindrical-clavate, with short furcate pedicel. *Ascospores* 10–16 × 2–5 µm ($\bar{x}$ = 14 × 3 µm, n = 20), fusiform, curved towards both ends, 1-septate, constricted at septum, hyaline to subhyaline, guttulate, with mucilaginous sheath. **Asexual morph** Hyphomycetous. *Conidiophores* aggregated into sporodochia or synnemata, without hyaline setae around the margin of conidiomata. *Conidiogenous cells* 7–15 × 1–2.5 µm ($\bar{x}$ = 12 × 2 µm, n = 20), monophialidic, hyaline, subulate. *Conidia* 3–8 × 1–3 µm ($\bar{x}$ = 5 × 2 µm, n = 40), slimy, aseptate, hyaline, oblong, guttulate, without a mucilaginous sheath.

Culture characteristics: Ascospores germinating on MEA within 12 h. Colonies on MEA, filamentous, hyaline, smooth and flat on surface media.

Material examined: THAILAND, Prachuap Khiri Khan Province, Bang Saphan District, on *Pandanus* sp., 30 July 2015, S. Tibpromma SF15-034 (MFLU 18-0014, **holotype**; HKAS 100839, **isotype**); ex-type living culture, MFLUCC 16-0366 = MFLUCC 16-0368 = KUMCC 16-0160.

GenBank numbers LSU: MH376742; ITS: MH388368; SSU: MH388332; TEF1: MH388402.

Notes: The sexual and asexual morphs of *Volutella thailandensis* fits well within the holomorphconcept for *Volutella* (Grafenhan et al. 2011; Seifert et al. 2011). In the phylogenetic tree (Fig. 74) based on the sequences of

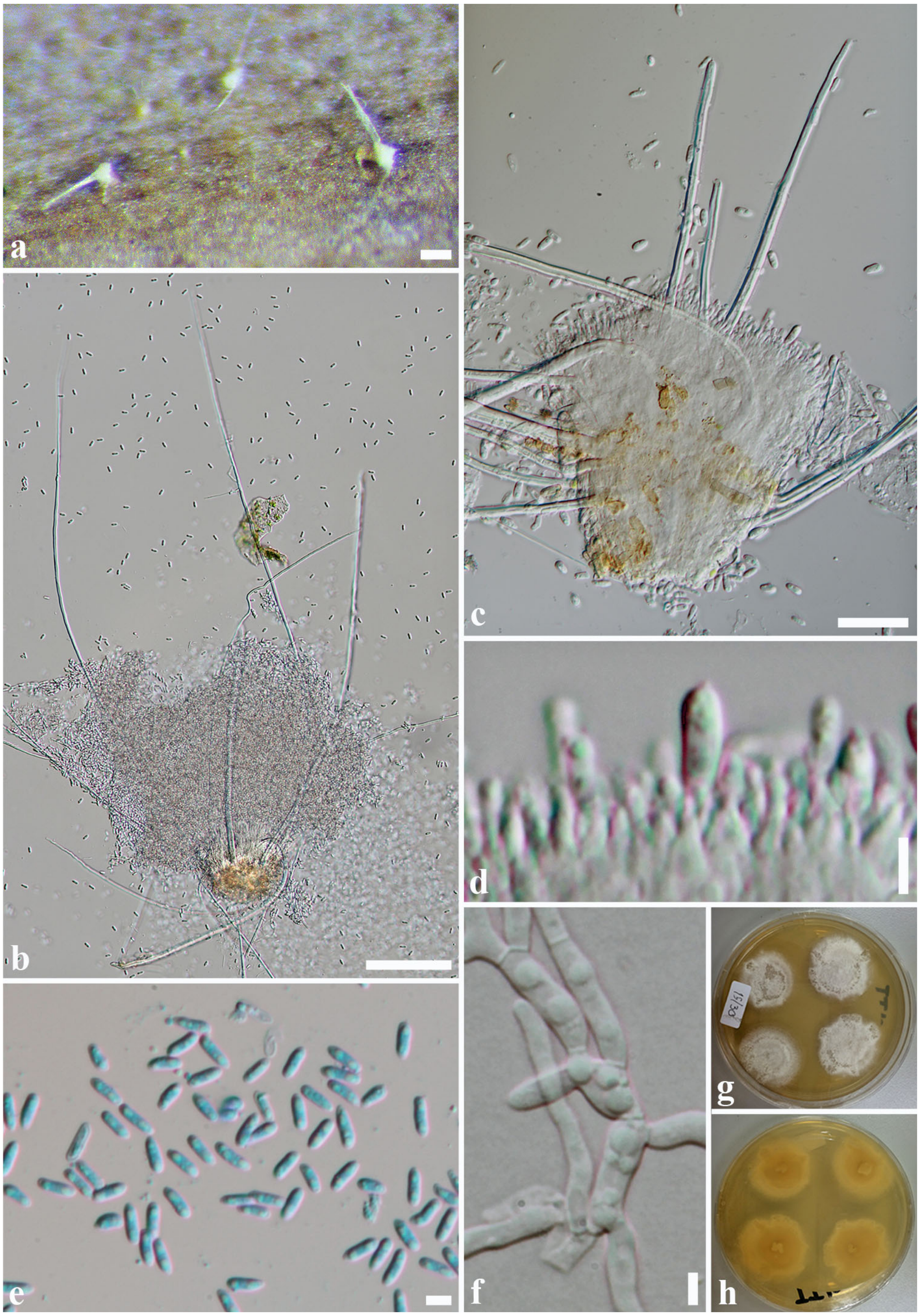


Fig. 82 ***Volutella krabiense*** (MFLU 16-1932, **holotype**). **a, b** Sporodochial conidiomata on dead leaves of *Pandanus* sp. **c, d** Conidiophores, conidiogenous cells and conidium. **e** Conidia strain with cotton blue. **f** Germinating conidium. **g, h** Colonies on MEA from above and below. Scale bars: **b** = 50 µm, **c** = 20 µm, **d–f** = 5 µm

multi-gene, *V. thailandensis* clusters with *V. krabiense*, but there are more than 30 bp (5.83%) differences in 514 ITS (+5.8S) nucleotides between the two species and thus indicating they are distinct species. In a BLASTn search on NCBI GenBank, the closest matches of ITS sequence of MFLUCC 16-0366 is *Volutella* sp. with 99% identity to the strain DoF21 (JQ388266).

Niessliaceae Kirschst.

Niessliaceae was introduced by Kirschstein (1939) with *Niesslia* Auersw. as the type genus. Members of this family are saprobic or parasitic on wood, leaves or lichens (Maharachchikumbura et al. 2016). The family was accepted in a narrow sense by Barr (1990b) and was separated from other families: Sphaeriaceae (Müller and von Arx 1962, 1973) and Trichosphaeriaceae (Barr 1983; Hawksworth et al. 1983). Eriksson and Hawksworth (1993), Hawksworth et al. (1995) and Samuels and Barr (1997) and accepted this family in the Hypocreales based on

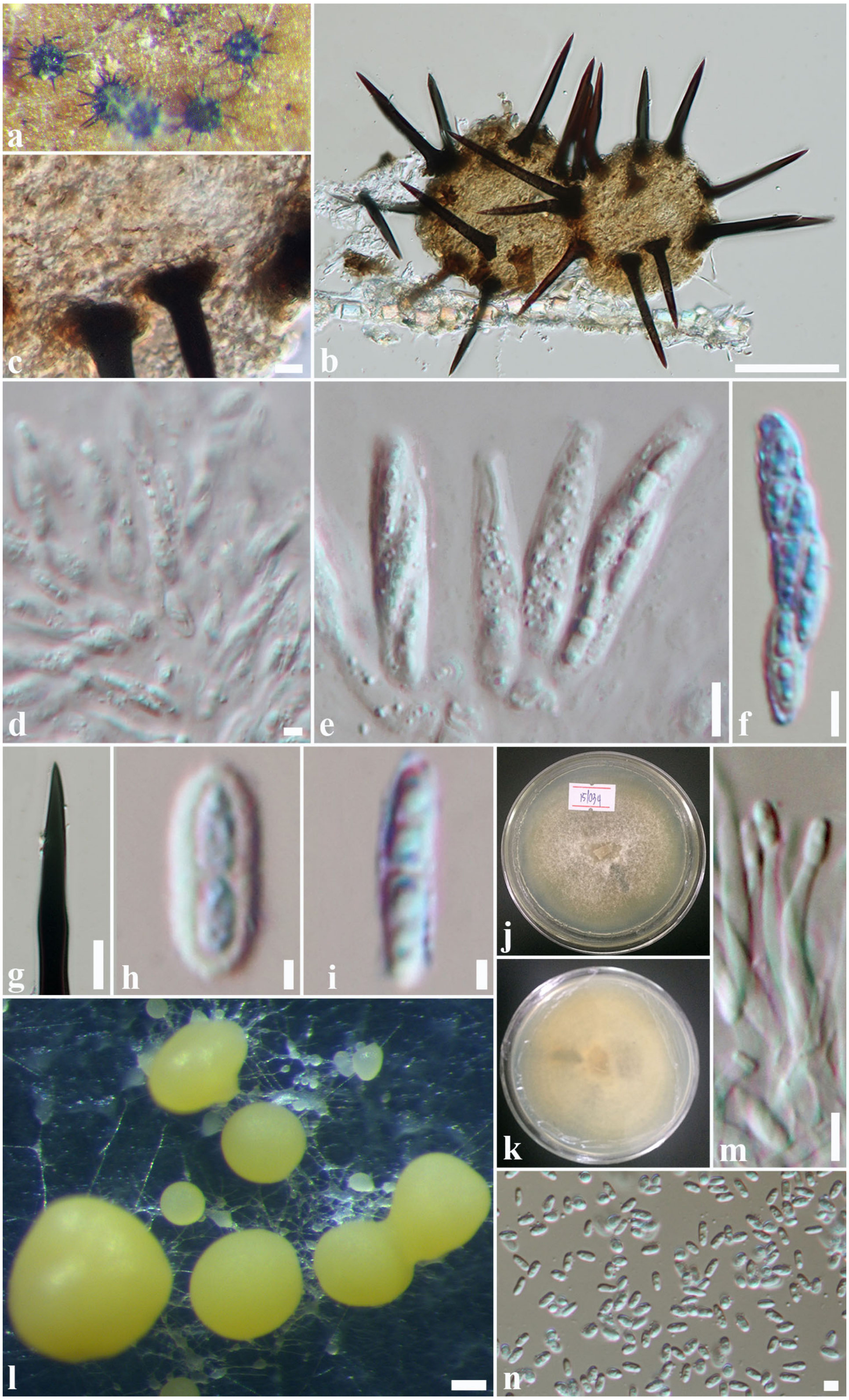


Fig. 83 ***Volutella thailandensis*** (MFLU 18-0014, **holotype**). **a** Appearance of ascomata on host substrate. **b** Ascomata. **c** Ascoma wall. **d** Hamathecium. **e** Asci. **f** Asci stained with cotton blue reagent. **g** Papilla. **h, i** Ascospores stained with cotton blue reagent. **j, k** Culture growing on MEA media. **l** Sporodochia formed in culture. **m** Conidiogenous cells and conidia formed in culture. **n** Conidia formed in culture. Scale bars: **b** = 50 µm, **c, e, f, m, n** = 5 µm, **d, h, i** = 2 µm, **g** = 10 µm, l = 200 µm

morphological features. Lumbsch and Huhndorf (2010) accepted 17 genera in the family and Jaklitsch and Voglmayr (2012) confirmed the placement of Niessliaceae in the Hypocreales by molecular data. An update for this family is provided in Maharachchikumbura et al.

(2015, 2016) and Wijayawardene et al. (2018). We introduce a new monotypic genus in this family.

Pseudohyaloseta Tibpromma & K.D. Hyde, ***gen. nov.***

Index Fungorum number: IF554542, *Facesoffungi number*: FoF04549

Etymology: name refers to the characteristics similar to *Hyaloseta*.

Type species: *Pseudohyaloseta pandanicola* Tibpromma & K.D. Hyde

Saprobic on dead or decaying leaves or wood in terrestrial habitats. **Sexual morph** *Ascomata* scattered to gregarious, superficial or semi-immersed, flat at the base, conspicuous on host surface, pigmented, shiny, usually flattened when dry, solitary or in small groups, globose to subglobose, deflated at the middle, with hyaline papilla, ostiole. *Peridium* composed of several layers, thin-walled; outer layers comprising thin-walled, yellow–brown to brown cells of *textura prismatica* and inner layer of larger, thin-walled, lightly pigmented or hyaline cells of *textura angularis*. *Hamathecium* of filiform, filamentous, unbranched, guttulate, septate paraphyses. *Asci* 6–8-spored, unitunicate, obclavate, pedicellate, with J-, apical ring. *Ascospores* cylindrical, curved towards both ends, 1-septate, slightly constricted at septum, hyaline to subhyaline, rough at the margin, guttulate, with a mucilaginous sheath. **Asexual morph** Undetermined.

Notes: The morphology of *Pseudohyaloseta* is similar to that of *Hyaloseta*. Based on phylogenic analysis, *Pseudohyaloseta* is well-separated from *Hyaloseta* (100% in ML, Fig. 74). There are more than 30 bp (> 5.60%) differences in 535 ITS (+5.8S) nucleotides and 14 bp (1.70%) in 819 LSU nucleotides between *Hyaloseta* and *Pseudohyaloseta*. Therefore, *Pseudohyaloseta* is introduced here as a new genus in Niessliaceae based on phylogenetic and morphological evidences.

Pseudohyaloseta pandanicola Tibpromma & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF554543, *Facesoffungi number*: FoF04550; Fig. 84

Etymology: named after the host genus, *Pandanus*.

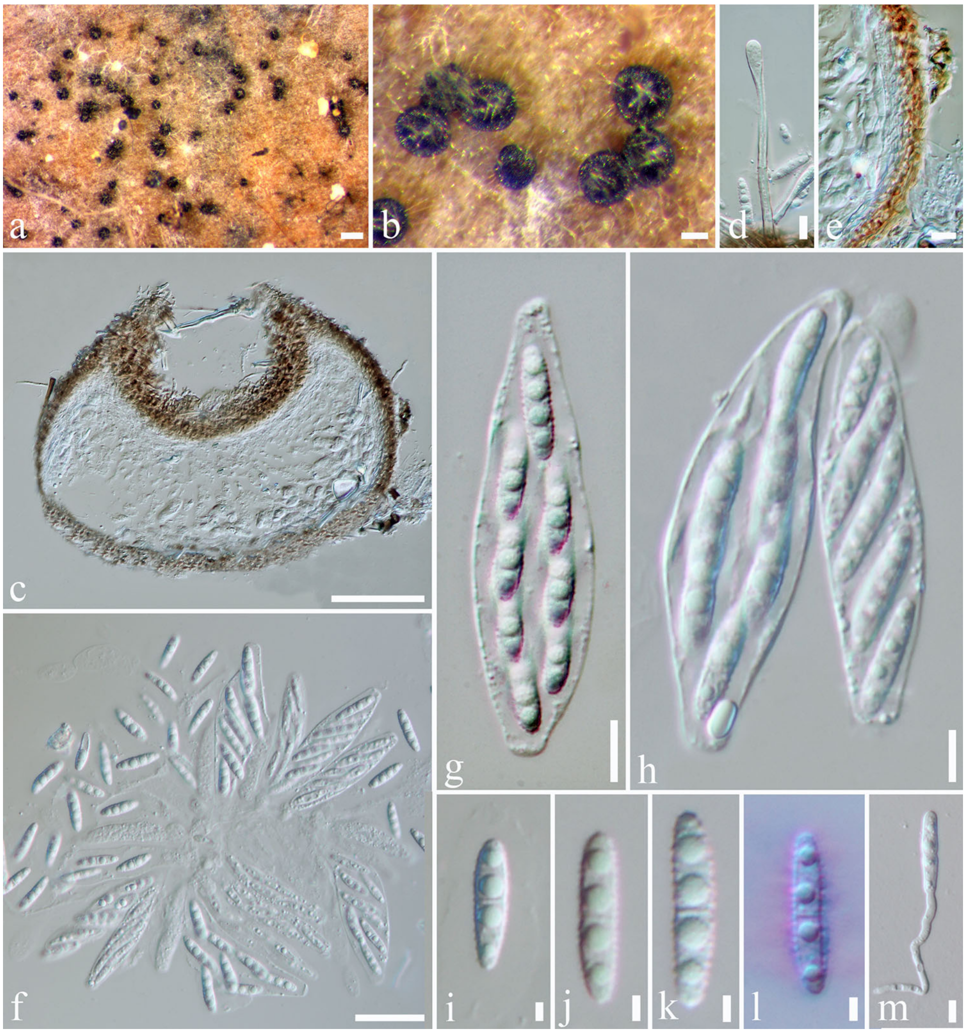


Fig. 84 ***Pseudohyaloseta pandanicola*** (MFLU 16-1882**, holotype**). **a, b** Appearance of ascomata on host substrate. **c** Section of ascoma. **d** Papilla. **e** Section of peridium. **f–h** Asci. **i–l** Ascospores. **m** Germinating ascospore. Scale bars: **a** = 200 μm, **b, c** = 50 μm, **d, e, g, h, m** = 5 μm, **f** = 20 μm, **i–l** = 2 μm

Holotype: MFLU 16-1882

Saprobic on dead roots of *Freycinetia javanica*. **Sexual morph** *Ascomata* 100–200 × 60–100 µm ($\bar{x}$ = 139 × 80 µm, n = 5), scattered to gregarious, superficial, flat at the base, conspicuous on host surface, black, shiny, solitary, uniloculate, globose to subglobose, compressed at the middle, with a hyaline papilla, ostiole. *Peridium* 9–15 µm wide, composed of several layers; outer layers comprising thin-walled, yellow–brown to brown of *textura prismatica* and inner layer of larger, thin-walled, lightly pigmented or hyaline cells of *textura angularis*. *Hamathecium* with 1–3.8 µm wide, filiform, filamentous, unbranched, guttulate, septate paraphyses. *Asci* 45–60 × 9–16 µm ($\bar{x}$ = 52 × 12 µm, n = 20), (6–)8-spored, unitunicate, obclavate, short-pedicellate, with J- apical ring. *Ascospores* 9–17 × 3–4 µm ($\bar{x}$ = 15 × 3.5 µm, n = 40), cylindrical, curved towards both ends, 1-septate, slightly constricted at septum, hyaline to subhyaline, rough at the margin, guttulate, with mucilaginous sheath. **Asexual morph** Undetermined.

Culture characteristics: Ascospores germinating on MEA within 12 h. Colonies on MEA, dark green to dark on the surface, dense, circular, with entire edge, raised, dark brown from below, with smooth margin.

Material examined: THAILAND, Phang Nga Province, Thap Put District, on *Freycinetia javanica* Blume., 17 December 2015, S. Tibpromma KB004 (MFLU 16-1882**, holotype**; HKAS 96233, **isotype**); ex-type living culture, MFLUCC 16-0316; Chiang Mai Province, Mae Taeng District, Mushroom Research Foundation, on *Pandanus* sp., 16 December 2017, S. Tibpromma P09 (MFLU 18-0028, **paratype**).

GenBank numbers LSU: MH376737; ITS: MH388363; TEF1: MH388398; RPB2: MH412733.

Notes: *Pseudohyaloseta pandanicola* is similar to *Hyaloseta nolinae* A.W. Ramaley, but can be differentiated from *H. nolinae* has 28–48 × 3.2–4.8 µm, oblong asci, and 5.6–7.2(9.6) × 2.4 µm, oblong-ellipsoid ascospores (Ramaley 2001). In the phylogenetic analysis, based on the multi-gene sequence analyses, *P. pandanicola* formed a separate branch from *H. nolinae*.

Stachybotryaceae L. Lombard & Crous

Stachybotryaceae was introduced by Crous et al. (2014) to accommodate *Myrothecium*, *Peethambara* and *Stachybotrys*. Castlebury et al. (2004) and Summerbell et al. (2011) showed those three genera form a monophyletic lineage, distinct from other families in the Hypocreales. There are 33 genera in the family (Wijayawardene et al. 2018). We collected taxa of Stachybotriaceae from Pandanaceae and confirm their identity in the order. In this paper, we introduce one new genus, *Pseudoornatispora* and a new species of *Parasarcopodium* and *Sirastachys* with an updated phylogeny (Fig. 74).

Parasarcopodium Mel'nik et al.

Parasarcopodium is a hyphomycetous genus, which was erected by Mel'nik et al. (2004) with *P. ceratocaryi* Mel'nik, S.J. Lee & Crous as the type species. *Parasarcopodium* was earlier placed in family Bionectriaceae (Mel'nik et al. 2004), but recently included in Stachybotryaceae (Maharachchikumbura et al. 2015). At present there are two epithets are listed in Index Fungorum (2018). *Parasarcopodium pandanicola* Tibpromma & K.D. Hyde has been previously recorded from Pandanaceae (Tibpromma et al. 2016a).

Parasarcopodium hongkongensis Tibpromma & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF554546, *Facesoffungi number*: FoF04553; Fig. 85

Etymology: named after Hong Kong, where the fungus was first discovered.

Holotype: HKAS 100859

Saprobic on dead leaves of *Pandanus* sp. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Conidiomata sporodochia* superficial on host surface scattered, solitary, orange, with long papilla. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 6–8.5 × 2–3 µm ($\bar{x}$ = 7.5 × 2.5 µm, n = 10), simple, smooth, enteroblastic, phialidic, ampulliform, hyaline, smooth-walled. *Conidia* 12–18 × 1.5–3 µm ($\bar{x}$ = 15 × 2 µm, n = 40), hyaline, filiform, straight to slightly curved, aseptate, smooth, thick-walled, distinctly guttulate, with an appendage at the base.

Culture characteristics: Conidia germinating on MEA within 12 h. Colonies on MEA reaching 9 cm diam., after 7 days at room temperature, circular, edge entire, white with brown, with dense, aerial mycelium on surface, rough with wrinkled, with small-dots, black; reverse of culture brown to black.

Material examined: HONG KONG, Tai Tam Tuk Reservoir, on *Pandanus* sp., 21 September 2016, S. Tibpromma HK02 (HKAS 100859, **holotype**); ex-type living culture, KUMCC 17-0267 = MFLUCC 17-0632; THAILAND, Krabi Province, Mueang Krabi District, on *Pandanus* sp., 14 December 2015, S. Tibpromma KB034 (MFLU 16-1912, **paratype**).

GenBank numbers LSU: MH376733; ITS: MH388359; SSU: MH388327; TEF1: MH388394.

Notes: *Parasarcopodium hongkongensis* has hyaline, filiform, straight to slightly curved, aseptate, basally appendaged conidia which are similar to the conidia of *P. pandanicola* Tibpromma & K.D. Hyde. However, they differ in size of conidiogenous cells and conidia. *Parasarcopodium hongkongensis* has conidiogenous cells 6–8.5 × 2–3 µm with conidia 12–18 × 1.5–3 µm, while

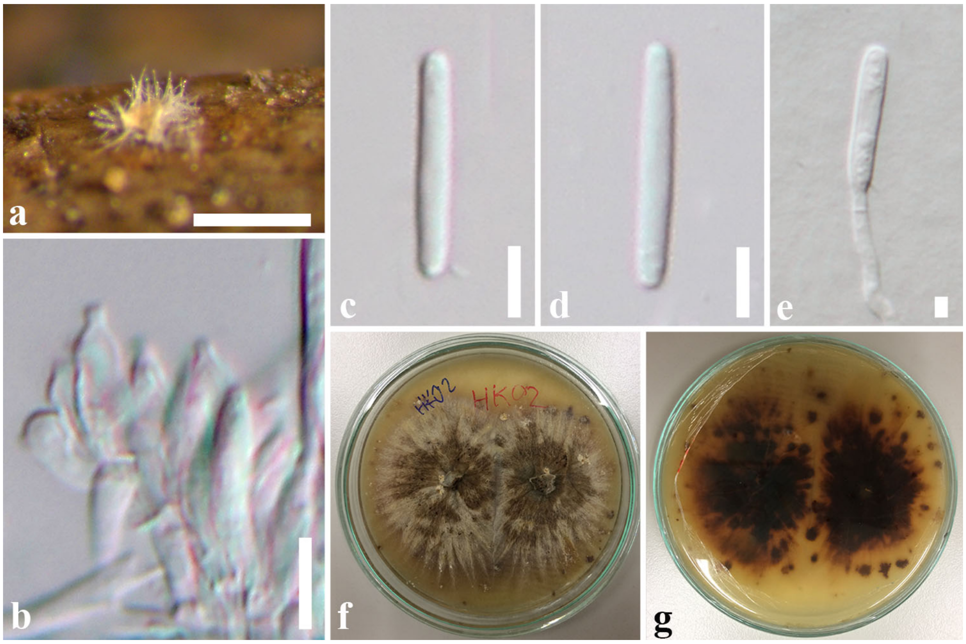


Fig. 85 ***Parasarcopodium hongkongensis*** (HKAS 100859, **holotype**). **a** Colony on dead leaves of *Pandanus* sp. **b** Conidiogenous cells with conidiophores. **c, d** Conidia with a small appendage in conidial base. **e** Germinating conidium. **f, g** Colonies on MEA from above and below. Scale bars: **a** = 500 µm. **b–e** = 5 µm

P. pandanicola has conidiogenous cells 5–14 × 3–4 µm with conidia 10–20 × 2–3 µm (Tibpromma et al. 2016a). Comparing SSU nucleotides of *P. hongkongensis* and *P. pandanicola* we found 29 bp (2.68%) differences in 1080 SSU nucleotides. Based on phylogeny *P. hongkongensis* is distinct from other species of *Parasarcopodium* with high support (98% in ML, Fig. 74). In a BLASTn search on NCBI GenBank, the closest matches of ITS sequence of KUMCC 17-0267 is *P. ceratocaryi* with 92% identity to the strain CBS 110664 (NR_154283).

