



# Fungal diversity notes 1717–1817: taxonomic and phylogenetic contributions on genera and species of fungal taxa

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## Abstract

As the continuation of Fungal Diversity Notes series, the current paper is the 16th contribution to this series. A total of 103 taxa from seven classes in *Ascomycota* and *Basidiomycota* are included here. Of these 101 taxa, four new genera, 89 new species, one new combination, one new name and six new records are described in detail along with information of hosts and geographic distributions. The four genera newly introduced are *Ascoglobospora*, *Atheliella*, *Rufoboletus* and *Tenuimyces*. Newly described species are *Akanthomyces xixiuensis*, *Agaricus agharkarii*, *A. allostipitatus*, *Amphisphaeria guttulata*, *Ascoglobospora marina*, *Astrothelium pseudostraminicolor*, *Athelia naviculisporea*, *Atheliella conifericola*, *Athelopsis subglaucina*, *Aureoboletus minimus*, *A. nanlingensis*, *Autophagomyces incertus*, *Beltrania liliiferae*, *Beltraniella jiangxiensis*, *Botryobasidium coniferarum*, *Calocybella sribuabanensis*, *Calonarius caesiofulvus*, *C. nobilis*, *C. pacificus*, *C. pulcher*, *C. subcorrosus*, *Cortinarius flaureifolius*, *C. floridaensis*, *C. subiodes*, *Crustomyces juniperi*, *C. scytinostromoides*, *Cystostereum subsirmaurense*, *Dimorphomyces seemanii*, *Fulvoderma microporum*, *Ginnsia laricicola*, *Gomphus zamorinorum*, *Halobyssothecium sichuanense*, *Hemileccinum duriusculum*, *Henningsomyces hengduanensis*, *Hygronarius californicus*, *Kneiffiella pseudoabditata*, *K. pseudoalutacea*, *Laboulbenia bifida*, *L. tschirnhausii*, *L. tuberculata*, *Lambertella dipterocarpacearum*, *Laxitextum subrubrum*, *Lyomyces austro-occidentalis*, *L. crystallina*, *L. guttulatus*, *L. niveus*, *L. tasmanicus*, *Marasmius centrocinnae*, *M. ferrugineodiscus*, *Megasporoporia tamilnaduensis*, *Meruliopsis crystallina*, *Metuloidea imbricata*, *Moniliophthora atlantica*, *Mystinariopsis ochrobrunnea*, *Neomycophora alishanensis*, *Nigrograna kunmingensis*, *Paracremonium aquaticum*, *Parahelicomyces dictyosporus*, *Peniophorella sidera*, *P. subreticulata*, *Phlegmacium fennicum*, *P. pallidocaeruleum*, *Pholiota betulicola*, *P. subcaespitosa*, *Pleurotheciella hyalospora*, *Pleurothecium aseptatum*, *Resupinatus porrigens*, *Russula chlorina*, *R. chrysea*, *R. cruenta*, *R. haematina*, *R. luteocarpa*, *R. sanguinolenta*, *Synnemellisia punensis*, *Tenuimyces bambusicola*, *Thaxterogaster americanoporphyropus*, *T. obscurivibratilis*, *Thermoascus endophyticus*, *Trechispora alba*, *T. perminisporea*, *T. subfarinacea*, *T. tuberculata*, *Tremella sairandhriana*, *Tropicoporus natarajanai*, *T. subramaniae*, *Usnea kriegiana*, *Wolfiporiella macrospora* and *Xylodon muchuanensis*. *Rufoboletus hainanensis* is newly transferred from *Butyriboletus*, while a new name *Russula albocarpa* is proposed for *Russula leucocarpa* G.J. Li & Chun Y. Deng an illegitimate later homonym of *Russula leucocarpa* (T. Lebel) T. Lebel. The new geographic distribution regions are recorded for *Agaricus bambusetorum*, *Bipolaris heliconiae*, *Crinipellis trichialis*, *Leucocoprinus cretaceus*, *Halobyssothecium cangshanense* and *Parasola setulosa*. Corresponding to morphological characters, phylogenetic evidence is also utilized to place the above-mentioned taxa in appropriate taxonomic positions. The current morphological and phylogenetic data is helpful for further clarification of species diversity and exploration of evolutionary relationships in the related fungal groups.

**Keywords** 95 new taxa · Six new records · *Ascomycota* · *Basidiomycota*

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Shi-Liang Liu and Xue-Wei Wang have contributed equally to this work.

**Ascomycota** Caval.-Sm.

**Dothideomycetes** O.E. Erikss & Winka.

**Muyocoprionales** Mapook, Boonmee & K.D. Hyde.

**Muyocoprionaceae** K.D. Hyde.

**1717. *Neomyleptodiscus alishanense*** Tennakoon, C.H. Kuo & K.D. Hyde, *sp. nov.* (Contributed by Danushka S. Tennakoon, Chang-Hsin Kuo and Kevin D. Hyde).

#### *Pleosporales* Barr.

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

**1718. *Halobyssothecium cangshanense*** (Z.L. Luo, X.J. Su & K.D. Hyde) M.S. Calabon, K.D. Hyde & E.B.G. Jones, *new geographical record* (Contributed by Yun Qing and Huang Zhang).

**1719. *Halobyssothecium sichuanense*** Y. Qing & H. Zhang, *sp. nov.* (Contributed by Yun Qing and Huang Zhang).

#### *Nigrogranaceae* Jaklitsch & Voglmayr.

**1720. *Nigrograna kunmingensis*** T.Y. Du & Tibpromma, *sp. nov.* (Contributed by Tian-Ye Du and Saowaluck Tibpromma).

**1721. *Nigrograna heveae*** R.F. Xu & Tibpromma, *new record for Thailand* (Contributed by Jing-Yi Zhang and Yong-Zhong Lu).

#### *Pleosporaceae* Nitschke.

**1722. *Bipolaris heliconiae*** Alcorn, *new record for India* (Contributed by PN Singh, KS Pawar and SK Singh.)

#### *Trypetheliales* Lücking, Aptroot & Sipman.

##### *Trypetheliaceae* Eschw.

**1723. *Astrothelium pseudostraminicolor*** S.H. Jiang, C. Zhang & J.C. Wei, *sp. nov.* (Contributed by Shu-Hua Jiang and Chao Zhang).

#### *Tubeufiales* Boonmee & K.D. Hyde.

##### *Tubeufiaceae* M.E. Barr.

**1724. *Parahelicomyces dictyosporus*** M.S. Calabon, E.B.G. Jones & K.D. Hyde, *sp. nov.* (Contributed by Mark S. Calabon, E.B. Gareth Jones, and Kevin D. Hyde).

#### *Eurotiomycetes* Tehler ex O.E. Eriksson & K. Winka.

##### *Eurotiales* G.W. Martin ex Benny & Kimbr.

##### *Thermoascaceae* Apinis.

**1725. *Thermoascus endophyticus*** T.M. Silva, C.S. Oliveira & J.D.P. Bezerra, *sp. nov.* (Contributed by Tati-ane M. da Silva, Cristina M. Souza-Motta and Jadson D.P. Bezerra).

#### *Laboulbeniomycetes* Engl.

##### *Laboulbeniales* Lindau.

##### *Laboulbeniaceae* G. Winter.

**1726. *Autophagomyces incertus*** W. Rossi & M. Leonardi, *sp. nov.* (Contributed by Walter Rossi and Marco Leonardi).

**1727. *Dimorphomyces seemanii*** W. Rossi & M. Leonardi, *sp. nov.* (Contributed by Walter Rossi and Marco Leonardi).

**1728. *Laboulbenia bifida*** W. Rossi & M. Leonardi, *sp. nov.* (Contributed by Walter Rossi and Marco Leonardi).

**1729. *Laboulbenia tschirnhausii*** W. Rossi & M. Leonardi, *sp. nov.* (Contributed by Walter Rossi and Marco Leonardi).

**1730. *Laboulbenia tuberculata*** W. Rossi & M. Leonardi, *sp. nov.* (Contributed by Walter Rossi and Marco Leonardi).

#### *Lecanoromycetes* O.E. Erikss. & Winka.

##### *Lecanorales* Nannf.

##### *Parmeliaceae* F. Berchtold & J. Presl.

**1731. *Usnea kriegieriana*** A. Gerlach & P. Clerc, *sp. nov.* (Contributed by Alice Gerlach).

#### *Leotiomycetes* O.E. Erikss. & Winka.

##### *Helotiales* Nannf.

##### *Rutstroemiaceae* Holst-Jensen, Koehn & Schmach.

**1732. *Lambertella dipterocarpacearum*** P.N. Singh, S.K. Singh & A.C. Lagashetti, *sp. nov.* (Contributed by P.N. Singh, S. K. Singh & A. C. Lagashetti).

#### *Sordariomycetes* O.E. Erikss. & Winka.

##### *Amphisphaeriales* D. Hawksw. & O.E. Erikss.

##### *Amphisphaeriaceae* G. Winter.

**1733. *Amphisphaeria guttulata*** J.Y. Zhang & Y.Z. Lu, *sp. nov.* (Contributed by Jing-Yi Zhang and Yong-Zhong Lu).

##### *Beltraniaceae* Nann.

**1734. *Beltrania liliiferae*** P. Razaghi, M. Raza & L. Cai, *sp. nov.* (Contributed by Parisa Razaghi, Mubashar Raza and Lei Cai).

**1735. *Beltraniella jiangxiensis*** P. Razaghi, M. Raza & L. Cai, *sp. nov.*

(Contributed by Parisa Razaghi, Mubashar Raza and Lei Cai).

##### *Hypocreales* Lindau.

##### *Bionectriaceae* Samuels and Rossman.

**1736. *Synnemellisia punensis*** K. S. Pawar, P. N. Singh, S. K. Singh, *sp. nov.*

(Contributed by K. S. Pawar, P. N. Singh & S. K. Singh).

##### *Cordycipitaceae* Kreisel ex G. H. Sung, J.M. Sung, Hywel-Jones & Spatafora.

**1737. *Akanthomyces xixiuensis*** X. C. Peng & T. C. Wen, *sp. nov.* (Contributed by Xing-Can Peng and Ting-Chi Wen).

##### *Nectriaceae* Tul. & C. Tul.

**1738. *Paracremonium aquaticum*** M.S. Calabon, E.B.G. Jones & K.D. Hyde, *sp. nov.* (Contributed by Mark S. Calabon, E.B. Gareth Jones and K.D. Hyde).



*Microascales* Luttr. ex Benny & R.K. Benj.

*Halosphaeriaceae* E. Müll. & Arx ex Kohlm.

**1739.** *Ascoglobospora* Abdel-Wahab, *gen. nov.* (Contributed by Mohamed A. Abdel-Wahab).

**1740.** *Ascoglobospora marina* Abdel-Wahab, *sp. nov.* (Contributed by Mohamed A. Abdel-Wahab).

*Pleurotheciales* Réblová & Seifert.

*Pleurotheciaceae* Réblová & Seifert.

**1741.** *Pleurothecium aseptatum* J. Ma & Y.Z. Lu, *sp. nov.* (Contributed by Jian Ma and Yong-Zhong Lu).

**Sordariomycetes, genus incertae sedis**

**1742.** *Pleurotheciella hyalospora* J. Ma & Y.Z. Lu, *sp. nov.* (Contributed by Jian Ma and Yong-Zhong Lu).

**Basidiomycota** R.T. Moore.

**Agaricomycetes** Doweld.

*Agaricales* Underw.

*Agaricaceae* Chevall.

**1743.** *Agaricus agharkarii* P.N. Singh, S.K. Singh, S. Rana & A.C. Lagashetti, *sp. nov.* (Contributed by P.N. Singh, S.K. Singh, S. Rana and A.C. Lagashetti)

**1744.** *Agaricus allostipitatus* E. Tarafder, A.K. Dutta & K. Acharya, *sp. nov.* (Contributed by Entaj Tarafder, Arun Kumar Dutta and Krishnendu Acharya).

**1745.** *Agaricus bambusetorum* H. Bashir & Niazi, *new host and geographical record* (Contributed by Entaj Tarafder, Arun Kumar Dutta and Krishnendu Acharya).

**1746.** *Leucocoprinus cretaceus* (Bull.) Locq., *new record for Thailand* (Contributed by Nakarin Suwannarach, Jaturong Kumla and Saisamorn Lumyong).

*Cortinariaceae* R. Heim ex Pouzar.

**1747.** *Calonarius caesiofulvus* Niskanen, Liimat. & M. E. Sm., *sp. nov.* (Contributed by Tuula Niskanen, Kare Liimatainen and Matthew E. Smith).

**1748.** *Calonarius nobilis* Niskanen & Liimat., *sp. nov.* (Contributed by Tuula Niskanen and Kare Liimatainen).

**1749.** *Calonarius pacificus* Niskanen, Liimat. & Bojantchev, *sp. nov.* (Contributed by Tuula Niskanen, Kare Liimatainen and Dimitar Bojantchev).

**1750.** *Calonarius pulcher* Niskanen, Liimat., & Bojantchev, *sp. nov.* (Contributed by Tuula Niskanen, Kare Liimatainen and Dimitar Bojantchev).

**1751.** *Calonarius subcorrosus* Niskanen & Liimat., *sp. nov.* (Contributed by Tuula Niskanen and Kare Liimatainen).

**1752.** *Cortinarius flaureifolius* Niskanen, Liimat. & M. E. Sm., *sp. nov.* (Contributed by Tuula Niskanen, Kare Liimatainen and Matthew E. Smith).

**1753.** *Cortinarius floridaensis* Niskanen, Liimat. & M. E. Sm., *sp. nov.* (Contributed by Tuula Niskanen, Kare Liimatainen and Matthew E. Smith).

**1754.** *Cortinarius subiodes* Niskanen, Liimat. & M. E. Sm., *sp. nov.* (Contributed by Tuula Niskanen, Kare Liimatainen and Matthew E. Smith).

**1755.** *Hygronarius californicus* Niskanen, Liimat., Bojantchev & Ammirati, *sp. nov.* (Contributed by Tuula Niskanen, Kare Liimatainen, Dimitar Bojantchev and Joe Ammirati).

**1756.** *Mystinariarius ochrobrunneus* Ammirati, Halling, Niskanen & Liimat., *sp. nov.* (Contributed by Joe Ammirati, Tuula Niskanen and Kare Liimatainen).

**1757.** *Phlegmacium fennicum* Kekki, Kytöv., Niskanen & Liimat., *sp. nov.* (Contributed by Tapio Kekki, Tuula Niskanen and Kare Liimatainen).

**1758.** *Phlegmacium pallidoceruleum* Niskanen, Liimat. & Bojantchev, *sp. nov.* (Contributed by Tuula Niskanen, Kare Liimatainen and Dimitar Bojantchev).

**1759.** *Thaxterogaster americanoporphyrus* Niskanen, Liimat. & Ammirati, *sp. nov.* (Contributed by Tuula Niskanen, Kare Liimatainen and Joe Ammirati).

**1760.** *Thaxterogaster obscurivibratilis* Niskanen, Liimat. & Ammirati, *sp. nov.* (Contributed by Tuula Niskanen, Kare Liimatainen and Joe Ammirati).

*Cystostereaceae* Jülich.

**1761.** *Crustomyces juniperi* S.L. Liu & L.W. Zhou, *sp. nov.* (Contributed by Shi-Liang Liu and Li-Wei Zhou).

**1762.** *Crustomyces scytinostromoides* S.L. Liu & L.W. Zhou, *sp. nov.* (Contributed by Shi-Liang Liu and Li-Wei Zhou).

**1763.** *Cystostereum subsirmaurensense* S.L. Liu & L.W. Zhou, *sp. nov.* (Contributed by Shi-Liang Liu and Li-Wei Zhou).

**1764.** *Tenuimyces* S.L. Liu & L.W. Zhou, *gen. nov.* (Contributed by Shi-Liang Liu and Li-Wei Zhou).

**1765.** *Tenuimyces bambusicola* S.L. Liu & L.W. Zhou, *sp. nov.* (Contributed by Shi-Liang Liu and Li-Wei Zhou).

**Incertainae sedis**

**1766.** *Henningsomyces hengduanensis* S.L. Liu & L.W. Zhou, *sp. nov.* (Contributed by Shi-Liang Liu and Li-Wei Zhou).

*Lyophyllaceae* Jülich.

**1767.** *Calocybella sribuabanensis* N. Suwannarach, J. Kumla & S. Lumyong, *sp. nov.* (Contributed by Nakarin Suwannarach, Jaturong Kumla and Saisamorn Lumyong).

*Marasmiaceae* Roze ex Kühner.

**1768.** *Crinipellis trichialis* (Lév.) Pat. ex Antonín, Ryoo & H.D. Shin, *new record for Thailand* (Contributed by Nakarin Suwannarach and Jaturong Kumla).

**1769.** *Marasmius centrocinnamomeus* J.S. Kim & Y.W. Lim, *sp. nov.* (Contributed by Ji Seon Kim and Young Woon Lim).

**1770. *Marasmius ferrugineodiscus*** J.S. Kim & Y.W. Lim, *sp. nov.* (Contributed by Ji Seon Kim and Young Woon Lim).  
**1771. *Moniliophthora atlantica*** N. A. Ramirez & Niveiro, *sp. nov.* (Contributed by Natalia Ramirez and Nicolás Niveiro).

**Pleurotaceae** Kühner.

**1772. *Resupinatus porrigens*** J. Z. Xu & Yu Li, *sp. nov.* (Contributed by Ji Ze Xu and Yu Li).

**Psathyrellaceae** Vilgalys, Moncalvo & Redhead.

**1773. *Parasola setulosa*** (Berk. & Broome) Redhead, Vilgalys & Hopple, *new record for Thailand* (Contributed by Nopparat Wannathes, Nakarin Suwannarach and Jaturong Kumla).

**Strophariaceae** Singer & A.H. Sm.

**1774. *Pholiota betulicola*** T. Bau & E.J. Tian, *sp. nov.* (Contributed by Tolgor Bau and Enjing Tian).

**1775. *Pholiota subcaespitosa*** E.J. Tian, *sp. nov.* (Contributed by Enjing Tian).

**Atheliales** Jülich.

**Atheliaceae** Jülich.

**1776. *Athelia naviculispota*** S.L. Liu & L.W. Zhou, *sp. nov.* (Contributed by Shi-Liang Liu and Li-Wei Zhou).

**Byssocorticiaceae** Jülich.

**1777. *Athelopsis subglaucina*** S.L. Liu & L.W. Zhou, *sp. nov.* (Contributed by Shi-Liang Liu and Li-Wei Zhou).

**Atheliales, genus incertae sedis**

**1778. *Atheliella*** S.L. Liu & L.W. Zhou, *gen. nov.* (Contributed by Shi-Liang Liu and Li-Wei Zhou).

**1779. *Atheliella conifericola*** S.L. Liu & L.W. Zhou, *sp. nov.* (Contributed by Shi-Liang Liu and Li-Wei Zhou).

**Boletales** E.-J. Gilbert.

**Boletaceae** Chevall.

**1780. *Aureoboletus minimus*** Ming Zhang, C.Q. Wang & T.H. Li, *sp. nov.* (Contributed by Ming Zhang).

**1781. *Aureoboletus nanlingensis*** Ming Zhang, C.Q. Wang & T.H. Li, *sp. nov.* (Contributed by Ming Zhang).

**1782. *Hemileccinum duriusculum*** Mei-Xiang Li, Zhu L. Yang & G. Wu, *sp. nov.* (Contributed by Mei-Xiang Li, Zhu L. Yang and Gang Wu).

**1783. *Rufoboletus*** N.K. Zeng & Zhi Q. Liang, *gen. nov.* (Contributed by Nian-Kai Zeng and Yun-Xiao Han).

**1784. *Rufoboletus hainanensis*** (N.K. Zeng, Zhi Q. Liang & S. Jiang) N.K. Zeng & Zhi Q. Liang, *comb. nov.* (Contributed by Nian-Kai Zeng and Yun-Xiao Han).

**Cantharellales** Gäum.

**Botryobasidiaceae** Jülich.

**1785. *Botryobasidium coniferarum*** S.L. Liu & L.W. Zhou, *sp. nov.* (Contributed by Shi-Liang Liu and Li-Wei Zhou).

**Gomphales** Jülich.

**Gomphaceae** Donk.

**1786. *Gomphus zamorinorum*** Krishnapriya K. & T.K.A. Kumar, *sp. nov.* (Contributed by K. Krishnapriya and T. K. Arun Kumar).

**Hymenochaetales** Oberw.

**Chaetoporellaceae** Jülich.

**1787. *Kneiffiella pseudoabditia*** Xue W. Wang & L.W. Zhou, *sp. nov.* (Contributed by Xue-Wei Wang and Li-Wei Zhou).

**1788. *Kneiffiella pseudoalutacea*** Xue W. Wang & L.W. Zhou, *sp. nov.* (Contributed by Xue-Wei Wang and Li-Wei Zhou).

**Hymenochaetaceae** Donk.

**1789. *Fulvoderma microporum*** Xue W. Wang & L.W. Zhou, *sp. nov.* (Contributed by Xue-Wei Wang and Li-Wei Zhou).

**1790. *Tropicoporus natarajaniae*** M. Kaliyaperumal, S. Gunaseelan, K. Kezo, Xue W. Wang & L.W. Zhou, *sp. nov.* (Contributed by Malarvizhi Kaliyaperumal, Sugantha Gunaseelan, Kezhocuyi Kezo, Xue-Wei Wang and Li-Wei Zhou).

**1791. *Tropicoporus subramaniae*** S. Gunaseelan, M. Kaliyaperumal, K. Kezo, Xue W. Wang & L.W. Zhou., *sp. nov.* (Contributed by Malarvizhi Kaliyaperumal, Sugantha Gunaseelan, Kezhocuyi Kezo, Xue-Wei Wang and Li-Wei Zhou).

**Schizoporaceae** Jülich.

**1792. *Lyomyces austro-occidentalis*** Xue W. Wang & L.W. Zhou, *sp. nov.* (Contributed by Xue-Wei Wang and Li-Wei Zhou).

**1793. *Lyomyces crystallina*** Xue W. Wang & L.W. Zhou, *sp. nov.* (Contributed by Xue-Wei Wang and Li-Wei Zhou).

**1794. *Lyomyces guttulatus*** Xue W. Wang & L.W. Zhou, *sp. nov.* (Contributed by Xue-Wei Wang and Li-Wei Zhou).

**1795. *Lyomyces niveus*** C.L. Zhao ex L.W. Zhou & Xue W. Wang, *sp. nov.* (Contributed by Li-Wei Zhou and Xue-Wei Wang).

**1796. *Lyomyces tasmanicus*** Xue W. Wang & L.W. Zhou, *sp. nov.* (Contributed by Xue-Wei Wang and Li-Wei Zhou).

**1797. *Xylodon muchuanensis*** Xue W. Wang & L.W. Zhou, *sp. nov.* (Contributed by Xue-Wei Wang and Li-Wei Zhou).

**Hymenochaetales, genus incertae sedis**

**1798. *Ginnsia laricicola*** Xue W. Wang & L.W. Zhou, *sp. nov.* (Contributed by Xue-Wei Wang and Li-Wei Zhou).

**1799. *Peniophorella sidera*** Xue W. Wang & L.W. Zhou, *sp. nov.* (Contributed by Xue-Wei Wang and Li-Wei Zhou).

**1800. *Peniophorella subreticulata*** Xue W. Wang & L.W. Zhou, *sp. nov.* (Contributed by Xue-Wei Wang and Li-Wei Zhou).

**Polyporales** Gäum.

**Irpicaceae** Spirin & Zmitr.

**1801. *Meruliopsis crystallina*** Xue W. Wang & L.W. Zhou, *sp. nov.* (Contributed by Xue-Wei Wang and Li-Wei Zhou).

**Laetiporaceae** Jülich.

**1802. *Wolfiporiella macrospora*** X.H. Ji, L.W. Zhou & S.L. Liu, *sp. nov.* (Contributed by Xiao-Hong Ji, Li-Wei Zhou and Shi-Liang Liu).

**Meruliaceae** Rea.

**1803. *Metuloidea imbricata*** R. Saha, A.K. Dutta & K. Acharya, *sp. nov.* (Contributed by Rituparna Saha, Arun Kumar Dutta and Krishnendu Acharya).

**Polyporaceae** Corda.

**1804. *Megasporoporia tamilnaduensis*** K. Kezo, M. Kaliyaperumal, S. Gunaseelan, Xue W. Wang & L.W. Zhou., *sp. nov.* (Contributed by Kezhocuyi Kezo, Malarvizhi Kaliyaperumal, Sugantha Gunaseelan, Xue-Wei Wang and Li-Wei Zhou).

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

**1805. *Laxitextum subrubrum*** R. Saha, A.K. Dutta & K. Acharya, *sp. nov.* (Contributed by Rituparna Saha, Arun Kumar Dutta and Krishnendu Acharya).

**Russulaceae** Lotsy.

**1806. *Russula albocarpa*** G.J. Li & Chun Y. Deng, *nom. nov.* (Contributed by Guo-Jie Li and Chun-Ying Deng).

**1807. *Russula chlorina*** G.J. Li & Chun Y. Deng, *sp. nov.* (Contributed by Guo-Jie Li and Chun-Ying Deng).

**1808. *Russula chrysea*** G.J. Li & Chun Y. Deng, *sp. nov.* (Contributed by Guo-Jie Li and Chun-Ying Deng).

**1809. *Russula cruenta*** G.J. Li & Chun Y. Deng, *sp. nov.* (Contributed by Guo-Jie Li and Chun-Ying Deng).

**1810. *Russula haematina*** G.J. Li & Chun Y. Deng, *sp. nov.* (Contributed by Guo-Jie Li and Chun-Ying Deng).

**1811. *Russula luteocarpa*** G.J. Li & Chun Y. Deng, *sp. nov.* (Contributed by Guo-Jie Li and Chun-Ying Deng).

**1812. *Russula sanguinolenta*** G.J. Li & Chun Y. Deng, *sp. nov.* (Contributed by Guo-Jie Li and Chun-Ying Deng).

**Trechisporales** K.H. Larss.

**Hydnodontaceae** Jülich.

**1813. *Trechispora alba*** S.L. Liu, G. He & L.W. Zhou, *sp. nov.* (Contributed by Shi-Liang Liu, Gang He and Li-Wei Zhou).

**1814. *Trechispora perminispora*** S.L. Liu & L.W. Zhou, *sp. nov.* (Contributed by Shi-Liang Liu and Li-Wei Zhou).

**1815. *Trechispora subfarinacea*** S.L. Liu & L.W. Zhou, *sp. nov.* (Contributed by Shi-Liang Liu and Li-Wei Zhou).

**1816. *Trechispora tuberculata*** S.L. Liu & L.W. Zhou, *sp. nov.* (Contributed by Shi-Liang Liu and Li-Wei Zhou).

**Tremellomycetes** Doweld.

**Tremellales** Fr.

**Tremellaceae** Fr.

**1817. *Tremella sairandhriana*** A. Thomas & T.K.A. Kumar, *sp. nov.* (Contributed by Anjitha Thomas and T. K. Arun Kumar).

## Introduction

Fungal taxonomy is a fundamental discipline that aims to recognize all fungi and clarify their kinships, viz. reconstruction of the Fungal Tree of Life (Zhou and May 2023). Since the publication of *Species Plantarum* in 1753 (Linnaeus 1753), fungi have been considered to be a low-level branch of plants and have been systematically explored for more than 250 years. The known species are no more than 10% of the total number of fungi estimated in various scenarios (Hawksworth 2001; Blackwell 2011; Dai et al. 2015; Hawksworth and Lücking 2017; Wu et al. 2019; Hyde 2020c, 2022). In contrast, however, the reduction of biodiversity is increasing due to habitat loss and climate change in the Anthropocene (Díaz et al. 2019; Wei 2021; Exposito-Alonso et al. 2022). Therefore, it is important to record species from all fungal groups for their conservation and utilization.

Traditionally, new fungal taxa are introduced by taxonomists who focus on specific fungal groups among for example, agarics, poroid species, corticioid species, plant pathogens and aquatic fungi. This leads to new taxa scattered in many papers (one or two new taxa per paper), and thus some of new taxa published in these papers may become buried in the copious publications, some obscure. For example, an order name *Xenasmatales* Jülich erected in 1981 (Jülich 1981) was published as a new order *Xenasmatales* K.Y. Luo & C.L. Zhao recently (Luo and Zhao 2022a). The latter is not valid (Note 2 to Art. 6 of the International Code of Nomenclature for algae, fungi, and plants; Turland et al. 2018). Therefore, the Fungal Diversity Notes series provides an outlet to promote newly described taxa at and above the species level (Ariyawansa et al. 2015; Liu et al. 2015a; Hyde et al. 2016; etc.).

In this paper we follow standard taxonomic protocols (Aime et al. 2021) when introducing new taxa. The authors follow the guidelines for describing new species for Basidiomycetes (He et al. 2021) and ascomycetes (Chethana et al. 2021; Maharachchimbura et al. 2021; Pem et al. 2021).

As the continuation of FDN series, this paper introduces, four new genera, 89 new species, one new combination and one new name. In addition, six new records are also included to provide distribution and host information for previously known species. This information is crucial for further preserving and utilizing fungal species (Hyde et al. 2007, 2019). Moreover, along with these new taxa, brief notes on higher taxa are provided for supplementing related taxonomic knowledge.

## Materials and methods

The studied fungal materials were collected from Asia, Europe, North America, South America and Oceania, and are preserved in various fungaria or herbaria (see Taxonomy section for acronyms following Index Herbariorum: <http://sweetgum.nybg.org/science/ih/>). Morphological examination and phylogenetic analyses were performed following standard fungal taxonomic procedures (Aime et al. 2021; Shen et al. 2021, 2023); the detailed procedures are similar to previous FDN series (Boonmee et al. 2021). The new taxa are registered in Index Fungorum (Index Fungorum 2023) and Faces of Fungi databases (Jayasiri et al. 2015).

