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Mycosphere Notes 413–448: Dothideomycetes associated with woody oil plants in China

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Abstract

This is the ninth in a series of Mycosphere notes wherein we provide notes on various fungal taxa in Dothideomycetes. In this set of notes, we focus on species associated with woody oil plants, which are important in terms of food security, ecology, agriculture and for industrial manufacturing. Eighty-five fungal taxa were identified in three orders (Muyocopronales, Pleosporales and Valsariales). Thirty-four species (belonging to 16 families) were identified in Pleosporales, one species was classified in Valsariales and one species was recognized in Muyocopronales. We introduce two new genera *Oleaginea* (Lophiostomataceae) and *Neobrevicollum* (Neohendersoniaceae) and 16 new species, *Acrocalymma paeoniae*, *Corynespora idesiae*, *Flabellascoma pistaciae*, *Loculosulcatispora paeoniae*, *Lophiostoma oleae*, *Montagnula verniciae*, *Neobrevicollum oleae*, *Neocucurbitaria pistaciicola*, *Nigrograna acericola*, *Ni. oleae*, *Ni. sichuanensis*, *Ni. verniciae*, *Oleaginea sichuanensis*, *Palmiascoma acericola*, *Paramonodictys paeoniae*, *Pseudothyridariella idesiae*. New host/country records are provided for *Acrocalymma pterocarpi*, *Angustimassarina kunmingense*, *Austropleospora ochracea*, *Crassiparies quadrisporus*, *Loculosulcatispora hongheensis*, *Lophiotrema hydei*, *Lophiotrema neoarundinaria*, *Lophiostoma chiangraiense*, *Lophiostoma japonica*, *Lophiostoma montanae*, *Montagnula donacina*, *Muyocopron lithocarpi*, *Neokalmusia aquibrunnea*, *Neovaginatispora fuckelii*, *Nigrograna hydei*, *Ni. locuta-pollinis*, *Ni. magnoliae*, *Pseudochaetosphaeronema chiangraiense*, *P. magnoliae*, and *Valsaria insitiva*. Three new asexual/sexual morph connections were made for *Acrocalymma pterocarpi*, *Austropleospora ochracea* and *Loculosulcatispora hongheensis*. A morphological description of one known species, *Nigrograna locuta-pollinis*, is provided. All taxa are described and illustrated, and phylogenetic trees are presented to show their phylogenetic placements.

Key words – 2 new genera – 16 new species – 20 new records – molecular phylogeny – multi-gene – taxonomy

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Introduction

'Woody oil plants' is the general term for the fruits, leaves or seeds of woody plants that can be used for oil extraction, are rich in nutritious resources and have a wide range of varieties around the world (Dai et al. 2015). They play vital roles in the fields of ecology, agriculture, and functional food manufacturing. Woody oil plants are usually divided into several groups; 1) edible woody oil plants: e. g. *Olea europaea* L., 2) industrial oil plants: e. g. *Swida walteri* (Wanger.) Sojak, 3) aromatic oil plants: e. g. *Illicium verum* Hook. f., 4) medicinal oil plants: e.g. *Semiliquidambar cathayensis* Chang, and 5) biomass fuel oil plants: e. g. *Jatropha curcas* L., *Malania oleifera* Chun & S.K. Lee, *Horsfieldia hainanensis* Merr. The woody oil plants identified in China belong to 151 families, 697 genera and 1,553 species, accounting for 5% of seed plants (Ma et al. 2009). Because of the intrinsic value of woody oil plants, they have been significantly cultivated in China in recent years. In 2020, the output of oil from woody plants reached 8.521 million tons, accounting for 4.27% of the total annual output of economic forest products in China (China forestry and grassland yearbook 2021).

With gradual expansion of the woody oil plantation area, the incidence of fungal diseases has increased. Pathogens such as *Colletotrichum* and pestalotiod species cause anthracnose diseases of *Camellia oleifera* Abel. (Li et al. 2016, Liu et al. 2021), *Botryosphaeria dothidea* causes branch rot and decay of *Juglans regia* L. (Zhang et al. 2020), while *Cycloconium oleaginum* is the causal agent of freckle disease of olive (She et al. 2020). In addition, Yu et al. (2018) reported a highly diverse endophytic fungal community associated with *Camellia oleifera*, and some of which act as biocontrol agents. The endophytic fungi *Alternaria*, *Arthrinium*, *Botryosphaeria*, *Colletotrichum* and *Pestalotiopsis* were also reported from woody oil plants (Li et al. 2018, 2021). Most studies have focused on diversity and ecology of pathogens and endophytes associated with woody oil plants and there are relatively few studies on the diversity of saprobes. During a survey of fungi on woody oil plants in Sichuan Province, we have previously reported four *Melomastia* species (*M. fusispora*, *M. oleae*, *M. sichuanensis* and *M. winteri*) from dead branches of olive and 31 strains of pestalotiod fungi from the diseased branches of *Camellia oleifera*, *Olea europaea*, *Paeonia suffruticosa* Andrews, *Sapium sebiferum* (L.) Roxb. and *Vernicia fordii* (Hemsl.) Airy Shaw (Li et al. 2022a, b), which reveal a potential high diversity of fungi on such plants.

This is the ninth paper in the series of Mycosphere Notes and treats 36 Dothideomycetes taxa associated with woody oil plants in China. All taxa described herein are based on morphological characterization and phylogenetic analyses.

Materials & Methods

Sample collection, morphological examination, and isolation

Fresh specimens were collected from woody-oil plantations in Sichuan Province, China during 2020 and 2021. Morphological examination and isolation followed the methods provided by Liu et al. (2010).

The strains isolated in this study were deposited at the China General Microbiological Culture Collection Center (CGMCC), Beijing, China and the University of Electronic Science and Technology Culture Collection (UESTCC), Chengdu, China. Herbarium specimens were deposited at Herbarium of Cryptogams, Kunming Institute of Botany Academia Sinica (KUN-HKAS), Kunming, China and Herbarium, University of Electronic Science and Technology (HUEST), Chengdu, China.

DNA extraction, PCR amplification and DNA sequencing

Fresh mycelia were scraped from 14 d old fungal colonies growing on PDA at 25 °C and stored in 1.5 mL sterilized microcentrifuge tubes. Genomic DNA was extracted using the EZ geneTM fungal gDNA kit (GD2416) following the manufacturer's protocol. DNA amplifications were performed by polymerase chain reaction (PCR). PCR amplifying condition and the primers used in this study are provided in Table 1. Purification and sequencing of PCR products were carried out at Beijing Tsingke Biological Engineering Technology and Services Co. (Beijing, China). All newly generated sequences were submitted to GenBank.

Table 1 Genes/loci used in the study with their PCR primers and protocols.

Gene/Loci	**Primers**	**Initial denaturation**	**PCR protocol**	**Final extension**	**References**
Internal transcribed spacer (ITS)	ITS5/ITS4	94 °C, 4 min	(94 °C, 45 sec; 56 (55) °C, 45 sec; 72 °C, 1 min) × 35 cycles	72 °C, 10 min	White et al. (1990)
Large subunit (LSU)	LR0R/LR5				Rehner & Samuels (1994)
Small subunit (SSU)	NS1/NS4				Vilgalys & Hester (1990)
Elongation factor-1 alpha (*tef1*)	EF1-983/EF1-2218	94 °C, 3 min	(94 °C, 30 sec; 55 (53) °C, 45 sec; 72 °C, 1 min) × 35 cycles		Rehner et al. (2005)
Beta tubulin (*tub2*)	Bt2a/Bt2b				Glass & Donaldson (1995)
	T1/T22				
RNA polymerase II second large subunit (*rpb2*)	fRPB2-5F/fRPB2-7cR	95 °C, 5 min	(95 °C, 45 sec; 52 (55) °C, 1 min; 72 °C, 1.5 min) × 35 cycles		Liu et al. (1999)

Phylogenetic analyses

The sequences were assembled by BioEdit v.7.2.6.1. Multiple alignments derived in this study were analyzed with similar sequences, acquired from GenBank BLASTn queries and relevant publications. All gene sequences were downloaded from NCBI (http://www.ncbi.nlm.nih.gov/, accessed on 10 February 2023) and aligned by MAFFT v.7 (http://mafft.cbrc.jp/alignment/server/, accessed on 10 February 2023) (Katoh et al. 2019). TrimAI.v1.2rev59 was used to optimize the alignment of sequences (Capella-Gutiérrez et al. 2009).

The single-gene datasets were examined for topological incongruence among loci and the conflict-free alignments were concatenated into a multi-locus alignment which was subjected to maximum-likelihood (ML) and Bayesian (BI) phylogenetic analyses. MrModeltest 2.3 was performed for each locus to estimate the best-fit evolutionary model under the Akaike Information Criterion (AIC) (Nylander 2004). The CIPRES Science Gateway platform (Miller et al. 2010) was used to perform RAxML and Bayesian analyses. ML analyses were made with RAxML-HPC2 on XSEDE v.8.2.10 (Stamatakis 2014) using the GTR+GAMMA swap model with 1000 bootstrap repetitions. Bayesian analyses were performed setting GTR+I+G for two million generations, sampling at every 1,000 generations, ending the run automatically when the standard deviation of split frequencies dropped below 0.01, with a burning fraction of 0.25. Phylograms were visualized with the FigTree v1.4.0 program (Rambaut 2012) and reorganized in Adobe Illustrator® CS5 (Version 15.0.0, Adobe®, San Jose, CA, USA).

Results

Taxonomy

Dothideomycetes

For the treatment of Dothideomycetes, we have followed Hongsanan et al. (2020) and Wijayawardene et al. (2022), and the review papers (Jayawardena et al. 2021, Maharachchikumbura et al. 2021, Pem et al. 2021) were taken as references.

Muyocopronales Mapook, Boonmee & K.D. Hyde, Phytotaxa 265 (3): 230.
Muyocopronaceae K.D. Hyde, Fungal Diversity (2013) 63:164

MycoBank number: MB 804506; Facesoffungi number: FoF 08090

Notes – Muyocopronaceae was introduced by Luttrell (1951) and included in the order Hemisphaeriales. Subsequently, Mapook et al. (2016) established a new order Muyocopronales to accommodate the Muyocopronaceae as the type family. There are ten genera accommodated in Muyocopronaceae: *Arxiella*, *Leptodiscella*, *Muyocopron*, *Muyocopromyces*, *Mycoleptodiscus*, *Neocochlearomyces*, *Neomycoleptodiscus*, *Paramycoleptodiscus*, *Pseudopalawania*, and *Setoapiospora* (Wijayawardene et al. 2022). Muyocopronaceae species are saprobes and endophytes of a wide range of hosts worldwide.

Muyocopron lithocarpi Mapook, Boonmee & K.D. Hyde, Phytotaxa 265 (3): 235 Fig. 1

MycoBank number: MB 551618; Facesoffungi number: FoF 01890

Saprobic on decaying branches of *Paeonia suffruticosa* Andrew. Sexual morph: *Ascomata* 150–170 × 130–170 µm ($\bar{x}$ = 165 × 150 µm, n = 10), superficial, coriaceous, solitary, or scattered, circular, flattened, dark spotted. *Ostiole* 26–38 µm wide, central. *Peridium* 33–36 µm thick, outer layer comprising dark brown to black, pseudoparenchymatous, occluded cells of *textura angularis*, inner layer comprising yellow-brown cells of *textura angularis*. *Hamathecium* 1.8–2.3 µm wide, comprising numerous, cylindrical, hyaline, septate, branched pseudoparaphyses. *Asci* 58–70 × 27–30 µm ($\bar{x}$ = 64 × 28.5 µm, n = 20), 8-spored, bitunicate, broadly cylindrical to ovoid, without or with cylindrical pedicel. *Ascospores* 17–19 × 10–12 µm ($\bar{x}$ = 18 × 11 µm, n = 20), overlapping 2–3 seriate, hyaline to yellowish, aseptate, ellipsoid to obovoid, granular, with 1–2 large guttules. Asexual morph: Not observed.

Known distribution – China, South Korea, Thailand.

Culture characteristics – Ccs on PDA reach 30 mm diam. after 14 d at 25 °C, colonies cream white, circular, slightly raised, dense at the centre; reverse yellow.

Material examined – China, Sichuan Province, Leshan city, Shizhong district, N 29°42'44.3484", E 103°52'41.8079", elevation 444 m, on branches of *Paeonia suffruticosa* (Paeoniaceae), 23 July 2021, W.L. Li, YMD 341 (HUEST 23.0091), living culture UESTCC 23.0091; *ibid*., YMD 343 (HUEST 23.0092), living culture UESTCC 23.0092.

GenBank numbers – UESTCC 23.0091 = LSU: OR253283, ITS: OR253124, SSU: OR253197; UESTCC 23.0092 = LSU: OR253284, ITS: OR253125, SSU: OR253198.

Notes – *Muyocopron lithocarpi* was introduced by Mapook et al. (2016) from dead leaves of *Lithocarpus lucidus* (Roxb.) Rehder in Thailand, and is characterized by small, superficial black spots, central ostiolate ascomata, ellipsoid asci with or without a cylindrial pedicel, and oval to ellipsoid, hyaline ascospores. The new collections obtained in this study morphologically fit well with *Muyocopron lithocarpi*. Phylogenetic analysis of combined ITS, LSU and SSU showed that our two new collections clustered with other collections of *M. lithocarpi* but are associated with a different host (Fig. 2). This is the first record of *M. lithocarpi* from *Paeonia suffruticosa* in China.

Pleosporales Luttrell ex M.E. Barr

Acrocalymmaceae Crous & Trakun., IMA Fungus 5 (2): 404 (2014)

MycoBank number: MB 810837; Facesoffungi number: FoF 08135

Notes – Acrocalymmaceae was introduced in Trakunyingcharoen et al. (2014) to accommodate a single genus *Acrocalymma*, which is characterized by globose conidiomata with a long pycnidial beak, and hyaline, or becoming pale brown with age, cylindrical to fusiform, aseptate, or 1–3-septate conidia, bearing mucoid appendage at one or both ends. The sexual morph of this group comprises globose to subglobose, ostiolate ascomata, a peridium with *textura angularis* cells, cylindric-clavate asci, and hyaline, fusiform, 1-septate ascospores which are surrounded by a thick, distinct sheath. Currently only four sexual morphs were reported, viz. *A. chuxiongense*, *A. hongheense*, *A. pterocarpi*, and *A. walker* (Crous et al. 2014, Jayasiri et al. 2019, Mortimer et al. 2021, Liu et al. 2022). Members of Acrocalymmaceae comprises endophytes, pathogens, and saprobes on terrestrial and rarely submerged plants (Zhang et al. 2012, Dong et al. 2020).

Acrocalymma paeoniae W.L. Li & Jian K. Liu sp. nov. Fig. 3

MycoBank number: MB 849142; Facesoffungi number: FoF 14415

Etymology – The specific epithet '*paeoniae*' refers to the host genus *Paeonia*, from which the holotype was collected.

Saprobic on decaying branches of *Paeonia suffruticosa*. Sexual morph: Not observed. Asexual morph: *Conidiomata* 60–130 µm high, 110–190 µm diam. ($\bar{x}$ = 95 × 150 µm, n = 5), pycnidial, dark brown, immersed to semi-erumpent, globose, with a central ostiole. *Conidiomatal wall* 13–22 µm wide, of unequal thickness, composed of dark brown to black cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells or with a single supporting cell. *Conidiogenous cells* 5.5–7.5 × 4–5 µm ($\bar{x}$ = 6.5 × 4.5 µm, n = 20), lining the inner cavity, hyaline, dolliform or ampulliform, enterblastic, phialidic, with prominent periclinal thickening at apex, guttulate. *Conidia* 19–21 × 4–5 µm ($\bar{x}$ = 20 × 4.5 µm, n = 20), hyaline, smooth, guttulate, solitary, straight, subcylindrical, obtusely rounded, with flaring mucoid appendages at both ends, visible in water mounts, aseptate, thin-walled.

Culture characteristics – Conidia germinate on PDA within 24 h. Colonies on PDA reach 30 mm diam. at 25 °C after 7 d, circular, thick and dense, white; reverse pale brown to yellow brown.

Material examined – China, Sichuan Province, Meishan city, Dongpo district, N 29°57'33.6347", E 103°49'52.1448", elevation 358 m, on branches of *Paeonia suffruticosa*, 29 October 2021, W.L. Li, YMD 531 (HKAS 127157, holotype), ex-type culture CGMCC 3.24440 = UESTCC 23.0011.

GenBank numbers – CGMCC 3.24440 = LSU: OR253308, SSU: OR253217, ITS: OR253149.

Notes – Multi-gene phylogenetic analysis indicated that *Acrocalymma paeoniae* nested within Acrocalymmaceae and formed a distinct clade sister to the clade of *A. bipolare*, *A. chuxiongensis*, *A. medicaginis* and *A. pterocarpi* with 82% ML/0.99 BYPP support (Fig. 5). Morphologically, *A. paeoniae* can be distinguished from *A. bipolare* and *A. medicaginis* by its larger conidia (19–21 µm vs. 9–12 µm vs. 13–15 µm, respectively). Moreover, the conidia of *A. medicaginis* become pale olivaceous and 1-septate with age, which were not observed in other *Acrocalymma* species. *Acrocalymma paeoniae* shares similar conidial shape, size and color to *A. pterocarpi*, but differs in having dolliform or ampulliform conidiogenous cells with prominent periclinal thickening at apex, while *A. pterocarpi* has cylindrical to subcylindrical conidiogenous cells.

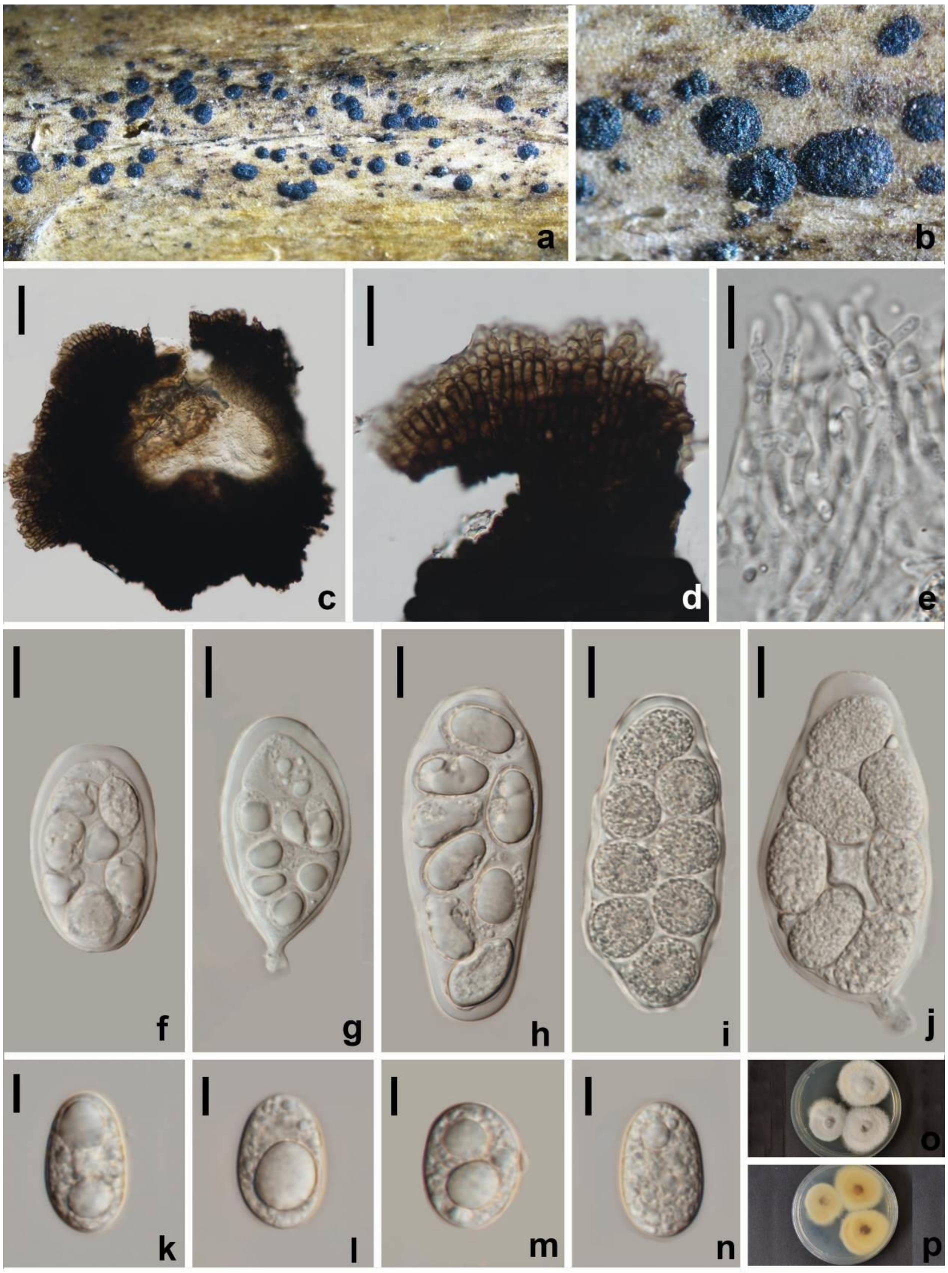

Figure 1 – *Muyocopron lithocarpi* (HUEST 23.0091). a, b Appearance of ascomata on host surface. c Vertical section through ascoma. d Peridium. e Hamathecium. f–j Asci. k–n Ascospores. o Colonies on PDA from above. p Colonies on PDA from below. Scale bars: c = 50 µm, d–j = 10 µm, k–n = 5 µm.

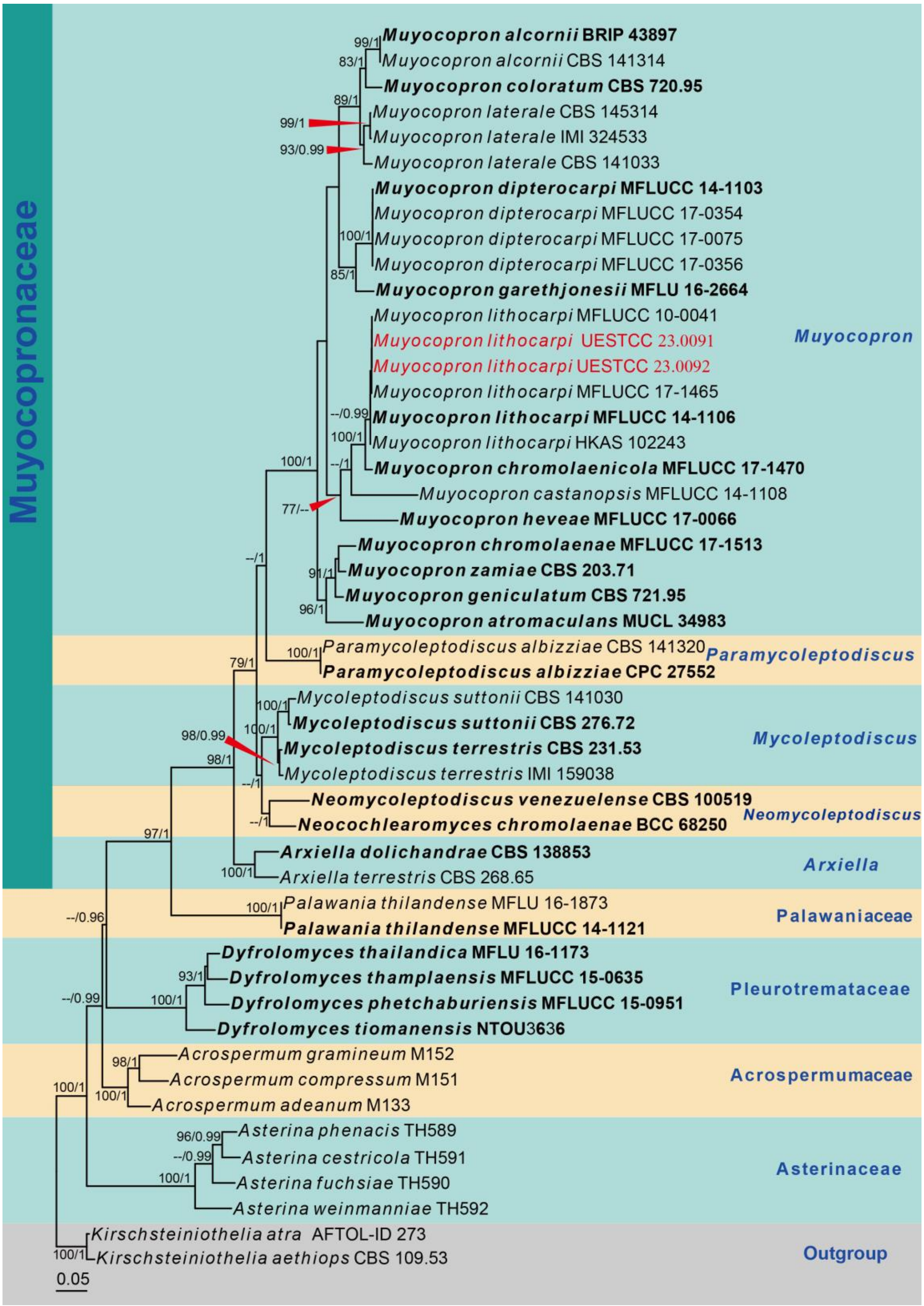

Figure 2 – Phylogram generated from maximum likelihood analysis based on combined LSU, SSU and ITS sequence data. Forty-nine strains are included in the combined sequence analyses, which comprise 3,188 characters with gaps. *Kirschsteiniothelia aethiops* CBS 109.53 and *K. atra* AFTOL-ID 273 are used as outgroup taxa. Tree topology of ML analysis is similar to BI analysis. The best scoring RAxML tree with a final likelihood value of -16053.974425 is presented. Proportion of gaps and completely undetermined characters in this alignment are 54.47% with 1,161 distinct alignment patterns. Estimated base frequencies were as follows; A = 0.239465, C = 0.248740, G = 0.302816, T = 0.208979; substitution rates AC = 1.467992, AG = 2.595213, AT = 1.351387, CG = 1.285683, CT = 5.382653, GT = 1.000000; gamma distribution shape parameter α = 0.645582.

Bootstrap support values for ML ≥ 75% and BYPP ≥ 0.95 are defined as ML/BYPP above the nodes. Hyphens (--) represent support values less than 75% in ML and 0.95 in BI. Newly generated sequences are in red and ex-type strains are in bold.

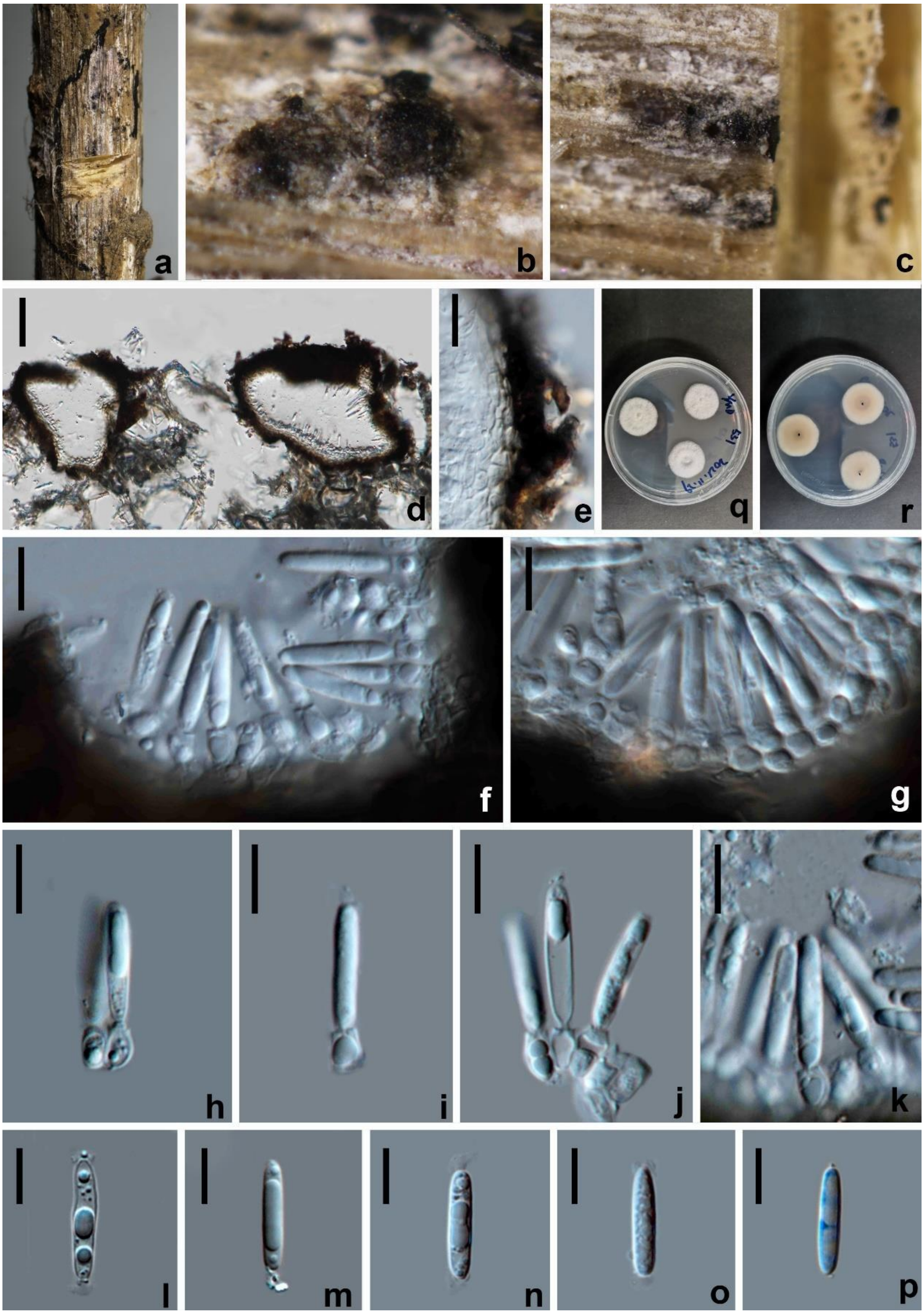

Figure 3 – *Acrocalymma paeoniae* (HKAS 127157, holotype). a–c Appearance of conidiomata on natural substrate. d Vertical section of conidiomata. e Pycnidial wall. f–k Conidiogenous cells and developing conidia. l–p Conidia (p in cotton blue). q Colonies on PDA from above. r Colonies on PDA from below. Scale bars: d = 20 µm, e–p = 10 µm.

Acrocalymma pterocarpi Jayasiri, E.B.G. Jones & K.D. Hyde, Mycosphere 10(1):20 (2019)

Fig. 4

MycoBank number: MB 555528

Saprobic on decaying branches of *Paeonia suffruticosa*. Sexual morph: Not observed. Asexual morph: *Conidiomata* 120–180 µm high, 60–110 µm diam. ($\bar{x}$ = 150 × 80 µm, n = 5), pycnidial, dark brown, immersed, globose, with a central ostiole. *Pycnidia wall* 13–14 µm wide, composed of dark brown to black cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 6–7 × 3–4 µm ($\bar{x}$ = 6.5 × 3.5 µm, n = 20), lining the inner cavity, hyaline, smooth, cylindrical to subcylindrical, enterblastic, annelledic, percurrently proliferating 1–2 times at apex, discrete. *Conidia* 20–24 × 4.5–5 µm ($\bar{x}$ = 22 × 4.5 µm, n = 20), hyaline, smooth, solitary, subcylindrical, straight, obtusely rounded at apex and base, 2–4 guttules, with flaring mucoid appendages at both ends, aseptate, thin-walled.

Culture characteristics – Conidia germinate on PDA within 24 h. Colonies on PDA reach 80 mm diam. at 25 °C after 14 d, circular, thick and dense, first white, turning pale brown to yellow brown, zonate; reverse cream at margin, dark brown at middle and yellow brown at center.

Material examined – China, Sichuan Province, Mianyang city, Santai county, N 31°05'21.84", E 105°06'38.23", elevation 377 m, on branches of *Paeonia suffruticosa*, 18 December 2021, W.L. Li, YMD 452 (HKAS 127158), living culture UESTCC 23.0012 = CGMCC 3.24961; *ibid*., YMD 459 (HUEST 23.0013), living culture UESTCC 23.0013.

GenBank numbers – CGMCC 3.24961 = LSU: OR253300, ITS: OR253141, SSU: OR253213; UESTCC 23.0013 = LSU: OR253300, ITS: OR253142.

Notes – The sexual morph of *Acrocalymma pterocarpi* was introduced by Jayasiri et al. (2019) from *Pterocarpus indicus* seed pods in Thailand, but it failed to produce asexual morph in culture and only chlamydospores were observed. Das et al. (2020) isolated a strain of *A. pterocarpi* from soil in Korea, however, the same result was obtained. In this study, our new collection has a close affinity to *A. pterocarpi* in the phylogenetic analysis (Fig. 5) and a comparison of ITS, LSU, SSU sequence data show a few nucleotide differences. However, we cannot compare the morphological characteristics of our strains with those of *A. pterocarpi* as it is only known by the sexual morph. As the morphology of our collections fits well with the genetic concept of *Acrocalymma*, we identify the new collection as *A. pterocarpi* and report the asexual morph for the first time.

Amorosiaceae K.M. Thambugala & K.D. Hyde, Fungal Diversity 74: 252 (2015)

MycoBank number: MB 551277; Facesoffungi number: FoF 01084

Notes – Amorosiaceae was established by Thambugala et al. (2015) to accommodate two genera, *Amorosia* and *Angustimassarina*. Subsequently, *Amorocoelophoma* (Jayasiri et al. 2019) and *Alfoldia* (Crous et al. 2019) were introduced in this family. *Angustimassarina* is the largest genus with twelve epithets listed in Index Fungorum (2023). *Angustimassarina* species may be parasitic on other fungi and appear to grow within the ascomata of other ascomycetes (Thambugala et al. 2015). It has a narrow geographical distribution, with most species reported in Italy and Germany (De Silva et al. 2022). Recently, Jayawardena et al. (2022) isolated *A. kunmingense* from *Camellia semiserrata* in Yunnan province, China. In this study, a new collection of *A. kunmingense* is reported from *Juglans regia* in Sichuan province.

Angustimassarina kunmingense H.D. Yang & K.D. Hyde, Fungal Diversity 117: 18 (2023)

Fig. 6a, b

MycoBank number: MB 559764; Facesoffungi number: FoF 11804

Saprobic on decaying branches of *Juglans regia* L. Sexual morph: *Ascomata* 410–440 × 200–220 µm ($\bar{x}$ = 420 × 210 µm, n = 10), semi-immersed to immersed, solitary or in small groups, lageniform, subglobose, with or without a long neck, visible as black dots on the host surface, conspicuous at the surface, papillate, ostiolate. *Ostiole* 92–97 µm wide, with a pore-like opening. *Peridium* 21.5–24.5 µm wide, comprised of pale brown 3–5 layers of *textura angularis*.

Hamathecium comprising 1.6–2.2 µm wide, numerous, septate, hyaline, smooth, pseudoparaphyses. *Asci* 76–93 × 10.5–12 µm ($\bar{x}$ = 84.5 × 11 µm, n = 20), 8-spored, bitunicate, fissitunicate, cylindric-clavate, slightly curved, with a short pedicel, apex rounded with a minute ocular chamber, smooth-walled. *Ascospores* 17–21 × 3.5–4.5 µm ($\bar{x}$ = 19 × 4 µm, n = 20), one seriate at the base, overlapping 2-seriate at the apex, fusiform, hyaline, 1-septate at the centre, with 4 large guttules, cell above the median septum slightly wider than the lower, tapering towards the ends, deeply constricted at the septum, smooth-walled, thick- or thin-walled, surrounded by a mucilaginous sheath, 11.5–15 µm wide. Asexual morph: Not observed.

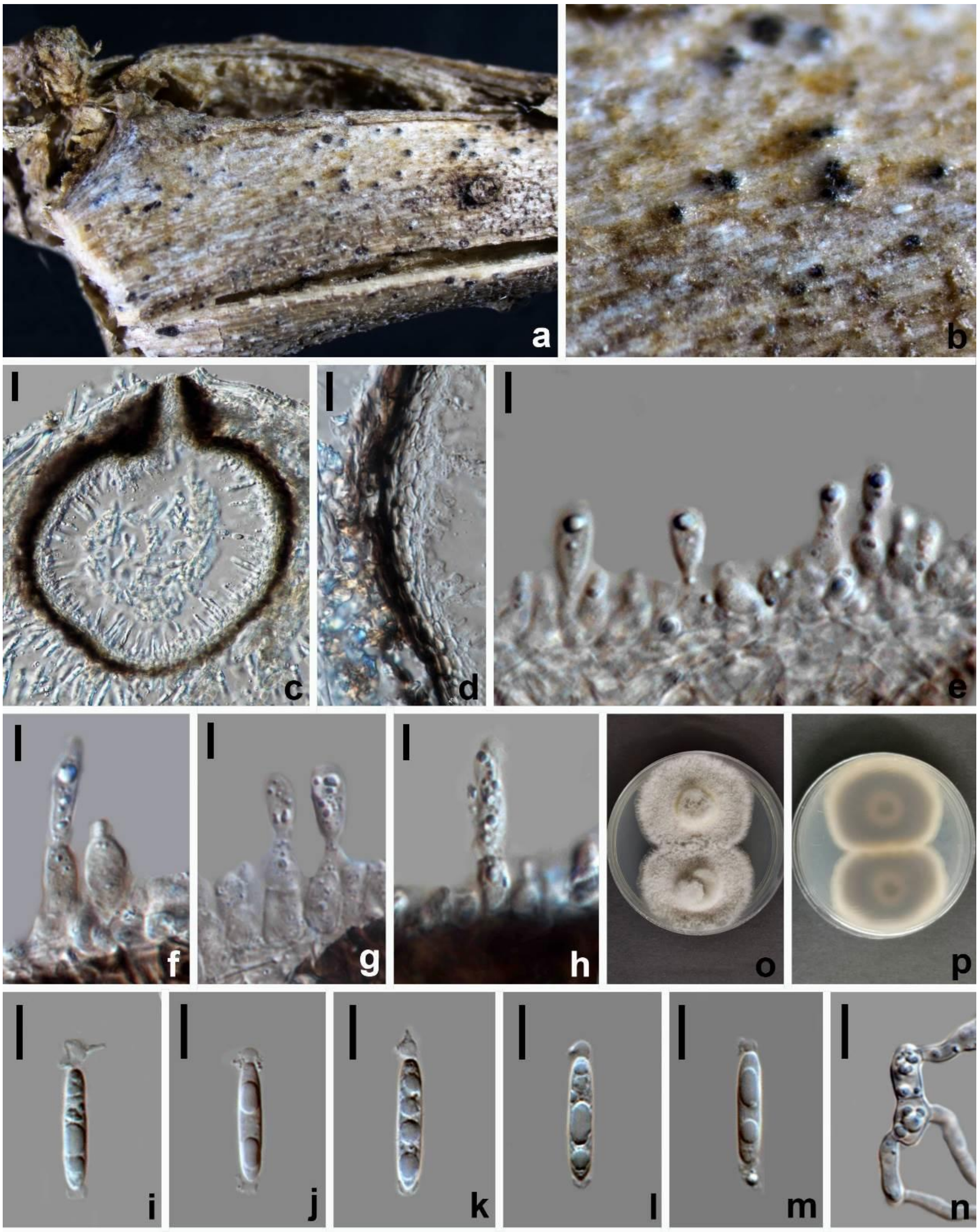

Figure 4 – *Acrocalymma pterocarpi* (HKAS 127158, asexual morph). a, b Appearance of conidiomata on natural substrate. c Vertical section of conidioma. d Pycnidial wall. e–h Conidiogenous cells and developing conidia. i–m Conidia. n Germinated conidia. o Colonies on PDA from above. p Colonies on PDA from below. Scale bars: c = 20 µm, d, e, i–n = 10 µm, f–h = 5 µm.

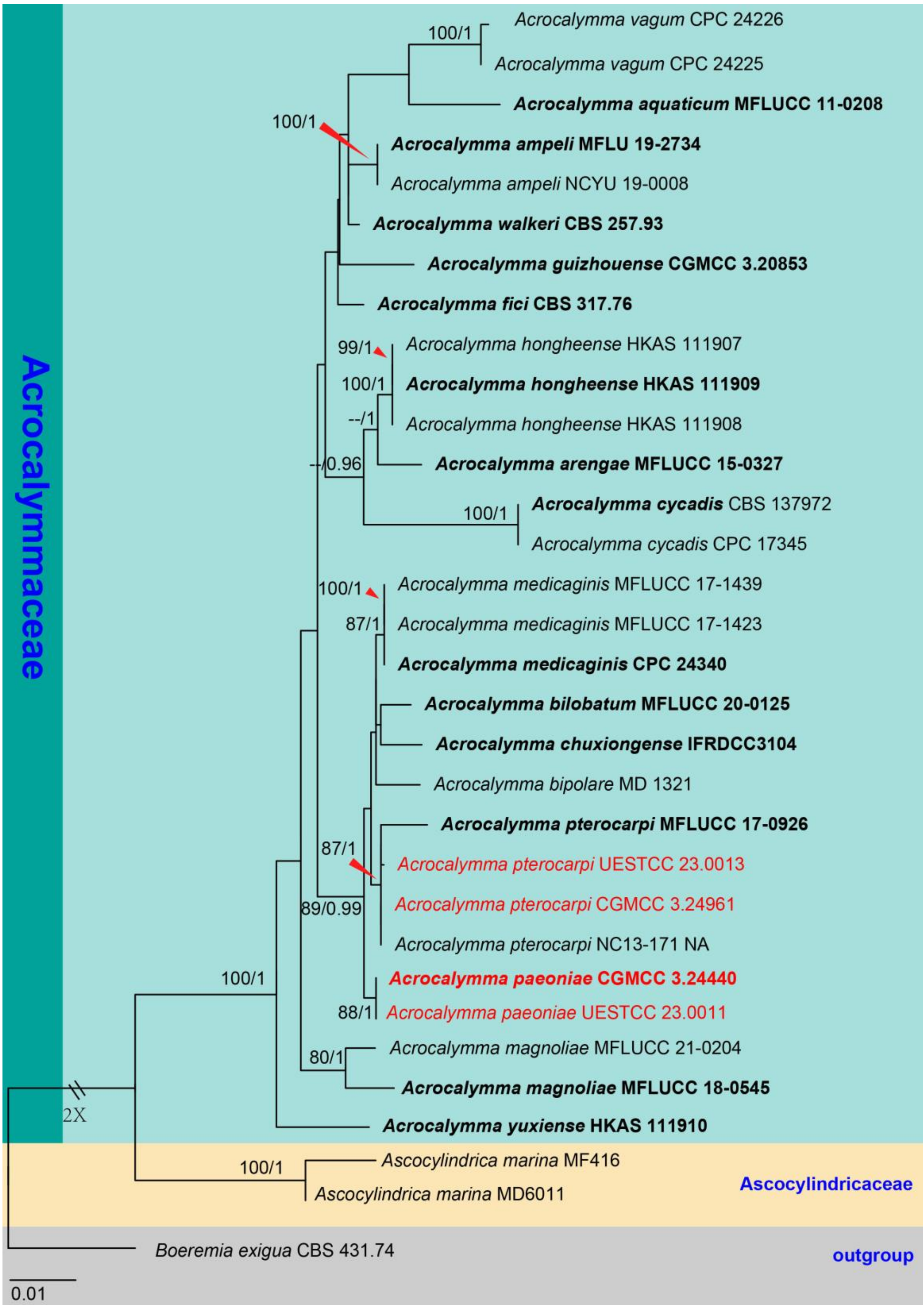

Figure 5 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU and SSU sequence data. Thirty-two strains are included in the combined sequence analyses, which comprise 2,408 characters with gaps. *Boeremia exigua* CBS 431.74 is used as the outgroup taxon. Tree topology of ML analysis is similar to BI analysis. The best scoring RAxML tree with a final likelihood value of -5983.665314 is presented. Proportion of gaps and completely undetermined characters in this alignment are 26.15% with 379 distinct alignment patterns. Estimated base frequencies were as follows; A = 0.251597, C = 0.213578, G = 0.272287, T = 0.262537; substitution rates AC = 2.327611, AG = 2.456290, AT = 2.844116, CG = 1.022202, CT = 8.506061,

GT = 1.000000; gamma distribution shape parameter α = 0.684582. Bootstrap support values for ML ≥ 75% and BYPP ≥ 0.95 are mentioned as ML/BYPP above the nodes. Hyphens (--) represent support values less than 75% in ML and 0.95 in BI. Newly generated sequences are in red and ex-type strains are in bold.

Figure 6a – *Angustimassarina kunmingense* (HKAS 127159), shape I. a–c Appearance of ascomata on host surface. d, e Vertical section through the ascomata. f Peridium. g Hamathecium. h–k Asci. l–q Ascospores (q stained in Indian ink, showing sheath). r Colonies on PDA from above. s Colonies on PDA from below. Scale bars: d, e = 100 µm, f–k = 10 µm, l–q = 5 µm.

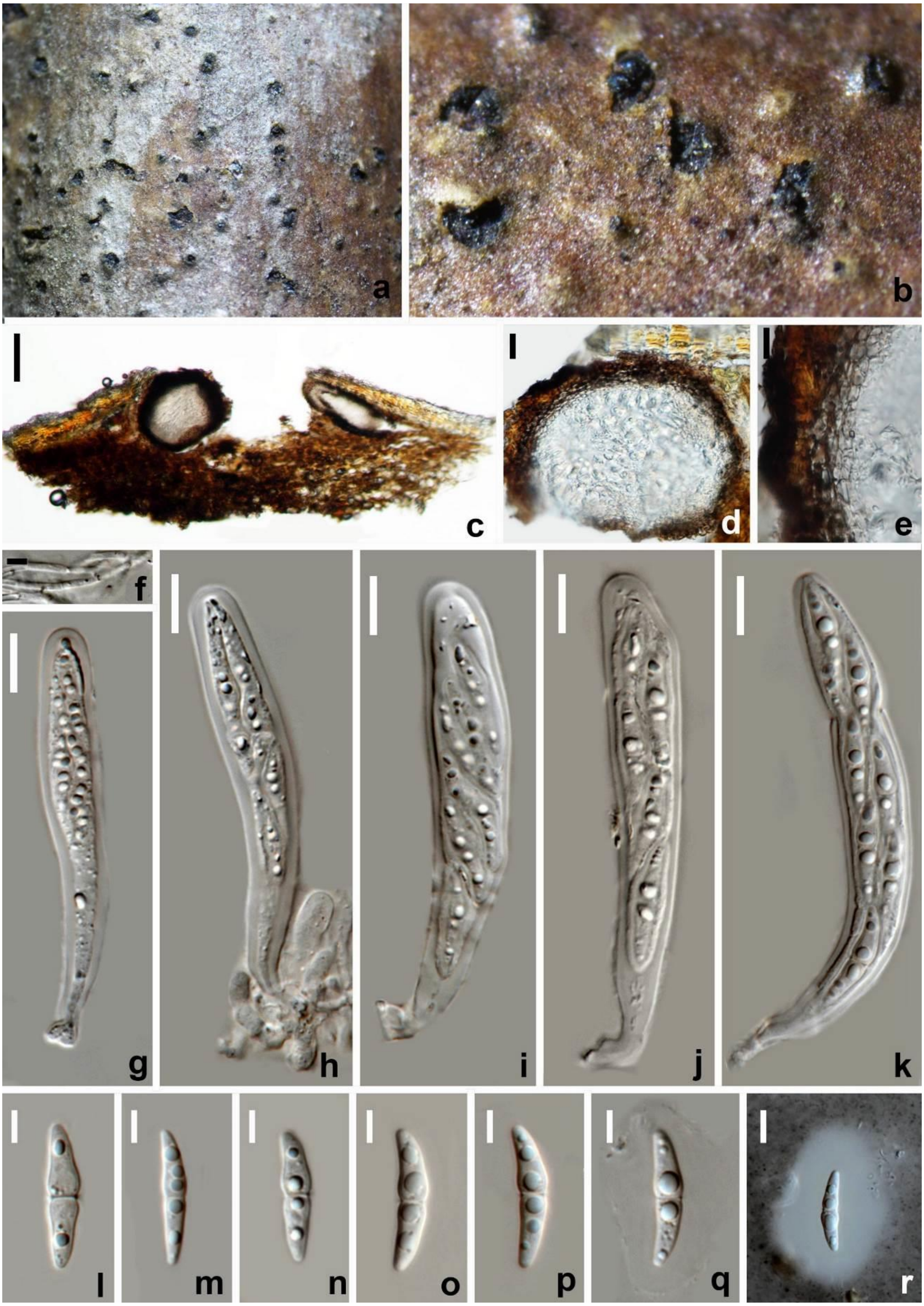

Figure 6b – *Angustimassarina kunmingense* (HUEST 23.0015), shape II. a, b Appearance of ascomata on host surface. c, d Vertical section through the ascomata. e Peridium. f Hamathecium. g–k Asci. l–r Ascospores (r stained in indian ink, showing sheath). Scale bars: c = 100 μm, d = 20 μm, e–k = 10 μm, l–r = 5 μm.