Pseudoornatispora Tibpromma & K.D. Hyde, ***gen. nov.***

Index Fungorum number: IF555336, *Facesoffungi number*: FoF04551

Etymology: name refers to the characteristics similar to *Ornatispora*.

Type species: *Pseudoornatispora krabiense* Tibpromma & K.D. Hyde

Saprobic on dead or decaying leaves, wood in terrestrial habitats. **Sexual morph** *Ascomata* scattered or gregarious, superficial or semi-immersed with flat base, conspicuous on host surface, back, shiny, globose to subglobose, covered by dark brown, papilla, with or without ostiole, with hyaline setae-like periphyses. *Peridium* composed of several layers; outer layers comprising thick-walled, pale brown to brown cells of *textura angularis*; inner layers of larger, thin-walled, lightly pigmented or hyaline cells of *textura angularis*. *Hamathecium* with filiform, cellular, branched or unbranched, guttulate, aseptate paraphyses. *Asci* 6–8-spored, unitunicate, cylindrical-clavate, with club shape pedicel, J- apical ring. *Ascospores* fusiform, curved towards both end, 1-septate, constricted at septum, hyaline to subhyaline, rough at the margin, guttulate, with mucilaginous sheath. **Asexual morph** Hyphomycetous. *Conidiophores* aggregated in dense fascicles. *Conidiogenous cells* holoblastic, phialidic, discrete, cylindrical, hyaline, conical at apex. *Conidia* ellipsoid, hyaline to subhyaline, tapering to conical apex, aseptate, guttules, without mucilaginous sheath, smooth-walled.

Notes: *Pseudoornatispora* is introduced as a monotypic genus to accommodate *P. krabiense* based on morphology (sexual and asexual morphs) and phylogenetic analysis. The sexual morph *Pseudoornatispora* is similar to *Ornatispora* (≡ *Stachybotrys*) K.D. Hyde, Goh, Joanne E. Taylor, J. Fröhl. in ascomata and ascospores characters, which are black ascomata with seta and ostioles, and hyaline, 1-septate and verrucose ascospores (Hyde et al. 1999), but this genus has never been sequenced and is probably polyphyletic. The asexual morph of *Pseudoornatispora* is morphologically similar to *Peethambara* Subram. & Bhat, but these two genera are phylogenetically apart in multi-gene phylogenetic analysis. Fresh collections are needed.

Pseudoornatispora krabiense Tibpromma & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF555337, *Facesoffungi number*: FoF04552; Figs. 86, 87

Etymology: named after Krabi Province, where the fungus was first discovered.

Holotype: MFLU 16-1892

Saprobic on dead leaves of *Pandanus* sp. **Sexual morph** *Ascomata* 150–200 × 165–180 µm ($\bar{x}$ = 172 × 172.5 µm,

Fig. 86 ***Pseudoornatispora krabiense*** (MFLU 16-1892, **holotype**). **a, b** Appearance of ascomata on host substrate. **c** Ascoma. **d** Section of ascoma. **e** Section of peridium. **f** Ostiole. **g** Papilla. **h–i** Asci. **j** Paraphyses. **k**–**n** Ascospores. **o** Germinating ascospore. **p, q** Colonies on MEA from above and below. Scale bars: **a, b** = 100 µm, **c, d** = 50 µm, **e, g–i** = 10 µm, **f** = 20 µm, **j–o** = 5 µm

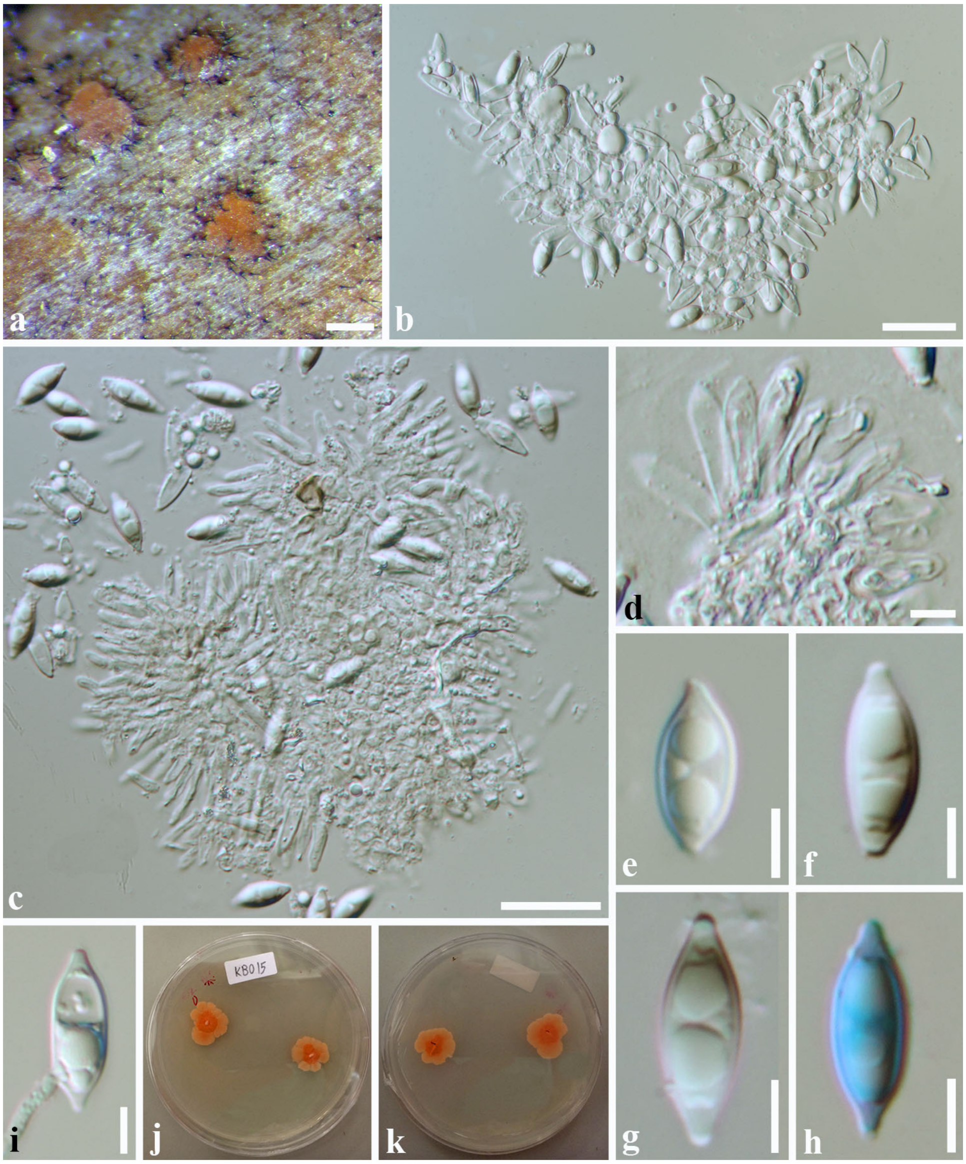


Fig. 87 ***Pseudoornatispora krabiense*** (MFLUCC 16-0318). **a** Colonies on dead leaves of *Pandanus* sp. **b, c** Conidiogenous cells and conidia. **d** Conidiogenous cells. **e–g** Conidia. **h** Conidium strained in cotton blue reagent. **i** Germinating conidium. **j, k** Colonies on MEA from above and below. Scale bars: **a** = 200 µm, **b, c** = 20 µm, **d–i** = 5 µm

n = 5), scattered to gregarious, superficial, flat on the base, conspicuous on host surface, back, shiny, solitary, uniloculate, globose to subglobose, covered by dark septate setae, papillate, centrally located ostiole with pore-like opening and with hyaline periphyses. *Peridium* 20–30 µm wide, composed of several layers; outer layers comprising thick-walled, pale brown to brown of *textura angularis* and inner layers of larger, thin-walled, lightly pigmented or hyaline cells of *textura angularis*. *Hamathecium* composed of 4–5 µm wide, filiform, cellular, unbranched, guttulate, aseptate paraphyses. *Asci* 70–130 × 15–20 µm ($\bar{x}$ = 89.5 × 17 µm, n = 10), (6–)8-spored, unitunicate, cylindrical-clavate, with club-shaped pedicel, with J- apical ring. *Ascospores* 26–43 × 5–17 µm ($\bar{x}$ = 34.5 × 9.5 µm, n = 30), fusiform, curved towards both ends, 1-septate, constricted at septum, hyaline to subhyaline, rough at the margin, guttulate, with mucilaginous sheath. **Asexual morph** Hyphomycetous. *Conidiophores* aggregated in dense fascicles, sporodochial. *Conidiogenous cells* 9–15 × 3–4 µm ($\bar{x}$ = 11 × 3.5 µm, n = 10), holoblastic, phialidic, discrete, cylindrical, smooth, hyaline, with conical apex. *Conidia* 10–17 × 4–6 µm ($\bar{x}$ = 14.6 × 5 µm, n = 30), ellipsoid, solitary, hyaline, tapering to conical apex and base, aseptate, smooth, guttulate, slimy, without a mucilaginous sheath, smooth-walled.

Culture characteristics: Ascospores germinating on MEA within 12 h. Colonies on MEA, orange pink, with irregular, curled, flat and dry on media surface, orange pink in reverse.

Material examined: THAILAND, Krabi Province, Mueang Krabi District, on *Pandanus* sp., 15 December 2015, S. Tibpromma KB014 (MFLU 16-1892, **holotype**;

HKAS 96242, **isotype**); ex-type living culture, MFLUCC 16-0317; Krabi Province, Mueang Krabi District, on *Pandanus* sp., 15 December 2015, S. Tibpromma KB015 (MFLU 16-1893; HKAS 96243, **paratype**); living culture, MFLUCC 16-0318 = KUMCC 16-0139.

GenBank numbers MFLUCC 16-0317 LSU: MH376721; ITS: MH388348; SSU: MH388315; TEF1: MH388383; RPB2: MH412729. MFLUCC 16-0318 LSU: MH376722; ITS: MH388349; SSU: MH388316; TEF1: MH388384; RPB2: MH412730.

Notes: The sexual morph of *Pseudoornatispora krabiense* is similar to *Stachybotrys* which has superficial, globose ascomata covered with numerous setae, clavate, pedicellate asci, and ellipsoidal, 1-septate and verrucose ascospores (Corda 1837; Wang et al. 2015). However, *P. krabiense* differs as ascospores are rough at the margin and guttulate and have a mucilaginous sheath. The sexual morph of *Pseudoornatispora krabiense* is similar to *Stachybotrys* in having superficial, globose ascomata, covered with numerous setae, clavate, pedicellate asci, and ellipsoidal, 1-septate and verrucose ascospores (Corda 1837). *Pseudoornatispora krabiense* is similar to *Ornatispora novae-zelandiae* Whitton, K.D. Hyde & McKenzie, but *O. novae-zelandiae* has narrowly clavate, 8-spored asci, with an apical refractive ring and discoid, narrowly ellipsoid to ellipsoid or fusoid and verrucose ascospores (Whitton et al. 2012), while *P. krabiense* differs in having cylindrical-clavate, (6–)8-spored asci, with a club-shaped pedicel and J- apical ring, and fusiform ascospores, which are rough at the margin, guttulate, and with mucilaginous sheath.

Sirastachys L. Lombard & Crous

Sirastachys was introduced by Lombard et al. (2016) to accommodate *S. phaeospora* L. Lombard & Crous. *Sirastachys* is a stachybotrys-like fungus that forms synnemata in culture. Phylogenetic analyses showed that *Sirastachys* forms a well-supported clade distantly related to *Stachybotrys* (Lombard et al. 2016). At present, there are eight epithets are listed in Index Fungorum (2018). *Sirastachys pandanicola* L. Lombard & Crous has been reported from Singapore on a decaying leaf of *Pandanus* sp. (Lombard et al. 2016).

Sirastachys phangngaensis Tibpromma & K.D. Hyde, ***sp. nov***.

Index Fungorum number: IF554549, *Facesoffungi number*: FoF04556; Fig. 88

Etymology: named after Phang Nga Province, where the fungus was first discovered.

Holotype: MFLU 16-0544

Saprobic on dead leaf of *Pandanus* sp. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Mycelium* composed of septate, branched, smooth, subhyaline, hyphae. *Conidiophores* 35–46 × 2–3 µm ($\bar{x}$ = 42.6 × 2.4 µm, n = 10), wider at the base, determinate, macronematous, solitary or in groups, erect, unbranched, septate, hyaline, smooth-walled. *Conidiogenous cells* 4–7 × 1.5–2 µm ($\bar{x}$ = 5.6 × 1.7 µm, n = 10), phialidic, ellipsoid, discrete, light pink, often with conspicuous collarettes and producing conidia singly or successively in basipetal succession. *Conidia* 3.5–4 × 1.5–2 µm ($\bar{x}$ = 3.6 × 1.7 µm, n = 30), blastic-phialidic, ovoid to ellipsoidal, aseptate, guttulate, reddish–brown to green–brown, rough-walled, slimy (Fig. 89).

Culture characteristics: on MEA reaching 9 cm diam., after 2 weeks at room temperature, circular with filiform, flat on media surface, cream with rough and wrinkled.

Material examined: THAILAND, Phang Nga Province, Mueang Phang Nga District, on dead leaf of *Pandanus* sp., 6 December 2014, S. Tibpromma & K.D. Hyde SF14-039 (MFLU 16-0544, **holotype;** HKAS 100832, **isotype**); ex-type living culture, MFLUCC 15-0680.

GenBank numbers LSU: MH376739; ITS: MH388365; TEF1: MH388400; RPB2: MH412735.

Notes: In blast homology searches of the ITS sequences, *Sirastachys phangngaensis* matches with *S. phaeospora* L. Lombard & Crous (CBS 100155) with 98% identity. *Sirastachys phaeospora* has hyaline to pale olivaceous brown to dark brown conidia, smooth to verrucose, ellipsoidal to obovoid to cylindrical (Lombard et al. 2016). We also compared *Sirastachys phangngaensis* with *S. pandanicola* morphologically. They have similar conidiogenous cells size 6–9 × 2–4 µm with conidia 3–4 × 2–3 µm, obovoid to ellipsoidal, darkly olivaceous (Lombard et al. 2016). A synopsis of *Sirastachys* species are shown in Table 4. *Sirastachys* can form synnemata in culture but *Sirastachys phangngaensis* does not show synnematous conidiophores habit in culture. In a BLASTn search on NCBI GenBank, the closest matches of ITS sequence of MFLUCC 15-0680 is *S. phaeospora* with 98% identity to the strain CBS 136167 (KU846667).

Microascales Luttr. ex Benny & Kimbr.

Microascaceae Luttr. ex Malloch

Microascaceae was proposed by Luttrell (1951) with validly published by Latin descriptions by Malloch (1970) and Benny and Kimbrough (1980). The sexual and asexual characteristics were reviewed by Malloch (1970). The taxonomic placement of Microascaceae using molecular data is shown by Réblová et al. (2011) and Maharachchikumbura et al. (2015). There are 21 genera in the family (Wijayawardene et al. 2018). We collected *Parascedosporium putredinis* from Pandanaceae in Thailand and provided new molecular data for this species.

Parascedosporium Gilgado et al.

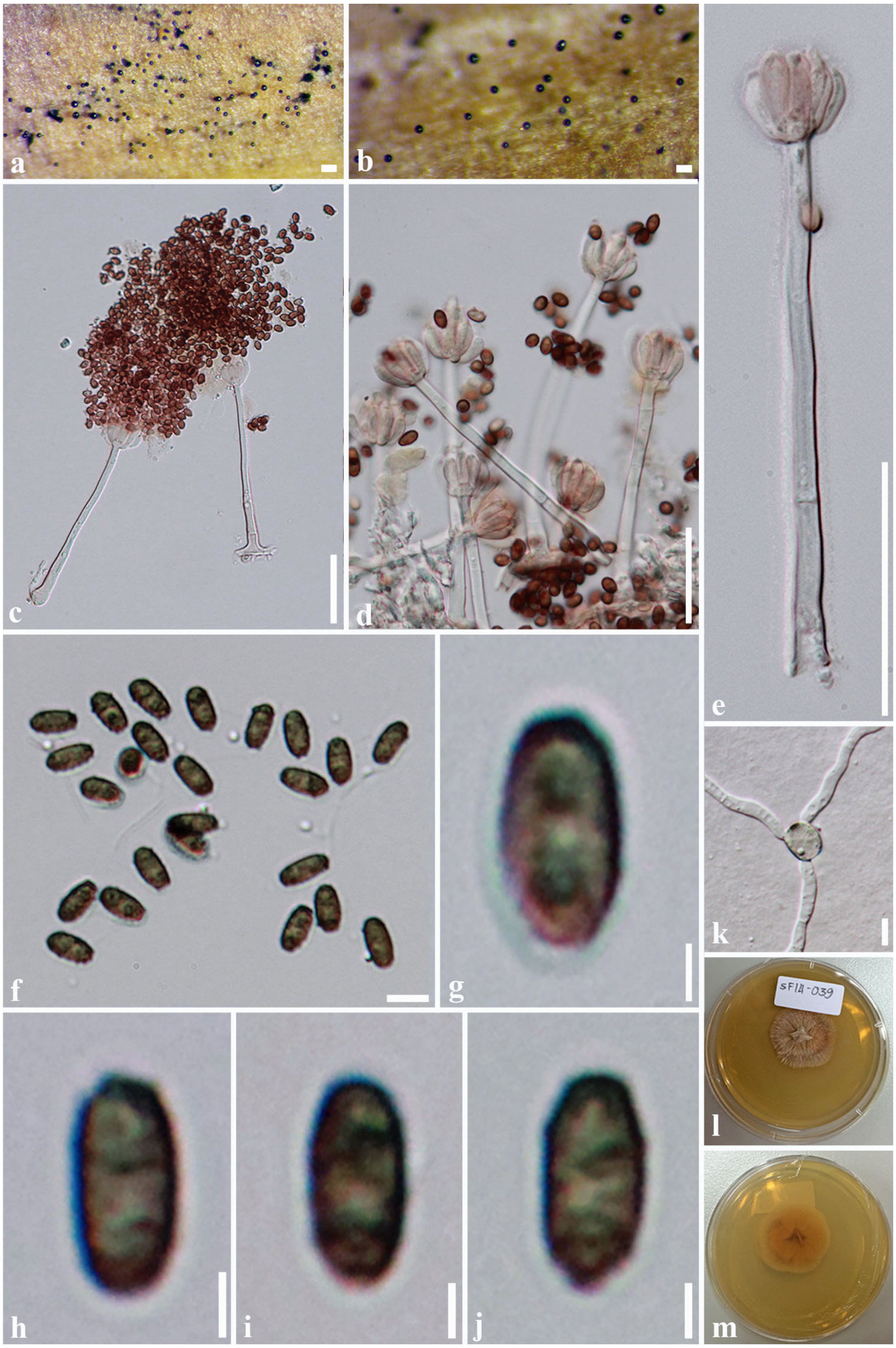


Fig. 88 ***Sirastachys phangngaensis*** (MFLU 16-0544, **holotype**). **a, b** Colonies on dead leaves of *Pandanus* sp. **c–e** Conidiophores, conidiogenous cells and conidia. **f–j** Conidia. **k** Germinating conidium. **l, m** Colony on MEA from above and below. Scale bars: **a** = 100 µm, **b** = 50 µm, **c–e** = 20 µm, **f, k** = 5 µm, **g–j** = 1 µm

Parascedosporium was introduced by Gilgado et al. (2007) to accommodate *P. tectonae* (C. Booth) Gilgado, Gené, Cano & Guarro. *Parascedosporium* shows morphology similar to *Scedosporium* (Gilgado et al. 2007). Later, *Parascedosporium* was segregated from *Scedosporium* and its synnematous synanamorph *Graphium* on the basis of morphology (Lackner and de Hoog 2011). The sexual morph of this genus is unknown (Seifert et al. 2011). *Parascedosporium* has twelve epithets are listed in Index Fungorum (2018) and this is the first report of *Parascedosporium* from Pandanaceae.