## Taxonomy

### Ascomycota Caval.-Sm.

**Notes:** Ascomycota is not only the largest phylum in the fungal kingdom, but also one of the most diverse and common phylum in eukaryotes (Kirk et al. 2008). The species are widely distributed in a variety of terrestrial and aquatic environments. Cavalier-Smith (1998) officially introduced Ascomycota, which consists of two subphyla (Hemiascomycotina and Euascomycotina), seven classes and nine subclasses. Schoch et al. (2009) provided an outline of Ascomycota including three subphyla (Pezizomycotina, Saccharomycotina and Taphrinomycotina), 16 classes and ten subclasses. Schoch et al. (2009) explored the origin and evolutionary relationship of species within the whole phylum through phylogenetic methods. Recently, Wijayawardene et al. (2018) provide an updated outline of Ascomycota, which includes three subphyla, 19 classes, and approximately 6600 genera.

### Dothideomycetes O.E. Erikss. & Winka.

**Notes:** Dothideomycetes is the largest class in Ascomycota, including two subclasses (Dothideomycetidae and Pleosporomycetidae), 33 orders and 174 families. It also comprises a highly diverse group of freshwater fungi. There are 1022 genera in Dothideomycetes (Wijayawardene et al. 2018). Species in this class are characterized mainly by

bitunicate asci (two wall layers, Hyde et al. 2013). In recent years, with the development of molecular technology, more and more scholars used phylogenetic analysis methods to modified Dothideomycetes lineage. Lumbsch and Huhndorf (2010) accepted 41 families consisting of 249 genera in Dothideomycetes. Hyde et al. (2013) introduced ten new families in Dothideomycetes and provided the corresponding descriptions, notes and illustrations based on the phylogenetic tree. Wijayawardene et al. (2014) listed 23 orders, 110 families and 1295 genera of Dothideomycetes following the International Code of Nomenclature for Algae, Fungi, and Plants (ICN; Melbourne Code), which addresses the nomenclature of pleomorphic fungi, became effective from 30 July 2011. They also provided a phylogenetic tree for 23 orders and 75 families. Hongsanan et al. (2020a) further provided an overall phylogenetic tree of families in Dothideomycetes based on combined analysis of LSU, SSU, *rpb2* and *tef1* sequence data and phylogenetic trees for each order in Dothideomycetidae and Pleosporomycetidae.

### *Muyocoprionales* Mapook, Boonmee & K.D. Hyde.

**Notes:** *Muyocoprionales* was introduced by Mapook et al. (2016) to accommodate the *Muyocoprionaceae* as the type family. This order was related to *Acrospemales* and *Dyfrulomycetales*, but morphologically differs in having superficial, flattened, carbonaceous, brittle ascomata, cellular pseudoparaphyses that are longer than the asci and ellipsoid to ovate, unicellular ascospores (Hongsanan et al. 2020a; Mapook et al. 2020). To date, only *Muyocoprionaceae* is accepted in this order and divergence time has been estimated as 171 million years ago (Mya) (Hongsanan et al. 2020a; Wijayawardene et al. 2022).

### *Muyocoprionaceae* K.D. Hyde.

**Notes:** This family was invalidly introduced by Luttrell (1951) and re-established by Hyde et al. (2013) with a single genus *Muyocopron*. *Muyocoprionaceae* members are commonly found as saprobes on dead leaves, twigs and stems, thus playing important roles in decomposition (Hongsanan et al. 2020a; Tennakoon et al. 2021). Currently, this family comprises nine genera *Arxiella*, *Leptodiscella*, *Mycoleptodiscus*, *Muyocopron*, *Neocochlearomyces*, *Neomycoleptodiscus*, *Paramycoleptodiscus*, *Setoapiospora*, and *Pseudopalawania* (Hongsanan et al. 2020a; Wijayawardene et al. 2022). In this study, we follow the recent treatment of Mapook et al. (2020) for *Muyocoprionaceae*.

### *Neomycoleptodiscus* Hern.-Restr., J.D.P. Bezerra & Crous.

**Notes:** *Neomycoleptodiscus* was introduced by Hernández-Restrepo et al. (2019) to accommodate *Neomycoleptodiscus venezuelense* as the type species. The type species was found on leaf litter of *Gynerthera caribensis* in Venezuela. *Neomycoleptodiscus* is distinguished from

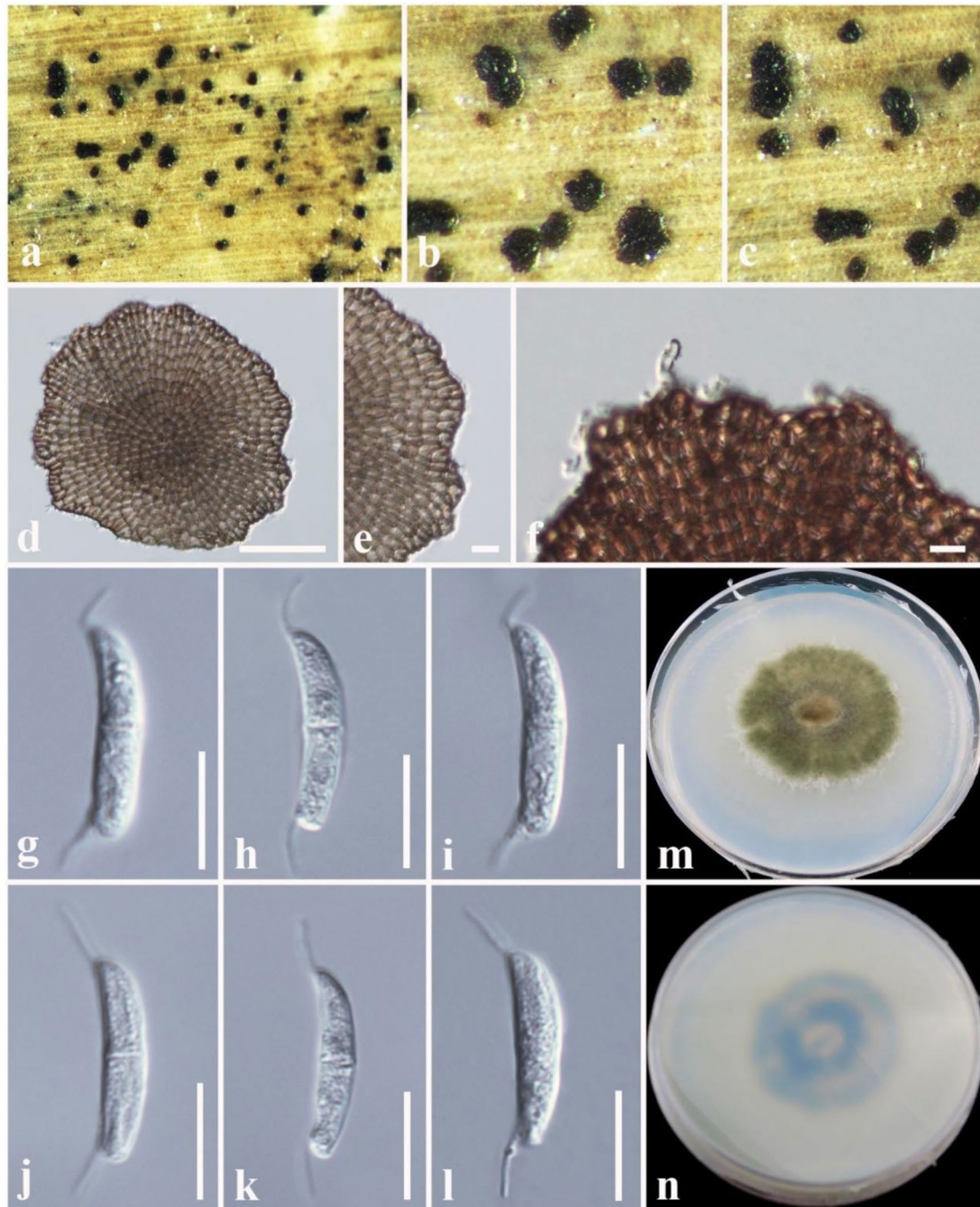


*Mycoleptodiscus* by having dark brown conidiogenous cells and conidia which are curved at the apex, and truncate at the base, whereas *Mycoleptodiscus* has brown conidiogenous cells and conidia with recurved ends (Hernández-Restrepo et al. 2019). Currently, this genus has two species, viz. *Neomycoleptodiscus pertusus* and *N. venezuelense*. However, molecular data are available only for the type species. In this

study, we introduce *Neomycoleptodiscus alishanense* as the third species of this genus.

*Neomycoleptodiscus alishanense* Tennakoon, C.H. Kuo & K.D. Hyde, *sp. nov.*

*Index Fungorum* Number: IF559582; *Facesoffungi* number: FoF10790; Fig. 1



**Fig. 1** *Neomycoleptodiscus alishanense* (MFLU 19-2732, **holotype**). **A** and **b** Appearance of conidiomata on host. **c** Close-up of conidiomata. **d** Thyriothecia. **E** and **f** Thyriothecium wall and conidiogenous

cells. **g–l** Conidia. **m** Colony from above. **n** Colony from below. Scale bars: **d** = 50  $\mu$ m, **e**, **f** = 20  $\mu$ m, **g–l** = 10  $\mu$ m

**Etymology:** The epithet "*alishanense*" refers to the local mountain (Ali Shan), from where the taxon was collected.

**Holotype:** MFLU 19-1732.

**Saprobic** on senescent leaves of *Trachycarpus fortunei*. **Sexual morph:** Undetermined. **Asexual morph:** Coelomycetous. *Conidiomata* sporodochial, 120–150 µm high, 130–160 µm in diam. ( $\bar{x}$  = 135 × 145 µm,  $n$  = 30), superficial, dark brown to black, circular, dull, undulate, umbonate, rough. *Conidiogenous cells* evanescent. *Conidia* 16–19 × 3–4 µm ( $\bar{x}$  = 17.5 × 3.6 µm,  $n$  = 30), 1-septate, cylindrical, hyaline, guttulate, straight or slightly curved, with filamentous appendages at both ends, 7–7.6 µm long, 0.4–1 µm wide, smooth-walled.

**Culture characteristics:** Colonies on PDA reaching 15 mm diameter after 2 weeks at 25 °C, colonies medium dense, circular, convex, surface slightly smooth with entire edge, effuse, velvety to hairy, margin well-defined and curled, colony from above: grey at the margin, brown at the centre; reverse, light brown to grey at the margin, brown to black at the centre; mycelium grey to greenish with tufting; not producing pigments in PDA.

**Material examined:** China, Taiwan Province, Chiayi, Fanlu Township area, Dahu forest, on dead leaves of *Trachycarpus fortunei*, 6 August 2019, D.S. Tennakoon, GSP014A (MFLU 19-2732, **holotype**), ex-type living culture, MFLUCC 19-0390; *ibid.*, 11 August 2019, GSP014B (NCYU 19-0006, **paratype**), NCYUCC 19-0391; *ibid.*, 13 August 2019, GSP014C (NCYU 19-0401), NCYUCC 19-0392.

**GenBank numbers:** MFLUCC 19-0390: ITS = ON024153, LSU = ON024150; NCYUCC 19-0391: ITS = ON024154, LSU = ON024151; NCYUCC 19-0392: ITS = ON024155, LSU = ON024152.

**Notes:** The characteristics of our collection (MFLU 19-2732 and NCYU 19-0006) tally with the type of *Neomycoleptodiscus* in having superficial, dark brown to black, circular, sporodochial conidiomata and 1-septate, cylindrical, hyaline, straight or slightly curved conidia with filamentous appendages at both ends (Hernández-Restrepo et al. 2019). Multi-gene phylogeny (LSU, SSU and ITS) generated herein indicates that our collection forms a strongly supported lineage sister to the clade containing *N. venezuelense* and *Mycoleptodiscus endophyticus* (85% ML, 1.00 BYPP, Fig. 2). Our collection can be distinguished from *N. venezuelense* in having smaller conidia (16–19 × 3–4 µm), whereas *N. venezuelense* has larger conidia (18–27 × 3–5 µm). In addition, a comparison of the 632 nucleotides across the ITS (+5.8S) gene region of our collection and *N. venezuelense* (CBS 100519) reveals 21 base pair differences (3.32%). Therefore, based on both morphology and phylogenetic evidence, we introduce our collections as a new species, *N. alishanense* from dead leaves of *Trachycarpus fortunei* (Arecaceae). *Mycoleptodiscus endophyticus* was introduced

by Tibpromma et al. (2018) from healthy leaves of *Freycinetia* sp. (Pandanaaceae) as an endophytic species based on mycelial characteristics. However phylogenetically, *M. endophyticus* has a close relationship with *Neomycoleptodiscus* species (Hernández-Restrepo et al. 2019). Therefore, further taxonomic work is needed to precisely resolve identification and relationships between *M. endophyticus* and *Neomycoleptodiscus* species.

### **Pleosporales** Luttr. ex M.E. Barr

**Notes:** *Pleosporales* (Barr 1987) is an order of the class Dothidiomycetes within the division Ascomycota. It is estimated to contains 91 families and 655 genera (Wijayawardene et al. 2022). The majority of species are saprobes on decaying plant material in freshwater (Shearer et al. 2009), marine (Suetrong et al. 2009) or terrestrial environments, but some species are also associated with living plants as parasites, epiphytes or endophytes (Zhang et al. 2009). The best studied species cause plant diseases on important agricultural crops e.g. *Cochliobolus heterostrophus*, causing southern corn leaf blight on maize, *Phaeosphaeria nodorum* (*Stagonospora nodorum*) causing glume blotch on wheat, sorghum and on various other host plants (Ellis 1971; Sivanesan 1987; Berbee et al. 1999). Some species of this order are coprophilous found on animal dung (Kruys et al. 2006) and a few members occur as lichens (Nelsen et al. 2009).

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

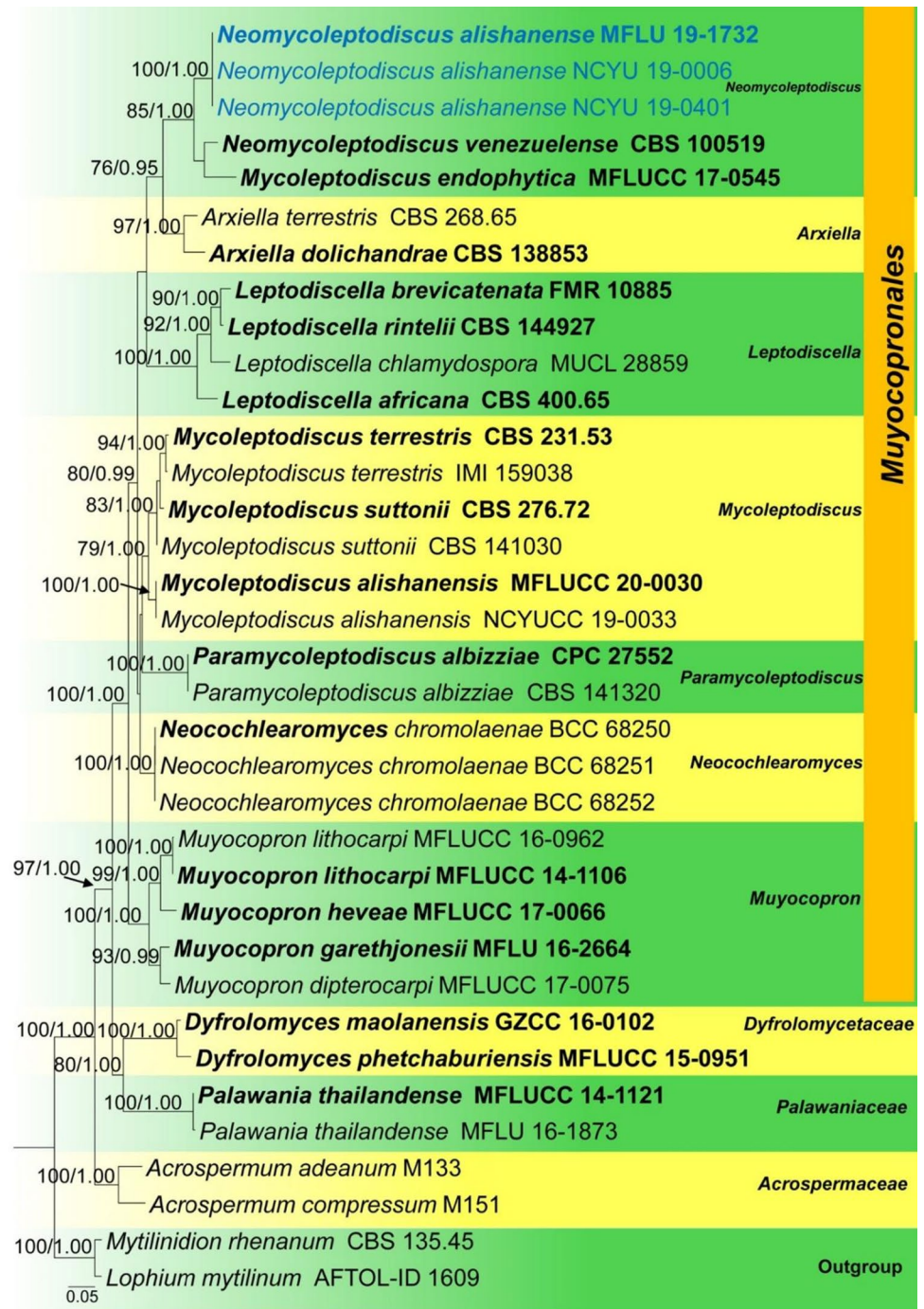
**Notes:** *Lentitheciaceae* was introduced by Zhang et al. (2009) to accommodate *Katumotaa*, *Keissleriella* and *Lentithecium*. Phylogenetically, the family is highly-supported as monophyletic in *Pleosporales* (Wanasinghe et al. 2014; Tanaka et al. 2015; Liu et al. 2017a). The species in this family have lenticular ascomata, fusiform to filiform, hyaline to pale yellow, 1-septate ascospores, sometimes becoming 3-septate when mature, rarely multiseptate (Zhang et al. 2009; Hyde et al. 2013). According to the latest report, there are 14 genera in *Lentitheciaceae*, viz. *Darksidea*, *Halobyssothecium*, *Katumotaa*, *Keissleriella*, *Lentithecium*, *Murilenthicium*, *Neophiosphaerella*, *Phragmocamarosporium*, *Pleurophoma*, *Poaceascoma*, *Pseudomurilenthicium*, *Setoseptoria*, *Tingoldiigo* and *Towyspora* (Hongsan et al. 2020a).

### **Halobyssothecium** Dayar., E.B.G. Jones & K.D. Hyde.

**Notes:** *Halobyssothecium* was introduced by Dayarathne et al. (2018) to accommodate *H. obiones*, which was previously regarded as *Byssothecium obiones*. The species in *Halobyssothecium* have subglobose or ellipsoidal, immersed to semi-immersed, ostiolate, carbonaceous, dark brown to black ascomata, septate, branched pseudoparaphyses,



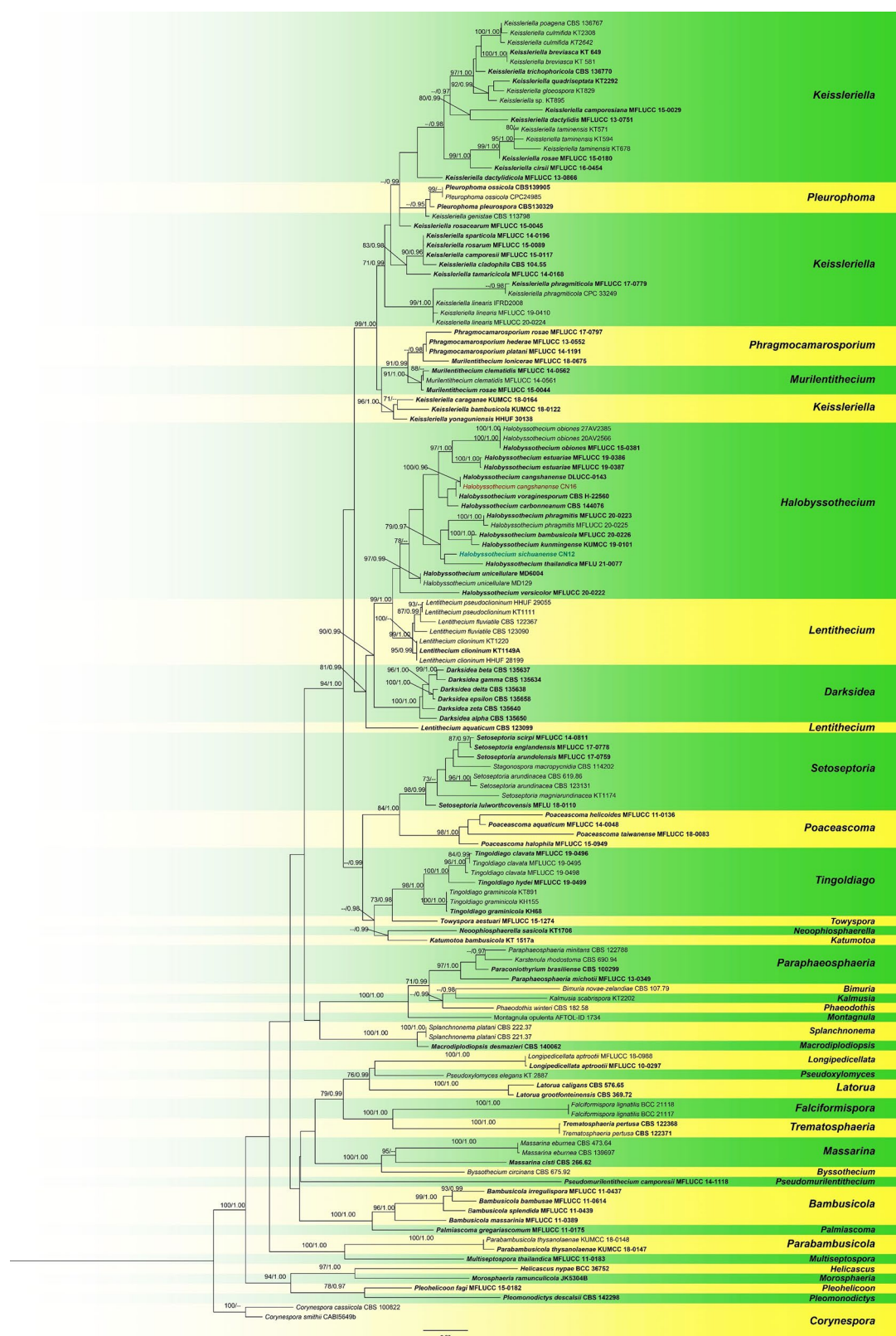
**Fig. 2** The best scoring RAXML tree with a final likelihood value of  $-14,874.014066$  for combined dataset of LSU, SSU and ITS sequence data. The topology and clade stability of the combined gene analyses was compared to the single gene analyses. The tree is rooted with *Lophium mytilinum* (AFTOL-ID 1609) and *Mytilinidion rhenanum* (CBS 135.45). The matrix had 1024 distinct alignment patterns with 36.09% undetermined characters and gaps. Estimated base frequencies were as follows; A=0.241588, C=0.238793, G=0.293284, T=0.226335; substitution rates AC=1.340756, AG=2.207875, AT=1.322261, CG=1.183116, CT=5.116204, GT=1.000000; gamma distribution shape parameter  $\alpha=0.586892$ . Ex-type strains are in bold and newly generated sequences are in red. Bootstrap support values for ML equal to or greater than 60% and BYPP equal to or greater than 0.90 are given above the nodes



8-spored, clavate to subcylindrical, short pedicellate asci, without an apical apparatus and versicolored, septate ascospores. Dayarathne et al. (2018) suggested that the most distinct character of this genus were the versicolored ascospores with brown central cells and hyaline end cells, which was similar to *Byssothecium*. Subsequently, Calabon et al. (2021) collected three new *Halobyssothecium* species and also transferred *Lentithecium cangshanense*, *L. carbonneanum*, *L. kunmingense*, *L. unicellulare*, and *L.*

*voraginesporum* to *Halobyssothecium* based on the result of their phylogeny. Hyde et al. (2021) introduced *H. thailandicum* from submerged wood in Thailand. *Halobyssothecium bambusicola*, *H. kunmingense*, *H. phragmitis* and *H. unicellulare* are asexual morphs, while *H. cangshanense*, *H. carbonneanum*, *H. thailandicum* and *H. voraginesporum* possess brown ascospores with uniform color, which differs from the original description of the genus. Bootstrap support values for *Halobyssothecium* in the phylogenetic tree





of Calabon et al. (2021) had low maximum likelihood and maximum parsimony lower than 50% and Bayesian posterior probabilities less than 0.90, which is in agreement

with Hyde et al. (2021) and this study (Fig. 3). Therefore, more studies need to be done to confirm whether *Halobyssothecium* is monophyletic. Herein we follow Calabon et al.

**Fig. 3** The best scoring Maximum Likelihood (RAxML) tree of family Lentitheciaceae, based on LSU, SSU, ITS and TEF1- $\alpha$  sequence dataset. The tree is rooted with *Corynespora smithii* (CABI5649b) and *Corynespora cassiicola* (CBS 100822). Maximum likelihood support values greater than 70% and Bayesian posterior probabilities greater than 0.95 are shown near the nodes. Newly strain in this study is shown in red, and new species is shown in blue. Ex-type strains are shown in bold. The optimal score of RAxML analysis results  $\ln L = -36,913,321,704$ . Estimated base frequencies are as follows: A=0.238921, C=0.248704, G=0.273797, T=0.238578; substitution rates AC=1.113695, AG=2.495521, AT=1.345905, CG=1.136632, CT=5.923529, GT=1.000000; gamma distribution shape parameter  $\alpha = 0.220373$

(2021) and Hyde et al. (2021), with eleven species in the genus.

***Halobyssothecium cangshanense*** (Z.L. Luo, X.J. Su & K.D. Hyde) M.S. Calabon, K.D. Hyde & E.B.G. Jones, Mycol. Progr. 20: 715 (2021).

*Index Fungorum number*: IF 558092; *Facesoffungi number*: FoF 09434; Fig. 4

*Saprobic* on decaying bamboo in freshwater habitats. **Sexual morph**: *Ascomata* 170–270  $\mu\text{m}$  high, 150–250  $\mu\text{m}$  in diam., scattered or clustered, semi-immersed to partially erumpent, conical or subglobose, black, papillate in the center, ostiolate. *Peridium* 20–30  $\mu\text{m}$  wide, composed of several layers of pseudoparenchymatous cells, arranged in a *textura angularis*, hyaline to subhyaline at the inner part, pigmented at the outer part. *Pseudoparaphyses* 2.5–3.5  $\mu\text{m}$  wide, numerous, septate, embedded in a mucilaginous matrix. *Asci* 65–114  $\times$  9–12  $\mu\text{m}$  ( $\bar{x} = 87.8 \times 10.8 \mu\text{m}$ ,  $n = 15$ ), 8-spored, bitunicate, clavate, pedicellate, with a rounded apex and an ocular chamber. *Ascospores* 15.5–19.5  $\times$  3.5–5.5  $\mu\text{m}$  ( $\bar{x} = 17.6 \times 4.5 \mu\text{m}$ ,  $n = 20$ ), 1–2-seriate, broadly fusiform, straight or slightly curved, yellowish brown, 1-septate in the central, slightly constricted at the septum, upper cell wider, guttulate when young, smooth-walled. **Asexual morph**: Undetermined.

*Culture characteristics*: On PDA, colony circular on the whole, germinating within 24 h, reaching 40 mm in 1 month at room temperature (25 °C), dark brown from above and below, surface rough and dry, umbonate, with dense brown mycelium in the middle, sparse mycelium in the regular edge.

*Material examined*: China, Sichuan Province, Yibin, Changning river, on submerged bamboo, 29 March 2021, Y. Qing, CN16 (IFRD, **new record for China**).

*GenBank numbers*: LSU = KU991149, SSU = KU991150.

*Notes*: *Halobyssothecium cangshanense* was originally introduced as *Lentithecium cangshanense* by Su et al. (2016) from Yunnan Province, China, and subsequently transferred to *Halobyssothecium* by Calabon et al. (2021)

based on phylogenetic analysis. Phylogenetically, our isolate clusters with *H. cangshanense* with strong support. Morphologically, our isolate fits the characters of *H. cangshanense* except for the slightly narrower conidia (3.5–5.5  $\mu\text{m}$  vs. 6–7  $\mu\text{m}$ ). This is the first time to report it from Sichuan Province, China.

***Halobyssothecium sichuanense*** Y. Qing & H. Zhang, *sp. nov.*

*Index Fungorum number*: IF 559791; *Facesoffungi number*: FoF 12672; Fig. 5

*Etymology*: Referring to this species collected from Sichuan.

*Holotype*: CN12 (IFRD).

*Saprobic* on decaying wood in freshwater habitats.