Culture characteristics – Ascospores germinate on PDA within 24 h and germ tubes produced from both ends of spores. Colonies on PDA reach 60 mm diam. after 14 d at 25 °C, circular, margin undulate, dense, surface slightly rough, effuse, velvety to hairy, pale brown; reverse pale brown at the margin, dark brown in the centre.

Material examined – China, Sichuan Province, Guangyuan city, Chaotian district, N 32°41'05.48", E 106°01'22.40", elevation 628 m, on branches of *Juglans regia* (Juglandaceae), 19 April 2021, W.L. Li, HT 227 (HKAS 127159), living culture UESTCC 23.0014 = CGMCC 3.24434; *ibid*., HT 224 (HUEST 23.0015), living culture UESTCC 23.0015; *ibid*., HT 228 (HUEST 23.0016), living culture UESTCC 23.0016; *ibid*., HT 232 (HUEST 23.0017), living culture UESTCC 23.0017.

GenBank numbers – CGMCC 3.24434 = LSU: OR253324, ITS: OR253166, SSU: OR253221, UESTCC 23.0015 = ITS: OR253167, SSU: OR253222; UESTCC 23.0016 = LSU: OR253326, ITS: OR253168, SSU: OR253223; UESTCC 23.0017 = LSU: OR253325, ITS: OR253169, SSU: OR253224.

Notes – Four strains isolated from dead branches of *Juglans regia* show two different shapes of ascomata and ascospores. Shape I (Fig. 6a): lageniform ascomata with long neck, round ostiole and thick-walled ascospores; shape II (Fig. 6b): subglobose ascomata and thin-walled ascospores. Phylogenetic analysis shows that the new collections are phylogenetically related to the ex-type strain of *Angustimassarina kunmingense* (Fig. 7), which was introduced by Jayawardena et al. (2022) from a dead stem of *Camellia semiserrata*. Morphologically, the shape II of our collection is almost identical to the holotype of *A. kunmingense*. A comparison of the LSU, ITS, SSU and *tef1* gene regions of KUNCC 22-10799 and CGMCC 3.24434 revealed only few nucleotide differences. Therefore, we identified our new collection as *A. kunmingense* and this is the first report of this species on *Juglans regia*.

Bambusicolaceae D.Q. Dai & K.D. Hyde, in Hyde et al., Fungal Divers. 63: 49 (2013).

MycoBank number: MB 804293; Facesoffungi number: FoF 00586

Notes – Bambusicolaceae was introduced by Hyde et al. (2013) to accommodate *Bambusicola*. Following consecutive studies, *Leucaenicola*, *Longipedicellata*, *Neobambusicola* and *Palmiascoma* were accepted in this family (Crous et al. 2014, Liu et al. 2015, Jayasiri et al. 2019). However, *Neobambusicola* and *Longipedicellata* were excluded from Bambusicolaceae and transferred to Sulcatisporaceae and Longipedicellataceae, respectively (Tanaka et al. 2015, Phukhamsakda et al. 2016). Wijesinghe et al. (2020) introduced *Corylicola* in Bambusicolaceae. In the latest taxonomy of Bambusicolaceae, four genera: *Bambusicola*, *Corylicola*, *Leucaenicola* and *Palmiascoma* are accommodated (Wijayawardene et al. 2022). *Palmiascoma* was introduced to accommodate *P. gregariascomum* with both asexual and sexual morphs isolated from palm by Liu et al. (2015).

Palmiascoma acericola W.L. Li & Jian K. Liu sp. nov. Fig. 8

MycoBank number: MB 849144; Facesoffungi number: FoF 14416

Etymology – The specific epithet '*acericola*' refers to the host genus *Acer*, from which the holotype was collected.

Saprobic on decaying branches of *Acer truncatum* Bunge. Sexual morph: *Ascomata* 170–240 × 180–210 µm ($\bar{x}$ = 210 × 200 µm, n = 10), immersed to erumpent, gregarious to dense, crowded, less commonly solitary, compressed globose, with flat base, brown to dark brown. *Ostiole* 36.5–48 µm wide, central, papillate, with a crest-like apex and a pore-like opening, filled with hyaline periphyses. *Peridium* 26–38 µm thick, composed of 3–5 layers of brown-walled cells of *textura angularis*. *Hamathecium* comprising 2.2–2.8 µm wide, cylindrical, hyaline, septate, branched pseudoparaphyses. *Asci* 63–69 × 9.5–11 µm ($\bar{x}$ = 66 × 10 µm, n = 20), 8-spored, bitunicate, fissitunicate, cylindric-clavate, elongated and cylindrical pedicellate, with a furcate base, apically rounded. *Ascospores* 12–14 × 3.5–4.5 µm ($\bar{x}$ = 13 × 4 µm, n = 20), biseriate, fusiform to ellipsoid, with rounded ends, uniseptate, slightly constricted at the septum, rough-walled, guttulate. Asexual morph: Not observed.

Culture characteristics – Ascospores germinate on PDA within 24 h and germ tubes produced from both ends of spores. Colonies on PDA reach 80 mm diam. after 14 d at 25 °C, medium dense, circular, convex, surface slightly rough with entire edge, effuse, velvety to hairy, margin well-defined, colony from both above and below: white to greyish at the margin, white in the centre.

Material examined – China, Sichuan Province, Chengdu city, Pidu district, N 30°49'26.76", E 103°47'41.64", elevation 442 m, on branches of *Acer truncatum* (Aceraceae), 19 May 2021, W.L. Li, YBF 98 (HKAS 127160, holotype), ex-type culture UESTCC 23.0020 = CGMCC 3.24963; *ibid*., YBF 97 (HUEST 23.0018), living culture UESTCC 23.0018; *ibid*., on a branch of *Pistacia chinensis* Bunge (Aceraceae), 19 May 2021, W.L. Li, HLM 160 (HUEST 23.0019), living culture UESTCC 23.0019; *ibid*., Guangyuan city, Chaotian district, N 32°41'05.48", E 106°01'22.40", elevation 628 m, on a branch of *Vernicia fordii* (Euphorbiaceae), 19 April 2021, W.L. Li, HT 205 (HUEST 23.0021), living culture UESTCC 23.0021.

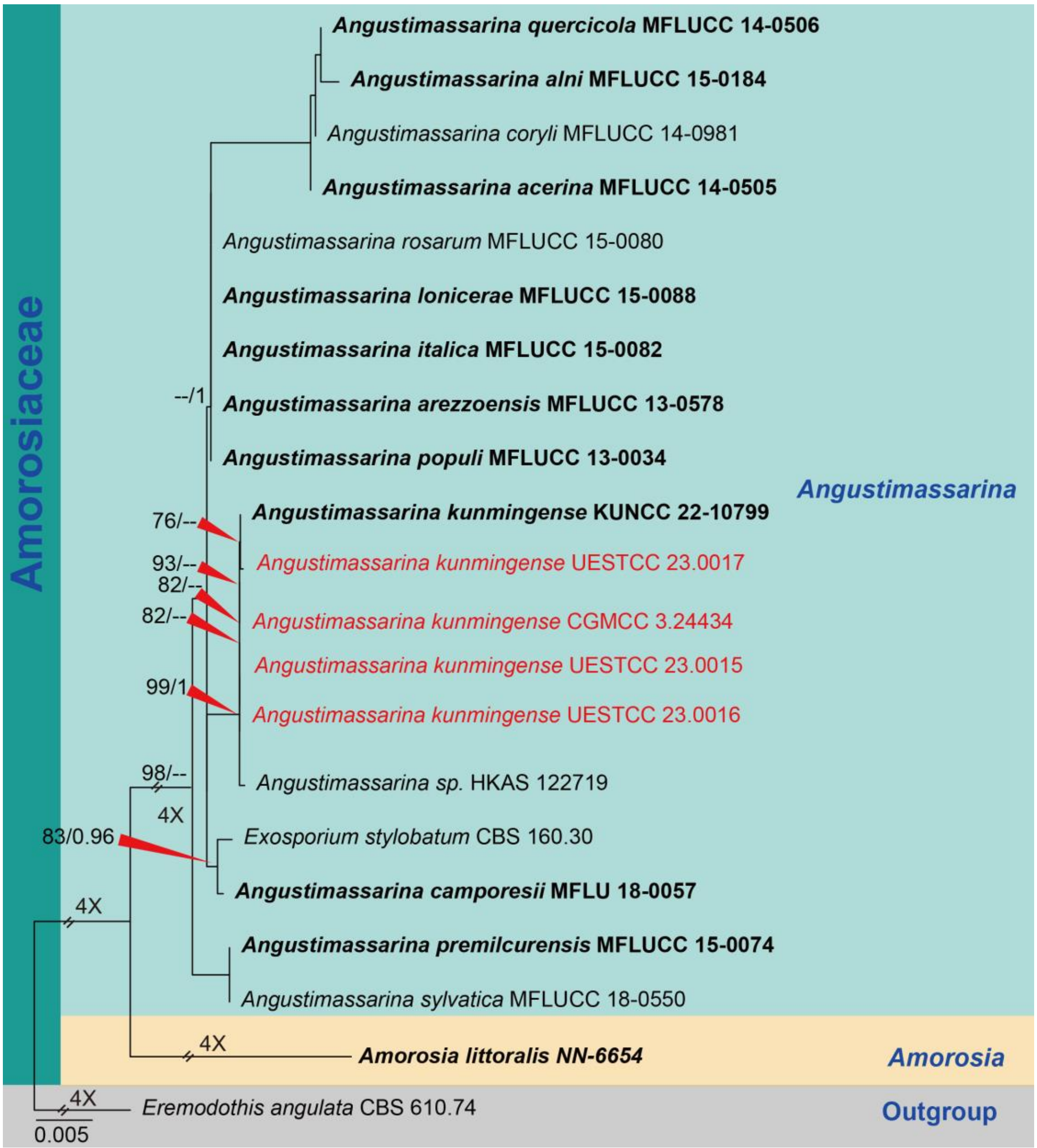

Figure 7 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU and SSU sequence data. Twenty-one strains are included in the combined sequence analyses, which comprise 3,075 characters with gaps. *Eremodothis angulata* CBS 610.74 is used as the outgroup taxon. Tree topology of ML analysis is similar to BI analysis. The best scoring RAxML tree with

a final likelihood value of -6146.283473 is presented. Proportion of gaps and completely undetermined characters in this alignment are 26.37% with 297 distinct alignment patterns. Estimated base frequencies were as follows; A = 0.244511, C = 0.242134, G = 0.270274, T = 0.243081; substitution rates AC = 1.138013, AG = 1.276197, AT = 0.966009, CG = 0.892014, CT = 4.831395, GT = 1.000000; gamma distribution shape parameter α = 0.895248. Bootstrap support values for ML ≥ 75% and BYPP ≥ 0.95 are mentioned as ML/BYPP above the nodes. Hyphens (--) represent support values less than 75% in ML and 0.95 in BI. Newly generated sequences are in red and ex-type strains are in bold.

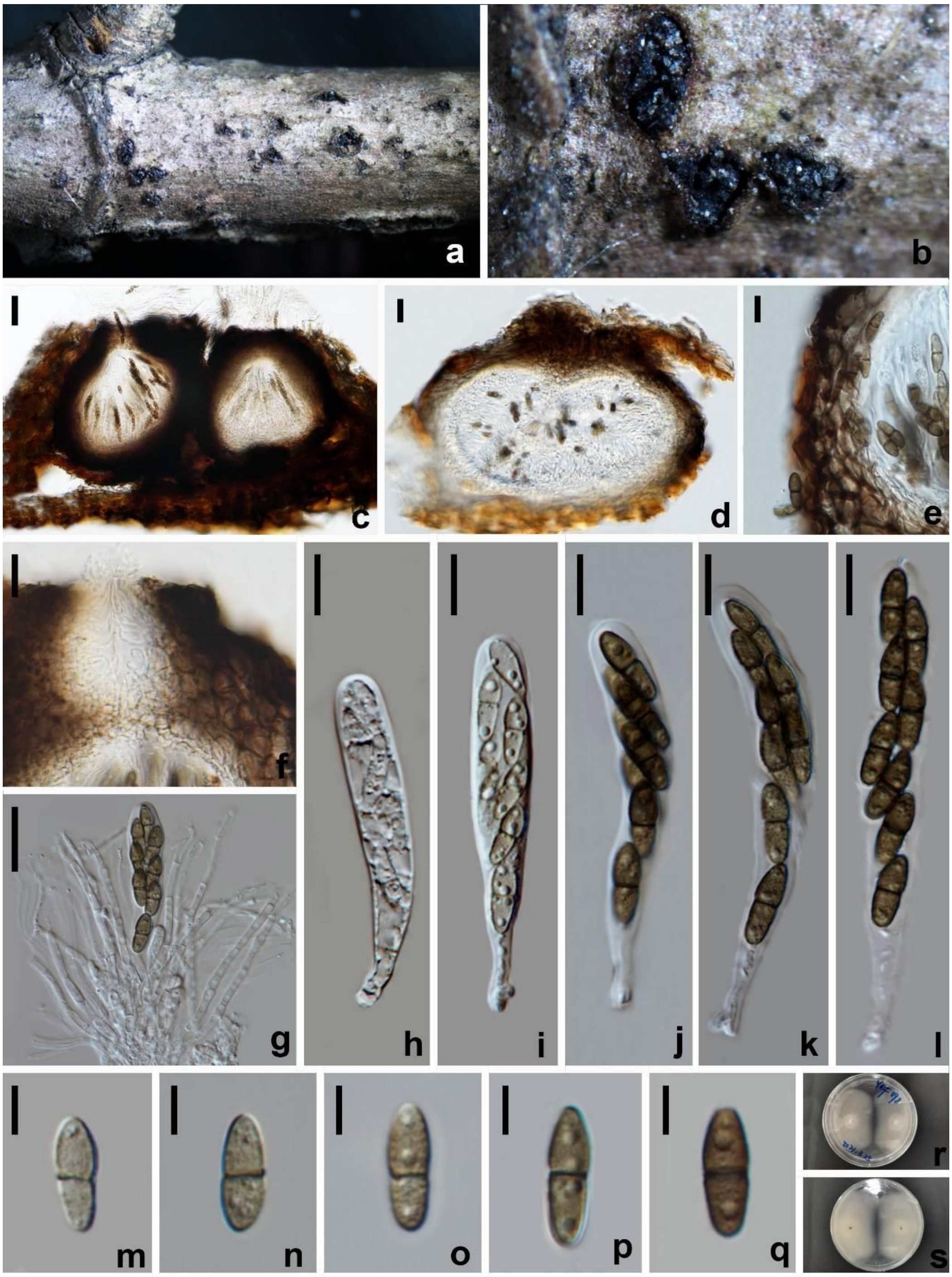

Figure 8 – *Palmiascoma acericola* (HKAS 127160, holotype). a, b Appearance of ascomata on host surface. c, d Vertical section through the ascomata. e Peridium. f Ostiole. g Hamathecium. h–l Asci. m–q Ascospores. r Colonies on PDA from above. s Colonies on PDA from below. Scale bars: c = 50 μm, d, f, g = 20 μm, e, h–l = 10 μm, m–q = 5 μm.

GenBank numbers – CGMCC 3.24963 = LSU: OR253251, ITS: OR253099, SSU: OR253178, *rpb2*: OR262121; UESTCC 23.0018 = LSU: OR253250, ITS: OR253098, SSU: OR253177, *rpb2*: OR262120; UESTCC 23.0019 = LSU: OR253263, ITS: OR253110, SSU: OR253188, *rpb2*: OR251135; UESTCC 23.0021 = LSU: OR253268, ITS: OR253114, SSU: OR253191

Notes – Multi-gene phylogenetic analysis indicated four strains of *Palmiascoma acericola* clustered with the type strains of *P. qujingense* (KUMCC 19-0201) with 99% ML/1.00 BYPP (Fig. 9). A comparison of sequence data between *P. acericola* (UESTCC 23.0020) and *P. qujingense* (KUMCC 19-0201) show 9 bp (1.9%) and 42 bp (4.2%) nucleotide differences in ITS and *rpb2*, respectively, while no base pair difference in LSU and SSU. Morphologically, *P. acericola* is similar to *P. qujingense* in having immersed to semi-immersed ascomata, cylindric-clavate asci with an elongated pedicel, broadly fusiform to ellipsoid, 1-septate ascospores. However, *P. acericola* has smaller ascomata than *P. qujingense* (170–240 × 180–210 µm vs. 280–400 × 200–300 µm). Additionally, the ascospores of *P. acericola* are rough-walled while those of *P. qujingense* are smooth-walled.

Corynesporascaceae Sivan., Mycological Research 100: 786 (1996)

MycoBank number: MB 81981; Facesoffungi number: FoF 12737

Notes – Corynesporascaceae was introduced by Sivanesan (1996) to accommodate a monotypic genus *Corynesporasca*, and *Co. caryotae* was designed as the type species. In several studies, *Corynespora* was considered as the asexual morph of *Corynesporasca* (Sivanesan 1996). However there is no enough evidence to support this conclusion. In the latest taxonomy of Dothiodeomycetes, *Corynespora* and *Corynesporasca* were classified into the family *Corynesporascaceae* as two distinct genera (Hongsanan et al. 2020).

Corynespora idesiae W.L. Li & Jian K. Liu sp. nov. Fig. 10

MycoBank number: MB 849145; Facesoffungi number: FoF 14413

Etymology – The specific epithet '*idesiae*' refers to the host genus *Idesia*, from which the holotype was collected.

Saprobic on decaying branches of *Idesia polycarpa* Maxim. Sexual morph: Not observed. Asexual morph: Hyphomycetous. *Colonies* effuse, brown to dark brown and hairy. *Mycelium* semi-immersed to immersed, composed of branched, septate, pale brown to brown, smooth-walled hyphae. *Conidiophores* 173–258 × 8.5–11 µm ($\bar{x}$ = 215.5 × 9.5 µm, n = 15), macronematous, mononematous, unbranched, erect, straight or flexuous, cylindrical, smooth, brown to dark brown, septate, with up to 3 successive cylindrical extensions. *Conidiogenous cells* 41–56 × 5–8.5 µm ($\bar{x}$ = 48.5 × 7 µm, n = 15), integrated, terminal, monotretic, cylindrical, pale brown to brown, smooth. *Conidia* 110–186 × 10–12 µm ($\bar{x}$ = 148 × 11 µm, n = 15), acrogenous, solitary, subcylindrical, rounded at the apex, straight or slightly curved, 10–20-distoseptate, pale olivaceous, smooth, tapering towards to the apex, truncate at the base, with a darkened scar at the base, sometimes with percurrent proliferation which forms another conidium from the conidial apex.

Culture characteristics – Conidia germinae on PDA within 24 h and germ tubes produced from all cells. Colonies on PDA reach 30 mm diam. at 25 °C after 14 d, circular, velvety, fluffy, subhyaline at centre, cream at margin; reverse yellow brown at center, dark grey at middle, cream at margin.

Material examined – China, Sichuan Province, Yaan city, Tianquan county, N 30°05'37.08", E 102°54'24.33", elevation 612 m, on branches of *Idesia polycarpa*, 29 October 2021, W.L. Li, STZ 498 (HKAS 127161, holotype), ex-type culture UESTCC 23.0022 = CGMCC 3.24438; *ibid*., HLM 498b (HUEST 23.0023), living culture UESTCC 23.0023.

GenBank numbers – CGMCC 3.24438 = LSU: OR253305, ITS: OR253146, *rpb2*: OR253753; UESTCC 23.0023 = LSU: OR253306, ITS: OR253147, *rpb2*: OR253754.

Notes – Multi-gene phylogenetic analysis indicated that two strains of *Corynespora idesiae* clustered with *C. lignicola* with 99% ML and 1.00 BYPP support (Fig. 11). Morphologically, *C. idesiae* resembles *C. lignicola* in having mononematous and unbranched conidiophores, and cylindrical, distoseptate and pale olivaceous conidia. Nonetheless, *C. idesiae* can be distinguished from *C. lignicola* by shorter conidiophores (173–258 µm vs. 470–670 µm).

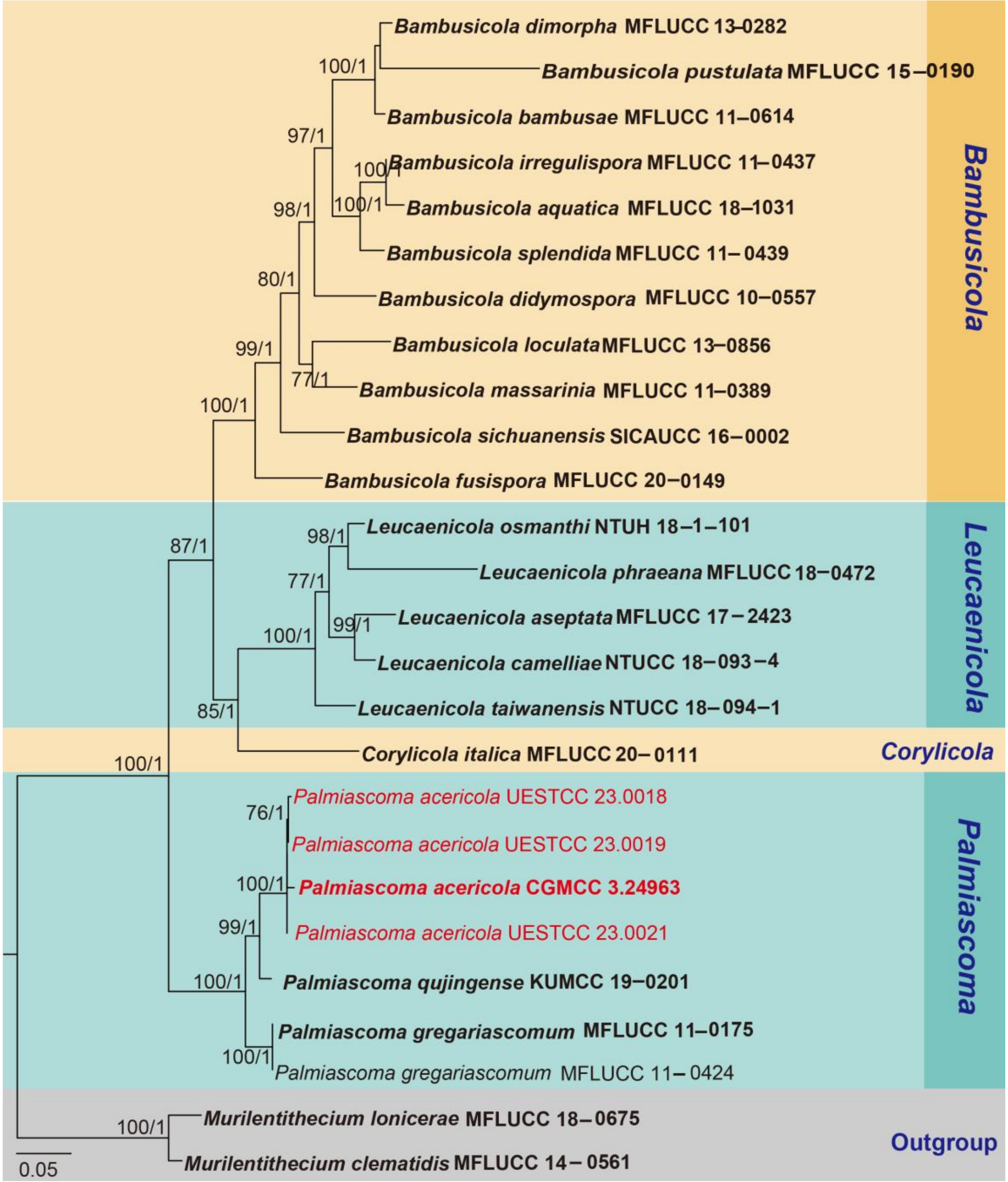

Figure 9 – Phylogram generated from maximum likelihood analysis based on combined LSU, SSU, ITS and *rpb2* sequence data. Twenty-six strains are included in the combined sequence analyses, which comprise 3,657 characters with gaps. *Murilentithecium clematidis* MFLUCC 14-0561 and *M. lonicerae* MFLUCC 18-0675 are used as outgroup taxa. Tree topology of ML analysis is similar to BI analysis. The best scoring RAxML tree with a final likelihood value of -25703.719340 is presented. Proportion of gaps and completely undetermined characters in this alignment are 12.92% with 953 distinct alignment patterns. Estimated base frequencies were as follows; A = 0.087127, C = 0.033474, G = 0.088612, T = 0.058542; substitution rates AC = 0.312229, AG = 2.081526, AT = 3.217693, CG = 0.095403, CT = 0.138768, GT = 0.260191; gamma distribution shape parameter α = 0.146122. Bootstrap support values for ML ≥ 75% and BYPP ≥ 0.95 are defined as ML/BYPP above the nodes. Hyphens (--) represent support values less than 75% in ML and 0.95 in BI. Newly generated sequences are in red and ex-type strains are in bold.

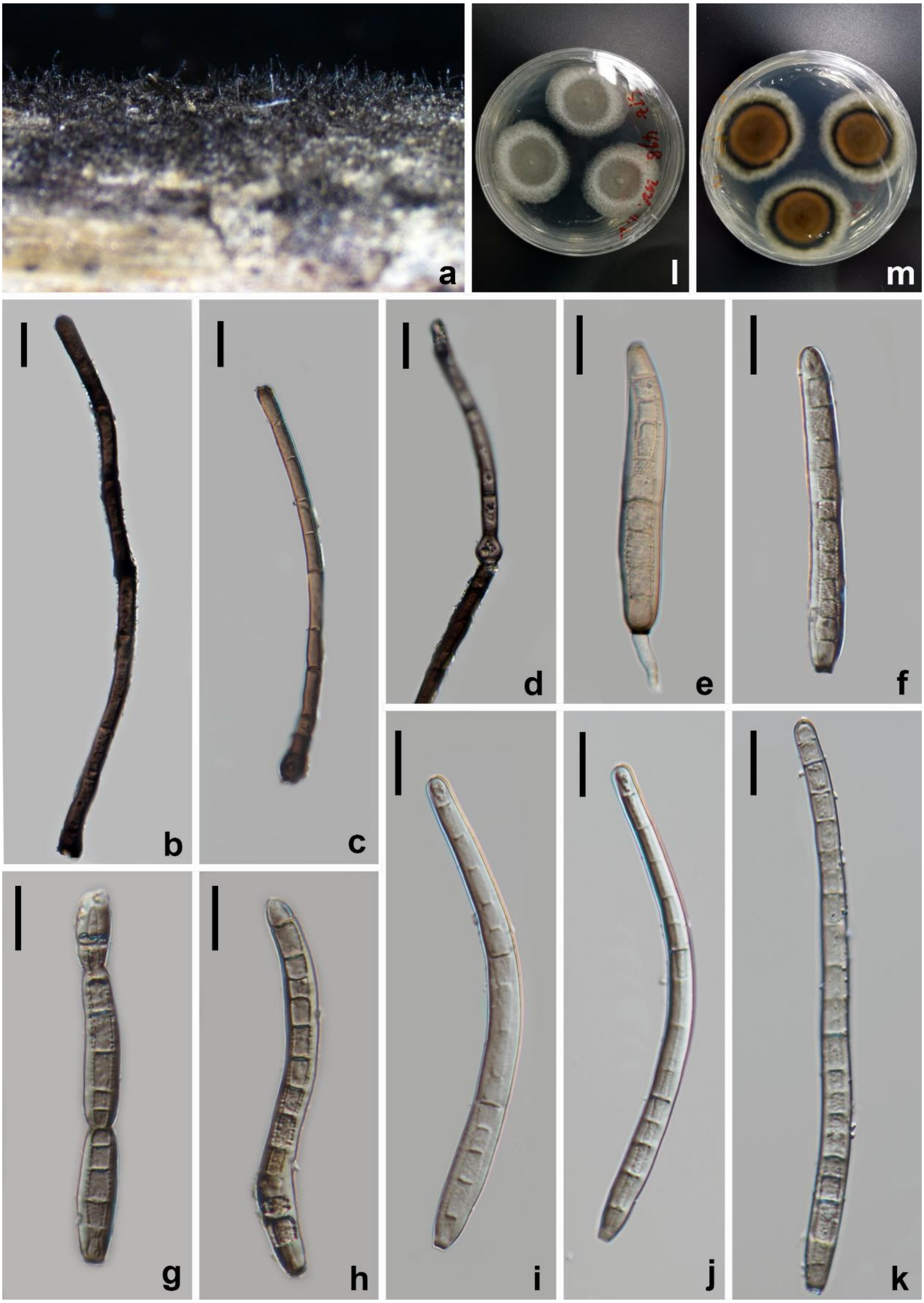

Figure 10 – *Corynespora idesiae* (HKAS 127161, holotype). a Appearance of colony on host surface. b–d Conidiophores and conidiogenous cells. e–k Conidia. l Colonies on PDA from above. m Colonies on PDA from below. Scale bars: b–k = 20 μm.

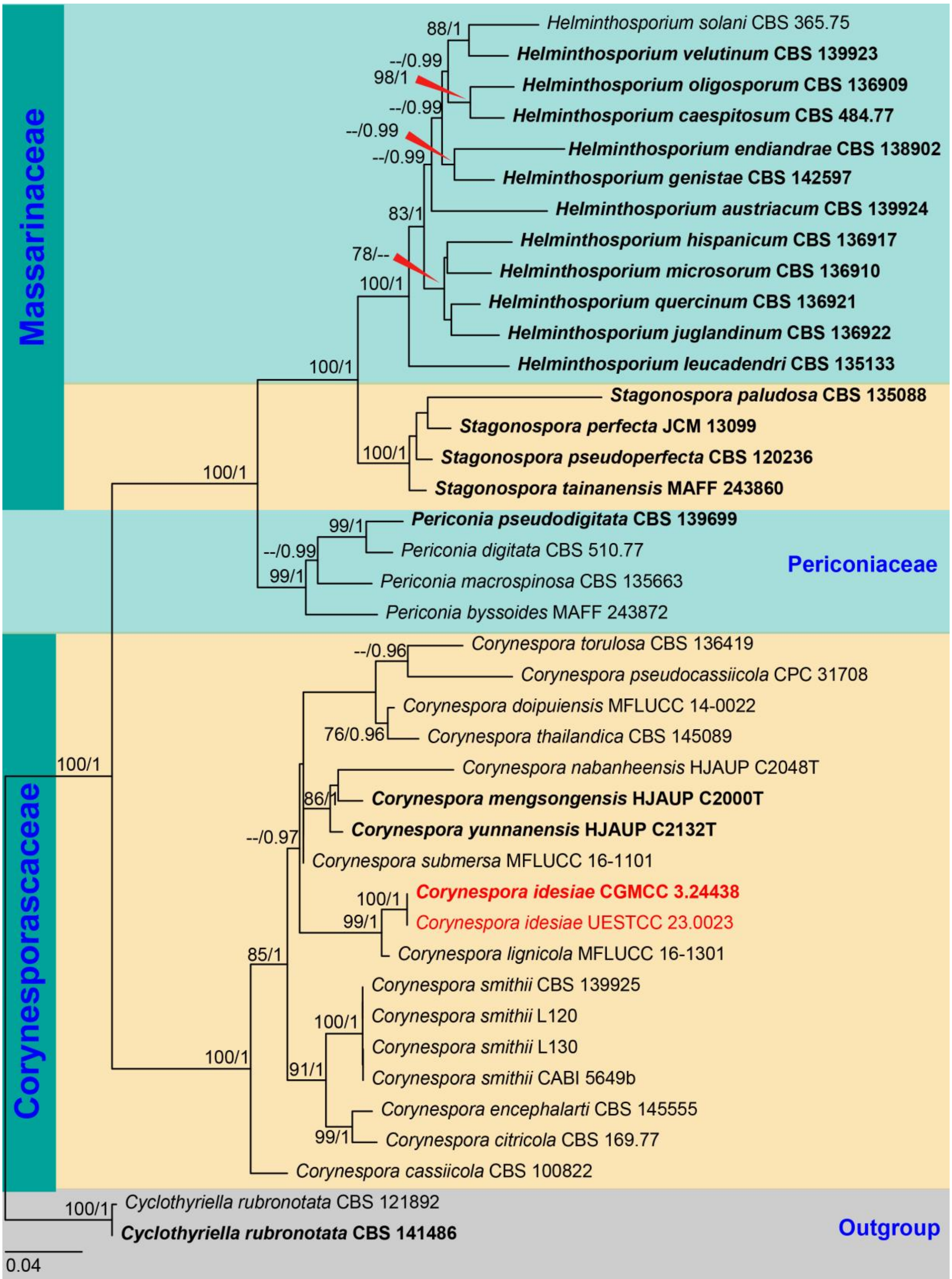

Figure 11 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU and SSU sequence data. Forty strains are included in the combined sequence analyses, which comprise 5,124 characters with gaps. *Cyclothyriella rubronotata* CBS 121892 and *C. rubronotata* CBS 141486 are used as outgroup taxa. Tree topology of ML analysis is similar to BI analysis. The best scoring RAxML tree with a final likelihood value of -24798.829502 is presented. Proportion of gaps and completely undetermined characters in this alignment are 42.78% with 1637 distinct alignment patterns. Estimated base frequencies were as follows; A = 0.238508, C = 0.261869, G = 0.265930, T = 0.233693; substitution rates AC = 1.264679, AG = 2.847659, AT = 1.321126,

CG = 1.023455, CT = 7.027562, GT = 1.000000; gamma distribution shape parameter α = 0.613420. Bootstrap support values for ML ≥ 75% and BYPP ≥ 0.95 are defined as ML/BYPP above the nodes. Hyphens (--) represent support values less than 75% in ML and 0.95 in BI. Newly generated sequences are in red and ex-type strains are in bold.

Cucurbitariaceae G. Winter [as Cucurbitarieae], Rabenh. Krypt.-Fl., Edn 2 (Leipzig) 1.2: 308. 1885.

MycoBank number: MB 80667; Facesoffungi number: FoF 08179

Notes – Cucurbitariaceae was introduced by Winter (1885), with *Cucurbitaria* as the type genus, and characterized by ostiolate ascomata aggregated on a basal pseudostromatic structure. Hamathecium composed of wide persistent filaments, fissitunicate, cylindrical to cylindrical-clavate asci and dark, phragmosporous or muriform ascospores. Asexual morph characterized by phoma-like, setose pycnidia, and hyaline, aseptate conidia. After a series of familial revision, 13 genera were accepted in Cucurbitariaceae, including five sexual genera (*Cucitella*, *Fenestella*, *Rhytidiella*, *Seltsamia* and *Syncarpella*), three asexual genera (*Astragalicola*, *Allocucurbitaria* and *Paracucurbitaria*) and five holomorphic genera (*Cucitella*, *Cucurbitaria*, *Neocucurbitaria*, *Parafenestella* and *Synfenestella*).

Neocucurbitaria pistaciicola W.L. Li & Jian K. Liu sp. nov. Fig. 12

MycoBank number: MB 849146; Facesoffungi number: FoF 14417

Etymology – The specific epithet ‘*pistaciicola*’ refers to the host genus *Pistacia*, from which the holotype was collected.

Saprobic on decaying branches of *Pistacia chinensis* Bunge. Sexual morph: *Ascomata* 230–260 × 240–300 µm ($\bar{x}$ = 240 × 270 µm, n = 10), globose to subglobose, with flattened base, solitary, immersed, uniloculate, excreting dark brown to black masses of ascospores on host surface, ostiolate. *Ostiole* central, short and broadly papillate, inconspicuous at the surface, black, filled with hyaline periphyses. *Peridium* 27–36 µm thick, composed of several layers of pale brown to dark brown cells of *textura angularis*. *Hamathecium* consisting of 1.5–2 µm wide, numerous, filamentous, septate pseudoparaphyses, branched and enclosed in a gelatinous matrix, hyaline, smooth. *Asci* 154–197 × 31–34 µm ($\bar{x}$ = 175.5 × 32.5 µm, n = 20), 4 or 8-spored, bitunicate, fissitunicate, cylindrical to clavate, with a cylindrical and eccentric pedicel, apically rounded, with a small ocular chamber. *Ascospores* 36.5–45 × 9.5–13 µm ($\bar{x}$ = 41 × 11 µm, n = 20), 1-seriate in 4-spored asci, 2-seriate in 8-spored asci, muriform, ellipsoid to broadly fusiform, with rounded ends, hyaline to pale brown when young, becoming dark brown at maturity, deeply constricted at the middle traverse septum, the upper part is larger than the lower part, guttules in each cell, no mucilaginous sheath observed when immersed in Indian ink. Asexual morph: Not observed.

Culture characteristics – Ascospores germinate on PDA within 24 h and germ tubes produced from any cell. Colonies on PDA reach 80 mm diam. at 25 °C after 14 d, circular, thick and dense, first white, turning dull olivaceous brown to brownish grey from the centre, zonate; aerial hyphae forming loose greyish mesh; reverse dark grey to black.

Material examined – China, Sichuan Province, Chengdu city, Pidu district, N 30°49'26.76", E 103°47'41.64", elevation 442 m, on branches of *Pistacia chinensis*, 23 January 2021, W.L. Li, HLM 158 (HKAS 127162, holotype), ex-type culture CGMCC 3.24431 = UESTCC 23.0025.

GenBank numbers – CGMCC 3.24431 = LSU: OR253261, ITS: OR259025, SSU: OR242657, *tef1*: OR266098, *rpb2*: OR262125; UESTCC 23.0025 = LSU: OR253262, ITS: OR253109, SSU: OR253187, *tef1*: OR266099, *rpb2*: OR251134.

Notes – Multi-gene phylogenetic analysis indicated that *Neocucurbitaria pistaciicola* form a sister clade with *N. variabilis* with 87% ML/1.00 BYPP support (Fig. 13). The asexual morph of *N. variabilis* was originally isolated from plant debris in freshwater in Spain (Magaña-Dueñas et al. 2021), but its sexual morph has not been reported. *Neocucurbitaria pistaciicola* fits well with the genetic concept of *Neocucurbitaria*, characterized by immersed and uniloculate ascomata, cylindrical to clavate asci with a pedicel, and ellipsoid to broadly fusiform and muriform ascospores. However, *N. pistaciicola* differs from other *Neocucurbitaria* species in having 4-spored and 8-spored asci when mature, and with a cylindrical and eccentric pedicel (Jaklitsch et al. 2018). Additionally, most *Neocucurbitaria* species display uniseriately arranged asci, while ascospores of *N. pistaciicola* are sometimes biseriately arranged in the asci.

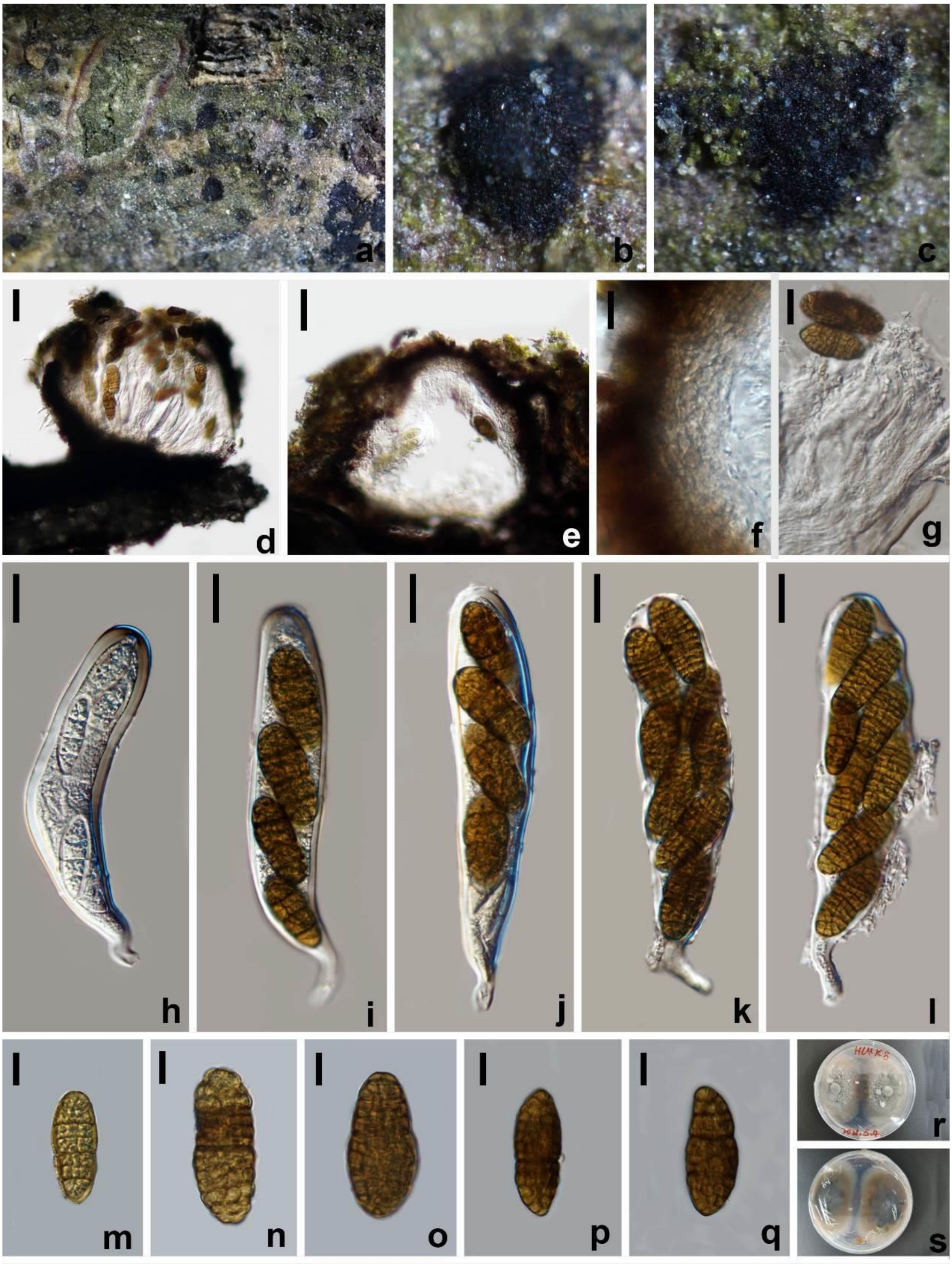

Figure 12 – *Neocucurbitaria pistaciicola* (HKAS 127162, holotype). a–c Appearance of ascomata on host surface. d, e Vertical section through ascomata. f Peridium. g Hamathecium. h–l Asci. m–q Ascospores. r Colonies on PDA from above. s Colonies on PDA from below. Scale bars: d, e = 50 µm, f, h–q = 10 µm, g = 20 µm.

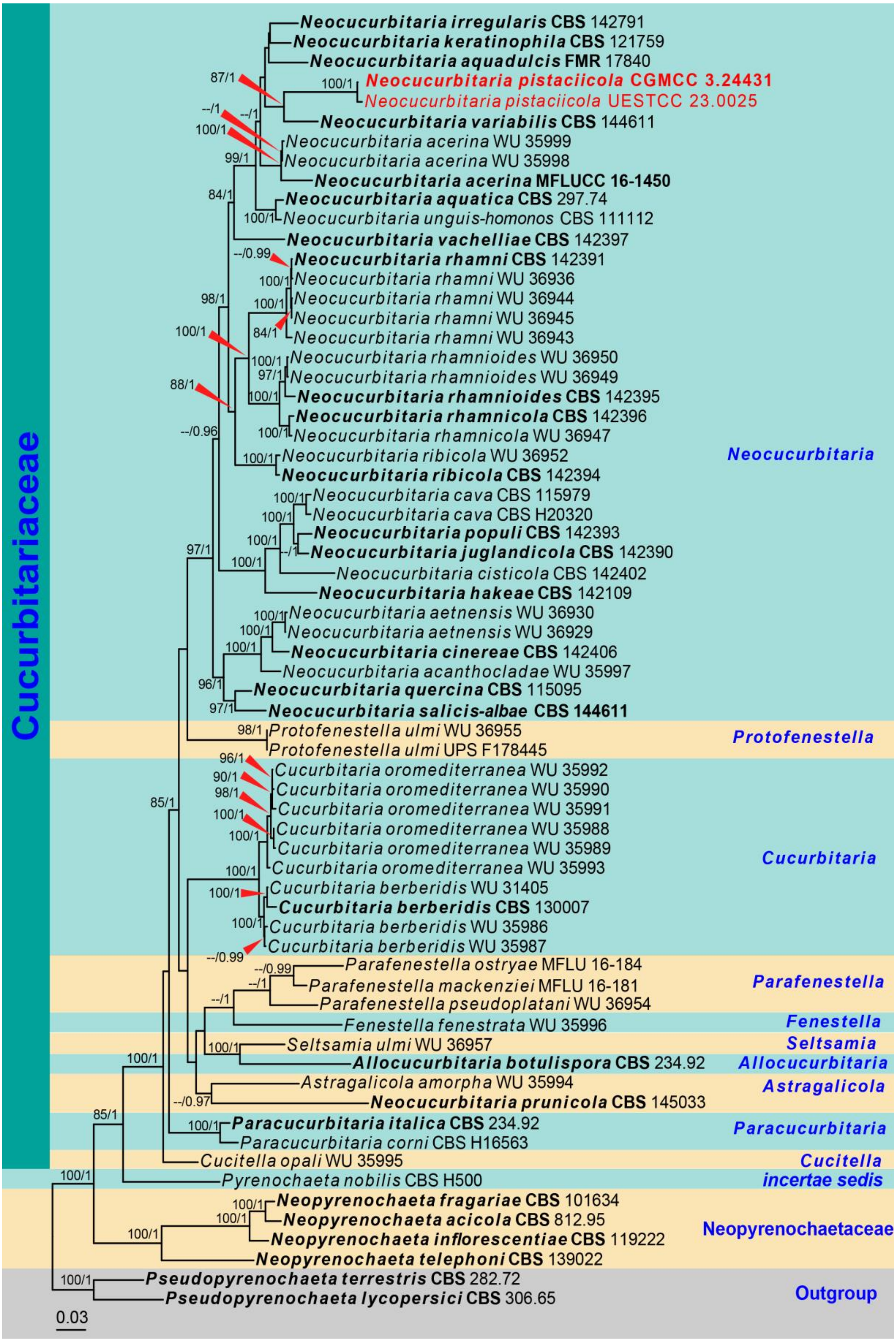

Figure 13 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, SSU, *rpb2*, *tef1* and *tub2* sequence data. Sixty-six strains are included in the combined sequence analyses, which comprise 7,513 characters with gaps. *Pseudopyrenochaeta lycopersici* CBS 306.65

and *P. terrestris* CBS 282.72 are used as outgroup taxa. Tree topology of ML analysis is similar to BI analysis. The best scoring RAxML tree with a final likelihood value of -63664.024897 is presented. Proportion of gaps and completely undetermined characters in this alignment are 35.95% with 1870 distinct alignment patterns. Estimated base frequencies were as follows; A = 0.087127, C = 0.033474, G = 0.088612, T = 0.058542; substitution rates AC = 0.312229, AG = 2.081526, AT = 3.217693, CG = 0.095403, CT = 0.138768, GT = 0.260191; gamma distribution shape parameter α = 0.139760. Bootstrap support values for ML ≥ 75% and BYPP ≥ 0.95 are defined as ML/BYPP above the nodes. Hyphens (--) represent support values less than 75% in ML and 0.95 in BI. Newly generated sequences are in red and ex-type strains are in bold.