Parascedosporium putredinis (Corda) Lackner and de Hoog, IMA Fungus 2 (1): 44 (2011)

Facesoffungi number: FoF04557; Fig. 90

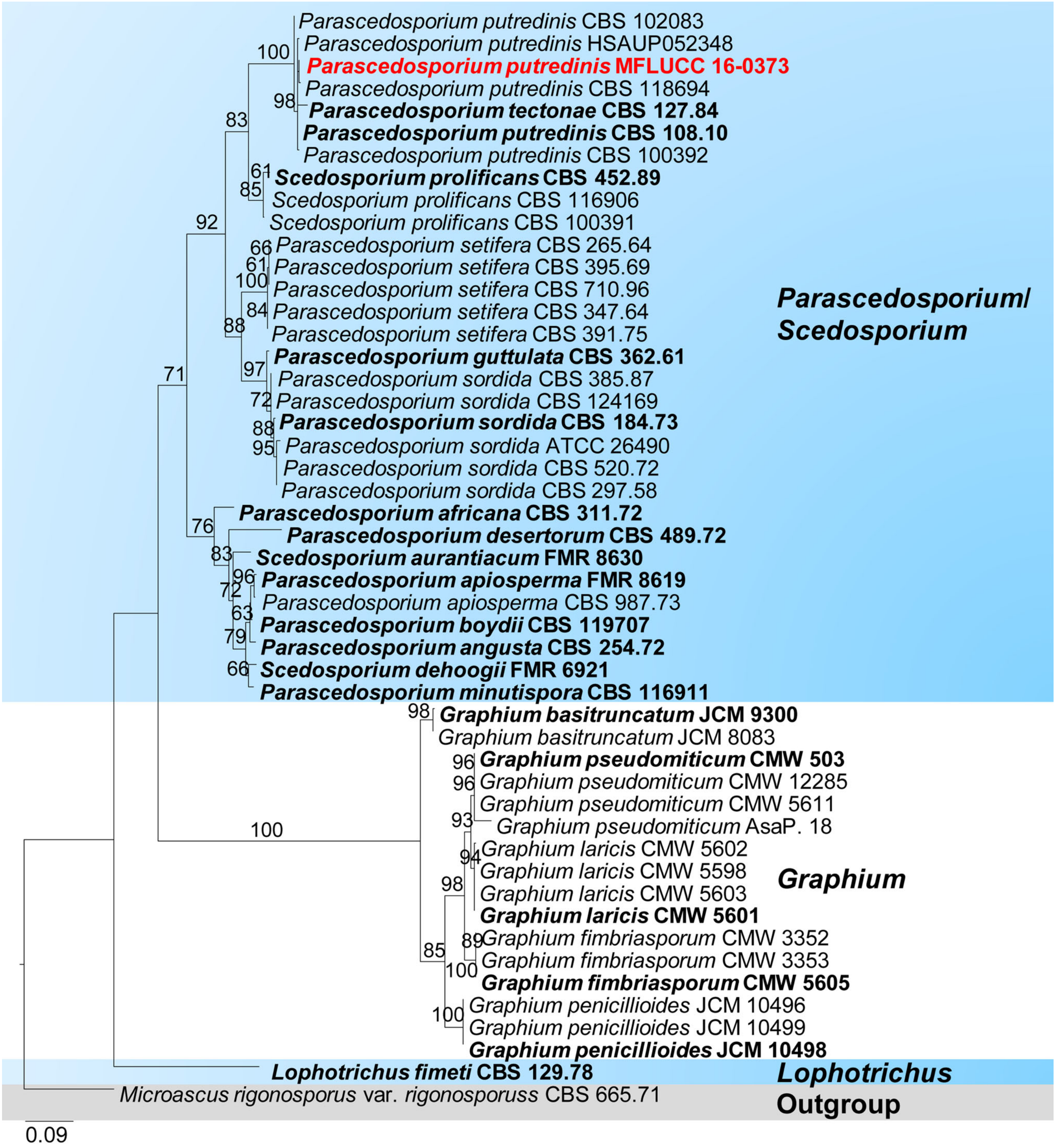


Fig. 89 Phylogram generated from maximum likelihood analysis of ITS sequenced data. Related sequences were obtained from Lackner and de Hoog (2011). Fourty-nine strains are included in the combined sequence analysis, which comprise 589 characters with gaps. *Microascus rigonosporus var. rigonosporuss* (CBS 665.71) is used as the outgroup taxon. The best scoring RAxML tree with a final likelihood value of − 3685.984786 is presented. The matrix had 330 distinct alignment patterns, with 16.30% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.227200, C = 0.292880, G = 0.246760, T = 0.233160; substitution rates AC = 1.819950, AG = 3.705991, AT = 2.078108, CG = 1.765696, CT = 5.084148, GT = 1.000000; gamma distribution shape parameter α = 0.382819. Bootstrap support values for ML equal to or greater than 60% is given above the nodes. The newly generated sequence is in red

Table 4 Synopsis of *Sirastachys* species and new isolate from this study is indicated in bold

Taxa	Conidia			References
	Size (μm)	Shape	Colour	
S. castanedae	5 × 3	Obovoid	Dark olivaceous to dark brown	Lombard et al. (2016)
S. cylindrospora	9 × 2	Cylindrical	Hyaline	Lombard et al. (2016)
S. longispora	8.8–12 × 2–2.4	Hyaline to olivaceous brown	Hyaline to olivaceous brown	Matsushima (1975) and Lombard et al. (2016)
S. pandanicola	4 × 2	Obovoid to ellipsoidal	Dark olivaceous	Lombard et al. (2016)
S. phaeospora	4 × 3	Obovoid to ellipsoidal	Dark olivaceous to dark brown	Lombard et al. (2016)
S. phangngaensis	**3.6 × 1.7**	**Ovoid to ellipsoidal**	**Reddish brown to green–brown**	**This study**
S. phyllophila	5 × 2	Ellipsoidal	Dark olivaceous	Lombard et al. (2016)
S. pseudolongispora	10 × 2	Hyaline to olivaceous brown	Hyaline to olivaceous brown	Lombard et al. (2016)

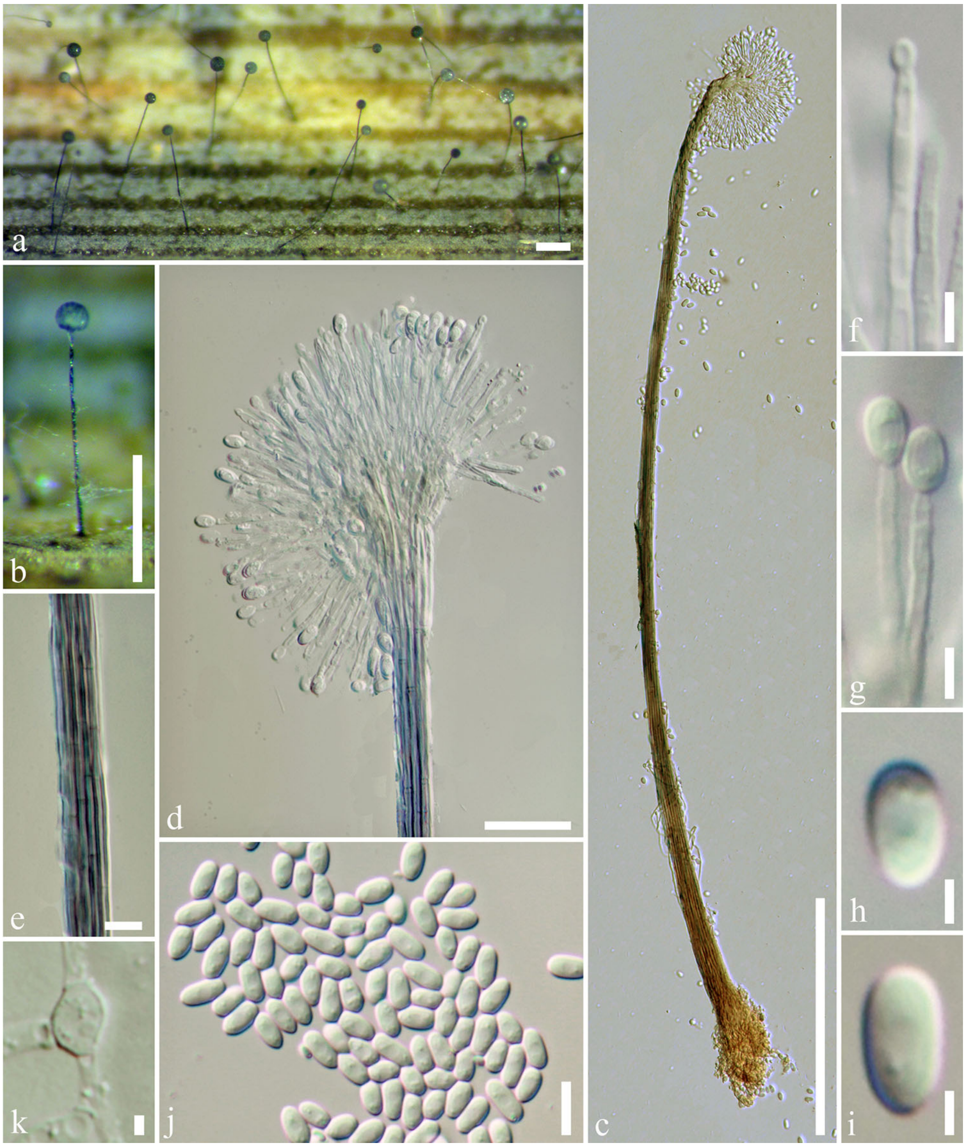


Fig. 90 ***Parascedosporium putredinis*** (MFLU 16-0545). **a, b** Synnemata on host substrate. **c** Conidiogenous cells with conidiophores and conidia. **d** Close up conidiogenous cells with conidia. **e** Conidiophores. **f, g** Conidiogenous cells with conidia. **h–j** Conidia. **k** Germinating conidium. Scale bars: **a, b** = 200 μm, **c** = 100 μm, **d** = 10 μm, **e, f–g** = 2 μm, **h, i, k** = 1 μm, **j** = 5 μm

Saprobic on dead leaves of *Pandanus* sp. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Synnemata* 540–600 × 7.5–15 µm ($\bar{x}$ = 587 × 8.5 µm, n = 5), scattered but abundant, arising from the host plant. *Stipes* pale to dark brown, (68–)88–140(–151) × (23–)60–97 µm. *Conidiophores* 450–500 × 9–13 µm ($\bar{x}$ = 469.6 × 11 µm, n = 5), with multi-branches. *Conidiogenous cells* annellate, brown, septate. *Conidia* 3–5 × 1–3 µm ($\bar{x}$ = 4 × 2 µm, n = 40), aseptate, hyaline, cylindrical to obovoid, hyaline, produced in mucilaginous mass on synnemata.

Culture characteristics: Conidia germinating on PDA within 12 h. Colonies on PDA circular, entire edge with white to cream, raised on surface media. Sporulating in culture after 3 months which produce conidia similar in shape to those recorded on natural dead leaves.

Material examination: THAILAND, Krabi Province, Mueang Krabi District, on dead leaf of *Pandanus* sp., 8 December 2014, S. Tibpromma & KD Hyde SF14-044 (MFLU 16-0545, HKAS 100834); living culture, MFLUCC 16-0373 = KUMCC 16-0157.

GenBank numbers LSU: MH260311; ITS: MH275077; SSU: MH260351.

Notes: *Parascedosporium putredinis* (MFLUCC 16-0373) from dead leaf of *Pandanus* sp. showed morphological similarities to *P. putredinis* (CBS 108.10) (Lackner and de Hoog 2011). Phylogenetic analysis confirmed our collection is *P. putredinis*.

Subclass Savoryellomycetidae Hongsanan et al.

Savoryellales Boonyuen et al.

Savoryellaceae Jaklitsch & Réblová

Savoryellaceae (Halosphaeriales) was invalidly erected by Ranghoo (1998) in her PhD thesis, then Jaklitsch and Réblová (2015) formally introduced Savoryellaceae (Savoryellales) with *Savoryella* E.B.G. Jones & R.A. Eaton as the type genus. There are six genera in the family (Wijayawardene et al. 2018). We describe two new species of *Canalisporium* and provide an updated tree for the family (Fig. 91).

Canalisporium Nawawi & Kuthub.

Canalisporium was introduced with *C. caribense* as the type species (Nawawi and Kuthubutheen 1989). Twelve epithets are listed in Index Fungorum (2018), but only seven species have sequences available in GenBank. Three species of *Canalisporium* have been found previously on Pandanaceae. *Canalisporium caribense* var. *caribense* (Hol.-Jech. & Mercado) Nawawi & Kuthub. and *C. elegans* Nawawi & Kuthub. were recorded on *Freycinetia* and *Pandanus* species (McKenzie and Hyde 1997; Goh et al. 1998; Whitton et al. 2012), while *C. exiguum* Goh & K.D. Hyde was found on *Pandanus penetrans* in Thailand (Thongkantha et al. 2008). Whitton et al. (2012) provided a key to the genus and a synoptic table.

Canalisporium krabiense Tibpromma & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF554550, *Facesoffungi number*: FoF04558; Fig. 92

Etymology: named after Krabi Province, where the fungus was first discovered.

Holotype: MFLU 16-1888

Conidiomata sporodochia on natural substrate scattered on leaf sheath of *Pandanus* sp. in small group, punctiform, pulvinate, granular, black, velvety. *Mycelium* immersed in the substrate, composed of branched, septate, smooth, hyaline hyphae. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Conidiophores* 2–20 × 3–6 µm ($\bar{x}$ = 10 × 5 µm, n = 20), micronematous or semi-macronematous, mononematous, fasciculate, aseptate, hyaline, smooth. *Conidiogenous cells* holoblastic, integrated, terminal, determinate. *Conidia* 27–50 × 22–32 µm ($\bar{x}$ = 40 × 27.4 µm, n = 40), acrogenous, solitary, broadly ellipsoidal to obovoid in surface view, fusiform to obclavate in lateral view, flattened, one-cell thick, muriform with 8–12 cells, smooth, olivaceous brown to brown, with 1 straight vertical septum and 4–6 rows of transverse septa, slightly constricted at septa, dark and thickly banded at septa, canals in the septa obscured by dark pigmentation in face view, visible in side view; basal cell subhyaline to pale brown, cuneiform, thin-walled. Conidial secession rhexolytic.

Material examined: THAILAND, Krabi Province, Mueang Krabi District, on leaf sheath of *Pandanus* sp., 16 December 2017, S. Tibpromma KB010 (MFLU 16-1888, **holotype**; HKAS 96238, **isotype**).

GenBank numbers LSU: MH260283; ITS: MH275051.

Notes: *Canalisporium krabiense* clustered with *C. thailandensis* and *C. exiguum. Canalisporium krabiense* differs from *C. exiguum* in conidial size, number of rows of cells and colour. Conidia of *C. krabiense* are 27–50 × 22–32 µm, with 4–6 rows of cells, while those of *C. exiguum* are 18–25 × 13–15 × 5–8 µm, with 2–3(–4) rows of cells (Goh et al. 1998). In a BLASTn search on NCBI GenBank, the closest matches of ITS sequence of MFLU 16-1888 is *C. exiguum* with 99% identity to the strain SS00809 (GQ390296).

Canalisporium thailandensis Tibpromma & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF554551, *Facesoffungi number*: FoF04559; Fig. 93

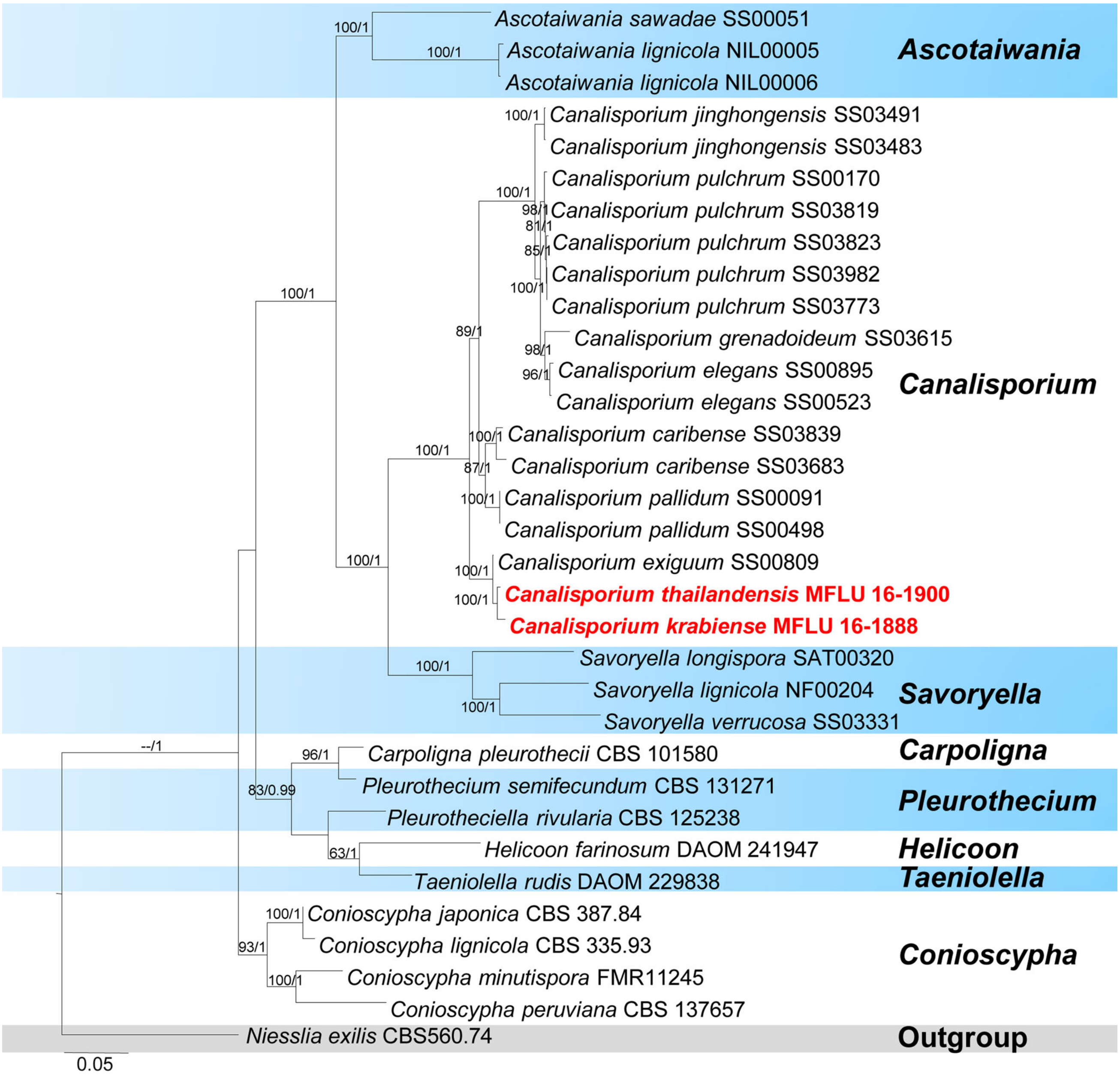


Fig. 91 Phylogram generated from maximum likelihood analysis of combined ITS, LSU and SSU sequence data. Related sequences were obtained from Sri-indrasutdhi et al. (2010a, b) and Boonyuen et al. (2011). Thirty-three strains are included in the combined sequence analysis, which comprise 2936 characters with gaps. *Niesslia exilis* (CBS560.74) is used as the outgroup taxon. Tree topology of the ML analysis was similar to the BYPP. The best scoring RAxML tree with a final likelihood value of − 16595.878216 is presented. The matrix had 1187 distinct alignment patterns, with 19.20% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.231716, C = 0.252553, G = 0.301318, T = 0.214412; substitution rates AC = 1.494718, AG = 2.678433, AT = 1.590940, CG = 1.066185, CT = 5.489636, GT = 1.000000; gamma distribution shape parameter α = 0.258630. Bootstrap support values for ML equal to or greater than 60% and BYPP equal to or greater than 0.95 are given above the nodes. Newly generated sequences are in red

Etymology: named after Thailand, where the fungus was first discovered.

Holotype: MFLU 16-1900

Saprobic on dead leaf sheath of *Pandanus* sp. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Colonies* on natural substrate, in small groups, blackish brown, velvety, glistening, conidia readily liberated when disturbed. *Mycelium* immersed in the substrate, composed of branched, septate, smooth, hyaline hyphae. *Conidiophores* 39–60 × 13–17.5 µm ($\bar{x}$ = 51.5 × 15 µm, n = 20), mononematous, fasciculate, septate, deeply constricted at septa, hyaline, smooth. *Conidiogenous cells* 11–13 × 9–

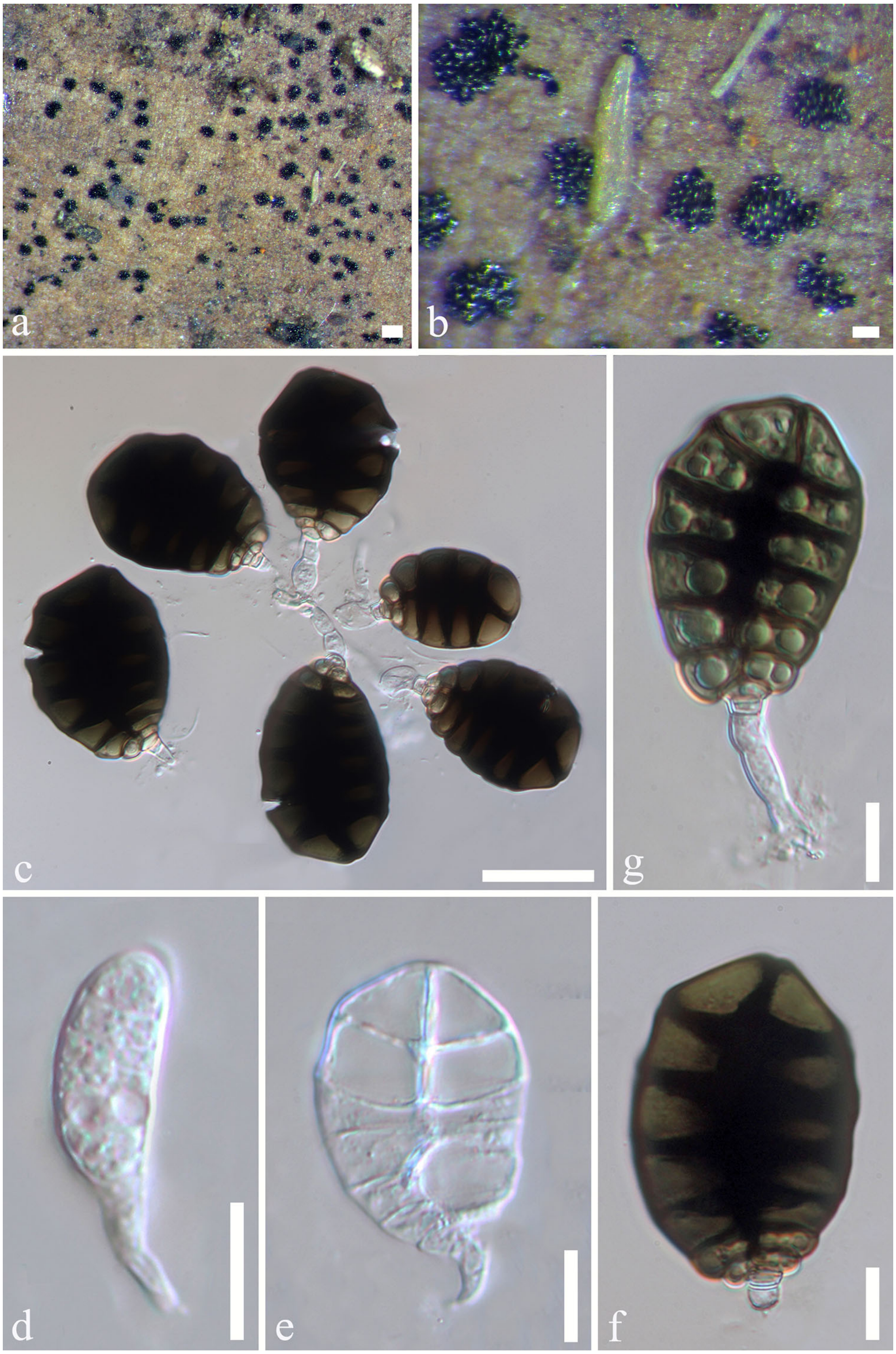


Fig. 92 ***Canalisporium krabiense*** (MFLU 16-1888, **holotype**). **a, b** Colonies on dead leaf sheath of *Pandanus* sp. **c, g** Conidiophores, conidiogenous cells and conidia. **d–g** Conidia at different stages of maturity. Scale bars: **a** = 200 µm, **b** = 50 µm, **c** = 20 µm, **d–g** = 10 µm

13 µm ($\bar{x}$ = 12 × 11 µm, n = 20), holoblastic, monoblastic, integrated, terminal, determinate, globose to oval connected in a chain, with guttules, hyaline. *Conidia* 22.5–31 × 17–22 µm ($\bar{x}$ = 28 × 19 µm, n = 20), acrogenous, solitary, broadly ellipsoidal to obovoid, flattened, one-cell thick, muriform with 8–10 cells, smooth, yellow–brown to brown, with 1 straight column of vertical septa and 4–5 rows of cells, slightly constricted at septa, dark and thickly banded at septa, septa obscured by dark pigmentation in face view and visible in side view; basal cell subhyaline to pale brown, cuneiform, thin-walled.