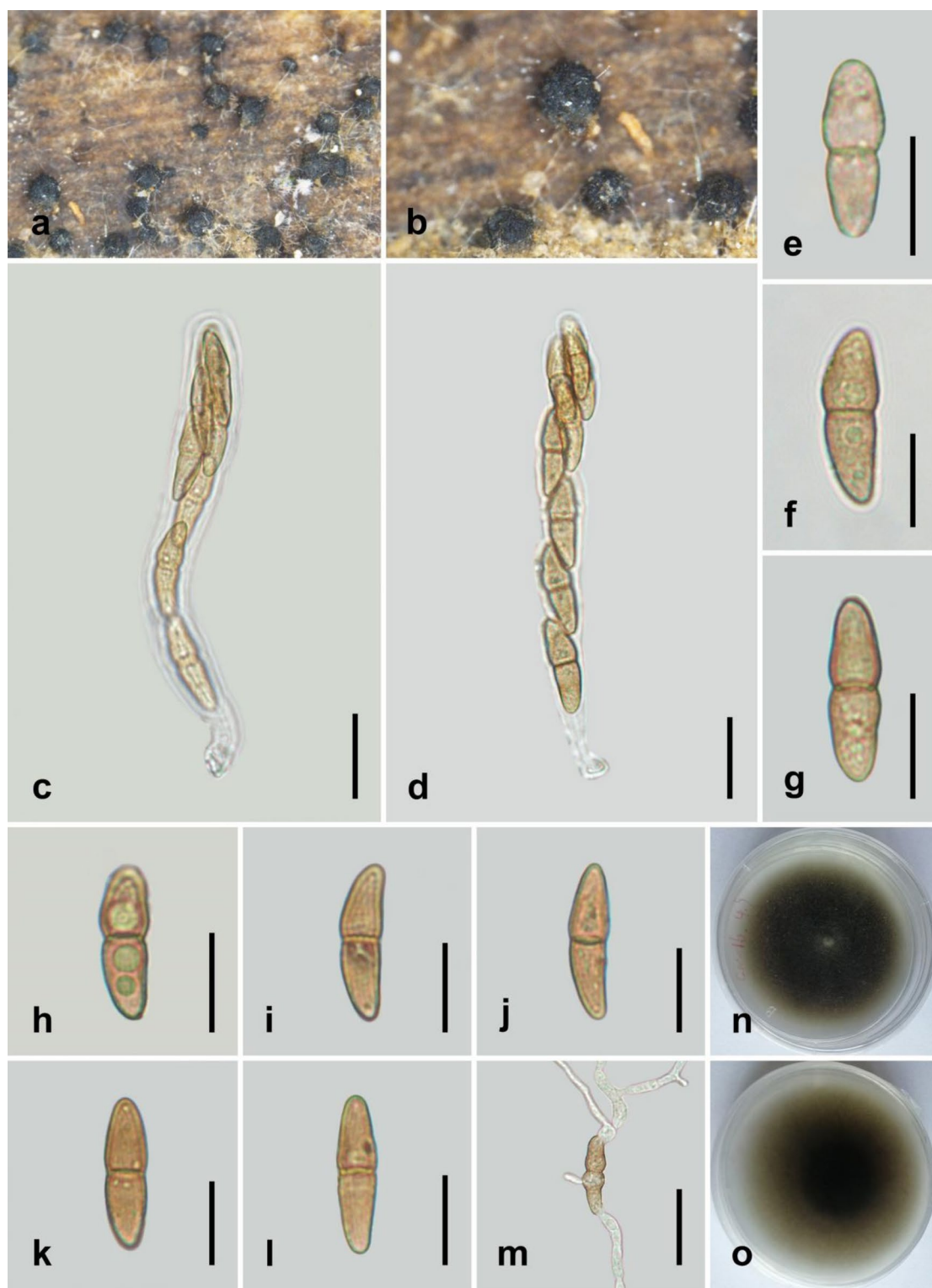
**Sexual morph**: Undetermined. **Asexual morph**: *Conidiomata* 90–180  $\mu\text{m}$  high, 180–310  $\mu\text{m}$  in diam, pycnidial, scattered, semi-immersed to superficial, ellipsoidal, dark brown to black, unilocular, sometimes white at the top, ostiolate. *Conidiomatal wall* 19–35  $\mu\text{m}$ , composed of thick-walled, dark brown cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 3–7  $\times$  2–4  $\mu\text{m}$ , holoblastic, determinate, cylindrical to subcylindrical, aseptate, hyaline, smooth-walled. *Conidia* 8–15  $\times$  6–8  $\mu\text{m}$  ( $\bar{x} = 12.4 \times 6.7 \mu\text{m}$ ,  $n = 20$ ), ellipsoidal to ovoidal, aseptate, rarely 1-septate, hyaline, thin-walled, smooth, with one large guttule or several smaller ones in each cell.

*Culture characteristics*: On PDA, colony circular, conidia germinated within 24 h, reaching 23 mm in 1 month at room temperature (25 °C), grey to brown from above, dark brown from below, surface rough and dry, umbonate, with dense white mycelium in the middle, regular edge.

*Material examined*: China, Sichuan Province, Yibin, Changning River, on submerged wood, 29 March 2021, Y. Qing, CN12 (IFRD, **holotype**).

*GenBank numbers*: ITS = ON124829, LSU = ON124829.

*Notes*: *Halobyssothecium sichuanense* is a distinct species and close to the sexual species *H. thailandica* (Fig. 3). *Halobyssothecium bambusicola*, *H. kunmingense*, *H. phragmitis* and *H. unicellulare* are also known from their asexual morphs. *Halobyssothecium sichuanense* morphologically differs from *H. bambusicola* and *H. phragmitis* in conidial shape (ellipsoidal to ovoidal in *H. sichuanense* vs. globose to obovate in *H. bambusicola* vs. ovoid to fusoid-ellipsoidal in *H. phragmitis*, Calabon et al. 2021); from *H. kunmingense* in having smaller conidiomata (210–250  $\mu\text{m}$  high vs. 90–180  $\mu\text{m}$  high, Dong et al. 2020); and from *H. unicellulare* in having larger conidia (8–15  $\times$  6–8  $\mu\text{m}$  vs. 6–9  $\times$  4–5  $\mu\text{m}$ ) and cylindrical to subcylindrical conidiogenous cells as compared to globose, subglobose to pear-shaped ones in *H. unicellulare* (Hyde et al. 2016). All of the four known



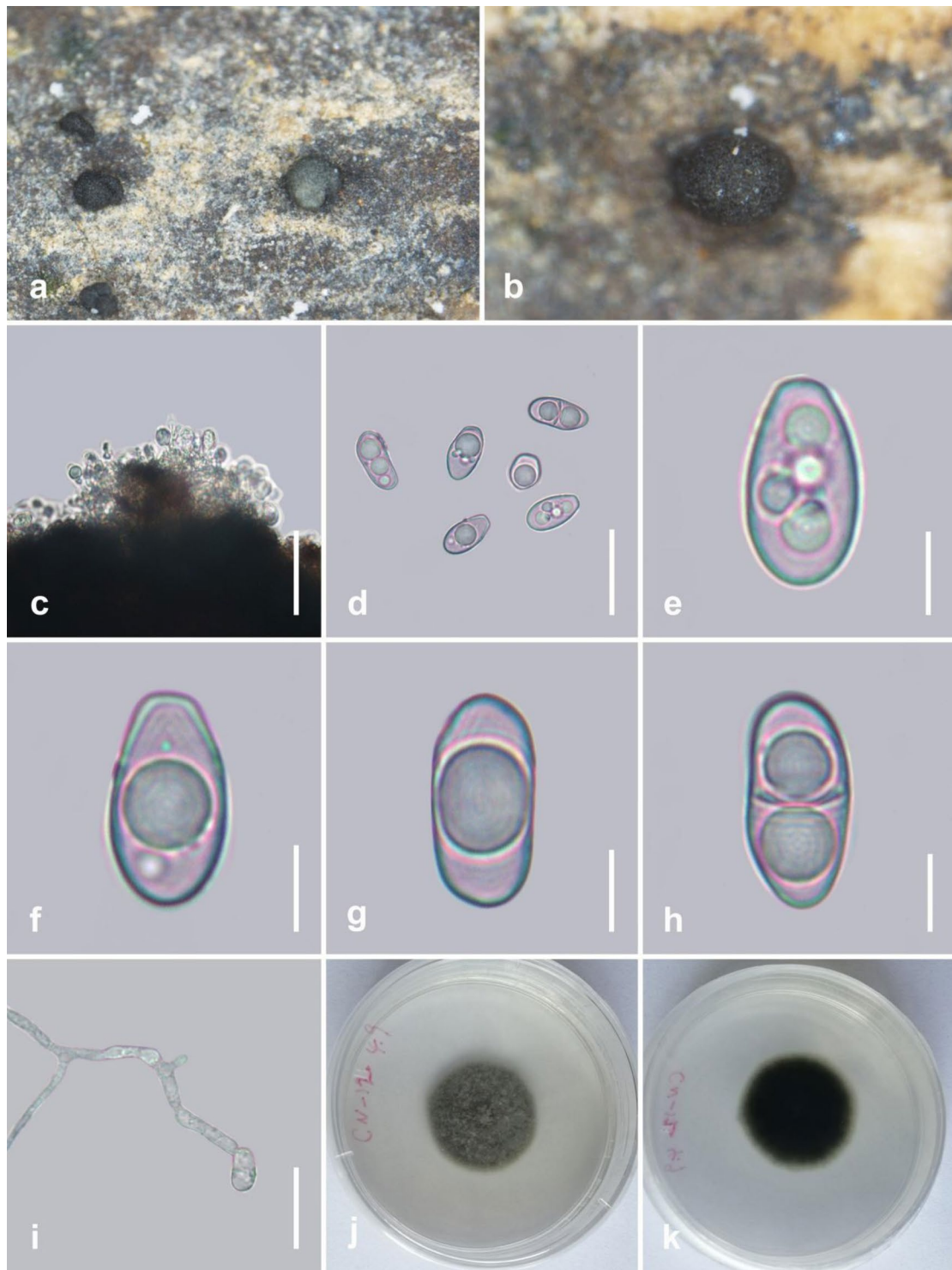
**Fig. 4** *Halobyssothecium cangshanense*. **a, b** Colonies on substrate. **c, d** Asci. **e–l** Ascospores. **m** Germinating ascospore on PDA. **n** Surface view of culture on PDA. **o** Reverse view of culture on PDA. Scale bar: **c, d** = 15  $\mu$ m, **e–l** = 10  $\mu$ m, **m** = 25  $\mu$ m

asexual species are phylogenetically distinguished from our new isolate. Therefore, it is introduced as a new species *H. sichuanense*.

**Nigrogranaceae** Jaklitsch & Voglmayr.

*Notes:* *Nigrogranaceae* was established by Jaklitsch and Voglmayr (2016) to accommodate *Nigrograna* based on its





**Fig. 5** *Halobyssothecium sichuanense* (CN12, holotype). **a, b** Colonies on substrate. **c** Developing conidia attach to conidiogenous cell. **d–h** Conidia. **i** Germinating conidia on PDA. **j** Surface view

of culture on PDA. **k** Reverse view of culture on PDA. Scale bar: **c** = 35  $\mu$ m, **i** = 20  $\mu$ m, **d–h** = 5  $\mu$ m

unique morphology. *Nigrograna* is the monotypic genus of *Nigrogranaceae* and it is considered to be a geographically and ecologically diverse group (Kolařík et al. 2017;

Kolařík 2018). The divergence time estimates for this family are given as crown age of 72 Mya (44–124 Mya) and

stem age of 131 Mya (86–180 Mya) during the Cretaceous period (Liu et al. 2017a; Mapook et al. 2020).

**Nigrograna** Gruyter, Verkley & Crous.

**Notes:** *Nigrograna* was introduced by de Gruyter et al. (2013) with *N. mackinnonii* as the type species. Based on the related molecular data of *N. mackinnonii* and the type species of *Biatrispora* (*B. marina*), Ahmed et al. (2014) synonymized *Nigrograna* under *Biatrispora*, and *N. mackinnonii* was transferred to *Biatrispora*. Later, Jaklitsch and Voglmayr (2016) found three new collections clustered with the above two *Biatrispora* species in the molecular study, but the new collections were different morphologically and ecologically from *B. marina*; therefore, they established the family *Nigrogranaceae* to accommodate *Nigrograna*, and *N. mackinnonii* was designated as the type species (Zhang et al. 2020). Subsequently, Kolařík et al. (2018) synonymized four endophytic species of *Biatrispora*, viz. *B. antibiotica*, *B. carollii*, *B. peruviansis* and *B. yasuniana* under *Nigrograna*. Members of this genus have been recorded from a wide range of hosts, i.e. marine and terrestrial habitats as saprobes, endophytes, and pathogens (Hyde et al. 2017; Tibpromma et al. 2017; Kolařík 2018; Zhao et al. 2018; Dayaratne et al. 2020; Zhang et al. 2020; Boonmee et al. 2021). *Nigrograna* is characterized by black ascomata, clavate, short pedicellate asci and pale to chocolate brown, asymmetric, fusoid to narrowly ellipsoid septate ascospores (Zhang et al. 2020; Boonmee et al. 2021). Currently, the genus includes 20 species epithets in Index Fungorum (2022). All of these species were confirmed with molecular data.

***Nigrograna kunmingensis*** T.Y. Du & Tibpromma, *sp. nov.*

**Index Fungorum number:** IF559865; **Facesoffungi number:** FoF 12956; **Fig. 6**

**Etymology:** named after the city Kunming from which the holotype was collected.

**Holotype:** ZHKU 22-0141.

**Saprobic** on dead stems of *Gleditsia sinensis*. **Sexual morph:** Ascomata 300–500 µm high × 390–450 µm diam. ( $\bar{x}$  = 356 × 413 µm,  $n$  = 10), aggregated in a disc, immersed in substrate, appearing as black irregular protrusions and cracks, subglobose to globose, brown to dark brown, hairs of ascomata 2–3.5 wide, brown, septate, branched. *Ostiole* inconspicuous, without papilla. *Peridium* 20–60 µm wide, comprising several layers, thick-walled cells, comprising brown to dark brown cells of *textura angularis*. *Hamathecium* comprising 1.5–2.5 µm wide, filiform, hyaline, septate, branched pseudoparaphyses. *Asci* (56–)65–80 × 10–12.5(–14) µm ( $\bar{x}$  = 70.3 × 11.4 µm,  $n$  = 20), bitunicate, fissionate, 8-spored, cylindrical to clavate, straight or slightly curved, with a short pedicel, apically rounded. *Ascospores* 13–16 × 5–6(–7) µm ( $\bar{x}$  = 14 × 5.4 µm,  $n$  = 30), uniseriate, brown to dark brown, broadly fusiform

or inequilateral, with slightly obtuse ends, upper part or second cell slightly wider, 3-septate when mature, slightly constricted at the septum, straight or slightly curved, guttulate, without appendages. **Asexual morph:** Undetermined.

**Culture characteristics:** Ascospores germinated on PDA within 24 h at 28 °C and germ tubes were produced from several cells. Mycelium raised, entire, white aerial hyphae; yellow to brown in reverse.

**Material examined:** China, Yunnan Province, Kunming City, Kunming Institute of Botany, on dead stems of *Gleditsia sinensis*, 24 March 2021, S.C. Karunaratna, KMD8 (ZHKU 22-0141, **holotype**); ex-type living culture: ZHKUCC 22-0242, ZHKUCC 22-0243.

**GenBank numbers:** ZHKUCC 22-0242: LSU = OP456379, ITS = OP456214, SSU = OP456382, TEF1- $\alpha$  = OP471608. ZHKUCC 22-0243: LSU = OP456380, ITS = OP484334, SSU = OP456383, TEF1- $\alpha$  = OP471609.

**Notes:** In the present phylogenetic analyses, *Nigrograna kunmingensis* clusters with the sister taxon *N. magnoliae* (MFLUCC 20-0020, MFLUCC 20-0021) with 100% ML and 1.00 PP statistical support (Fig. 7). *Nigrograna kunmingensis* and *N. magnoliae* are similar in the shape and size of asci and ascospores. However, *N. kunmingensis* differs from *N. magnoliae* in having ascomata with hairs, aggregated in a disc, immersed in the substrate, septate and branched pseudoparaphyses, and uniseriate, brown to dark brown, broadly fusiform or inequilateral ascospores, while *N. magnoliae* has immersed to erumpent ascomata, septate pseudoparaphyses, and uni to bi-seriate, yellowish-brown to brown, ellipsoid ascospores (Wanasinghe et al. 2020). Therefore, based on both phylogenetic analyses and morphological comparison, *N. kunmingensis* associated with *Gleditsia sinensis* is introduced as a new species from China.

***Nigrograna heveae*** R.F. Xu & Tibpromma, *Mycosphere* 14: 663–744 (2023).

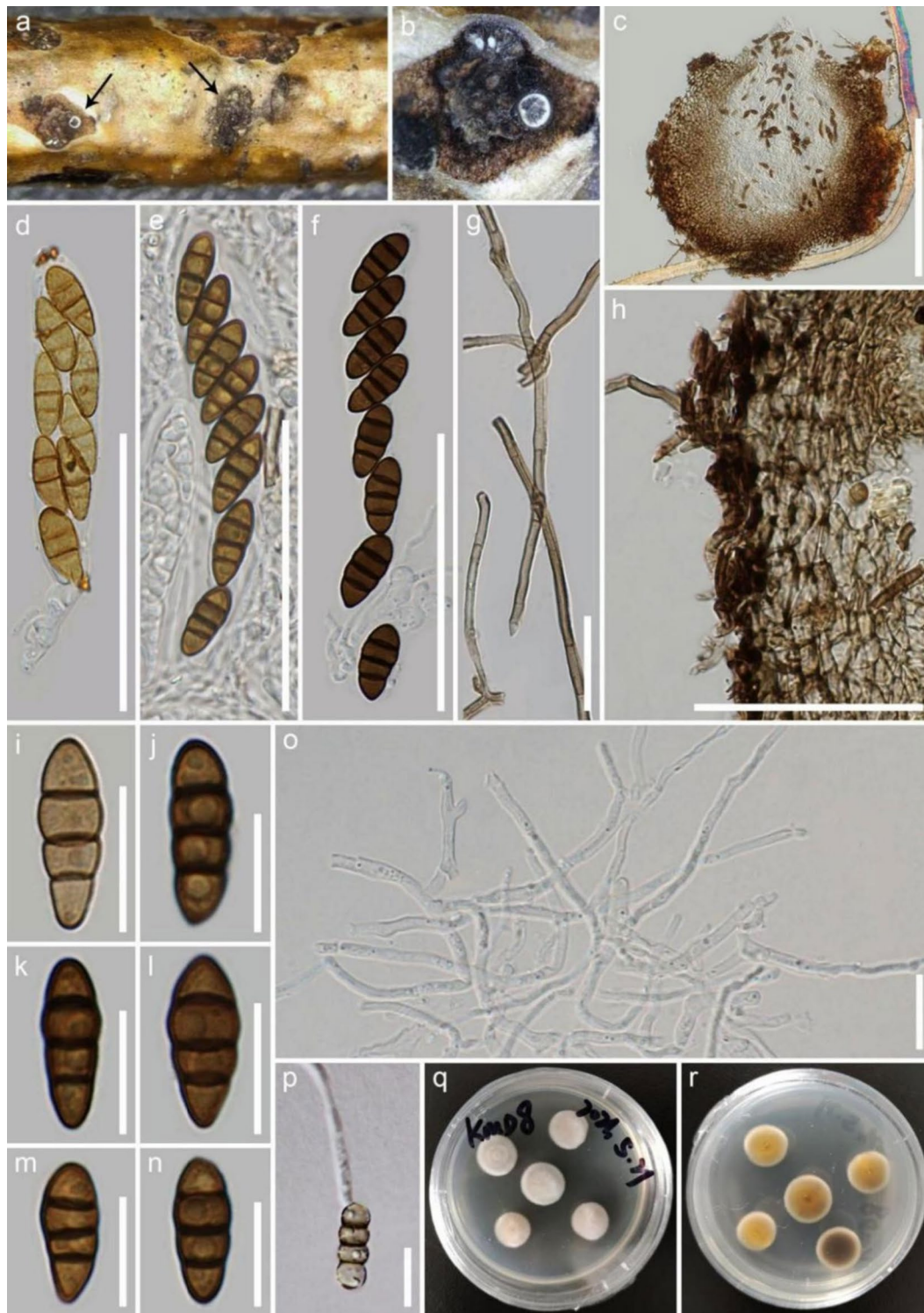
**Index Fungorum number:** IF559985; **Facesoffungi number:** IF559985; **Fig. 8**

**Holotype:** ZHKU 22-0152.

**Saprobic** on dead branch. **Sexual morph:** undetermined. **Asexual morph:** Coelomycetous. *Conidiomata* immersed in natural host, visible as black spots, solitary, scattered or aggregated, globose to depressed globose, papillate. *Conidiophores* arising from the wall, up to 28 µm long, and mainly 3 µm wide, in palisadic arrangement, filiform, septate, 1 to 3-celled, hyaline, unbranched or sparsely branched. *Conidiogenous cells* 4–12.5 × 1–3 µm ( $\bar{x}$  = 7.5 × 2.5 µm,  $n$  = 10), terminal phialide, cylindrical, hyaline. *Conidia* 3–4 × 1.5–2 µm ( $\bar{x}$  = 3.5 × 1.8 µm,  $n$  = 20), oblong to cylindrical, unicellular, with 1–2 small guttules, hyaline, smooth-walled.

**Culture characteristics:** Conidia germinating on PDA within 12 h and germ tube produced from conidia. Colonies



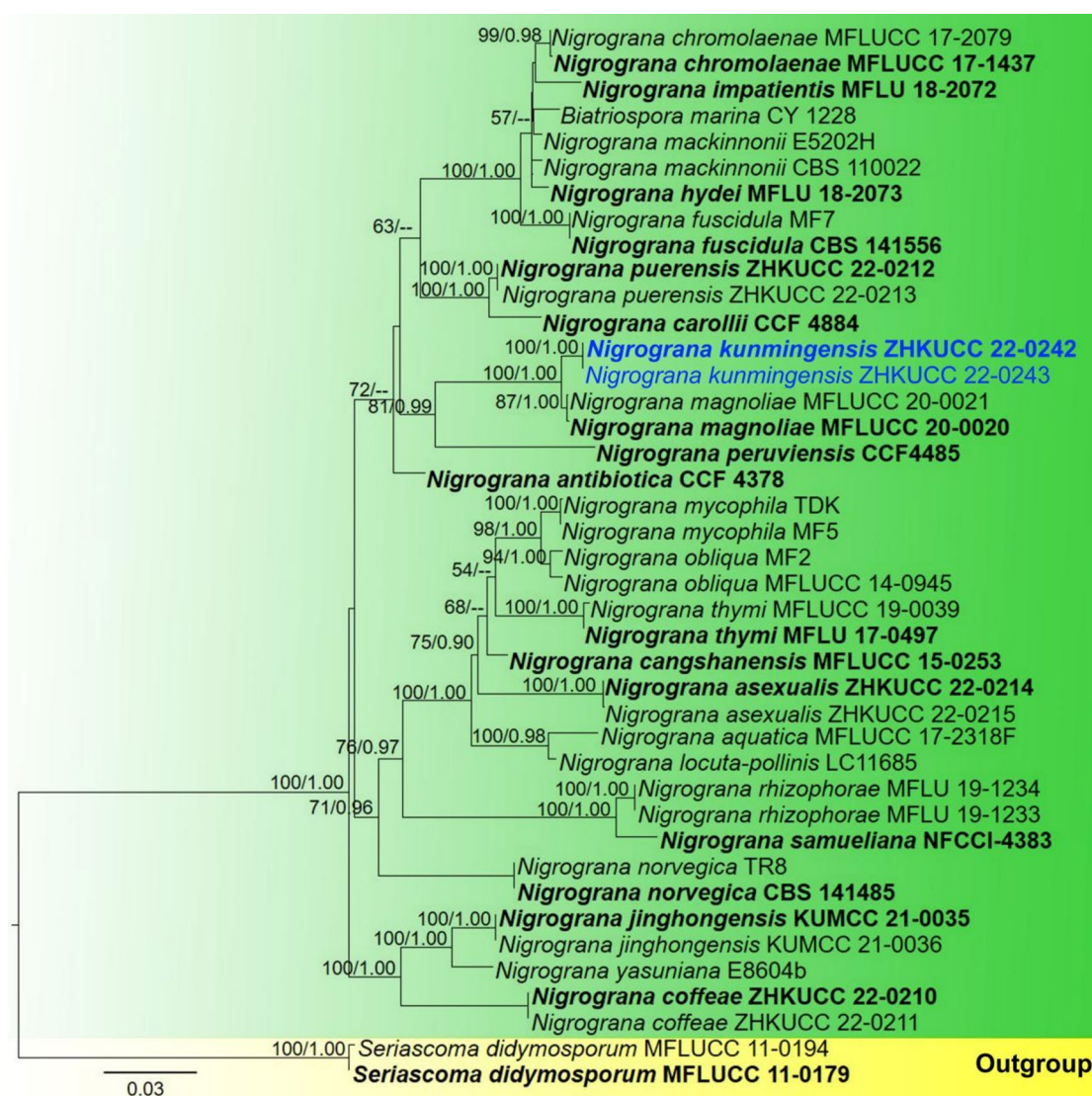


**Fig. 6** *Nigrograna kunmingensis* (ZHKU 22-0141, **holotype**). **a, b** Appearance of ascomata on the substrate. **c** A section through ascoma. **d–f** Asci. **g** Hairs of an ascoma. **h** Peridium. **i–n** Ascospores.

**o** Pseudoparaphyses. **p** Germinating ascospore. **q, r** Colony on PDA from above and below. Scale bars: **c** = 200  $\mu$ m, **d–f** = 50  $\mu$ m, **g** = 20  $\mu$ m, **h** = 50  $\mu$ m, **i–p** = 10  $\mu$ m

growing on PDA, reaching 20 mm diam. in 10 days at 25 °C, circular, flat, entire edge with a protuberance in the center,

brown to yellowish towards the edge in reverse and not producing pigment in culture.



**Fig. 7** Phylogram generated from maximum likelihood analysis based on a combined dataset of LSU, ITS, SSU, TEF1 and RPB2 sequence data of *Nigrograna*. Forty-one strains are included in the combined sequence analysis, which comprises 3961 characters with gaps. Tree topology of the ML analysis was similar to the BYPP. The best scoring RAXML tree with a final likelihood value of  $-15,644.521340$  is presented. The matrix had 949 distinct alignment patterns, with 30.90% of undetermined characters or gaps. Estimated base frequencies were as follows: A=0.249098, C=0.246692, G=0.264559,

T=0.239652; substitution rates: AC=1.741432, AG=5.232798, AT=1.725788, CG=1.315174, CT=13.366562, GT=1.000000; gamma distribution shape parameter  $\alpha=0.546634$ . Bootstrap support values for ML equal to or greater than 50% and BYPP equal to or greater than 0.90 are given above the nodes. The ex-types are in black bold; while the new isolates are in blue. The tree is rooted with *Seriascoma didymosporum* (MFLUCC 11-0179) and *S. didymosporum* (MFLUCC 11-0194)

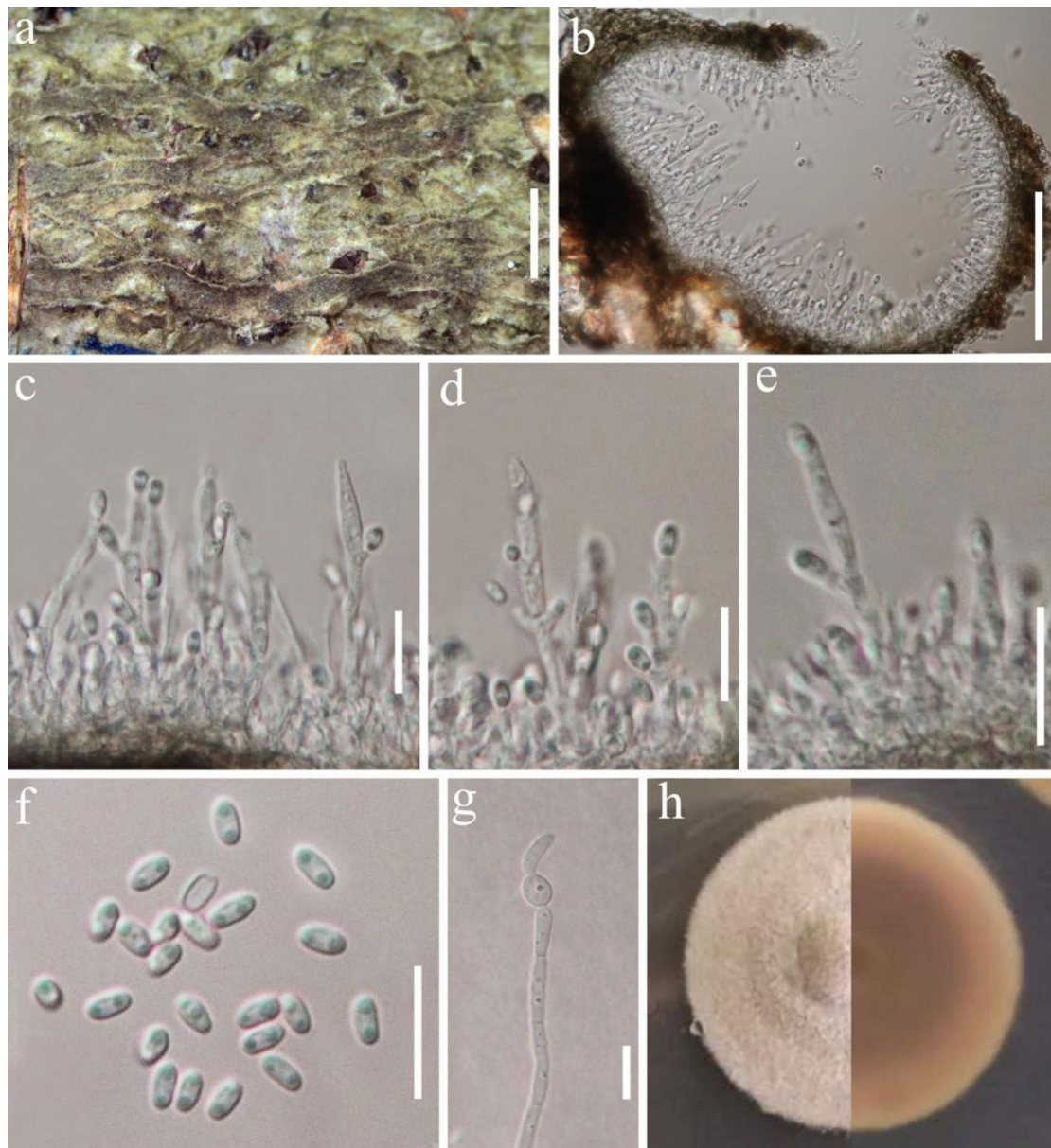
**Material examined:** Thailand, Chiangrai Province, Mae Fah Luang University, on dead branch in a forest, 07 January 2019, J.Y. Zhang, TF01-2 (MFLU 19-1393), living culture, ex-type living culture, MFLUCC 22-0051 (**new record for Thailand**).