Didymosphaeriaceae Munk, Dansk bot. Ark. 15(no. 2): 128 (1953).

MycoBank number: MB 80702; Facesoffungi number: FoF 00200

Notes – Didymosphaeriaceae species have a cosmopolitan distribution, and are saprobic, pathogenic or endophytic on woody and herbaceous plants. This family was established by Munk (1953) and typified by *Didymosphaeria*. Hongsanan et al. (2020) accepted 32 genera in Didymosphaeriaceae.

Austropleospora ochracea L.S. Dissan, J.C. Kang & K.D. Hyde, Phytotaxa 491(3): 223 (2021)

Fig. 14

MycoBank number: MB 557841; Facesoffungi number: FoF 00936

Saprobic on decaying branches of *Acer truncatum* Bunge. Sexual morph: Not observed. Aesexual morph: Coelomycetous. *Conidiomata* 230–300 × 300–340 µm ($\bar{x}$ = 260 × 320 µm, n = 10), pycnidial, solitary, immersed or semi-immersed, unilocular or multilocular, central ostiole. *Conidophores* reduced to conidiogenous cells. *Conidiogenous cells* 4–5.5 × 3–4.5 µm ($\bar{x}$ = 4.5 × 3.7 µm, n = 10), lining the inner conidiomatal cavity, inconspicuous, hyaline, ampulliform to doliiform, phialidic. *Conidia* 4.5–7 × 3–4.5 µm ($\bar{x}$ = 5.5 × 3.5 µm, n = 30), ellipsoid, hyaline to brown, with two small oil-droplets at each end, aseptate, smooth- and thick-walled.

Known distribution – Guizhou Province, China

Culture characteristics – Conidia germinate on PDA within 24 h. Colonies on PDA 30 mm diam. after 2 weeks at 25 °C, cream white at the margin, pale brown to yellowish brown in the center; reverse thin, flat, pale brown to yellowish brown.

Material examined – China, Sichuan Province, Chengdu city, Pidu district, N 30°49'26.76", E 103°47'41.64", elevation 442 m, on branches of *Acer truncatum*, 19 March 2021, W.L. Li, YBF 106 (HUEST 23.0031), living culture UESTCC 23.0031; *ibid*., 5 March 2021, YBF 39 (HUEST 23.0034), living culture UESTCC 23.0034; *ibid*., University of Electronic Science and Technology of China (UESTC), Qingshuihe campus, N 30°45'24.74", E 103°55'21.108", elevation 638 m, on a branch of *Trachycarpus fortunei*, 24 November 2020, W.L. Li, W126 (HUEST 23.0032), living culture UESTCC 23.0032; *ibid*., Guangyuan city, Qingchuan county, N 32°41'54.56", E 106°04'45.37", elevation 638 m, on branches of *Vernicia fordii*, 20 April 2021, W.L. Li, YT 174 (HUEST 23.0033), living culture UESTCC 23.0033.

GenBank numbers – UESTCC 23.0031 = LSU: OR253255, ITS: OR253103, SSU: OR253181, *tef1*: OR251062, *rpb2*: OR262127; UESTCC 23.0032 = LSU: OR253316, SSU: OR253218, *tef1*: OR263573; UESTCC 23.0034 = LSU: OR253239, ITS: OR253087; UESTCC 23.0033 = LSU: OR253265, ITS: OR253112, SSU: OR253190, *tef1*: OR251062.

Notes – *Austropleospora ochracea* with its sexual morph was introduced by Dissanayake et al. (2021), isolated from dead twigs of an undetermined host in Guizhou Province, China. In the multi-gene phylogeny, our four new isolates clustered together with the ex-type of *A. ochracea* with 91% ML/1.00 BYPP support (Fig. 15). The BLASTn searches of the LSU sequence of our strain resulted in 100% similarity with *A. ochracea* HMAS 248367, the *tef1* showed 99.78% similarity with *A. ochracea* GZCC 19-0430, and ITS BLASTn results appeared 99.64% similarity with *A. ochracea* HMAS 248367. Thus, we accept the new collection as the asexual morph of *A. ochracea*, discovered on woody oil plants for the first time.

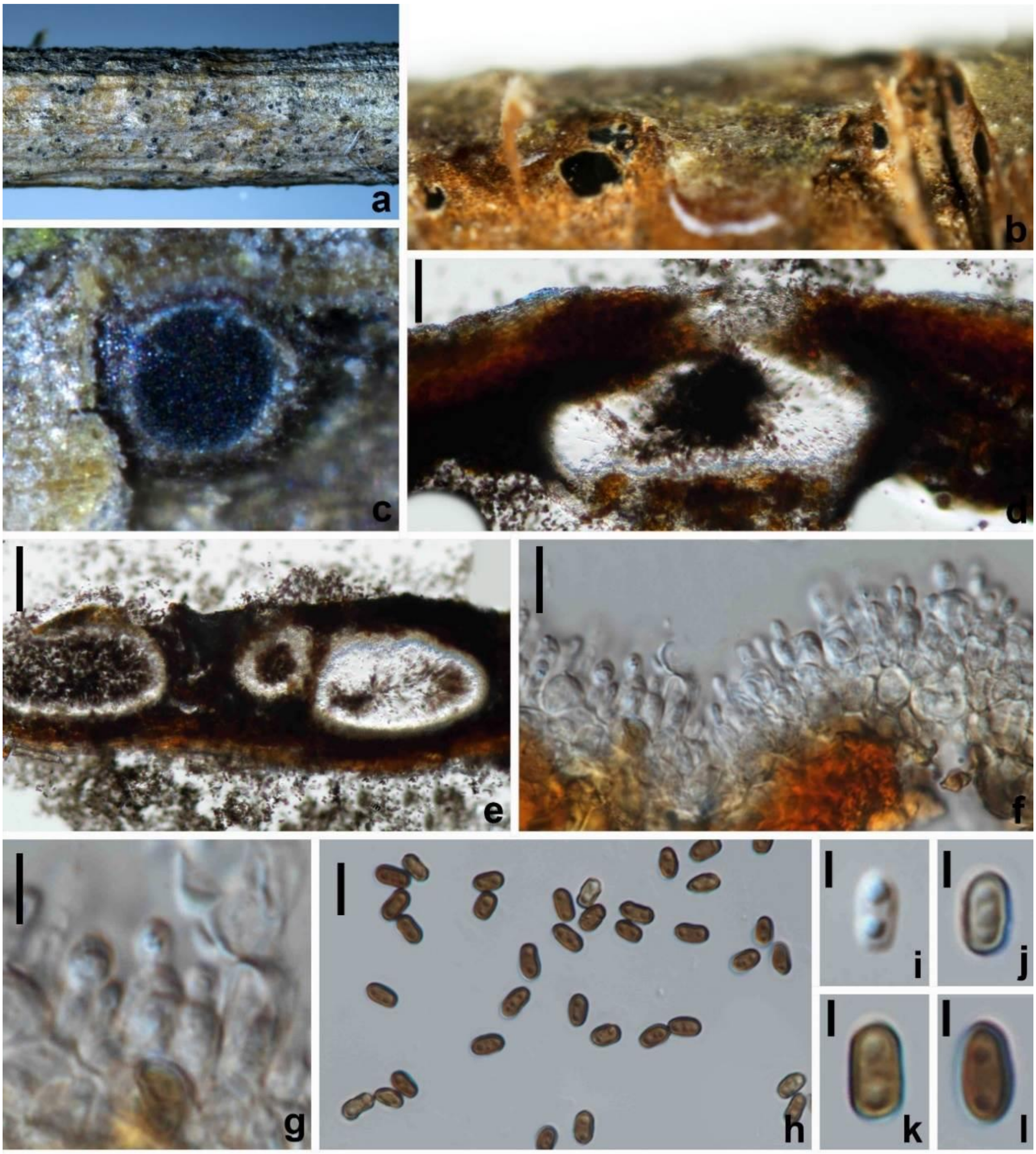

Figure 14 – *Austropleospora ochracea* (HUEST 23.0031). a–c Appearance of conidiomata on natural substrate. d, e Vertical section of conidiomata. f, g Conidiogenous cells and developing conidia. h–l Conidia. Scale bars: d, e = 100 µm, f–h = 10 µm, i–l = 2.5 µm.

Montagnula donacina (Niessl) Wanas., E.B.G. Jones & K.D. Hyde, Fungal Biology 120 (11): 1365 (2016) Fig. 16

MycoBank number: MB 626421; Facesoffungi number: FoF 04638

Saprobic on decaying branches of *Paeonia suffruticosa*. Sexual morph: *Ascomata* 370–430 × 220–360 µm ($\bar{x}$ = 400 × 290 µm, n = 10), immersed to semi-immersed, solitary, scattered or in small groups, unilocular, globose, brown to dark brown, ostiolate. *Ostiole* 63–65 µm wide, papillate, central. *Peridium* 33–39 µm thick, multi-layered, outer layer comprising dark brown, thick-walled cells of *textura angularis*, inner layer composed of pale brown, thin-walled cells of *textura angularis*. *Hamathecium* 2–2.5 µm wide, composed of numerous, hyaline, filamentous, branched, septate, pesudoparaphyses, and embedded in a gelatinous matrix. *Asci* 99–114 × 11–12 µm ($\bar{x}$ = 106.5 × 11.5 µm, n = 20), 8-spored, bitunicate, fissitunicate, cylindric-clavate with an elongate pedicel, apically rounded, with a tiny ocular chamber. *Ascospores* 14.5–16.5 × 5–6 µm ($\bar{x}$ = 15.5 × 5.5 µm, n = 20), overlapping, 1–2 seriate, fusiform, pale to dark brown, uniseptate, deeply constricted at the septum, guttulate, thick- and smooth-walled, without terminal appendages. Asexual morph: Not observed.

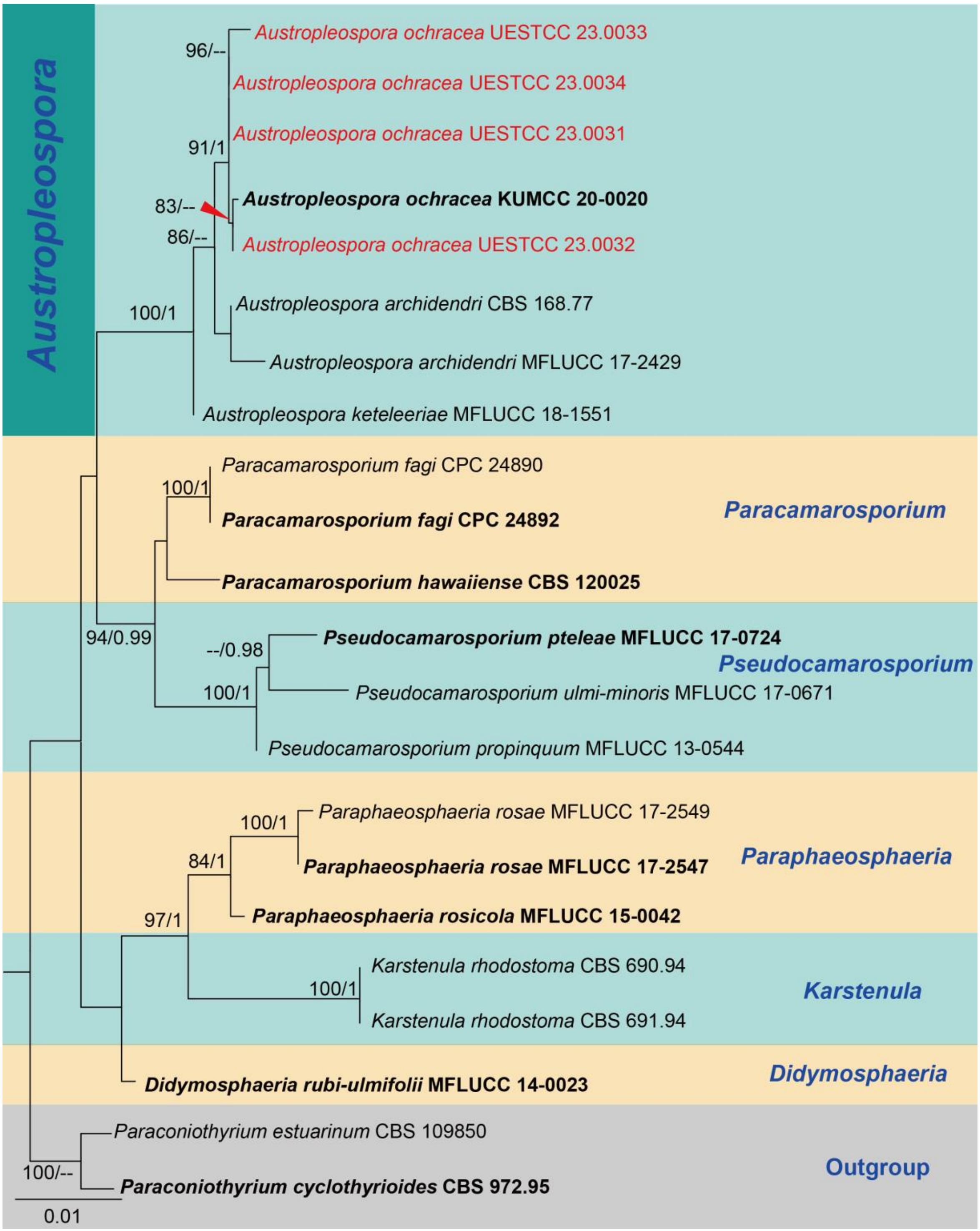

Figure 15 – Phylogram generated from maximum likelihood analysis based on combined LSU, SSU, ITS and *tef1* sequence data. Twenty-two strains are included in the combined sequence analyses, which comprise 3,302 characters with gaps. *Paraconiothyrium cyclothyrioides* CBS 972.95 and *P. estuarinum* CBS 109850 are used as outgroup taxa. Tree topology of ML analysis is similar to BI analysis. The best scoring RAxML tree with a final likelihood value of -6364.761725 is presented. Proportion of gaps and completely undetermined characters in this alignment are

23.13% with 299 distinct alignment patterns. Estimated base frequencies were as follows; A = 0.238529, C = 0.245119, G = 0.270434, T = 0.245917; substitution rates AC = 0.884887, AG = 1.065917, AT = 0.843771, CG = 0.920942, CT = 6.617746, GT = 1.000000; gamma distribution shape parameter α = 0.990764. Bootstrap support values for ML ≥ 75% and BYPP ≥ 0.95 are defined as ML/BYPP above the nodes. Hyphens (--) represent support values less than 75% in ML and 0.95 in BI. Newly generated sequences are in red and ex-type strains are in bold.

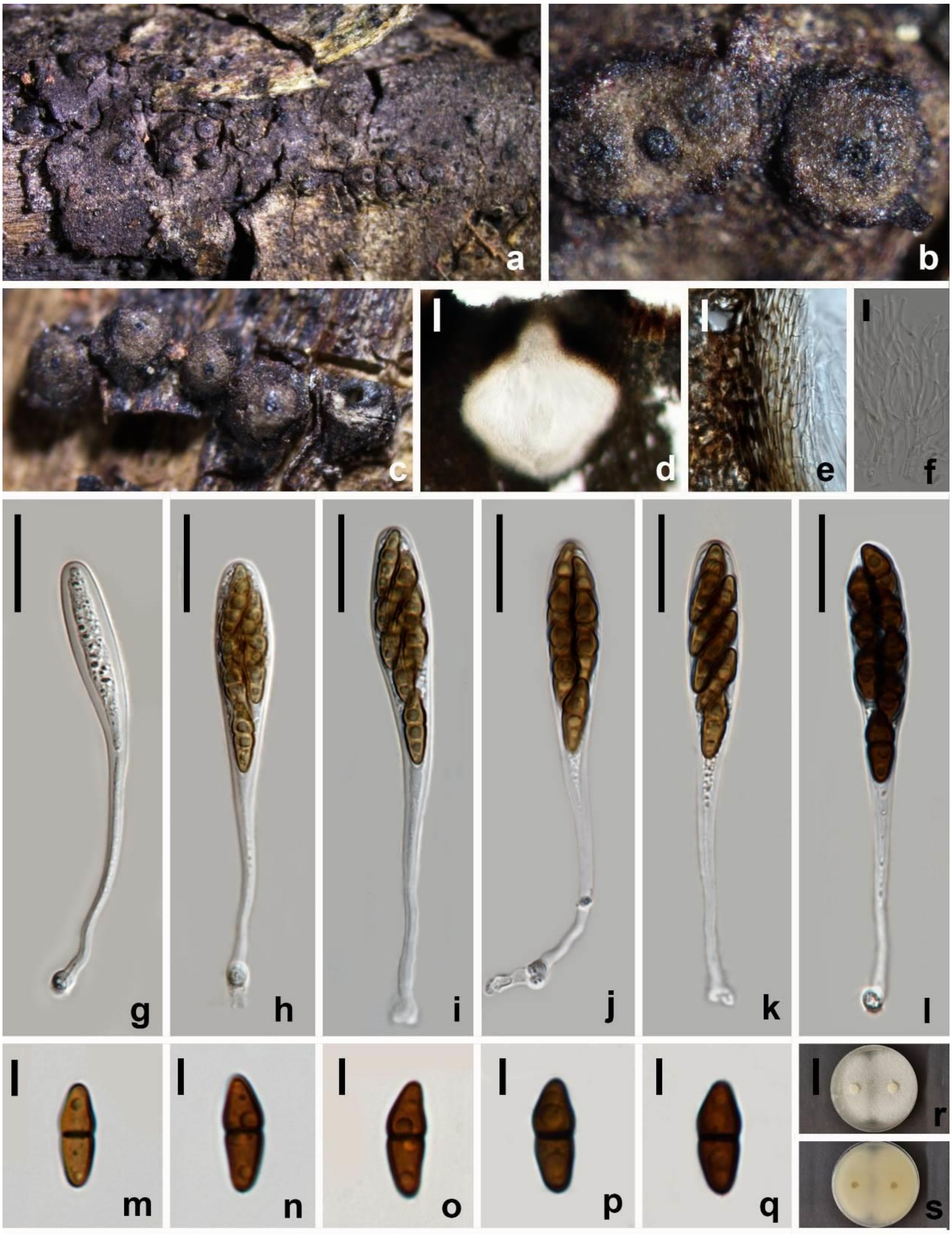

Figure 16 – *Montagnula donacina* (HUEST 23.0030). a–c Appearance of ascomata on host surface. d Vertical section through the ascoma. e Peridium. f Hamathecium. g–l Asci. m–q Ascospores. r Colonies on PDA from above. s Colonies on PDA from below. Scale bars: d = 100 μm, e, f = 10 μm, g–l = 20 μm, m–q = 5 μm.

Known distribution – China, Thailand

Culture characteristics – Conidia germinate on PDA within 24 h. Colonies on PDA reach 80 mm diam. after 14 d at 25 °C, effuse, hairy, grey-white from above, yellowish white from below.

Material examined – China, Sichuan Province, Mianyang city, Youxian district, N 31°25'22.18", E 104°48'57.99", elevation 800 m, on a branch of *Paeonia suffruticosa*, 10 June 2021, W.L. Li, YMD 313 (HUEST 23.0030), living culture UESTCC 23.0030.

GenBank numbers – UESTCC 23.0030 = LSU: OR253279, ITS: OR253120, SSU: OR253194, *tef1*: OR251171, *rpb2*: OR251143.

Notes – *Montagnula donacina* was introduced to accommodate *Munkovalsaria donacia* by Wanasinghe et al. (2016). Recently, Sun et al. (2023) synonymized *M. chromolaenicola*, *M. puerensis, M. saikhuensis* and *M. thailandica* under *M. donacia* based on DNA sequence data and overlapping morphological characteristics. *Montagnula donacina* was characterized by immersed to erumpent, globose ascomata, bitunicate, fissitunicate, elongate-clavate to short cylindrical asci, long pedicellate, bearing biseriate, uniseptate, light brown to blackish brown ascospores without a mucilaginous sheath. Multi-gene phylogenetic analysis shows that our new isolate UESTCC 23.0030 (Fig. 18) clustered with *M. donacina* strains. We, thus classify the new collection within *M. donacina*.

Montagnula verniciae W.L. Li & Jian K. Liu sp. nov. Fig. 17

MycoBank number: MB 849147; Facesoffungi number: FoF 14414

Etymology – The specific epithet '*verniciae*' refers to the host genus *Vernicia*, from which the holotype was collected.

Saprobic on decaying branches of *Vernicia fordii* (Hemsl) Airy Shaw. Sexual morph: *Ascomata* 320–360 × 300–330 µm ($\bar{x}$ = 340 × 320 µm, n = 10), immersed, visible as black spots, surrounded by a pale-yellow halo on the surface, solitary, scattered, globose or subglobose, wide papillate, dark reddish brown, ostiolate. *Peridium* 28–39 µm thick, comprising an inner layer of hyaline cells of *textura angularis,* and an outer layer of reddish-brown cells of *textura angularis. Hamathecium* 1.8–2.2 µm wide, hyaline, septate, anastomosing at the apex, branched, filamentous pesudoparaphyses. *Asci* 91–98 × 15–18 µm ($\bar{x}$ = 94.5 × 16.5 µm, n = 20), 8-spored, bitunicate, fissitunicate, clavate, with a long pedicel with knob-like to furcate base, apically rounded, with a small ocular chamber. *Ascospores* 19.5–23 × 7.5–9 µm ($\bar{x}$ = 21 × 8 µm, n = 20), 1–2-seriate, overlapping, initially hyaline to reddish-brown, ellipsoidal to fusiform with rounded and subhyaline ends, uniseptate, slightly constricted at the septum, straight to curved, enlarged at the upper cell, smooth-walled, with guttules. Asexual morph: Not observed.

Culture characteristics – Colonies on PDA 30 mm diam. after 4 weeks at 25 °C, dirty white to pale brown at the margin, pale brown to yellowish brown in the centre; reverse thin, flat, pale brown.

Material examined – China, Sichuan Province, Guangyuan city, Qingchuan county, N 32°41'54.56", E 106°04'45.37", elevation 638 m, on branches of *Vernicia fordii,* 20 April 2021, W.L. Li, YT240 (HKAS 127164, holotype), ex-type culture UESTCC 23.0028 = CGMCC 3.24435; *ibid*., YT240b (HUEST 23.0029, isotype), living culture UESTCC 23.0029.

GenBank numbers – CGMCC 3.24435 = LSU: OR253273, ITS: OR269139, SSU: OR253192, *tef1*: OR251166, *rpb2*: OR251141; UESTCC 23.0029 = LSU: OR253274, ITS: OR269140, SSU: OR253193, *tef1*: OR251167, *rpb2*: OR251142

Notes – Multi-gene phylogenetic analysis indicated that *Montagnula verniciae* forms a distinct clade within *Montagnula* (Fig. 18). The morphological characters of *M. verniciae* fits well with *Montagnula* species in having immersed ascomata with a small papilla, multi-layered peridium comprising cells of *textura angularis*, cellular pseudoparaphyses and bitunicate, fissitunicate, clavate asci with a long pedicel and bearing septate and yellowish-brown to brown ascospores. However, *M. verniciae* differs from other species of *Montagnula* in having distinct translucent areas at both ends of the ascospores.

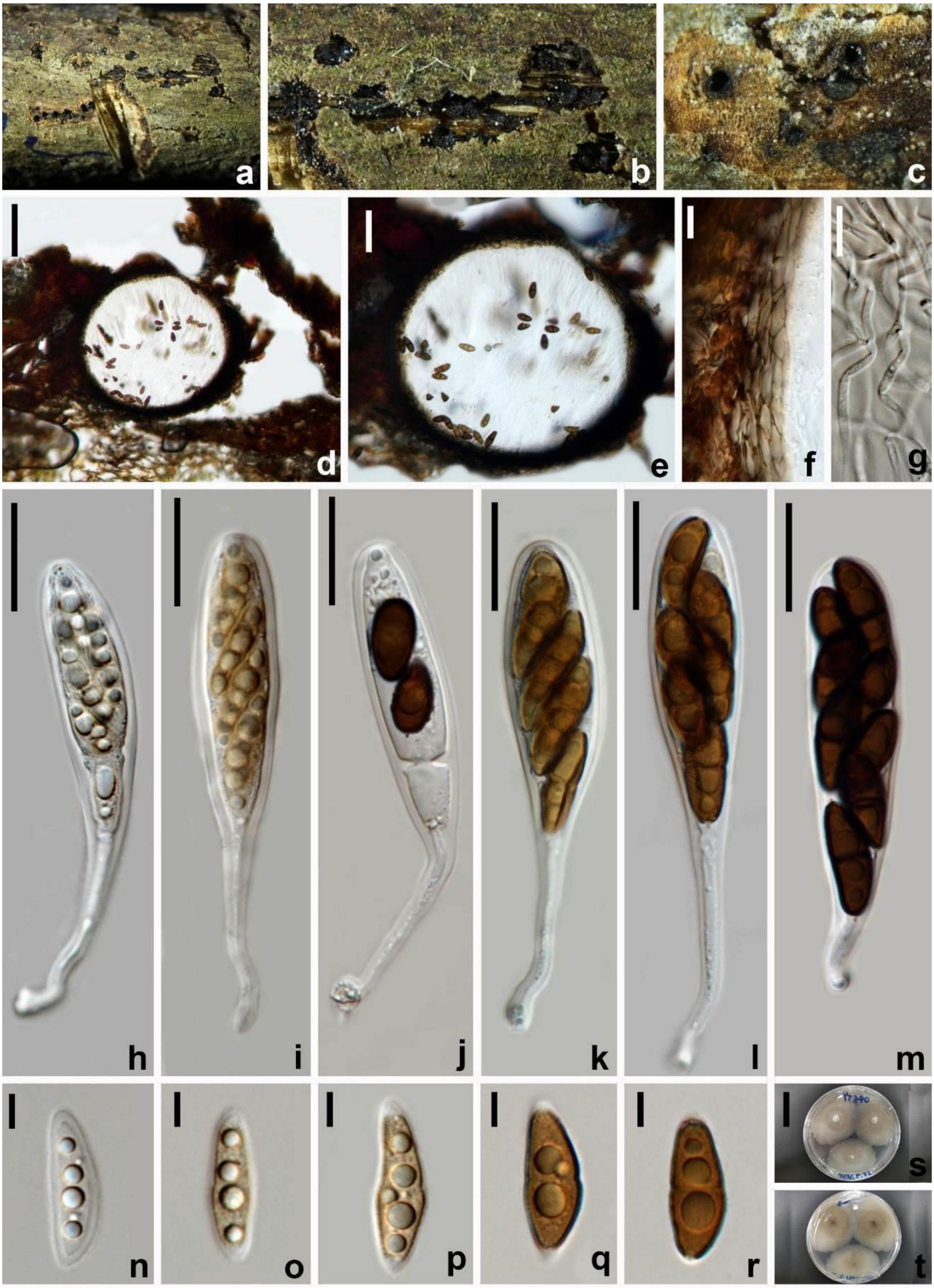

Figure 17 – *Montagnula verniciae* (HKAS 127164, holotype). a–c Appearance of ascomata on host surface. d, e Vertical section through ascoma. f Peridium. g Hamathecium. h–m Asci. n–r Ascospores. s Colonies on PDA from above, t Colonies on PDA from below. Scale bars: d = 100 μm, e = 50 μm, f, g = 10 μm, h–m = 20 μm, n–r = 5 μm.

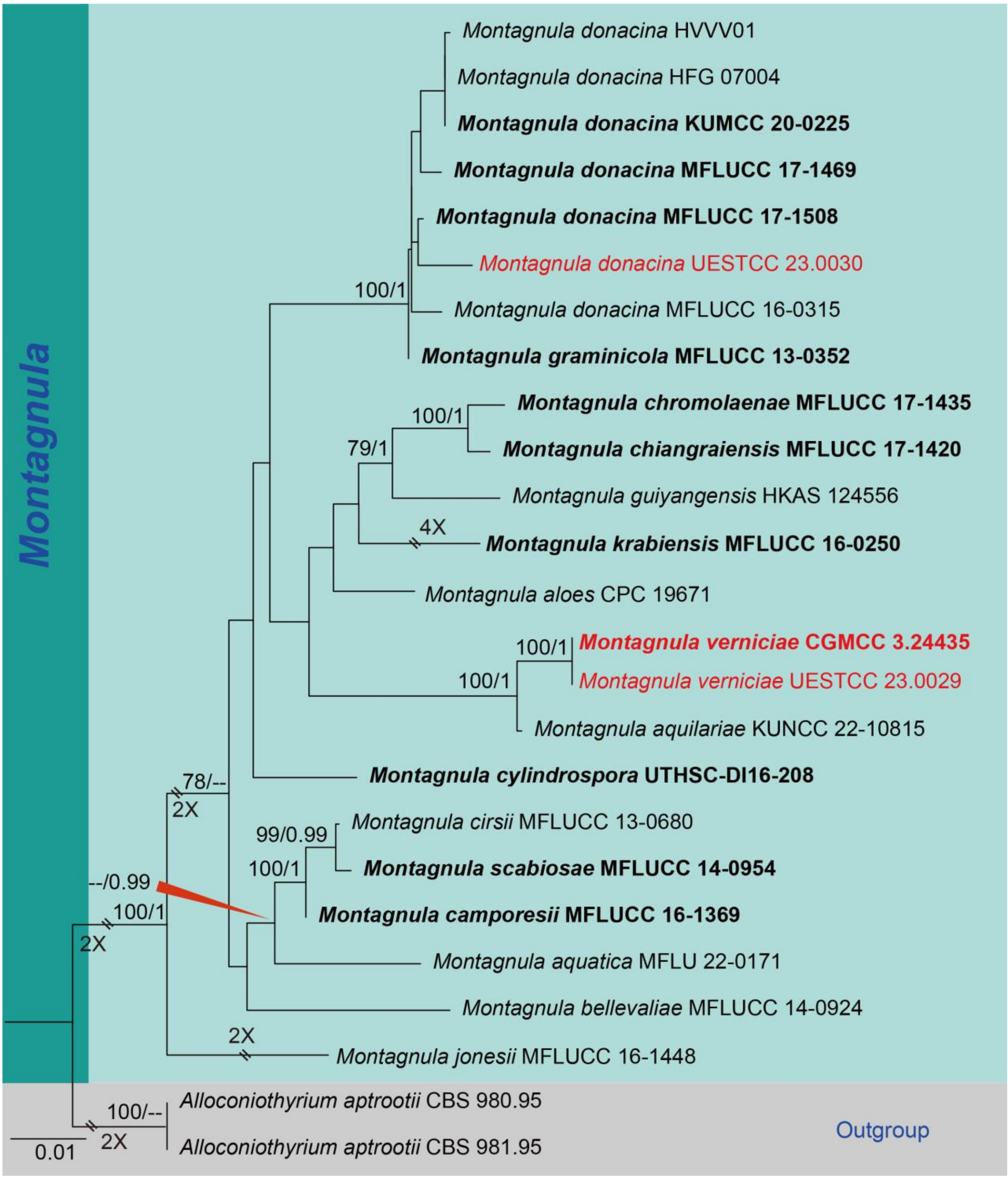

Figure 18 – Phylogram generated from maximum likelihood analysis based on combined LSU, SSU, ITS and *tef1* sequence data. Twenty-five strains are included in the combined sequence analyses, which comprise 3,360 characters with gaps. *Alloconiothyrium aptrootii* CBS 980.95 and *A. aptrootii* CBS 981.95 are used as outgroup taxa. Tree topology of ML analysis is similar to BI analysis. The best scoring RAxML tree with a final likelihood value of -9620.298714 is presented. Proportion of gaps and completely undetermined characters in this alignment are 22.71% with 621 distinct alignment patterns. Estimated base frequencies were as follows; A = 0.241394, C = 0.252438, G = 0.271067, T = 0.235101; substitution rates AC = 1.707952, AG = 2.421688, AT = 1.504214, CG = 1.111675, CT = 8.521535, GT = 1.000000; gamma distribution shape parameter α = 0.675307. Bootstrap support values for ML ≥ 75% and BYPP ≥ 0.95 are defined as ML/BYPP above the nodes. Hyphens (--) represent support values less than 75% in ML and 0.95 in BI. Newly generated sequences are in red and ex-type strains are in bold.

Neokalmusia aquibrunnea J. Yang, Jian K. Liu & K.D. Hyde, Fungal Diversity 119: 37 (2023) Fig. 19

MycoBank number: MB 559449; Facesoffungi number: FoF12782

Saprobic on decaying branches of *Trachycarpus fortunei* (Hook, f.) H. Wendl. Sexual morph: *Ascomata* 290–400 × 240–360 µm ($\bar{x}$ = 340 × 300 µm, n = 10), solitary, scattered or in groups of 1–3, immersed, globose to subglobose, coriaceous, clypeus brown to dark brown on host surface with ascomata breaking through slightly raised cracks at the centre. *Ostiole* 44.5–59 µm wide, central, periphysate. *Peridium* 27.5–46 µm thick, comprising host and fungal tissue, composed of brown and thick-walled to hyaline and thin-walled cells of *textura angularis*. *Hamathecium* 1.5–2 µm wide, numerous, dense, branches, septate, embedded in a gelatinous matrix. *Asci* 69.5–81 × 7.5–10 µm ($\bar{x}$ = 75 × 8.5 µm, n = 20), 8-spored, bitunicate, fissitunicate, cylindrical, apically rounded, with a small ocular chamber and a long pedicel. *Ascospores* 12.5–14 × 3.5–4 µm ($\bar{x}$ = 13 × 3.5 µm, n = 20), 1–2 seriate, broad fusiform, straight or slightly curve, with larger upper cell and elongate lower cell, uniseptate, deeply constricted at the septum, golden brown, smooth, guttulate. Asexual morph: Not observed.

Culture characteristics – Colonies on PDA reach 6 mm diam. after 14 d at 24 °C, dark grey to brown, circular, surface slightly rough with an entire edge, reverse yellowish brown to greyish brown, not producing pigments in PDA.

Material examined – China, Sichuan Province, Chengdu city, University of Electronic Science and Technology of China (UESTC) campus (Qingshuihe), N 30°45'24.74", E 103°55'21.10", elevation 638 m, on branches of *Trachycarpus fortunei*, 25 November 2020, W.L. Li, WD128 (HKAS 127163), living cultures UESTCC 23.0026 = CGMCC 3.24441; *ibid*., WD128b (HUEST 23.0027), living culture UESTCC 23.0027.

GenBank numbers – CGMCC 3.24441 = LSU: OR253317, ITS: OR253159, SSU: OR253219, *tef1*: OR263574; UESTCC 23.0027 = LSU: OR253318, ITS: OR253160, SSU: OR253220, *tef1*: OR263575.

Notes – Based on the morphological traits and molecular evidence (Fig. 20), our strains (CGMCC 3.24441 and UESTCC 23.0027) are identified as *Neokalmusia aquibrunnea*. *Neokalmusia aquibrunnea* was described by Yang et al. (2023), isolated from decaying submerged bamboo culms in freshwater habitats. In this study, we report a new host record of *N. aquibrunnea* and extend its habitat from freshwater ecosystem to terrestrial.

Lophiotremataceae K. Hiray. & Kaz. Tanaka, Mycoscience 52: 405 (2011)

Notes – Lophiotremataceae was established by Hirayama & Tanaka (2011) to accommodate the type genus *Lophiotrema*, which was initially placed under Lophiostomataceae. Hashimoto et al. (2017) revised Lophiotremataceae and accepted another five genera *Atrocalyx*, *Crassimassarina*, *Cryptoclypeus*, *Galeaticarpa*, and *Pseudocryptoclypeus* in this family based on morphology and molecular analyses. Currently, eight genera are accepted in Lophiotremataceae by Wijayawardene et al. (2022).

Lophiotrema hydei J.F. Zhang, J.K. Liu & Z.Y. Liu, Phytotaxa 379 (2): 172 (2018) Fig. 21

MycoBank number: MB 555509

Saprobic on decaying branches of *Vernicia fordii.* Sexual morph: *Ascomata* 200–220 × 210–230 µm ($\bar{x}$ = 210 × 220 µm, n = 10), solitary or gregarious, immersed to erumpent through host tissue, carbonaceous, globose to subglobose, brown to dark brown, ostiolate. *Ostiole* 65–82 µm wide, central, crest-like, periphysate. *Peridium* 27.5–35 µm wide, composed of 3–4 layers of flattened, brown-walled, angular pseudoparenchymatous cells. *Hamathecium* 2.1–2.6 µm wide, numerous, filamentous, septate, branched, cellular pseudoparaphyses. *Asci* 73.5–78 × 7–8 µm ($\bar{x}$ = 75.5 × 7.5 µm, n = 20), 8-spored, bitunicate, fissitunicate, cylindrical to clavate, with a swollen pedicel, apically rounded, with a minute ocular chamber. *Ascospores* 17–20 × 2.5–3.5 µm ($\bar{x}$ = 18.5 × 3 µm, n = 20), uniseriate, partially overlapping, fusiform, with acute ends, hyaline, straight or slightly curved, uniseptate, constricted at the septa, narrow towards both ends, smooth-walled, with guttules, surrounded by a thin mucilaginous sheath. Asexual morph: Not observed.

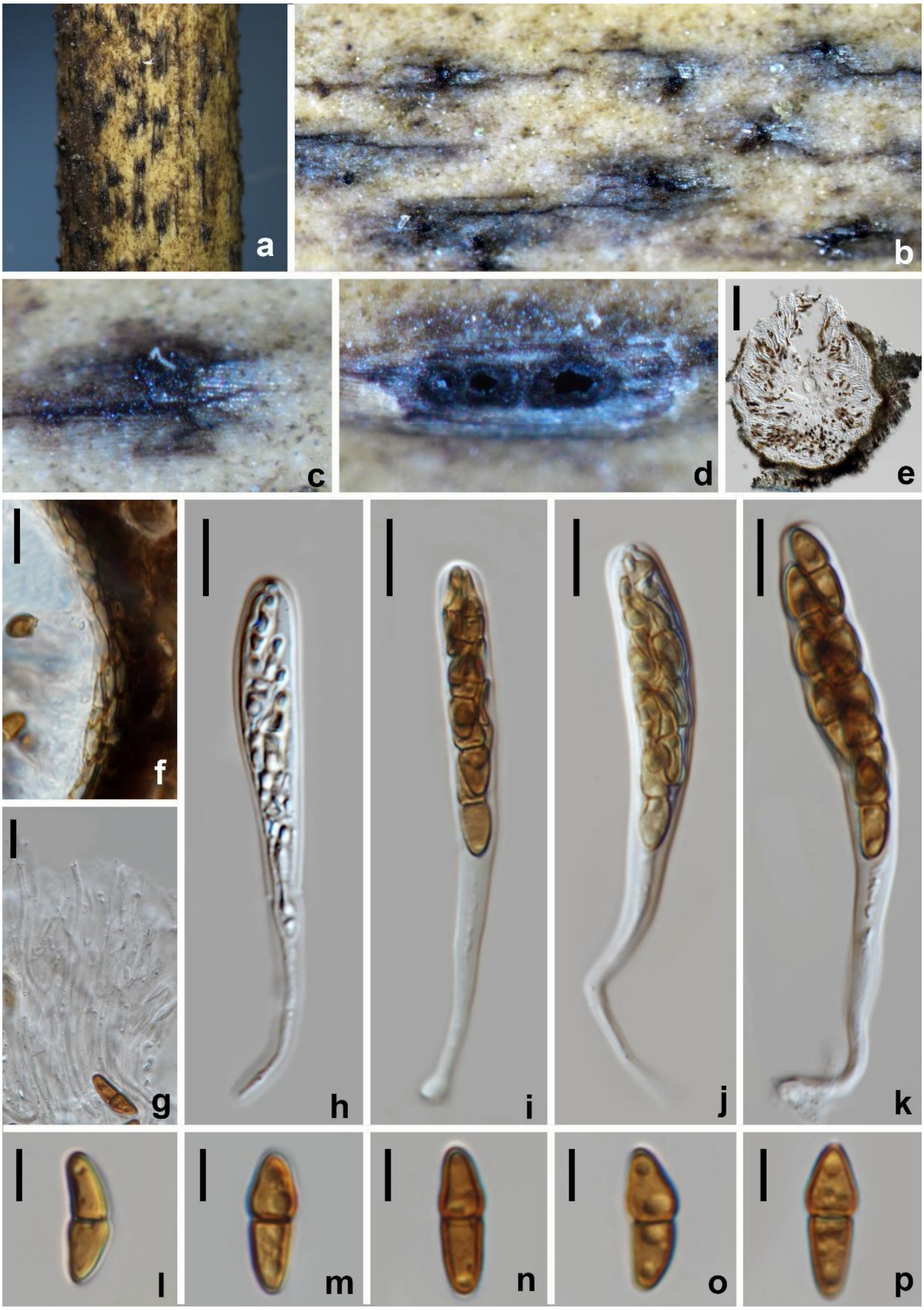

Figure 19 – *Neokalmusia aquibrunnea* (HKAS 127163). a–d Appearance of ascomata on host surface. e Vertical section through ascoma. f Peridium. g Hamathecium. h–k Asci. l–p Ascospores. Scale bars: e = 50 µm, f–k = 10 µm, l–p = 5 µm.

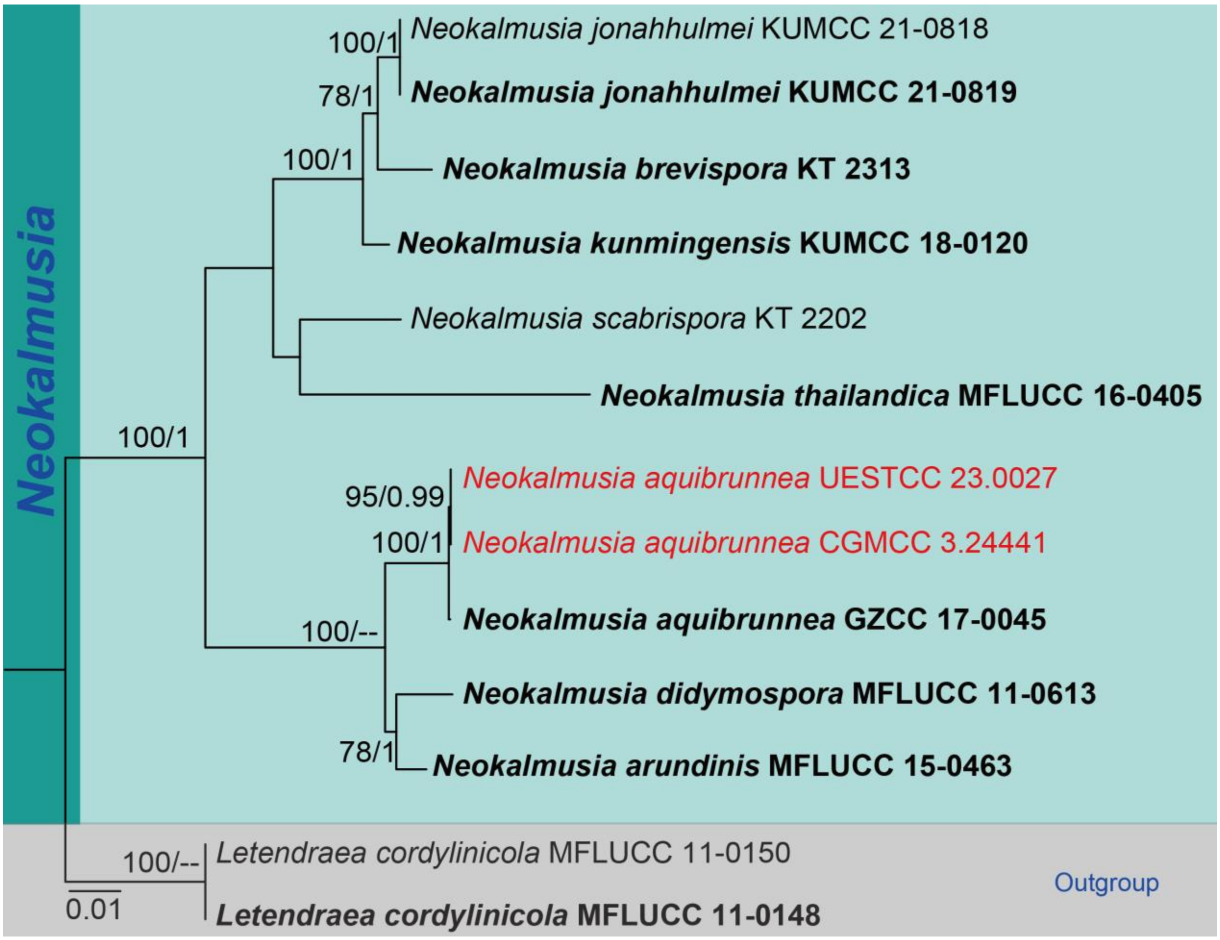

Figure 20 – Phylogram generated from maximum likelihood analysis based on combined LSU, SSU, ITS and *tef1* sequence data. Thirteen strains are included in the combined sequence analyses, which comprise 3,371 characters with gaps. *Letendraea cordylinicola* MFLUCC 11-0148 and *L. cordylinicola* MFLUCC 11-0150 are used as outgroup taxa. Tree topology of ML analysis is similar to BI analysis. The best scoring RAxML tree with a final likelihood value of -7553.756133 is presented. Proportion of gaps and completely undetermined characters in this alignment are 23.13% with 299 distinct alignment patterns. Estimated base frequencies were as follows; A = 0.235764, C = 0.254991, G = 0.272188, T = 0.237057; substitution rates AC = 1.637181, AG = 2.478489, AT = 1.634864, CG = 1.579299, CT = 14.091718, GT = 1.000000; gamma distribution shape parameter α = 0.469060. Bootstrap support values for ML ≥ 75% and BYPP ≥ 0.95 are defined as ML/BYPP above the nodes. Hyphens (--) represent support values less than 75% in ML and 0.95 in BI. Newly generated sequences are in red and ex-type strains are in bold.

Culture characteristics – Colonies on PDA reach 14–17 mm diam. after 2 weeks at 25 °C, colonies circular, medium dense, slightly raised to umbonate, dull, smooth, slightly radiating; from above, white to yellowish-grey at the margin, yellowish-grey to dark grey in the centre; from below: pale yellowish to yellowish-brown at the margin, dark brown at the center, not producing pigmentation in agar.

Material examined – China, Sichuan Province, Guangyuan city, Qingchuan county, N 32°41'54.56", E 106°04'45.37", elevation 638 m, on a branch of *Vernicia fordii*, 20 April 2021, W.L. Li, YT 171 (HUEST 23.0061), living culture UESTCC 23.0061; *ibid*., Leshan city, Wutongqiao district, N 29°24.44'，E 103°49.38'，elevation, 365 m, on branches of *Camellia oleifera*, 23 July 2021, W.L. Li, YC 348 (HUEST 23.0060), living culture UESTCC 23.0060; *ibid*., YC 356 (HUEST 23.0059), living culture UESTCC 23.0059.

GenBank numbers – UESTCC 23.0059 = LSU: OR253288, ITS: OR253129, SSU: OR253201, *tef1*: OR251177, *rpb2*: OR251147; UESTCC 23.0060 = LSU: OR253286, ITS:

OR253127, SSU = OR253200, *tef1*: OR251175, *rpb2*: OR251145; UESTCC 23.0061 = LSU: OR253264, ITS: OR253111, SSU: OR253189, *tef1*: OR251161, *rpb2*: OR251136.