Material examined: THAILAND, Krabi Province, Mueang Krabi District, on dead leaf sheath of *Pandanus*

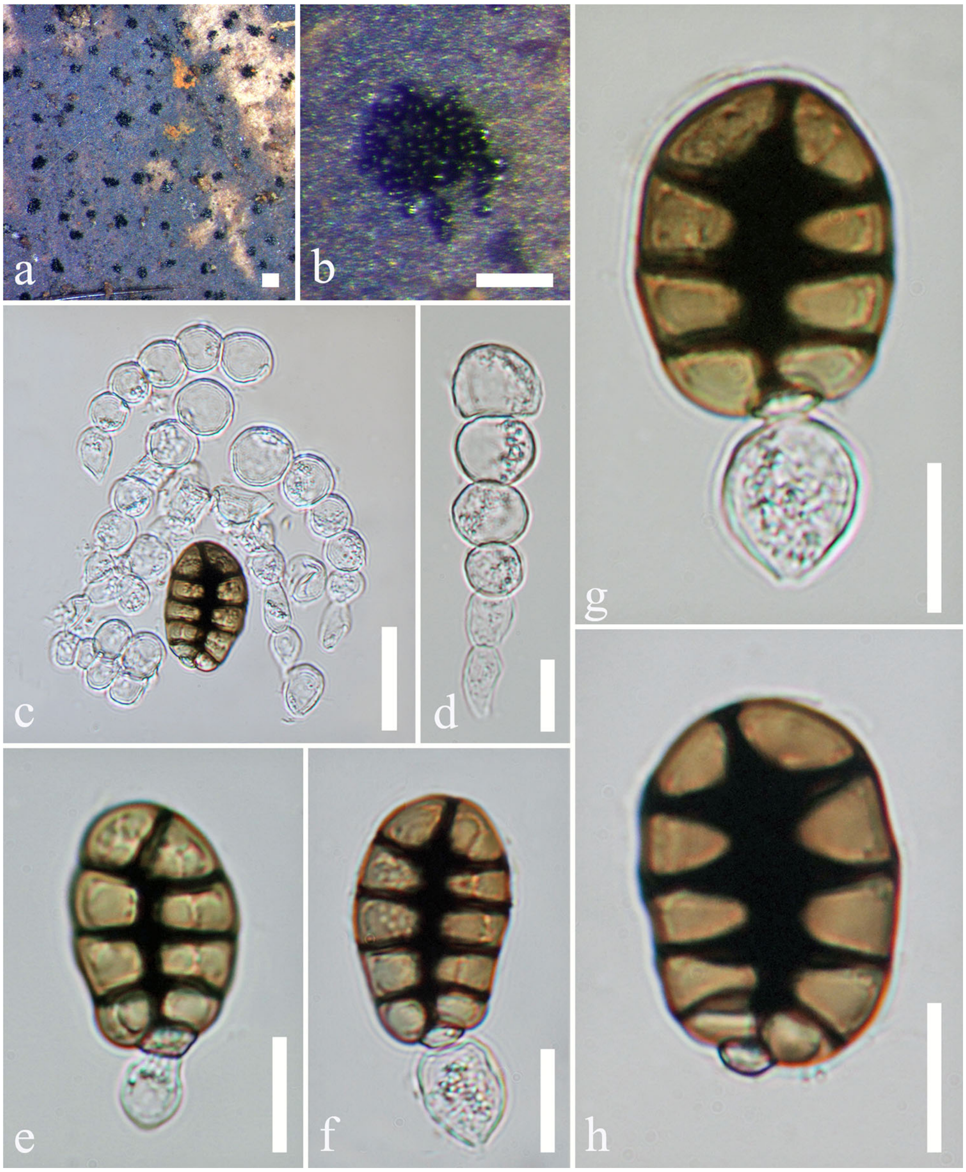


Fig. 93 ***Canalisporium thailandensis*** (MFLU 16-1900, **holotype**). **a, b** Colonies on dead leaf sheath of *Pandanus* sp. **c** Conidiophores, conidiogenous cells and conidium. **d** Conidiophore and conidiogenous cells. **e–h** Conidia. Scale bars: **a** = 200 µm, **b** = 100 µm, **c** = 20 µm, **d–h** = 10 µm

sp., 16 December 2017, S. Tibpromma KB022 (MFLU 16-1900, **holotype**; HKAS 96249, **isotype**).

GenBank numbers LSU: MH260284; ITS: MH275052.

Notes: *Canalisporium thailandensis* differs from other *Canalisporium* species by globose to oval conidiogenous cells connected in a chain, which is a unique character for *Canalisporium* (Sri-indrasutdhi et al. 2010a, b). Phylogenetic analysis also supported this as a distinct new species with high bootstrap support (100% in ML, 1.00 in BYPP, Fig. 91). In a BLASTn search on NCBI GenBank, the closest matches of ITS sequence of MFLU MFLU 16-1900 is *C. exiguum* with 99% identity to the strain SS00809 (GQ390296).

Subclass Sordariomycetidae O.E. Erikss & Winka (= Meliolomycetidae P.M. Kirk & K.D. Hyde)

Chaetosphaeriales Huhndorf et al.

Chaetosphaeriaceae Réblová et al.

Chaetosphaeriaceae was erected by Réblová et al. (1999) with *Chaetosphaeria* Tul. & C. Tul. as the type genus (Tulasne and Tulasne 1863). Several authors have carried out morphological studies of the genus (Munk 1953; Booth 1957; Müller and von Arx 1962; Saccardo 1883; Samuels et al. 1997; Réblová et al. 1999). Maharachchikumbura et al. (2016) listed 37 genera in this family and mentioned that the limits of the family are confused and more work with molecular support is needed to resolve the accepted genera. We introduce new species of Chaetosphaeriaceae in the genera *Dictyochaeta*, *Menisporopsis* and *Thozetella*, which were collected on Pandanaceae from Thailand and China.

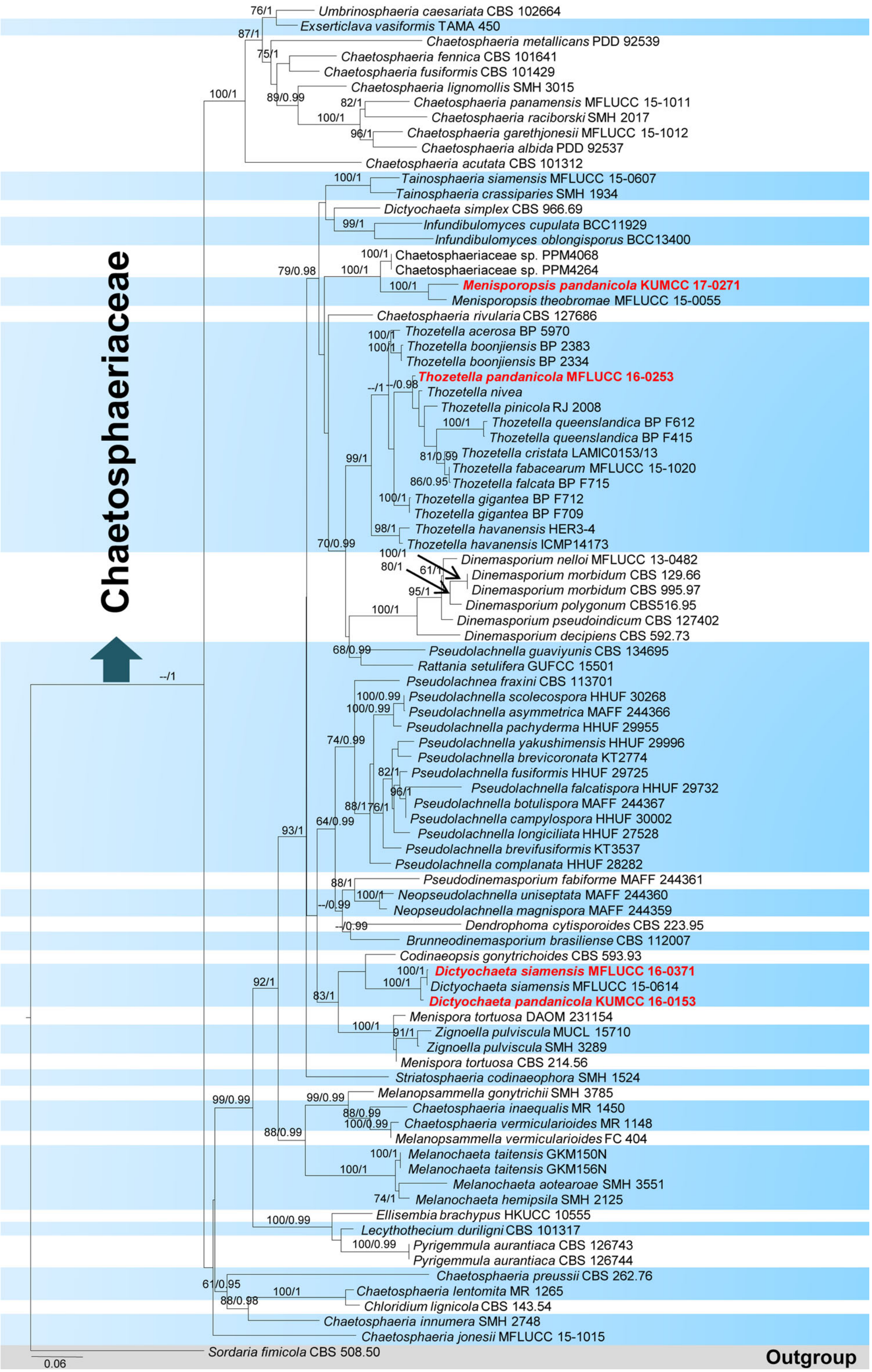


Fig. 94 Phylogram generated from maximum likelihood analysis based on combined LSU, and ITS partial sequence data. Eighty-nine strains are included in the sequence analysis, which comprise 1803 characters with gaps. Single gene analysis was carried out and compared with each species, to compare the topology of the tree and clade stability. *Sordaria fimicola* (Sordariaceae) is used as the outgroup taxon. Tree topology of the ML analysis was similar to the BYPP. The best scoring RAxML tree with a final likelihood value of − 18027.584016 is presented. The matrix had 880 distinct alignment patterns, with 27.96% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.233040, C = 0.260279, G = 0.300714, T = 0.205967; substitution rates AC = 1.320651, AG = 2.076856, AT = 1.962948, CG = 0.818781, CT = 6.443592, GT = 1.000000; gamma distribution shape parameter α = 0.238273. Bootstrap support values for ML equal to or greater than 60% and BYPP equal to or greater than 0.95 are given above the nodes. Newly generated sequences are in red

Dictyochaeta Speg.

Dictyochaeta was erected by Spegazzini (1923) with *D. fuegiana* Speg. as type species. It is characterised by conidia that are hyaline, smooth, typically falcate but can be ellipsoidal, clavate, fusoid, or cylindrical, 0–1(–3)-septate, and often with setulae (Gamundi et al. 1977; Kuthubutheen and Nawawi 1991a, b, c, d). Index Fungorum (2018) listed 101 epithets for *Dictyochaeta*. Several species (*Dictyochaeta fertilis*, *D. parva*, *D. renispora* and *D. simplex*) have been recorded on Pandanaceae (Whitton

Fig. 95 ***Dictyochaeta pandanicola*** (HKAS 101807, **holotype**). **a** Colonies on dead leaves of *Pandanus* sp. **b–d** Conidiophores and conidiogenous cells. **e–g** Conidia. **h** Germinating conidium. **i, j** Colonies on PDA from above and below. Scale bars: **a** = 100 µm, **b–d** = 10 µm, **e–h** = 5 µm

et al. 2012). An updated phylogenetic tree for the family Dictyochaetaceae is presented (Fig. 94).

Dictyochaeta pandanicola Tibpromma & K.D. Hyde, ***sp. nov***.

Index Fungorum number: IF554520, *Facesoffungi number*: FoF04530; Fig. 95

Etymology: named after the host genus, *Pandanus*.

Holotype: HKAS 101807

Saprobic on dead leaf of *Pandanus* sp. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Mycelium* partly superficial composed of septate, branched, smooth, hyaline hyphae. *Conidiophores* 65–260 × 5–10 µm ($\bar{x}$ = 142.5 × 7 µm, n = 10), erect, straight or slightly flexuous, in groups of 4–6 arising from common basal stroma, brown to dark brown at base, hyaline to pale brown towards apex, septate, smooth. *Conidiogenous cells* 15–33 × 6–8 µm ($\bar{x}$ = 25.5 × 7 µm, n = 20), mono- or polyphialidic, terminal, integrated, cylindrical, hyaline to pale brown, smooth, with conspicuous, flared collarettes. *Conidia* 16–26 × 4–6 µm ($\bar{x}$ = 23 × 4.4 µm, n = 20), allantoid, conical at ends, hyaline, guttulate, with one setula at each end, 8–13.5 µm long.

Culture characteristics: Colonies on PDA attaining 9 cm diam., within 2 weeks at room temperature, grey to dark grey, irregular, undulate edge with curled on media surface, raised on media.

Material examined: CHINA, Yunnan Province, Xishuangbanna, Nabanhe, on fallen dead and decaying leaves of *Pandanus* sp., 2 August 2016, S. Tibpromma NBH22 (HKAS 101807, **holotype**); ex-type living culture, KUMCC 16-0153 = MFLUCC 17-0563.

GenBank numbers LSU: MH376710; ITS: MH388338; SSU: MH388307; TEF1: MH388373.

Notes: In our phylogenetic analysis, *Dictyochaeta pandanicola* is well-separated from other *Dictyochaeta* species with high bootstrap support (100% in ML, 1 in BYPP, Fig. 94). Morphologically, *D. pandanicola* is similar to *D. siamensis* J. Yang, K.D. Hyde & J.K. Liu. but differs in *D. siamensis* has setae, 4–6 septate conidiophores with 17.5 × 3 µm conidia, aggregated in slimy mass at the apex of the conidiophore, with 7–12 µm long setulae (Liu et al. 2016). In a BLASTn search on NCBI GenBank, the closest matches of ITS sequence of KUMCC 16-0153 is *D. siamensis* with 99% identity to the strain MFLU 15-1149 (NR_154016).

Dictyochaeta siamensis J. Yang, K.D. Hyde & J.K. Liu, Mycological Progress 15 (10): 1159 (2016)

Facesoffungi number: FoF04531; Fig. 96

Saprobic on dead leaf of *Pandanus* sp. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Mycelium* partly superficial, composed of septate, branched, smooth, hyaline hyphae. *Setae* up to 400 µm long, erect, straight or slightly flexuous, simple, smooth, septate, brown to dark brown, terminating with an acute tip, unbranched. *Conidiophores* 43.5–87 × 2.5–6 µm ($\bar{x}$ = 67 × 4 µm, n = 10), erect, straight or slightly flexuous, in groups of 4–6 arising from common basal stroma, dark brown at base, pale brown towards apex, 4–6 septate, unbranched. *Conidiogenous cells* mono- or polyphialidic, terminal, integrated, cylindrical, smooth, with conspicuous, flared collarettes. *Conidia* 8–17 × 2–5 µm ($\bar{x}$ = 13 × 3 µm, n = 20), allantoid, cylindrical or long fusiform, conical at both ends, hyaline, aseptate, guttulate, with one setula at each end 1–10 µm long.

Culture characteristics: Colonies on MEA attaining 9 cm diam., within 2 weeks at room temperature, dark green, circular, entire edge with convex on media surface, flossy with velvety.

Material examined: THAILAND, Prachuap Khiri Khan Province, Bang Saphan District, Sai Khu Waterfall, on dead leaf of *Pandanus* sp., 30 July 2015, S. Tibpromma & K.D Hyde SF15-022 (MFLU 16-0553; HKAS 96279); living culture, MFLUCC 16-0371.

GenBank numbers LSU: MH376711; ITS: MH388339; SSU: MH388308; TEF1: MH388374.

Notes: In the phylogenetic analysis our isolate grouped with *Dictyochaeta siamensis* with high bootstrap support (100% in ML, 1 in BYPP, Fig. 94). Our isolate shares similar morphology to *D. siamensis* (MFLU 15-1149) in septate, unbranched setae, 4–6-septate, unbranched conidiophores and hyaline, aseptate, cylindrical or long fusiform conidia, with setulae at both ends (Liu et al. 2016).

Menisporopsis S. Hughes

Menisporopsis was introduced with single species *M. theobromae* S. Hughes (Hughes 1952). *Menisporopsis* is characterized by synnematous conidiophores that surround a single sterile, erect seta with falcate conidia has one or more setulae at each end (Hughes 1952; Pirozynski and Hodges 1973; Varghese and Rao 1978; Rao and de Hoog 1986). There are ten epithets are listed in Index Fungorum (2018). Two species, *M. pirozynskii* Varghese & V.G. Rao and *M. theobromae* S. Hughes have been reported from Pandanaceae (Whitton et al. 2012).

Menisporopsis pandanicola Tibpromma & K.D. Hyde, ***sp. nov***.

Index Fungorum number: IF554522, *Facesoffungi number*: FoF04533; Fig. 97

Etymology: named after the host genus, *Pandanus*.

Holotype: HKAS 100862

Saprobic on dead leaf of *Pandanus* sp. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Mycelium* partly superficial, composed of septate, branched, smooth, hyaline hyphae. *Setae* 344–375 × 7–10.5 µm, erect, straight or slightly flexuous, simple, smooth, septate, brown to dark brown at the base, pale brown towards the apex. *Conidiophores* 85–100 × 14.5–23 µm ($\bar{x}$ = 93 × 19 µm, n = 5), synnematous encircling the setae, erect, straight or slightly flexuous, pale brown, septate, smooth. *Conidiogenous cells* 8–29 × 0.5–2 µm ($\bar{x}$ = 17 × 1.5 µm, n = 20), polyphialidic, terminal, integrated, cylindrical, smooth. *Conidia* 17–22 × 2–3 µm ($\bar{x}$ = 19 × 2.5 µm, n = 40), lunate, conical at both ends, aseptate, guttulate, aggregated into a slimy mass, hyaline, with (1–)2 setula at each end, 4–12 µm long.

Culture characteristics: Conidia germinating on MEA within 12 h. Colonies growing show on MEA, circular, entire edge with white to cream, raised on surface media.

Material examined: HONG KONG, Lantau Island, Pui O Beach, on *Pandanus* sp., 20 September 2016, S. Tibpromma HK011 (HKAS 100862, **holotype**); ex-type living culture, KUMCC 17-0271 = MFLUCC 17-0638.

GenBank numbers LSU: MH376726; ITS: MH388353; SSU: MH388320; TEF1: MH388388; RPB2: MH412732.

Notes: In the phylogenic tree *Menisporopsis pandanicola* clustered with *M. theobromae* (MFLU 15-1168) (100% in ML, 1 in BYPP). *Menisporopsis pandanicola* has conidia 19 × 3 µm, with one or two setulae at each end

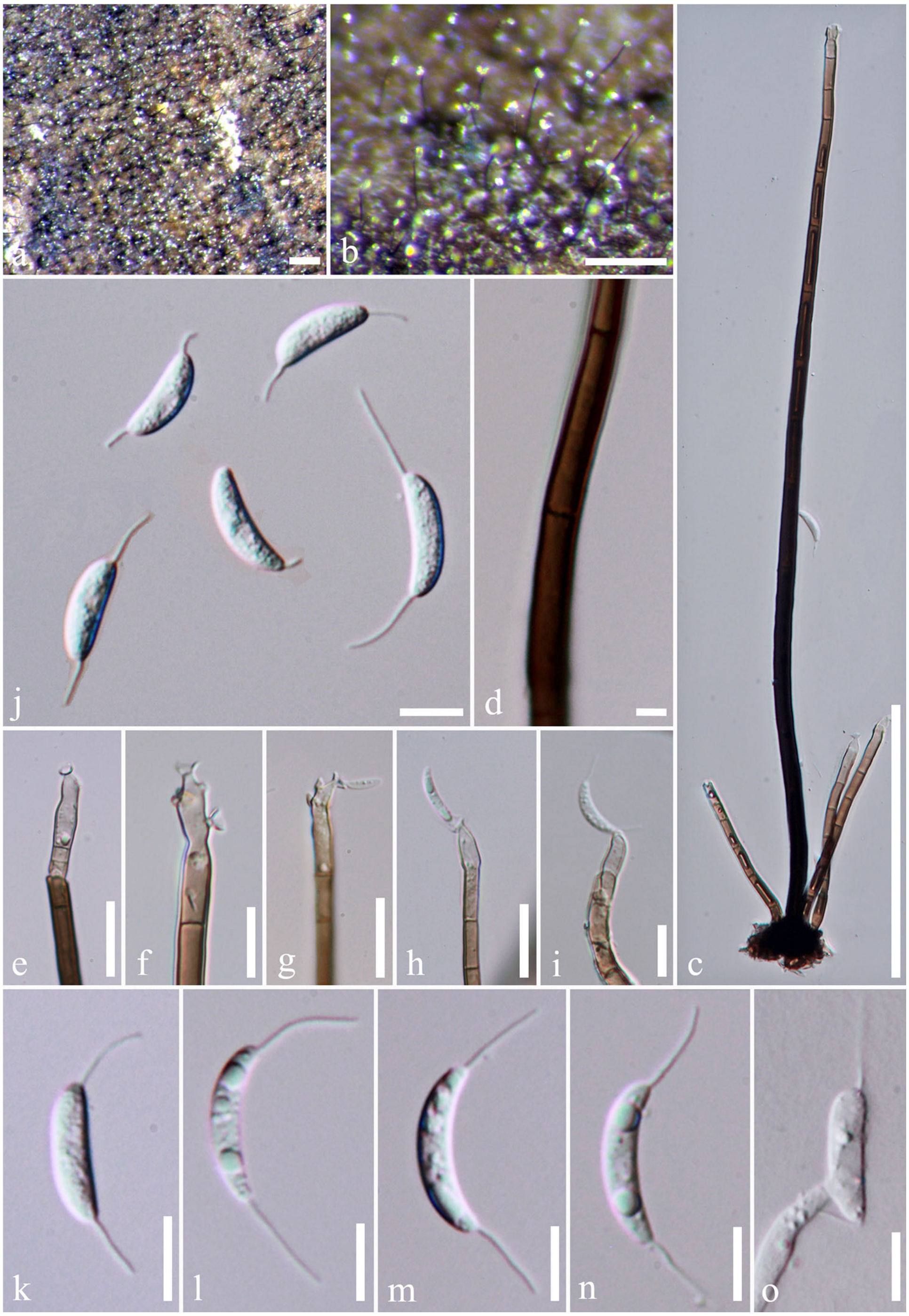


Fig. 96 ***Dictyochaeta siamensis*** (MFLU 16-0553). **a, b** Colonies on dead leaves of *Pandanus* sp. **c–f** Conidiogenous cells with conidiophores. **d** Setae-walled. **e–i** Conidiogenous cells with conidiophores and conidia. **j–n** Conidia. **o** Germinating conidium. Scale bars: **a, b** = 200 µm, **c** = 100 µm, **d** = 2 µm, **e–i** = 10 µm, **j–o** = 5 µm

measuring 4–12 µm long, while *M. theobromae* has conidia 17 × 2.5 µm, setula with a single setula at each end measuring 6–7.5 µm long (Liu et al. 2016). We also compared ITS and LSU nucleotides and found that they are different 20 bp (4.08%) in 490 ITS (+5.8S) nucleotides and 10 bp (1.23%) in 808 LSU nucleotides. In a BLASTn search on NCBI GenBank, the closest matches of ITS sequence of KUMCC 17-0271 is *M. theobromae* with 95% identity to the strain MFLUCC 15-0055 (KX609957).

Thozetella Kuntze

Thozetella was introduced with *T. nivea* (Kuntze 1891) as the type species. The *Thozetella* is characterised by conidiophores that are grouped into short conspicuous sporodochia or short synnemata and terminated by phialidic conidiogenous cells. There are 22 epithets are listed in Index Fungorum (2018). Whitton et al. (2012) provided a synoptic table to 17 species of *Thozetella*. *Thozetella*

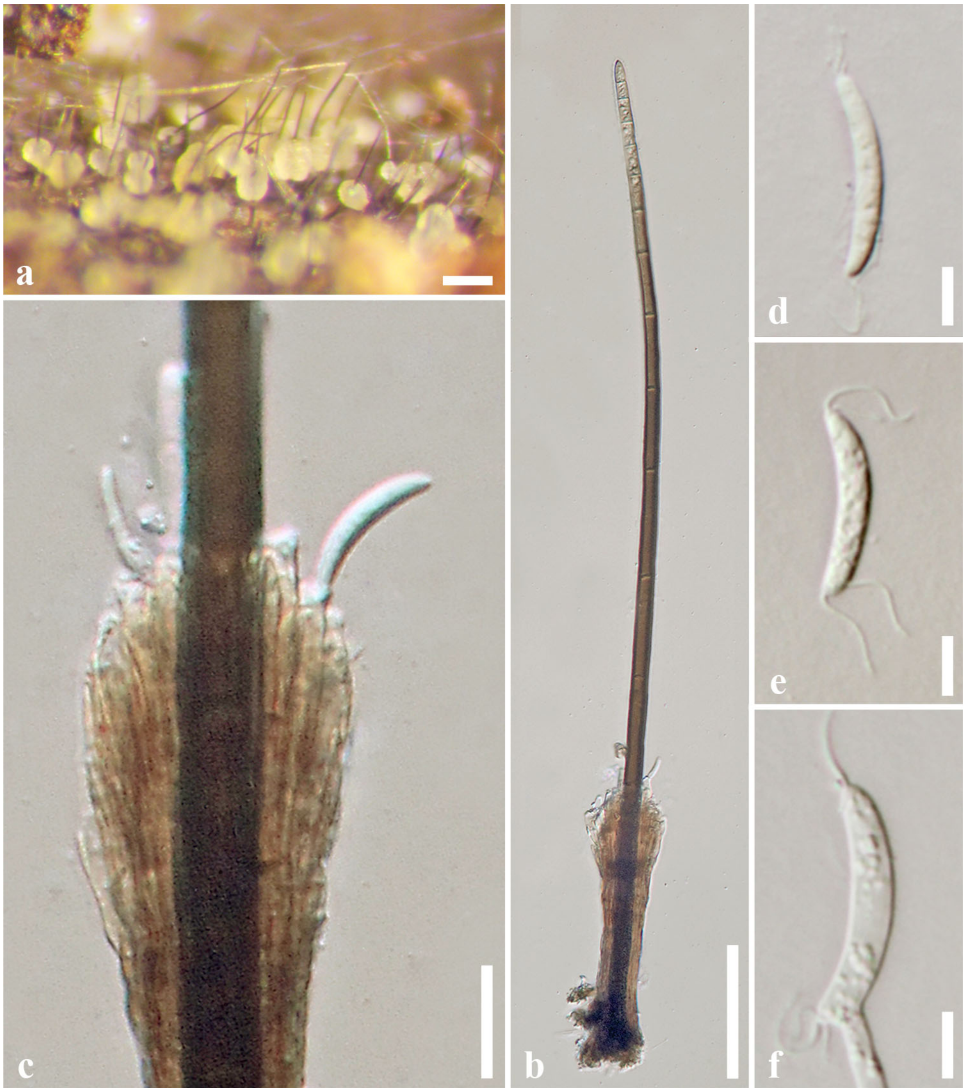


Fig. 97 ***Menisporopsis pandanicola*** (HKAS 100862, **holotype**). **a** Colonies on dead leaves of *Pandanus* sp. **b** Setae with conidiophores, conidiogenous cells and conidia. **c** Conidiogenous cells with conidia. **d, e** Conidia. **f** Germinating conidium. Scale bars: **a** = 100 µm, **b** = 10 µm, **c** = 50 µm, **d–f** = 5 µm

serrata Whitton, McKenzie & K.D. Hyde has been reported from Pandanaceae (Whitton et al. 2012).