**GenBank numbers:** LSU=OQ101584, ITS=OQ101581, TEF1 $\alpha$ =OQ054804.

**Notes:** Morphologically, our collection (MFLUCC 22-0051) matches with generic concept of *Nigrograna* and is similar to *N. fuscidula* in the shape of conidiophores,

conidiogenous cells and conidia (Jaklitsch & Voglmayr 2016). However, our collection differs from *N. fuscidula* in having shorter conidiophores (up to 28  $\mu\text{m}$  vs. up to 55  $\mu\text{m}$ , Jaklitsch & Voglmayr 2016). In the phylogenetic tree, our isolate (MFLUCC 22-0051) clustered as sister taxon to the strains of *Nigrograna heveae* (ZHKUCC 22-0284 and ZHKUCC 22-0285) with support (100% ML/1.00 PP, Fig. 9). The comparison of LSU, ITS, and TEF1 $\alpha$  sequences between our isolate and type strain (ZHKUCC 22-0285) showed 99.77% (850/852 bp), 99.34% (907/913 bp) and





**Fig. 8** *Nigrograna heveae* (MFLU 19-1393). **a** Superficial conidiomata on unidentified plant substrate. **b** Section of conidioma. **c–e** Conidiophores and conidiogenous cells. **f** Conidia. **g** Germinating conidium. **h** Colony on PDA. Scale bars: **a** = 1000  $\mu$ m, **b** = 50  $\mu$ m, **c–g** = 10  $\mu$ m

99.79% (939/941 bp) sequence similarity, respectively. Based on the molecular evidence and phylogenetic result, we recognize they are the same species. *Nigrograna heveae* was introduced with its ascomycetous sexual morph on the stem of *Hevea brasiliensis* (Euphorbiaceae) in China (Hyde et al. 2023). In this study, we identify our collection as *N. heveae* with coelomycetous asexual morph and report a new record of the species in Thailand.

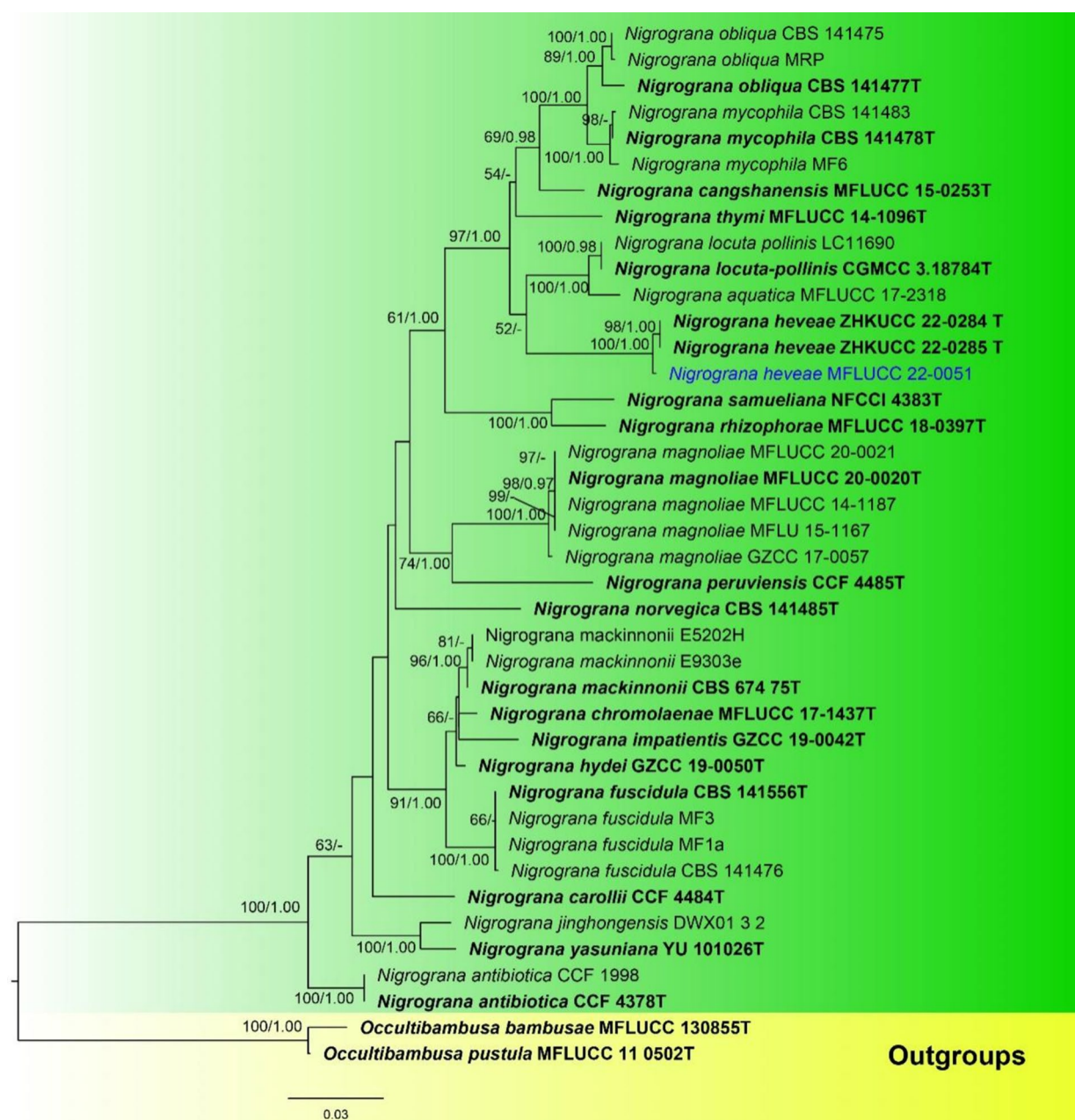
#### *Pleosporaceae* Nitschke.

**Notes:** *Pleosporaceae* (Nitschke 1869), includes 36 genera and 769 species (Kirk et al. 2008), and the species are

cosmopolitan. They are parasites or saprobes on wood and dead herbaceous stems or leaves (Sivanesan 1984). This includes the genera like *Alternaria*, *Bipolaris*, *Cochliobolus*, *Curvularia*, *Drechslera*, *Helminthosporium*, *Exserohilum* and *Pleospora*.

#### *Bipolaris* Shoemaker.

**Notes:** *Bipolaris* was established by Shoemaker (1959) and comprises 69 species according to Wijayawardene et al. (2022). *Bipolaris* species cause leaf spots, leaf blights, root rots, foot rots and other disease symptoms in the family Poaceae, including rice, maize, wheat and



**Fig. 9** Phylogram generated from maximum likelihood analysis based on combined ITS and TEF1 $\alpha$  sequence data. 40 taxa were included in the combined analyses, which comprised 1382 characters (ITS: 493 bp, TEF1 $\alpha$ : 889 bp) after alignment. The best scoring RAxML tree with a final likelihood value of -5723.168531 is presented. The matrix had 441 distinct alignment patterns, with 15.59% of undetermined characters or gaps. Estimated base frequencies were as follows: A=0.224465, C=0.293279, G=0.250321, T=0.231935;

substitution rates: AC=2.046193, AG=3.037116, AT=2.343899, CG=0.810670, CT=9.890958, GT=1.000000; gamma distribution shape parameter  $\alpha$ =0.176114. Bootstrap support values for ML equal to or greater than 50% and BYPP equal to or greater than 0.95 are given above the nodes. The tree is rooted with *Occultibambusa bambusae* MFLUCC 13-0855 and *O. pustula* MFLUCC 11-0502. The newly-generated strain is shown in blue. Ex-type strains are indicated by black and bold

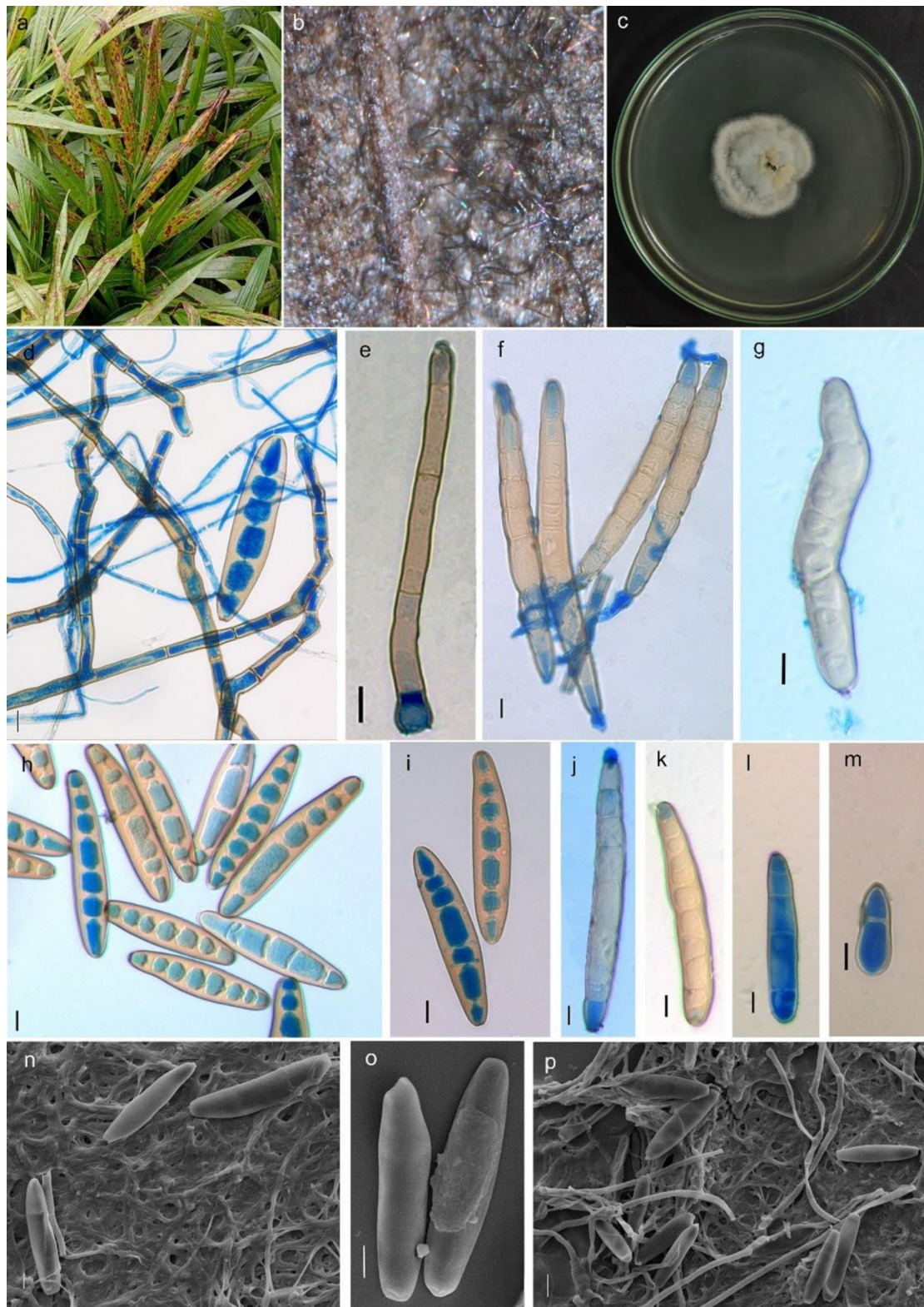
sorghum and on some other host plants (Ellis 1971; Sivanesan 1987; Berbee et al. 1999). We follow the recent treatment of Bhunjun et al. (2020) and Wijayawardene et al. (2022).

*Bipolaris heliconiae* Alcorn, Aust. Syst. Bot. 9(5): 814 (1996).

*Mycobank number*: MB 436839; *Facesoffungi number*: FoF11035; Fig. 10

*Holotype*: AMH10416.





**Fig. 10** *Bipolaris heliconiae* NFCCI 5165 (AMH10416, holotype). **a** Substratum (leaf of *Dypsis lutescens*). **b** Stereomicroscopic surface view of infected leaf. **c** Colony morphology on PDA (front view on 7th days). **d** Branched conidiophores. **e** An unbranched cylindrical

cal conidiophore. **f–m** Different types of conidia. **n–o** SEM images of conidia. **p** SEM images of branched conidiophores with numerous conidia. Scale bars **d–o** = 10  $\mu\text{m}$ , **p** = 20  $\mu\text{m}$

*Colour code follows:* Methuen Handbook of Colour (Kornerup and Wanscher 1978).

On leaf of *Dypsis lutescens* in terrestrial habitats. *Infection spots* amphiphilous, fructifications amphigenous, small, circular, dark brown, latter collapse to each other. **Sexual morph:** Undetermined. **Asexual morph:** stromatal cells 2–5 in groups, light to olivaceous brown (7D8). *Setae* and *hyphopodia* absent. *Conidiophores* superficial, straight to curved, solitary or in groups, unbranched to rarely dichotomously branched, basal cell of conidiophores slightly bulbous, geniculate in fertile region, scars slightly thickened, smooth walled, light brown (7D8), 2–12 septate,  $103.30\text{--}335.50 \times 7.0\text{--}16.5 \mu\text{m}$ . *Conidia* acropleurogenous, cylindrical, clavate to obclavate, smooth walled, light brown (7D8), transversely septate, 1–11 septate, hilum slightly thickened, non-protuberant, base truncate, tip obtuse,  $43.0\text{--}192.0 \times 7.5\text{--}17.0 \mu\text{m}$ .

*In-vitro culture*, vegetative hyphae, unbranched to branched, septate, thin and thick, pigmented, subhyaline to very light olivaceous brown (7D8),  $3.0\text{--}9.0 \mu\text{m}$  wide. *Chlamydospores* absent. *Setae* and *hyphopodia* absent. *Conidiophores* arising from superficial hyphae, macronematous, mononematous, unbranched to dichotomously branched, straight to flexuous, multi-septate, smooth walled, scars slightly thickened, light olivaceous brown (7D8), up to  $612.0 \times 9.5 \mu\text{m}$ . *Conidia* acropleurogenous, straight to slightly curved, clavate to obclavate, non-protuberant, hilum slightly thickened, olivaceous to light olivaceous brown (7D8), transversely septate, smooth walled, base truncate, tip obtuse, pseudoseptate, 3–7 septate, inner cells discoid,  $72.5\text{--}10.0 \times 15.5\text{--}21.5 \mu\text{m}$ .

*Culture characteristics:* On semi-synthetic agar medium PDA (Potato Dextrose Agar) greyish white (5A1), greyish brown (5A2) reaching 3 cm diam in 8 days at 25 °C, with irregular margin, puffy, surface filamentous.

*Material examined:* India, Maharashtra, Pune District, on infected leaves of *Dypsis lutescens* (Arecaceae), 5 September 2021, P.N. Singh, AMH10416 (**holotype**); ex-type living culture, NFCCI5165 (National Fungal Culture Collection of India- WDCM 932, **new record for India**).

*GenBank numbers:* ITS = ON028647, LSU = ON032299, TEF1- $\alpha$  = ON148454.

*Notes:* The present taxon is distinct from type species *Bipolaris heliconiae* (BRIP 17186) (Alcorn 1996) in having smaller conidia ( $72.65\text{--}99.75 \times 15.72\text{--}21.55 \mu\text{m}$  with 3–7 septa vs.  $65\text{--}150 \times 15\text{--}19 \mu\text{m}$  with 7–10 septa). In addition to this, the conidia of NFCCI 5165 are clavate to obclavate, whereas conidia of BRIP 17186 are fusoid to clavate fusoid. *Bipolaris heliconiae* (NFCCI 5165) clusters with *Bipolaris heliconiae* (BRIP 17189) and *B. heliconiae* (BRIP 17186) (Alcorn 1996) with 97% bootstrap support. On megablast analysis, our ITS sequence is showing 99% similarity (397/400) with 1 gap (0%) with both *Bipolaris*

*heliconiae* (BRIP 17189) and *Bipolaris heliconiae* (BRIP 17186) (Fig. 11).

However, based on similarity of morphological characteristics, and phylogenetic analysis, the present collection is confirmed as *Bipolaris heliconiae* (Alcorn 1996). This is the first report of *Bipolaris heliconiae* from India.

### *Trypetheliales* Lücking, Aptroot & Sipman.

*Notes:* The order *Trypetheliales* was established by Aptroot et al. (2008) to accommodate the lichen-forming family *Trypetheliaceae* (Hyde et al. 2013), and recently another family, *Polycoccaceae*, including lichenicolous fungi, was included in this order (Ertz et al. 2015). The order is characterized by perithecioid ascomata solitary or aggregated in the pseudostromata, branched and anastomosing paraphyses forming a network, and hyaline or rarely brown ascospores, transversely septate to muriform often with diamond-shaped lumina (Aptroot et al. 2008; Hyde et al. 2013; Ertz et al. 2015).

### *Trypetheliaceae* Eschw.

*Notes:* *Trypetheliaceae* now includes 18 genera and more than 400 species (Hongšan et al. 2020b). Most members in this family were found in tropical lowland to lower montane, rain forest, dry forest, and savanna habitats, but a few species extended into temperate regions.

### *Astrothelium* Eschw.

*Notes:* The genus *Astrothelium* includes pyrenocarpous lichen-forming fungi within *Trypetheliaceae* (Harris 1984, 1995). It is originally restricted to species with lateral, fused ostioles and transversely septate ascospores. In its revised delimitation, the genus comprises the majority of species in the *Trypetheliaceae* (Aptroot and Lücking 2016), with variable ascoma arrangement and ascospore septation (Hongšan et al. 2020b). In both its traditional and its current circumscription, the genus has a pantropical distribution (Harris 1984; Awasthi 1991; Aptroot et al. 2008; Hyde et al. 2013).

*Astrothelium pseudostraminicolor* S.H. Jiang, C. Zhang & J.C. Wei, **sp. nov.**

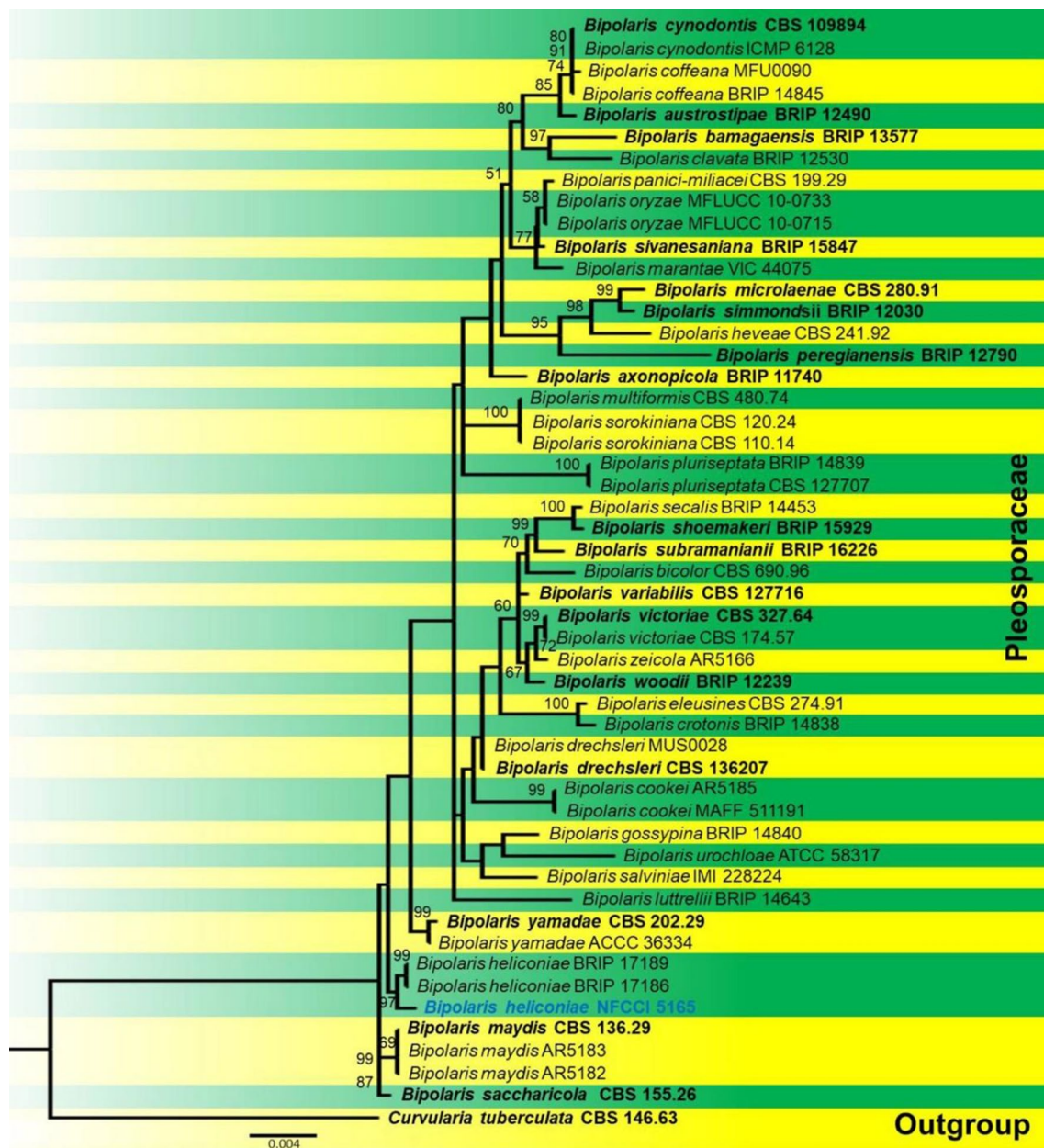
*Mycobank number:* MB 841113; *Facesoffungi number:* FoF 13377; Figs. 12, 13

*Etymology:* The epithet “pseudostraminicolor” refers to the similarity with *Astrothelium straminicolor*.

*Holotype:* HMAS – L 151080.

*Thallus* crustose, corticate, olive-green to yellowish, shiny, uneven to bullate, continuous, cortex distinct, prothallus not observed, 0.2–0.4 mm thick, covering areas up to 8 cm in diam., not inducing gall formation of the host bark. *Algae* trentepohlioid. *Ascomata* perithecia, conical or pyriform, black, 0.3–0.7 mm in diam., erumpent,





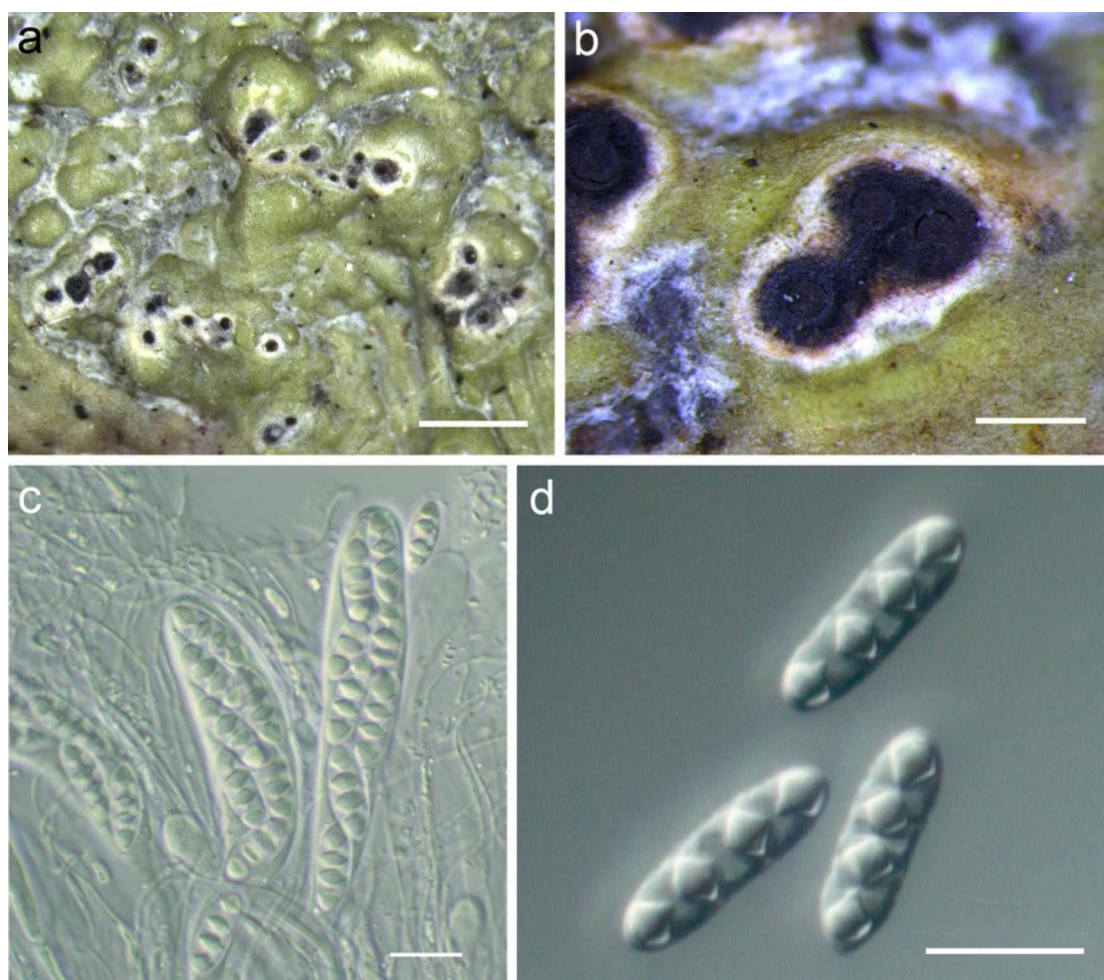
**Fig. 11** Phylogenetic tree of *Bipolaris heliconiae* (NFCCI 5165) constructed based on combined sequence data of ITS, LSU and TEF by Maximum-Likelihood method. *Curvularia tuberculata* CBS 146.63 was used as out-group. The analysis involved 51 nucleotide sequences. Evolutionary analyses were conducted in IQ-TREE multicore version 1.6.11 (Nguyen et al. 2015) by the Maximum-Likeli-

hood method using the best suitable model (TITNe+R2 model). Newly generated sequence is in blue. One-thousand bootstrap replicates were analyzed to get ultrafast bootstrap values, and the values above 50% were represented on nodes in the tree. Ex-type strains are in bold and new isolate is in blue

covered by thallus except for dark ostiolar area surrounded by whitish rim, solitary or aggregated in pseudostromata. *Pseudostromata* rounded to irregular, erumpent to prominent, covered by a thallus layer, with flattened top. *Ostiole* appearing as blackish dot, eccentric, fused, 30–100 µm in diam. *Ascomata* Wall carbonized, black, 20–90 µm thick. *Hamathecium* composed of densely anastomosing, net-like paraphyses, interspersed with oil drops. *Asci* cylindrical

to clavate, 120–140 × 16–21 µm. *Ascospores* 8 per ascus, biseriate to irregular, hyaline, transversely 3-septate, 17–30 × 6–10 µm, fusiform, ends rounded, lumina diamond-shaped, surrounded by a smooth gelatinous sheath, 2–8 µm wide. *Pycnidia* not seen.

**Chemistry:** Thallus UV-. Pseudostromata UV-. No substance detected by TLC.



**Fig. 12** *Astrothelium pseudostraminicolor* (HMAS–L 151080, **holotype**). **a** Thallus with ascomata. **b** Pseudostromata and ostioles. **c** asci. **d** ascospores. Scale bars: **a** = 0.1 mm, **b** = 0.2 mm, **c** = 20  $\mu$ m, **d** = 10  $\mu$ m

**Habitat and distribution:** The new species grows on the bark of tropical and subtropical regions, and is currently only found in China.

**Material examined:** China, Guangxi Province, Xing'an county, Maoershan National Nature Reserve, 25° 52' 10" N, 110° 24' 47" E, 2025 m alt., on bark, 21 August 2017, X.L. Wei, R.D. Liu, X. Qian, Y.B. Zuo, X.M. Cheng 20191091 (HMAS–L 151080, **holotype**); *ibid.*, XA2017068 (HMAS–L 0139996).

**GenBank numbers:** HMAS–L 151080: ITS = OM001629; HMAS–L 0139996: ITS = OM001628.

**Notes:** This species keys out in the recent world key (Aptroot 2021) in key K at couplet 6. It is similar to *Astrothelium straminicolor*, but the latter often has prominent pseudostromata, laterally covered by a thallus, with one to several groups of fused ascomata forming broad, flat, dark ostiolar areas often fused in a lobate pattern (Aptroot and Lücking 2016). Another similar species is *A. pyrenastrosulphureum*, but its pseudostromata are often prominent, covered by a

thallus, with one to several groups of fused ascomata with dark, papilliform, always separate ostiolar areas, but without a whitish rim (Aptroot and Lücking 2016).