Notes – In the phylogenetic analyses, three new isolates were clustered with *Lophiotrema hydei* with full bootstrap support (100% ML/1.00 BYPP) (Fig. 23). Morphologically, these collections similarity well with *L. hydei* in having carbonaceous ascomata with crest-like ostioles, clindrical to clavate asci with short pedicels, and fusiform ascospores with acute ends. Thus, we identify our collections as *L. hydei*, which is reported from *Vernicia fordii* for the the first time.

Lophiotrema neoarundinaria Y. Zhang ter, Kaz. Tanaka & K.D. Hyde, Stud. Mycol. 64: 97 (2009) Fig. 22

MycoBank number: MB 836880

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

Saprobic on decaying branches of *Acer truncatum* Bunge. Sexual morph: *Ascomata* 200–270 × 170–200 µm ($\bar{x}$ = 240 × 180 µm, n = 10), solitary, scattered, immersed to semi-immersed, globose to subglobose, dark brown to black, ostiolate. *Ostiole* 102–130 µm wide, central, rounded, black, with a crest-like opening, filled with hyaline periphyses. *Peridium* 17–24 µm thick, multi-layered, outer layers composed of thick-walled and pale brown cells of *textura angularis* fused with the host tissue, inner layers comprising hyaline, thin-walled cells of *textura angularis*. *Hamathecium* 1.8–2.4 µm wide, composed of numerous, filamentous, hyaline, septate, branched pseudoparaphyses. *Asci* 90–97 × 8–9.5 µm ($\bar{x}$ = 93.5 × 8.5 µm, n = 20), 8-spored, bitunicate, fissitunicate, cylindrical to clavate, apically rounded, with a cylindrical pedicel. *Ascospores* 29.5–30 × 3.5–5 µm ($\bar{x}$ = 29.5 × 4 µm, n = 20), 1–2 seriate, overlapping, fusiform, with acute ends, hyaline, straight to curved, 3-septate, constricted at the middle septum and slightly constricted at the remaining septa, smooth-walled, guttulate. Asexual morph: Not observed.

Known distribution – China, Japan

Culture characteristics – Colonies on PDA reach 30 mm diam within 21 d at 25 °C in the dark, floccose, with irregular margin, smoke grey; reverse olivaceous grey to olivaceous black.

Material examined – China, Sichuan Province, Chengdu city, Pidu district, N 30°49'26.76", E 103°47'41.64", elevation 442 m, on branches of *Acer truncatum*, 19 March 2021, W.L. Li, YBF 86 (HUEST 23.0058), living culture UESTCC 23.0058; *ibid*., YBF 87 (HUEST 23.0055), living culture UESTCC 23.0055; *ibid*., YBF 89 (HUEST 23.0054), living culture UESTCC 23.0054; *ibid*., Chengdu city, Shuangliu district, N 30°19'57.04", E 103°59'46.66", elevation 432 m, on branches of *Olea europaea*, 30 January 2021, GL 003 (HUEST 23.0053), living culture UESTCC 23.0053; *ibid*., 27 March 2021, GL 123 (HUEST 23.0057), living culture UESTCC 23.0057; *ibid*., Leshan city, Shizhong district, N 29°42.44', E 103°52.41′, elevation 444 m, on a branch of *Paeonia suffruticosa*, 23 July 2021, W.L. Li, 377 (HUEST 23.0056), living culture UESTCC 23.0056.

GenBank numbers – UESTCC 23.0053 = LSU: OR253230, SSU: OR253170; UESTCC 23.0054 = LSU: OR253247, ITS: OR253095, SSU: OR253176, *tef1*: OR251057; UESTCC 23.0055 = LSU: OR253246, ITS: OR253094, SSU: OR253175, *tef1*: OR251056; UESTCC 23.0056 = LSU: OR253290, ITS: OR253131, SSU: OR253203, *tef1*: OR251179; UESTCC 23.0057 = LSU: OR253256, ITS: OR253104, SSU: OR253182, *tef1*: OR251156; UESTCC 23.0058 = LSU: OR253245, ITS: OR253093, SSU: OR253174, *tef1*: OR251055.

Notes – *Lophiotrema neoarundinaria* was previously introduced as *Didymosphaeria arundinariae* by Ellis & Everhart (1892), collected from *Arundinaria* sp. in USA. The taxonomic placement of this species was updated by Zhang et al. (2009) by transferring to *Lophiotrema* based on both morphology and phylogeny. Boonmee et al. (2021) isolated *L. neoarundinaria* from *Prunus* sp. in Yunnan Province, China. In this study, six strains isolated from *Acer truncatum* and *Olea europaea* grouped with the other strains of *L. neoarundinaria* in the multi-gene phylogenetic tree (Fig. 23). Morphologically, the new collection shares similar morphological characters to the type strain of *L. neoarundinaria*. We, therefore identify the new collection as *L. neoarundinaria*, which is the first report from *Acer truncatum* and *Olea europaea*.

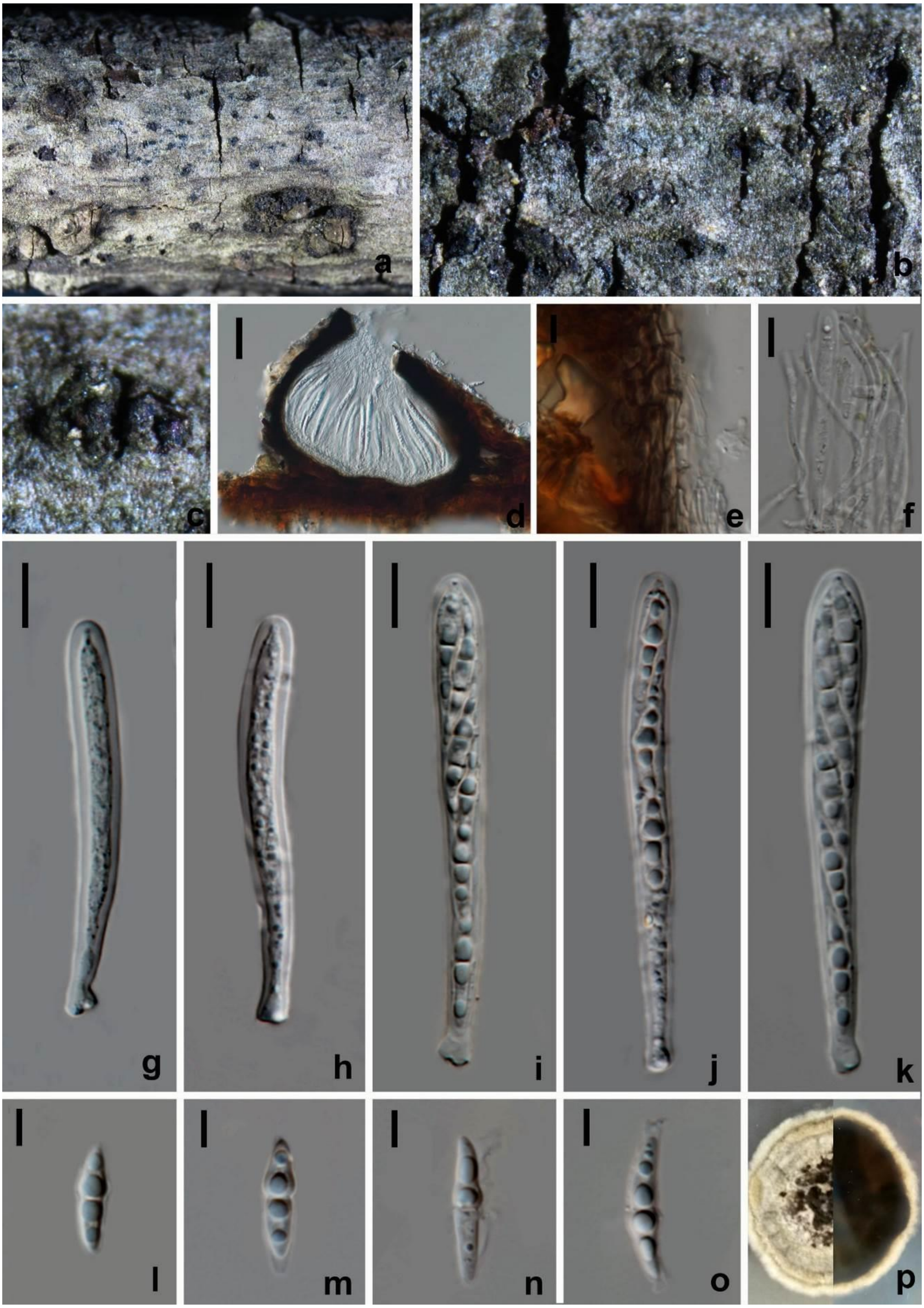

Figure 21 – *Lophiotrema hydei* (HUEST 23.0061). a–c Appearance of ascomata on host surface. d Vertical section through ascoma. e Peridium. f Hamathecium. g–k Asci. l–o Ascospores. p Upper and reverse view of the colony on PDA after 14 d. Scale bars: d = 50 µm, e, l–o= 5 µm, f–k = 10 µm.

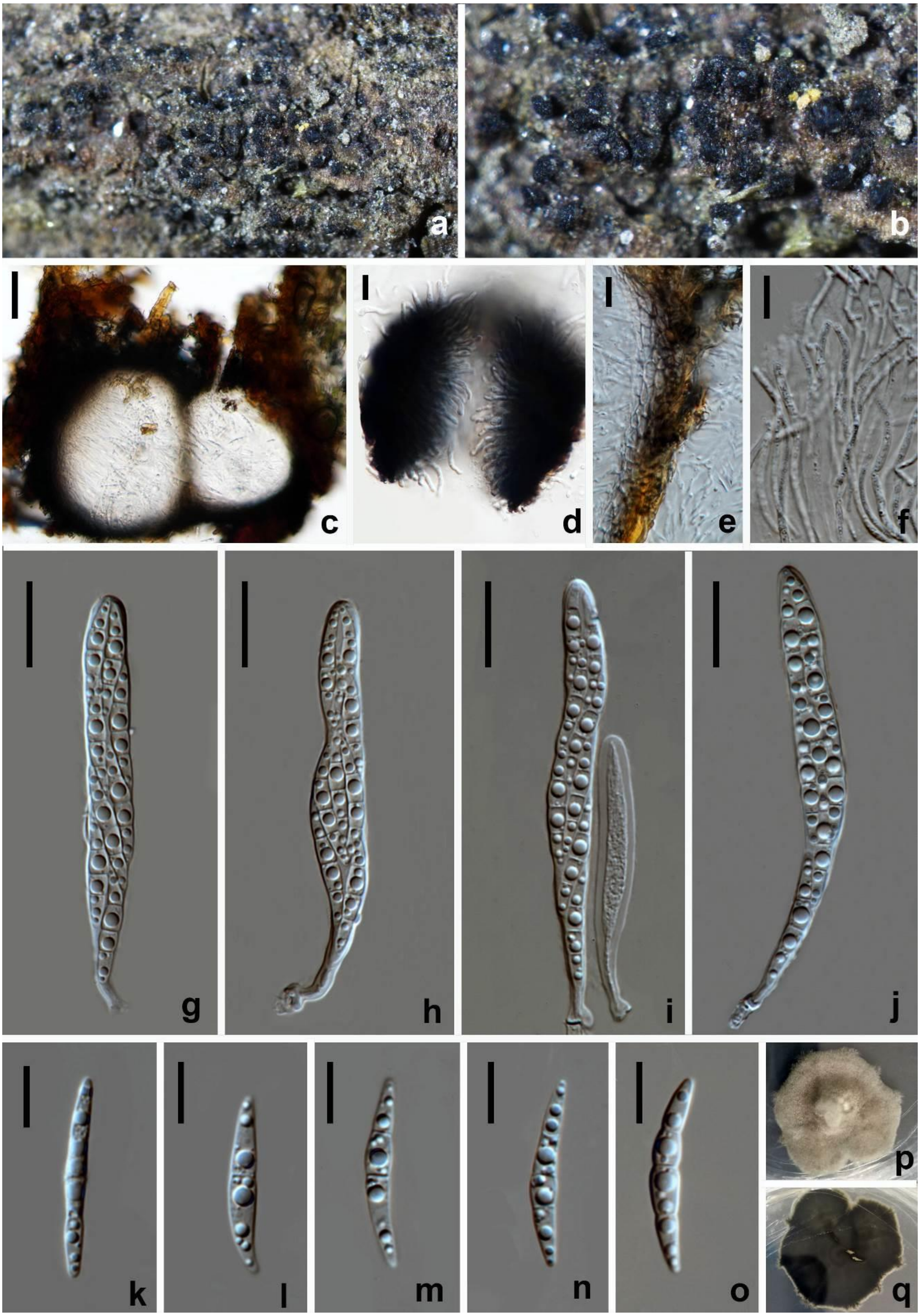

Figure 22 – *Lophiotrema neoarundinaria* (HUEST 23.0058). a, b Appearance of ascomata on host surface. c Vertical section through ascomata. d Ostiole. e Peridium. f Hamathecium. g–j Asci. k–o Ascospores. p Colony on PDA from above, q Colony on PDA from below. Scale bars: c, d = 20 μm, e–j = 10 μm, k–o = 5 μm.

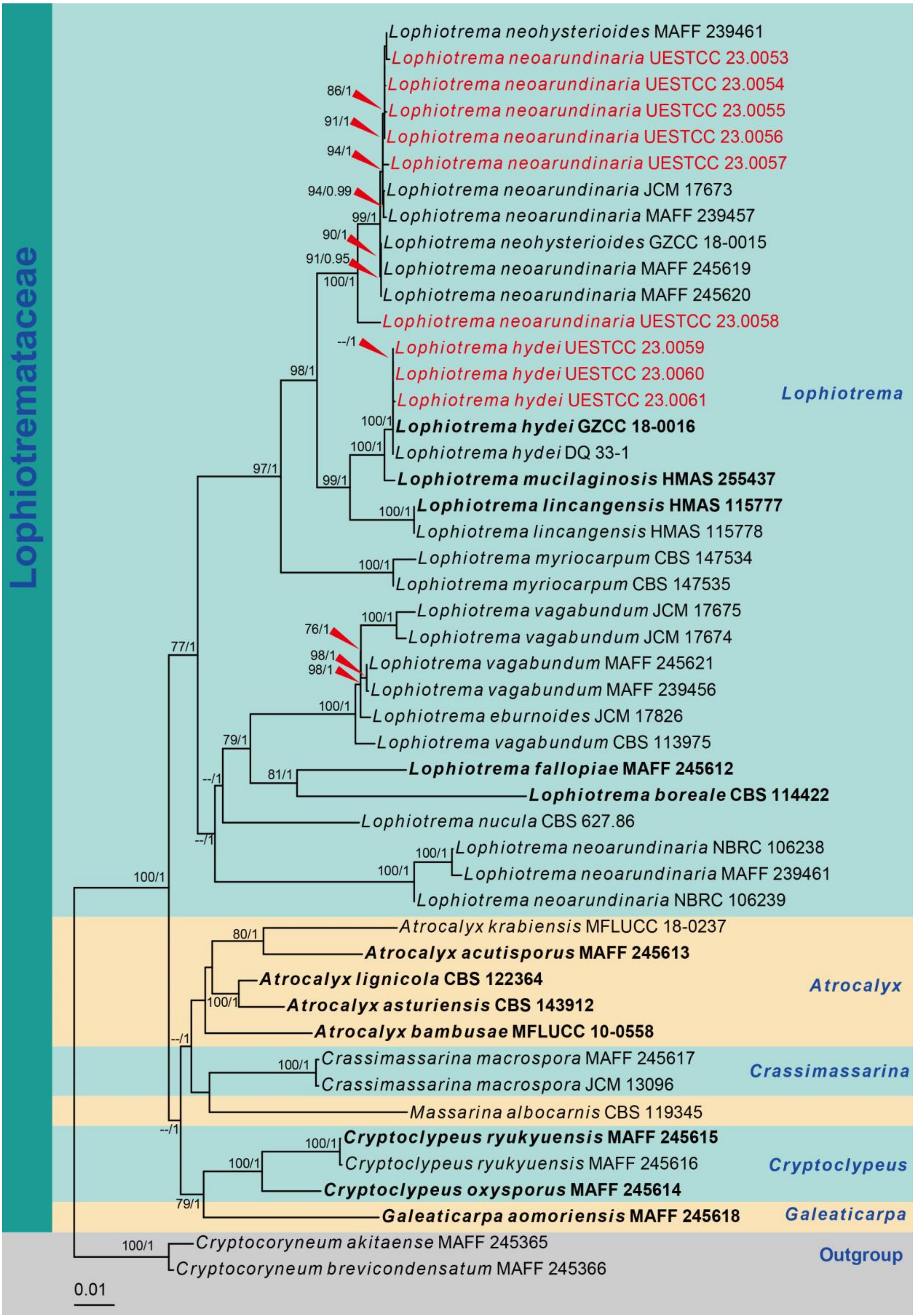

Figure 23 – Phylogram generated from maximum likelihood analysis based on combined SSU, ITS, LSU, *tef1* and *rpb2* sequence data. Forty-eight strains are included in the combined sequence analyses, which comprise 4,759 characters with gaps. *Cryptocoryneum akitaense* MAFF 245365 and *C. brevicondensatum* MAFF 245366 are used as outgroup taxa. Tree topology of ML analysis

is similar to BI analysis. The best scoring RAxML tree with a final likelihood value of -20218.930039 is presented. Proportion of gaps and completely undetermined characters in this alignment are 10.89% with 1144 distinct alignment patterns. Estimated base frequencies were as follows; A = 0.248228, C = 0.257422, G = 0.267016, T = 0.227334; substitution rates AC = 1.619356, AG = 4.654165, AT = 1.445045, CG = 1.467844, CT = 11.087042, GT = 1.000000; gamma distribution shape parameter α = 0.531310. Bootstrap support values for ML ≥ 75% and BYPP ≥ 0.95 are defined as ML/BYPP above the nodes. Hyphens (--) represent support values less than 75% in ML and 0.95 in BI. Newly generated sequences are in red and ex-type strains are in bold.

Lophiostomataceae Sacc., Syll. fung. (Abellini) 2: 672 (1883).

MycoBank number: MB 80966; Facesoffungi number: FoF 00796

Notes – Lophiostomataceae was introduced by Nitschke (1869) with *Lophiostoma* as the type genus. This family has been classified in different orders by various authors (von Arx et al. 1950, Luttrell 1973, Barr 1987, Holm 1988, Barr 1992, Kirk et al. 2008). Most species of Lophiostomataceae mainly occur on twigs, stems or bark of woody plants and herbaceous plants in terrestrial and aquatic environment (Holm 1988, Thambugala et al. 2015). Hongsanan et al. (2020) accepted 28 genera in this family. In the latest treatment, Andreasen et al. (2021) accepted 11 genera in Lophiostomataceae. Other 14 genera (*Alpestrisphaeria*, *Biappendiculispora*, *Capulatispora*, *Coelodictyosporium*, *Guttulispora*, *Lophiohelichrysum*, *Lophiopoacea*, *Neopaucispora*, *Neotrematosphaeria*, *Platystomum*, *Pseudocapulatispora*, *Pseudolophiostoma*, *Pseudoplatystomum* and *Sigarispora*) were synonymized under *Lophiostoma*. In this study, we introduce a new genus, three new species and four new records in Lophiostomataceae.

Flabellascoma pistaciae W.L. Li & Jian K. Liu, sp. nov. Fig. 24

MycoBank number: MB 849149; Facesoffungi number: FoF 14418

Etymology – The specific epithet ‘pistaciae’ refers to the host genus *Pistacia*, from which the holotype was collected.

Saprobic on decaying branches of *Pistacia chinensis*. Sexual morph: *Ascomata* 340–420 × 320–390 µm ($\bar{x}$ = 380 × 360 µm, n = 10), superficial, appear as black spots, coriaceous, solitary, scattered, or in small groups of 2–3, black walled, roughened, globose to obpyriform, papillate, ostiolate. *Ostiole* 59–75 µm wide, central, with a crest-like apex and a pore-like opening. *Peridium* 50–59 µm wide, composed of 5–6 layers of brown-walled cells of *textura angularis*. *Hamathecium* 2.5–3 µm wide, filamentous, branched, septate pseudoparaphyses. *Asci* 71–80 × 9.5–11.5 µm ($\bar{x}$ = 75.5 × 10.5 µm, n = 20), 8-spored, bitunicate, fissitunicate, cylindrical-clavate, straight or slightly curved, a short pedicel with knob-like or obtuse base, apically rounded, with an ocular chamber. *Ascospores* 13–21 × 4–5 µm ($\bar{x}$ = 14 × 4.5 µm, n = 20), 1–2-seriate, hyaline, broadly fusiform with obtuse ends, uniseptate, deeply constricted at the septum, curved, the lower cell often broader than the upper one, containing four refractive globules; sheath drawn out to form polar appendages, 2.4–4.3 × 1.8–2.3 µm ($\bar{x}$ = 3.3 × 2 µm, n = 10). Asexual morph: Not observed.

Culture characteristics – Ascospores germinate on PDA within 24 h and germ-tube produced from one or both sides of the ascospore. Colonies on PDA reach 20 mm diam. after 14 d at 25 °C, colonies circular, medium dense, surface smooth with sinuate edge, velvety, colony from above white at the margin, with white greyish to gray in the centre; from below: white brown to light brown at the margin, dark grey to blackish in the middle, white greyish to gray in the centre; not producing pigmentation in agar.

Material examined – China, Sichuan Province, Chengdu city, Pidu district, N 30°49'26.76", E 103°47'41.64", elevation 442 m, on branches of *Pistacia chinensis*, 19 March 2021, W.L. Li, GL 102 (HKAS 127166, holotype), ex-type culture UESTCC 23.0048 = CGMCC 3.24429; *ibid*., GL 102b (HUEST 23.0049), living culture UESTCC 23.0049; *ibid*., Shuangliu district, N 30°19'57.04", E 103°59'46.66", elevation 432 m, on a branch of *Camellia oleifera* Abel, 24 November 2021, W.L. Li, YC 537 (HUEST 23.0050), living culture UESTCC 23.0050.

GenBank numbers – CGMCC 3.24429 = LSU: OR253253, ITS: OR253101, SSU: OR253179; *tef1*: OR251060, *rpb2*: OR262122, UESTCC 23.0049 = LSU: OR253254, ITS: OR253102, SSU: OR253180, *tef1*: OR251061, *rpb2*: OR262123; UESTCC 23.0050 = LSU: OR253310, ITS: OR253151, SSU: OR242658, *tef1*: OR251155.

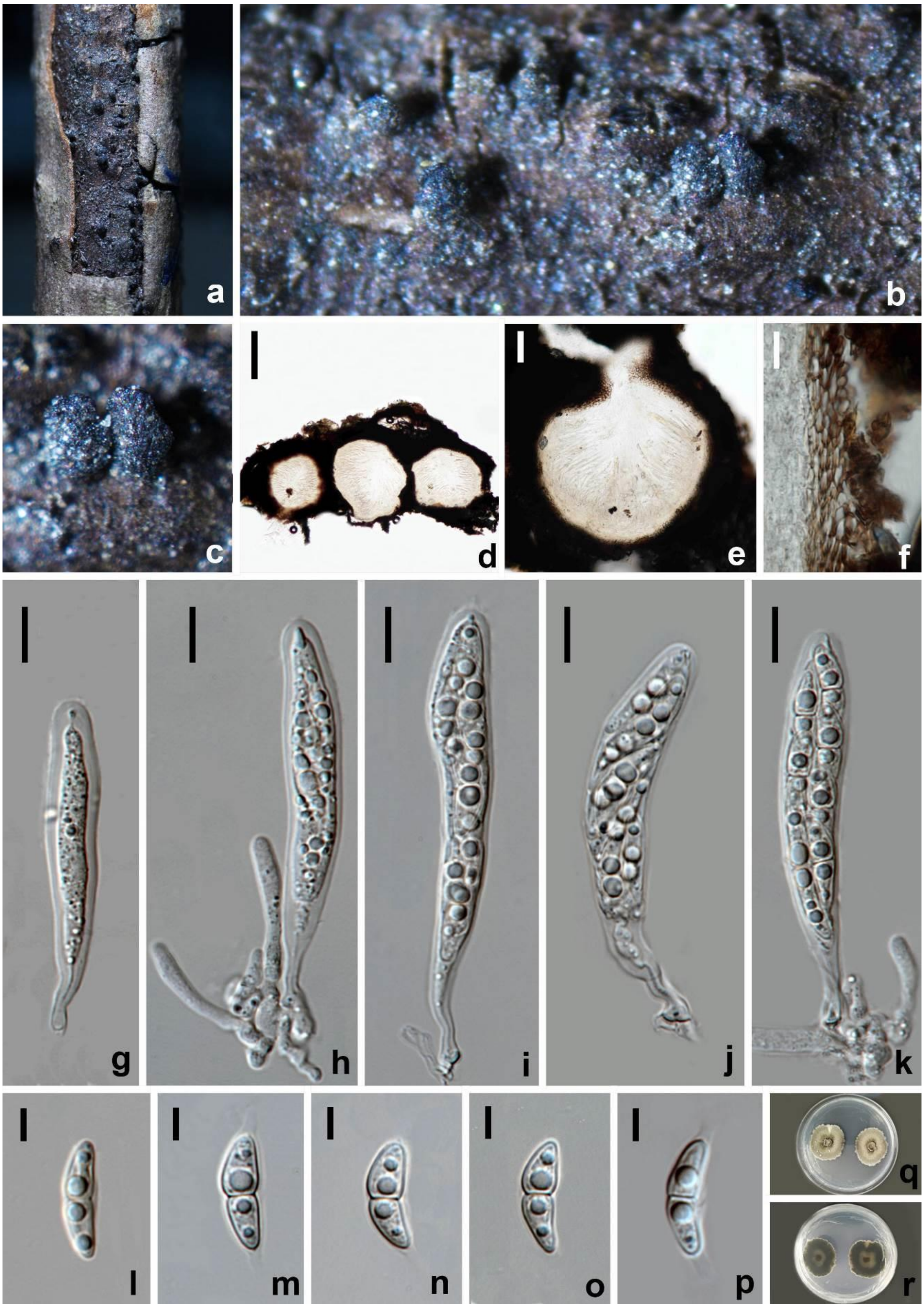

Figure 24 – *Flabellascoma pistaciae* (HKAS 127166, holotype). a–c Appearance of ascomata on host surface. d, e Vertical section through ascomata. f Peridium. g–k Asci. l–p Ascospores. q Colonies on PDA from above. r Colonies on PDA from below. Scale bars: d = 100 µm, e = 50 µm, f–k = 10 µm, l–p = 5 µm.

Notes – In the phylogenetic analysis, *Flabellascoma pistaciae* clustered with *F. fusiforme* with 98% ML/1.00 BYPP support (Fig. 31). *Flabellascoma pistaciae* is morphologically similar to *F. fusiforme* in having superficial, dark brown to black ascomata with crest-like neck, cylindrical-clavate asci and fusiform, hyaline ascospores with a polar sheath. However, *F. pistaciae* differs in having multilocular ascostromata. Additionally, the ascospores of *F. pistaciae* are curved, deeply constricted at the septum, while in *F. fusiforme* they are straight and slightly constricted at the septum.

Lophiostoma chiangraiense (Phukhams. & K.D. Hyde) W.L. Li & Jian K. Liu, comb. nov.

Fig. 25

= *Pseudolophiostoma chiangraiense* Phukhams. & K.D. Hyde, Fungal Diversity 102: 49 (2020)

MycoBank number: MB 849827

Saprobic on decaying branches of *Olea europaea*. Sexual morph: *Ascomata* 300–320 × 180–230 µm ($\bar{x}$ = 310 × 210 µm, n = 10), solitary, scattered, immersed, subglobose or compressed, brown to dark brown, with a well-developed clypeus. *Ostiole* 48.5–66 µm wide, opening by a pore, central, elongated and laterally compressed, irregular walled, black, filled with hyaline periphyses. *Peridium* 36.5–45 µm thick, two layers, outer layer composed of 3(–4) layers of *textura angularis*, dark-walled cells, inner layer composed of small, brown-walled cells of *textura prismatica. Hamathecium* 1.5–2 µm wide, composed of numerous, filamentous, hyaline, branched, septate pseudoparaphyses. *Asci* 86–92.5 × 12–14.5 µm ($\bar{x}$ = 89 × 13.5 µm, n = 20), 8-spored, bitunicate, fissitunicate, cylindric-clavate, with a short pedicel, apically rounded, with a tiny ocular chamber. *Ascospores* 28–30 × 5–6 µm ($\bar{x}$ = 29 × 5.5 µm, n = 20), uniseriate, overlapping, fusiform with acute ends, slightly curved, 1-septate, deeply constricted at the septum, guttulate, smooth-walled, with sheath drawn-out to form polar appendages. Asexual morph: Not observed.

Known distribution – Thailand

Culture characteristics – Ascospores germinate on PDA within 24 h. Colonies growing slowly on PDA, reach 20 mm in 14 d at 25°C, white to pale white, velvety, hairy; reverse olivaceous, with sinuate pale brown edge.

Material examined – China, Sichuan Province, Chengdu city, Shuangliu district, N 30°19'57.04", E 103°59'46.66", elevation 432 m, on a branch of *Olea europaea*, 30 January 2021, W.L. Li, GL 19 (HUEST 23.0037), living culture UESTCC 23.0037.

GenBank numbers – UESTCC 23.0037 = LSU: OR253234, ITS: OR253082, SSU: OR253173, *tef1*: OR262142, *rpb2*: OR262131.

Notes – *Lophiostoma chiangraiense* was originally isolated from *Clematis fulvicoma* and was described and treated in detail in Phukhamsakda et al. (2020). In the phylogeny of the concatenated alignment, our isolate (UESTCC 23.0037) clustered together with the type strain of *L. chiangraiense* with 91% ML/1.00 BYPP support (Fig. 31). Morphologically, the new isolate displays similar morphological characteristics with *L. chiangraiense* in having immersed, subglobose ascomata with a well-developed clypeus, broad cylindrical to cylindrical-clavate asci with furcate pedicel and broad-fusiform, hyaline ascospores with polar appendages. We, therefore, identified the new isolate as *L. chiangraiense,* as the first report in China.

Lophiostoma japonicum (Thambugala,Wanasinghe, Kaz. Tanaka & K.D. Hyde) Andreasen, Jaklitsch & Voglmayr, Persoonia 46: 256 (2021) Fig. 26

= *Biappendiculispora japonica* Thambug. et al., Fungal Diversity 74: 214 (2015)

MycoBank number: MB 838983

Saprobic on decaying branches of *Paeonia suffruticosa*. Sexual morph: *Ascomata* 280–410 × 330–400 µm ($\bar{x}$ = 350 × 370 µm, n = 10), immersed, only the ostiolar neck visible on the host surface, solitary, scattered, unilocular, globose to subglobose, brown to dark brown, papillate, ostiolate. *Ostiole* 75–125 µm wide, central, with crest-like papilla and a pore-like opening. *Peridium* 27.5–41.5 µm thick, comprised of several layers with brown to dark brown cells of *textura angularis*. *Hamathecium* 2.2–3 µm wide, comprising numerous, filiform, broadly cellular pseudoparaphyses, branched and anastomosing, embedded in gelatinous matrix. *Asci* 92–101 × 12–15 µm ($\bar{x}$ = 96.5 × 13.5 µm, n = 20), 8-spored, bitunicate, fissitunicate, cylindrical to cylindric-clavate, with an elongate and cylindrical pedicel, apically rounded with an ocular chamber. *Ascospores* 28–31 × 5–6 µm ($\bar{x}$ = 29.5 × 5.5 µm, n = 20), 1–2 seriate, overlapping, fusiform with acute ends, 5–7-septate, constricted at the septa, guttulate, initially hyaline, becoming yellowish brown at maturity, smooth-walled, with cylindrical appendages at both ends. Asexual morph: Not observed.

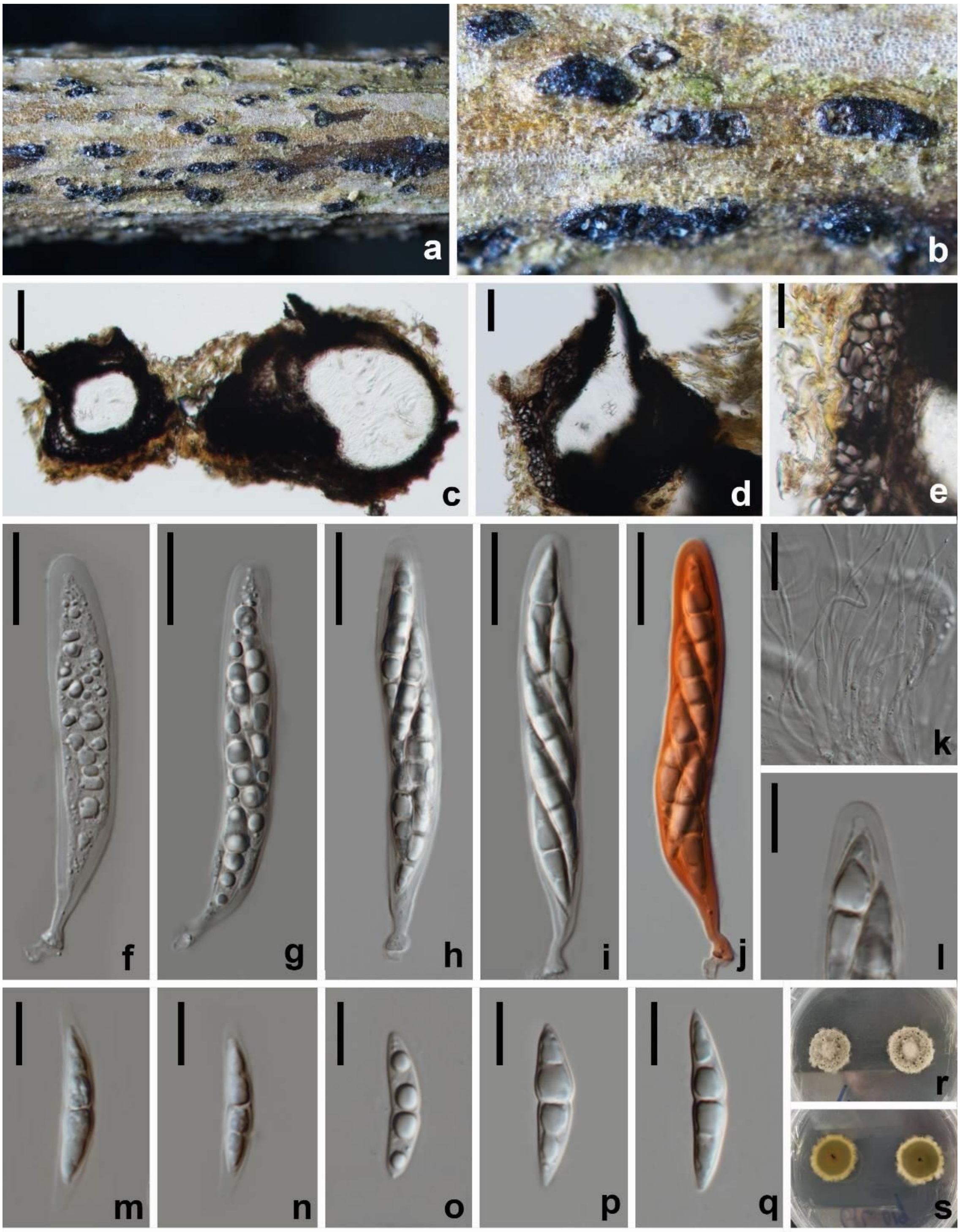

Figure 25 – *Lophiostoma chiangraiense* (HUEST 23.0037). a, b Appearance of ascomata on host surface. c, d Vertical section through ascomata. e Peridium. f–j Asci (j in congo red).

k Hamathecium. l Ocular chamber. m–q Ascospores. r Colonies on PDA from above. s Colonies on PDA from above. Scale bars: c = 100 µm, d = 50 µm, e–k = 20 µm, l–q = 10 µm.

Known distribution – China, Japan

Culture characteristics – Ascospores germinate on PDA within 24 h and germ tubes produced from several septa. Colonies on PDA, flat to effuse, surface white, reverse yellowish-orange, dense, aerial, surface smooth, with an entire edge.

Material examined – China, Sichuan Province, Mianyang city, Youxian district, N 31°25'22.18", E 104°48'57.99", elevation 470 m, on a branch of *Paeonia suffruticosa*, 10 September 2021, W.L. Li, YMD 469 (HUEST 23.0040), living culture UESTCC 23.0040.

GenBank numbers – UESTCC 23.0040 = LSU: OR253234, ITS: OR253143, SSU: OR253214, *tef1*: OR251151, *rpb2*: OR253752.

Notes – *Lophiostoma japonicum* was first described as *Lophiostoma caulium* var. f by Tanaka & Harada (2003). Thambugala et al. (2015) examined the holotype material and established the genus *Biappendiculispora* to accommodate it. Recently, *Biappendiculispora japonica* was transferred as *Lophiostoma japonicum* (Andreasen et al. 2021). In our phylogenetic tree, the new isolate UESTCC 23.0040 clustered together with three strains of *L. japonicum* (KT 573, KT 686-1P and MFLUCC 17-2450) with 89% ML support (Fig. 31). Morphologically, UESTCC 23.0040 shares similar morphological features with the holotype of *L. japonicum* (HHUF 27313) having immersed to semi-immersed ascomata, cylindric-clavate asci and fusiform, 5–7-septate ascospores with appendages at both ends. The length of the appendage is slightly different among the new isolate and the holotype (KT 573) and paratype (MFLUCC 17-2450) of *L. japonica*. The length difference of the appendages appeares to vary depending on the condition of the substrates. Based on morphology and molecular phylogeny, we identify strain UESTCC 23.0040 as *L. japonicum*.

Lophiostoma japonicum was mainly found on herbaceous plants in Japan. Bao et al. (2019) reported this species on decaying wood from a freshwater habitat for the first in China. Here we report *Lophiostoma japonicum* on *Paeonia suffruticosa* for the first time.

Lophiostoma montanae **(**Phukhams. Sue & K.D. Hyde) Andreasen, Jaklitsch & Voglmayr, Persoonia 46: 259 (2021) Fig. 27

= *Sigarispora montanae* Phukhams. Sue et al., Fungal Diversity 102: 55 (2020)

MycoBank number: MB 838991

Saprobic on decaying branches of *Paeonia suffruticosa*. Sexual morph: *Ascomata* 220–240 × 290–330 µm ($\bar{x}$ = 230 × 310 µm, n = 10), solitary, immersed, coriaceous, black, globose to subglobose, ostiolate. *Ostiole* 63.5–83 µm wide, rounded or split-like, central, papillate, with a crest-like apex and a pore-like opening, surrounded by a small blackened pseudoclypeus, irregular walled, filled with hyaline periphyses. *Peridium* 29–38.5 µm wide, wider at the apex, thinner at the base, composed of 6–8 outer layers of brown-walled cells of *textura angularis*. *Hamathecium* 1.5–2.5 µm wide, numerous, filamentous, branched, septate pseudoparaphyses, embedded in a gelatinous matrix. *Asci* 80–88 × 12.5–15 µm ($\bar{x}$ = 84 × 13.5 µm, n = 20), 8-spored, bitunicate, fissitunicate, cylindrical-clavate, with a short and bulbous pedicel, rounded at the apex, with an ocular chamber. *Ascospores* 22–24 × 4.9–5.8 µm ($\bar{x}$ = 23 × 5 µm, n = 20), biseriate, partially overlapping, fusiform, tapering towards the ends, hyaline when young, becoming yellowish brown at maturity, 5-septate, constricted at the middle septum, cells above the middle septum swollen, guttulate, smooth-walled, sheath drawn out 6.9–10.5 µm long at both ends, with a lateral pad-like structure within the sheath, up to 2 µm wide at side. Asexual morph: Not observed.

Known distribution – China, Thailand

Culture characteristics – Ascospores germinate on PDA within 12 h and germ tubes produced from ascospores. Colonies on PDA reach 80 mm in 14 d at 25 °C, circular, with flat surface, white to pale white, with fimbriate edge, smooth; reverse pale brown to yellow. Producing a yellow water-soluble pigment.

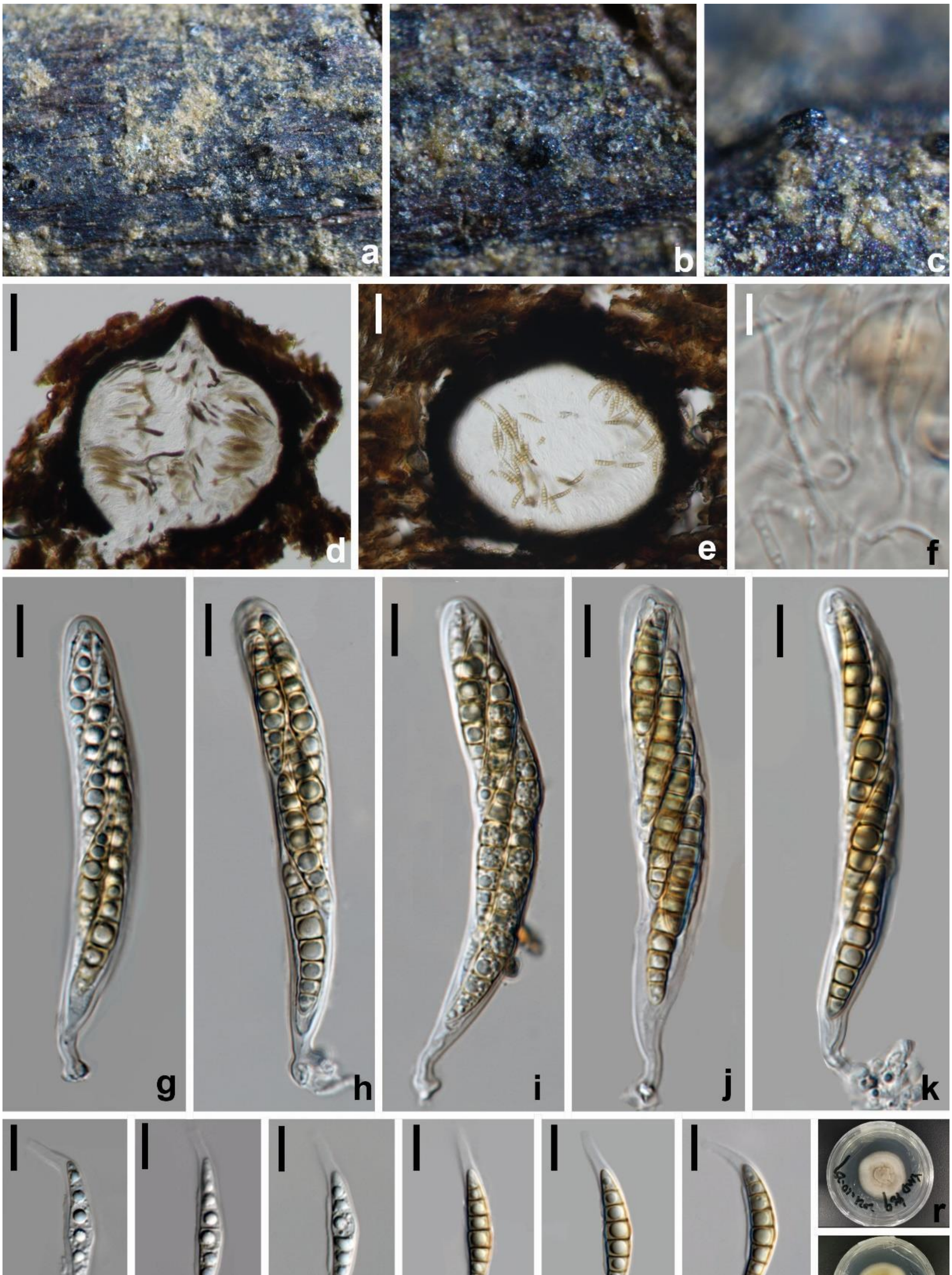

Figure 26 – *Lophiostoma japonicum* (HUEST 23.0040). a–c Appearance of ascomata on host surface. d, e Vertical section through ascomata. f Hamathecium. g–k Asci. l–q Ascospores. r Colony on PDA from above. s Colony on PDA from below. Scale bars: d, e = 50 µm, f, l–q = 10 µm, g–k = 20 µm.

Material examined – China, Sichuan Province, Mianyang city, Youxian district, N 31°25'22.18", E 104°48'57.99", elevation 470 m, on branches of *Paeonia suffruticosa*, 10 September 2021, W.L. Li, YMD 446 (HUEST 23.0038), living culture UESTCC 23.0038; *ibid*., YMD 447 (HUEST 23.0039), living culture UESTCC 23.0039.

GenBank numbers – UESTCC 23.0038 = LSU: OR253296, ITS: OR253137, SSU: OR253209, *rpb2*: OR253750; UESTCC 23.0039 = LSU: OR253297, ITS: OR253138, SSU: OR253210, *tef1* = OR251148, *rpb2*: OR253751.

Notes – *Lophiostoma montanae* was introduced by Phukhamsakda et al. (2020) from dead stems of *Clematis montana*. Two isolates obtained in this study clustered with the ex-type of *L. montanae* (MFLUCC 16-0999) in the phylogenetic analyses of combined ITS, LSU, SSU, *rpb2* and *tef1* sequence data (Fig. 31). We identified our collection as *L. montanae* based on morphology and phylogeny. *Lophiostoma montanae* is reported on *Paeonia suffruticosa* for the first time.

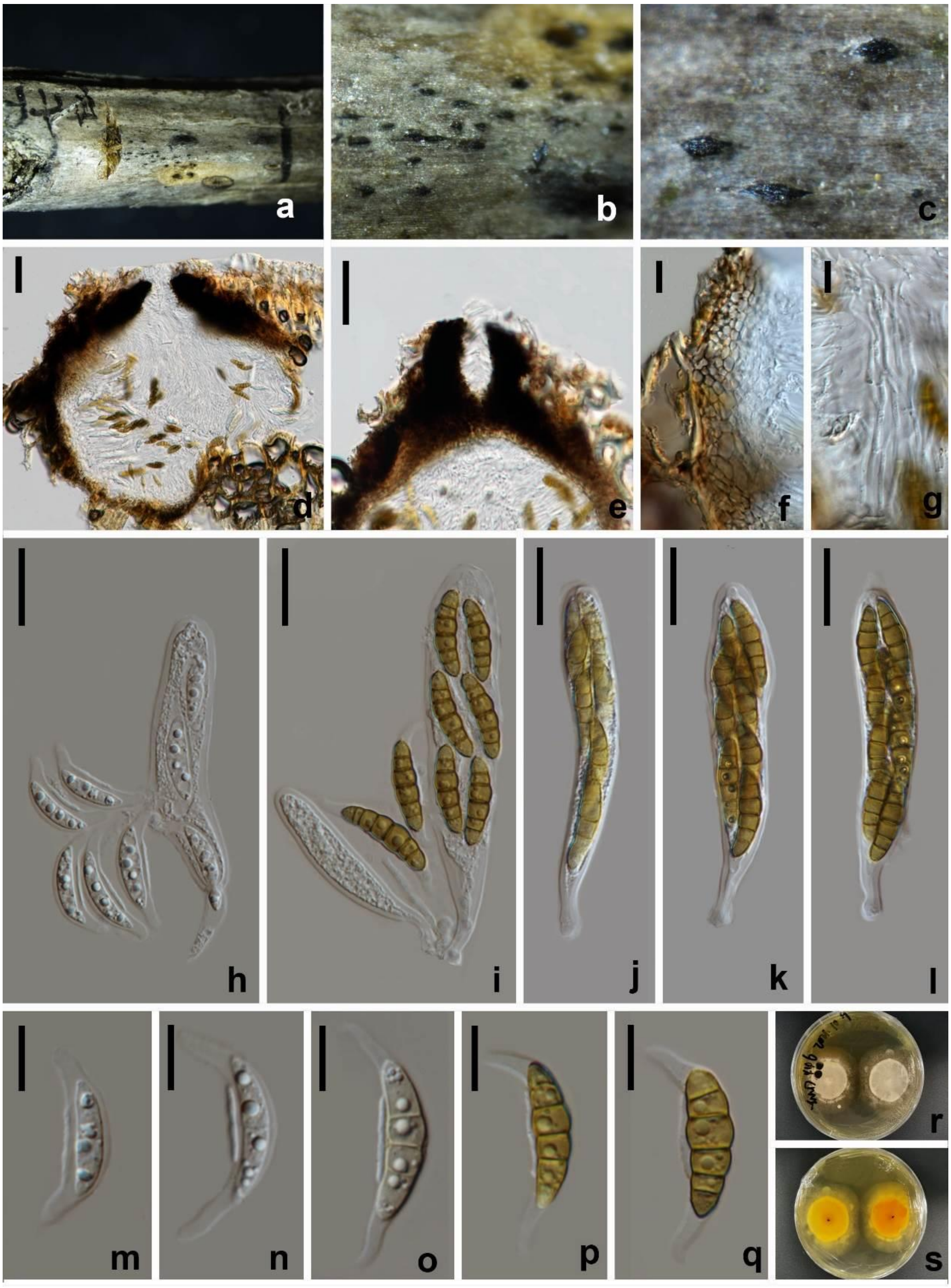

Figure 27 – *Lophiostoma montanae* (HUEST 23.0038). a–c Appearance of ascomata on host

surface. d, e Vertical section through ascomata. f Peridium. g Hamathecium. h–l Asci. m–q Ascospores. r Colonies on PDA from above. s Colonies on PDA from below. Scale bars: d, e = 50 µm, f, g, m–q = 10 µm, h–l = 20 µm.