Thozetella pandanicola Tibpromma & K.D. Hyde, ***sp*. *nov***.

Index Fungorum number: IF554521, *Facesoffungi number*: FoF04532; Fig. 98

Etymology: named after the host genus, *Pandanus*.

Holotype: MFLU 16-1898

Saprobic on dead leaves of *Pandanus* sp. *Mycelium* superficial, white to yellow–white. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 3–6 × 2–3.5 µm ($\bar{x}$ = 4.7 × 2.4 µm, n = 10), enteroblastic, phialidic, doliiform, smooth, hyaline. *Conidia* 17–21 × 2–3 µm ($\bar{x}$ = 19 × 2.4 µm, n = 30, fusiform, hyaline, acute apex, aseptate, smooth, guttulate, with flexuous appendage at each end 6–9 µm long, without a mucilaginous sheath.

Culture characteristics: Conidia germinating on MEA within 12 h. Colonies on MEA, circular, entire with curled, white to cream, smooth and raised on surface media. Mycelium superficial, flossy.

Material examined: THAILAND, Krabi Province, Mueang Krabi District, on *Pandanus* sp., 16 December 2017, S. Tibpromma KB020 (MFLU 16-1898, **holotype**; HKAS 96247, **isotype**); ex-type living culture, MFLUCC 16-0253.

GenBank numbers LSU: MH376740; ITS: MH388366; SSU: MH388330.

Notes: *Thozetella serrata* has been recorded on decaying leaves of *Pandanus furcatus* in Hong Kong. *Thozetella serrata* has fusoid almost straight conidia, 11.5–17 × 2–3 µm (Whitton et al. 2012), while *T. pandanicola* has fusiform conidia, 17–21 × 2–3 µm. The phylogeny showed *T. pandanicola* well-separated from other species in *Thozetella* (0.98 in BYPP, Fig. 94). In a BLASTn search on NCBI GenBank, the closest matches of

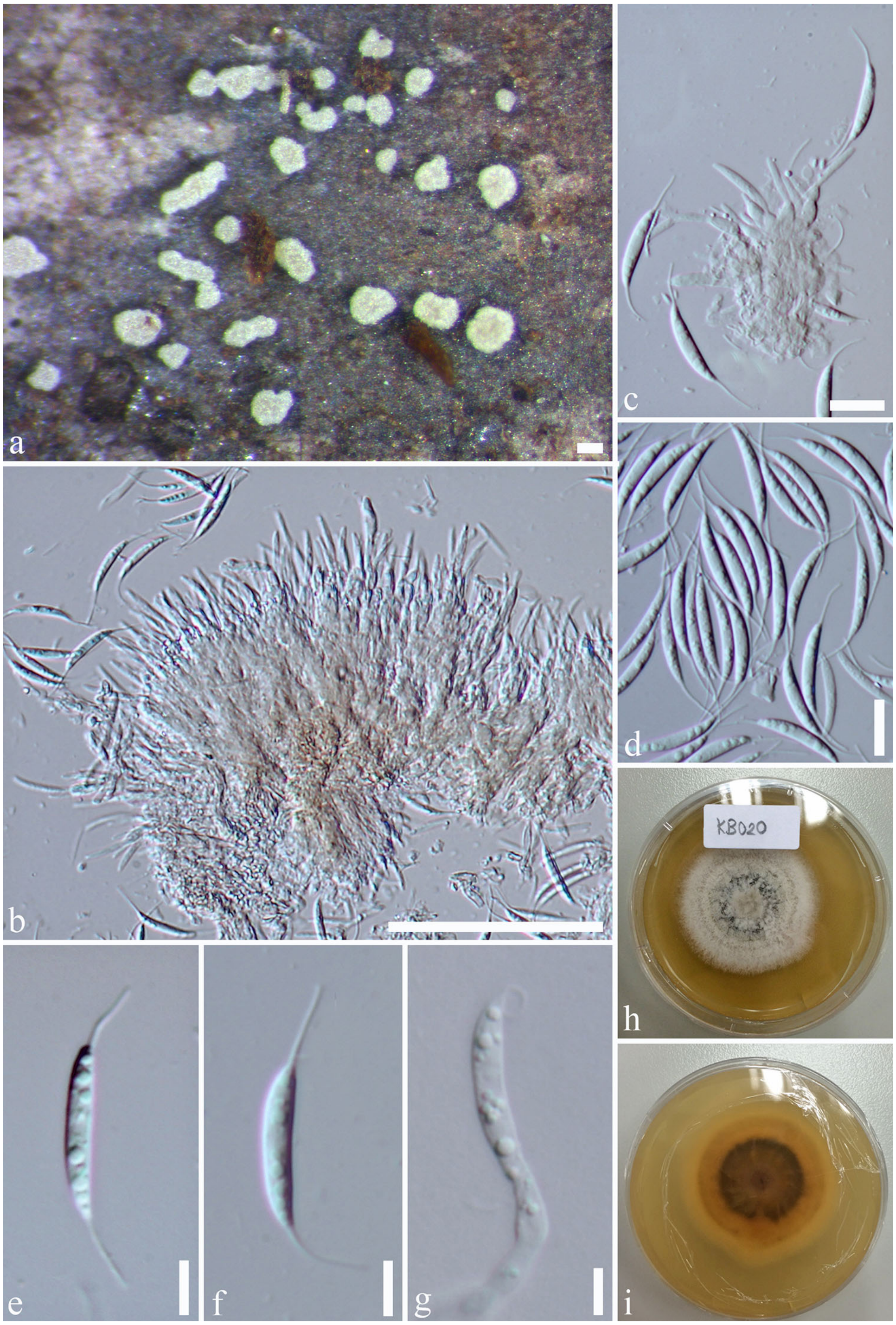


Fig. 98 ***Thozetella pandanicola*** (MFLU 16-1898, **holotype**). **a** Colonies on dead leaves of *Pandanus* sp. **b, c** Conidiogenous cells with conidiophores and conidia. **d–f** Conidia. **g** Germinating conidium. **h, i** Colony on MEA from above and below. Scale bars: **a** = 100 µm, **b** = 50 µm, **c, d** = 10 µm, **e–g** = 5 µm

ITS sequence of MFLUCC 16-0253 is *Thozetella* sp. with 96% identity to the strain C20-79 (KJ439080).

Sordariales Chadef. ex D. Hawksw. & O.E. Erikss.

Chaetomiaceae G. Winter

Chaetomiaceae was erected by Winter (1885a, b) (as Chaetomiea) with *Chaetomium* Kunze. as the type genus. Members of this family are ubiquitous, commonly residing in soil, on lignin and cellulosic or similar materials and some species are also human opportunistic pathogens (von Arx et al. 1986; Mukerji and Manoharachary 2010; Ahmed et al. 2015b). The placement of this family is not clear and it has been placed in various orders such as Chaetomiales (Ames 1961; Alexopoulos 1962; Mukerji 1968), Sphaeriales (Barr 1976; Müller and von Arx 1973), and later Sordariales (Hawksworth and Wells 1973; Mehrotra and Aneja 1990). Huhndorf et al. (2004), Liu (2011) and

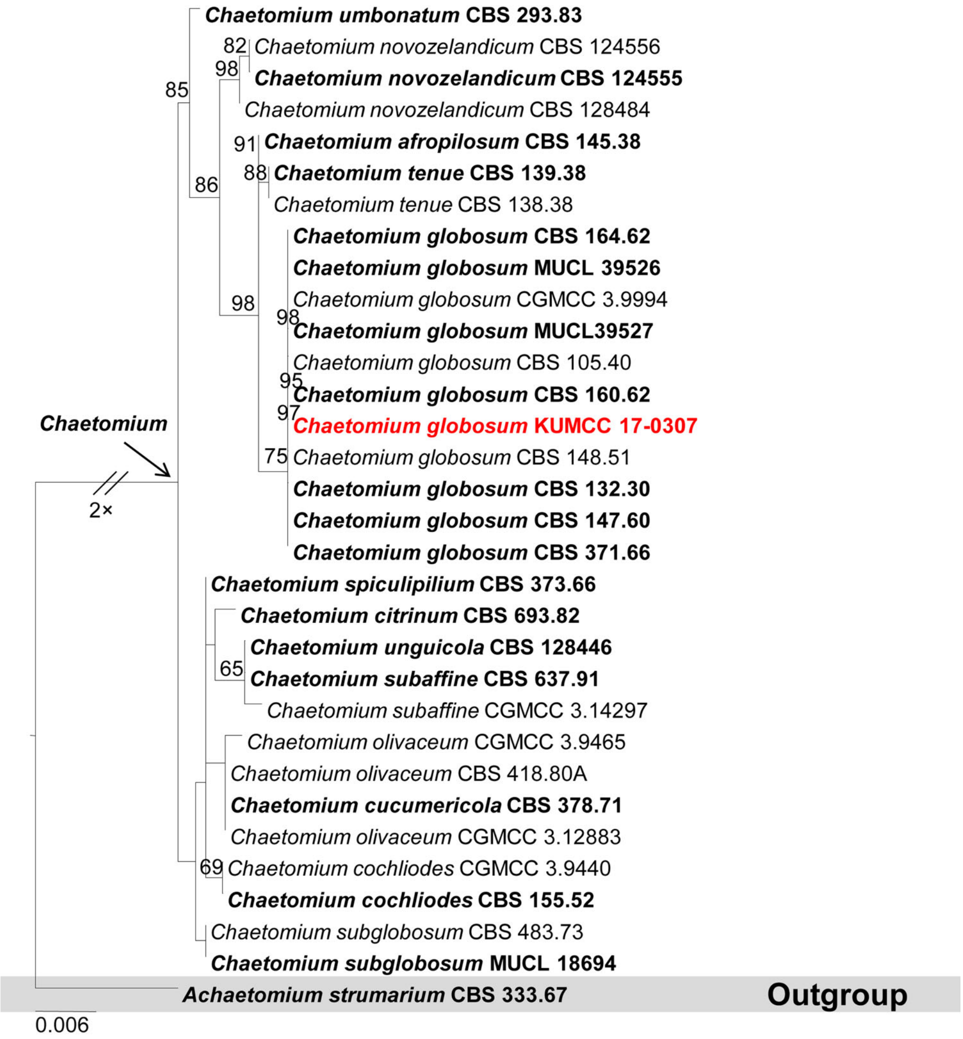


Fig. 99 Phylogram generated from maximum likelihood analysis of combined ITS and LSU sequenced data. Related sequences were obtained from Wang et al. (2016). Thirty-two strains are included in the sequence analysis, which comprise 1113 characters with gaps. *Achaetomium strumarium* (CBS 333.67) is used as the outgroup taxon. The best scoring RAxML tree with a final likelihood value of − 2044.666920 is presented. The matrix had 68 distinct alignment patterns, with 28.05% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.228029, C = 0.270995, G = 0.282117, T = 0.218859; substitution rates AC = 3.702498, AG = 4.553243, AT = 4.549924, CG = 8.172223, CT = 30.986343, GT = 1.000000; gamma distribution shape parameter α = 0.020000. Bootstrap support values for ML equal to or greater than 65% is given above the nodes. The newly generated sequence is in red

Maharachchikumbura et al. (2015) used molecular data to resolve the relationship of Chaetomiaceae in the order Sordariales and there are twenty-six genera in the family (Wijayawardene et al. 2018). We collected the type species, *Chaetomium globosum* from *Pandanus* sp. in Thailand and provide illustrations and a phylogenic analysis (Fig. 99).

Chaetomium Kunze

Chaetomium globosum Kunze is the type species of *Chaetomium*. The special characteristic of *Chaetomium* is its ascoma covered with hairs or setae (Hawksworth and Wells 1973). Many *Chaetomium* species are potential biological control agents and can produce bioactive metabolites (Soytong et al. 2001; Pieckova 2003; Wang et al. 2012; Li et al. 2014). Currently, there are 435 epithets are listed in Index Fungorum (2018). We report *Chaetomium globosum* from Pandanaceae.

Chaetomium globosum Kunze ex Fr., Systema Mycologicum 3: 255 (1829)

Facesoffungi number: FoF04560; Fig. 100

Saprobic on dead leaf of *Pandanus* sp. with immersed perithecia and later opening by a pore with white-pruinose margin on host surface. **Sexual morph** *Ascomata* 600–710 × 425–480 µm ($\bar{x}$ = 666 × 460.5 µm, n = 5), superficial to semi-immersed with thick aerial hyphae or exposed, ostiolate, covered with black ascomatal hairs, oval or ellipsoid, without papilla. *Ascomatal wall* brown to black, composed of hypha-like cells, *textura intricata* in surface view. *Terminal hairs* 3–7 µm, finely punctate to verrucose, pale brown, hypha-like, flexuous or undulate, sometimes geniculate. *Asci* 16–29 × 4–6 µm ($\bar{x}$ = 21 × 5 µm, n = 10), 8-spored, cylindrical to cylindric-clavate, long-pedicel, apically rounded. *Ascospores* 4–5 × 2–4 µm ($\bar{x}$ = 4.5 × 3 µm, n = 40), overlapping, globose to subglobose, hyaline, becoming brown with age, aseptate, rough, not surrounded by a mucilaginous sheath. **Asexual morph** Undetermined.

Culture characteristics: Ascospore germinating on MEA within 12 h. Colonies on MEA, circular, undulate

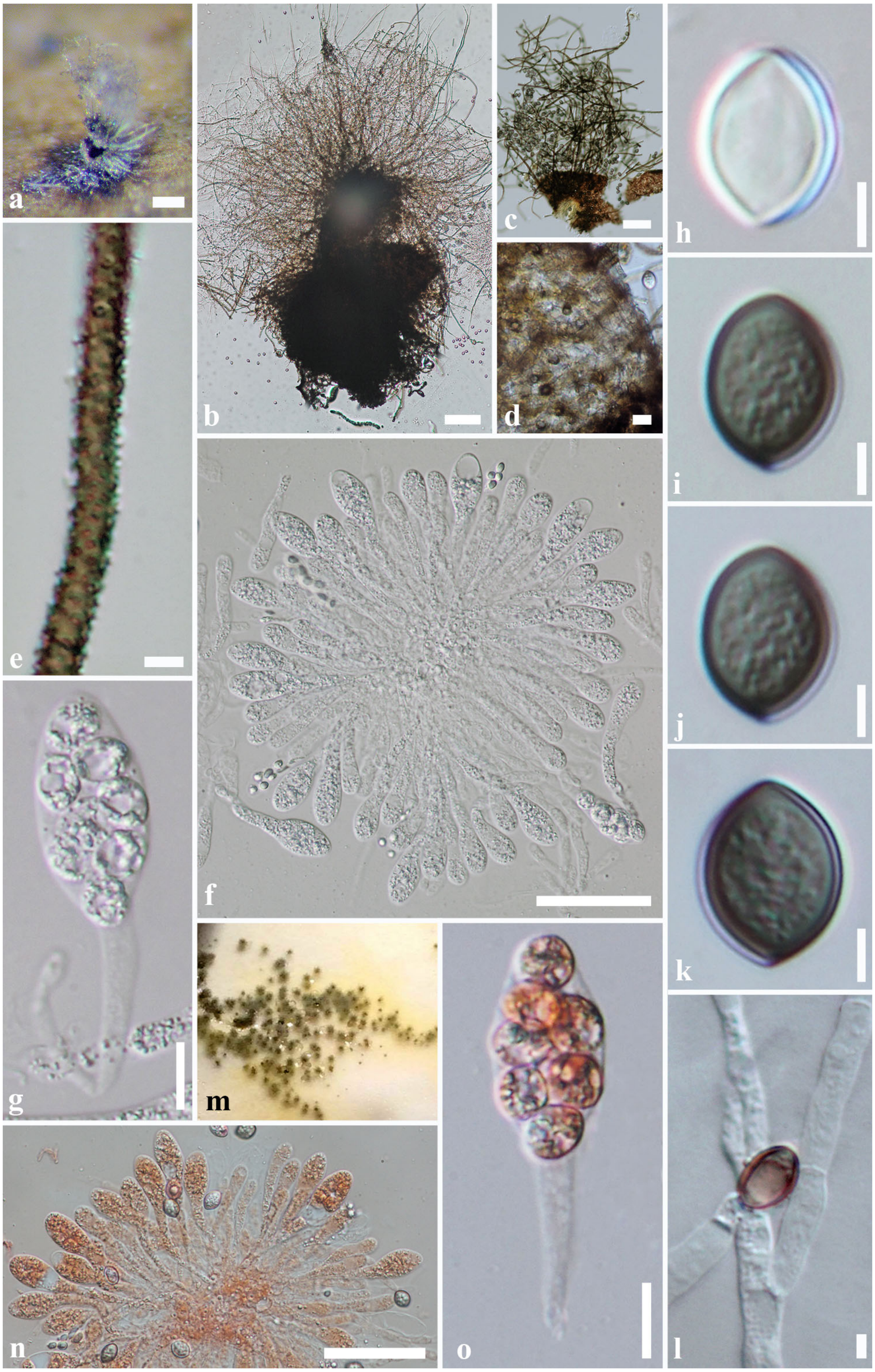


Fig. 100 ***Chaetomium globosum*** (MFLU 18-0015). **a** Colony on dead leaf of *Pandanus* sp. **b** Ascomata. **c** Upper part of terminal ascomatal hairs. **d** Structure of ascomatal wall in surface view. **e** Basal part of terminal ascomatal hair. **f, g** Asci. **h–k** Ascospores. **l** Germinating ascospore. **m** Colony on MEA. **n, o** Asci formed in culture (stained with congo red reagent). Scale bars: **b** = 100 μm, **c, f, n** = 50 μm, **d, g, o** = 10 μm, **e, h–l** = 5 μm

with white to yellow–white, smooth and raised on surface media. Mycelium superficial, velvety.

Material examined: THAILAND, Prachuap Khiri Khan Province, Bang Saphan District, Sai Khu Waterfall, on *Pandanus* sp., 30 July 2015, S. Tibpromma SF15-039 (MFLU 18-0015; HKAS 100841); living culture, KUMCC 17-0307.

GenBank numbers LSU: MH260286; ITS: MH275054; SSU: MH260332.

Notes: *Chaetomium* is a cosmopolitan genus with more than 150 species (Asgari and Zare 2011a, b; Zhang et al.

2012). *Chaetomium globosum* has been isolated previously from *Pandanus odoratissimus* and *P. penetrans* in Thailand (Thongkantha et al. 2008). *Chaetomium globosum* is commonly found in natural environments worldwide and can be a causal agent of emerging fungal infections (Sugiyama et al. 2008). The closest hits using a BLASTn search on NCBI GenBank of the ITS sequence were 99% similar to *Chaetomium globosum* (Accession numbers KT780353; KY132157; KY132151).

Subclass Xylariomycetidae O.E. Erikss & Winka

Amphisphaeriales D. Hawksw. & O.E. Erikss.

Beltraniaceae Nann.

Beltraniaceae was established by Nannizzi (1934) to accommodate a single genus *Beltrania* Penzig. Maharachchikumbura et al. (2016) accepted *Beltrania*, *Beltraniella*, *Beltraniomyces*, *Beltraniopsis*, *Parapleurotheciopsis*, *Porobeltraniella*, *Pseudobeltrania* and *Subramaniomyces* in the family. Later, Rajeshkumar et al. (2016) accepted an additional genus *Hemibeltrania* in the family and Lin et al. (2017) introduced *Subsessila* to this family. Species in Beltraniaceae are generally hyphomycetous and commonly isolated as saprobes (Seifert et al. 2011; Crous et al. 2015b; Maharachchikumbura et al. 2016). We describe two new species of *Beltraniella* and a new *Beltrania* species, collected on Pandanaceae in Thailand.

Beltrania Penz.

Beltrania was established with *B. rhombic* Penz. as the type species, found on *Citrus limonum* in Italy by Penzig (1882). The characteristics of this genus are setae with radially lobed basal cells, conidiophores with separating cells and biconic conidia with a hyaline transverse band and an apical tubular appendage. Pirozynski (1963) provided an illustrated monograph. *Beltrania rhombica* was found on *Pandanus* sp. from Mauritius (Dulymamode et al. 2001). There are 18 epithets for *Beltrania* are listed in Index Fungorum (2018).

Beltrania krabiensis Tibpromma & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF554512, *Facesoffungi number*: FoF04523; Fig. 101

Etymology: named after Krabi Province, where the fungus was first discovered.

Holotype: MFLU 16-1913

Saprobic on dead leaves of *Pandanus* sp. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Setae* erect, brown, thick-walled, indistinctly septate, straight to somewhat flexuous, conical at the apex, globose at basal cell. *Conidiophores* 43–86 × 2–4 µm, aggregated in dense fascicles, pale brown, cylindrical, septate, unbranched, straight to variously curved, proliferating sympodially at apex. *Conidiogenous cells* terminal, subhyaline, smooth, holoblastic, polyblastic, with several flat tipped denticles. *Separating cells* 7–8.5 × 3–4 µm ($\bar{x}$ = 8 × 3.4 µm, n = 10), subhyaline, finely roughened, with several apical, flat-tipped denticles. *Conidia* 17–23 × 5–8 µm ($\bar{x}$ = 20 × 7.5 µm, n = 20, including apical appendage), biconic, aseptate, solitary, subhyaline to pale brown, with distinct granules, without median transverse band, apical appendage 4–8 µm long, tapering to an acutely rounded tip, smooth, without a mucilaginous sheath.

Culture characteristics: Conidia germinating on MEA within 24 h. Colonies on MEA, filamentous with curled edge, raised on the media surface with white, smooth and flossy. Mycelium superficial, velvety.

Material examined: THAILAND, Krabi Province, Mueang Krabi District, on *Pandanus* sp., 4 December 2017, S. Tibpromma KB035 (MFLU 16-1913, **holotype**; HKAS 96262, **isotype**); ex-type living culture, MFLUCC 16-0257.

GenBank numbers LSU: MH260280; ITS: MH275048; SSU: MH260328.

Notes: Based on phylogenetic analysis, *Beltrania krabiensis* (69% in ML, 0.90 in BYPP) and clustered with *B. pseudorhombica* Crous & Y. Zhang. *Beltrania krabiensis* has 7–8.5 × 3–4 µm separating cells, subhyaline to pale brown conidia, without median transverse band, 17–23 × 5–8 µm, 4–8 µm apical appendages, while *B. pseudorhombica* has 7–12 × 5–6 µm separating cells, pale brown conidia with a distinct median transverse band of lighter pigment, (20–)22–25(–26) × (7–)8(–9) µm, 7–11 × 1 µm apical appendages. In a BLASTn search on NCBI GenBank, the closest matches of ITS sequence of MFLUCC 16-0257 is *Beltrania* sp. with 99% identity to the strain 114.2.1 (KP133187).

Beltraniella Subram.

Subramanian (1952) proposed *Beltraniella*, with *B. odinae* Subram. as the type species. *Beltraniella* is characterised by setiform conidiophores and polyblastic, sympodial, denticulate conidiogenous cells, lageniform conidia with a truncate base, rostrate apex, and a hyaline transverse band at the equatorial zone (Subramanian 1952). There are 25 epithets are listed in Index Fungorum (2018). *Beltraniella* has not been previously reported on Pandanaceae.