#### ***Tubeufiales* Boonmee & K.D. Hyde.**

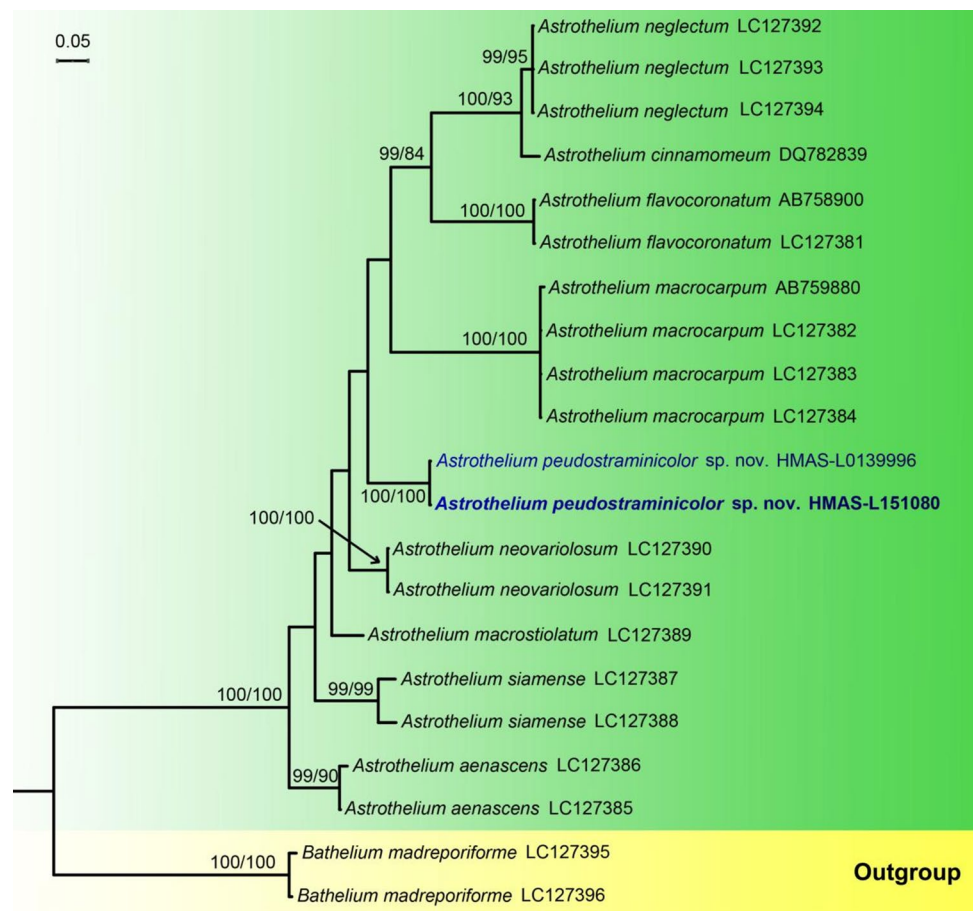
**Notes:** Boonmee et al. (2014) established *Tubeufiales* based on multi-locus phylogeny and morphology. *Tubeufiales* comprises three families: *Bezerromycetaceae* (3 genera), *Tubeufiaceae* (47 genera) and *Wiesneriomycetaceae* (6 genera, Wijayawardene et al. 2022). The latest treatments and updated accounts of *Tubeufiales* by Hongsanan et al. (2020b) was followed in this paper.

#### ***Tubeufiaceae* M.E. Barr.**

**Notes:** *Tubeufiaceae*, typified by *Tubeufia*, was introduced by Barr (1979), who accepted an additional five genera: *Letendrae*, *Melioliphila*, *Podonectria*, *Rebentischia* and *Thaxteriella*. Various authors later introduced and accepted other genera in *Tubeufiaceae* (Rossman 1987;



**Fig. 13** Phylogenetic tree showing the internal phylogeny of *Astrothelium*, constructed through Bayesian analysis based on ITS with an alignment length of 455 bp. Bayesian inference posterior probabilities above 95% (left) and Maximum likelihood bootstrap support above 70% (right) are shown at nodes (B–PP / ML–BP)



Kirk et al. 2001; Lumbsch and Huhndorf 2010; Boonmee et al. 2014; Brahmanage et al. 2017; Chaiwan et al. 2017; Liu et al. 2018; Lu et al. 2018). Forty-seven genera are presently included in *Tubeufiaceae* with *Acanthostigma* (60 species) and *Tubeufia* (ca. 60 species) being the most speciose genera (Dong et al. 2020). For the latest treatments and updated accounts of *Tubeufiaceae* see Hongsanan et al. (2020b).

#### *Parahelicomyces* Goh.

**Notes:** Lu et al. (2018) introduced *Pseudohelicomyces* with *P. talbotii* as type species and included four others, *P. aquaticus*, *P. hyalosporus*, *P. paludosus* and *P. indicus*. Phookamsak et al. (2019) and Jayasiri et al. (2019) introduced two more species, *P. menglunicus* and *P. quercus*, respectively. The former was observed from unidentified seed in China, while the latter from fruit pericarp of *Quercus* in Thailand. Later, Hsieh et al. (2021) collected *Pseudohelicomyces talbotii* from decaying culm of *Miscanthus floridulus* in Taiwan, China and an unidentified wood submerged in a stream. Since *Pseudohelicomyces* under *Tubeufiaceae* was a homonym of *Pseudohelicomyces* belonging to *Hymenogastraceae* (Agaricales, Agaricomycetes, Valenzuela and Garnica 2000). Hsieh et al. (2021) renamed the genus as

*Parahelicomyces*, and transferred *Pseudohelicomyces talbotii* and the other six illegitimate *Pseudohelicomyces* species. Currently, *Parahelicomyces* species are accepted, and all have molecular sequence data. *Parahelicomyces* thrives in terrestrial and freshwater habitats (Jayasiri et al. 2019; Calabon et al. 2022). Four species were reported in the latter: *Parahelicomyces aquaticus* (Lu et al. 2018), *P. hyalosporus* (Luo et al. 2017) and *P. talbotii* (Lu et al. 2018; Hsieh et al. 2021). In this paper, we introduce one novel species of *Parahelicomyces* with unique morphology from *Spartina* sp. in salt marsh habitat in Thailand.

***Parahelicomyces dictyosporus*** M.S. Calabon, E.B.G. Jones & K.D. Hyde, *sp. nov.*

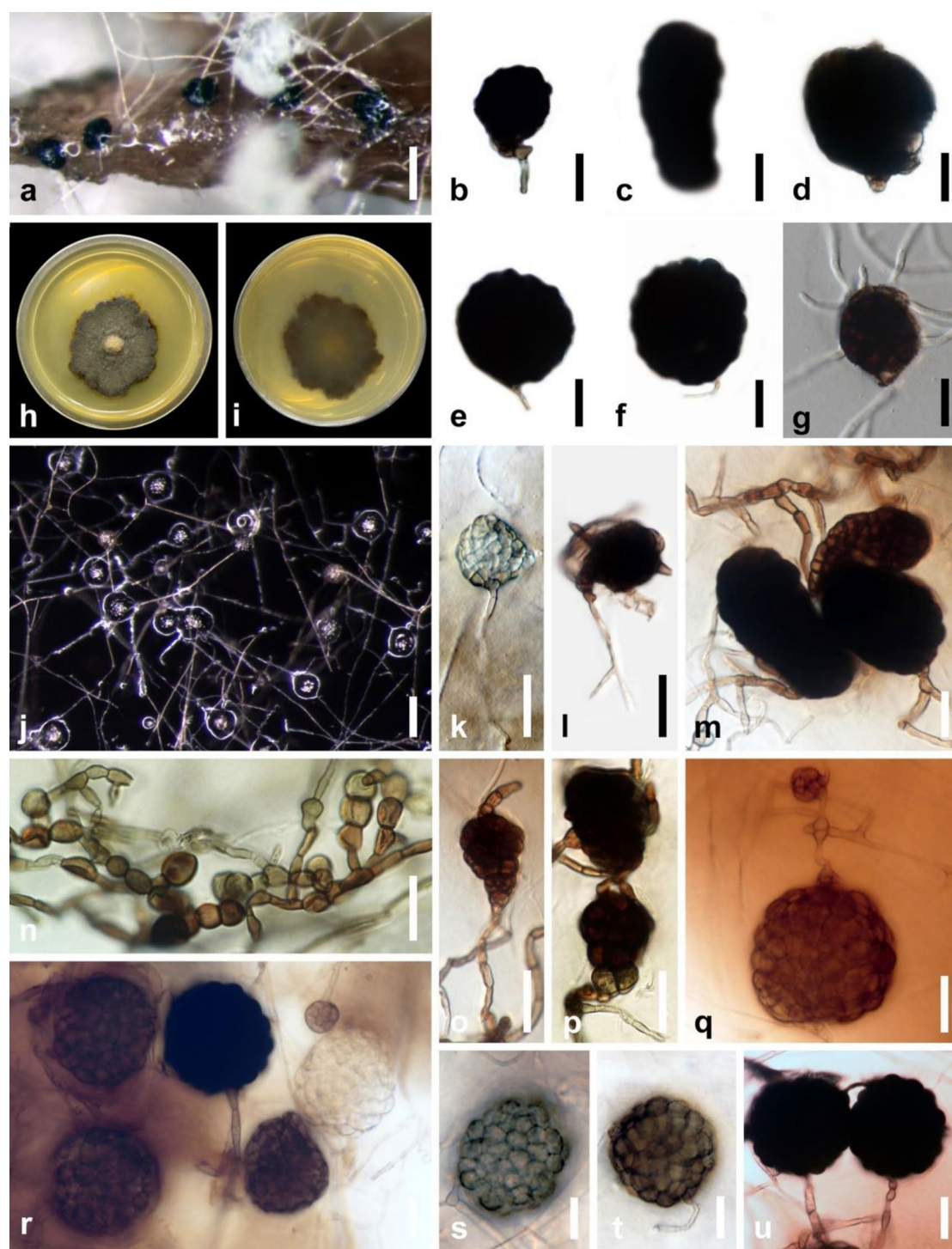
**Index Fungorum number:** IF 559841; **Facesofungi number:** FoF 12738; **Fig. 14**

**Etymology:** “dictyosporus” referring to dictyospores of this fungus.

**Holotype:** MFLU 22-0119.

**Saprobic** on submerged decaying wood in a freshwater stream. **Sexual morph:** Undetermined. **Asexual morph:** Hyphomycetous, dictyosporous. **Conidiophores** lacking. **Conidiogenous cells** holoblastic, monoblastic, integrated, cylindric, apical, hyaline to pale brown. **Dictyospores**





**Fig. 14** *Parahelicomyces dictyosporus* (MFLU 22-0119, **holotype**). **a** Colonies in natural substrates. **b–f** Dictyochlamydospores. **g** Germinated conidium. **h, i** Colonies on MEA from surface and in reverse.

**j** Dictyochlamydospores in culture. **k–q** Development of dictyochlamydospores. **r–u** Dictyochlamydospores. Scale bars: **a, j** = 100  $\mu$ m, **b–g, k–u** = 20  $\mu$ m

40–70  $\times$  25–70  $\mu$ m ( $\bar{x}$  = 52.3  $\times$  43.1  $\mu$ m,  $n$  = 20) acrogenous, carbonaceous, friable, solitary, mostly globose, subglobose to ovoid indistinctly dictyoseptate, verrucose, brown when young, dark brown to black when matured.

**Culture characteristics:** Conidia germinating on malt extract agar (MEA) and producing germ tubes within 24 h. Colonies growing on MEA, circular, with flat surface, edge entire to filiform, reaching 30–35 mm in 4 weeks at 25  $^{\circ}$ C,

from above brown to dark brown, from below dark brown. Mycelia superficial and partially immersed, branched, septate, hyaline to pale brown. Sporulation in culture. *Conidiophores* lacking. *Conidiogenous cells* holoblastic, monoblastic, integrated, cylindric, apical, hyaline to pale brown. *Dictyospores*  $35\text{--}70 \times 25\text{--}70\text{ }\mu\text{m}$  ( $\bar{x} = 53.1 \times 45.2\text{ }\mu\text{m}$ ,  $n = 50$ ) acrogenous, carbonaceous, friable, solitary, variable in shape, broadly oval to ellipsoidal when young, mostly globose when mature, indistinctly dictyoseptate, verrucose, hyaline to pale brown when young, dark brown to black when matured.

**Habitat and distribution:** *Parahelicomyces dictyosporus* was observed from submerged decaying culms of *Spartina* sp. in tropical saltmarsh area, and is currently only found in Thailand.

**Material examined:** Thailand, Prachuap Khiri Khan, Pran Buri,  $12^\circ 23' 43.0''\text{N}$   $99^\circ 58' 28.3''\text{E}$ , on submerged decaying culms of *Spartina* sp. (Poaceae), 20 July 2019, M.S. Calabon, MCFWBB (MFLU 22-0119, **holotype**), ex-type living culture, MFLUCC 22-0080.

**GenBank numbers:** ITS = OP216409, LSU = OP216404, TEF1- $\alpha$  = OP251194, RPB2 = OP251198.

**Notes:** The isolate MFLU 22-0119 is morphologically similar with *Tubeufia dictyospora* (MFLU 17-1173) with globose to subglobose dictyospores but the latter has a larger dictyospores [ $60\text{--}100 \times 60\text{--}70(80)\text{ }\mu\text{m}$  vs.  $40\text{--}70 \times 25\text{--}70\text{ }\mu\text{m}$ ] (Lu et al. 2018). NCBI BLASTn of the sequences of isolate MFLUCC 22-0119 showed the this is closely related to *Parahelicomyces*: LSU (*P. hyalosporus* CBS 283.51, 99.51%), ITS (*P. aquaticus* MFLUCC 16-0234, 92.20%), TEF1- $\alpha$  (*P. aquaticus* MFLUCC 16-0234, 98.46%; *P. quercus* MFUCC 17-0895, 98.02%), and RPB2 (*P. hyalosporus* AFTOL-ID, 94.30%). The multi-locus phylogenetic analysis placed the isolate within *Parahelicomyces* in a subclade with a terrestrial species *P. Chiangmaiensis* and the freshwater species *P. aquaticus* (Fig. 15). In pairwise nucleotide comparisons of *P. dictyosporus* with the sister taxon *P. Chiangmaiensis* (MFUCC 21-0159), there is a nucleotide differences of 3.36% (13 bp) in ITS (of 387 nucleotides altogether), 1.86% (16 bp) in TEF1- $\alpha$  (of 861 nucleotides altogether), and 3.26% (26 bp) in RPB2 (of 797 nucleotides altogether). *Parahelicomyces dictyosporus* is a dictyosporous species and this morphological character is unique compared to other *Parahelicomyces* species with cylindrical, branched conidiophores, and acropleurogenous, helicoid conidia. *Parahelicomyces dictyosporus* is the first species of *Parahelicomyces* reported from marine habitats, and the third species recorded from aquatic environments in Thailand, wherein *Para. aquaticus* and *Para. talbotii* were earlier recorded by Lu et al. (2018).

**Eurotiomycetes** Tehler ex O.E. Eriksson & K. Winka.

**Notes:** For the latest treatments and updated accounts of Eurotiomycetes, see Wijayawardene et al. (2022).

**Eurotiales** G.W. Martin ex Benny & Kimbr.

**Notes:** The order *Eurotiales* has many species with economically important uses and negative impacts on human activities (Houbraken et al. 2020); currently, it has five accepted families harbouring about 28 genera (Wijayawardene et al. 2022).

**Thermoascaceae** Apinis.

**Notes:** The family *Thermoascaceae* was introduced by Apinis (1967), and it has been recently revisited based on morphology and phylogeny; currently, this family has two accepted genera, *Paecilomyces* and *Thermoascus* (Houbraken et al. 2020; Wijayawardene et al. 2022).

**Thermoascus** Mische.

**Notes:** The genus *Thermoascus* has 12 records in Index Fungorum and MycoBank databases (3 July 2022), and about seven species are accepted in this genus (Houbraken et al. 2020; Wijayawardene et al. 2022). Species in this genus are thermophilic and morphologically characterised by the “production of orange-yellow, brown or red-brown, soft cleistothecia formed in a more or less continuous crust-like layer with a pseudoparenchymatous wall”, and the anamorph can be absent or differ significantly (Houbraken et al. 2020).

**Thermoascus endophyticus** T.M. Silva, C.S. Oliveira & J.D.P. Bezerra, *sp. nov.*

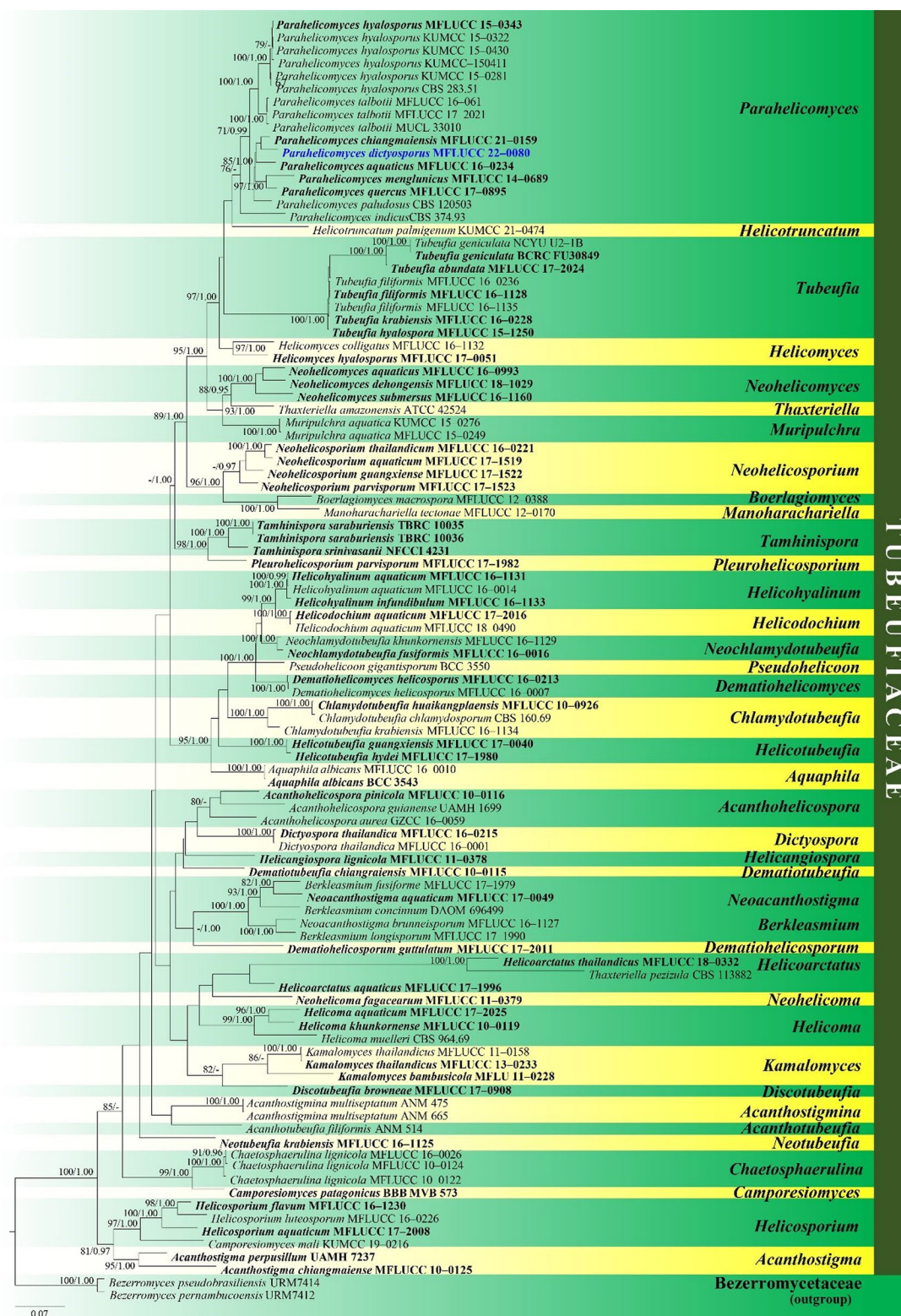
**Mycobank number:** MB 846409; **Facesoffungi number:** FoF 13376; Fig. 16

**Etymology:** The epithet “endophyticus” refers to the fungus’s lifestyle, which was found to occur endophytically in *Brosimum gaudichaudii*.

**Holotype:** UFG 34289.

Cleistothecial ascomata, globose to subglobose, light brown to brown, abundantly present with colony age (178–)418(–465)  $\times$  (108–)372(–465)  $\mu\text{m}$ . *Asci* globose to subglobose, 8-spored,  $13.5\text{--}16.5 \times 11\text{--}13.5\text{ }\mu\text{m}$ . *Ascospores* ellipsoids, ornamented, light brown to brown with age (5.5–)8  $\times$  (4–)5.5  $\mu\text{m}$ . *Conidiophores* straight to flexuous, septate, branched, hyaline, smooth-walled, abundantly present at the initial colony growth stage (40.5–)108–148(–216)  $\times$  (4–)5.5  $\mu\text{m}$ . *Phialides* ampulliform with a cylindrical basal portion and tapering to a thin neck, hyaline, smooth-walled, in groups of two to three (occasionally one) on short metulae, single phialides are occasionally born directly on the hyphae (13.5–)16–19(–21.5)  $\times$  (3–)5.5  $\mu\text{m}$ . *Conidia* cylindrical, occasionally subglobose, aseptate, hyaline to light brown with age, smooth walled, produced in chains (5.5–)8–11  $\times$  3(–5.5)  $\mu\text{m}$ . *Chlamydospores* not observed.





**Culture characteristics:** Colonies on PDA, MEA and DG18 growing fast and attaining a diameter of 90 mm at 25 °C after 1 week in the dark and growing up to 70 mm on CZ. On PDA, colonies are plane, floccose, whitish,

yellowish to orange and orange with age, exudate yellowish; reverse yellowish to orange. On MEA, colonies are plane, slightly cottonose, whitish, salmon to orange with age, concentric circles, exudate salmon to orange; reverse

**Fig. 15** Phylogram generated from maximum likelihood analysis based on combined LSU, ITS, TEF1- $\alpha$ , and RPB2 sequence data representing Tubeufiaceae (Tubeufiales). One hundred strains are included in the combined analyses which comprised 3726 characters (806 characters for LSU, 967 characters for ITS, 910 characters for TEF1- $\alpha$ , and 1043 characters for RPB2) after alignment. *Bezeromyces pernambucoensis* (URM7412) and *Bezeromyces pseudo-brasiliensis* (URM7414) in Tubeufiaceae (Tubeufiales) were used as the outgroup taxa. The best scoring RAxML tree with a final likelihood value of -44,231.079169 is presented. The matrix had 1741 distinct alignment patterns, with 33.38% of undetermined characters or gaps. Estimated base frequencies were as follows: A=0.242684, C=0.256704, G=0.264190, T=0.236422; substitution rates: AC=1.008141, AG=3.810958, AT=1.774984, CG=0.705605, CT=6.978420, GT=1.000000; gamma distribution shape parameter  $\alpha$ =0.240917. Bootstrap support values for ML equal to or greater than 70% are given above the nodes (left side). Bayesian posterior probabilities (BYPP) equal to or greater than 0.95 are given above the nodes (right side). Ex-type strains are in bold and newly generated sequences are in blue

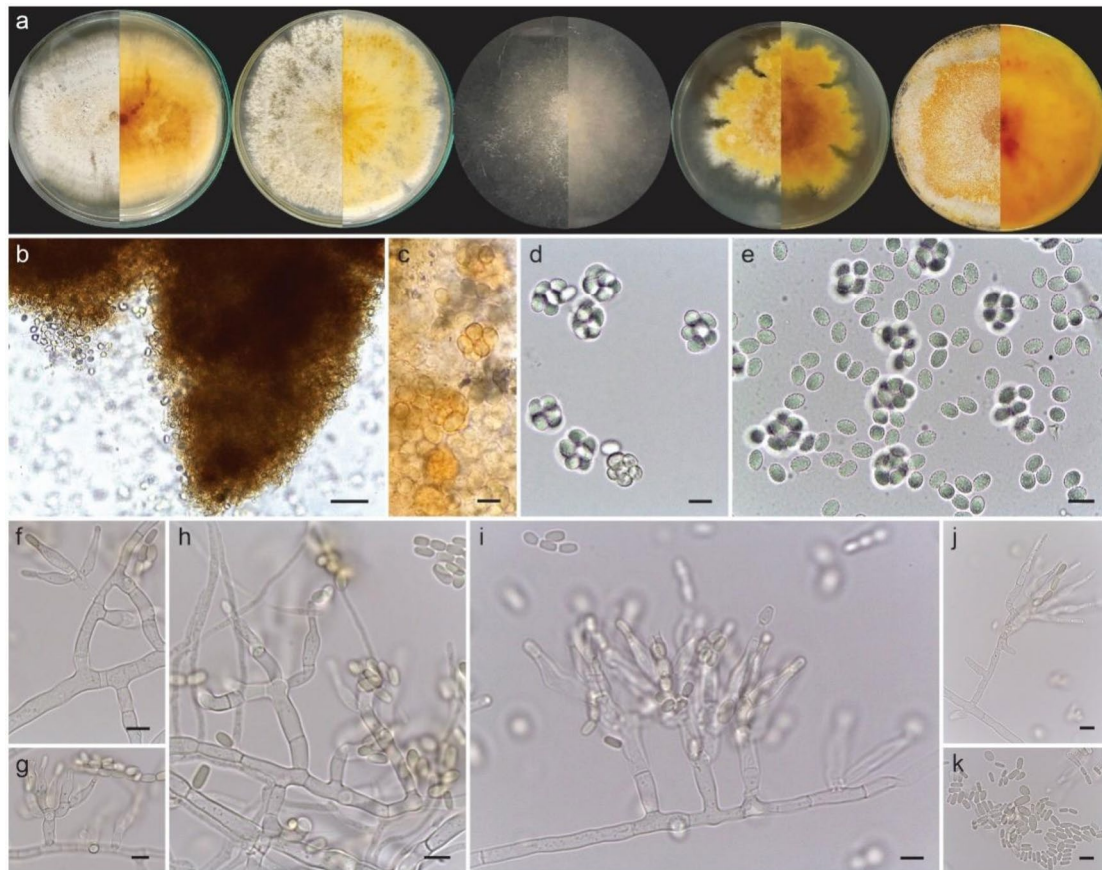
brownish to orange. On DG18, colonies are slightly cottony, whitish to light orange with age, exudate not observed; reverse white and yellowish to orange. On CZ, colonies are

plane, floccose, yellowish to orange, exudate not observed; reverse light brown to orange. At 36 °C after 1 week in the dark, colonies on PDA, MEA and DG18 growing fast and attaining a diameter of 90 mm and morphologically similar as described at 25 °C.

**Habitat and distribution:** The new species occur endophytically in branches of *Brosimum gaudichaudii* Trécul (Moraceae) and is currently only found in Brazil's Cerrado biome.

**Material examined:** Brazil, Goiás state, Goiânia municipally, Escola de Agronomia of the Universidade Federal de Goiás, 16° 35' 58.5" S, 49° 16' 45.8" W, isolated as an endophyte from branches of *Brosimum gaudichaudii* (Moraceae), 20 October 2020, T. M. Silva & J.D.P. Bezerra (UFG 34289, **holotype**), ex-type living culture, FCCUFG 19 = URM 8565, *ibid.*, FCCUFG 20 and FCCUFG 21.

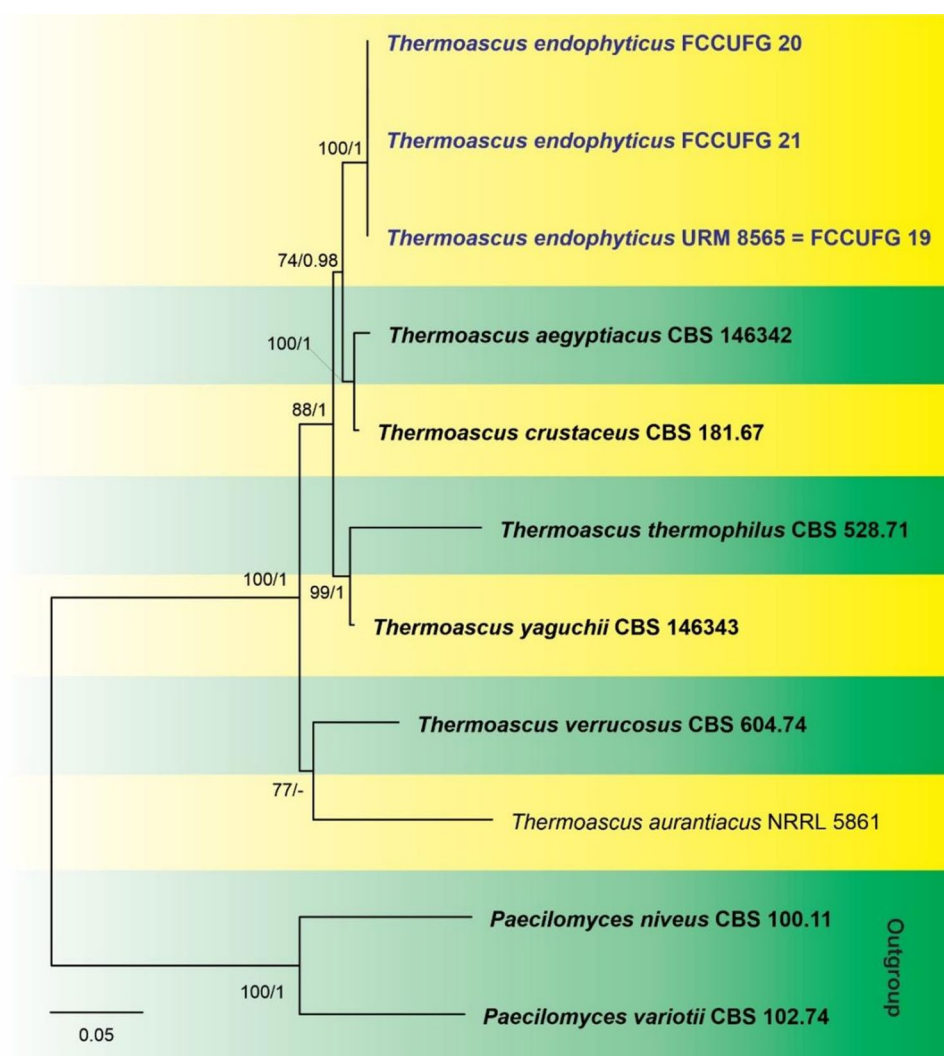
**GenBank numbers:** FCCUFG 19 = URM 8565: ITS = OP325230, CAL = OP351562, TUB2 = OP351559, RPB2 = OP351565; FCCUFG 20: ITS = OP325231, CAL = OP351563, TUB2 = OP351560, RPB2 = OP351566; FCCUFG 21: ITS = OP325232, CAL = OP351564, TUB2 = OP351561, RPB2 = OP351567.