Lophiostoma oleae W.L. Li & Jian K. Liu sp. nov. Fig. 28

MycoBank number: MB 849152; Facesoffungi number: FoF 14409

Etymology – The specific epithet '*oleae*' refers to the host genus *Olea*, from which the holotype was collected.

Saprobic on decaying branches of *Olea europaea*. Sexual morph: *Ascomata* 190–210 × 110–160 µm ($\bar{x}$ = 200 × 130 µm, n = 10), solitary or in small groups, semi-immersed, globose or subglobose, coriaceous to carbonaceous, dark brown to black, with a developed pseudoclypeus, ostiolate. *Ostiole* 105–129 µm wide, with a crest-like apex and opening by a pore, central, elongated and laterally compressed, surrounded by a small blackened pseudoclypeus, irregular walled, filled with hyaline periphyses. *Peridium* 20–47 µm wide, uniform, wider and heavily pigmented at the apex, composed of 2–3 layers of *textura angularis* and *textura prismatica*. *Hamathecium* 2.4–3.2 µm wide, composed of numerous, dense, filamentous, branched, septate, cellular pseudoparaphyses, embedded in a gelatinous matrix. *Asci* 72–78 × 9.5–12.5 µm ($\bar{x}$ = 75 × 11.5 µm, n = 20) 8-spored, bitunicate, fissitunicate, clavate to cylindrical, with a short pedicel, apically rounded, with an ocular chamber. *Ascospores* 20–22.5 × 3.5–4 µm ($\bar{x}$ = 21 × 3.5 µm, n = 20), biseriate or partially overlapping, hyaline, fusiform, tapering towards the ends, rounded at the end, 1-septate, slightly constricted at the septum, with one guttule in each cell, surrounded by a mucilaginous sheath, 2–2.5 µm thick. Asexual morph: Not observed.

Culture characteristics – Ascospores germinate on PDA within 48 h. Colonies on PDA reach 40 mm diam. in 14 d at 25 °C, circular, effuse, velvety to hairy, initially white, becoming pale brown to dark brown in the centre, yellowish brown in media from below, with dark brown inner circular edge.

Material examined – China, Sichuan Province, Chengdu city, Shuangliu district, N 30°19'57.04", E 103°59'46.66", elevation 432 m, on branches of *Olea europaea*, 30 January 2021, W.L. Li, GL 17 (HKAS 127165, holotype), ex-type culture UESTCC 23.0035 = CGMCC 3.24426; *ibid*., GL 12 (HUEST 23.0036), living culture UESTCC 23.0036.

GenBank numbers – CGMCC 3.24426 = LSU: OR253233, ITS: OR253081, SSU: OR253172, *tef1*: OR262141, *rpb2*: OR262130; UESTCC 23.0036 = LSU: OR253231, SSU: OR253171, *tef1*: OR262139, *rpb2*: OR262129.

Notes – In the phylogenetic analyses, two strains of *Lophiostoma oleae* (CGMCC 3.24426 and UESTCC 23.0036) formed a sister clade to *L. obtusisporum* with 99% ML/1.00 BYPP support (Fig. 31). Morphologically, both *L. oleae* and *L. obtusisporum* share the presence of immersed ascomata with a crest-like neck, cylindrical-clavate asci and fusiform, 1-euseptate, hyaline ascospores. However, *L. oleae* differs from *L. obtusisporum* in having smaller ascomata (190–210 × 110–160 µm vs. 350–400 × 250–350 µm), smaller asci (72–78 × 9.5–12.5 µm vs. 103–140 × 8–15 µm) and smaller ascospores (20–22.5 × 3.5–4 µm vs. 23.5–31.5 × 4–7 µm). Furthermore, the sheath of *L. obtusisporum* extends to form polar appendages with a lateral pad-like structure, while in *L. oleae*, the sheath entirely surrounds the ascospores.

Neovaginatispora fuckelii (Sacc.) A. Hashim., K. Hiray. & Kaz. Tanaka, Studies in Mycology 90: 188 (2018) Fig. 29

MycoBank number: MB 551535

Basionym: *Lophiostoma fuckelii* Sacc., Michelia 1 (no. 3): 336 (1878)

≡ *Vaginatispora fuckelii* (Sacc.) Thambugala, Fungal Diversity 74: 242 (2015)

= *Lophiostoma pulveraceum* Sacc., Michelia 1: 336 (1878)

= *Didymosphaeria lophospora* Sacc. & Speg., Michelia 1: 376 (1878)

= *Lophiosphaera mendax* Rehm, Ann. Myc. 5: 544 (1907)

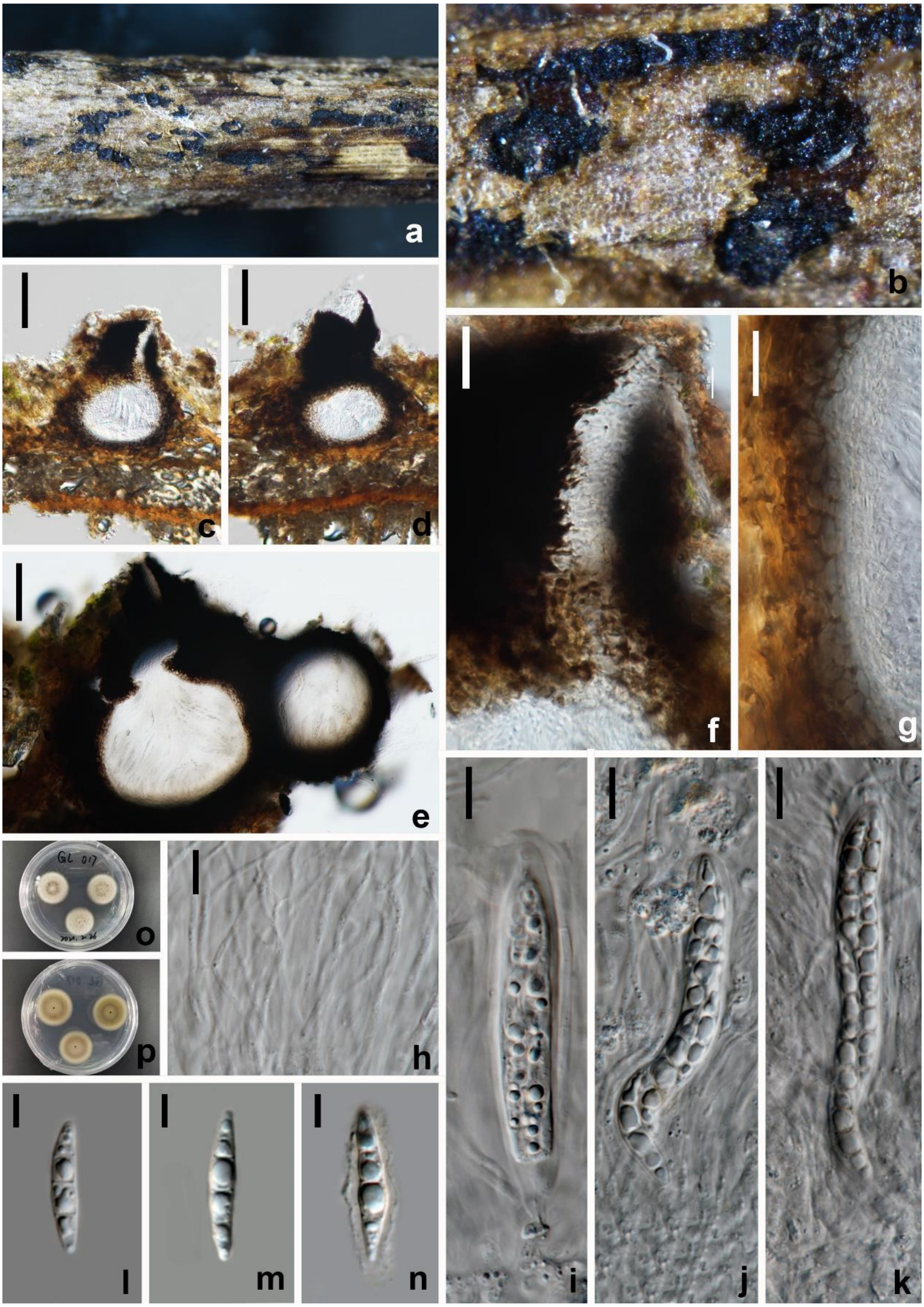

Figure 28 – *Lophiostoma oleae* (HKAS 127165, holotype). a–b Appearance of ascomata on host surface. c–e Vertical section through the ascomata. f Ostiolar canal. g Peridium. h Hamathecium. i–k Asci. l–n Ascospores. o Colonies on PDA from above. p Colonies on PDA from below. Scale bars: c–e = 100 µm, f–k = 10 µm, l–n = 5 µm.

Saprobic on decaying branches of *Camellia oleifera*. Sexual morph: *Ascomata* 120–150 × 130–160 µm ($\bar{x}$ = 145 × 145 µm, n = 10), immersed, only the ostiolar necks visible on the host surface, solitary, scattered, unilocular, globose to subglobose, brown to dark brown, papillate, ostiolate. *Ostiole* 49–58 µm wide, central, filled with hyaline periphyses. *Peridium* 10–15 µm thick, two layers, outer layer composed of brown to dark brown, thick-walled cells of *textura angularis*; inner layer composed of hyaline to lightly pigmented cells of *textura prismatica*. *Hamathecium* 1.8–2.2 µm wide, comprising numerous, filiform, hyaline, anastomosed pseudoparaphyses, guttulate. *Asci* 65–74 × 7–8 µm ($\bar{x}$ = 69.5 × 7.5 µm, n = 20), 8-spored, bitunicate, fissitunicate, cylindrical to clavate, with elongate and cylindrical pedicel, apically rounded, with a minute ocular chamber. *Ascospores* 14.5–16.5 × 3–4 µm ($\bar{x}$ = 15.5 × 3.5 µm, n = 20), 1–2 seriate, partially overlapping, hyaline, fusiform, with obtuse ends, 1–3-septate at median, constricted at the septa, straight or slightly curved, smooth-walled, guttulate, with cap-like, globose appendages at each end. Asexual morph: Not observed.

Known distribution –China, Germany, Japan, Sweden, Switzerland, UK.

Culture characteristics – Ascospores germinate on PDA within 48 h at 25 °C. Colonies on PDA reach 20 mm after 14 d at 25 °C, cream-gray, circular, rough and flat on the surface, with slightly radial striations, without aerial mycelium; reverse pale brown.

Material examined – China, Sichuan Province, Leshan city, Wutongqiao district, N 29°24'43.82", E 103°49'38.12", elevation 365 m, on a branch of *Camellia oleifera*, 23 July 2021, W.L. Li, YC 352 (HUEST 23.0047), living culture UESTCC 23.0047; *ibid*., Shizhong district, N 29°42'44.34", E 103°52'41.80", elevation 444 m, on branches of *Paeonia suffruticosa*, 3 July 2021, W.L. Li, YMD 344 (HUEST 23.0046), living culture UESTCC 23.0046; *ibid*., YMD 370 (HUEST 23.0043), living culture UESTCC 23.0043; *ibid*., Mianyang city, Youxian district, N 31°25'22.18", E 104°48'57.99", elevation 470 m, on branches of *Paeonia suffruticosa*, 23 July 2021, W.L. Li, YMD 445 (HUEST 23.0041), living culture UESTCC 23.0041; *ibid*., YMD 471 (HUEST 23.0044), living culture UESTCC 23.0044; *ibid*., Chengdu city, Jintang county, N 30°35'16.3032", E 104°43'59.0304", elevation 509 m, on a branch of *Idesia polycarpa*, 13 August 2021, W.L. Li, STZ 387 (HUEST 23.0042), living culture UESTCC 23.0042; *ibid*., Guangyuan city, Chaotian district, N 32°41.08′, E 106°45.15′, elevation 707 m, on a branch of *Juglans nigra*, 19 April 2021, W.L. Li, 221 (HUEST 23.0045), living culture UESTCC 23.0045.

GenBank numbers – UESTCC 23.0041 = LSU: OR253295, ITS: OR253136, SSU: OR253208, *rpb2*: OR253749; UESTCC 23.0042 = LSU: OR253291, ITS: OR253132, SSU: OR253204, *tef1*: OR263567, *rpb2*: OR253748; UESTCC 23.0043 = LSU: OR253289, ITS: OR253130, SSU: OR253202, *tef1*: OR251178; UESTCC 23.0044 = LSU: OR253303, ITS: OR253144, SSU: OR253215, *tef1*: OR251152; UESTCC 23.0045 = LSU: OR253271, ITS: OR253115, SSU: OR251165; UESTCC 23.0046 = LSU: OR253285, ITS: OR253126, SSU: OR253199, *tef1*: OR251174, *rpb2*: OR251144; UESTCC 23.0047 = LSU: OR253287, ITS: OR253128, *tef1*: OR251176, *rpb2*: OR251146

Notes – *Neovaginatispora fuckelii* was introduced by Hashimoto et al. (2018) and was previously misidentified with the genus *Lophiostoma*. Thambugala et al. (2015) transferred *Lophiostoma fuckelii* to the genus *Vaginatispora* based on "*Lophiostoma fuckelii* JCM 17672" which formed a sister clade with *V. aquatica.* Later, *Vaginatispora fuckelii* was excluded from *Vaginatispora* and transferred to the genus *Neovaginatispora* by Hashimoto et al. (2018). *Neovaginatispora fuckelii* has a wide geographical distribution in the Northern Hemisphere (Wang et al. 2004, Thambugala et al. 2015, Tennakoon et al. 2018) and has been reported from both aquatic and terrestrial habitats (Bao et al. 2019).

In the phylogenetic analyses, seven strains isolated from *Camellia oleifera*, *Idesia polycarpa*, *Juglans nigra* and *Paeonia suffruticosa* grouped with the clade of *Neovaginatispora fuckelii* (Fig. 31). The new collection (UESTCC 23.0047) is morphologically similar to *N. fuckelii* in having immersed to erupment ascomata, cylindrical to clavate asci, and 1-septate, hyaline, fusiform ascospores with globose appendages at both ends. To our knowledge, these are the first records of *N. fuckelii* on *Camellia oleifera*, *Idesia polycarpa*, *Juglans nigra* and *Paeonia suffruticosa* in China.

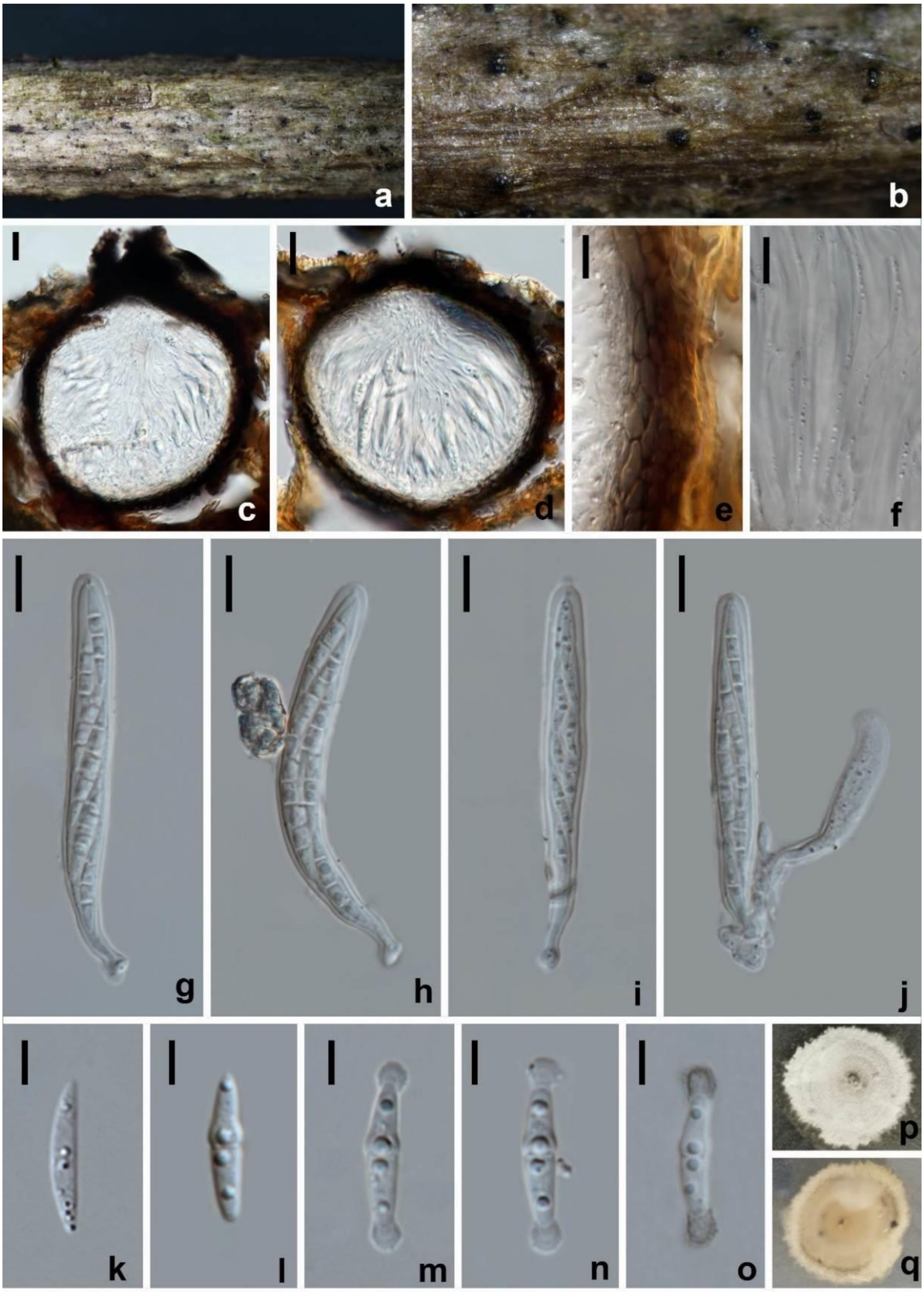

Figure 29 – *Neovaginatispora fuckelii* (HUEST 23.0047). a, b Appearance of ascomata on host surface. c, d Vertical section through ascomata. e Peridium. f Hamathecium. g–j Asci. k–o Ascospores. p Colony on PDA from above. q Colony on PDA from below. Scale bars: c, d = 20 µm, e–j = 10 µm, k–o = 5 µm.

Oleaginea W.L. Li & Jian K. Liu, gen. nov.

MycoBank number: MB 849150; Facesoffungi number: FoF 14411

Etymology – Name reflects the host genus, *Olea* from which the holotype was collected.

Type species – *Oleaginea sichuanensis*

Saprobic on decaying wood. Sexual morph: *Ascomata* solitary or in small groups, uniloculate, immersed to semi-immersed, globose to subglobose, coriaceous, dark brown to black, papillate, ostiolate. *Ostiole* central, dark brown, filled with short periphyses. *Peridium* multilayered, composed of dark brown cells of *textura prismatica*, outer layer heavily pigmented, the inner layer hyaline. *Hamathecium* filiform, unbranched, septate, hyaline, smooth, cellular pseudoparaphyses. *Asci* 8-spored, bitunicate, fissitunicate, clavate, with a short pedicel, apically rounded, with an ocular chamber. *Ascospores* biseriate, fusiform to ellipsoid, hyaline, septate, deeply constrict at the septum, with large guttules in each cell, smooth. Asexual morph: Not observed.

Notes – *Oleaginea* is established herein as a monotypic genus in Lophiostomataceae to accommodate *Oleaginea sichuanensis*, which was isolated from *Olea europaea* in Sichuan Province, China. *Oleaginea* mainly differs from other genera in Lophiostomataceae in having hyaline, 1-septate, broadly fusiform to ellipsoid ascospores, lacking a mucilaginous sheath and terminal appendages. In our phylogenetic tree, though *O. sichuanensis* forms a sister clade to the *Dimorphiopsis* clade, species residing in these two clades are morphologically distinct. Therefore, a new genus is introduced to accommodate *O. sichuanensis*.

Oleaginea sichuanensis W.L. Li & Jian K. Liu, sp. nov. Fig. 30

MycoBank number: MB 849151; Facesoffungi number: FoF 14412

Etymology – 'sichuanensis' refers to Sichuan Province, where the species was collected.

Saprobic on decaying branches of *Olea europaea*. Sexual morph: *Ascomata* 350–420 × 300–320 µm ($\bar{x}$ = 390 × 310 µm, n = 10), solitary or in small groups, uniloculate, immersed to semi-immersed, globose to subglobose, coriaceous, dark brown to black, rough-walled, papillate, ostiolate. *Ostiole* 106–118 µm wide, central, dark brown, filled with short periphyses. *Peridium* 25–33 µm wide, multilayered, composed of 3–4 layers of dark brown cells of *textura prismatica*, outer layer heavily pigmented, the inner layer hyaline. *Hamathecium* 1.5–2.2 µm wide, filiform, unbranched, septate, hyaline, smooth, cellular pseudoparaphyses. *Asci* 106–121 × 14.5–18.5 µm ($\bar{x}$ = 113.5 × 16.5 µm, n = 20), 8-spored, bitunicate, fissitunicate, clavate, short pedicellate, apically rounded, with an ocular chamber. *Ascospores* 21.5–27 × 6–7.5 µm ($\bar{x}$ = 24 × 6.5 µm, n = 20), biseriate, broad fusiform to ellipsoid, ends rounded, hyaline, 1-septate, deeply constrict at the septum, containing four refractive globules, smooth. Asexual morph: Not observed.

Culture characteristics – Ascospores germinate on PDA within 72 h and germ-tube is produced from the septum of ascospore. Colonies on PDA reach 20 mm diam. after 21 d at 25 °C, colonies circular, medium dense, velvety to woolly, white to pale yellowish; from below white to light brown, no pigmentation on agar.

Material examined – China, Sichuan Province, Chengdu city, Pidu district, N 30°19'57.04", E 103°59'46.66", elevation 432 m, on branches of *Olea europaea*, 30 January 2021, W.L. Li, GL 35 (HKAS 127167, holotype), ex-type culture CGMCC 3.24427 = UESTCC 23.0052.

GenBank numbers – CGMCC 3.24427 = LSU: OR253236, ITS: OR253084, *tef1*: OR262145, rpb2: OR262132; UESTCC 23.0052 = LSU: OR253237, ITS: OR253085, *tef1*: OR262147, rpb2: OR262133.

Notes – The BLASTn searches of the LSU sequence of *Oleaginea sichuanensis* resulted in 95.78% similarity with *Lophiostoma alpigenum* (GKM 1091b) and *L. quadrinucleatum* (GKM 1233). The ITS showed 82.99% similarity with *Dimorphiopsis brachystegiae* (327/394, 29 gaps). *tef1* BLASTn results appeared 92.14% similarity with *Lophiostoma arundinis* (AFTOL-ID 1606) while the *rpb2* BLASTn results indicated 83.51% similarity with *Lophiostoma compressum* (OF 256913). The multi-gene analyses implied *O. sichuanensis* within Lophiostomataceae and sister to *Dimorphiopsis brachystegiae* (Fig. 31). *Dimorphiopsis* comprises only one species and it is pathogenic on leaves of *Brachystegia spiciformis* (Fabaceae) in Zambia. However, no sexual morph was reported in this genus (Crous et al. 2013). *Oleaginea sichuanensis* mainly differs from other genera in Lophiostomataceae in having hyaline, 1-septate, broadly fusiform to ellipsoid ascospores, lacking a mucilaginous sheath and terminal appendages.

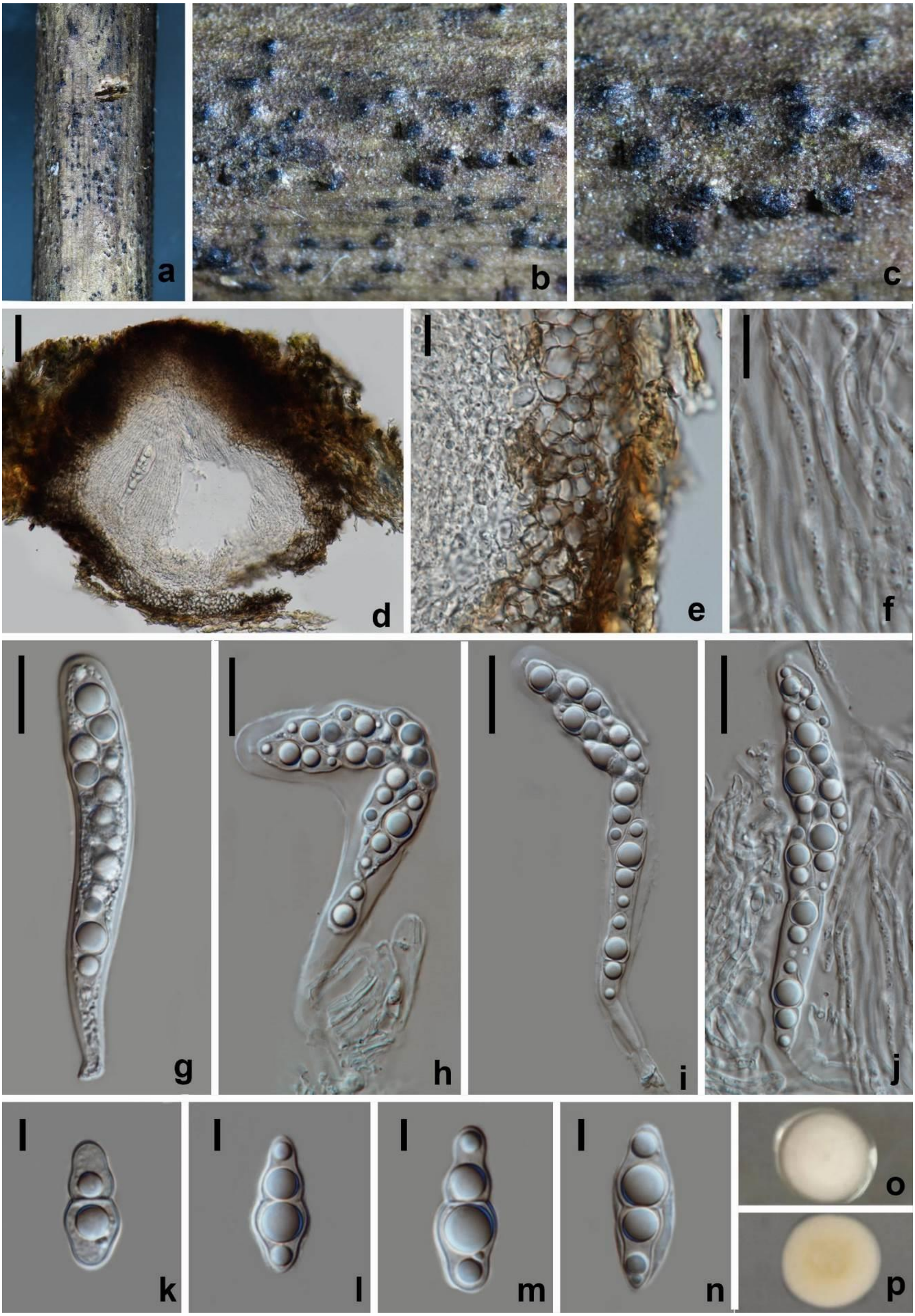

Figure 30 – *Oleaginea sichuanensis* (HKAS 127167, holotype). a–c Appearance of ascomata on host surface. d Vertical section through ascoma. e Peridium. f Hamathecium. g–j Asci. k–n Ascospores. o Colony on PDA from above. p Colony on PDA from below Scale bars: d = 50 μm, e, f = 10 μm, g–j = 20 μm, k–n = 5 μm.

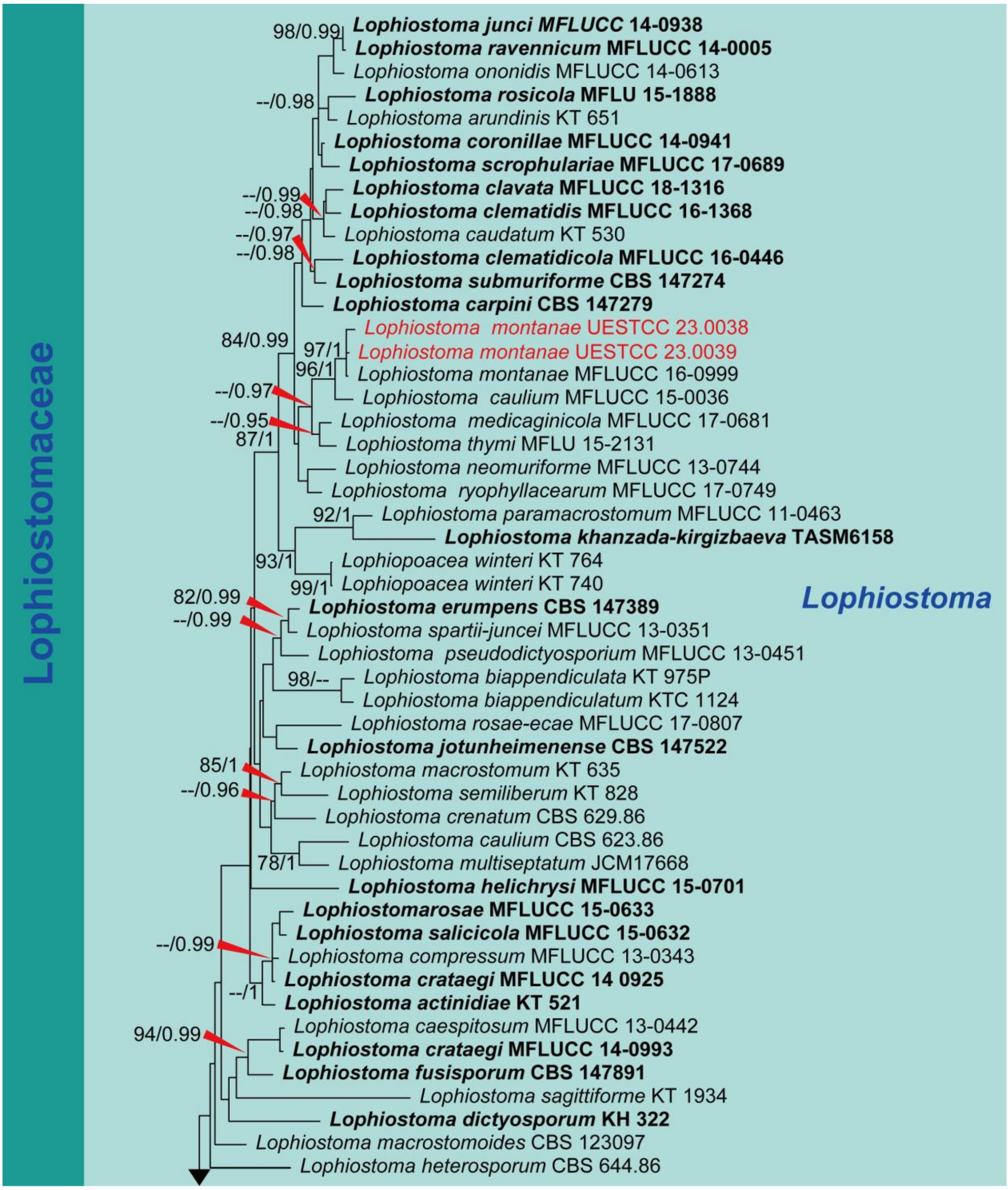

Figure 31 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, SSU and *tef1* sequence data. One hundred and forty-one strains are included in the combined sequence analyses, which comprise 4,301 characters with gaps. *Cryptocoryneum japonicum* HHUF 30482, *C. japonicum* KT3300 and *C. pseudorilstonei* CBS 113641 are used as outgroup taxa. Tree topology of ML analysis is similar to BI analysis. The best scoring RAxML tree with a final likelihood value of -48277.416310 is presented. Proportion of gaps and completely undetermined characters in this alignment are 25.27% with 2,153 distinct alignment patterns. Estimated base frequencies were as follows; A = 0.248841, C = 0.247651, G = 0.267841, T = 0.235668; substitution rates AC = 1.520871, AG = 3.839654, AT = 1.386573, CG = 1.342904, CT = 8.732284, GT = 1.000000; gamma distribution shape parameter α = 0.508101. Bootstrap support values for ML ≥ 75% and BYPP ≥ 0.95 are defined as ML/BYPP above the nodes. Hyphens (--) represent support values less than 75% in ML and 0.95 in BI. Newly generated sequences are in red and ex-type strains are in bold.

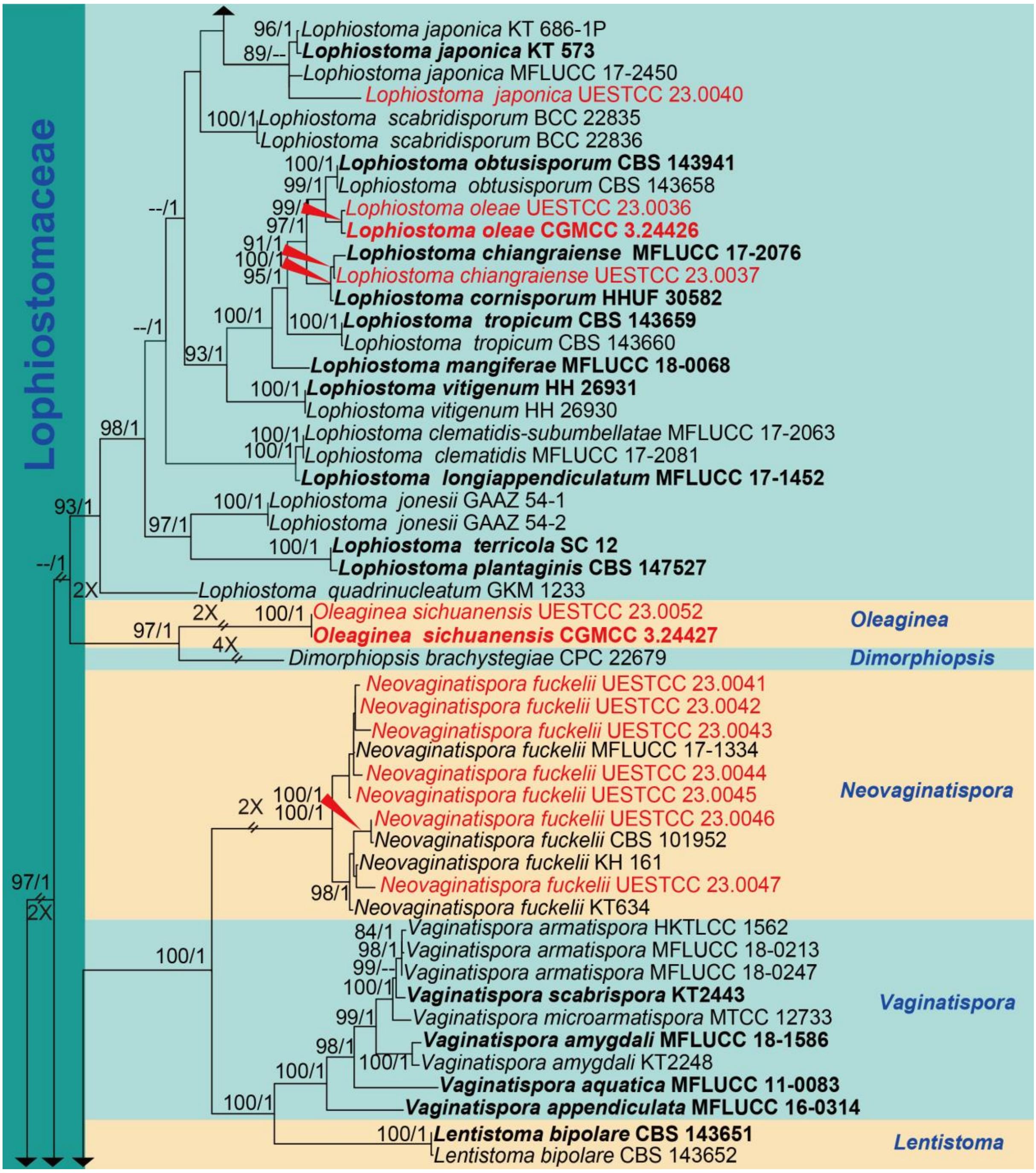

Figure 31 – Continued.

Macrodiplodiopsidaceae Voglmayr, Jaklitsch & Crous, IMA Fungus 6(1): 178 (2015).

MycoBank number: MB 812794; Facesoffungi number: FoF 08291

Note – Macrodiplodiopsidaceae, typified by *Macrodiplodiopsis* with *Macrodiplodiopsis desmazieri*, was introduced by Crous et al. (2015) to accommodate *Macrodiplodiopsis* and *Pseudochaetosphaeronema*. Later, *Camarographium* and *Pseudomonodictys* were introduced in this family (Ariyawansa et al. 2015, Tanaka et al. 2015). However, *Camarographium* was classified into Pleosporales genera *incertae sedis* while *Pseudomonodictys* was allocated to the family Parabambusicolaceae. Later, Wijayawardene et al. (2022) accepted *Macrodiplodiopsis* and *Pseudochaetosphaeronema* in Macrodiplodiopsidaceae. Species of Macrodiplodiopsidaceae have a cosmopolitan distribution on a wide range of plant hosts, encompassing endophytes, saprobes and plant pathogens (Zhang et al. 2016, Hyde et al. 2020). Intriguingly, some species are known to cause infections in humans (Ahmed et al. 2014).

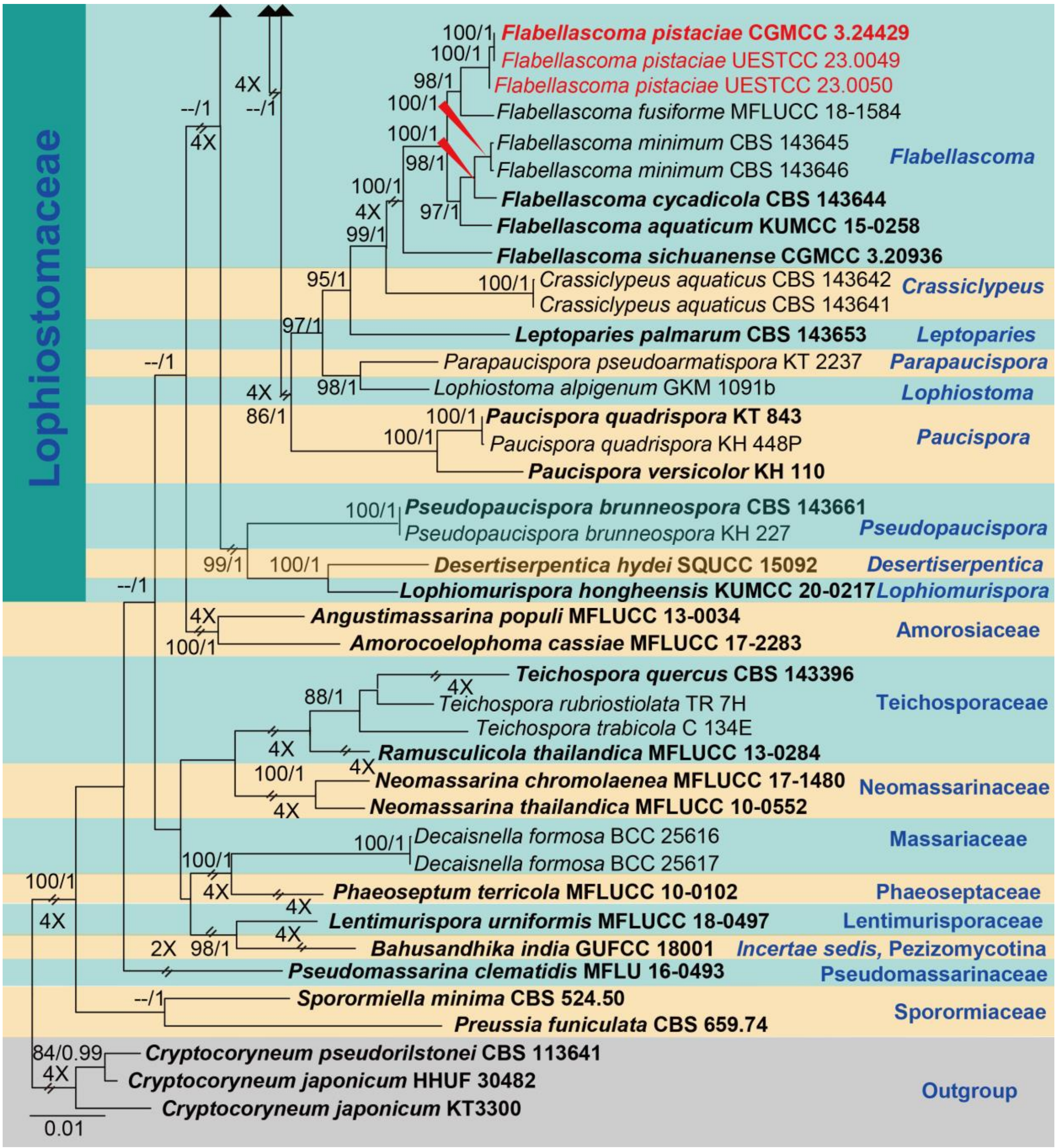

Figure 31 – Continued.

Pseudochaetosphaeronema chiangraiense Wijesinghe, Boonmee & K.D. Hyde, Fungal Divers 111: 75 (2021) Fig. 32

MycoBank number: MB 558549

Saprobic on decaying branches of *Olea europaea*. Sexual morph: *Ascomata* 260–280 × 190–210 µm ($\bar{x}$ = 270 × 200 µm, n = 10), solitary, scattered, immersed, uniloculate, black, globose to subglobose, coriaceous. *Peridium* 27.5 × 36 µm thick, comprising two layers, outer layer heavily pigmented, comprising blackish to dark brown cells of *textura angularis*, inner layer composed of pale brown, thin-walled cells of *textura angularis*. *Hamathecium* 2–3 µm wide, comprising numerous, filamentous, unbranched, septate pseudoparaphyses. *Asci* 83–102 × 23.5–28 µm ($\bar{x}$ = 92.5 × 25.5 µm, n = 20), 8-spored, bitunicate, fissitunicate, cylindrical to clavate, with a short pedicel, apically rounded, with a well-developed ocular chamber. *Ascospores* 28.5–29 × 7.5–10.5 µm ($\bar{x}$ = 28.5 × 9 µm, n = 20), overlapping 2–3 seriate, broadly fusiform, with obtuse ends, hyaline, medially 1-septate, deeply constricted at the septum, guttulate, thick- and smooth-walled. Asexual morph: Not observed.

Known distribution – Thailand

Culture characteristics – Ascospores germinate on PDA within 48 h and germ tubes produced from all sides. Colonies on PDA reach 20 mm diam. after 14 d at 25 °C, colonies circular to irregular, medium dense, flat or effuse, slightly raised, with sinuate edge, fluffy, gray-white; reverse dark brown; not producing pigments in agar.

Material examined – China, Sichuan Province, Chengdu city, Shuangliu district, N 30°19'57.04", E 103°59'46.66", elevation 438 m, on a branch of *Olea europaea*, 27 March 2021, W.L. Li, GL 143 (HUEST 23.0065), living culture UESTCC 23.0065.

GenBank numbers – UESTCC 23.0065 = LSU: OR253260, ITS: OR253108, SSU: OR253186, *tef1*: OR251160.

Figure 32 – *Pseudochaetosphaeronema chiangraiense* (HUEST 23.0065). a–d Appearance of ascomata on host surface. e Hamathecium. f Vertical section through ascoma. g Peridium, h–l Asci. m–p Ascospores. q Colonies on PDA from above. r Colonies on PDA from below. Scale bars: d = 50 µm, e–j = 10 µm, k–n = 5 µm.

Notes – *Pseudochaetosphaeronema chiangraiense* was introduced by Boonmee et al. (2021) from dead leaves of *Tamarindus* sp. in Thailand. It was characterized by immersed, uniloculate ascomata, cylindrical to obclavate asci with short pedicel and 1-septate, thick-walled, fusiform ascospores with pointed ends. Our new isolate UESTCC 23.0065 resembles *P. chiangraiense* in terms of the shape and size of ascospores, asci and ascomata. While the new collection displays more characters (e. g. ascospore can produce yellow pigments when mature), a feature not observed in *P. chiangraiense* (MFLU 21-0083). In the multi-gene phylogenetic analysis, our new collection clustered with the ex-type strain of *P. chiangraiense* with full bootstrap support (100% ML/1.00 BYPP) (Fig. 34). There are no base pair differences of the ITS nucleotides which confirmed that the new collection is *P. chiangraiense* (Jeewon & Hyde 2016). Thus, *P. chiangraiense* is reported as a new report from China on *Olea europaea*.

Pseudochaetosphaeronema magnoliae N.I. de Silva, Lumyong & K.D. Hyde, Mycosphere 13(1): 985 (2022) Fig. 33

MycoBank number: MB 559518; Facesoffungi number: FoF 10716

Saprobic on decaying branches of *Olea europaea*. Sexual morph: Not observed. Asexual morph: *Conidiomata* 160–180 × 120–140 µm ($\bar{x}$ = 170 × 130 µm, n = 10), superficial, scattered, gregarious, hemispherical, black, glabrous, apapillate, inconspicuous ostiolate. *Conidiomatal wall* 42–50 µm wide, with 2 strata, composed of several layers of brown to dark brown cells of *textura angularis*, heavily pigmented towards the outer layers. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 9–10 × 2–3 µm ($\bar{x}$ = 9.5 × 2.5 µm, n = 20), hyaline, enteroblastic, phialidic, ampulliform to subcylindrical or lageniform, with a moderate periclinal thickening in collarette zone, indeterminate, thick- and smooth-walled. *Conidia* 20–23 × 4.5–7 µm ($\bar{x}$ = 21.5 × 6 µm, n = 20), hyaline, guttulate, fusiform, with a rounded or obtuse apex and a truncate base, straight, aseptate, thick- and smooth-walled.