Beltraniella pandanicola Tibpromma & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF554513, *Facesoffungi number*: FoF04524; Fig. 102

Etymology: named after the host genus, *Pandanus*.

Holotype: MFLU 18-0039

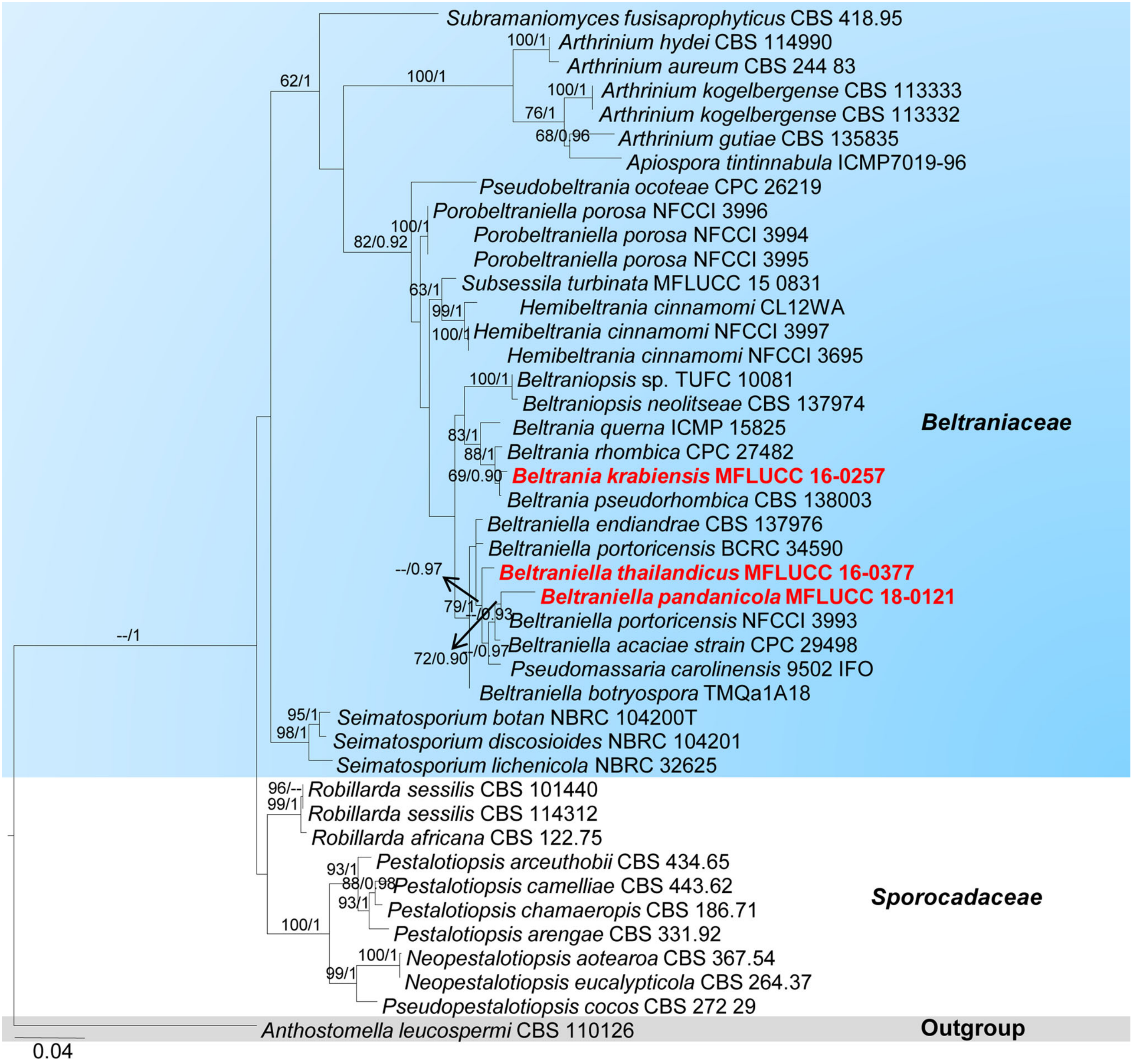


Fig. 101 Phylogram generated from maximum likelihood analysis based on combined LSU and ITS sequence data. Related sequences were obtained from Lin et al. (2017). Forty-three strains are included in the combined sequence analysis, which comprise 1365 characters with gaps. *Anthostomella leucospermi* (CBS 110126) is used as the outgroup taxon. Tree topology of the ML analysis was similar to the BYPP. The best scoring RAxML tree with a final likelihood value of − 6451.337345 is presented. The matrix had 478 distinct alignment patterns, with 20.17% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.249145, C = 0.216405, G = 0.265430, T = 0.269020; substitution rates AC = 1.149297, AG = 2.533695, AT = 2.034519, CG = 1.003899, CT = 5.840755, GT = 1.000000; gamma distribution shape parameter α = 0.167365. Bootstrap support values for ML equal to or greater than 60% and BYPP equal to or greater than 0.90 are given above the nodes. Newly generated sequences are in red

Saprobic on dead leaves of *Pandanus* sp. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Setae* 114–200 × 5–6 µm, erect, cylindrical, dark brown, 2–4-septate, thick-walled, straight to flexuous, conical at the tip, unbranched, smooth. *Conidiophores* 20–42 × 2–5 µm ($\bar{x}$ = 26 × 4 µm, n = 10), subcylindrical, pale brown, smooth, arising from base of setae, straight to flexuous, septate. *Conidiogenous cells* 6–10 × 3–4.5 µm ($\bar{x}$ = 8 × 4 µm, n = 10), terminal or lateral, discrete, subcylindrical to somewhat clavate, subhyaline to pale brown, smooth, polyblastic, with 2–4 denticulate conidiogenous loci. *Conidia* 14–24 × 4–6 µm ($\bar{x}$ = 17.6 × 5 µm, n = 20), solitary, hyaline to subhyaline, biconic, aseptate, round at attenuated base, smooth-walled, without a transverse band and mucilaginous sheath or appendage.

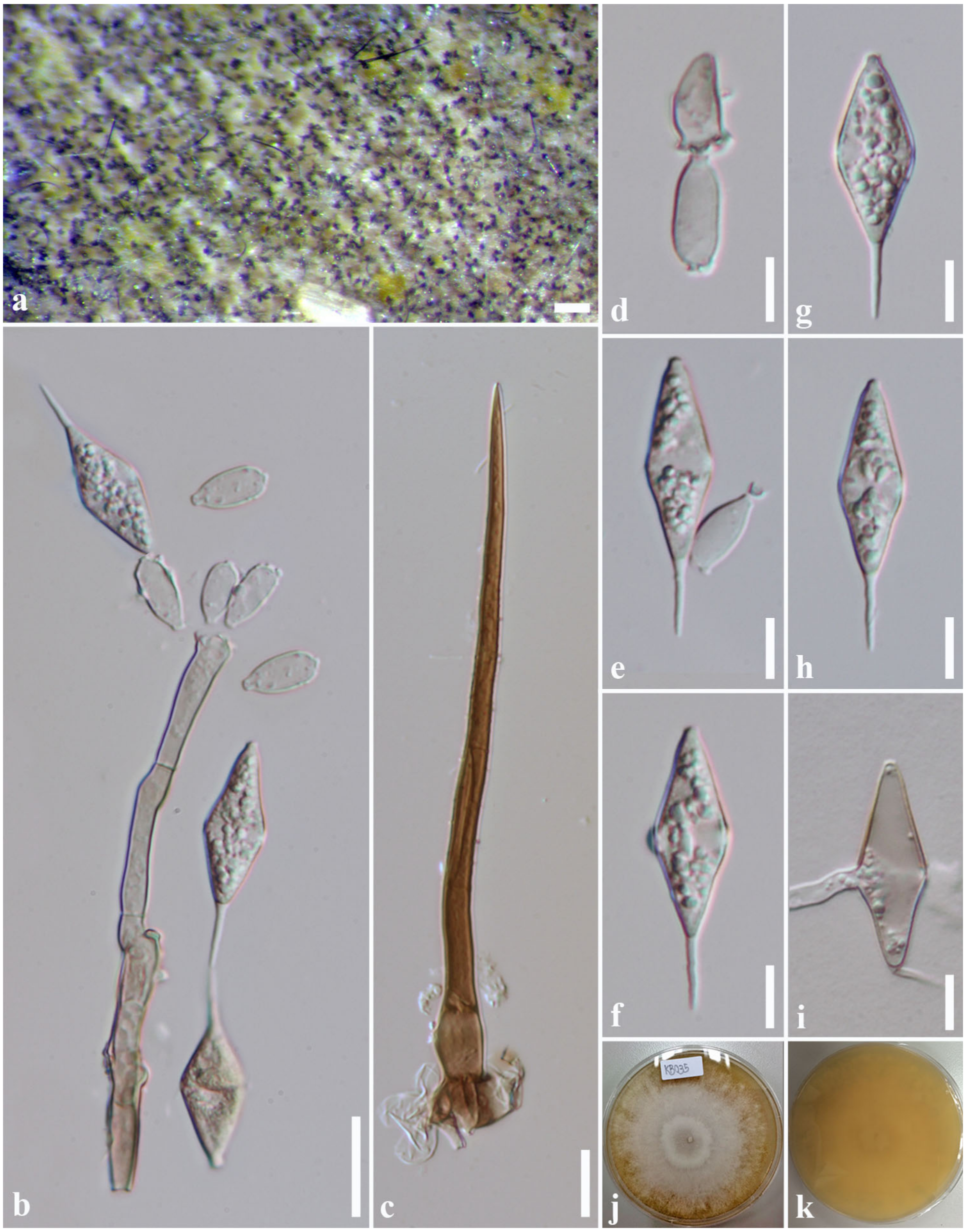


Fig. 102 ***Beltrania krabiensis*** (MFLU 16-1913, **holotype**). **a** Colonies on dead leaves of *Pandanus* sp. **b** Conidiogenous cells with conidiophores and conidia. **c** Seta. **d** Conidiogenous cells. **e–h** Conidia. **i** Germinating conidium. **j, k** Colony on MEA from above and below. Scale bars: **a** = 100 µm, **b, c** = 10 µm, **d–i** = 5 µm

Culture characteristics: Conidia germinating on MEA within 12 h. Colonies on MEA, circular with filamentous-like, filamentous edge, flay on surface media, powdery, white to grey.

Material examined: THAILAND, Phuket Province, Thalang District, on fallen dead and decaying leaves of *Pandanus* sp., 19 December 2017, N. Chaiwan P20 (MFLU 18-0039, **holotype**); ex-type living culture, MFLUCC 18-0121.

GenBank numbers LSU: MH260281; ITS: MH275049; SSU: MH260329.

Notes: *Beltraniella pandanicola* is group together with *B. portoricensis* (F. Stevens) Piroz. & S.D. Patil and *B. acacia* Crous. *Beltraniella portoricensis* has subhyaline to olivaceous conidia with a hyaline transverse band (Rajeshkumar et al. 2016), while *B. acacia* has conidia with median transverse bands of lighter pigments and apical appendages tapering to an acutely rounded tip (Crous et al. 2016b). The conidia of *B. pandanicola* lack both an apical appendage and a median transverse band. In a BLASTn search on NCBI GenBank, the closest matches of ITS sequence of MFLUCC 18-0121 is *B. fertilis* with 99% identity to the strain MRC 4-1 (MF580248).

Beltraniella thailandicus Tibpromma & K.D. Hyde, ***sp. nov***.

Index Fungorum number: IF554514, *Facesoffungi number*: FoF04522; Fig. 103

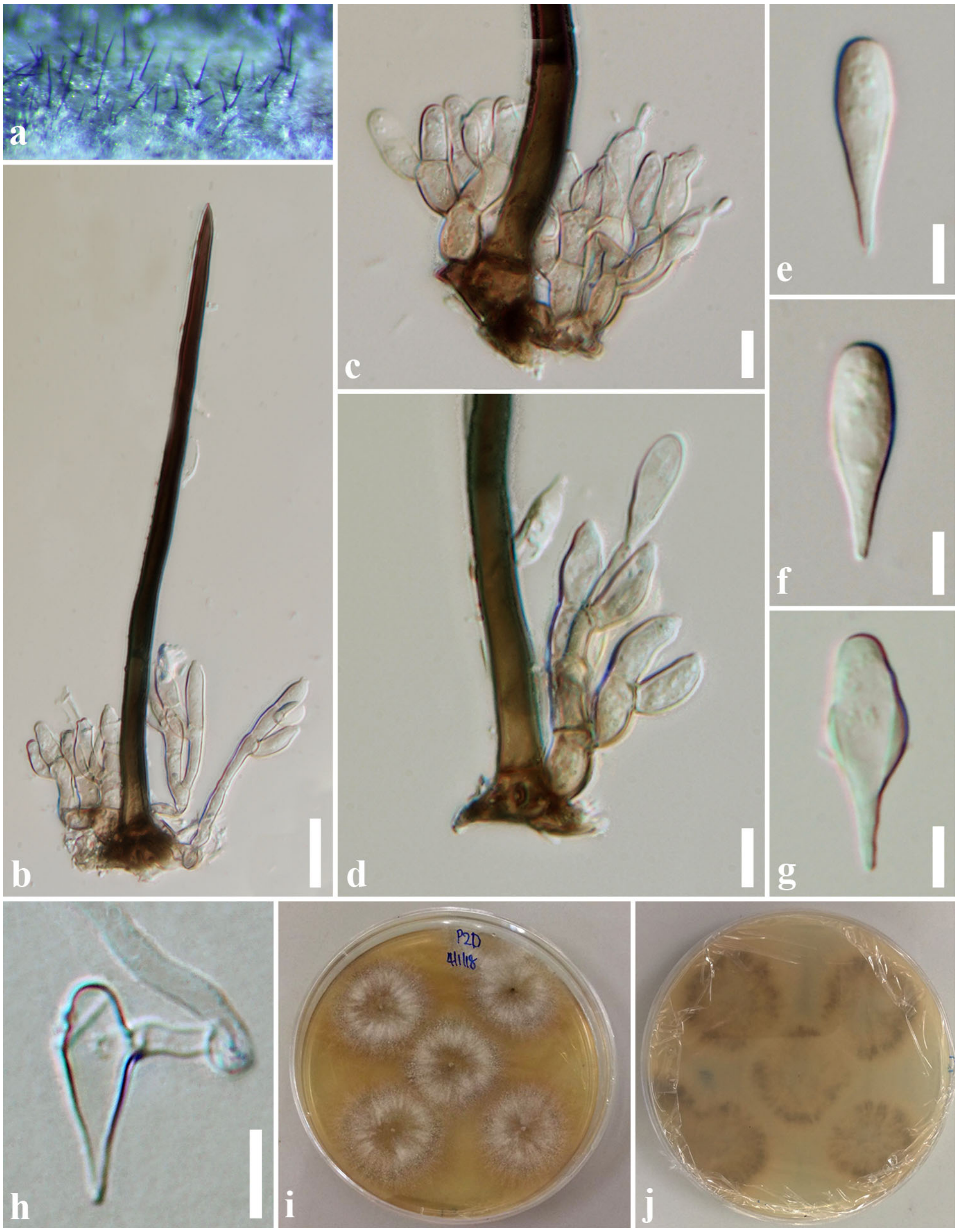


Fig. 103 ***Beltraniella pandanicola*** (MFLU 18-0039, **holotype**). **a** Colonies on dead leaves of *Pandanus* sp. **b–d** Setae, Conidiogenous cells with conidiophores and conidia. **e–g** Conidia. **h** Germinating conidium. **i, j** Colonies on MEA from above and below. Scale bars: **b–d** = 10 µm, **e–h** = 5 µm

Etymology: named after Thailand, where the fungus was first discovered.

Holotype: MFLU 16-1878

Saprobic on dead leaves of *Pandanus* sp. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Setae* 100–118 × 3–4 µm, erect, cylindrical, dark brown, 1–2-septate, thick-walled, straight to flexuous, conical at the tip, unbranched. *Conidiophores* subcylindrical, pale brown, smooth, arising base of setae, straight to flexuous, aseptate. *Conidiogenous cells* 4.5–7.5 × 2–3 µm ($\bar{x}$ = 6 × 2.6 µm, n = 10), terminal or lateral, discrete, subcylindrical to somewhat clavate, pale brown, smooth, polyblastic, sympodial, with 1–4 denticulate conidiogenous loci. *Conidia* 10–25 × 3–6 µm ($\bar{x}$ = 16 × 4 µm, n = 30), solitary, hyaline to subhyaline, kite-like, aseptate, smooth, without a hyaline transverse band, mucilaginous sheath or appendage.

Culture characteristics: Conidia germinating on MEA within 24 h. Colonies on MEA, circular, entire edge with curled, raised on surface media, rough, grey with black at the curled, hard.

Material examined: THAILAND, Chonburi Province, Bang Lamung District, on *Pandanus* sp., 18 July 2016, W. Jaidee PTY03 (MFLU 16-1878, **holotype**; HKAS 96272, **isotype**); ex-type living culture, MFLUCC 16-0377 = KUMCC 17-0300.

GenBank numbers LSU: MH260282; ITS: MH275050; SSU: MH260330.

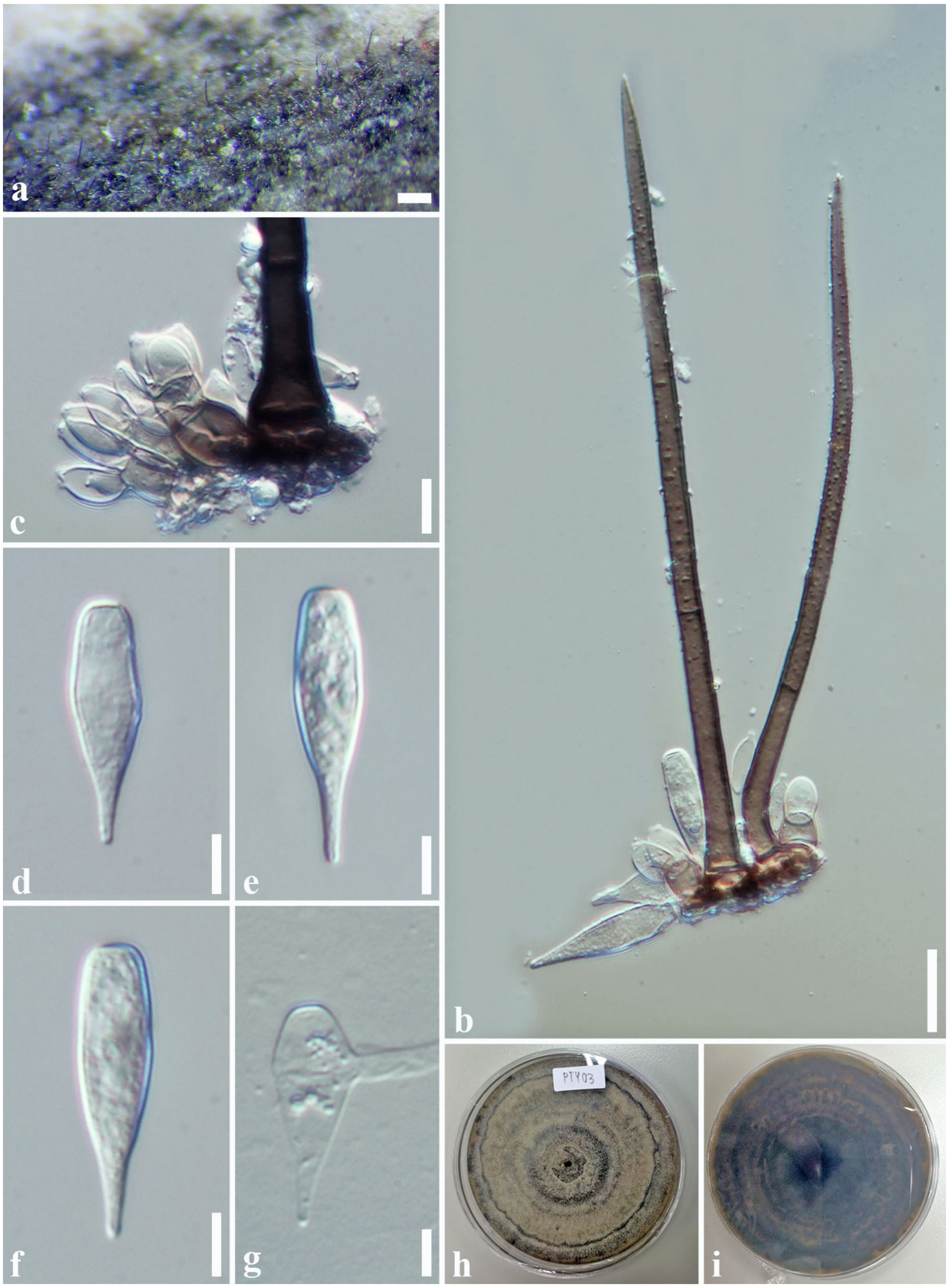


Fig. 104 ***Beltraniella thailandicus*** (MFLU 16-1878, **holotype**). **a** Colonies on dead leaves of *Pandanus* sp. **b, c** Setae, Conidiogenous cells with conidiophores and conidia. **d–f** Conidia. **g** Germinating conidium. **h, i** Colony on MEA from above and below. Scale bars: **a** = 100 µm, **b, c** = 10 µm, **d–g** = 5 µm

Notes: In the phylogenetic analyses, *Beltraniella thailandicus* is distinct from other species of *Beltraniella* (0.97 in BYPP, Fig. 101). It shares similar conidial morphology to *B. portoricensis* but differs by absence of a hyaline transverse band in the conidia (Rajeshkumar et al. 2016). In a BLASTn search on NCBI GenBank, the closest matches of ITS sequence of MFLUCC 16-0377 is *Beltraniella* sp. with 98% identity to the strain 111.3.3 (KP133179).

Sporocadaceae Corda

Sporocadaceae was established by Corda (1842) with *Sporocadus* Corda (1839) as type genus. *Sporocadus* was synonymized under *Seimatosporium* by Maharachchikumbura et al. (2016). Maharachchikumbura et al. (2015) and Senanayake et al. (2015) updated the family. Members of the family are saprobes, endophytes, or foliar pathogens in tropical and temperate regions (Nag Raj 1993; Tanaka et al. 2011). There are 22 genera in the family (Wijayawardene et al. 2018). We describe three new species of *Neopestalotiopsis* and two new species of *Pestalotiopsis* collected from Pandanaceae.

Neopestalotiopsis Maharachch. et al.