**Fig. 16** *Thermoascus endophyticus* (UFG 34289, **holotype**). **a** Colonies (verse and reverse) on MEA, PDA, DG18 and CZ at 25 °C after 1 week in the dark and PDA after 30 days. **b** Cleistothecial ascomata

and ascospores. **c–e** Asci and ascospores. **f–j** Conidiophores and conidia. **k** Conidia. Scale bars: **b** = 50  $\mu$ m, **c–k** = 10  $\mu$ m





**Fig. 17** Phylogram generated from maximum likelihood analysis based on combined ITS, TUB2, CAL and RPB2 sequence data representing *Thermoascus* in *Thermoascaceae*, *Eurotiales*. Eleven strains are included in the combined analyses which comprised 2815 characters (610 characters for ITS, 533 characters for TUB2, 625 characters for CAL and 1047 characters for RPB2) after alignment. *Paecilomyces niveus* (CBS 100.11) and *Paecilomyces variotii* (CBS 102.74) in *Thermoascaceae* (*Eurotiales*) were used as the outgroup taxa. The best scoring RAxML tree with a final likelihood value of -9050.155654 is presented. The matrix had 699 distinct alignment

patterns, with 20.42% of undetermined characters or gaps. Estimated base frequencies were as follows: A=0.212703, C=0.286868, G=0.279343, T=0.221086; substitution rates: AC=0.719132, AG=1.931043, AT=0.828377, CG=0.434883, CT=3.720518, GT=1.000000; gamma distribution shape parameter  $\alpha$ =0.268628. Bootstrap support values for ML equal to or greater than 70% and Bayesian posterior probabilities (BYPP) equal to or greater than 0.95 are given near nodes. Ex-type strains are in bold and newly generated sequences (*Thermoascus endophyticus*) are in blue

**Notes:** The new species is phylogenetically placed in a well-supported clade (ML-BS = 100% and BYPP = 1), having *Thermoascus aegyptiacus* and *Thermoascus crustaceus* as related species (Fig. 17). Morphologically, *T. endophyticus* differs from *T. aegyptiacus* by the size of cleistothecia (250–550  $\mu$ m), asci (14–18  $\times$  11–15  $\mu$ m) and ascospores (6.0–8.5  $\times$  4.0–5.5  $\mu$ m) in the teleomorph; and in the anamorph by the size of conidiophores (50–300  $\times$  5–7  $\mu$ m),

phialides (12–30  $\times$  3–6  $\mu$ m) and conidia (4.5–11  $\times$  3–4  $\mu$ m) (Salar and Aneja 2007). The new species also differs from *T. crustaceus* by the size of orange cleistothecia (300–900  $\mu$ m diameter), asci (16–20  $\times$  13–15  $\mu$ m) and ascospores (6.5–8  $\times$  5–6.5  $\mu$ m) in the teleomorph; in the anamorph by the size of conidiophores (up to 1000  $\mu$ m long, 7–12  $\mu$ m wide at the base and 4–5  $\mu$ m at the apex), phialides (15–30  $\mu$ m long) and conidia (6–10  $\times$  3–6  $\mu$ m, Stolk 1965).

**Laboulbeniomyces** Engl.**Laboulbeniales** Lindau.

**Notes:** This order includes more than 2100 species described as obligate ectosymbionts on Arthropods. Wijayawardena et al. (2022) accepted three families viz. *Ceratomycetaceae*, *Euceratomycetaceae* and *Laboulbeniaceae* in this order.

**Laboulbeniaceae** G. Winter.

**Notes:** Goldmann and Weir (2018) based on SSU rDNA sequence data identified this family to consist of mostly terrestrial and sexually reproducing taxa with simple or compound endogenous antheridia. Santamaria & Pedersen (2021) accepted 147 genera in this family.

**Autophagomyces** Thaxt.

**Notes:** After the revision by Benjamin (2001), the concept of this genus was narrowed to 12 species, nine of which occur on *Coleoptera Anthicidae* and the others on *Phalacridae* and *Scaphiidae*. The seven characteristics listed by Benjamin for *Autophagomyces* in the limited concept are: (1) cell III very close or in contact with cell I; (2) cell I and II separated by a transverse cross wall; (3) 1–3 free, slender appendages borne from cell III; (4) absence of the remain of the original spore apex; (5) trichogyne consisting of 2 or rarely 3 cells; (6) trichogynic remnant not visible; and (7) perithecium with five tiers of outer wall cells. No DNA sequence is available for any species in *Autophagomyces*.

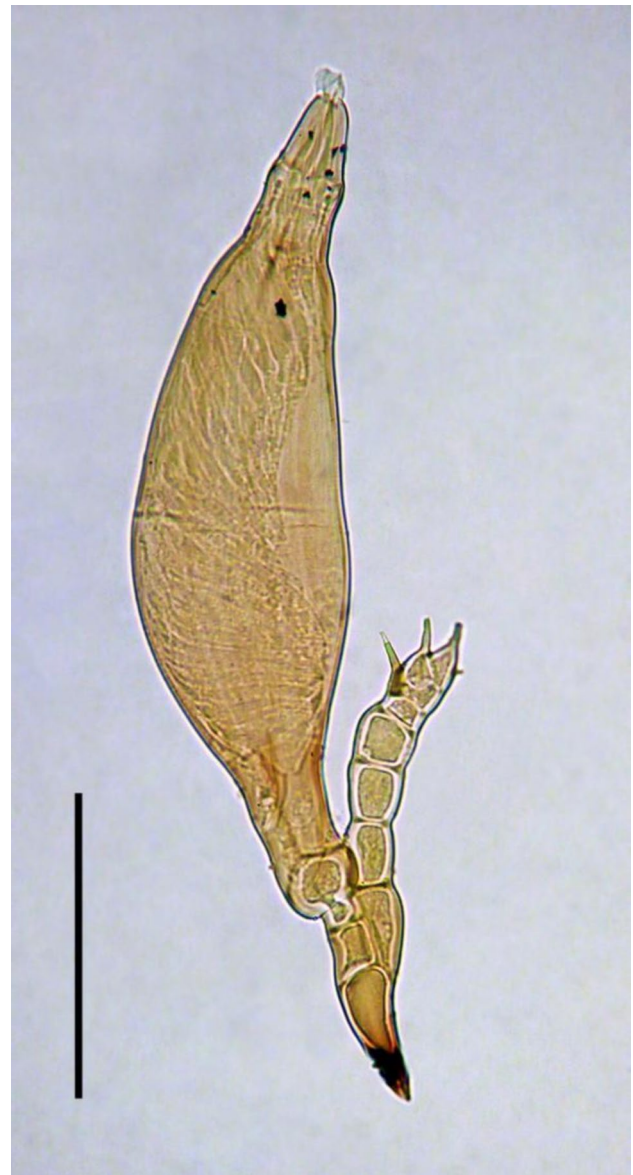
**Autophagomyces incertus** W. Rossi & M. Leonardi, *sp. nov.*

*Index Fungorum* number: 559783; *Facesoffungi* number: FoF 12769; Fig. 18

**Etymology:** From Latin, meaning uncertain, because of the uncertain taxonomic position of the new species.

**Holotype:** CAMB WR2471.

*Thallus* uniformly straw-yellow. *Basal cell of the receptacle* (cell I) tapered downward to hyaline and aciculate tip of foot. *Cell II* quadrangular, slightly longer than broad, its outer margin slightly concave. *Cell III* relatively large, wedge-shaped, united on the inside to cell II, reaching the base of cell VI and the top of cell I. *Appendage* simple, free, consisting of 5 superposed cells, the lower two of which are slightly longer than broad, the third subquadrate, the fourth much smaller and broader than long, bearing an antheridium on the inner side, while the fifth, slightly larger than the fourth, bears two antheridia. *Antheridia* with a very narrow and slightly curved efferent tube, the terminal one bearing a tiny and hardly visible spine. *Cell VI* short, about as long as maximum width, abruptly constricted at the base. *Cell VII* and basal cells relatively large and elongate, forming together a stipe



**Fig. 18** *Autophagomyces incertus* (FI WR2471, **holotype**). Scale bars: 100  $\mu$ m

slightly exceeding the ascigerous part of the perithecial body. *Perithecium* slightly asymmetrical, with the ventral side more convex, broadest below the middle, than tapering upwards, becoming abruptly narrower just above the median tier of the outer wall cells, than nearly uniform in width, the *tip* rather abruptly and symmetrically tapered, the *apex* rounded. Length from foot to perithecial apex 285–330  $\mu$ m; length from foot to tip of uppermost antheridium 160–165  $\mu$ m; perithecium, including basal cells 200–225  $\times$  70–75  $\mu$ m.

**Material examined:** Australia, New South Wales, Headwaters Lookout Barrington Tops, in leaf litter, 19 January 1992, leg. V. Lorimer, on the dorsal side of the abdomen

of *Palimbolus* sp. (Coleoptera, Staphylinidae, Pselaphinae) CAMB WR2471 (**holotype**).

**Notes:** Utilizing the key given by Tavares (1985), the inclusion of this fungus within the genus *Autophagomyces* is out of question. The new species also displays at least five of the seven characteristics listed by Benjamin (2001) for *Autophagomyces* in the limited concept. A sixth remains uncertain, because the structure of the trichogyne is not visible in the available thalli. The only feature in contrast with Benjamin's concept of the genus is the presence of a spinous process on the appendage, which is not, in our opinion, a conclusive feature. The fact that the spine, which is actually the remain of the original spore apex, is sometimes minute and evanescent, and has been observed in only one of almost 700 recognized species of *Laboulbenia* (Dima et al. 2021) and in only one of the 91 species of *Rhachomyces* (Santamaria et al. 2020; Buyck et al. 2021) would seem to support our opinion.

### *Dimorphomyces* Thaxt.

**Notes:** Dioecious genus consisting of 29 recognized species, of which the most recently described is *D. caroliniae* (Rossi 2010). The female thallus consists of a row of small cells bordered below by an extension of the basal cell; these cells produce from their upper side either

perithecia or secondary appendages. The male thallus is much smaller, being composed of a few celled receptacle, compound flask-shaped antheridia and a simple appendage. The majority of the hosts of *Dimorphomyces* are rove beetles (Coleoptera, Staphylinidae), but a few species are found on other insect families (viz. Carabidae and Tenebrionidae), one on ants and two on mites. No DNA sequence is available for any of the species in *Dimorphomyces*.

### *Dimorphomyces seemanii* W. Rossi & M. Leonardi, *sp. nov.*

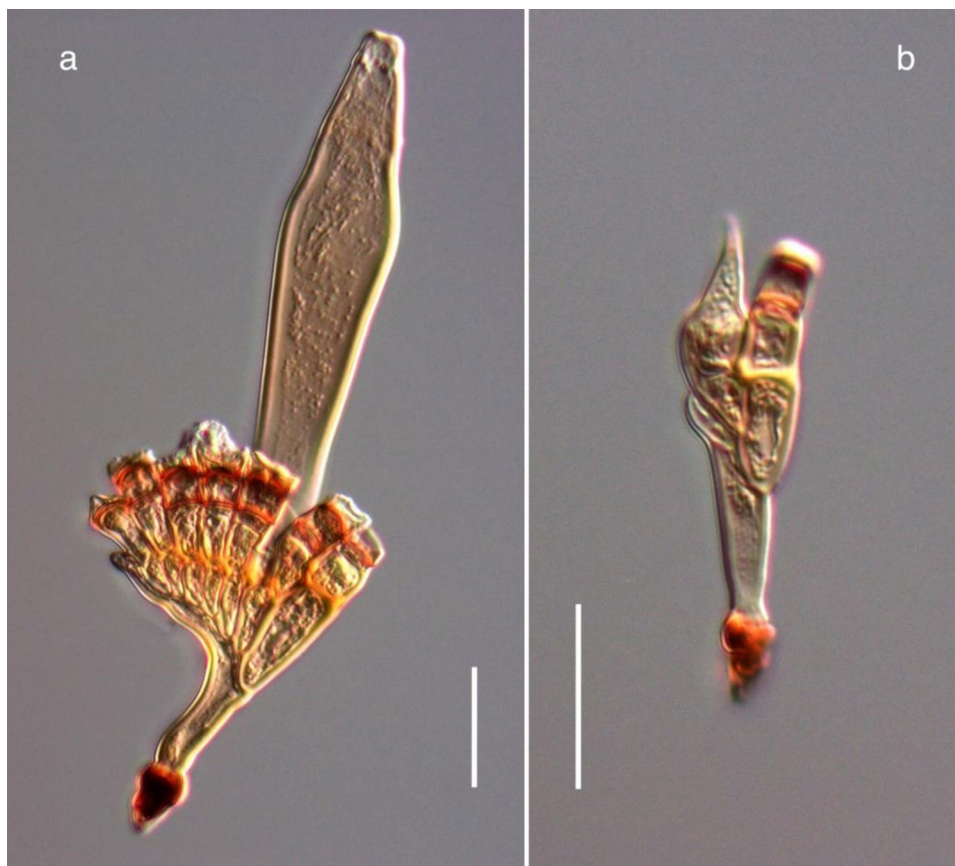
*Index Fungorum* number: 559784; *Facesoffungi* number: FoF 12924; Fig. 19

**Etymology:** Named after the Australian acarologist Owen D. Seeman, who supplied us with the materials utilized for the description of this new species.

**Holotype:** CAMB WR2471.

**Female thallus** broadly fan-shaped, tinged with amber yellow. Lower portion of the *basal cell* (Cell I) forming a well-defined stalk. *Cell II* distinctly longer than broad, regularly enlarging from below upwards. *Primary appendage* consisting of three cells, the lower of which is quadrangular in outline, slightly to distinctly longer than broad, the following smaller, pale gray and barrel-shaped, delimited above and below by thick, dark septa, the uppermost cell hyaline

**Fig. 19** *Dimorphomyces seemanii* (FI WR3782, **holotype**). **a** mature female thallus, with broken terminal cell of the appendages. **b** male thallus. Scale bars: 25 µm





rounded or slightly longer than broad; the uppermost cell is usually missing in mature thalli. *Secondary receptacle* usually curved, forming an almost right angle with the primary receptacle, consisting of a row of 7–10 gradually smaller cells bearing one or two perithecia or three celled appendages similar to the primary appendage. *Perithecia* paler than the receptacle, subfusiform, with a truncate apex. Length from foot to perithecial apex 120–175  $\mu\text{m}$ ; perithecium, including stalk cell 110  $\times$  25  $\mu\text{m}$ .

*Male thallus* translucent, tinged with very pale yellow. *Basal cell of the receptacle* slender and elongate, separated from the shorter and stockier suprabasal cell by a very oblique septum. *The latter cell* gives rise distally to the appendage and bears laterally the short antheridial stalk-cell and a small rounded cell which protrudes outwards under the antheridium. *Appendage* similar to those of the female thalli. *Antheridium* flask-shaped, with the venter almost rounded, rather abruptly distinguished from the strongly tapering and slightly outcurved neck. Length from foot to antheridial apex 67  $\mu\text{m}$ .

*Material examined*: Australia, SE Queensland, Lamington N. P., rainforest, 1142 m, 28.259°S, 153.162°E, 27 January 2008, leg. C. Burwell, on *Micromegistus* sp. (*Acarina*, *Parantennulidae*) WR3782 (**holotype**). NE New South Wales, Gibraltar Range, pitfall trap, 450 m, 29° 32' S, 152° 22' E, 1980–1981, leg. G.B. Monteith, on *Micromegistus* sp., WR3783.

*Notes*: The new species is very different from *Dimorphomyces clavulifer* and *D. triangularis*, the other two species occurring on mites. Among other differences, both the latter fungi have much longer appendages and much shorter perithecia. *Dimorphomyces seemanii* is easily distinguishable from all other species in the same genus for the spherical distal cell of the appendages and the rounded cell protruding under the antheridium.

An undescribed species of *Dimorphomyces* on an undescribed species *Micromegistus* associated with the ground beetle *Trichosternus subvirens* was reported for the first time by Seeman and Nahrung (2000), who also provided a drawing of the new fungus in Fig. 1a on page 5.

#### *Laboulbenia* Mont. & C.P. Robin.

*Notes*: With about 700 species, *Laboulbenia* is by far the largest genus among the *Laboulbeniales*, representing almost one third of all species in the order. The species of *Laboulbenia* occur on various families of beetles (*Coleoptera*), but are also found on flies (*Diptera*), true bugs (*Hemiptera*), ants (*Hymenoptera*), termites (*Isoptera*), cockroaches (*Blattodea*), crickets (*Orthoptera*), and mites (*Acarina*) (Kaishian et al. 2020; Kong et al. 2020; Santamaria and Pedersen 2021). Very few published sequences of species in this large genus are available to date, with most of the taxa, including the type species, lacking this molecular information.

**Fig. 20** *Laboulbenia bifida* (FI WR3571, **holotype**). Scale bars: 100  $\mu\text{m}$



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

*Index Fungorum number*: 559786; *Facesoffungi number*: FoF 12925; Fig. 20

*Etymology*: From Latin *bifidus* = bifid, divided in two parts, referring to the outer appendage consisting of two subequal branches.

*Holotype*: FI WR3571.

*Basal cell* (cell I) grayish yellow, relatively small, about twice longer than maximum width, tapering below. *Suprabasal cell* (II) paler and much larger than the former, dirty yellow, almost twice longer than broad, slightly enlarging upwards. *Cell III* much smaller than cell II, bicolored, with the lower portion concolorous with the underlying cell and the upper grayish yellow, distinctly darker. *Cell IV* as long as cell III but slightly wider, dark gray, becoming paler on the inner side. *Cell V* small, shield-shaped and yellowish. *Insertion cell* black and thick. Outer appendage consisting of a dirty yellow, relatively large, broader than long and irregularly quadrangular basal cell, bearing distally two simple and elongate branches. The latter are similar except in color, the outer one being darker in the lower portion, with the two lowermost cells dark gray, the third light gray, the others dirty yellow. *Cell VI* quadrangular, distinctly shorter than the flanking cell III. *Perithecium* more than half free, about two and a half times longer than broad, irregularly yellowish gray, darker above its basal cells, not abruptly tapering to the tip, ending in a hyaline and subtruncate apex pointing outwards, subtended by a blackish area more extended on the ventral side and darker on the dorsal. Length from foot to perithecial apex 325–425 µm; longest appendage 275 µm; perithecium 175–195 × 65–75 µm.

*Material examined*: New Zealand, South Island, mouth of Taieri River, under driftwood, sandy beach, January 2007, J. Nunn, on various parts of the body of *Otagonia chathamensis* Bordon (Coleoptera, Staphylinidae), FI WR3571 (**holotype**).

*Notes*: Although *Laboulbenia*, with almost 700 species, is by far the largest genus among the *Laboulbeniales*, the species of this genus occurring on *Staphylinidae* are just over thirty. None of these fungi bear an outer appendage consisting of two subequal branches arising from the basal cell, which makes *Laboulbenia bifida* distinguishable at first sight. The new species might be compared only with *L. micrandra*, with which it shares a bifurcate outer appendage, an inner appendage lacking sterile branches, and a septum between cells IV and V not reaching cell III. However, the latter species, parasitic on *Lobrathium* sp. from Ecuador, is distinctly smaller and slenderer, with the outer appendage dividing above the second cell (not above the first, as in *Laboulbenia bifida*), and with very different perithecial tip and apex (Rossi 2011).

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

*Index Fungorum number*: 559788; *Facesoffungi number*: FoF 12927; Fig. 21

*Etymology*: Named after the German dipterologist Michael von Tschirnhaus, who supplied us with the flies bearing the new parasites.

*Holotype*: CAMB WR3382.

*Basal cell* (cell I) large brownish yellow, short, trapezoidal, slightly broader than long. *Suprabasal cell* (cell II) concolorous with the former but much longer, slightly and evenly enlarging from below upwards. *Stalk cell of the appendage* (cell III + IV + V) darker, slightly longer than broad, with the outer margin distinctly convex and the inner united to the stalk- and basal cells of the perithecium. *Insertion cell* small, dark brown, nearly isodiametric, adherent to the base of the perithecium on the inner side, bearing apically four cells, of which the two outer ones are larger and more elongate. These cells give rise to short and irregularly ramified branches ending in elongate antheridia or slender, hyaline and curled branchlets. *Stalk cell of the perithecium* (cell VI) almost flattened. *Perithecium*, with its basal cells, chestnut brown, becoming paler above and below, flask-shaped, the inflated venter evenly tapering to the long neck, ending with two large, short, cylindrical, truncate and symmetrically diverging outgrowths, which are subtended by a rounded prominence on the ventral side. Length from insect surface to perithecial apex 360–430 µm; length from insect surface to tip of longest appendage 290 µm; perithecium 215–270 × 85–105 µm.

*Material examined*: Australia, Queensland, Carnarvon National Park, Mt. Moffatt Camp Site along small creek, 10 October 2002, M. von Tschirnhaus, on the head of an undescribed species of *Apotropina* (Diptera, Chloropidae), CAMB WR3382 (**holotype**), FI WR3383.

*Notes*: *Laboulbenia tschirnhausii* clearly belongs to a small group of species occurring on flies characterized by rhizoids penetrating the body of the host insects and by an undivided stalk-cell of the appendage. This group includes *L. dahlii*, *L. curtonoti*, *L. penetrans* and *L. perforans* (Thaxter 1901; Rossi and Kirk-Spriggs 2011; Rossi and Leonardi 2018; Rossi et al. 2019). *Laboulbenia tschirnhausii* differs from all the latter parasites for its stockier habitus, the nearly isodiametric stalk-cell of the appendage, the more inflated perithecial venter, and especially the peculiar perithecial outgrowths.

The thalli of *Laboulbenia tschirnhausii* were all found projecting forward from the head of the host insects, which means that the transfer of the sticky spores from a parasitized insect to other members of the same species did not happen during sexual contacts. Actually, although sexual contacts represent the more frequent method by which *Laboulbeniales* pass from one host to another, these fungi

**Fig. 21** *Laboulbenia tschirnhausii* (FI WR3382, **holotype**). **a** group of 5 mature thalli. **b** tip of perithecium, enlarged. **c** tuft of thalli emerging from the face of the host insect (paratype MLUH Dipt-Chlor 0021 m—photo by A. Stark). Scale bars: **a**= 100  $\mu$ m, **b**= 25  $\mu$ m



take advantage also of other contacts resulting from social behaviors not directly related with mating. The contacts by means of the antennae, which are frequent among insects, seems to be the way utilized by *Laboulbenia tschirnhausii*. Several other *Laboulbeniales* benefit from this behavior. For example, among the species occurring on flies can be cited *Stigmatomyces hydrelliae* and the above mentioned *Laboulbenia dahlia* (Thaxter 1901; Weir and Rossi 1995).

The description of a new species bearing haustoria penetrating the host insect gives us the opportunity to briefly comment on a recent paper that deals with this topic (Haelewaters et al. 2022). In this paper the authors suggest that species with haustoria are older than the species without haustoria and that the latter are derived from the former. However, phylogenetic analyses based on DNA sequence

data have shown that the genera bearing haustoria are scattered through the phylogenetic tree and do not occupy a basal position relative to genera without (evident) haustoria (Goldmann and Weir 2018). This pattern clearly suggests that the character ‘haustorium’ evolved independently in different clades of Labulbeniomycetes. Moreover, under the term ‘haustoria’ are grouped very different structures. For example, the genera *Herpomyces* and *Hesperomyces*, have inconspicuous haustoria originating from the foot, while the haustoria of *Laboulbenia* and *Rhizomyces*, when present, are in comparison very large, sometimes very long and ramified, originating from the basal cell [these four genera are present in the tree of Goldmann and Weir (2018)]. Therefore, it is possible that these different types of haustoria do not represent homologous structures. While the evolutionary origin of



**Fig. 22** *Laboulbenia tuberculata* (FI WR4035, **holotype**). **a** mature thallus. **b** mature thallus enlarged. **c** immature thallus with focus on warts. Scale bars: 25  $\mu$ m



haustoria certainly needs further research, the hypothesis by Haelewaters et al. (2022) is clearly not supported by available data.

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

*Index Fungorum* number: 559787; *Facesoffungi* number: FoF 12926; Fig. 22

*Etymology*: From Latin *tuberculatus*, which means “covered with wart-like projections”.

*Holotype*: FI WR4035.

*Basal cell* (cell I) of the receptacle slender and elongate, with almost parallel margins, hyaline above the foot, then gradually darkening from below upwards becoming brown in the upper portion, its surface distinctly warty. *Suprabasal cell* (cell II) with a wavy surface, broadly pentagonal, much shorter and paler than the basal, from which is separated by a thick, blackish septum looking like a prominent ring. Similar septa, but shorter and symmetrically oblique, divide cell II from cell III and cell VI. *Cell III* about as long as cell II but distinctly narrower, dark brown, its surface covered with large, dark warts, the warty surface extending to cell VI and to the lower, outer portion of cell IV. The latter as long as cell III but slightly broader and somewhat paler. *Cell V* very small and lens-like. *Insertion cell* thick, subtended by a paler line. *Outer appendage* consisting of a basal cell almost twice longer than broad followed by a linear series of hyaline cells gradually longer and slenderer. *Inner appendage*

consisting of a small and flattened basal cell giving rise to a short cell oriented inwards and bearing distally a pair of falcate antheridia. *Cell VI* rhombic, shorter than the adjacent cell III. *Perithecium* colored pale brown, darker in the lower portion, adnate to the receptacle for 3/5 of its length, oblong, slightly inflated, its surface slightly undulate, the darker tip abruptly distinguished, ending in rounded and subhyaline lips, one of which is larger than the others. Length from foot to perithecial apex 160–180  $\mu$ m; length from foot to tip of longest appendage 420  $\mu$ m; perithecium 60–63  $\times$  23–25  $\mu$ m.

*Material examined*: Papua New Guinea, Western Province, Yaromdeng tem, Cave near Finim tel, 9 November 1975, leg. Ph. Chapman, on *Altagonum sphodrum* Darlington (Coleoptera, Carabidae), FI WR4035 (**holotype**), FI WR4036.

*Notes*: The large, irregularly arranged dark warts that cover most of the surface of the receptacle make it possible to distinguish at first sight *Laboulbenia tuberculata* from any other described species. Smaller warts on the surface of the receptacle are found in *L. tuberculifera* and *L. rugosa*, but in the latter species the warts are found only on cells III, IV and V, while in the former these are restricted to cell II (Thaxter 1908; Rossi and Leonardi 2020). The surface of the receptacle of *Laboulbens scabra* is also completely covered with warts, but in this case the warts are small, uniformly distributed and concolorous with the remaining parts of the thallus (Kong et al. 2020).

**Lecanoromycetes** O.E. Erikss. & Winka.

**Notes:** Lecanoromycetes is the largest and most varied class of lichenized fungi with 15,131 species and 701 genera. It includes four subclasses (Acarosporomycetidae, Candelariomycetidae, Lecanoromycetidae, Ostropomycetidae), 17 orders and 75 families. This class includes orders predominantly or exclusively lichenized, with the exception of *Ostropales* (Lücking et al. 2017). Species in this class are characterized mainly by their ascohymenial ascomatal ontogeny, with a predominance of apothecial fruiting bodies, although of diverse construction and shape. In most lineages, asci have a multilayered ascus wall of which two layers are thick enough to be visible with light microscopy and display different types of dehiscence (Miadlikowska et al. 2006). Members of Lecanoromycetes form bipartite symbiotic associations with a broad range of photobionts, representing chlorococcalean algae, filamentous algae and cyanobacteria. Molecular studies have substantially challenged phenotypically based groupings applied to previous classifications, as well as resolved placement of many sterile taxa, and taxa with uncertain taxonomic affiliation. Kraichak et al. (2018) proposed a revised classification, based on temporal banding approach, of orders and families in the two major subclasses of Lecanoromycetes with seven orders in Lecanoromycetidae and eight in Ostropomycetidae.

**Lecanorales** Nannf.

**Notes:** *Lecanorales* was introduced by Nannfeldt (1932) to accommodate the *Lecanoraceae* as the type family. It is the largest order of lichen fungi with 6231 species and 234 genera distributed into 19 families (Lücking et al. 2017). The main ascus dehiscence, structural differences, and staining reactions of the tholus induced by Lugol's iodine was used to name ascus type according to genera (e.g. *Lecanora*-type, *Bacidia*-type, *Acarospora*-type) although with little agreement on naming conventions. A *Lecanora*-type ascus may have been ancestral in the *Lecanorales*. (Ekman et al. 2008).

**Parmeliaceae** F. Berchtold & J. Presl.

**Notes:** *Parmeliaceae* is the largest family of lichenized fungi, with 2765 species and 77 genera (Lücking et al. 2016). The family belongs to the core of the *Lecanorales* closely related to other large families like the *Lecanoraceae* and *Cladoniaceae* (Crespo et al. 2007). *Parmeliaceae* includes morphologically very diverse lichens, including crustose (e.g., *Protoparmelia*), peltate (e.g., *Omphalodiella*), subcrustose (e.g., *Karoowia*), foliose (e.g., *Parmelia*), umbilicate (e.g., *Xanthomaculina*), fruticose (e.g., *Usnea*) or subfruticose (e.g., *Almbornia*) species and even lichenicolous fungi devoid of any own photosynthetic partner, such as *Phacopsis* and *Nesolechia* (Crespo et al. 2007) tested hypotheses of phylogenetic relationships in *Parmeliaceae* based on morphology and molecular biology (three

ribosomal markers and the nuclear gene RPB1). In this study, they point out that the species of *Usnea* are strongly supported as a monophyletic group and that six more monophyletic clades were found in *Parmeliaceae*: alectorioide, cetrarioid, hypogymnioid, letharioid, parmelioid and psiloparmelioid. A review of the family *Parmeliaceae* is provided by Thell et al. (2012).