Known distribution – Thailand

Culture characteristics – Conidia germinate on PDA within 24 h. Germ tubes produced from both ends of conidia. Colonies on PDA reach 20 mm diam. after 14 d at 25 °C, colonies circular, medium dense, flat or effuse, slightly raised, with an irregular edge, gray white; reverse blackish brown; not producing pigments in agar.

Material examined – China, Sichuan Province, Chengdu city, Shuangliu district, N 30°19'57.04", E 103°59'46.66", elevation 445 m, on branches of *Olea europaea*, 24 August 2021, W.L. Li, GL 426 (HKAS 127169), living culture UESTCC 23.0064 = CGMCC 3.24436; *ibid*., GL 427 (HUEST 23.0063), living culture UESTCC 23.0063; *ibid*., GL 417 (HUEST 23.0062), living culture UESTCC 23.0062.

GenBank numbers – CGMCC 3.24436 = LSU: OR253293, ITS: OR253134, SSU: OR253206; UESTCC 23.0062 = LSU: OR253292, ITS: OR253133, SSU: OR253205, *tef1*: OR263568; UESTCC 23.0063 = LSU: OR253294, ITS: OR253135, SSU: OR253207, *tef1*: OR263569.

Notes – The morphological characteristics of our collection resembles *Pseudochaetosphaeronema magnoliae* having uniloculate, globose to subglobose pycnidia, enteroblastic, and cylindrical conidiogenous cells and aseptate, hyaline conidia with several guttules. Multi-gene phylogeny indicates that our collection clusters with the ex-type of *P. magnoliae* (MFLUCC 18-0707) with 100% ML/1.00 BYPP support (Fig. 34). Therefore, we report our collection as a new host record of *P. magnoliae* from *Olea europaea* in China.

Neohendersoniaceae A. Giraldo & Crous, Mycol. Progr. 16: 343 (2017)

MycoBank number: MB 818515; Facesoffungi number: FoF 07373

Notes – Neohendersoniaceae was introduced by Giraldo et al. (2017) with *Neohendersonia* as the type genus. Tanaka et al. (2017) accepted *Brevicollum*, *Crassiparies*, *Medicopsis* and *Neohendersonia* in this family based on phylogenetic analysis. Crous et al. (2019) introduced *Neomedicopsis* in Neohendersoniaceae, which has a close phylogenetic relation to the genus

Medicopsis. In this study, a new genus *Neobrevicollum* and a new host record of *Crassiparies quadrisporus* are introduced.

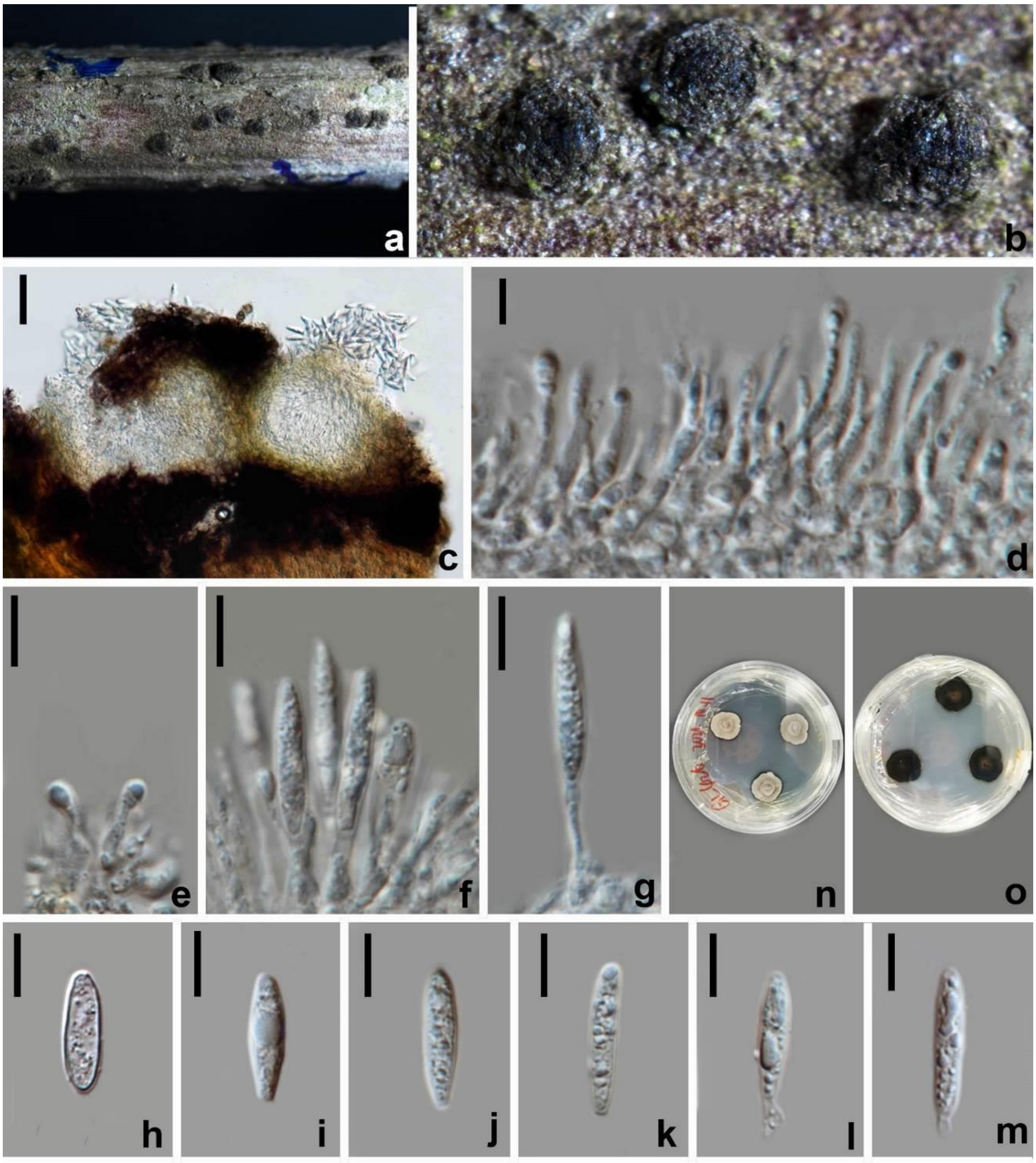

Figure 33 – *Pseudochaetosphaeronema magnoliae* (HKAS 127169). a, b Appearance of conidiomata on natural substrate. c Vertical section of conidiomata. d–g Conidiogenous cells and developing conidia. h–m Conidia. n Colonies on PDA from above. o Colonies on PDA from below. Scale bars: c = 50 µm, d–m = 10 µm.

Crassiparies quadrisporus M. Matsum, K. Hiray & Kaz. Tanaka, Fungal Diversity 78: 63 (2016)
Fig. 35

MycoBank number: MB 825295

Saprobic on decaying branches of *Olea europaea*. Sexual morph: *Ascomata* 270–300 × 230–300 µm ($\bar{x}$ = 280 × 270 µm, n = 10), immersed, scattered, solitary, globose or subglobose, brown to dark brown. *Ostiole* 48–51 µm wide, central. *Peridium* 30–49 µm thick, multi-layered, outer layer comprising dark brown, thick-walled cells of *textura angularis*, inner layer composed of pale brown, thin-walled cells of *textura angularis*. *Hamathecium* 2–2.5 µm wide, numerous, cylindrical, hyaline, rarely branched. *Asci* 75–80 × 16.5–18 µm ($\bar{x}$ = 77.5 × 17 µm, n = 20), 4-spored, bitunicate, fissitunicate, clavate, with elongate pedicel. *Ascospores* 26–30 × 6.5–7.5 µm ($\bar{x}$ = 28 × 7 µm, n = 20), 1–2 seriate, partially overlapping, hyaline, broadly fusiform, 1–3-septate, deeply constricted at the middle septa, smooth-walled. Asexual morph: Not observed.

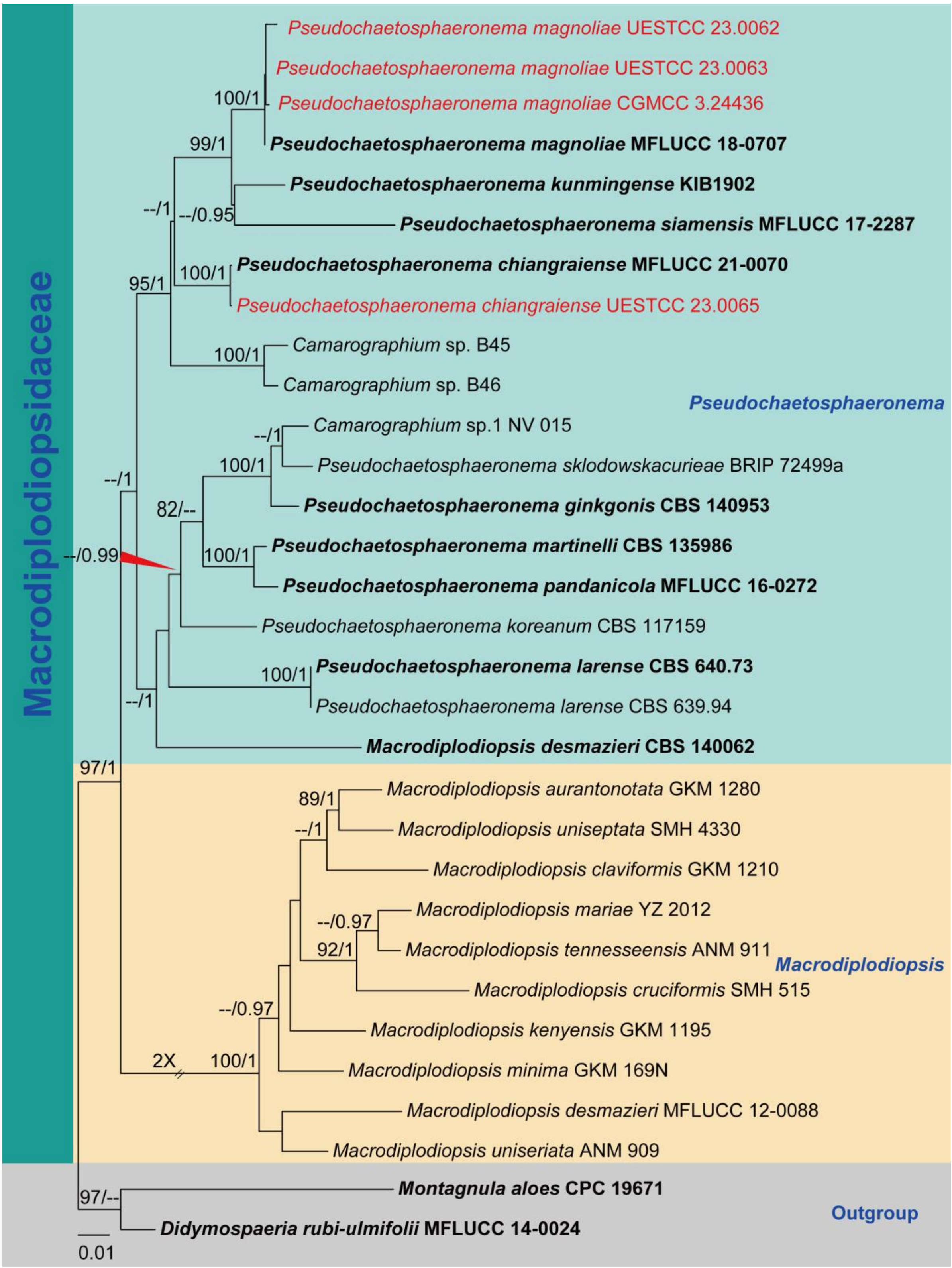

Figure 34 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, SSU and *tef1* sequence data. Thirty-one strains are included in the combined sequence analyses, which comprise 3,329 characters with gaps. *Didymosphaeria rubi-ulmifolii* MFLUCC 14-0024 and *Montagnula aloes* CPC 19671 are used as outgroup taxa. Tree topology of ML analysis is similar to

BI analysis. The best scoring RAxML tree with a final likelihood value of -11405.554410 is presented. Proportion of gaps and completely undetermined characters in this alignment are 37.46% with 742 distinct alignment patterns. Estimated base frequencies were as follows; A = 0.240052, C = 0.249934, G = 0.275173, T = 0.234841; substitution rates AC = 1.335876, AG = 3.576916, AT = 2.022954, CG = 1.410021, CT = 11.118337, GT = 1.000000; gamma distribution shape parameter α = 0.532606. Bootstrap support values for ML $\geq$ 75% and BYPP $\geq$ 0.95 are defined as ML/BYPP above the nodes. Hyphens (--) represent support values less than 75% in ML and 0.95 in BI. Newly generated sequences are in red and ex-type strains are in bold.

Known distribution – China, Japan, Thailand

Culture characteristics – Colonies on PDA reach 20 mm diam. after 14 d at 25 °C, colonies pale brown, circular, entire margin, slightly raised, flat and rough on the surface, dense at the centre; reverse, dark brown from the centre of the colony, gray white at margin.

Material examined – China, Sichuan Province, Chengdu city, Shuangliu district, N 30°19'57.04", E 103°59'46.66", elevation 438 m, on a branch of *Olea europaea*, 27 March 2021, W.L. Li, GL 137 (HUEST 23.0066), living culture UESTCC 23.0066.

GenBank numbers – UESTCC 23.0066 = LSU: OR253259, ITS: OR253107, SSU: OR253185, *tef1*: OR251159.

Notes – *Crassiparies quadrisporus* was introduced by Li et al. (2016) from dead twigs of *Acer* sp. in Japan, and was characterized by immersed to superficial ascomata, scattered or in groups of 2–3, 2-strata peridium, 4-spored asci and 2-celled, broadly fusiform ascospores. Senwanna et al. (2021) observed *C. quadrisporus* on twigs of *Hevea brasiliensis* while Yang et al. (2022) reported this species from *Mangifera indica.* Our collection is morphologically similar to the holotype of *C. quadrisporus*. The only difference is that our collection contains 4-celled ascospores. Phylogenetically, the new collection clustered with *C. quadrisporus* isolates with 88% ML/1.00 BYPP support (Fig. 37). A comparison of ITS, LSU, SSU and *tef1* sequence data between our strain and the ex-type strain of *C. quadrisporus* show a few nucleotide differences. We, therefore, identify our isolate as *C. quadrisporus*, which is the first report on *Olea europaea* in China.

Neobrevicollum W.L. Li & Jian K. Liu, gen. nov.

MycoBank number: MB 849238; Facesoffungi number: FoF 14410

Etymology – The name refers to the similarity to the genus *Brevicollum*

Type species – *Neobrevicollum oleae*

Saprobic on decaying branches of *Olea europaea*. Sexual morph: *Ascomata* solitary, uniloculate, immersed, with visible black shiny ostioles, globose or subglobose, coriaceous, thick-walled, brown to dark brown, ostiolate. *Ostiole* central, papillate. *Peridium* equally thickened, multi-layered, composed of 2–3 light brown to dark brown cells of *textura angularis*, heavily pigmented at the outer layers. *Hamathecium* comprising numerous, hyaline, septate, branched pseudoparaphyses. *Asci* 8-spored, bitunicate, fissitunicate, cylindric-clavate, with a short pedicel, apically rounded with an ocular chamber. *Ascospores* fusiform, 1–3-septate, with obtuse ends, constricted at the middle septum, straight or slightly curved, hyaline, guttulate, surrounded by a mucilaginous sheath. Asexual morph: Not observed.

Notes – *Neobrevicollum*, which was isolated from *Olea europaea* in China is established as a monotypic genus in Neohendersoniaceae. The type species *Neobrevicollum oleae* is characterized by cylindrical to obclavate asci with an elongate and cylindrical pedicel, fusiform, hyaline and 1–3-septate ascospores. *Neobrevicollum* is morphologically similar to *Brevicollum* and *Crassiparies* in having broad fusiform and hyaline ascospores. However, *Brevicollum* has 3–5-septate, hyaline or brown ascospores, surrounded by a rounded mucilaginous sheath. *Crassiparies* has hyaline, 1–3-septate ascospores without a mucilaginous sheath, while *Neobrevicollum* has 1–3-septate, hyaline ascospores with a mucilaginous sheath. Phylogenetic analysis based on combined ITS, LSU, SSU and *tef1* sequence data indicates that our isolate of *Neobrevicollum oleae* formed a distinct subclade from *Amarenographium solium* and *Brevicollum* spp. (Fig. 37). Unfortunately, no sexual morph was reported in *Amarenographium*.

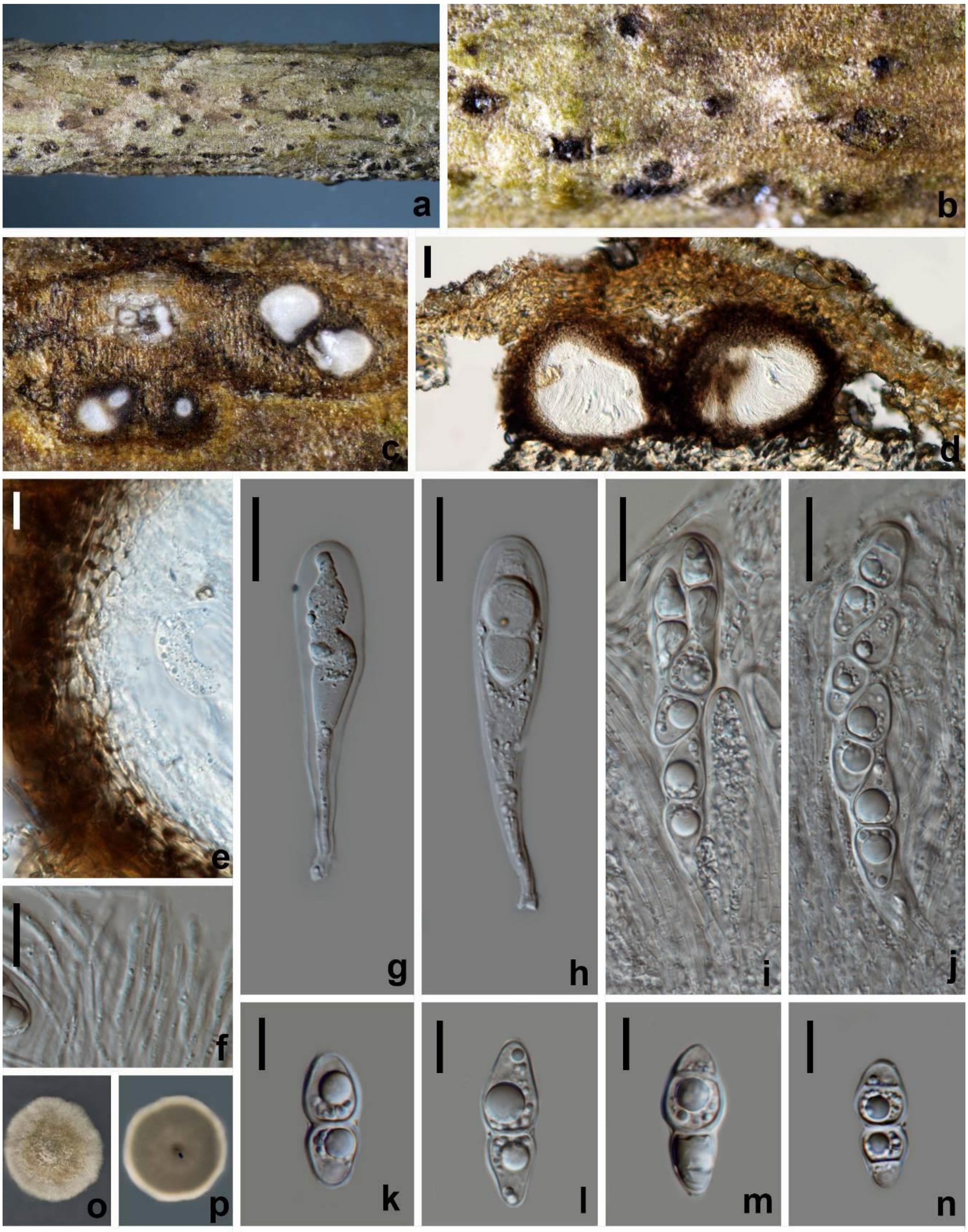

Figure 35 – *Crassiparies quadrisporus* (HUEST 23.0066). a–c Appearance of ascomata on host surface. d Vertical section through ascomata. e Peridium. f Hamathecium. g–j Asci. k–n Ascospores. o Colony on PDA from above. p Colony on PDA from below. Scale bars: d = 50 µm, e, f = 10, g–j = 20 µm, k–n = 5 µm.

Neobrevicollum oleae W.L. Li & Jian K. Liu, sp. nov. Fig. 36

MycoBank number: MB 849239; Facesoffungi number: FoF 14429

Etymology – Name reflects the host plant *Olea* from which the holotype was collected.

Saprobic on decaying branches of *Olea europaea*. Sexual morph: *Ascomata* 230–270 × 200–230 µm ($\bar{x}$ = 250 × 215 µm, n = 10), solitary, uniloculate, immersed, with visible black shiny ostioles, globose or subglobose, coriaceous, thick-walled, brown to dark brown, ostiolate. *Ostiole* central, papillate. *Peridium* 18 × 25 µm, of equally thickened, composed of 2–3 layers, light brown to dark brown cells of *textura angularis*, heavily pigmented at the outer layers. *Hamathecium* composed of 1.8–2 µm wide, numerous, hyaline, branched pseudoparaphyses. *Asci* 105–135 × 18–23 µm ($\bar{x}$ = 120 × 20 µm, n = 20), bitunicate, fissitunicate, cylindrical to obclavate, with a cylindrical pedicel, apically rounded, with a small ocular chamber. *Ascospores* 23–26 × 5.5–7 µm ($\bar{x}$= 24.5 × 6 µm, n = 20), 8-spored, uniseriate, partially overlapping, fusiform, 1–3-septate, with obtuse ends, constricted at the septa, straight or slightly curved, hyaline, with a mucilaginous sheath, 4–5.5 µm, guttulate. Asexual morph: Not observed.

Culture characteristics – Colonies on PDA reach 20 mm diam. after 14 d at 25 °C, colonies pale brown, circular, entire margin, slightly raised, dense at the centre; reverse, dark brown from the centre of the colony, pale brown at margin.

Material examined – China, Sichuan Province, Chengdu city, Shuangliu district, N 30°19'57.04", E 103°59'46.66", elevation 438 m, on branches of *Olea europaea*, 5 March 2021, W.L. Li, GL 131 (HKAS 127170, holotype), ex-type culture UESTCC 23.0067 = CGMCC 3.25054; *ibid*., GL 133 (HUEST 23.0068), living culture UESTCC 23.0068.

GenBank numbers – CGMCC 3.25054 = LSU: OR253257, ITS: OR253105, SSU: OR253183, *tef1*: OR251157, UESTCC 23.0068 = LSU: OR253258, ITS: OR253106, SSU: OR253183, *tef1*: OR251158.

Notes – BLASTn searches of the ITS sequence of *Neobrevicollum oleae* resulted in 86.84% similarity with *Brevicollum hyalosporum* MAFF 243400. The LSU showed 97.78% similarity with *B. hyalosporum* MFLUCC 18-0306, and *tef1* BLASTn results appeared at 91.53% similarity with *Crassiparies quadrisporus* KUMCC 21-0341, while SSU BLASTn results indicated 97.44% similarity with *Amarenographium solium* MFLU12-0059. The multi-gene analyses showed *N. oleae* nested within Neohendersoniaceae and sister to *A. solium* (Fig. 37). *Neobrevicollum oleae* mainly differs from other genera in this family in having hyaline, 1–3-septate ascospores, with a mucilaginous sheath.

Nigrogranaceae Jaklitsch & Voglmayr, Stud. Mycol. 85: 54 (2016)

MycoBank number: MB 817780; Facesoffungi number: FoF 08317

Notes – Nigrogranaceae was proposed by Jaklitsch et al. (2016) to accommodate the monotypic genus *Nigrograna*. A taxonomic and phylogenetic revision of *Nigrograna* showed that the genus has a close affinity to Apiosporaceae (Wang et al. 2017). Species accommodated in Nigrogranaceae are saprobic, pathogenic or endophytic on plant tissues, occasionally infecting humans (De Gruyter 2012, Tibpromma et al. 2017, Kolařík 2018, Zhao et al. 2018) and have been reported from aquatic, terrestrial and marine habitats (Hyde et al. 2017, Tibpromma et al. 2017, Dayarathne et al. 2020)

Nigrograna acericola W.L. Li & Jian K. Liu sp. nov. Fig. 38

MycoBank number: MB 849155; Facesoffungi number: FoF 14407

Saprobic on decaying branches of *Acer truncatum*. Sexual morph: *Ascomata* 390–410 × 210–280 µm ($\bar{x}$ = 400 × 240 µm, n = 10), immersed, scattered, solitary, visible as shiny black dots on the host surface, globose or compressed, coriaceous, dark brown to black, ostiolate. *Ostiole* 30–54 µm wide, with a crest-like apex, central, filled with hyaline periphyses. *Peridium* 30–35 µm wide, composed of 2–3 layers of flattened, thin-walled cells of *textura angularis*. *Hamathecium* 1.8–2 µm wide, composed of numerous, filamentous, hyaline, unbranched pseudoparaphyses. *Asci* 78–85 × 9–11 µm ($\bar{x}$ = 81.5 × 10 µm, n = 20), 8-spored, bitunicate, fissitunicate, cylindrical to clavate, short pedicellate, apically rounded, with a minute ocular chamber. *Ascospores* 15–17 × 5–6 µm ($\bar{x}$ = 16 × 5.5 µm, n = 20), biseriate or partially overlapping, pale brown to yellow brown, fusoid to fusiform, with obtuse ends, tapering towards the ends, 1–3-euseptate, slightly constricted at the middle septum, guttulate, smooth-walled. Asexual morph: Not observed.

Culture characteristics – Colonies on PDA reach 20 mm diam. after 14 d at 25 °C, colonies pale brown, circular, flat, edge entire, margin well-defined; reverse, dark brown, with a light brown margin.

Figure 36 – *Neobrevicollum oleae* (HKAS 127170, holotype). a, b Appearance of ascomata on host surface. c Vertical section through ascoma. d Peridium. e, f Hamathecium (f in cotton blue). g–j Asci (i, j in cotton blue). k Ascus apex stained in cotton blue. l Ascus stipe stained in cotton blue. m–r Ascospores (p, q stained in cotton blue; r stained in indian ink). s Colonies on PDA from above. t Colonies on PDA from below. Scale bars: c = 50 µm, d–f, k, l, m–r = 10 µm, g–j = 20 µm.

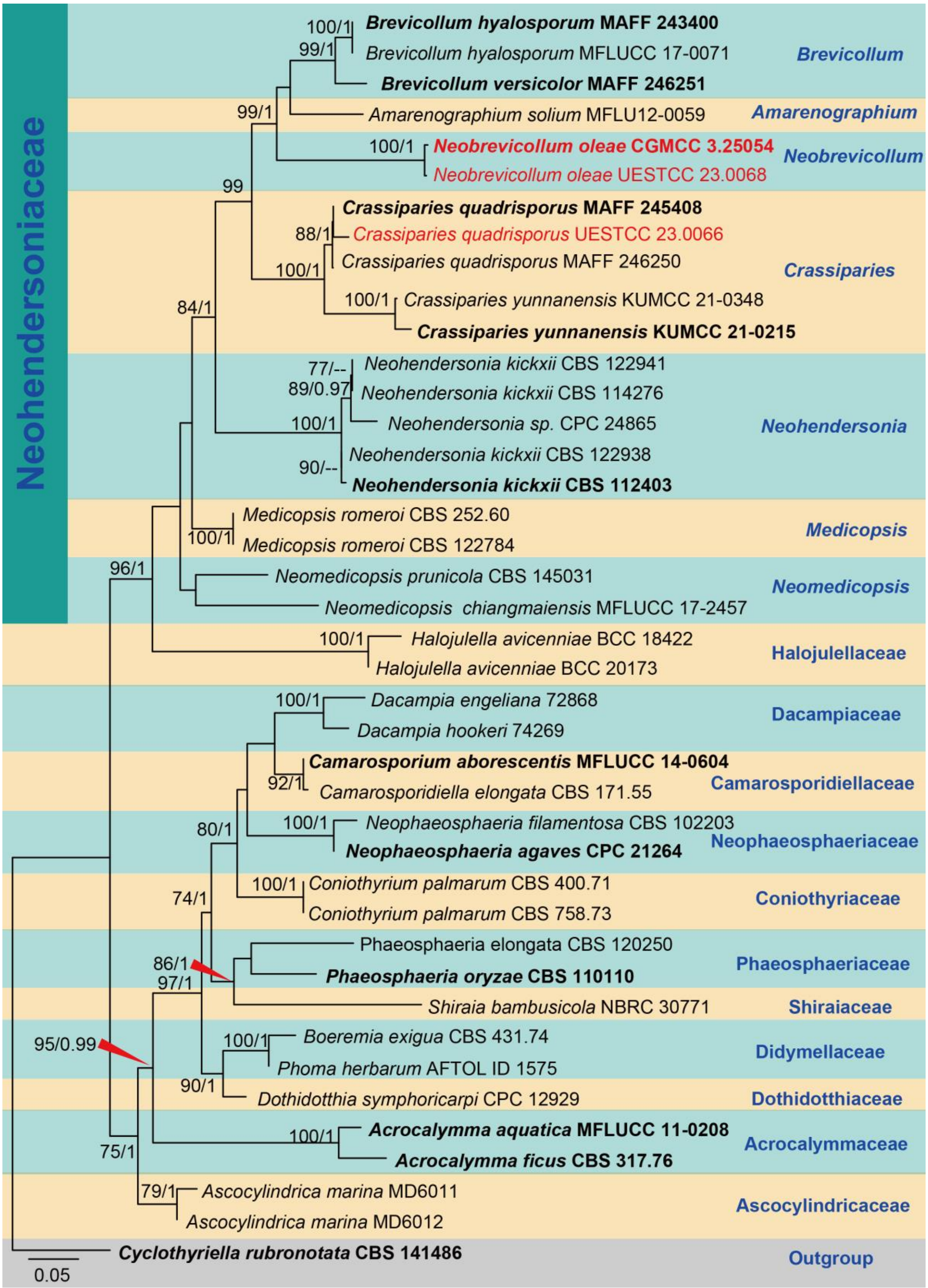

Figure 37 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, SSU and *tef1* sequence data. Forty-one strains are included in the combined sequence analyses, which comprise 3,364 characters with gaps. *Cyclothyriella rubronotata* CBS 141486 is used as the outgroup taxon. Tree topology from ML analysis was similar to BI analysis. The best scoring RAxML tree with a final likelihood value of -11405.554410 is presented. Proportion of gaps and completely undetermined characters in this alignment are 37.46% with 742 distinct alignment patterns. Estimated base frequencies were as follows; A = 0.240052, C = 0.249934, G = 0.275173, T = 0.234841; substitution rates AC = 1.335876, AG = 3.576916, AT = 2.022954, CG = 1.410021,

CT = 11.118337, GT = 1.000000; gamma distribution shape parameter α = 0.532606. Bootstrap support values for ML ≥ 75% and BYPP ≥ 0.95 are defined as ML/BYPP above the nodes. Hyphens (--) represent support values less than 75% in ML and 0.95 in BI. Newly generated sequences are in red and ex-type species are in bold.

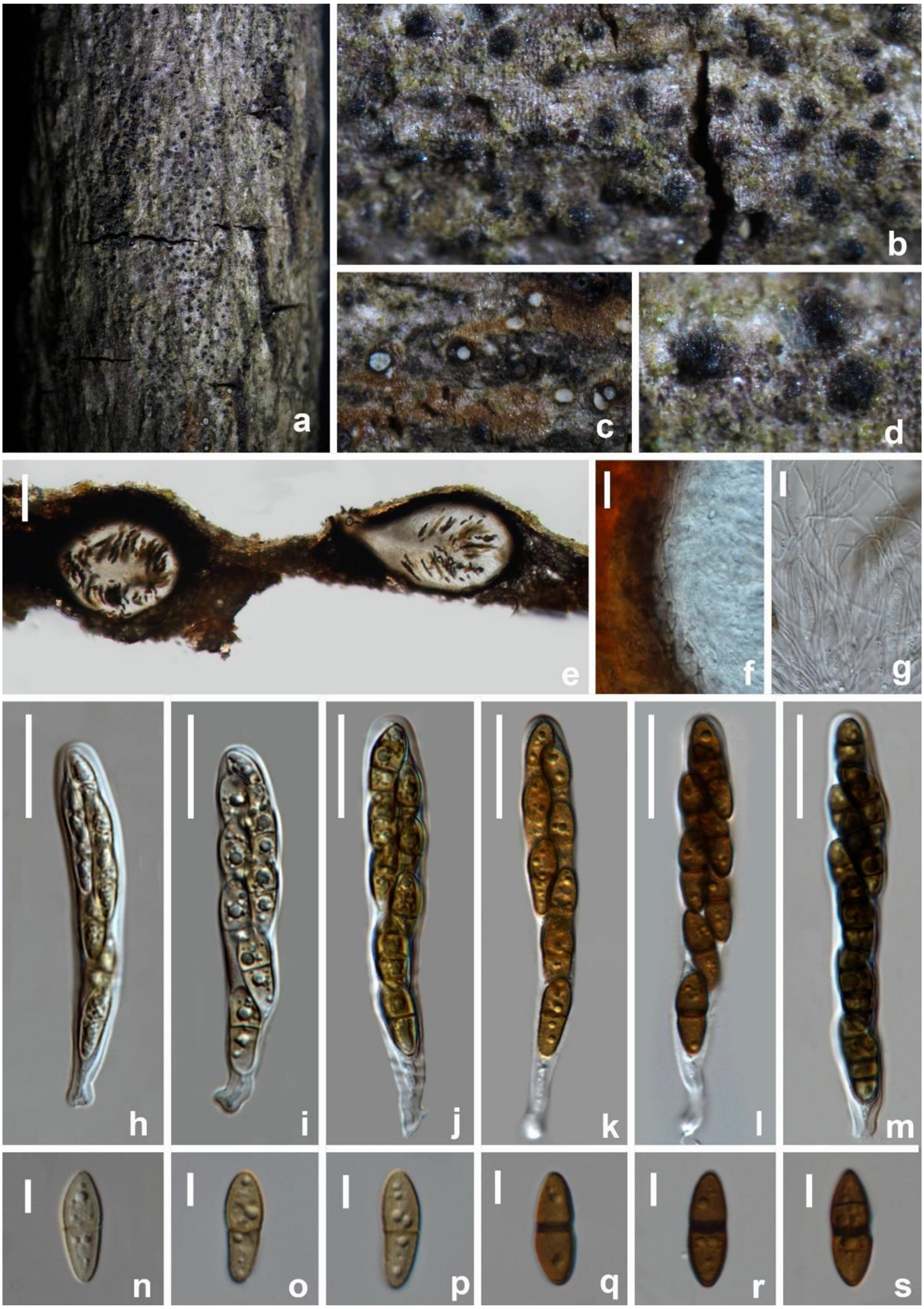

Figure 38 – *Nigrograna acericola* (HKAS 127171, holotype). a–d Appearance of ascomata on host surface. e Vertical section through ascomata. f Peridium. g Hamathecium. h–m Asci. n–s Ascospores. Scale bars: e = 100 µm, f, g = 10 µm, h–m = 20 µm, n–s = 5 µm.

Material examined – China, Sichuan Province, Chengdu city, Pidu district, N 30°49'26.76", E 103°47'41.64", elevation 442 m, on branches of *Acer truncatum*, 1st December 2021, W.L. Li, YBF 560 (HKAS 127171, holotype), ex-type culture UESTCC 23.0069 = CGMCC 3.24957.

GenBank numbers – CGMCC 3.24957 = LSU: OR253312, ITS: OR253153, *tef1*: OR263572

Notes – In the phylogenetic analyses, *Nigrograna acericola* clustered in a distinct, well-supported clade closely related to the strains of *N. magnoliae* (Fig. 45). However, a comparison of sequence data between ex-types of *N. acericola* and *N. magnoliae* shows differences of 3 bp (0.06%), 26 bp (3.1%), and 38 bp (4.2%) in ITS, LSU and *tef1* gene regions, respectively. The morphological characteristics of *N. acericola* agree with *Nigrograna* species in having solitary, immersed ascomata, clavate to cylindrical asci with a short stipe and fusoid to ellipsoid, septate ascospores. *Nigrograna acericola* differs from its phylogenetically related species *N. magnoliae* in having larger ascomata (390–410 × 210–280 µm vs. 200–300 × 100–150 µm).

Nigrograna hydei J.F. Zhang, Jian K. Liu & Z.Y. Liu Mycol Progress 19:1369 (2020)

Fig. 39

MycoBank number: MB 556749

Saprobic on decaying branches of *Paeonia suffruticosa*. Sexual morph: *Ascomata* 220–380 × 100–180 µm ($\bar{x}$ = 300 × 140 µm, n = 10), scattered, solitary, immersed, visible as black dots on the host surface, globose or subglobose, with long necks, uniloculate. *Ostiole* 55–72.5 µm wide, central, filled with hyaline periphyses. *Peridium* 21.5–39 µm thick, consisting several layers of lightly pigmented cells of *textura angularis*. *Hamathecium* 2.3–2.6 µm wide, comprising numerous, filiform, hyaline pseudoparaphyses. *Asci* 43–45 × 6–7.5 µm ($\bar{x}$ = 44 × 6.5 µm, n = 20), 8-spored, bitunicate, fissitunicate, clavate, pedicellate with an obtuse to furcate base, apically rounded, with a well-developed ocular chamber, clearly seen at immature state. *Ascospores* 12.5–14 × 3.5–5 µm ($\bar{x}$ = 13 × 4 µm, n = 20), 1–2 seriate, partially overlapping, fusoid to clavate, pale brown, 1–3-septate, constricted at the middle septum. Asexual morph: Not observed.

Known distribution – India, South Korea, Thailand.

Culture characteristics – Colonies on PDA reach 30 mm diam. after 14 d at 25 °C, circular, with dense, velvety, white mycelium on the surface, becoming yellow with age; in reverse dark brown in the middle, entire margin yellowish.

Material examined – China, Sichuan Province, Miangyang city, Youxian district, N 31°25'22.18", E 104°48'57.99", elevation 470 m, on a branch of *Paeonia suffruticosa*, 10 September 2021, W.L. Li, YMD 496 (HUEST 23.0078), living culture UESTCC 23.0078.

GenBank numbers – UESTCC 23.0078 = LSU: OR253304, ITS: OR253145, *tef1*: OR251153

Notes – *Nigrograna hydei* was introduced by Zhang et al. (2020) from unidentified hosts in Krabi Province, Thailand. The characteristics of our collection fits well with the ex-type strain of *N. hydei* in having immersed ascomata with long necks, clavate asci, knot-like pedicel, and fusoid to ellipsoid, 3-septate ascospores. In the multi-gene phylogeny, our new collection clustered with the ex-type strain of *N. hydei* (GZCC 19-0050) with full support (100% ML/1.00 BYPP) (Fig. 45). Therefore, we conclude that this is the first record of *N. hydei* from China as well as the first report on *Paeonia suffruticola*.

Nigrograna locuta-pollinis F. Liu & L. Cai, Mycosphere 9(6): 1097 (2018) Fig. 40

MycoBank number: MB 824507

Saprobic on decaying branches of *Acer truncatum*. Sexual morph: *Ascomata* 210–250 × 190–250 µm ($\bar{x}$ = 230 × 220 µm, n = 10), immersed, only the ostiolar necks visible on the host surface, solitary, scattered, globose to subglobose, dark brown to black. *Ostiole* central, crest-like, elongated, filled with hyaline periphyses. *Peridium* 36–56 µm thick, consisting of several layers of thick-walled, dark brown to lightly pigmented cells of *textura angularis*. *Hamathecium* comprising 2–2.3 µm wide, numerous, filiform, branched, hyaline pseudoparaphyses. *Asci* 37.5–47 × 6.5–9 µm ($\bar{x}$ = 42 × 8 µm, n = 20), 8-spored, bitunicate, fissitunicate, clavate, short pedicellate with a swollen base, apically rounded. *Ascospores* 11.5–14.5 × 3–4.5 µm ($\bar{x}$ = 13 × 4 µm, n = 20), 1–2-seriate, fusoid to broad fusiform, straight or curved, 3-septate, pale brown to dark brown, constricted at each septum. Asexual morph: Not observed.

Known distribution – China

Culture characteristics – Colonies on PDA reach 20 mm diam. after 14 d at 25 °C, colonies circular, margin entire, dense, surface smooth, velvety appearance, cream at the margin, pale brown in the centre; reverse reddish brown, with a pale brown edge; producing a yellow water-soluble pigment.

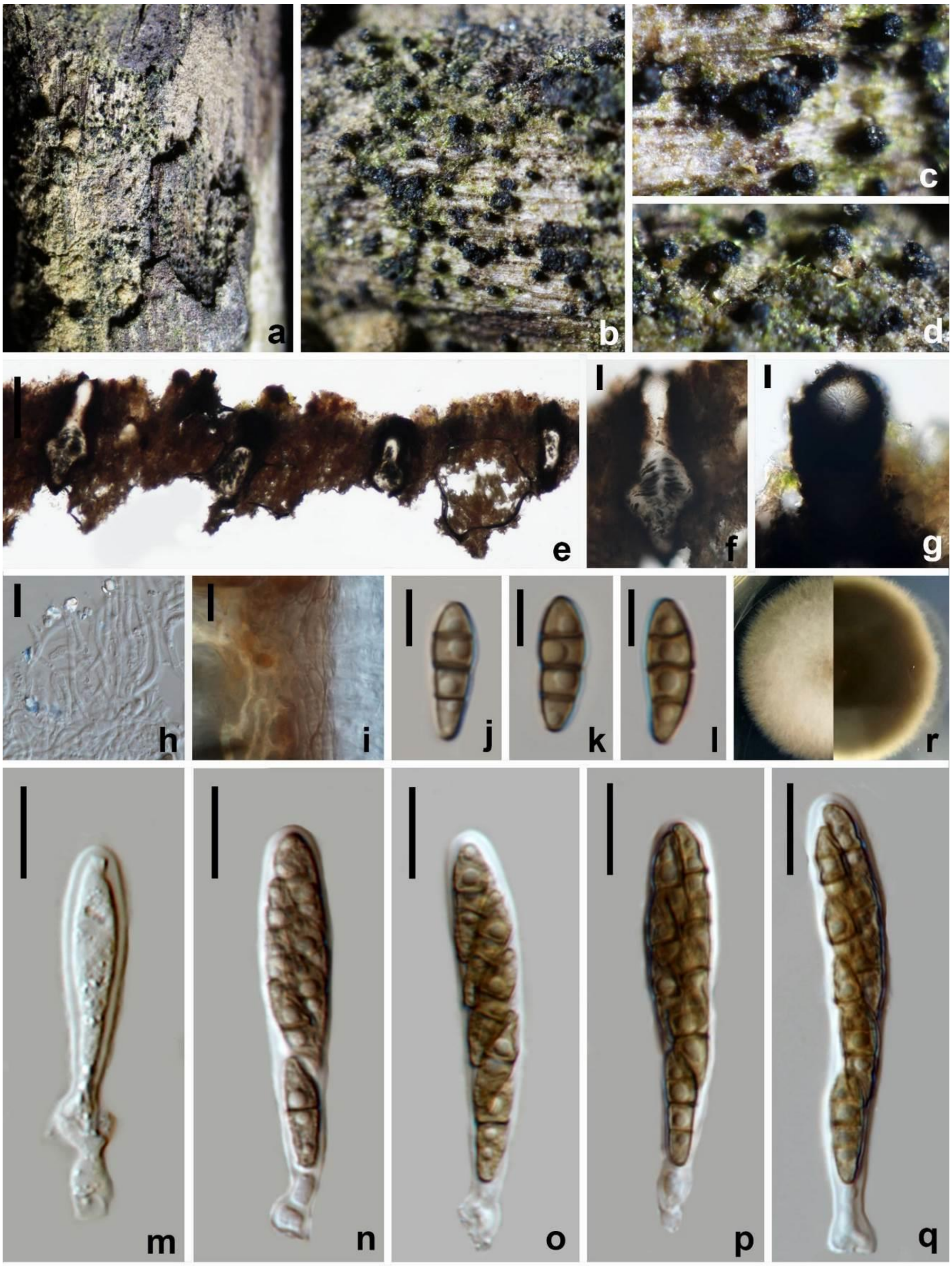

Figure 39 – *Nigrograna hydei* (HUEST 23.0078). a–d Appearance of ascomata on host surface. e, f Vertical section through ascomata. g Ostiole. h Hamathecium. i Peridium. j–l Ascospores. m–q Asci. r Upper and reverse view of the colony on PDA after 14 d. Scale bars: e = 200 µm, f = 50 µm, g = 20 µm, h, i, m–q = 10 µm, j–l = 5 µm.

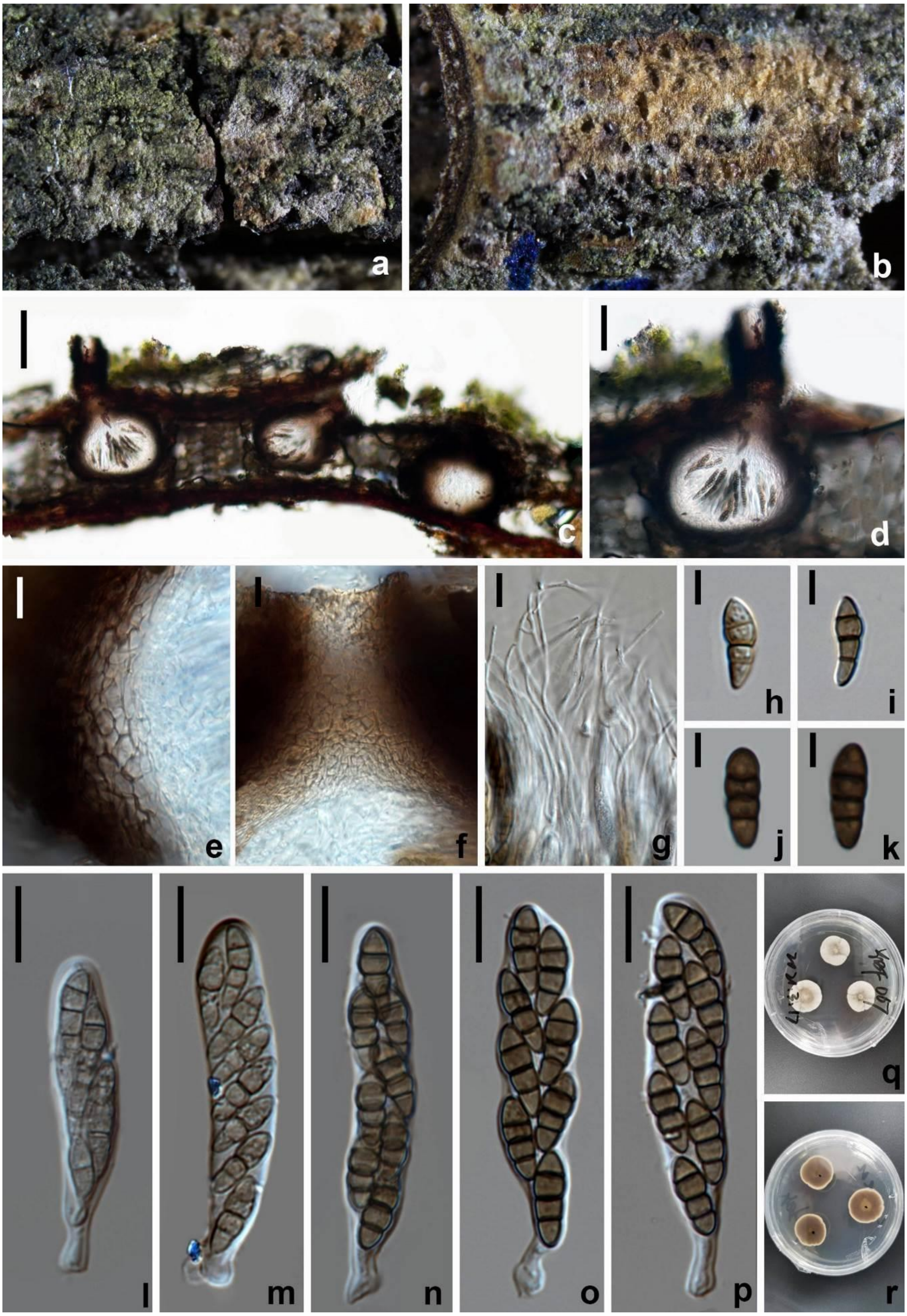

Figure 40 – *Nigrograna locuta-pollinis* (HUEST 23.0073, sexual morph). a, b Appearance of ascomata on host surface. c, d Vertical section through ascomata. e Peridium. f Ostiole. g Hamathecium. h–k Ascospores. l–p Asci. q Colonies on PDA from above. r Colonies on PDA from below. Scale bars: c = 100 µm, d = 50 µm, e–g, l–p = 10 µm, h–k = 5 µm.