Neopestalotiopsis was erected by Maharachchikumbura et al. (2014) with *N. protearum* (Crous & L. Swart)

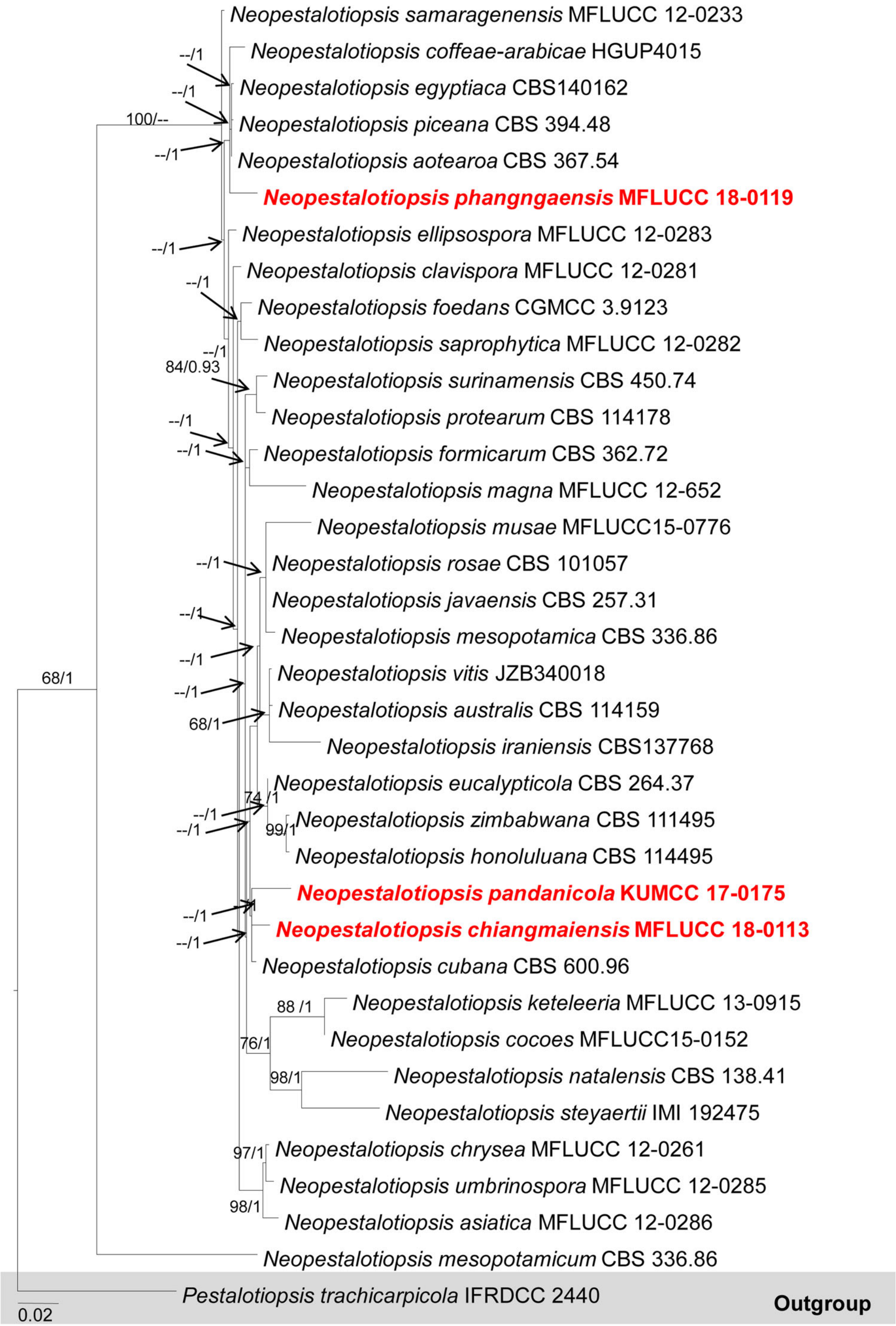


Fig. 105 Phylogram generated from maximum likelihood analysis based on combined ITS, TUB2 and TEF1 sequence data. Thirty-six strains are included in the combined sequence analysis, which comprise 1452 characters with gaps. *Pestalotiopsis trachicarpicola* (IFRDCC 2440) is used as the outgroup taxon. Tree topology of the ML analysis was similar to the BYPP. The best scoring RAxML tree with a final likelihood value of − 5392.679460 is presented. The matrix had 396 distinct alignment patterns, with 12.70% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.229675, C = 0.268221, G = 0.215256, T = 0.286848; substitution rates AC = 1.007965, AG = 3.841487, AT = 1.520713, CG = 0.561002, CT = 4.529758, GT = 1.000000; gamma distribution shape parameter α = 0.234364. Bootstrap support values for ML equal to or greater than 60% and BYPP equal to or greater than 0.90 are given above the nodes. Newly generated sequences are in red

Maharachch., K.D. Hyde & Crous As the type species. The characteristics of this genus are similar to *Pestalotiopsis* but can be distinguished from the latter by distinct phylogeny and versicolourous median cells (Maharachchikumbura et al. 2014). There are 31 epithets listed in Index Fungorum (2018). This is the first report of *Neopestalotiopsis* species from Pandanaceae.

Neopestalotiopsis chiangmaiensis Tibpromma & K.D. Hyde, ***sp. nov***.

Index Fungorum number: IF554515, *Facesoffungi number*: FoF04525; Fig. 105

Etymology: named after Chiang Mai Province, where the fungus was first discovered.

Holotype: MFLU 18-0026

Fig. 106 *Neopestalotiopsis chiangmaiensis* (MFLU 18-0026, **holotype**). **a** Appearance of conidiomata on dead leaves of *Pandanus* sp. **b** Conidiogenous cells with conidiophores and conidia. **c–h** Conidia. **i** Germinating conidium. **j, k** Colony on MEA from above and below. Scale bars: **b–i** = 5 µm

Saprobic on dead leaves of *Pandanus* sp. **Sexual morph** Undetermined. **Asexual morph** *Conidiomata sporodochia* on surface of substrate, scattered, dark brown, dull. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* holoblastic, filiform, smooth, thin-walled, hyaline, short. *Conidia* fusoid to ellipsoid, straight to slightly curved, 4-septate, 18–22 × 8–11 µm ($\bar{x}$ = 20 × 9 µm, n = 20); basal cell conic to obconic with obtuse end, subhyaline, thin-walled and verruculose at the basal cell, 4–5 µm long ($\bar{x}$ = 4.2 µm); three median cells, doliiform, concolorous, yellow to brown, together 12–17 µm long ($\bar{x}$ = 14 µm); second cell from base, yellow, 3.5–5 µm long ($\bar{x}$ = 4 µm); third cell, yellow–brown, 3.5–6 µm long ($\bar{x}$ = 4.6 µm); fourth cell, brown, 3–5 µm long ($\bar{x}$ = 4.4 µm); apical cell hyaline to subhyaline, conic, 3–5 µm long ($\bar{x}$ = 4 µm), with (2–)3 tubular apical appendages; appendages unbranched, 4–28 µm long ($\bar{x}$ = 14 µm); basal appendage present, 3–5 µm long ($\bar{x}$ = 4 µm).

Culture characteristics: Conidia germinating on MEA within 12 h. Colonies on MEA reaching 9 cm diam., after 7 days at room temperature, edge undulate, whitish, aerial mycelium on surface, floosy, velvety; reverse of culture yellow.

Material examined: THAILAND, Chiang Mai Province, Mae Taeng District, Mushroom Research Foundation, on *Pandanus* sp., 16 December 2017, S. Tibpromma P07 (MFLU 18-0026, **holotype**; HKAS 101795, **isotype**); ex-type living culture, MFLUCC 18-0113.

GenBank numbers TEF1: MH388404; TUB2: MH412725.

Notes: Based on multi-gene phylogenetic analysis, *Neopestalotiopsis chiangmaiensis* clusters with *N. pandanicola* and *N. cubana* Maharachch., K.D. Hyde & Crous (Fig. 106). *Neopestalotiopsis pandanicola* has 2(–3)

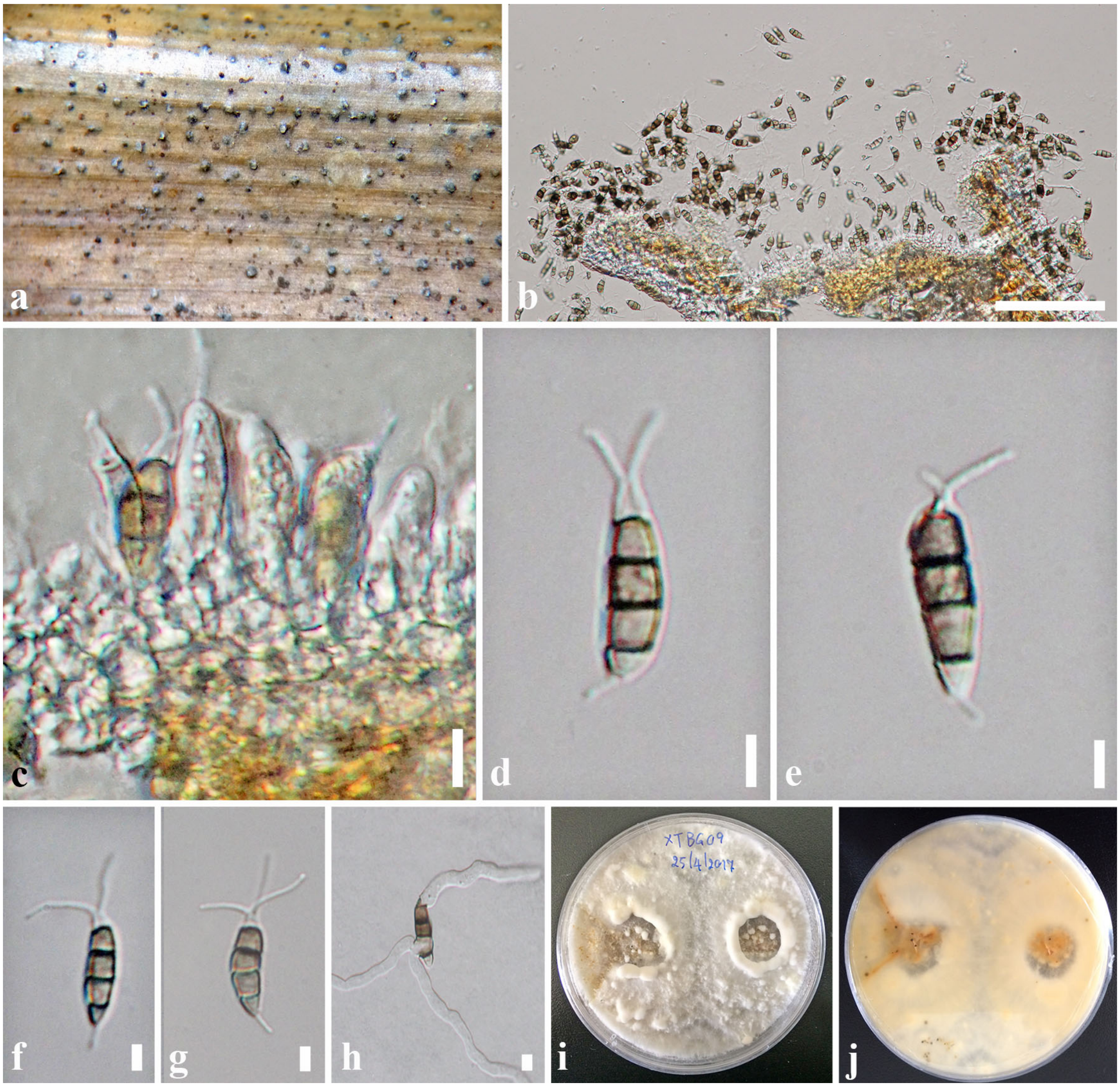


Fig. 107 ***Neopestalotiopsis pandanicola*** (HKAS 99617, **holotype**). **a** Appearance of conidiomata on dead leaves of *Pandanus* sp. **b** Section of conidiomata. **c** Conidiogenous cells with conidiophores and conidia. **d–g** Conidia. **h** Germinating conidium. **i, j** Colonies on MEA from above and below. Scale bars: **b** = 100 µm, **c–h** = 5 µm

tubular apical appendages 9.5–26 µm long, while *N. cubana* has 2–4 tubular apical appendages (19–)21–27 (–28) µm long (Maharachchikumbura et al. 2014). *Neopestalotiopsis chiangmaiensis* has (2–)3 tubular apical appendages; appendages unbranched, 4–28 µm long. In a comparison of the 512 TEF1 nucleotides of *N. chiangmaiensis* and *N. cubana* differed 6 bp (1.17%) and 441 TUB2 nucleotides differed 3 bp (0.68%). In a BLASTn search on NCBI GenBank, the closest matches of TEF1 sequence of MFLUCC 18-0113 is *N. clavispora* with 98% identity to the strain TOR-802-803-804 (KU096881), while the closest matches with the TUB2 sequence were with 99% identical *N. clavispora* strain JT11 (MG740724).

Neopestalotiopsis pandanicola Tibpromma & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF554516, *Facesoffungi number*: FoF04526; Fig. 107

Etymology: named after the host genus, *Pandanus*.

Holotype: HKAS 99617

Saprobic on dead leaves of *Pandanus* sp. **Sexual morph** Undetermined. **Asexual morph** *Conidiomata* 280–450 µm, acervulus, subepidermal in origin, with basal stroma, thin-walled comprising hyaline to pale brown cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* oval, smooth, thin-walled, hyaline, short. *Conidia* fusoid to ellipsoid, straight to slightly curved, 4-septate, 27–35 × 7.5–11 µm ($\bar{x}$ = 31 × 9 µm, n = 20); basal cell conic to obconic with obtuse end, sub-hyaline to pale brown, thin-walled and verruculose, 3.5–8 µm long ($\bar{x}$ = 6 µm); three median cells, doliiform, concolorous, brown, periclinal walls darker than rest of the cell, together 17–25 µm long ($\bar{x}$ = 21 µm); second cell from base 4.5–12.5 µm long ($\bar{x}$ = 8 µm); third cell 5–8 µm long ($\bar{x}$ = 7 µm); fourth cell 6–10 µm long ($\bar{x}$ = 8 µm); apical cell hyaline, conic to cylindrical 3–6 µm long ($\bar{x}$ = 4 µm), with 2(–3) tubular apical appendages; unbranched, 9.5–26 µm long ($\bar{x}$ = 17 µm); with single basal appendage 3–6 µm long ($\bar{x}$ = 5 µm), rarely absent, tubular, unbranched, centric.

Culture characteristics: Conidia germinating on PDA within 12 h. Colonies on PDA reaching 9 cm diam., after 7 days at room temperature, edge undulate, whitish, aerial mycelium on surface, floosy, velvety; reverse of culture yellow–white.

Material examined: CHINA, Yunnan Province, Xishuangbanna, on fallen dead and decaying leaves of *Pandanus* sp., 12 November 2016, T. Aluthwaththa XTBG09 (HKAS 99617, **holotype**); ex-type living culture, KUMCC 17-0175 = MFLUCC 17-2261.

GenBank numbers LSU: MH376727; SSU: MH388321; TEF1: MH388389; TUB2: MH412720.

Notes: *Neopestalotiopsis pandanicola* is morphologically similar to *N. javaensis* Maharachch., K.D. Hyde & Crous. Conidiogenous cells of *N. pandanicola* are filiform and short, while the conidiogenous cells of *N. javaensis* are ampulliform to lageniform and rugose-walled. *Neopestalotiopsis pandanicola* is phylogenetically closely related to *N. chiangmaiensis* (Fig. 106). However, this species differs from *N. pandanicola* by has smaller conidia (20 × 9 µm) and apical appendages. In a comparison of the 490 TEF1 nucleotides of *N. pandanicola* and *N. chiangmaiensis* differed 23 bp (4.69%). In a BLASTn search on NCBI GenBank, the closest matches of TEF1 sequence of KUMCC 17-0175 is *N. clavispora* with 99% identity to the strain TOR-802-803-804 (KU096881), while the closest matches with the TUB2 sequence were with 99% identical *N. clavispora* strain NM16311a (LC209221).

Neopestalotiopsis phangngaensis Tibpromma & K.D. Hyde, ***sp. nov***.

Index Fungorum number: IF554517, *Facesoffungi number*: FoF04527; Fig. 108

Etymology: named after Phang Nga Province, where the fungus was first discovered.

Holotype: MFLU 18-0037

Saprobic on dead leaves of *Pandanus* sp. **Sexual morph** Undetermined. **Asexual morph** *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* enteroblastic, annellidic, filiform, ampulliform, smooth, thin-walled,

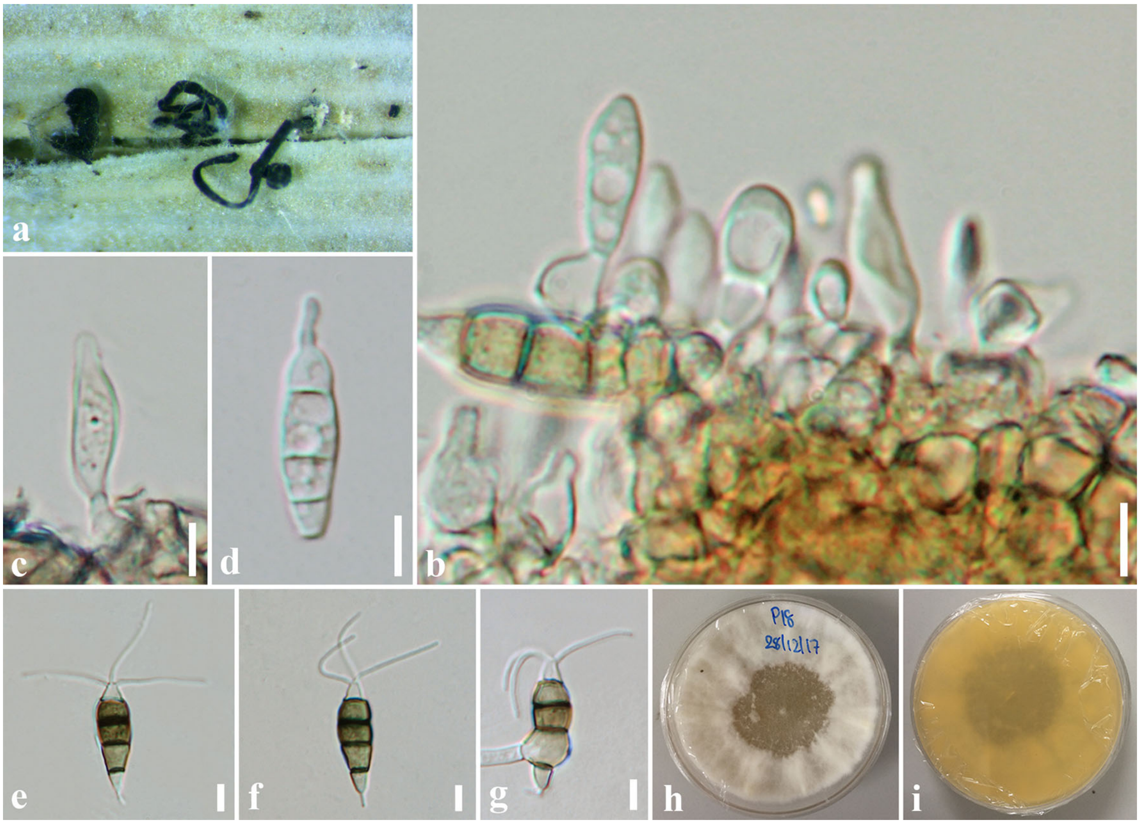


Fig. 108 ***Neopestalotiopsis phangngaensis*** (MFLU 18-0037, **holotype**). **a** Colonies on dead leaves of *Pandanus* sp. **b, c** Conidiogenous cells with conidiophores and conidia. **d–f** Conidia. **g** Germinating conidium. **h, i** Colony on MEA from above and below. Scale bars: **b–g** = 5 µm

hyaline, short. *Conidia* fusoid to ellipsoid, straight to slightly curved, 4-septate, 18–25 × 6–7.5 µm ($\bar{x}$ = 21 × 6.6 µm, n = 20); basal cell conic to obconic with obtuse end, hyaline, verruculose, 3–5 µm long ($\bar{x}$ = 4.3 µm); three median cells doliiform, concolorous, hyaline to subhyaline, becoming brown with age, septa and periclinal walls darker than rest of cells, together 13–15 µm long ($\bar{x}$ = 14 µm); second cell from base 3.5–5 µm long ($\bar{x}$ = 4.6 µm); third cell 2.5–5 µm long ($\bar{x}$ = 4.5 µm); fourth cell 4–5 µm long ($\bar{x}$ = 4.5 µm); apical cell hyaline, conic 3–4.5 µm long ($\bar{x}$ = 3.5 µm), with 3 tubular apical appendages; appendages unbranched, 16–24.5 µm long ($\bar{x}$ = 18 µm); basal appendage present 3–6 µm long ($\bar{x}$ = 3.9 µm), rarely absent, tubular, unbranched, centric.

Culture characteristics: Conidia germinating on MEA within 12 h. Colonies on MEA reaching 9 cm diam., after 7 days at room temperature, edge undulate, whitish, aerial mycelium on surface, floosy, velvety; reverse of culture yellow–white.

Material examined: THAILAND, Phang Nga Province, Thap Put District, on *Pandanus* sp., 20 December 2017, N. Chaiwan P18 (MFLU 18-0037, **holotype**; HKAS 101796, **isotype**); ex-type living culture, MFLUCC 18-0119.

GenBank numbers LSU: MH376728; ITS: MH388354; SSU: MH388322; TEF1: MH388390; TUB2: MH412721.

Notes: *Neopestalotiopsis phangngaensis* is well-separated from other species of *Neopestalotiopsis* in the combined gene phylogenetic analyses (Fig. 106). *Neopestalotiopsis phangngaensis* is similar to *N. eucalypticola* isolated from *Eucalyptus globules* in country name. However, *N. eucalypticola* has 1–2, long tubular apical appendages, which are sometimes branched (Maharachchikumbura et al. 2016), while *N. phangngaensis* has 5 tubular apical appendages which are unbranched. In a comparison of the 512 TEF1 nucleotides of *N. eucalypticola* and *N. phangngaensis* differed 5 bp (0.97%) and 441 TUB2 nucleotides differed 26 bp (5.89%). In a BLASTn search on NCBI GenBank, the closest matches of TEF1 sequence of KUMCC 17-0175 is *Neopestalotiopsis* sp. with 90% identity to the strain MMf-0011 (LC184190), while the closest matches with the TUB2 sequence were with 99% *Pestalotiopsis* sp. strain HGUP4077 (KF179298).

Pestalotiopsis Steyaert

Pestalotiopsis was erected by Steyaert (1949) with *P. guepinii* (Desm.) Steyaert as the type species. *Pestalotiopsis* are opportunistic pathogens, endophytes and saprobes (Hu et al. 2007; Maharachchikumbura et al. 2011, 2012, 2014). Steyaert (1949) split *Pestalotia* into three genera, namely *Pestalotia*, *Pestalotiopsis* and *Truncatella* based on conidial morphology. Maharachchikumbura et al. (2014), provided morphological and phylogeny. There are 309 epithets listed in Index Fungorum (2018). *Pestalotiopsis funerea* (Desm.) Steyaert and *P. guepinii* (Desm.) Steyaert have been reported from Pandanaceae (Whitton et al. 2012).

Pestalotiopsis krabiensis Tibpromma & K.D. Hyde, ***sp. nov*.**

Index Fungorum number: IF554518, *Facesoffungi number*: FoF04528; Fig. 109

Etymology: named after Krabi Province, where the fungus was first discovered.

Holotype: MFLU 16-1919

Saprobic on dead leaves of *Pandanus* sp. **Sexual morph** Undetermined. **Asexual morph** *Conidiophores* short, unbranched, reduced to conidiogenous cells. *Conidiogenous cells* discrete, holoblastic, simple, filiform, smooth, thin-walled, hyaline. *Conidia* fusoid to ellipsoid, straight to slightly curved, 4-septate, 19–25 × 4–6 µm ($\bar{x}$ = 21 × 5 µm, n = 30), basal cell conic to obconic with obtuse end, hyaline, thin-walled, verruculose, 3.5–5 µm long ($\bar{x}$ = 4 µm); three median cells, doliiform, concolorous, hyaline becoming yellow–white with age, septa and periclinal walls darker than rest of the cell, together 13–15 µm long ($\bar{x}$ = 13.7 µm); second cell from base 3–5 µm long ($\bar{x}$ = 4 µm); third cell 4–5.5 µm long ($\bar{x}$ = 4.6 µm); fourth cell 4–5 µm long ($\bar{x}$ = 4.3 µm); apical cell hyaline, conic 4–5.5 µm long ($\bar{x}$ = 4.5 µm), with 2(–3) tubular apical appendages; appendages arising from the apex of the apical cell, unbranched, 11–19 µm long ($\bar{x}$ = 15 µm); single basal appendage usually present, 2–4 µm long ($\bar{x}$ = 2.6 µm), tubular, unbranched, centric.

Culture characteristics: Conidia germinating on MEA within 12 h. Colonies on MEA reaching 9 cm diam., after 7 days at room temperature, edge undulate, whitish, aerial mycelium on surface, curled, fruiting bodies black after 2 months, concentric, floosy, velvety; reverse of culture yellow–white.

Material examined: THAILAND, Krabi Province, Mueang Krabi District, on *Pandanus* sp., 14 December 2015, S. Tibpromma KB041 (MFLU 16-1919, **holotype**; HKAS 96268, **isotype**); ex-type living culture, MFLUCC 16-0260 = KUMCC 16-0141.

GenBank numbers LSU: MH376734; ITS: MH388360; TEF1: MH388395; ACT: MH412715; TUB2: MH412722.