**Usnea** Dill. ex Adans.

**Notes:** The genus *Usnea* forms a strong supported clade (named “usneoid”) within the phylogeny of *Parmeliaceae* (Crespo et al. 2007) sister to *Cornicularia normoerica* (Divakar et al. 2015). *Usnea* is a fruticose lichen genus easily recognized by its thallus branches with radial symmetry, the presence of a central cartilaginous axis and the production of usnic acid in the cortex. The first major work about the genus *Usnea* was published by Motyka (1936), who published more than 750 names in his world monograph, many of them are now considered synonyms of well-known species (Clerc 1998). *Usnea* is among the ten richest genus among the lichenized fungi in number of species with 350 species (Lücking et al. 2016), but actually molecular phylogeny indicated that the number could be twice (Lücking et al. 2020). Modern revisions of the genus were done in Africa (e.g., Temu et al. 2019), Australia (e.g., Stevens 2004), Europe (e.g., Clerc and Otte 2018), India (e.g., Shukla et al. 2014), Japan, China and Russia (e.g., Ohmura 2001; Ohmura et al. 2017), New Zealand (e.g., Galloway 2007), North America (e.g. Herrera-Campos 2016), South America (e.g. Gerlach et al. 2020), and Polar regions (e.g. Wirtz et al. 2012).

**Usnea kriegeiriana** A. Gerlach & P. Clerc, *sp. nov.*

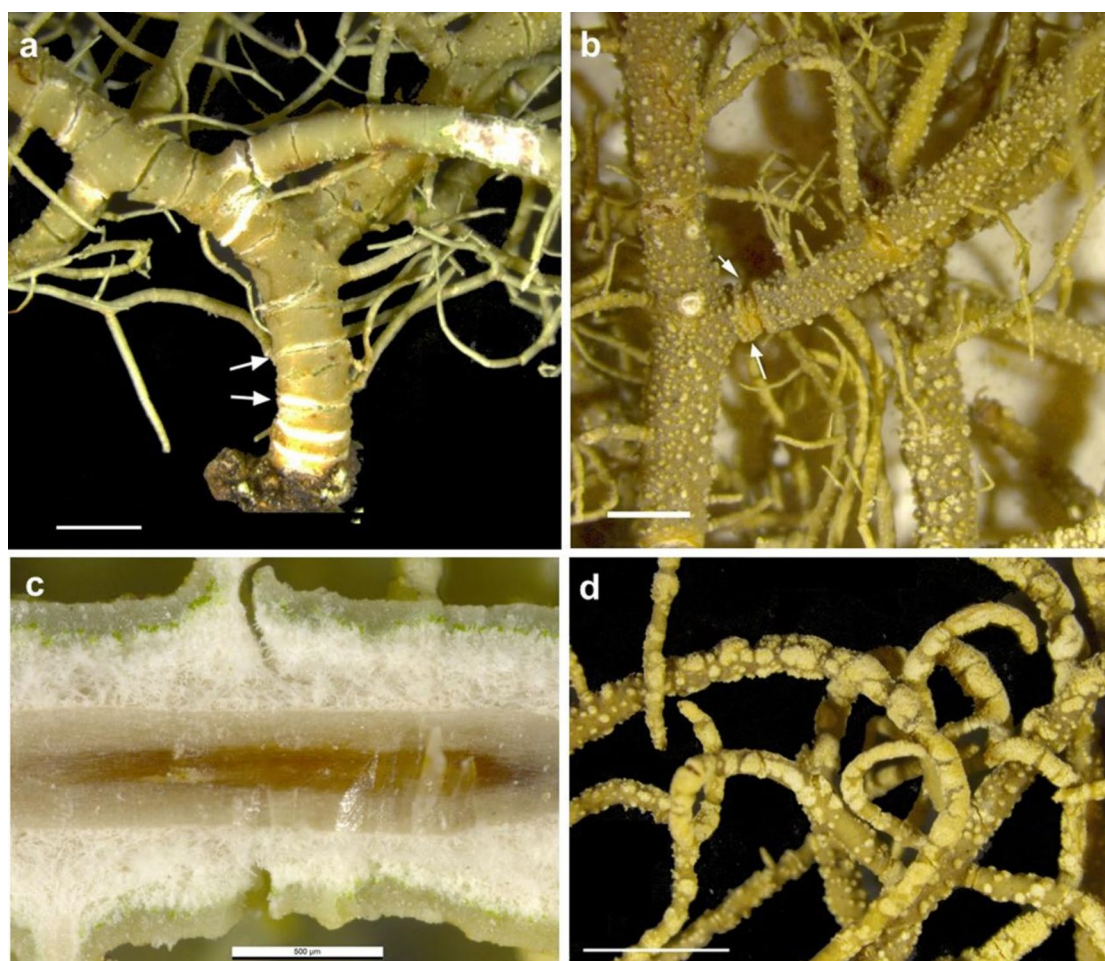
**Index Fungorum number:** IF 900342; **Facesoffungi number:** FoF 14476; **Fig. 23**

**Etymology:** In honor of the Brazilian Priest Leopoldo Krieger, retired botany teacher of the Federal University of Juiz de Fora (Brazil), who collected many *Usnea* specimens chiefly in the south of Minas Gerais and in the Paraná State. The oldest specimen of this new species was collected by him in 1975.

**Holotype:** 2016/P19 (ICN).

**Diagnosis:** Thallus shrubby, basal part with annular cracks, lateral branches not constricted at ramification point, main branches covered with eroded tubercles and convex soralia, cortex mat, thin to  $\pm$  thick (6.5–)7.5–9%–10.5(–11.5) and medulla with fumarprotocetraric acids as main medullar secondary metabolite.

Lichenized Ascomycota fungi corticolous on bark of *Araucaria angustifolia*, on exotical *Pinus* spp, or lignicolous on fences. *Thallus* shrubby, up to 10 cm long; ramifications mainly isotomic-dichotomous; basal part up to 0.5 cm long, concolorous to the main branches, sometimes paler or with a faint orange tinge, regularly with annular cracks;



**Fig. 23** *Usnea kriegeana*. **a** basal part with annular cracks (white arrows) ((2016/P19, **holotype**). **b** lateral branches slightly constricted at ramification point, with annular cracks (arrows) (*Krieger* 13474). **c**

section through thallus with matt cortex (**holotype**). **d** large and confluent soralia (*Krieger* 13474). Scales bars: **a**, **b**=2 mm, **c**=500  $\mu$ m, **d**=2 mm

main branches up to 1.8 mm diameter ( $n=16$ ), cylindrical to slightly irregular; branches segments cylindrical, sometimes slightly swollen; lateral branches not (main branches) to sometimes slightly constricted (secondary branches) at ramification point; annular cracks present, thin, often with medullar extrusions, sparse to frequent on the whole thallus, 1–2 annular cracks/0.5 cm; foveolae, depressions, maculae and pseudocyphellae absent; papillae absent or sparse; tubercles present, often numerous, verrucous, eroded at top; fibrils slender, unevenly distributed; fibercles sparse; soralia punctiform to large, convex, often circular or building elliptical to irregular masses of soralia, usually numerous on main branches, well delimited to confluent towards the apices of the branches, arising from the top of tubercles, with granular soredia; isidiomorphs usually numerous; isidiofibrils rare; *apothecia* and *pycnidia* not seen; *cortex* moderately thin to  $\pm$  thick [(6.5–)7.5–9%–10.5(–11.5)], mat ( $n=16$ ); medulla  $\pm$  thin to thick [19–25.5%–32(–48)], dense; *axis* sometimes with an orange tinge, thin to  $\pm$  thin

[(19–)24–31.5%–38.5(–40)]; A/M=0.6–1–2. Photobiont trebouxoid. Medulla K + yellow turning red. Secondary chemistry detected by thin layer chromatography: fumarprotocetraric acid,  $\pm$  protocetraric acid,  $\pm$  an unknown substance orange after charring Rf classes A/B/C: 1–2/2–3/1–2 (US2) ( $n=20$ ).

**Material examined:** Brazil, Santa Catarina: Alfredo Wagner, Reserva Particular do Patrimônio Natural Rio das Furnas, ca. 27° 40' 28.3" S, 49° 10' 37.9" W, ca. 900 m, on twigs, 13 May 2016, Gerlach et al., 2016/P19 (ICN, **holotype**), Bosque das Araucarias, sobre *Araucaria angustifolia*, ca. 900 m, 2016, Gerlach et al. P37 (G); Joinville, estrada das Laranjeiras, sobre mourão, 5 October 2013, Gerlach & Beilke 1133a (ICN); Urubici, Parque Nacional de São Joaquim, arredores do alojamento, ca. 1300 m, 03 February 2014, Gerlach & Alves 1327 (ICN); São Bento do Sul, APA Rio Vermelho, on *Araucaria angustifolia*, 12 March 2013, Gumboski 4269 (ICN). Espírito Santo, Domingos Martins, in Weide am Morro do Cruzeiro, 1200 m, 20° 26' S,



41° 00' W, 11 October 1988, Schäfer-Verwimp & Verwimp (G). Minas Gerais, Serra de Ibitipoca, 19 May 1975, Krieger 13474 (JPB). Paraná: Curitiba, en allant vers Vila Velha, 25°21'S, 49°34'W, 4 March 1989, Grundlehner (G). Rio Grande do Sul: Cambará do Sul, Parque Nacional dos Aparados da Serra, Cânion do Itaimbezinho, 30 April 1989, Fleig 3577 (ICN); *ibid.*, mata nebulosa próximo ao centro de visitantes, 14 March 2014, Gerlach & Akkerman 1403 (ICN). São Paulo, Zwischen Guapira und Apiaí, in einem Kleinen Pinus-Forest, an *Pinus* spec., 800 m, 23 August 1980, Kalb (G); Serra da Mantiqueira, Campos do Jordão, etwa 150 km nordöstlich von São Paulo, an freistehenden *Pinus* spec. 1700 m, 26 May 1978, Kalb & Plöbst (G).

**GenBank number:** ITS = MF669873.

**Notes:** *Usnea* is a ultradiverse genus with more than 450 species worldwide (Lücking et al. 2020) mainly corticolous species in Africa (e.g. Swinscow and Krog 1979; Temu et al. 2019), Europe (e.g. Clerc 1987, 2011; Halonen et al. 1998; Clerc and Otte 2018), Asia (e.g. Ohmura 2001, 2012; Stevens 2004; Ohmura and Clerc 2019), South America (e.g. Rodriguez et al. 2011; Truong et al. 2011, 2013; Truong and Clerc 2012, 2013, 2016; Gerlach et al. 2017, 2019a, b, 2020) and North America (e.g. Clerc 2007; Herrera-Campos 2016). The genus is characterized by the fruticose thallus, branches holding a central axis and the presence of usnic acid in the cortex (Clerc 1998). *Usnea kriegneriana* is characterized by the annulate and cracked basal part, the lateral branches that are not constricted at attachment point, the numerous tubercles eroded at the top, the large soralia, the mat cortex, the thin to thick medulla (22.5–25%–35) and the presence of fumarprotocetraric acid as main secondary substance in the medulla. The density of the annular cracks with medullar extrusion and isidiomorphs is variable in this species. The lateral branches are most of the time not constricted; only rarely slightly constricted at attachment point. The shape of the segments varies from slightly swollen to cylindrical. Soralia are convex and often well delimited on main branches. Well-developed specimens have confluent soralia that become larger up to the half of the branches diameter towards the apices. *Usnea kriegneriana* produces fumarprotocetraric often accompanied by protocetraric acid and an unknown substance (refereed as US2; only one specimen without protocetraric and another one without US2 were found) in the medulla.

*Usnea kriegneriana* is morphologically similar with *U. flammea*, which, however, differs mainly by the shape of the soralia, that are even with the cortex surface, and by the absence of tubercles (Clerc 2006). *Usnea subflammea* is similar by the presence of numerous tubercles, but it differs by the thicker cortex [12–16%; instead 7.5–9%–10.5(–11.5) in *U. kriegneriana*] and the soralia that do not enlarge (Clerc 2006). Moreover, *U. flammea* and *U. subflammea* have stictic acid in the medulla whereas *U. kriegneriana*

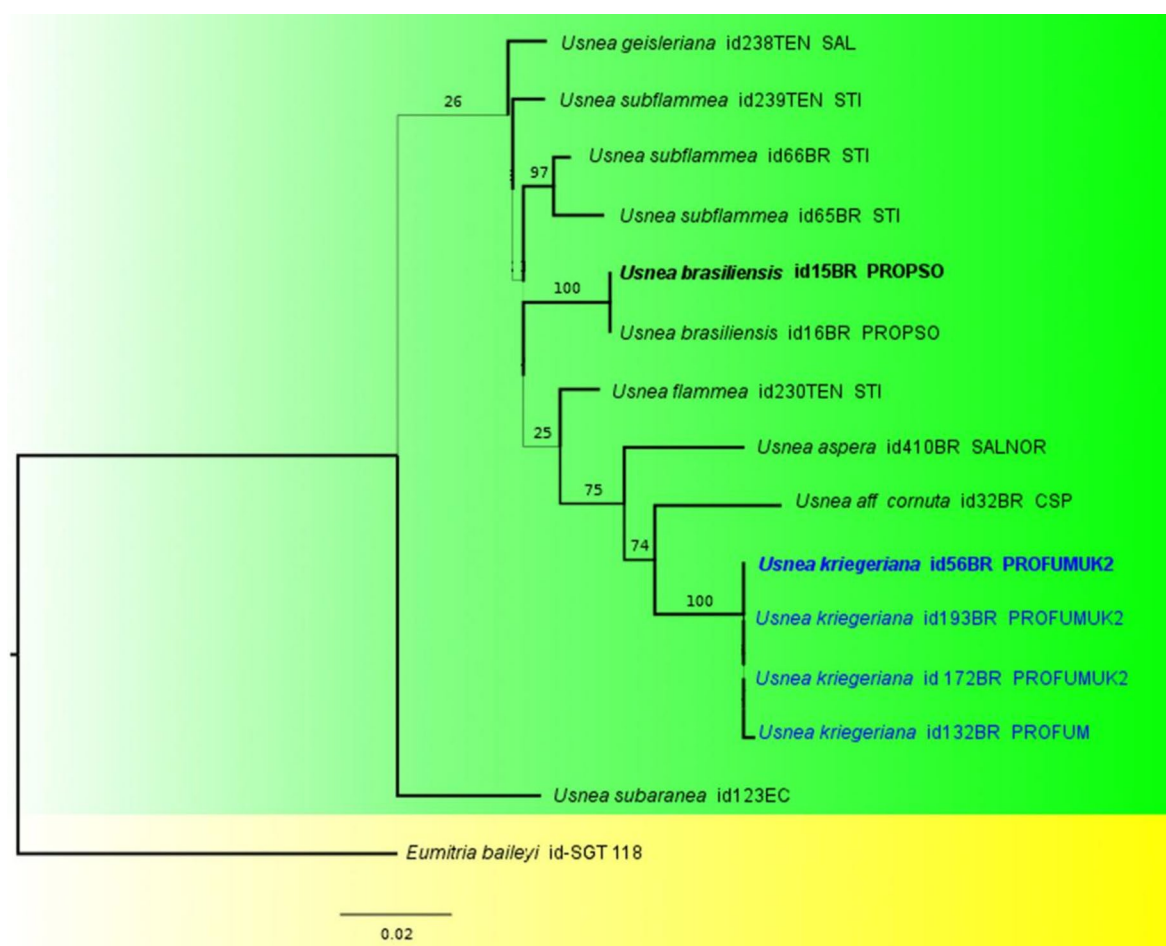
has fumarprotocetraric acid. Moreover, *Usnea kriegneriana* builds a strongly supported clade, unrelated to *Usnea flammea* and *U. subflammea* (Fig. 24; Fig. 1 as *Usnea* sp. 5 in Gerlach et al. 2019a).

Until our knowledge there are relatively few species with fumarprotocetraric acid as secondary metabolite recorded for South America: *Usnea aurantiaco-atra* belong to the *Neuropogon* group, differing by the saxicolous and by the fertile thallus. *U. bornmuelleri* is also saxicolous. *U. brasiliensis* differs from *U. kriegneriana* mainly by the CMA and by the absence of tubercles. *U. grandispora* is a fertile species without soralia. *Usnea pallida* is a erect-shrubby species belonging to the *Usnea articulata* group; *Usnea rubropallens* belonging to the *Usnea cornuta* aggregate and differ by the presence of a faint red pigment subcortical (see Gerlach et al. 2020 for more details); *U. subrubicunda* differs from *U. kriegneriana* by the vitreous cortex and the presence of a red pigment cortical; *U. vitrea* is a fertile species with apothecia and does not present vegetative propagules.

*Usnea kriegneriana* is relatively frequent in the mountainous areas above 900 m in *Araucaria* Forest. So far known only in Brazil (Southern and Southeast Region): Espírito Santo, Minas Gerais, Paraná, Rio Grande do Sul, Santa Catarina and São Paulo states.

#### **Leotiomycetes** O.E. Erikss. & Winka.

**Notes:** Eriksson and Winka (1997) introduced the class Leotiomycetes (Ascomycota) comprising of 4 orders, 19 families and 641 genera (Kirk et al. 2008). Leotiomycetes contains numerous species with anamorphs placed within the fungi imperfecti (deuteromycota), that have only recently found their place in the phylogenetic system. Earlier, Leotiomycetes was placed into Discomycetes clade (inoperculate Discomycetes). Molecular studies have recently shed lights to the still ambiguous systematics. Most researchers consider Leotiomycetes a sister group to Sordariomycetes in the phylogenetic tree of Pezizomycotina. Its division into sub-classes have received strong support by the molecular data, but the overall monophyly of Leotiomycetes is uncertain. The order *Lichinodiales* and family *Lichinodiaceae*, newly circumscribed by Prieto et al. (2019) to contain the cyanolichen genus *Lichinodium*, which is the first known group of lichenized fungi in the Leotiomycetes. Most Leotiomycetes form apothecia containing asci (seldom cleistothecia). The asci are found cylindrical and have no operculum. Hyaline spores are of various shapes, disperse through a circular apical pore (Prieto et al. 2019). Most of the genera in this class are saprophytic growing on a wide variety of substrates like dead plant materials, on dung as well as endophytes. Many of the genera belonging to Leotiomycetes, like *Botrytis*, *Erysiphe*, *Uncinula*, *Blumeria*, *Podosphaera*, *Phyllactinia*, *Diplocarpon*, *Scytalidium* etc. are well known to cause serious plant diseases on a variety of plants.



**Fig. 24** Maximum likelihood (ML) tree reconstruction, on RAXML Black Box on the CIPRES server. Outlined on yellow gradient is the outgroup. The new species are in blue. Specimens of *Usnea* used in

the study including voucher information, chemotype and GenBank accession numbers for the nuclear ribosomal internal transcribed spacer region (ITS) are available on supplementary information

### *Helotiales* Nannf.

**Notes:** *Helotiales* (Nannf 1932) is an order of the class Leotiomycetes within the division Ascomycota (Lumbsch and Hündorf 2007). According to the dictionary of fungi estimate, the order contains 10 families, 501 genera, and 3881 species (Kirk et al. 2008). This is the largest order of inoperculate discomycetes. The order is distinguished by its disc or cup-shaped apothecia. Most fungal genera of this order live as saprobes on dead logs, soil humus, manure and other organic matter. This order includes most fungi associated with ericoid mycorrhiza. Including *Rhizoscyphus ericae* (Zhang and Zhuang 2004), *Meliniomyces bicolor* (Hambleton and Sigler 2005) and *Cairneyella variabilis* (Midgley et al. 2016). Many of the fungi of this order are deadly severe plant pathogens such as *Sclerotinia sclerotiorum* causing lettuce drop and other diseases (de Bary 1884), *Monilinia fruticola* causing brown rot on stone fruits (Honey 1928), *Diplocarpon rosae* causing black spot of roses (Wolf 1912) and *Sclerotium cepivorum* causing soft rot of onions (Berkeley 1841).

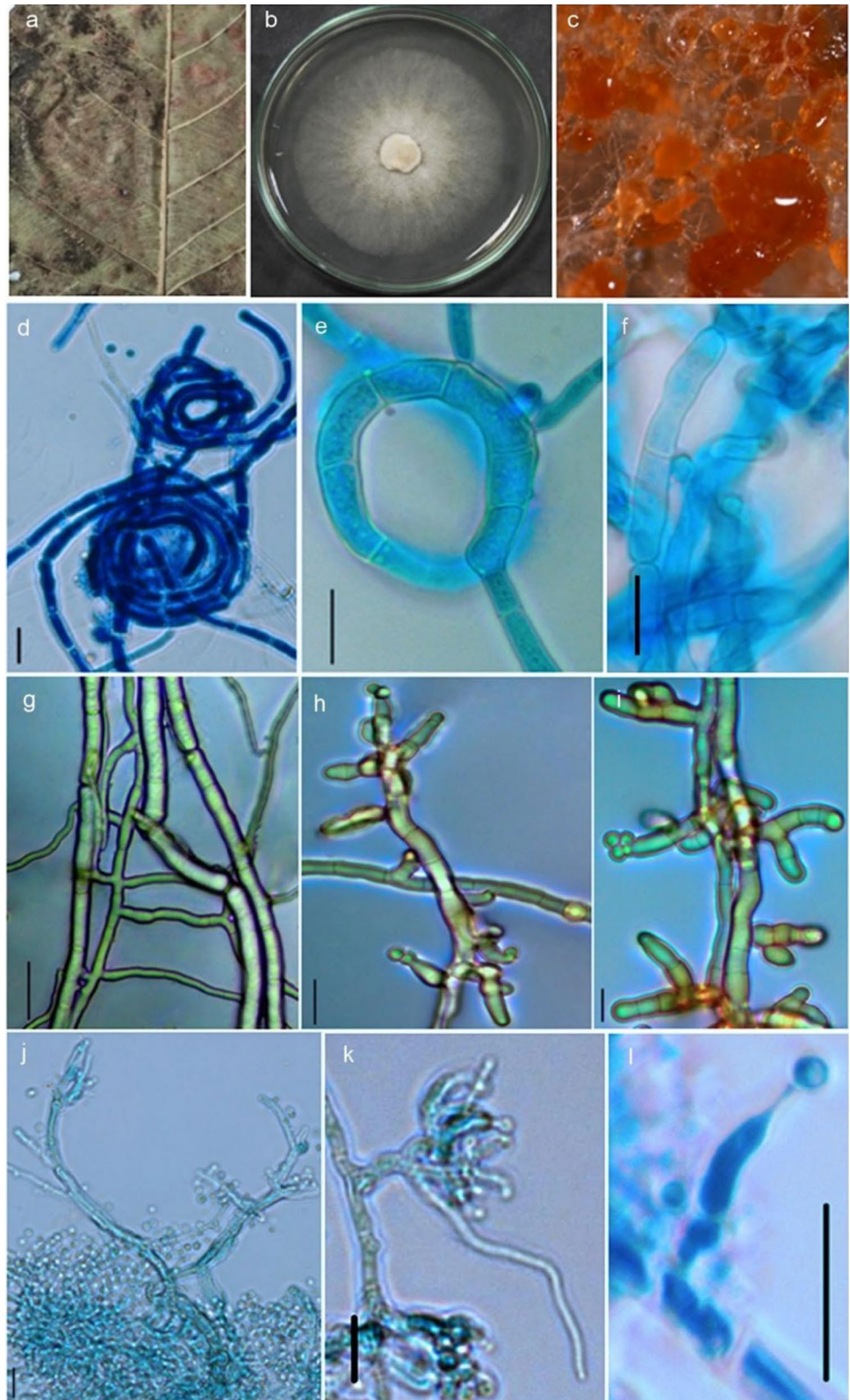
### *Rutstroemiaceae* Holst-Jensen, Koehn & Schmach.

**Notes:** The species in this family (Holst-Jensen et al. 1997) have a cosmopolitan distribution, especially in temperate areas (Cannon and Kirk 2007). This family includes the genera like *Dicephalospora*, *Lambertella*, *Lanzia*, *Poculum*, *Rutstroemia*, *Scleromitrella* etc.

### *Lambertella* Höhn.

**Notes:** The genus *Lambertella* was established by von Höhnelt (1918). The genus is characterized by the presence of a substratal stroma with epidermoid cells and an ectal excipulum composed of thin-walled prismatic cells. Pigmented ascospores are also one of the distinguishing characters of the genus *Lambertella* (Zhao et al. 2016a). It is one of the largest genera in the family *Rutstroemiaceae* consists of 78 species according to Index Fungorum records (<http://www.indexfungorum.org/names/Names.asp>). Studies have already shown the polyphyly in the genus *Lambertella* based on the phylogenetic analysis of ITS, LSU, and RPB2 regions suggesting its phylogenetic heterogeneity. However,

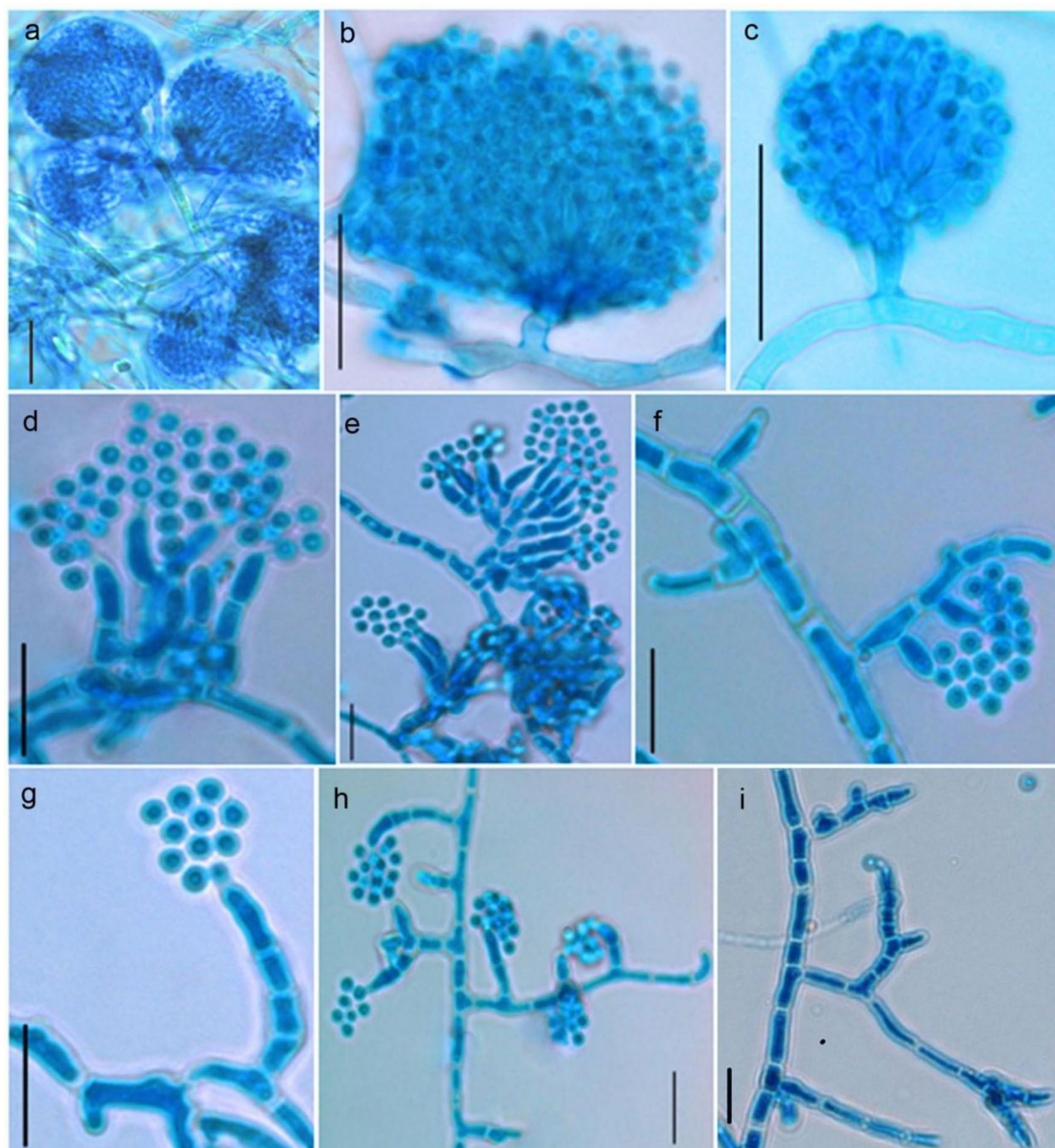
**Fig. 25** *Lambertella diptercarpacearum* (AMH10226, holotype). **a** Substratum (leaf of *Shorea*). **b** Colony morphology on PDA (front view on 5th days). **c** Stereomicroscopic surface view of colony showing dark orange shiny gleosporic mass of conidial heads. **d–g** Coiled and anastomosed hyphae. **h, i** Hyphae bearing developing phialides with conidia. **j, k** branched conidiophores with sterile arm. **l** Conidiophore with solitary phialide. Scale bars: **d–f** = 10  $\mu$ m, **g** = 20  $\mu$ m, **h** = 20  $\mu$ m, **i** = 5  $\mu$ m, **j, k** = 10  $\mu$ m, **l** = 20  $\mu$ m



a highly supported clade called *Lambertella* sensu stricto has been confirmed consists of species characterized by brown ascospores before discharged from asci (Zhao et al. 2016a).

*Lambertella diptercarpacearum* P.N. Singh, S.K. Singh & A.C. Lagashetti, *sp. nov.*





**Fig. 26** *Lambertella dipterocarpacearum* (AMH10226, **holotype**). **a–c** Conidiophores with conidial heads. **d–i** Different types of patterns of conidiophores and arrangement of conidia on phialides. Scale bars: **a** = 10  $\mu$ m, **b**, **c** = 20  $\mu$ m, **d–i** = 10  $\mu$ m

*Index Fungorum* number: IF900321; *Facesoffungi* number: FoF0773601; Figs. 25, 26

*Etymology*: specific epithet ‘*dipterocarpacearum*’ refers to the host family.