Material examined – China, Sichuan Province, Chengdu city, Pidu district, N 30°49'26.76", E 103°47'41.64", elevation 442 m, on branches of *Acer truncatum*, 19 March 2021, W.L. Li, YBF

67 (HUEST 23.0073), living culture UESTCC 23.0073; *ibid*., 1st December 2021, W.L. Li, 553 (HUEST 23.0074), living culture UESTCC 23.0074 = CGMCC 3.24424.

GenBank numbers – UESTCC 23.0073 = LSU: OR253242, ITS: OR253090, *tef1*: OR251053; UESTCC 23.0074 = LSU: OR253311, ITS: OR253152, *tef1*: OR263571.

Notes – *Nigrograna locuta-pollinis* was introduced by Zhang et al. (2018) based on their phylogenetic analyses. The fungus was isolated from hive-stored pollen of *Brassica campestris*, but no sporulation was observed in the culture. In our study, two new strains isolated from *Acer truncatum* were clustered with the ex-type strain of *N. locuta-pollinis* with 86% ML/1.00 BYPP support (Fig. 45). A comparison of sequence data between *N. locuta-pollinis* and the new strains show a few nucleotides differences in ITS, LSU and *tef1*. Thus, we identify our new collections as *N. locuta-pollinis*, and corresponding morphological descriptions and illustrations were provided.

Nigrograna magnoliae Wanas., PLoS One 15(7): 10 (2020) Fig. 41

MycoBank number: MB 557331

Saprobic on decaying branches of *Acer truncatum*. Sexual morph: *Ascomata* 100–300 × 180–250 µm ($\bar{x}$ = 200 × 210 µm, n = 10), immersed, scattered, solitary, visible as black dots on the host surface, uniloculate, globose to subglobose, ostiolate, papillate. *Ostiole* central or eccentric, with a crest-like apex, filled with hyaline periphyses. *Peridium* 15.5–19 µm thick, multi-layered, comprising dark brown or reddish brown to lightly pigmented cells of *textura angularis*. *Hamathecium* 1.5–2 µm wide, composed of numerous, filiform, hyaline, aseptate, rarely branched, guttulate, smooth-walled pseudoparaphyses. *Asci* 62–65 × 7.5–8.5 µm ($\bar{x}$ = 63.5 × 8 µm, n = 20), 8-spored, bitunicate, fissitunicate, clavate, with a short cylindrical pedicel, apically rounded, with a minute ocular chamber. *Ascospores* 14.5–16 × 4.5–5 µm ($\bar{x}$ = 15 × 4.5 µm, n = 20), 1–2 seriate, partially overlapping, fusoid to ellipsoid, tapering towards the blunt ends, yellow brown to dark brown, 3-septate, deeply constricted at septa, guttulate, smooth-walled. Asexual morph: Not observed.

Known distribution – China.

Culture characteristics – Colonies on PDA reach 20 mm diam. after 14 d at 25 °C, colonies pale brown, circular, flat, edge entire, margin well-defined; reverse dark brown from the centre of the colony, light brown at margin.

Material examined – China, Sichuan Province, Chengdu city, Pidu district, N 30°49'26.76", E 103°47'41.64", elevation 442 m, on branches of *Acer truncatum*, 5 March 2021, W.L. Li, YBF 054 (HUEST 23.0079), living culture UESTCC 23.0079; *ibid*., 19 March 2021, W.L. Li, YBF 084 (HUEST 23.0080), living culture UESTCC 23.0080; *ibid*., Guangyuan city, Chaotian district, N 32°41'5.48", E 106°45'15.76", elevation 623 m, on a branch of *Juglans regia*, 19 April 2021, W.L. Li, HT 231 (HUEST 23.0083), living culture UESTCC 23.0083; *ibid*., Mianyang city, Youxian district, N 31°22'28.88", E 104°50'42.00", elevation 398 m, on branches of *Olea europaea*, 10 June 2021, W.L. Li, GL 267 (HUEST 23.0081), living culture UESTCC 23.0081; *ibid*., GL 278 (HUEST 23.0082), living culture UESTCC 23.0082.

GenBank numbers – UESTCC 23.0079 = LSU: OR253240, ITS: OR253088; *tef1*: OR262144; UESTCC 23.0080 = LSU: OR253244, ITS: OR253092, *tef1*: OR251054; UESTCC 23.0081 = LSU: OR253276, ITS: OR253117, *tef1*: OR251169; UESTCC 23.0082 = LSU: OR253278, ITS: OR253119, *tef1*: OR251170; UESTCC 23.0083 = LSU: OR253272.

Notes – The asexual and sexual morph of *Nigrograna magnoliae* was introduced by Wanasinghe et al. (2020) from *Magnolia denudate*. Later, Zhang et al. (2020) reported this species from an aquatic habitat. Multi-gene phylogeny indicated that our collection clustered with other strains of *Nigrograna magnoliae* (Fig. 45). A comparison of ITS nucleotides show that our new collection is similar with the ex-type strain of *N. magnoliae*. Therefore, we identified our collection as *N. magnoliae*, which are reported from *Juglans regia* and *Olea europaea* for the first time.

Nigrograna oleae W.L. Li & Jian K. Liu sp. nov. Fig. 42

MycoBank number: MB 849157; Facesoffungi number: FoF 14406

Etymology – The specific epithet '*oleae*' refers to the host genus *Olea*, from which the holotype was collected.

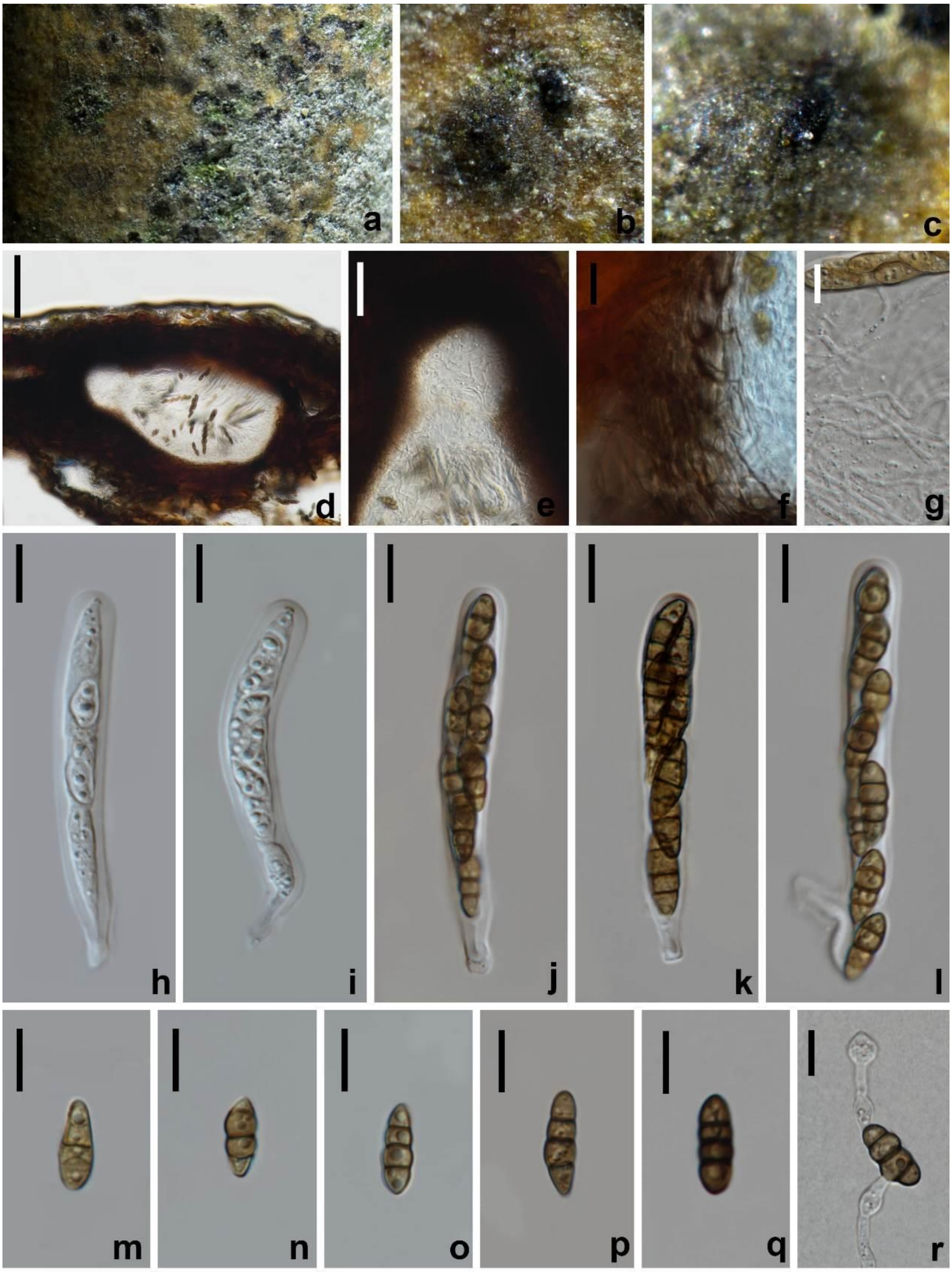

Figure 41 – *Nigrograna magnoliae* (HUEST 23.0079). a–c Appearance of ascomata on host surface. d Vertical section through ascoma. e Ostiole. f Peridium. g Hamathecium. h–l Asci. m–q Ascospores. r Germinated ascospore. Scale bars: d = 100 µm, e = 40 µm, f–r = 10 µm.

Saprobic on decaying branches of *Olea europaea*. Sexual morph: *Ascomata* 260–280 × 200–230 µm ($\bar{x}$ = 270 × 210 µm, n = 10), immersed to semi-immersed, solitary, scattered, often lying parallelly or obliquely to the bark or wood surface, with a cylindrical ostiolar neck, coriaceous, obpyriform, brown to dark brown. *Ostiole* 67–74 µm wide, central or eccentric, periphysate. *Peridium* 23–26 µm wide, consisting 6–7 layers of brown-walled cells of *textura angularis*. *Hamathecium* 1.5–2 µm wide, composed of numerous, filiform, septate, branched pseudoparaphyses. *Asci* 63.5–76 × 11–13.5 µm ($\bar{x}$ = 70 × 12 µm, n = 20), 8-spored, bitunicate, fissitunicate, cylindrical to clavate, with a short pedicel, apically rounded with a smaller ocular chamber. *Ascospores* 15–16.5 × 5.5–7 µm ($\bar{x}$ = 15.5 × 6 µm, n = 20), uni- to bi-seriatly arranged, fusoid to clavate, apical cell mostly obtuse, straight, 1-septate and pale brown to yellow-brown when young, becoming 3-septate, dark to chocolate-brown at maturation, constricted at the septa. Asexual morph: Not observed.

Culture characteristics – Colonies on PDA reach 20 mm diam. after 14 d at 25 °C, colonies circular, margin entire, dense, surface smooth, velvety appearance, cream white, pale brown in the centre; reverse gray white at the margin, brown in the centre; producing a yellow water-soluble pigment.

Material examined – China, Sichuan Province, Chengdu city, Shuangliu district, N 30°19'57.04", E 103°59'46.66", elevation 432 m, on branches of *Olea europaea*, 30 January 2021, W.L. Li, GL 14 (HKAS 127172, holotype), ex-type culture UESTCC 23.0070 = CGMCC 3.24423; *ibid*., GL 20 (HUEST 23.0072), living culture UESTCC 23.0072; *ibid*., Pidu district, on a branch of *Acer truncatum*, 5 March 2021, W.L. Li, GL 58 (HUEST 23.0071), living culture UESTCC 23.0071.

GenBank numbers – CGMCC 3.24423 = LSU: OR253232, ITS: OR253080, *tef1*: OR262140; UESTCC 23.0071 = LSU: OR253241, ITS: OR253089, *tef1*: OR262145; UESTCC 23.0072 = LSU: OR253235, ITS: OR253083, *tef1*: OR262143.

Notes – In the phylogenetic analyses, three strains of *Nigrograna oleae* clustered with *N. thymi* with 1.00 BYPP support (Fig. 45). However, a comparison of sequence data between *N. oleae* and *N. thymi* shows 7 bp (1.8%), 7 bp (0.8%), and 40 bp (4.3%) differences in ITS, LSU and *tef1* gene regions, respectively. Morphologically, *N. oleae* differs from *N. thymi* in having shorter asci (63.5–76 vs. 90–94 µm), as well as shorter ascospores (15–16.5 µm vs. 24–26 µm). Additionally, *N. thymi* possesses 4-septate ascospores with cuspate apex while *N. oleae* possesses 3-septate ascospores with rounded apex when mature.

Nigrograna sichuanensis W.L. Li & Jian K. Liu sp. nov. Fig. 43

MycoBank number: MB 849156; Facesoffungi number: FoF 14408

Etymology – ‘sichuanensis’ refers to Sichuan Province, where the species was collected.

Saprobic on decaying branches of *Idesia polycarpa* Maxim. Sexual morph: *Ascomata* 200–230 × 170–190 µm ($\bar{x}$ = 210 × 180 µm, n = 10), visible as black spots on the host, solitary, scattered, immersed, coriaceous, dark brown to black, globose to subglobose, surrounded by a small blackened pseudoclypeus, ostiolate. *Ostiole* 66–82 µm wide, central, periphysate. *Peridium* 32.5–36 µm wide, consisting of several layers of thick-walled, dark brown to lightly pigmented cells of *textura angularis*. *Hamathecium* 2–2.5 µm wide, numerous, cylindrical, septate, unbranched. *Asci* 47.5–49 × 6.5–7.5 µm ($\bar{x}$ = 48 × 7 µm, n = 20), 8-spored, bitunicate, fissitunicate, cylindrical to clavate, short pedicellate, apically rounded. *Ascospores* 9.5–11 × 3–4.5 µm ($\bar{x}$ = 10 × 3.5 µm, n = 20), overlapping, 1–2 seriate, fusiform to clavate, hyaline to brown, 1-septate when immature, becoming 3-euseptate when mature, straight or slightly curved, slightly constricted at septa. Asexual morph: Not observed.

Culture characteristics – Colonies on PDA reach 20 mm diam. after 14 d at 25 °C, colonies circular, margin entire, reverse dark brown, with pale brown edge; producing yellow water-solute pigment.

Material examined – China, Sichuan Province, Chengdu city, Pidu district, N 30°49'26.76", E 103°47'41.64", elevation 442 m, on branches of *Acer truncatum*, 19 March 2021, W.L. Li, YBF 92 (HKAS 127174, holotype), ex-type culture UESTCC 23.0075 = CGMCC 3.24424; *ibid*., GL 99 (HUEST 23.0076), living culture UESTCC 23.0076.

GenBank numbers – CGMCC 3.24424 = LSU: OR253248, ITS: OR253096, *tef1*: OR251058; UESTCC 23.0076 = LSU: OR253252, ITS: OR253100, *tef1*: OR251059

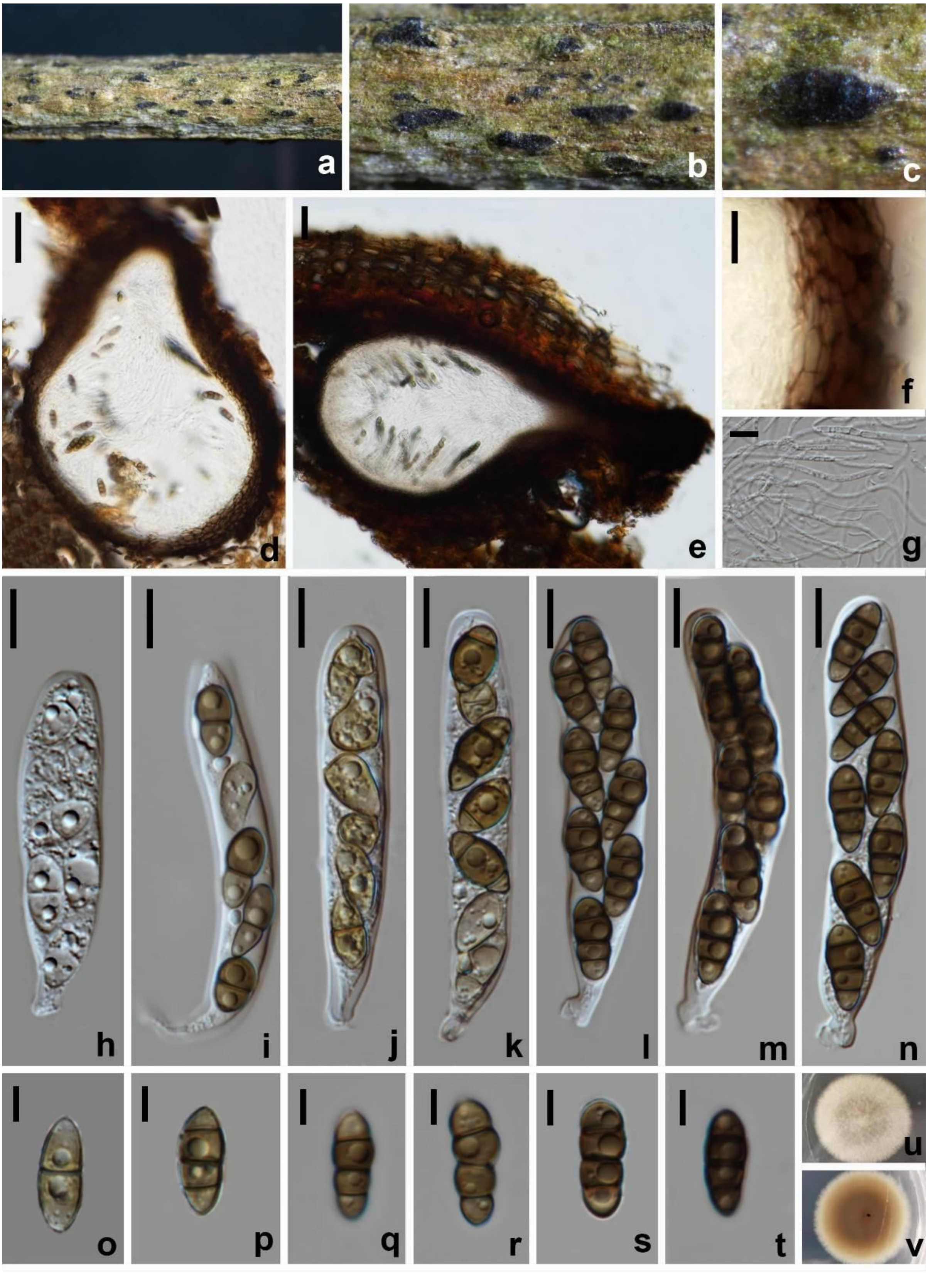

Figure 42 – *Nigrograna oleae* (HKAS 127172, holotype). a–c Appearance of ascomata on host surface. d, e Vertical section through ascomata. f Peridium. g Hamathecium. h–n Asci. o–t Ascospores. u Colony on PDA from above. v Colony on PDA from below. Scale bars: d, e = 40 µm, f–n = 10 µm, o–t = 5 µm.

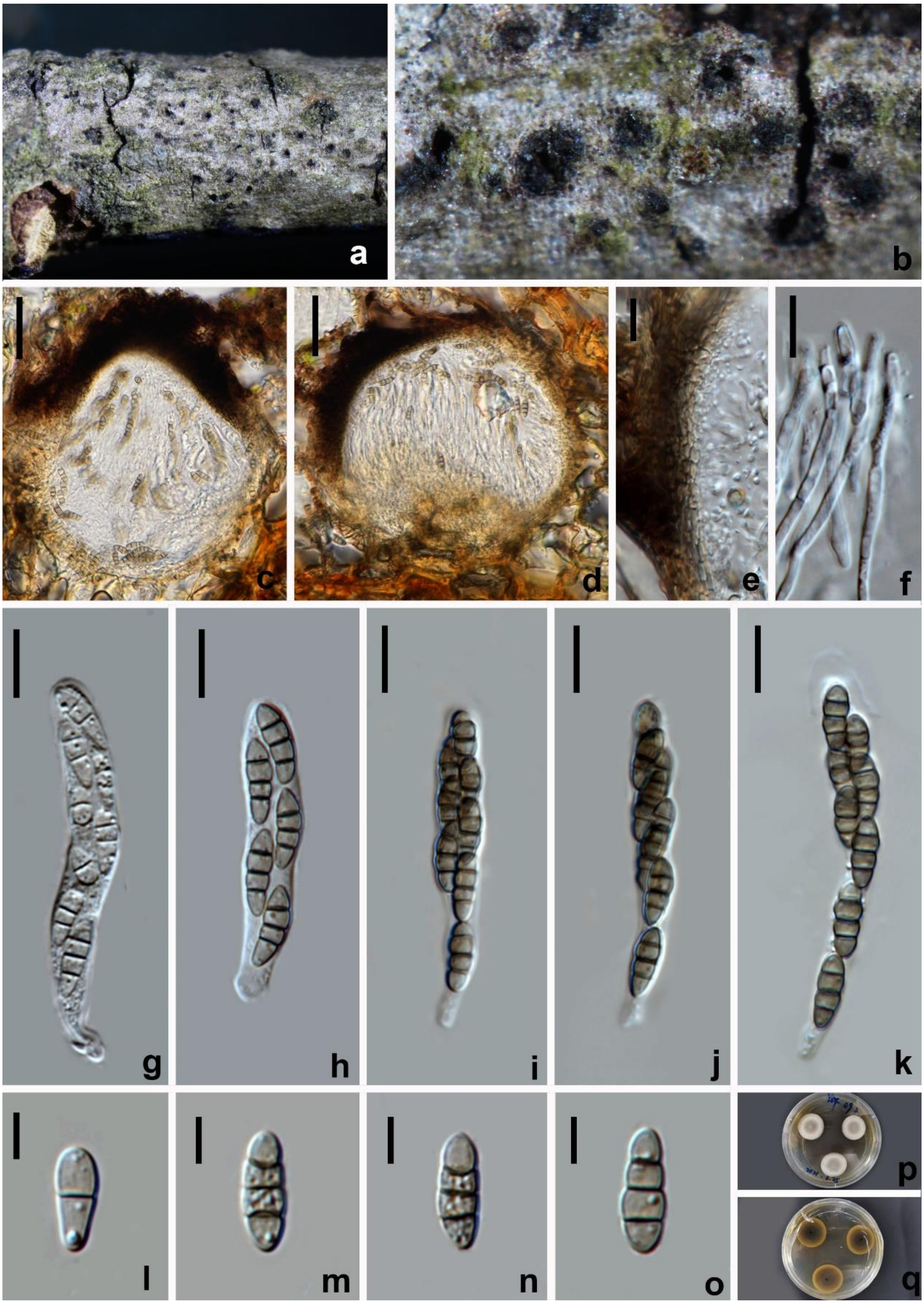

Figure 43 – *Nigrograna sichuanensis* (HKAS 127174, holotype). a, b Appearance of ascomata on host surface. c, d Vertical section through ascomata. e Peridium. f Hamathecium. g–k Asci. l–o Ascospores. p Colonies on PDA from above. q Colonies on PDA from below. Scale bars: c, d = 40 µm, e–k = 10 µm, l–o = 5 µm.

Notes – In the phylogenetic analyses, two strains of *Nigrograna sichuanensis* clustered with *N. locuta-pollinis* with absolute bootstrap support (100% ML/1.00 BYPP) (Fig. 45). A comparison of sequence data between *N. sichuanensis* and *N. locuta-pollinis* shows 12 bp (2.4%), 4 bp (0.5%), and 4 bp (0.5%) differences in ITS, LSU and *tef1* gene regions, respectively. Morphologically, *N. sichuanensis* is similar to *N. locuta-pollinis* in having immersed, globose to subglobose ascomata, clavate asci with a short pedicel and broad fusiform, 3-septate ascospores. However, *N. sichuanensis* has a well-developed clypeus, while *N. locuta-pollinis* has a well-developed, crest-like ostiolar neck lacking the clypeus. Additionally, the asci of *N. locuta-pollinis* are larger than those of *N. sichuanensis* (49–54 × 10–11 µm vs. 47.5–49 × 6.5–7.5 µm).

Nigrograna verniciae W.L. Li & Jian K. Liu sp. nov. Fig. 44

MycoBank number: MB 849158; Facesoffungi number: FoF 14428

Etymology – The specific epithet '*verniciae*' refers to the host genus *Vernicia*, from which the holotype was collected.

Saprobic on decaying branches of *Vernicia fordii* Hemsl. Sexual morph: *Ascomata* 340–360 × 350–370 µm ($\bar{x}$ = 350 × 360 µm, n = 10), semi-immersed to immersed, solitary or scattered, globose to subglobose, coriaceous, brown to dark brown, glabrous. *Ostiole* central, papillate, protruding from the substratum. *Peridium* 26.5–42 µm wide, comprising 5–6 layers of brown-walled cells of *textura angularis*. *Hamathecium* 1.8–2.2 µm wide, comprising filiform, hyaline, septate, branching pseudoparaphyses. *Asci* 57–66 × 9–10 µm ($\bar{x}$ = 61.5 × 9.5 µm, n = 20), 8-spored, bitunicate, fissitunicate, cylindrical to clavate, apically rounded, with knob-like to furcate pedicel. *Ascospores* 14–16 × 4–5 µm ($\bar{x}$ = 15 × 4.5 µm, n = 20), overlapping, 1–2 seriate, fusoid to narrowly ellipsoid, straight or slightly curved, grayish brown to dark brown, guttulate. Asexual morph: Not observed.

Culture characteristics – Colonies on PDA reach 40 mm diam. after 1 week at 25 °C, colonies irregular, undulate margin, flat, pale brown in the centre, cream at the margin; reverse, brown from the centre of the colony, cream at margin.

Material examined – China, Sichuan Province, Guangyuan city, Qingchuan county, N 32°41'54.56", E 106°04'45.37", elevation 638 m, on branches of *Vernicia fordii*, 20 April 2021, W.L. Li, HT 246 (HKAS 127175, holotype), ex-type culture UESTCC 23.0077 = CGMCC 3.24425.

GenBank numbers – CGMCC 3.24425 = LSU: OR253275, ITS: OR253116, *tef1*: OR251168.

Notes – In the phylogenetic analyses, *Nigrograna verniciae* clustered together with *N. asexualis* (ZHKUCC 22-0214) with 99% ML/1.00 BYPP support (Fig. 45). The base pair comparison of ITS showed 18 bp (3.9%) differences. The asexual morph of *N. asexualis* was introduced by Li et al. (2022) from *Coffea arabica* in Yunnan Province, China. However, we could not compare the morphological characteristics with *N. asexualis* (ZHKUCC 22-0214), since it lacks sexual morph record. *Nigrograna verniciae* resembles *N. mycophile* and *N. obliqua* in having immersed ascomata with a cylindrical neck, clavate asci and fusoid to ellipsoid ascospores. However, the ascomata of the latter two are often immersed in valsoid groups beneath the periderm of the host, and surrounded by a brown to olivaceous subiculum. Additionally, *Nigrograna verniciae* has smaller asci than *N. mycophila* and *N. obliqua* (57–66 × 9–10 µm vs. 72–85 × 11–13 µm vs. 65–83 ×9.5–12.2 µm, respectively).

Parabambusicolaceae Kaz. Tanaka & K. Hiray., Stud. Mycol. 82: 115 (2015).

MycoBank number: MB 811324; Facesoffungi number: FoF 06708

Notes – Parabambusicolaceae was introduced by Tanaka et al. (2015) to accommodate *Aquastroma* and *Parabambusicola*. Species of Parabambusicolaceae frequently occur on bamboo, but are also found on other hosts (Phukhamsakda et al. 2018). Based on morphology and phylogenetic analysis, nine genera *Aquastroma*, *Lonicericola*, *Multilocularia*, *Multiseptospora*, *Neoaquastroma*, *Parabambusicola*, *Paramonodictys*, *Paratrimmatostroma* and *Pseudomonodictys* are currently accepted in this family (Wijayawardene et al. 2022).

Paramonodictys paeoniae W.L. Li & Jian K. Liu sp. nov. Fig. 46

MycoBank number: MB 849159; Facesoffungi number: FoF 14404

Etymology – The specific epithet '*paeoniae*' refers to the host genus *Paeonia*, from which the holotype was collected.

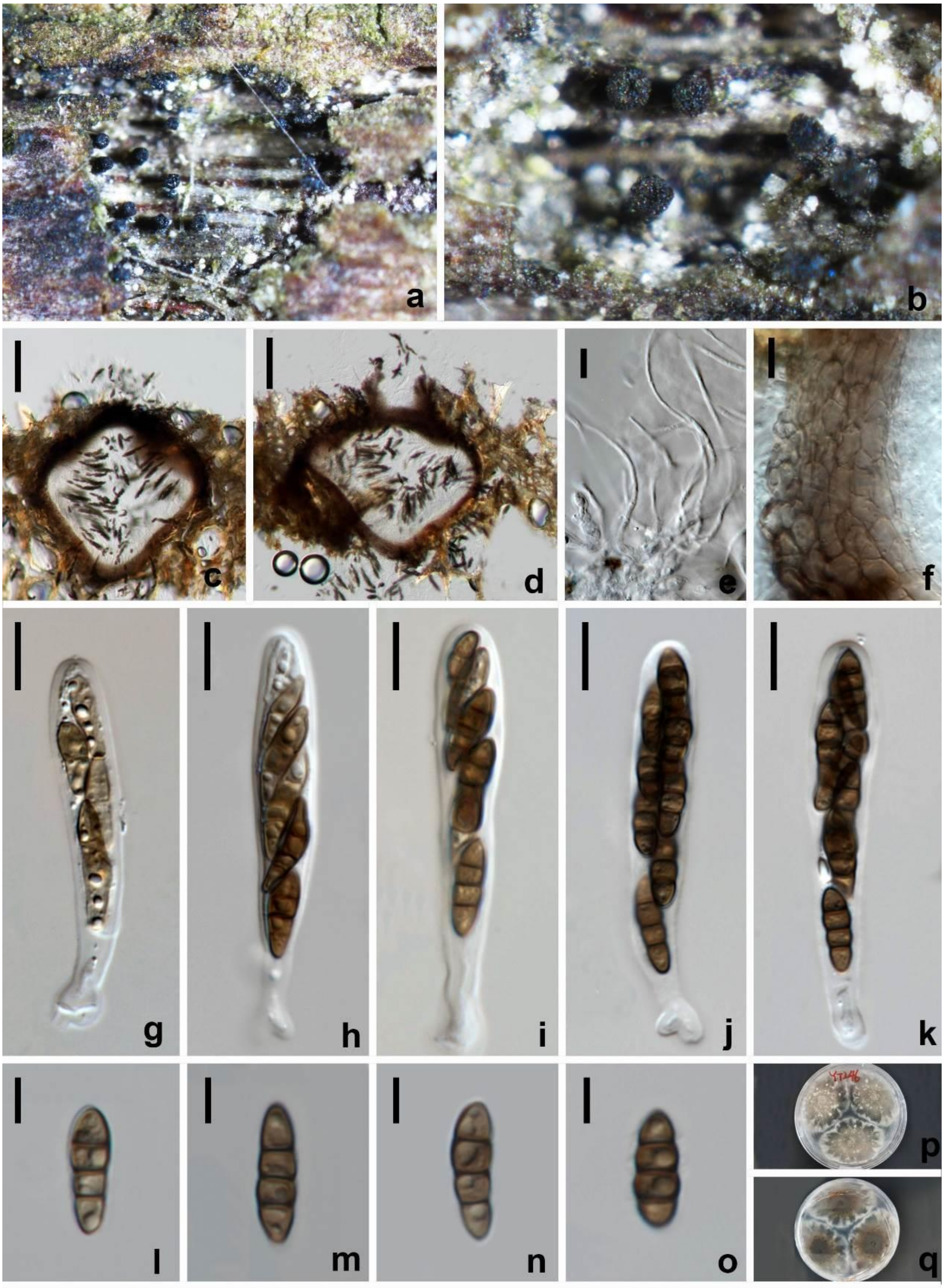

Figure 44 – *Nigrograna verniciae* (HKAS 127175, holotype). a, b Appearance of ascomata on host surface. c, d Vertical section through ascomata. e Hamathecium. f Peridium. g–k Asci. l–o Ascospores. p Colonies on PDA from above. q Colonies on PDA from below. Scale bars: c, d = 100 µm, e–k = 10 µm, l–o = 5 µm.

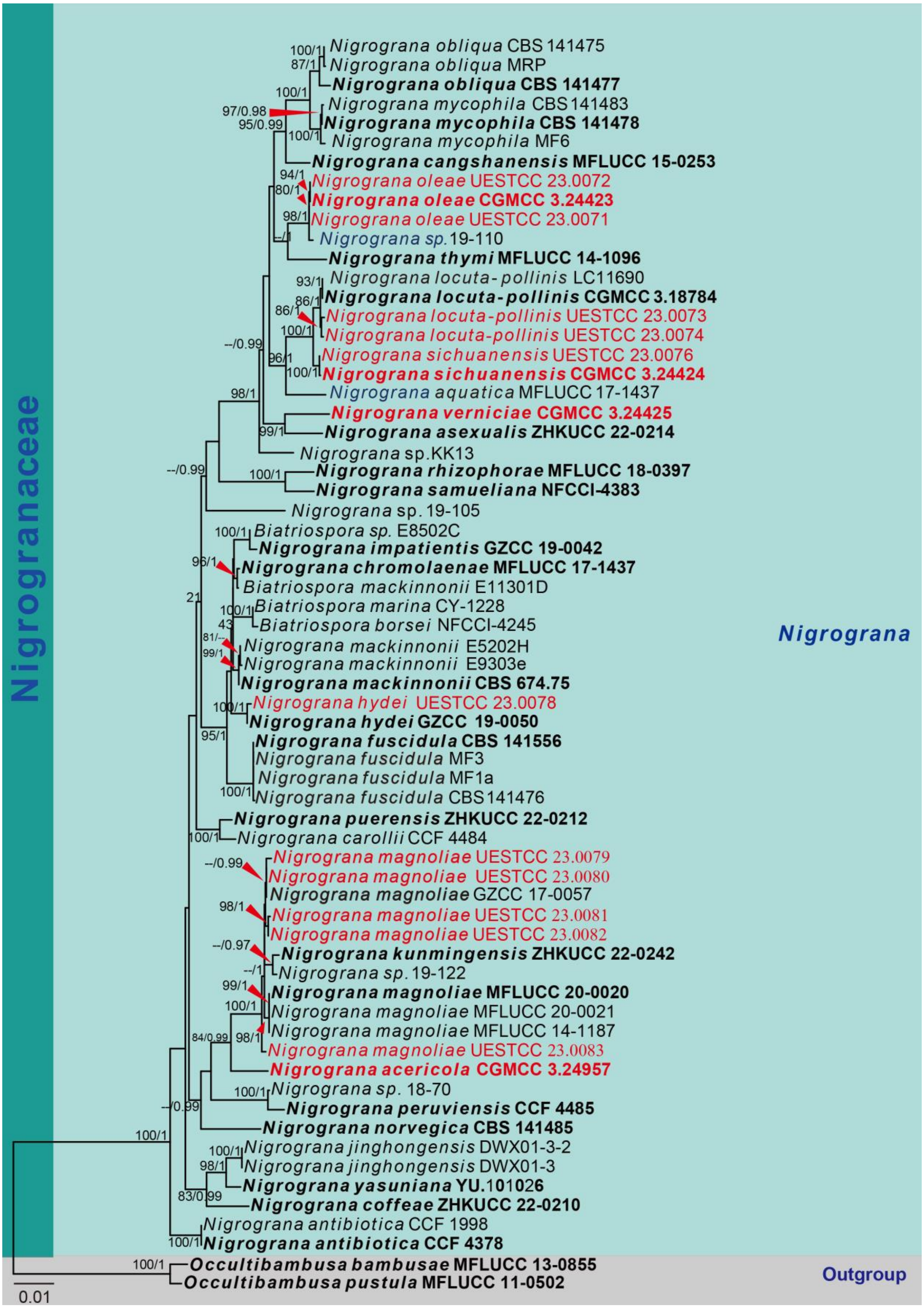

Figure 45 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, and *tef1* sequence data. Sixty-five strains are included in the combined sequence analyses, which comprise 2,312 characters with gaps. *Occultibambusa bambusae* MFLUCC 13-0855 and *O. pustula* MFLUCC 11-0502 are used as outgroup taxa. Tree topology of ML analysis is similar to BI analysis. The best scoring RAxML tree with a final likelihood value of -10389.941795 is

presented. Proportion of gaps and completely undetermined characters in this alignment are 15.85% with 697 distinct alignment patterns. Estimated base frequencies were as follows; A = 0.235174, C = 0.263723, G = 0.267412, T = 0.233691; substitution rates AC = 2.113529, AG = 3.517522, AT = 2.191070, CG = 1.008825, CT = 12.946138, GT = 1.000000; gamma distribution shape parameter α = 0.585694. Bootstrap support values for ML ≥ 75% and BYPP ≥ 0.95 are defined as ML/BYPP above the nodes. Hyphens (--) represent support values less than 75% in ML and 0.95 in BI. Newly generated sequences are in red and ex-type strains are in bold.

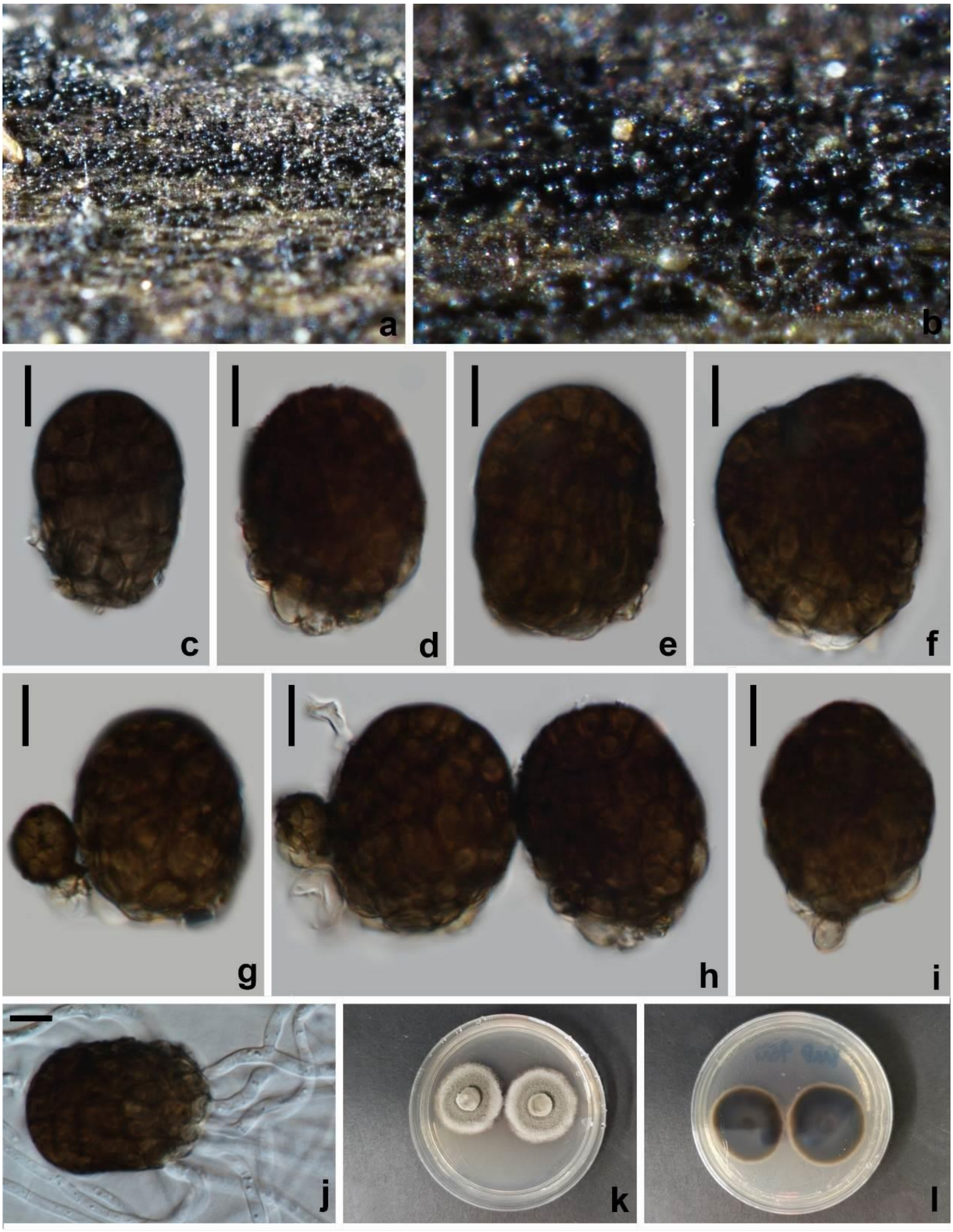

Figure 46 – *Paramonodictys paeoniae* (HKAS 127176, holotype). a, b Colonies on host surface. c–i Conidia. j Germinated conidium. k Colonies on PDA from above. l Colonies on PDA from below. Scale bars: c–j = 10 µm.

Saprobic on decaying branches of *Paeonia suffruticosa*. Sexual morph: Not observed. Asexual morph: Colonies on substrate effuse, superficial, erect, solitary, oboviod to oblong, visible as brownish to dark brown dots scattered on the host surface. *Mycelium* partially superficial. *Stromata* inconspicuous. *Conidiogenous cells* monoblastic, integrated, pale brown. *Conidia* 32–43 × 29.5–31 µm ($\bar{x}$ = 37.5 × 30 µm, n = 20), obovoid to subglobose, dictyosporous, muriform, thick-walled, irregularly multiseptate, brown to dark brown.

Culture characteristics – Conidia germinate on PDA within 24 h at 25 ℃, germ tubes arise from the base of the conidia. Colonies on PDA reach 25 mm diam. after 14 d at 25 °C, colonies circular, flat, edge entire, olivaceous, with cream white margin; reverse dark brown, with a light brown margin.

Material examined – China, Sichuan Province, Mianyang city, Youxian district, N 31°25'22.18", E 104°48'57.99", elevation 800 m, on branches of *Paeonia suffruticosa*, 10 September 2021, W.L. Li, YMD 450 (HKAS 127176, holotype), ex-type culture CGMCC 3.24437 = UESTCC 23.0085.

GenBank numbers – CGMCC 3.24437 = LSU: OR253298, ITS: OR253139, SSU: OR253211, *tef1*: OR251149, *rpb2*: OR253758; UESTCC 23.0085 = LSU: OR253299, ITS: OR253140, SSU: OR253212, *tef1*: OR251150, *rpb2*: OR253759.

Notes – The morphology of *Paramonodictys paeoniae* fits well with the generic concept of *Paramonodictys*, being characterized by monoblastic conidiogenous cells, dictyosporous, muriform, globose to subglobose, dark brown conidia. *Paramonodictys paeoniae* is similar to *P. solitarius* in the shape and size of conidia (Table 2), but the latter has olivaceous brown conidia attached to hyaline and subcylindrical stromata. *Paramonodictys paeoniae* is phylogenetically sister to *P. hongheensis* (Fig. 47), but the conidia of *P. paeoniae* are larger than those of *P. hongheensis* (32–43 × 29.5–31 µm vs.19–26 × 19–22 µm).

Table 2 Morphological comparison of *Paramonodictys* species.

***Paramonodictys* species**	**Conidia**			**Conidiogenous cells**	**References**
	size (µm)	**shape**	**color**	**size (µm)**	
P. hongheensis	19–26 × 19–22	subglobose to oval	pale-brown to yellow-brown	10–15 × 16–25	Yang et al. (2022)
P. paeoniae	32–43 × 29.5–31	subglobose to obovoid	brown to dark brown	–	This study
P. solitarius	50–87 × 40–61	globose or subglobose	olivaceous brown to dark brown	–	Hyde et al. (2020)
P. yunnanensis	47–70 × 35–47	obovoid to subglobose	brown to olivaceous brown	8–12 × 9–12	Yang et al. (2022)

Sulcatisporaceae Kaz. Tanaka & K. Hiray., Stud. Mycol. 82: 119 (2015)

MycoBank number: MB 814431; Facesoffungi number: FoF 06031

Notes – Sulcatisporaceae was introduced by Tanaka et al. (2015) to accommodate *Magnicamarosporium*, *Sulcatispora* and *Neobambusicola*. Members of this family are saprobic on dead twigs and stems (Crous et al. 2014, Tanaka et al. 2015, Phukhamsakda et al. 2017, Phookamsak et al. 2019). Presently, 13 species from seven genera viz. *Anthosulcatispora*, *Loculosulcatispora*, *Magnicamarosporium*, *Neobambusicola*, *Parasulcatispora*, *Pseudobambusicola* and *Sulcatispora* are accepted in the family (Tanaka et al. 2015, Phukhamsakda et al. 2017, Phookamsak et al. 2019). *Anthosulcatispora*, *Loculosulcatispora*, *Neobambusicola*, and *Sulcatispora* are holomorphic genera, while *Magnicamarosporium*, *Parasulcatispora* and *Pseudobambusicola* are reported as asexual genera.