Notes: In the phylogenetic analysis, *Pestalotiopsis krabiensis* forms a sister group to *P. pandanicola*. *Pestalotiopsis krabiensis* has larger conidia (21.1 × 5.2 µm) with mostly 2 apical appendages, while *P. pandanicola* has smaller conidia (15.1 × 3.6 µm) with 3 apical appendages. In a comparison of the 517 TEF1 nucleotides of *P. pandanicola* and *P. krabiensis* differed 1 bp (0.19%), 475 TUB2 nucleotides differed 17 bp (3.57%) and 577 ITS (+5.8S) nucleotides differed 1 bp (0.17%) which justifies these two isolates as two distinct taxa. In a BLASTn search

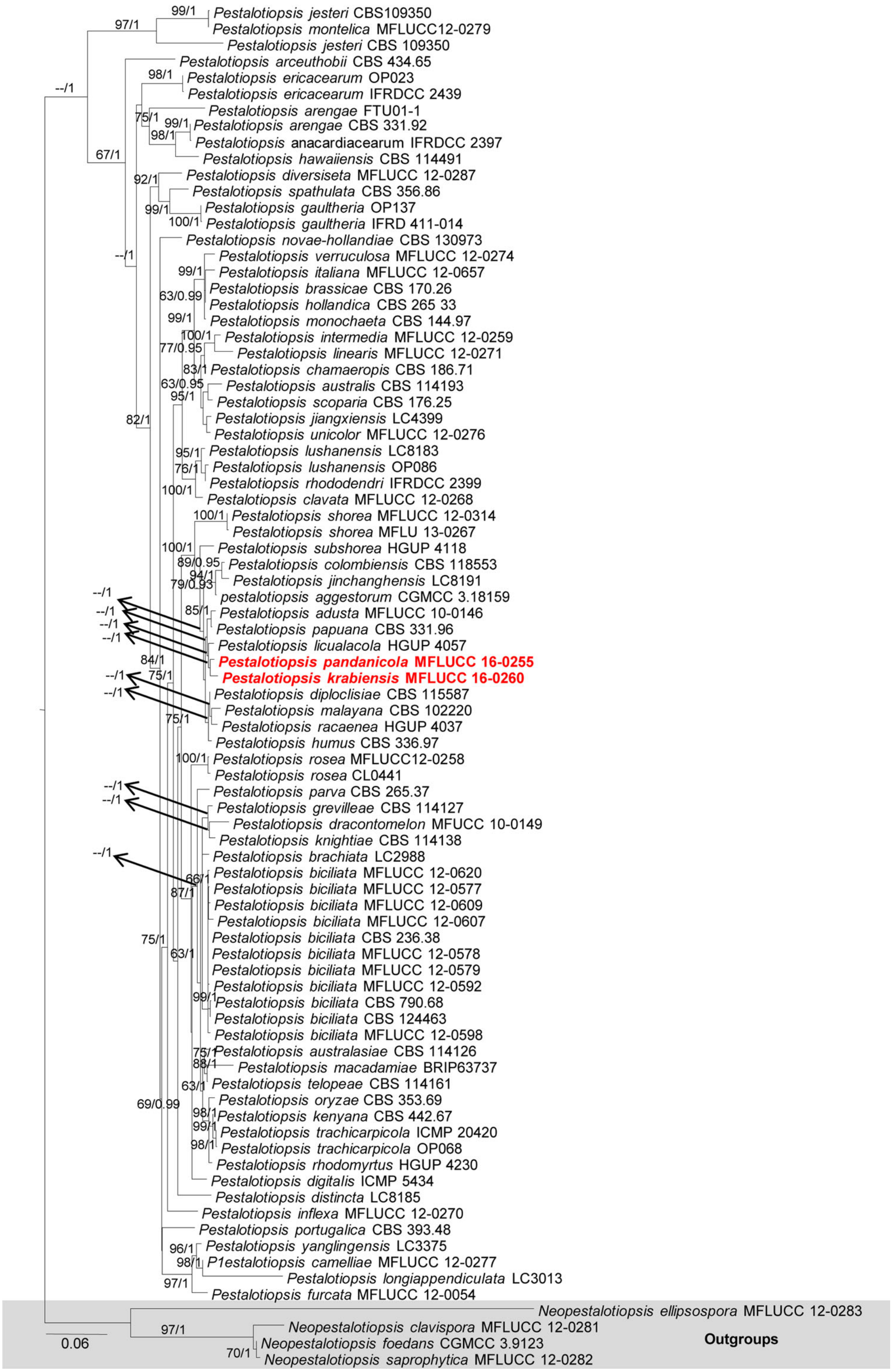


Fig. 109 Phylogram generated from maximum likelihood analysis based on combined ITS, TUB2 and TEF1 sequence data. Eighty-four strains are included in the combined sequence analysis, which comprise 1577 characters with gaps. *Pestalotiopsis trachicarpicola* (IFRDCC 2440) is used as the outgroup taxon. Tree topology of the ML analysis was similar to the BYPP. The best scoring RAxML tree with a final likelihood value of − 11764.880209 is presented. The matrix had 766 distinct alignment patterns, with 11.72% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.234091, C = 0.292387, G = 0.213607, T = 0.259915; substitution rates AC = 1.039520, AG = 3.238137, AT = 1.214322, CG = 0.889565, CT = 3.748492, GT = 1.000000; gamma distribution shape parameter α = 0.310200. Bootstrap support values for ML equal to or greater than 60% and BYPP equal to or greater than 0.90 are given above the nodes. Newly generated sequences are in red

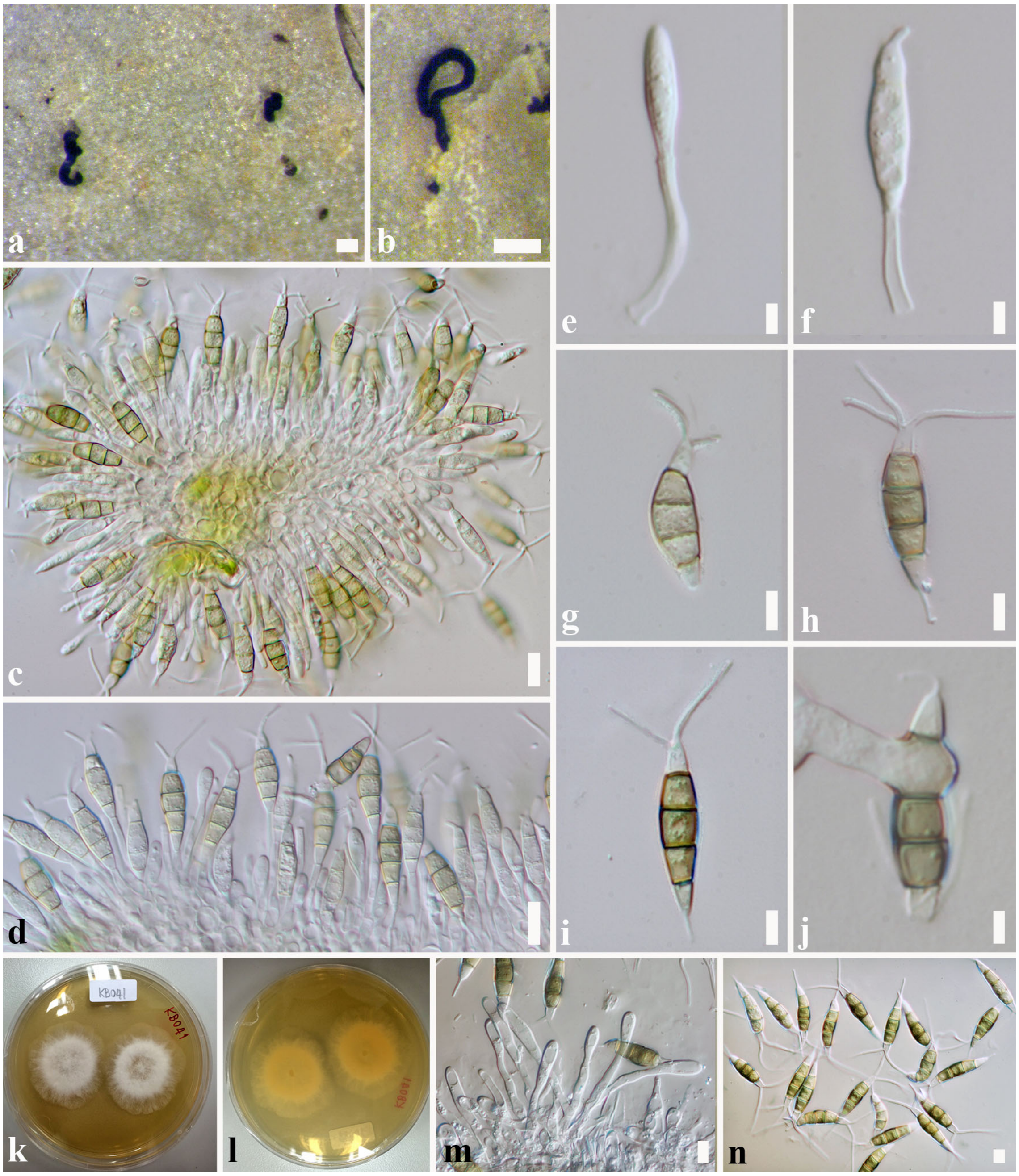


Fig. 110 ***Pestalotiopsis krabiensis*** (MFLU 16-1919, **holotype**). **a, b** Colonies on dead leaves of *Pandanus* sp. **c–f** Conidiogenous cells with conidiophores and conidia. **g–i** Conidia. **j** Germinating conidium. **k, l** Colonies on MEA from above and below. **m, n** Conidiogenous cells and conidia formed in culture. Scale bars: **a** = 100 µm, **b** = 200 µm, **c, d, m, n** = 10 µm, **e–j** = 5 µm

on NCBI GenBank, the closest matches of TEF1 sequence of MFLUCC 16-0260 is *P. adusta strain* with 99% identity to the strain MFLUCC 10-0146 (JX399071), while the closest matches with the TUB2 sequence were with 99% *P. adusta* strain LPJZ02 (KJ885549).

Pestalotiopsis pandanicola Tibpromma & K.D. Hyde, ***sp. nov***.

Index Fungorum number: IF554519, *Facesoffungi number*: FoF04529; Fig. 110

Etymology: named after the host genus, *Pandanus*.

Holotype: MFLU 18-0039

Saprobic on dead leaves of *Pandanus* sp. **Sexual morph** Undetermined. **Asexual morph** *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* discrete, holoblastic, simple, filiform, smooth, thin-walled, hyaline, and long. *Conidia* fusoid to ellipsoid, straight to slightly curved, 4-septate, 13–18 × 2.5–4.5 µm ($\bar{x}$ = 15.1 × 3.6 µm, n = 30), basal cell conic to obconic with obtuse end, hyaline, thin and verruculose, 2–4 µm long ($\bar{x}$ = 3.1 µm), with three median cells, doliiform, concolorous, yellow to pale brown, septa, together 8–11 µm long ($\bar{x}$ = 9.5 µm); second cell from base, pale brown, 2–4 µm long ($\bar{x}$ = 3 µm); third cell, pale brown, 2.5–4 µm long ($\bar{x}$ = 3 µm); fourth cell, pale brown, 5–6.5 µm long ($\bar{x}$ = 3.1 µm), apical cell hyaline, conic to sometimes cylindrical, 2–3 µm long ($\bar{x}$ = .4 µm), with (2–)3 tubular apical appendages; appendages arising from apex of the apical cell, unbranched, 3.5–8 µm long ($\bar{x}$ = 6.7 µm); basal appendage present, 1–4 µm long ($\bar{x}$ = 2.7 µm), single, tubular, centric.

Culture characteristics: Conidia germinating on MEA within 12 h. Colonies on MEA reaching 9 cm diam., after 7 days at room temperature, circular, edge entire, whitish to pale yellow, with dense, aerial mycelium on surface, fruiting bodies black; reverse of culture whitish to pale yellow.

Material examined: THAILAND, Krabi Province, Mueang Krabi District, on *Pandanus* sp., 14 December 2015, S. Tibpromma KB030 (MFLU 16-1908, **holotype**; HKAS 96257, **isotype**); ex-type living culture, MFLUCC 16-0255 = KUMCC 16-0140.

GenBank numbers LSU: MH376735; ITS: MH388361; TEF1: MH388396; ACT: MH412716; TUB2: MH412723.

Notes: *Pestalotiopsis pandanicola* clusters with *P. krabiensis* in the phylogenetic analysis (Fig. 111), which has been described from the same location. Therefore, we propose *P. pandanicola* as a new species in *Pestalotiopsis* based on morphology and phylogenic analysis which discussion at above. In a BLASTn search on NCBI GenBank, the closest matches of TEF1 sequence of MFLUCC 16-0255 is *P. adusta strain* with 94% identity to the strain MFLUCC 10-0146 (JX399071), while the closest matches with the TUB2 sequence were with 99% *P. uvicola* strain HHL-AG (HM573238).

Sordariomycetes orders *incertae sedis*

Vermiculariopsiellales Hern.-Restr. et al.

Vermiculariopsiellaceae Hern.-Rest. et al.

Vermiculariopsiellaceae was erected by Hernández-Restrepo et al. (2017) with *Vermiculariopsiella* Bender as the type genus based on phylogenetic analysis. *Echinosphaeria macrospora* Gawas, Bhat & K.D. Hyde. and *E. pteridis* S. Dharg. & Bhat. have been reported as sexual morphs of *Vermiculariopsiella* species based on culture techniques (Gawas et al. 2006; Dhargalkar and Bhat 2009), but need to be confirmed as the type species of *Echinosphaeria* is related to the family Helminthosphaeriaceae in the order Chaetosphaeriales (Miller and Huhndorf 2004; Miller et al. 2014). Morphological details for Helminthosphaeriaceae are provided by Hernández-Restrepo et al. (2017). We introduced a new species of *Vermiculariopsiella* collected from *Pandanus* sp.

Vermiculariopsiella Bender

Vermiculariopsiella spp. have been reported as asexual morphs of *Echinosphaeria macrospora* Gawas, Bhat & K.D. Hyde. and *E. pteridis* S. Dharg. & Bhat based on culture techniques (Gawas et al. 2006; Dhargalkar and Bhat 2009). However, Miller and Huhndorf (2004) and Miller et al. (2014) suggested that this relationship needed to be confirmed using molecular studies. Maharachchikumbura et al. (2016) showed that *Vermiculariopsiella* belonged to Microascales, genera *incertae sedis*. However, Hernández-Restrepo et al. (2017) introduced *Vermiculariopsiella* to Vermiculariopsiellaceae. *Vermiculariopsiella* has sporodochia with brown, erect setae dispersed throughout, and subhyaline conidiophores that give rise to phialidic conidiogenous cells with prominently curved apices, and hyaline, aseptate conidia (Crous et al. 2017). *Vermiculariopsiella* has 24 epithets are listed in Index Fungorum (2018). *Vermiculariopsiella* never has been reported from Pandanaceae.

Vermiculariopsiella hongkongensis Tibpromma & K.D. Hyde, ***sp. nov.***

Index Fungorum number: IF554552, *Facesoffungi number*: FoF04561; Fig. 112

Etymology: named after Hong Kong, where the fungus was first discovered.

Holotype: HKAS 100861

Saprobic on dead leaves of *Pandanus* sp. *Colonies* on natural substrate minute, brown, with erect, thick-walled, roughened, straight to flexuous, cylindrical and brown setae dispersed throughout sporodochium. **Sexual morph** Undetermined. **Asexual morph** Hyphomycetous. *Conidiophores* subcylindrical, septate, hyaline to subhyaline and dense. *Conidiogenous cells* 3.5–6 × 0.5–1.5 µm, terminal, subcylindrical, hyaline to subhyaline. *Conidia* 50–100 × 4–7.5 µm ($\bar{x}$ = 70 × 5 µm, n = 20), solitary, hyaline, guttulate, straight to slightly curved, oblong with conical at both end, smooth-walled, without mucilaginous sheath. *Setae* 150–175 × 1.5–3 µm, cylindrical, conical at the apex, pale brown, septate.

Culture characteristics: Conidia germinating on MEA within 12 h. Colonies on MEA, circular, edge entire, white to yellow with white flossy in some part, velvety, with raised on media.

Material examined: HONG KONG, around Tai Tam Tuk Reservoir Dam, on *Pandanus* sp., 21 September 2016, S. Tibpromma HK09 (HKAS 100861, **holotype**); ex-type living culture, KUMCC 17-0270, MFLUCC 17-0636.

GenBank numbers LSU: MH260327; ITS: MH275092; SSU: MH260365.

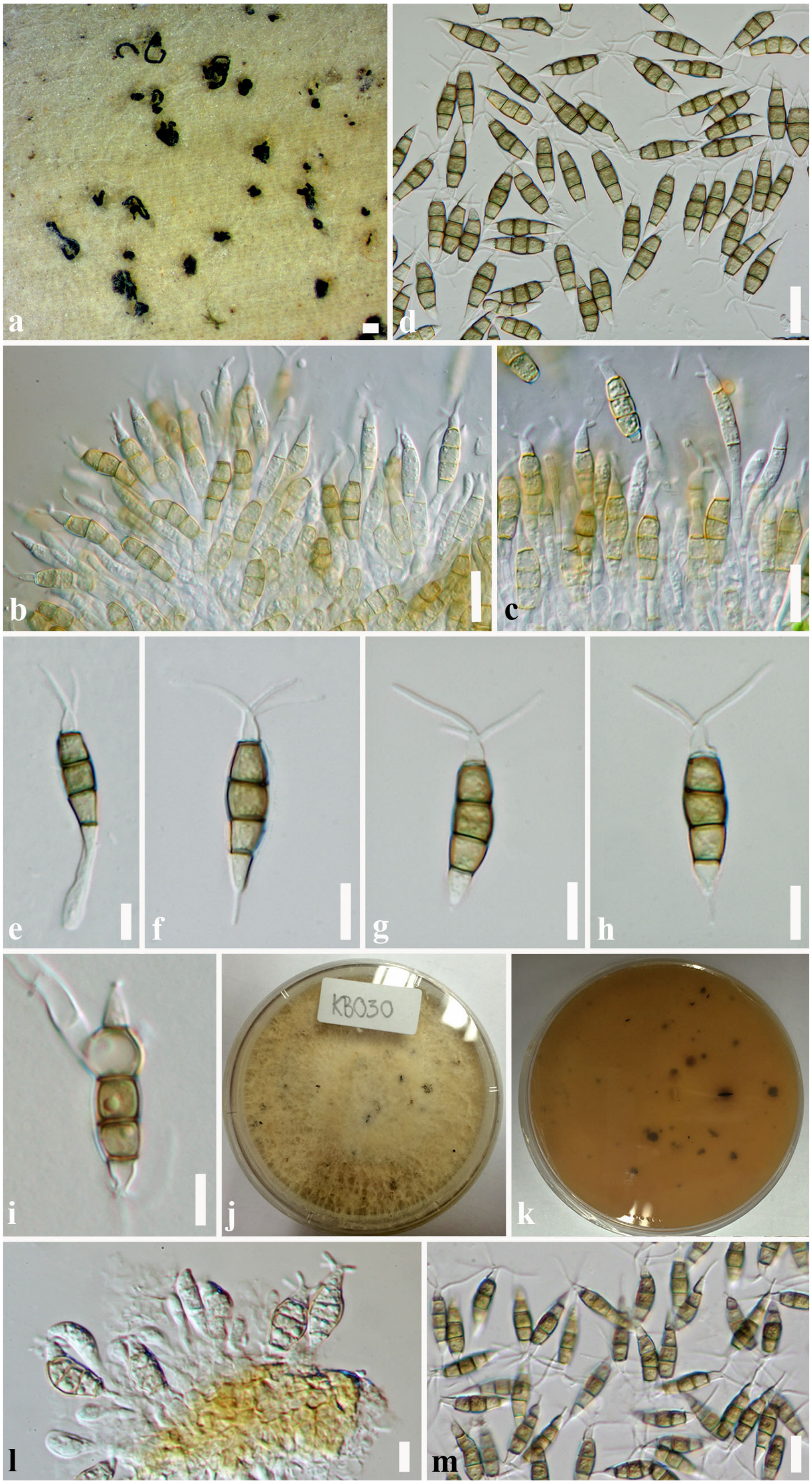


Fig. 111 ***Pestalotiopsis pandanicola*** (MFLU 16-1908, holotype). **a** Colonies on dead leaves of Pandanus sp. **b, c** Conidiogenous cells with conidiophores and conidia. **d–h** Conidia. **i** Germinating conidium. **j, k** Colony on MEA from above and below. **l** Conidiogenous cells with conidia formed in culture. **m** Conidia formed in culture. Scale bars: **b–d** = 10 lm, **e–i, l, m** = 5 lm

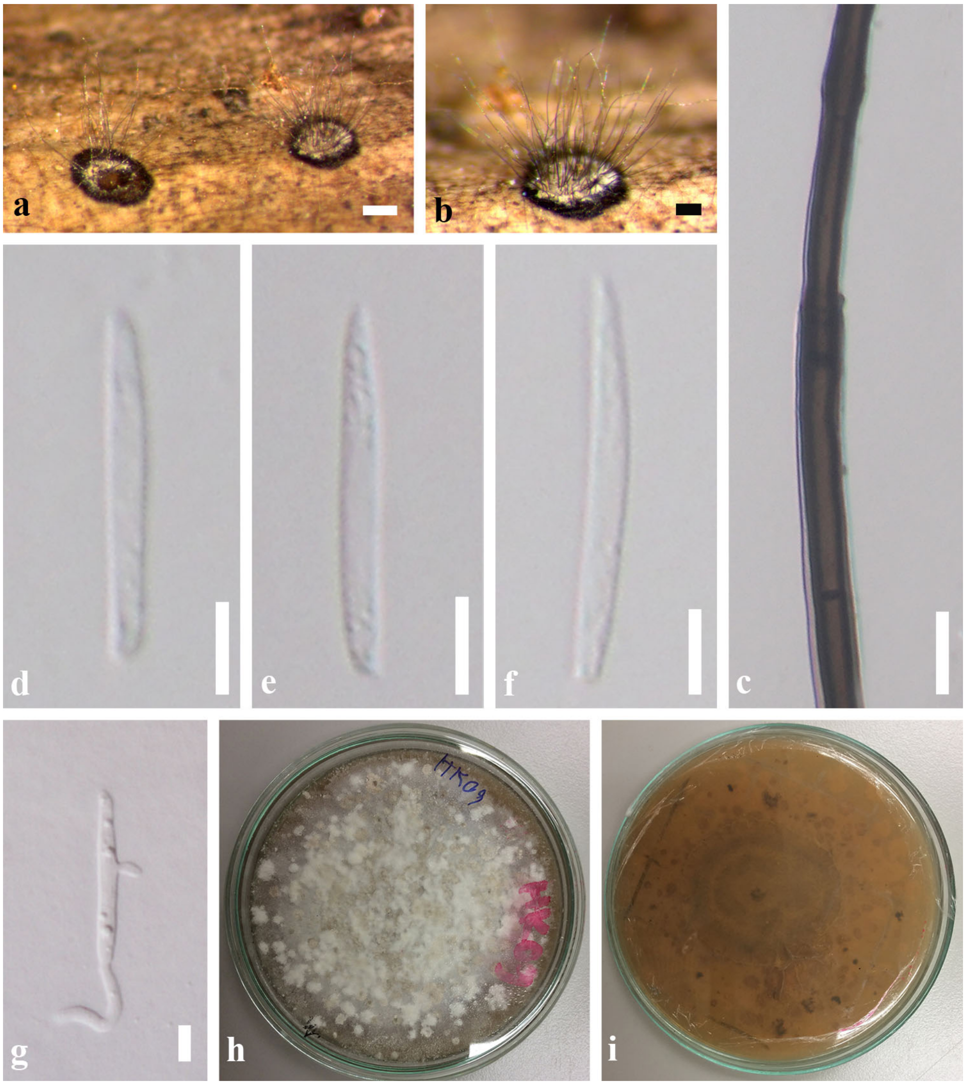


Fig. 112 ***Vermiculariopsiella hongkongensis*** (HKAS 100861, **holotype**). **a, b** Colonies on dead leaf of *Pandanus* sp. **c** Setae-walled. **d–f** Conidia. **g** Germinating conidium. **h, i** Colony on MEA from above and below. Scale bars: **a** = 200 µm, **b** = 100 µm, **b** = 10 µm, **c**, **g** = 5 µm, **d–f** = 2 µm

Notes: *Vermiculariopsiella* has never been reported from Pandanaceae. Based on phylogenetic analysis, *V. hongkongensis* is well-separated from other species of *Vermiculariopsiella* (0.99 in BYPP, Fig. 68). However, we compare the morphology *V. hongkongensis* with *V. acaciae* Crous & M.J. Wingf. and *V. immersa* (Desm.) Bender. but *V. acacia* has dimorphic conidia (Crous et al. 2016a), while *V. immerse* has fusoid to cylindrical conidia (Bender 1932). In a BLASTn search on NCBI GenBank, the closest matches of ITS sequence of KUMCC 17-0270 is *V. dichapetali culture* with 99% identity to the strain CBS:143440 (MH107924).

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