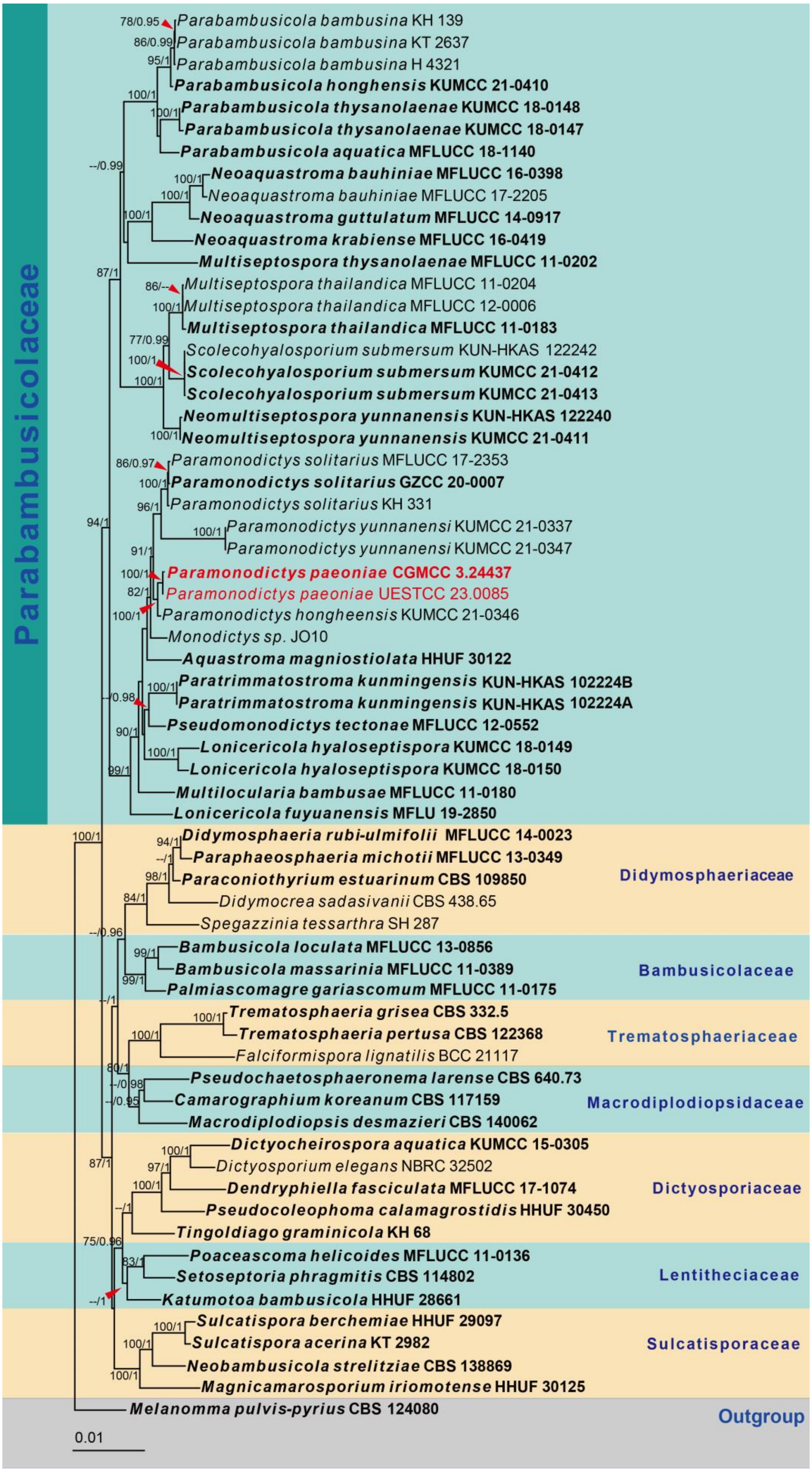

Figure 47 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU,

SSU and *tef1* sequence data. Sixty-five strains are included in the combined sequence analyses, which comprise 3,204 characters with gaps. *Melanomma pulvis-pyrius* CBS 124080 is used as the outgroup taxon. Tree topology from ML analysis is similar to BI analysis. The best scoring RAxML tree with a final likelihood value of -20845.470255 is presented. Proportion of gaps and completely undetermined characters in this alignment are 16.53% with 1143 distinct alignment patterns. Estimated base frequencies were as follows; A = 0.240053, C = 0.249770, G = 0.271530, T = 0.238646; substitution rates AC = 1.002161, AG = 2.581445, AT = 1.347365, CG = 1.062317, CT = 6.950391, GT = 1.000000; gamma distribution shape parameter α = 0.504660. Bootstrap support values for ML ≥ 75% and BYPP ≥ 0.95 are defined as ML/BYPP above the nodes. Hyphens (--) represent support values less than 75% in ML and 0.95 in BI. Newly generated sequences are in red and ex-type strains are in bold.

Loculosulcatispora hongheensis Wanas., J. Fungi 8 (375), 14 (2022). Fig. 48

MycoBank number: MB 843434

Saprobic on decaying branches of *Vernicia fordii* Hemsl. Sexual morph: Not observed. Asexual morph: Coelomycetous. *Conidiomata* 200–350 × 140–200 µm ($\bar{x}$ = 280 × 170 µm, n = 10), immersed or slightly erumpent to the host surface, dark brown to black, globose to subglobose, multilocular, lacking an ostiole. *Conidiomatal wall* 30–45 µm wide, unequally thickened, composed of 3–10 layers of brown-walled cells of *textura angularis*, heavily pigmented towards the outer layers. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 6.5–11 × 2–2.5 µm ($\bar{x}$ = 8.5 × 2.2 µm, n = 20), enteroblastic, cylindrical, smooth, hyaline, thin-walled, arising from the basal cavity. *Conidia* 10–12 × 3–4 µm ($\bar{x}$ = 11 × 3.5 µm, n = 20), ellipsoidal to obovoid, obtuse at both ends, hyaline, aseptate, smooth-walled with granular contents.

Culture characteristics – Colonies on PDA reach 30 mm diam. after 14 d at 25 °C, colonies circular, margin entire, dense, slightly raised, cream white; reverse white to cream at the margin, dark brown in the centre.

Material examined – China, Sichuan Province. Guangyuan city, Chaotian district N 32°41'5.48", E 106°01'22.40", elevation 444 m, on a branch of *Vernicia fordii*, 19 April 2021, W.L. Li, YT 204 (HKAS 127177), living culture UESTCC 23.0086 = CGMCC 3.24432.

GenBank numbers – CGMCC 3.24432 = LSU: OR253266, ITS: OR253226, *tef1*: OR251163, *rpb2*: OR251137.

Notes – The sexual morph of *Loculosulcatispora hongheensis* was introduced by Wanasinghe et al. (2022) from dead twigs of forest litter. Our new collection clustered with *L. hongheensis* (HKAS 122920 and HKAS 122921) with an absolute support (100% ML/1 BYPP) (Fig. 50). The BLASTn searches of the LSU sequence of our strain resulted in 100% similarity with *L. hongheensis* HKAS 122920, the *tef1* showed 99.67% similarity with *L. hongheensis* HKAS 122920, and ITS BLASTn results appeared at 99.53% similarity with *L. hongheensis* HKAS 122920. Thus, we accept the new collection as the asexual morph of *L. hongheensis*, which is discovered on *Vernicia fordii* for the first time.

Loculosulcatispora paeoniae W.L. Li & Jian K. Liu, sp. nov. Fig. 49

MycoBank number: MB 849160; Facesoffungi number: FoF 14405

Etymology – The specific epithet ‘*paeoniae*’ refers to the host genus *Paeonia*, from which the holotype was collected.

Saprobic on decaying branches of *Paeonia suffruticosa*. Sexual morph: *Ascomata* 120–150 × 140–160 µm ($\bar{x}$ = 140 × 150 µm, n = 10), solitary, scattered, immersed or slightly erumpent on the host, globose to subglobose, brown to dark brown, ostiolate. *Ostiole* 37 × 40 µm wide, central, papillate. *Peridium* 17.5–24 µm thick, composed of several layers of *textura angularis,* merged with the host tissues. *Hamathecium* 1.8–2.5 µm wide, composed of numerous, filamentous, rarely branched and anastomosed, hyaline pseudoparaphyses. *Asci* 71–80 × 8–11 µm ($\bar{x}$ = 75.5 × 9.5 µm, n = 20), bitunicate, fissitunicate, cylindro-obcavate, with a globose pedicel, apically rounded, with a minute ocular chamber. *Ascospores* 24–27 × 4–5 µm ($\bar{x}$ = 25.5 × 4.5 µm, n = 20), 8-spored, uniseriate, partially overlapping, fusiform, with obtuse ends, slightly curved, 1-septate, hyaline, smooth-walled, with 4 guttules, with or without a mucilaginous sheath. Asexual morph: Not observed.

Culture characteristics – Colonies on PDA reach 30 mm diam. after 14 d at 25 °C, colonies circular, margin entire, dense, slightly raised, cream white; reverse cream at the margin, yellowish brown in the middle, pale brown in the centre.

Material examined – China, Sichuan Province, Leshan city, Shizhong district, N 29°42'44.34", E 103°52'41.80", elevation 444 m, on branches of *Paeonia suffruticosa*, 23 July 2021, W.L. Li, YMD 331 (HKAS 127178, holotype), ex-type culture CGMCC 3.24433 = UESTCC 23.0089.

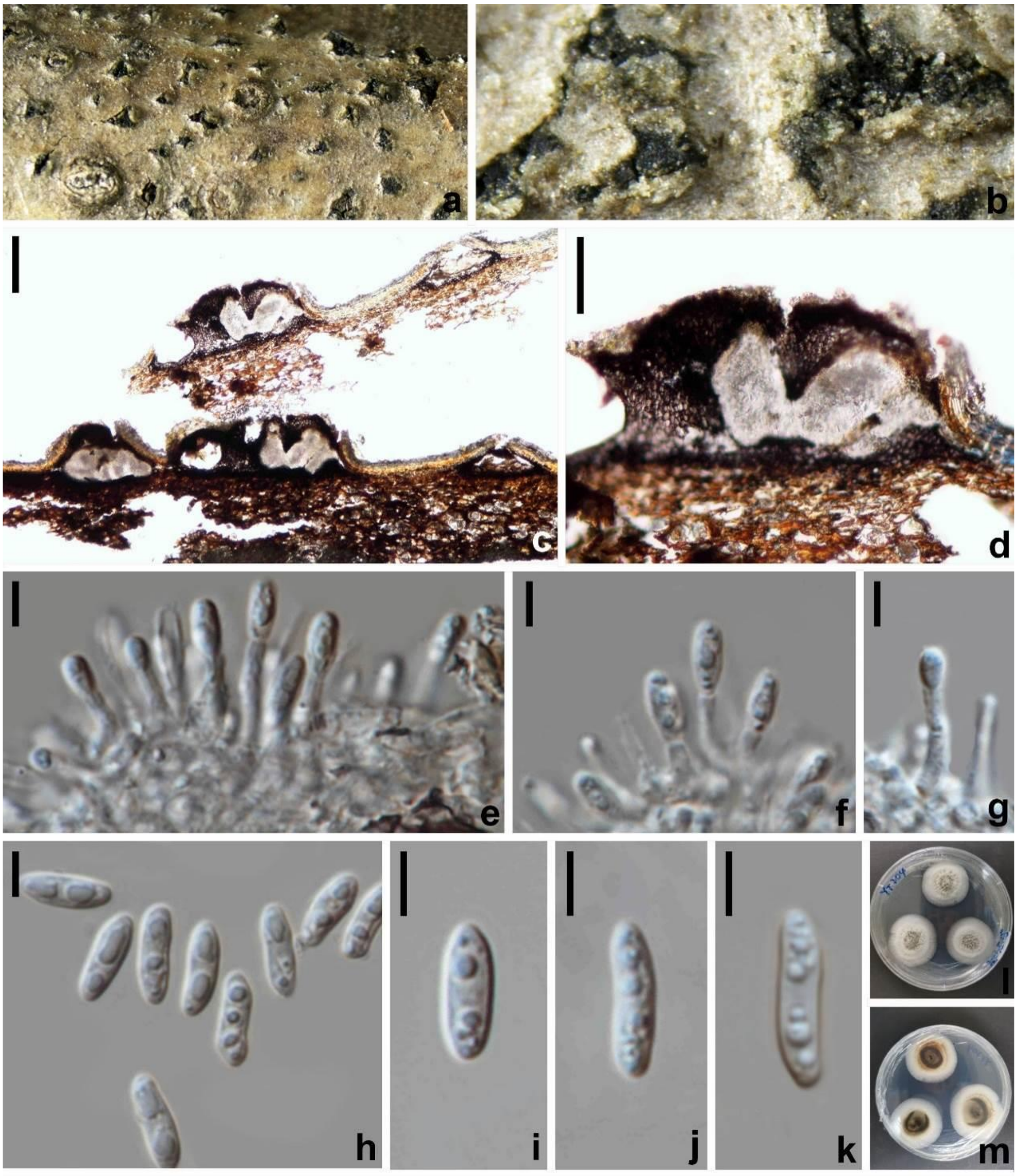

Figure 48 – *Loculosulcatispora hongheensis* (HKAS 127177, asexual morph). a, b Appearance of conidiomata on natural substrate. c, d Vertical section of conidiomata. e–g Conidiogenous cells and developing conidia. h–k Conidia. l Colonies on PDA from above. m Colonies on PDA from below. Scale bars: c = 200 μm, d = 100 μm, e–h = 10 μm, i–k = 5 μm.

GenBank numbers – CGMCC 3.24433 = LSU: OR253281, ITS: OR253122, SSU: OR253195, *tef1*: OR251172; UESTCC 23.0089 = LSU: OR253282, ITS: OR253122, SSU: OR253196, *tef1*: OR251173.

Notes – In the multi-gene phylogenetic analysis, *Loculosulcatispora paeoniae* formed a distinct clade in *Loculosulcatispora* and clustered with *L. hongheensis* and *L. thailandica* by 100% ML/1.00 BYPP (Fig. 50). *Loculosulcatispora paeoniae* shares similar morphological characters with the sexual morph of *L. hongheensis* in having cylindrical to clavate asci, and fusiform, uniseptate ascospores with a mucilaginous sheath. However, it differs in having a globose pedicel, while *L. hongheensis* has a cylindrical pedicel with truncate base. Additionally, ascospores of *L. paeoniae* have obuse ends, while they are acute in *L. hongheensis* (Wanasinghe et al. 2022).

Thyridariaceae Q. Tian & K.D. Hyde, Fungal Divers. 63: 254 (2013)

MycoBank number: MB 805172; Facesoffungi number: FoF 08374

Notes – Thyridariaceae was introduced by Hyde et al. (2013) to accommodate *Thyridaria*. Later, Jaklitsch & Voglmayr (2016) introduced *Parathyridaria* and accepted five genera viz. *Neoroussoella*, *Parathyridaria*, *Roussoella*, *Roussoellopsis* and *Thyridaria* in Thyridariaceae. Wanasinghe et al. (2018) introduced three genera, *Cycasicola*, *Neoconiothyrium* and *Pararoussoella*. However, *Neoconiothyrium* and *Pararoussoella* have been transferred to Roussoellaceae based on morphological data and phylogenetic analyses (Jayasiri et al. 2019, Phookamsak et al. 2019). Subsequently, *Thyridariella*, *Liua*, *Chromolaenomyces* and *Pseudothyridariella* were introduced in Thyridariaceae (Devadatha et al. 2018, Phookamsak et al. 2019, Mapook et al. 2020).

Pseudothyridariella idesiae W.L. Li & Jian K. Liu sp. nov. Fig. 51

MycoBank number: MB 849161; Facesoffungi number: FoF 14402

Etymology – The specific epithet refers to the host genus *Idesia*, from which the holotype was collected.

Saprobic on decaying branches of *Idesia polycarpa*. Sexual morph: Not observed. Asexual morph: *Conidiomata* 660–700 × 440–560 µm ($\bar{x}$ = 680 × 500 µm, n = 10), superficial, subglobose to globose, black, unilocular, thick-walled, surrounded by yellow, dense, hair-like setae, papillate. *Conidiomatal wall* 54–97 µm thick, composed of thick-walled, brown cells of *textura intricata* to *textura epidermoidea*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 6.5–9 × 3–4 µm ($\bar{x}$ = 7.5 × 3.5 µm, n = 10), hyaline, holoblastic, cylindrical to lageniform, indeterminate, thick- and smooth-walled. *Conidia* 16–18 × 6–8 µm ($\bar{x}$ = 17 × 7 µm, n = 20), cylindrical to ellipsoidal, broadly rounded at ends, occasionally swollen at the basal cell, 0–4 transverse septate, 1–2 longitudinal or oblique septa in the apical or second cell, hyaline to dark brown, straight, guttulate, smooth.

Culture characteristics – Conidia germinate on PDA within 24 h at 25 °C, germ tubes arise from all cells of conidia. Colonies on PDA reach 25 mm diam. after 14 d at 25 °C, colonies cream, circular, flat, slightly raised, dense at the centre, white at the margin; reverse, brown from the centre of the colony, cream at margin.

Material examined – China, Sichuan Province. Chengdu city, Chongzhou county, Huaiyuan town, N 30°42'58.0428", E 103°33'46.1088", elevation 685 m, on branches of *Idesia polycarpa*, 5 November 2021, W.L. Li, STZ 522 (HKAS 127179, holotype), ex-type culture UESTCC 23.0090 = CGMCC 3.24439.

GenBank numbers – CGMCC 3.24439 = LSU: OR253307, ITS: OR253148, SSU: OR253216, *tef1*: OR251154, *rpb2*: OR253762.

Notes – The multi-gene phylogenetic analysis shows that *Pseudothyridariella idesiae* is sister to the ex-type strain of *P. chromolaenae* (MFLUCC 17-1472) with 100% ML/1.00 BYPP support (Fig. 52). A comparison between *P. idesiae* and *P. chromolaenae* indicated 11 (2.2%), 6 (0.8%) and 11 (1.2%) nucleotide differences in the ITS, *rpb2*, *tef1*, respectively. However, it is not possible to compare the morphological characteristics of these two closely related species since *P. idesiae* was found as an asexual morph in nature, while *P. chromolaenae* was found as a sexual morph and has not produce its asexual morph in culture (Mapook et al. 2020). Based on the available evidence, *P. idesiae* was identified as a new species.

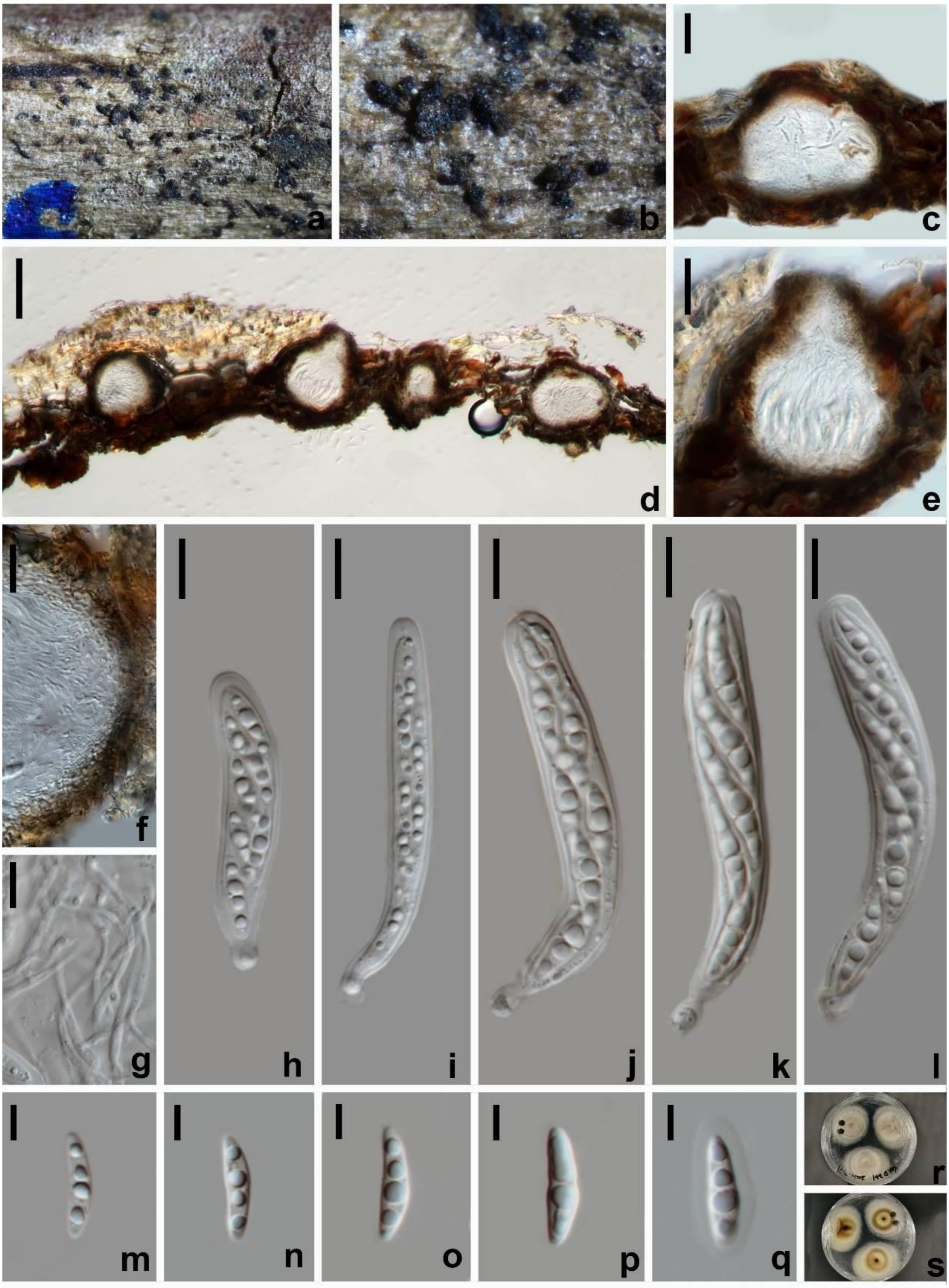

Figure 49 – *Loculosulcatispora paeoniae* (HKAS 127178, holotype). a, b Appearance of ascomata on host surface. c–e Vertical section through ascomata. f Peridium. g Hamathecium. h–l Asci. m–q Ascospores. r Colonies on PDA from above. s Colonies on PDA from below. Scale bars: c, e = 40 µm, d = 100 µm, f = 20 µm, g–l = 10 µm, m–q = 5 µm.

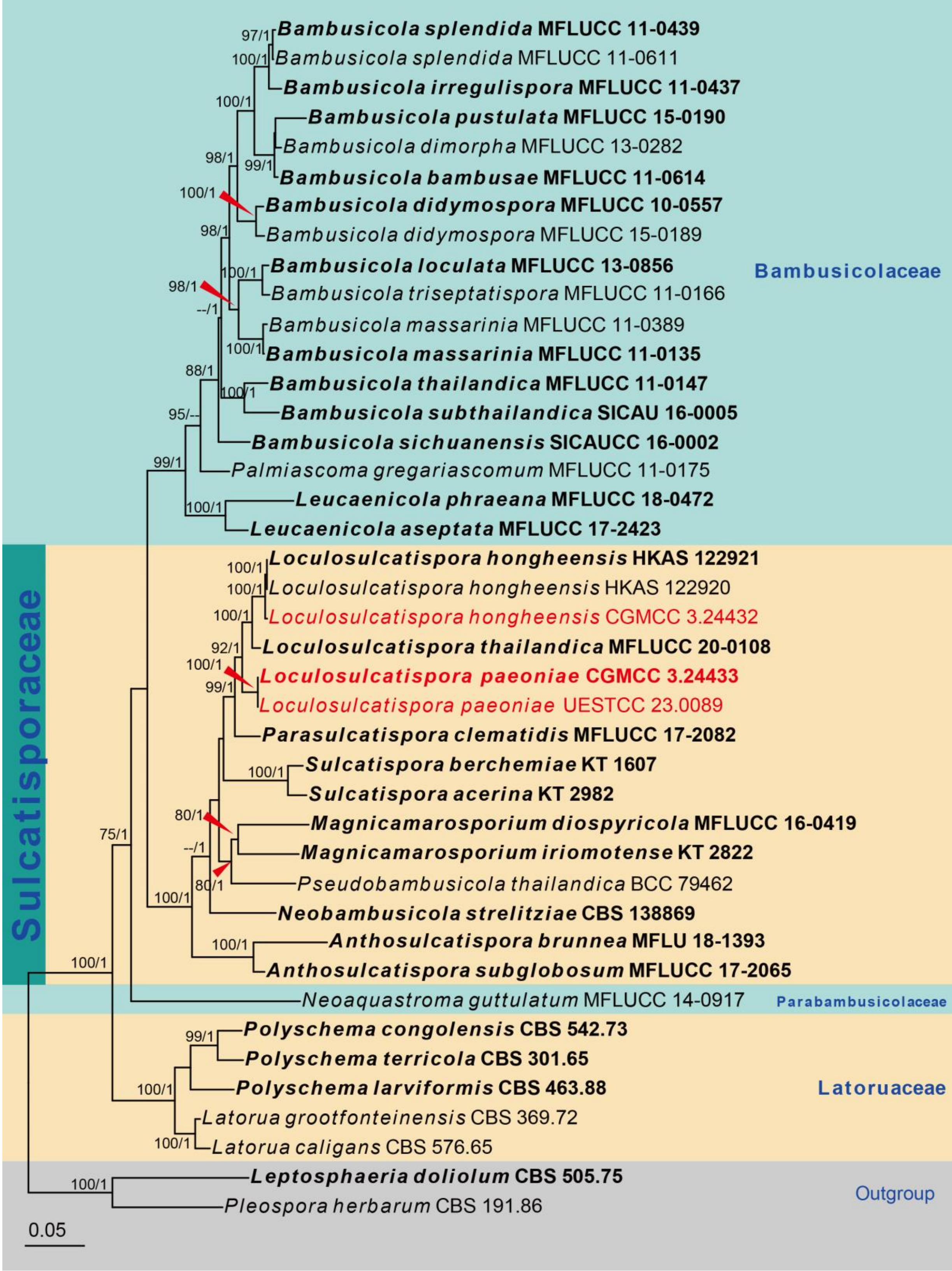

Figure 50 – Phylogram generated from maximum likelihood analysis based on combined SSU, LSU, ITS, *tef1* and *rpb2* sequence data. Forty strains are included in the combined sequence analyses, which comprise 4,457 characters with gaps. *Leptosphaeria doliolum* CBS 505.75 and *Pleospora herbarum* CBS 191.86 are used as outgroup taxa. Tree topology of ML analysis is similar to BI analysis. The best scoring RAxML tree with a final likelihood value of -25532.250304 is presented. Proportion of gaps and completely undetermined characters in this alignment are 27.26% and 1,599 number of distinct site patterns. Estimated base frequencies were as follows; A =

0.240301, C = 0.259495, G = 0.269728, T = 0.230476; substitution rates AC = 1.235353, AG = 2.936999, AT = 1.109122, CG = 0.909219, CT = 6.505446, GT = 1.000000; gamma distribution shape parameter α = 0.455759. Bootstrap support values for ML ≥ 75% and BYPP ≥ 0.95 are defined as ML/BYPP above the nodes. Hyphens (--) represent support values less than 75% in ML and 0.95 in BI. Newly generated sequences are in red and ex-type species are in bold.

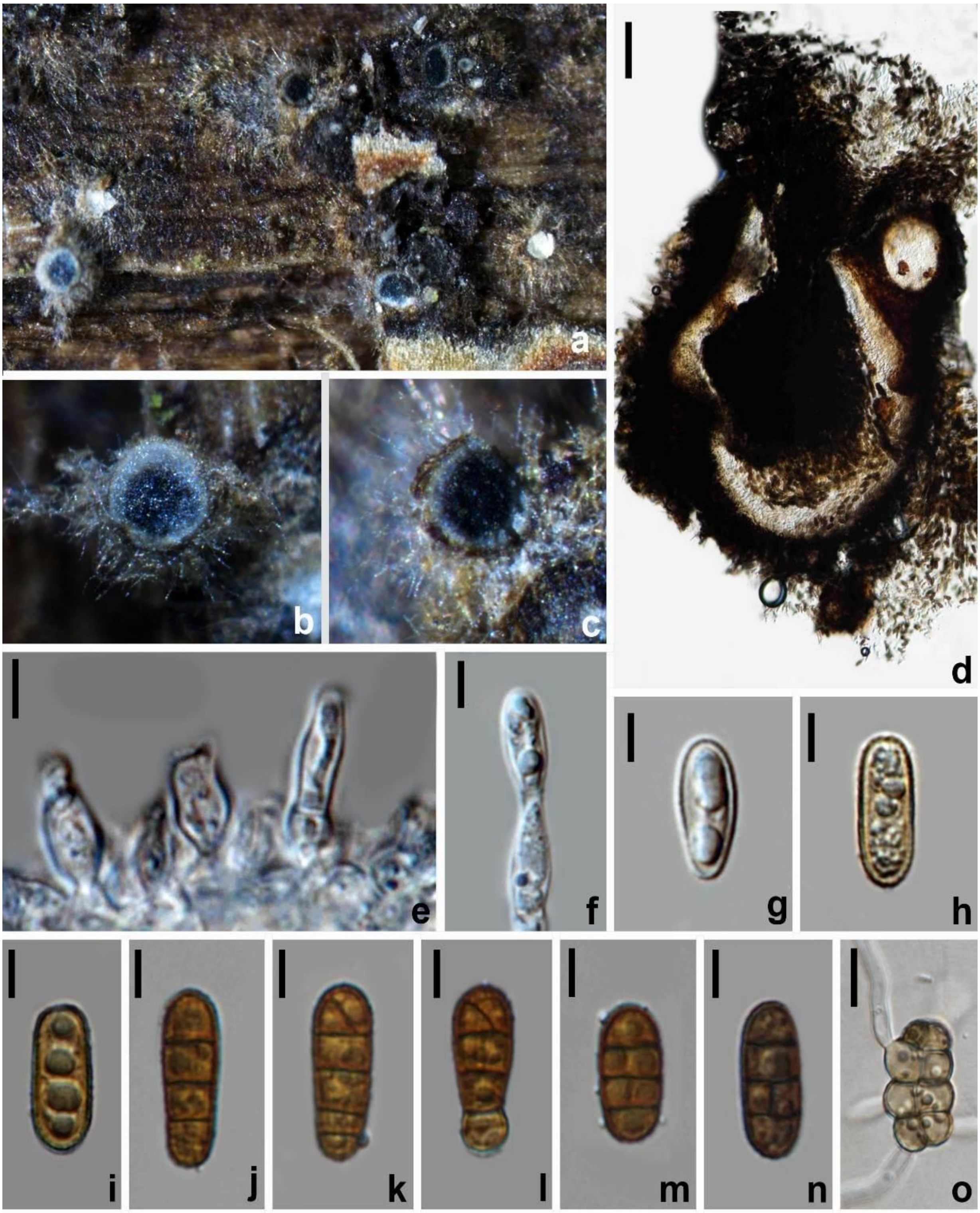

Figure 51 – *Pseudothyridariella idesiae* (HKAS 127179, holotype). a–c Appearance of conidiomata on natural substrate. d Vertical section of conidioma. e, f Conidiogenous cells and developing conidia. g–n Conidia. o Germinated conidium. Scale bars: d = 100 µm, e–n = 5 µm, o = 10 µm.

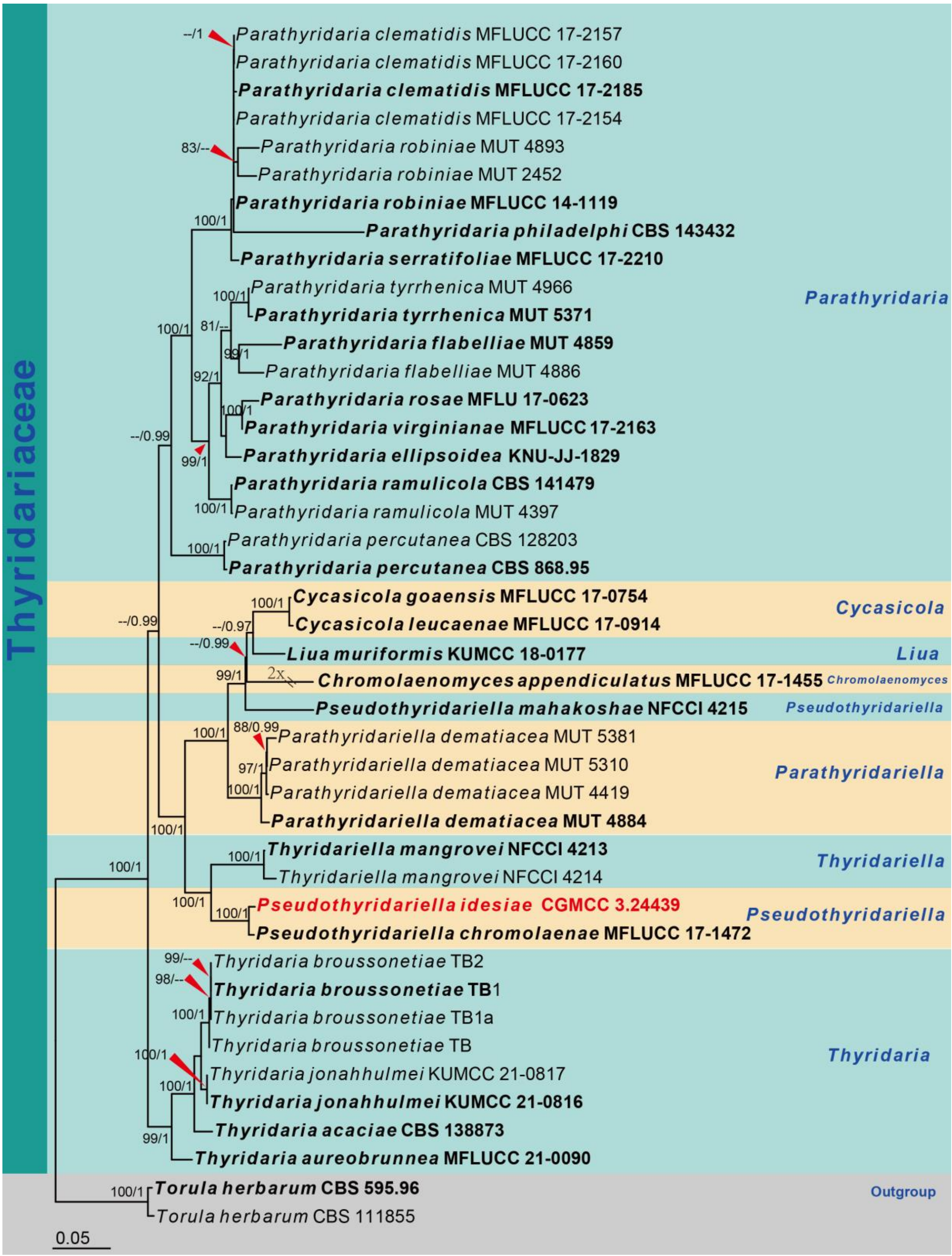

Figure 52 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, SSU, *tef1* and *rpb2* sequence data. Forty-three strains are included in the combined sequence analyses, which comprise 4,317 characters with gaps. *Torula herbarum* CBS 111855 and CBS 595.96 are used as outgroup taxa. Tree topology of ML analysis is similar to BI analysis. The best scoring RAxML tree with a final likelihood value of -22577.133520 is presented. Proportion of gaps and completely undetermined characters in this alignment are 19.25% with 1525 distinct alignment patterns. Estimated base frequencies were as follows; A = 0.248574, C = 0.257170, G = 0.268899, T = 0.225357; substitution rates AC = 1.143452, AG = 2.576414, AT = 1.269009, CG = 0.852776, CT = 5.835262, GT = 1.000000; gamma distribution shape parameter α = 0.518283.

Bootstrap support values for ML ≥ 75% and BYPP ≥ 0.95 are defined as ML/BYPP above the nodes. Hyphens (--) represent support values less than 75% in ML and 0.95 in BI. Newly generated sequences are in red and ex-type strains are in bold.

Valsariales Jaklitsch, K.D. Hyde & Voglmayr, Fungal Diversity 73: 167 (2015)
Valsariaceae Jaklitsch, K.D. Hyde & Voglmayr, Fungal Diversity,73: 167 (2015)

MycoBank number: MB 811901; Facesoffungi number: FoF 06561

Note – Valsariaceae was introduced by Jaklitsch et al. (2015) with *Valsaria insitiva* as the type species. Members of Valsariaceae have a worldwide distribution on various substrates as saprobes, plant pathogens or necrotrophs. Three genera, *Bambusaria*, *Myrmaecium* and *Valsaria* are accepted in this family. The spore ornamentation is an important character to differentiate genera within Valsariaceae, while the number of guttules and wall development has been used to segregate species of *Valsaria* (Pem et al. 2019).

Valsaria insitiva (Tode) Ces. & De Not., Comm. Soc. crittog. Ital. 205 (1863) Fig. 53

MycoBank number: MB 450784

Known distribution – Brazil, Canada, France, Germany, Georgia, India, New Zealand, Poland, Portugal, South Africa, Sri Lanka, USA.

Saprobic on decaying branches of *Camellia oleifera*. Sexual morph: *Stromata* pseudostromatic, erumpent from host surface, scattered or mostly gregarious, pustular at dehiscence, broadly conical or subglobose with a flattened base, enclosed on top by a thick pseudoparenchymatous black crust. *Ascomata* 270–290 × 120–140 µm ($\bar{x}$ = 280 × 130 µm, n = 10), 1–3 per individual cluster, vertical to oblique, subglobose to flask-shape. *Ostiole* 25–33 µm wide, central, cylindrical, interior periphysate, inconspicuous opening at the surface. *Peridium* 14–21 µm thick, pseudoparenchymatous, brown. *Hamathecium* 2–3.5 µm wide, numerous, simple, rarely septate, cylindrical, apically free. *Asci* 92–115 × 10.5–13.5 µm ($\bar{x}$ = 103.5 × 12 µm, n = 20), 8-spored, bitunicate, fissitunicate, dehiscent, cylindrical, short pedicellate, truncate or furcate, apex containing an ocular chamber and a pulvinate ring. *Ascospores* 14–15 × 7–8 µm ($\bar{x}$ = 14.5 × 7.5 µm, n = 20), uniseriate, ovate to ellipsoidal, golden to dark brown, 2-celled, with a dark middle, constricted at the septum, septum thicker than the cell wall, rough-walled. Asexual morph: Not observed.

Material examined – China, Sichuan Province, Chengdu city, Pidu district, N 30°19'49.84", E 103°59'45.61", elevation 442 m, on a branch of *Camellia oleifera*, 24 November 2021, W.L. Li, YC 536 (HUEST 23.0096), living culture UESTCC 23.0096; *ibid*., on a branch of *Pistacia chinensis*, 19 March 2021, W.L. Li, HLM 76 (HUEST 23.0093 = HKAS 127180, holotype), living culture UESTCC 23.0093 = CGMCC 3.24428; *ibid*., on a branch of *Acer truncatum*, 19 March 2021, W.L. Li, HLM 38 (HUEST 23.0094), living culture UESTCC 23.0094; *ibid*., University of Electronic Science and Technology of China (UESTC) campus (Qingshuihe), N 30°45'24.74", E 103°55'21.10", elevation 638 m, on a branch of *Trachycarpus fortunei*, 24 November 2021, W.L. Li, W120 (HUEST 23.0095), living culture UESTCC 23.0095.

GenBank numbers – UESTCC 23.0096 = LSU: OR253309, ITS: OR253150; CGMCC 3.24428 = LSU: OR253243, ITS: OR253091, *rpb2*: OR262135; UESTCC 23.0094 = LSU: OR253238, ITS: OR253086, *rpb2*: OR262134; UESTCC 23.0095 = LSU: OR253315, ITS: OR253158, *rpb2*: OR253755.

Notes – *Valsaria insitiva* was first described as *Sphaeria insitiva* by Tode et al. (1791). However, due to the lack of microscopic data of the original specimen, Ju et al. (1996) designated another specimen (*Valsaria insitiva* CBS 127882) from *Vitis* as the epitype of *S. insitiva*. Our new collection isolated from *Camellia oleifera* shares similar morphological characters to the ex-epitype strain of *V. insitiva*. They share pseudostromatic stromata, apically free pseudoparaphyses, an apical ring and ellipsoid ascospores with tuberculate surface ornamentation. Phylogenetically, the new strain forms a close relationship with *V. insitiva* with an absolute support (100% ML/1.00 BYPP) (Fig. 54). This is the first record of *V. insitiva* from woody oil plants in China.

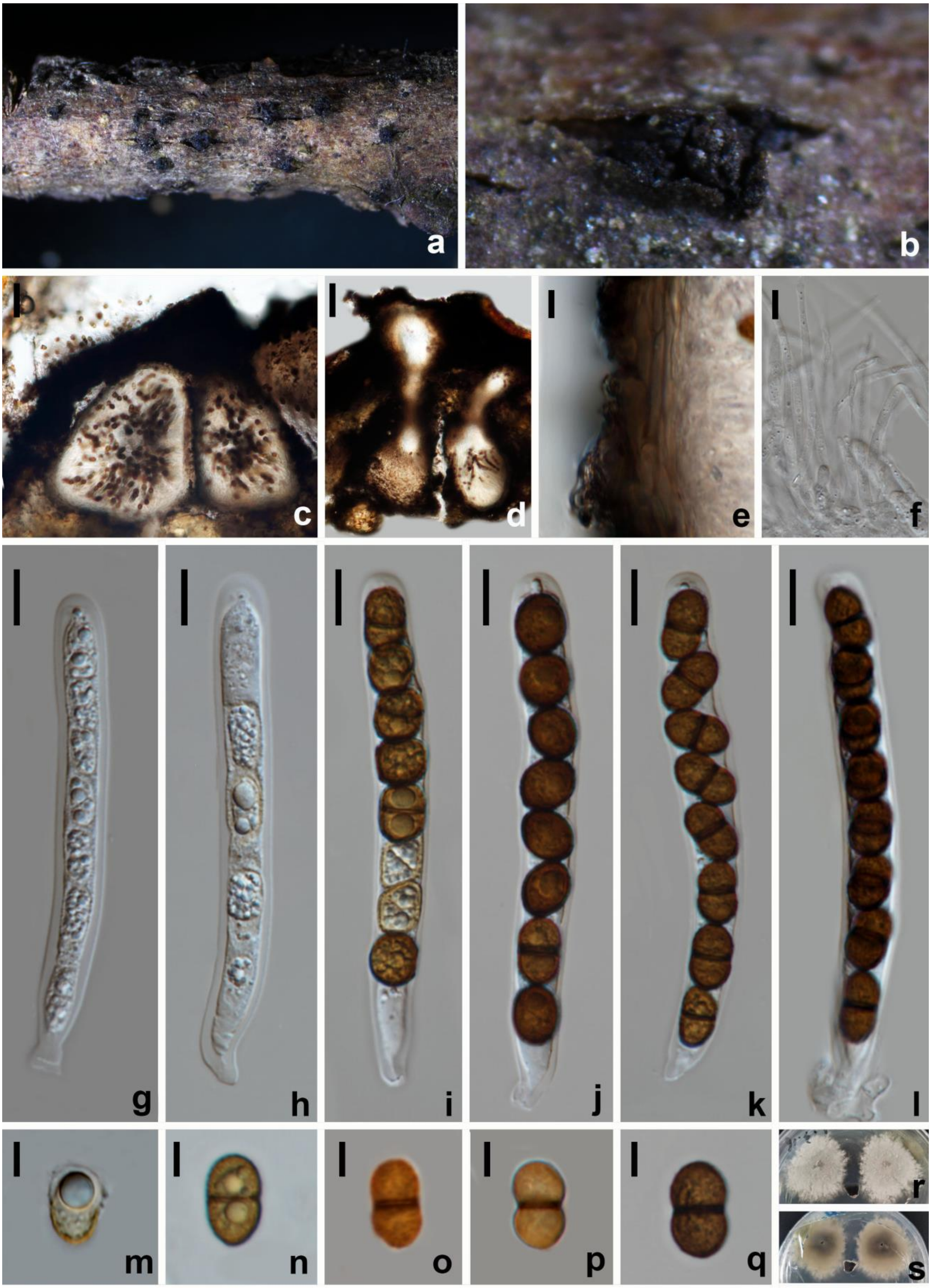

Figure 53 – *Valsaria insitiva* (HUEST 23.0096, new county record). a, b Appearance of ascomata on host surface. c, d Vertical section through ascostromata. e Peridium. f Hamathecium. g–l Asci. m–q Ascospores, r Colonies on PDA from above. s Colonies on PDA from below. Scale bars: c = 50 μm, d = 100 μm, e–q = 10 μm.

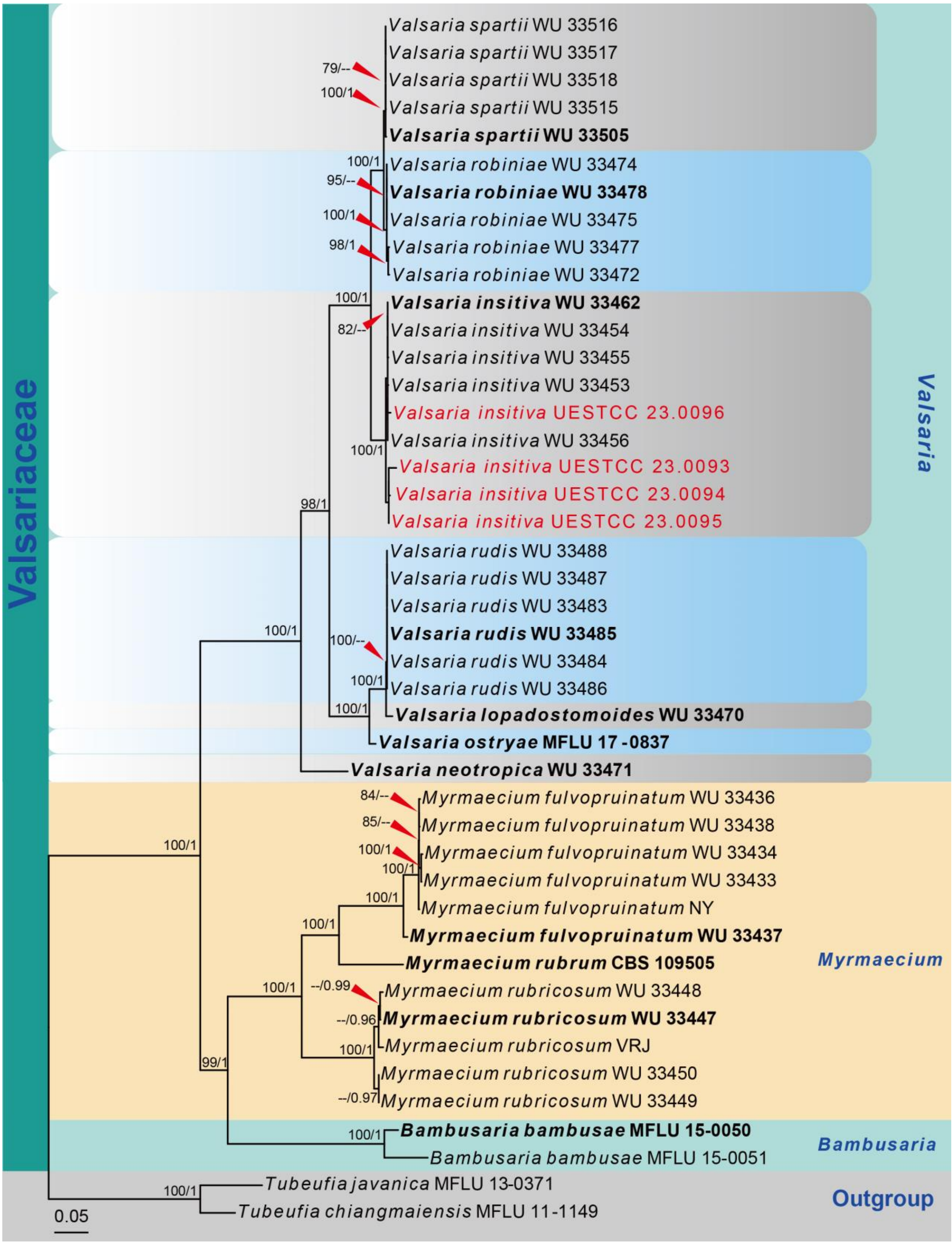

Figure 54 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU and *rpb2* sequence data. Forty-four strains are included in the combined sequence analyses, which comprise 2,592 characters with gaps. *Tubeufia chiangmaiensis* MFLU 11–1149 and *T. javanica* MFLU 13–0371 are used as outgroup taxa. Tree topology of ML analysis was similar to BI analysis. The best scoring RAxML tree with a final likelihood value of -21179.874899 is presented. Proportion of gaps and completely undetermined characters in this alignment are 8.51% with 926 distinct alignment patterns. Estimated base frequencies were as follows; A = 0.087127, C =

0.033474, G = 0.088612, T = 0.058542; substitution rates AC = 0.312229, AG = 2.081526, AT = 3.217693, CG = 0.095403, CT = 0.138768, GT = 0.260191; gamma distribution shape parameter α = 0.266310. Bootstrap support values for ML ≥ 75% and BYPP ≥ 0.95 are defined as ML/BYPP above the nodes. Hyphens (--) represent support values less than 75% in ML and 0.95 in BI. Newly generated sequences are in red and ex-type strains are in bold.

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