*Holotype*: AMH 10226.

*Colour code* follows: Methuen Handbook of Colour (Kornerup and Wanscher 1978).

On leaf phylloplane of *Shorea robusta* in terrestrial habitats. **Asexual morph**: vegetative hyphae smooth walled, branched, septate, anastomoses, sometimes coiled, subhyaline to light olivaceous up to 10.15  $\mu$ m wide. *Stroma* none. *Chlamydospores* absent. *Setae* and *hyphopodia*

absent. *Conidiophores* macronematous, mononematous, unbranched to dichotomously densely branched, straight, short, septate, smooth walled, subhyaline to light olivaceous, 4.5–138.90  $\times$  4–6.35  $\mu$ m, sometimes reduced into conidiogenous cells. Occasionally, a sterile arm is produced near axel of conidiophore. *Conidiogenous cells* holoblastic, terminal to lateral, determinate, polyblastic, ampulliform, persistent, aseptate, hyaline, 2.88–12.75  $\times$  1.61–7.20  $\mu$ m ( $\bar{x}$  = 6.30  $\times$  2.70  $\mu$ m,  $n$  = 30). *Phialides* solitary or aggregated, densely produced, ampulliform to lageniform, aseptate, sometimes single to multi-septate, smooth walled, hyaline, 2.59–22.92  $\times$  1.67–4  $\mu$ m ( $\bar{x}$  = 6.31  $\times$  2.73  $\mu$ m,  $n$  = 30).

*Conidia* mostly aggregated in slimy mass heads at the apex of phialides, sometimes produced in chains, globose to subglobose, smooth walled, sub-hyaline to light olivaceous,  $1.84\text{--}4.22 \times 1.81\text{--}2.80\text{ }\mu\text{m}$  ( $\bar{x} = 2.38 \times 2\text{ }\mu\text{m}$ ,  $n = 30$ ). **Sexual morph:** Undetermined.

**Culture characteristics:** on semi-synthetic agar medium PDA (Potato Dextrose Agar) white (1A1), reaching 6.5 cm diam. in 5 days at 25 °C, with irregular margin, surface filamentous, reverse light yellow (4A4). After aging light yellow (4A3), reverse light yellow (4A3). *Hyphae* septate, unbranched to branched, sometimes constricted near septa, smooth and thin walled, subhyaline to light olivaceous, 2–10.15  $\mu\text{m}$  wide.

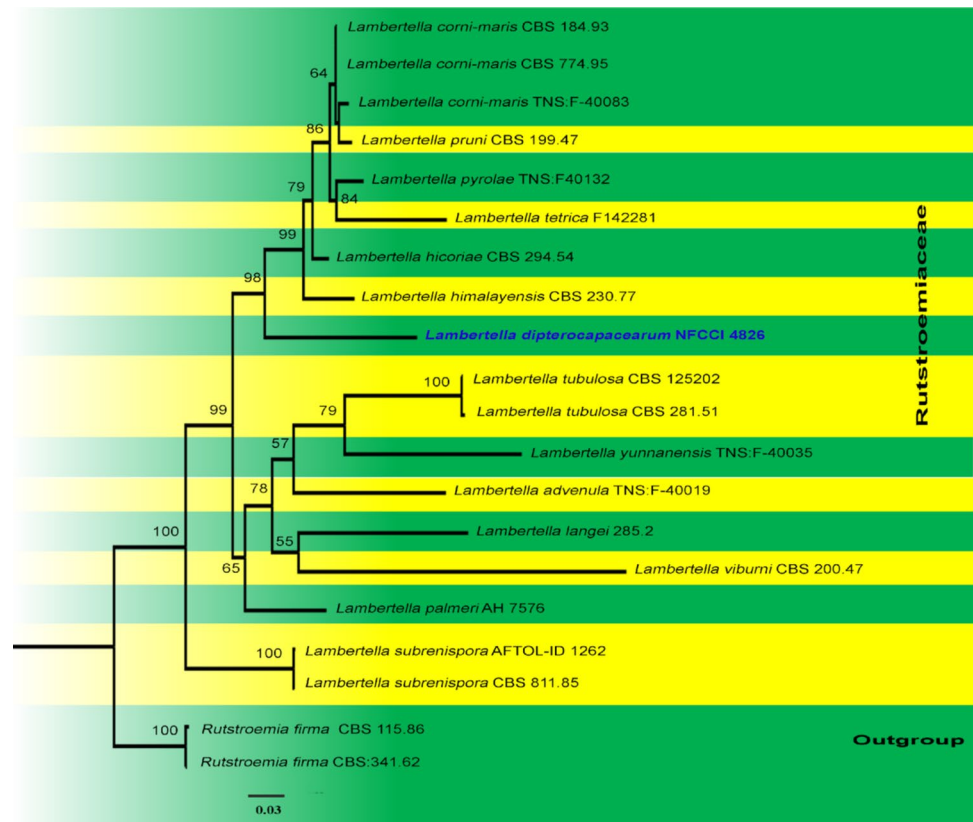
**Materials examined:** India, Uttar Pradesh, Gorakhpur District, on *Shorea robusta* (leaf infested with black mold), 5 May 2016, P.N. Singh, AMH10226 (**holotype**); ex type living culture, NFCCI 4826 (National Fungal Culture Collection of India-WDCM 932).

**GenBank Numbers:** AMH10226: ITS = MT227126, LSU = MT227018, RPB2 = OM313014.

**Notes:** The present taxon is morphologically distinct from allied species of *Lambertella*. All the species of *Lambertella* have been reported to be found in apothecial forms rather producing conidial stage. The sexual stage in the present taxon was not found. Therefore, it was not compared with the allied taxons of the genus *Lambertella*. The genus *Lambertella* is morphologically most closely related to anamorphs

of *Cadophora*, *Phialocephala*, *Mollerodiscus* and *Longia*. The present taxon is compared with *Cadophora fastigiata* (Lagerberg et al. 1927), which is the anamorph of the genus *Lambertella*. The *L. dipterothecae* was found in anamorphic state in having subhyaline to light olivaceous globose to subglobose conidia ( $1.84\text{--}4.22 \times 1.81\text{--}2.80\text{ }\mu\text{m}$ ) produced on tips of phialides in compact dark orangish gleosporic mass. In addition, densely produced phialides, conidiogenous cells, presence of coiled/anastomoses hyphae and sterile arms in axel of conidiophores are the distinct features of this taxon. These features are lacking in *Cadophora fastigiata*. Flask-shaped, light brown phialides that are produced laterally from hyphae and having funnel-shaped collarette conidiogenous cells in *C. fastigiata*. Conidia are generally oval to button shaped ( $3.0\text{--}5.5 \times 1.5\text{--}2.5\text{ }\mu\text{m}$ ). Thus, based on these morphological distinction, *L. dipterothecae*, is described here as species new to science. Phylogenetic analysis of ITS, LSU and RPB2 sequence data indicates that *L. dipterothecae* (NFCCI 4826), is a new species in *Rutstroemia*, which is different from other known species of *Lambertella* forming a sister clade to *Lambertella* sensu stricto (Zhao et al. 2016a) with strong ultrafast bootstrap value of 98 (Fig. 27). On megablast analysis, ITS sequence of *L. dipterothecae* showed 92% (485/525) identity and 13 gaps (2%) with *L. corni-marit* CBS 184.93 and *L. corni-marit* CBS 774.95, 92% (483/523) identity and 14 gaps (2%) with *L. himalayensis* CBS 230.77, 92% (471/512)

**Fig. 27** Phylogenetic tree of *Lambertella dipterothecae* (NFCCI 4826) by Maximum-Likelihood method based on combined sequence data of ITS, LSU and RPB2. *Rutstroemia firma* CBS 115.86 and *Rutstroemia firma* CBS 341.62 were used as outgroup. The analysis involved 20 nucleotide sequences. Evolutionary analyses were conducted in IQ-TREE multicore version 1.6.11 (Nguyen et al. 2015) by the Maximum-Likelihood method using the best suitable model (TIM2e + G4 model). Ex-type strains are in bold and newly generated sequence is in blue. One-thousand bootstrap replicates were analyzed to get ultrafast bootstrap values, and the values above 50% were represented on nodes in the tree



identity and 14 gaps (2%) with *L. pruni* CBS 199.47, 92% (472/511) identity and 12 gaps (2%) with *L. hicoloriae*, and 91% (472/519) identity and 12 gaps (2%) with *L. pyrolae*. To our knowledge, this was isolated for the first time from leaf of *Shorea* collected from Kusumi Forest, District Gorakhpur, Uttar Pradesh region in India. Moreover, this species is being reported for the first time from India.

### Sordariomycetes O.E. Erikss. & Winka.

**Notes:** The class Sordariomycetes was established by (Eriksson and Winka 1997). This is the second largest class of Ascomycota (Kirk et al. 2008; Maharachchikumbura et al. 2016). According to Kirk et al. (2008), 15 orders, 64 families, 1,119 genera and 10,564 species belong to class Sordariomycetes; however, as per the recent classification, the Sordariomycetes now comprises six subclasses, 28 orders, 90 families and 1,344 genera (Maharachchikumbura et al. 2015). Fungi of this class have worldwide distribution containing mostly terrestrial taxa including some pathogens causing disease to plants, arthropods and mammals along with some aquatic fungi (Maharachchikumbura et al. 2016). Main characteristic of large number of Sordariomycetes species is presence of flask-shaped hollow fruiting body containing inoperculate unitunicate asci (Zhang et al. 2006).

### Amphisphaeriales D. Hawksw. & O.E. Erikss.

**Notes:** Based on divergence time estimations provided by Samarakoon et al. (2016) and Hongsanan et al. (2017), *Amphisphaeriales* was supported as a distinct order in Xylariomycetidae and 17 families were accepted.

### Amphisphaeriaceae G. Winter.

**Notes:** The family *Amphisphaeriaceae* was established by Winter (1885) as '*Amphisphaerieae*' and later established as *Amphisphaeriaceae* to accommodate the type genus *Amphisphaeria* and its allies (Winter 1887). Members of *Amphisphaeriaceae* are saprobes on decaying wood in terrestrial, freshwater and marine habitats (Wang et al. 2004; Liu et al. 2015a; Senanayake et al. 2015; Samarakoon et al. 2019, 2020; Dissanayake et al. 2020; Hyde et al. 2020b). According to the latest update of *Amphisphaeriaceae* by Samarakoon et al. (2020), *Lepteutypa* was synonymized under *Amphisphaeria* based on holomorphic morphology and multigene phylogeny, and *Amphisphaeria* was accepted as the only genus in *Amphisphaeriaceae*.

### Amphisphaeria Ces. & De Not.

**Notes:** *Amphisphaeria*, the type genus of *Amphisphaeriaceae*, was introduced by Cesati and De Notaris (1863), and is typified by *A. umbrina* with asexual morph. Samarakoon et al. (2020) accepted 27 species among 287 epithets listed under *Amphisphaeria*. It should be noted that several

taxa were introduced as new to science within the genus *Amphisphaeria* with a weak bootstrap values support, which implied more fresh collections and isolations are expected in future studies (Samarakoon et al. 2019, 2020; Dissanayake et al. 2020).

***Amphisphaeria guttulata* J.Y. Zhang & Y.Z. Lu, sp. nov.**

**Index Fungorum number:** IF 900043; **Facesoffungi number:** FoF 13259; **Fig. 28**

**Etymology:** refers to the ascospores with guttules.

**Holotype:** MFLU 22-0078.

Saprobic on dead branch. **Sexual morph:** *Ascomata* 193–268 µm high × 104–208 µm in diam. ( $\bar{x}$  = 225 × 161 µm, n = 8), immersed, visible as black spots, surrounded by a grey halo area, solitary, scattered or aggregated, globose to subglobose, dark reddish brown, centric ostioles with periphyses. *Hamathecium* composed of paraphyses, septate, unbranched, 2.5–5 µm wide, not anastomosing, hyaline. *Perridium* comprising 4–7 layers of dark brown cells of *textura angularis*, 12.5–24 µm wide, thick-walled. *Asci* 77–88 × 8.5–12.5 µm ( $\bar{x}$  = 81 × 10.5 µm, n = 15), 8-spored, unitunicate, cylindrical, sessile, thin-walled, apically round. *Ascospores* 12–16 × 4.5–5.5 µm ( $\bar{x}$  = 14 × 5 µm, n = 20), uniseriate, partly overlapping, oblong or narrowly fusiform, 1-septate, 2-celled, slightly constricted at the septum, guttulate, pale brown, smooth-walled. **Asexual morph:** undetermined.

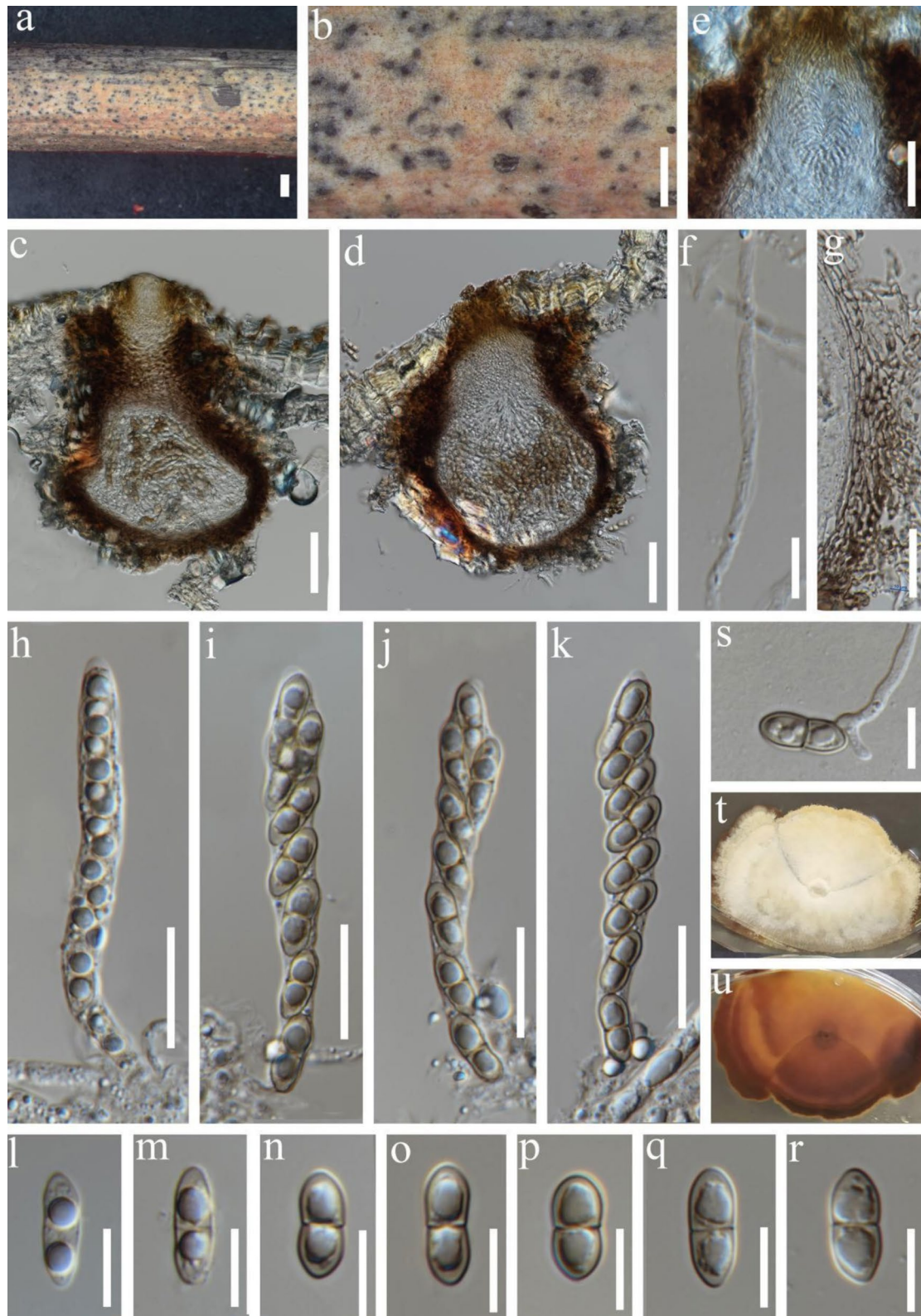
**Culture characteristics:** Ascospores germinated on WA within 12 h at 25–28 °C. The hyaline germ tube germinates from a point of one cell of the ascospores. Colonies growing on PDA, reaching 19 mm in diam. after two weeks at 25 °C, flat, section to fan shape at the surface, fimbriate margin with a smooth surface, yellowish white from above; cream yellow mycelium in the middle and brown yellow mycelium in the outer ring in reverse, and not producing pigment in the culture.

**Material examined:** Thailand, Loei Province, Chang Wat, Phu Kradueng, Tambon Huai Som (16° 55' 9" N, 101° 55' 21" E), on dead branch in a forest, 27 February 2020, J.Y. Zhang, Y196 (MFLU 22-0078, **holotype**); ex-type living culture, MFLUCC 22-0052.

**GenBank numbers:** MFLU 22-0078: LSU = OQ101583, ITS = OQ101582.

**Notes:** The morphological characteristics of the new isolate match well with the generic concept of *Amphisphaeria* and is most similar to *Amphisphaeria micheliae* in the shape of asci and ascospores (Samarakoon et al. 2020). However, it is recognized from *A. camelliae* by its shorter asci (77–88 × 8.5–12.5 µm vs. 92–135 × 7–10.5 µm) and smaller ascospores (12–16 × 4.5–5.5 µm vs. 15.5–21 × 6–7.5 µm, Samarakoon et al. 2020). The phylogenetic tree showed that the new collection formed a separate clade within the genus *Amphisphaeria*, and is sister to *A. yunnanensis* (Fig. 29). Therefore, we introduce the new collection as *Amphisphaeria guttulata* sp. nov.

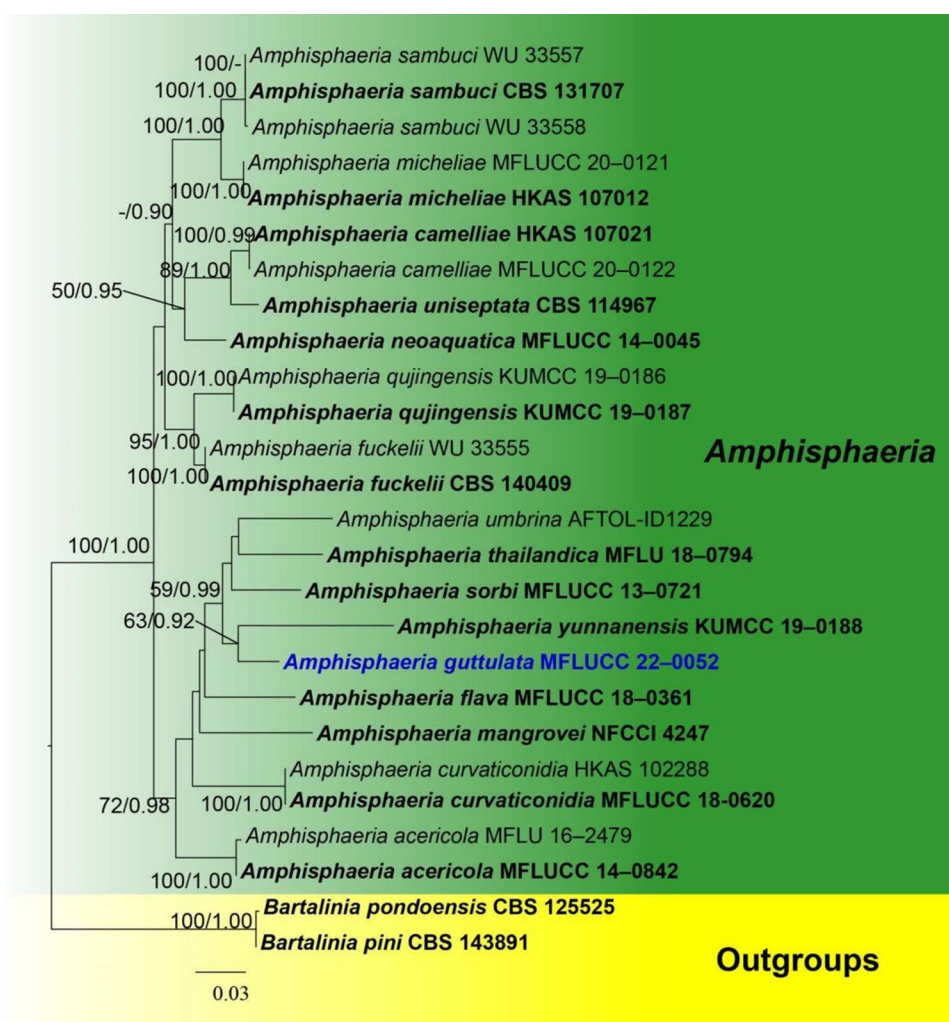




**Fig. 28** *Amphisphaeria guttulata* (MFLU 22-0078, holotype). **a, b** Ascomata on the substrate. **c, d** Vertical section of ascoma. **e** ostiole. **f** paraphyses. **g** peridium. **h–k** asci. **l–r** ascospores. **s** Germinating

ascospore. **t, u** Colony on PDA from above and below. Scale bars: **a, b** = 1000  $\mu$ m, **c–e** = 50  $\mu$ m, **g–k** = 20  $\mu$ m, **f, l–s** = 10  $\mu$ m

**Fig. 29** Phylogram generated from maximum likelihood analysis based on combined LSU and ITS sequence data. 26 taxa were included in the combined analyses, which comprised 1782 characters (LSU: 1160 bp, ITS: 622 bp) after alignment. The best scoring RAXML tree with a final likelihood value of -7242.965669 is presented. The matrix had 614 distinct alignment patterns, with 17.29% of undetermined characters or gaps. Estimated base frequencies were as follows: A=0.257803, C=0.216953, G=0.269172, T=0.256073; substitution rates: AC=0.829912, AG=2.560479, AT=1.266564, CG=0.816478, CT=4.838135, GT=1.000000; gamma distribution shape parameter  $\alpha=0.264935$ . Bootstrap support values for ML equal to or greater than 50% and BYPP equal to or greater than 0.90 are given above the nodes. The tree is rooted with *Bartalinia pondoensis* CBS 125525 and *B. pini* CBS 143891. The newly-generated strain is shown in blue and bold. Ex-type strains are indicated by black and bold



### **Beltraniaceae** Nann.

**Notes:** *Beltraniaceae* was introduced by Nannizzi (1934) to accommodate the genus *Beltrania* and allied genera including *Beltrania*, *Beltraniella*, *Beltraniopsis*, *Hemibeltrania*, *Parapleurotheciopsis*, *Porobeltraniella*, *Pseudobeltrania*, *Pseudosubramaniomyces* and *Subsessila* (Wijayawardene et al. 2022).

### **Beltrania** Penz.

**Notes:** Species of *Beltrania* are characterized by setae with radially lobed basal cells, conidiophores with separating cells, and biconic conidia with a hyaline transverse band and apical tubular appendage. There are 26 epithets for *Beltrania* listed in Index Fungorum (2022).

### **Beltrania liliiferae** P. Razaghi, M. Raza & L. Cai, *sp. nov.*

**Index Fungorum number:** IF 900337; **Facesoffungi number:** FoF 12673; **Fig. 30**

**Etymology:** The name refers to the host “*Magnolia liliifera*”.

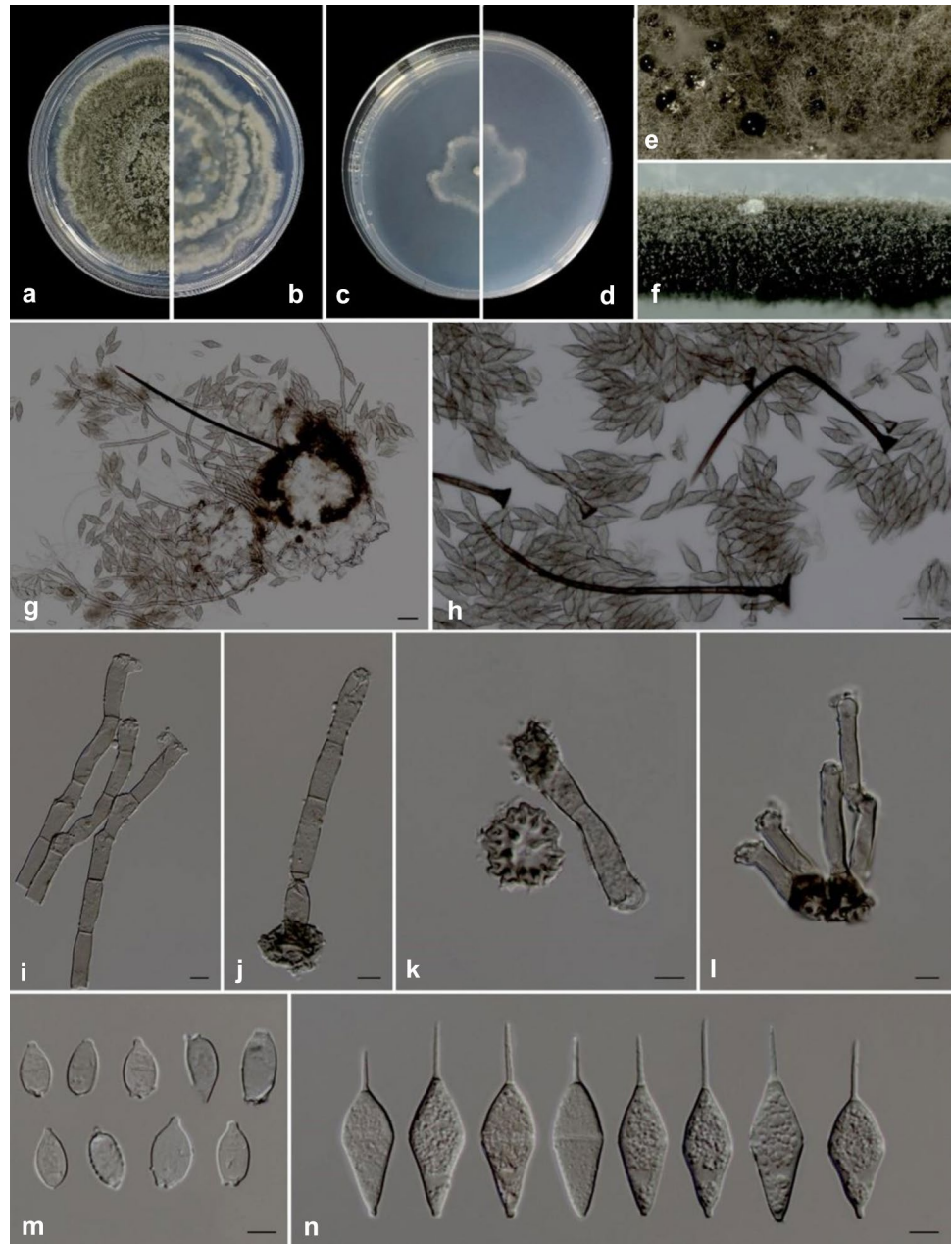
**Holotype:** HMAS 352088.

**Setae** numerous, erect, arising from radially lobed basal cells, straight to flexuous, unbranched, 2–6-septate, thick-walled, verrucose, dark brown to black, 155–207  $\mu\text{m}$  long, 4.5–7  $\mu\text{m}$  wide, tapering to a pointed apex. **Conidiophores** macronematous, mononematous, single or in small groups, erect, unbranched, hyaline to pale brown, smooth, straight to flexuous, mostly geniculate at the apical region, 2–12(–23) septate, 37–91(–380)  $\times$  4–7.5  $\mu\text{m}$ , arising from basal cells of setae or from separate dark brown, swollen, radially lobed cells, 11–19  $\mu\text{m}$  (av. = 13.47  $\pm$  2.32  $\mu\text{m}$ ) diam. **Conidiogenous cells** polyblastic, integrated, terminal, sympodial, with several flat-tipped denticles, cylindrical, clavate, subhyaline to pale brown, smooth (14.5–)18–24.5  $\times$  4.5–8.5  $\mu\text{m}$  (av. = 20.71  $\pm$  4.37  $\times$  6.11  $\pm$  1.35  $\mu\text{m}$ ). **Separating cells** hyaline, finely roughened, aseptate, ellipsoidal, obovoid, 9.5–13  $\times$  5–7  $\mu\text{m}$  (av. = 10.81  $\pm$  0.97  $\times$  5.68  $\pm$  0.47  $\mu\text{m}$ ), with several apical, flat-tipped denticles. **Conidia** arise directly from conidiogenous cells or from separating cells, acrogenous, biconic, rhomboidal, aseptate, solitary, smooth, pale brown to pale smoky-brown with a



**Fig. 30** *Beltrania liliiferae* (HMAS 352088, **holotype**).

**a–d** Upper and reverse views of cultures on PDA and SNA after 1 week of inoculation, respectively. **e** Exudate droplets on PDA. **f** Conidiophores and setae on pine needle on SNA. **g, h** Setae, conidiophores, conidiogenous cells and conidia. **i–l** Conidiophores and radial lobed basal cells of conidiophores. **m** Separating cells. **n** Conidia. Scale bars: **g, h** = 20  $\mu$ m, **i–n** = 5  $\mu$ m



hyaline to subhyaline equatorial transverse band, with distinct granules, rounded or 1-denticulate at base,  $20\text{--}25 \times 8.5\text{--}10\text{ }\mu\text{m}$  (av. =  $22.66 \pm 1.39 \times 9.36 \pm 0.51\text{ }\mu\text{m}$ ), apical appendage  $7\text{--}12\text{ }\mu\text{m}$  (av. =  $8.94 \pm 1.29\text{ }\mu\text{m}$ ) long, tapering to an acutely rounded tip. **Sexual morph:** Undetermined.

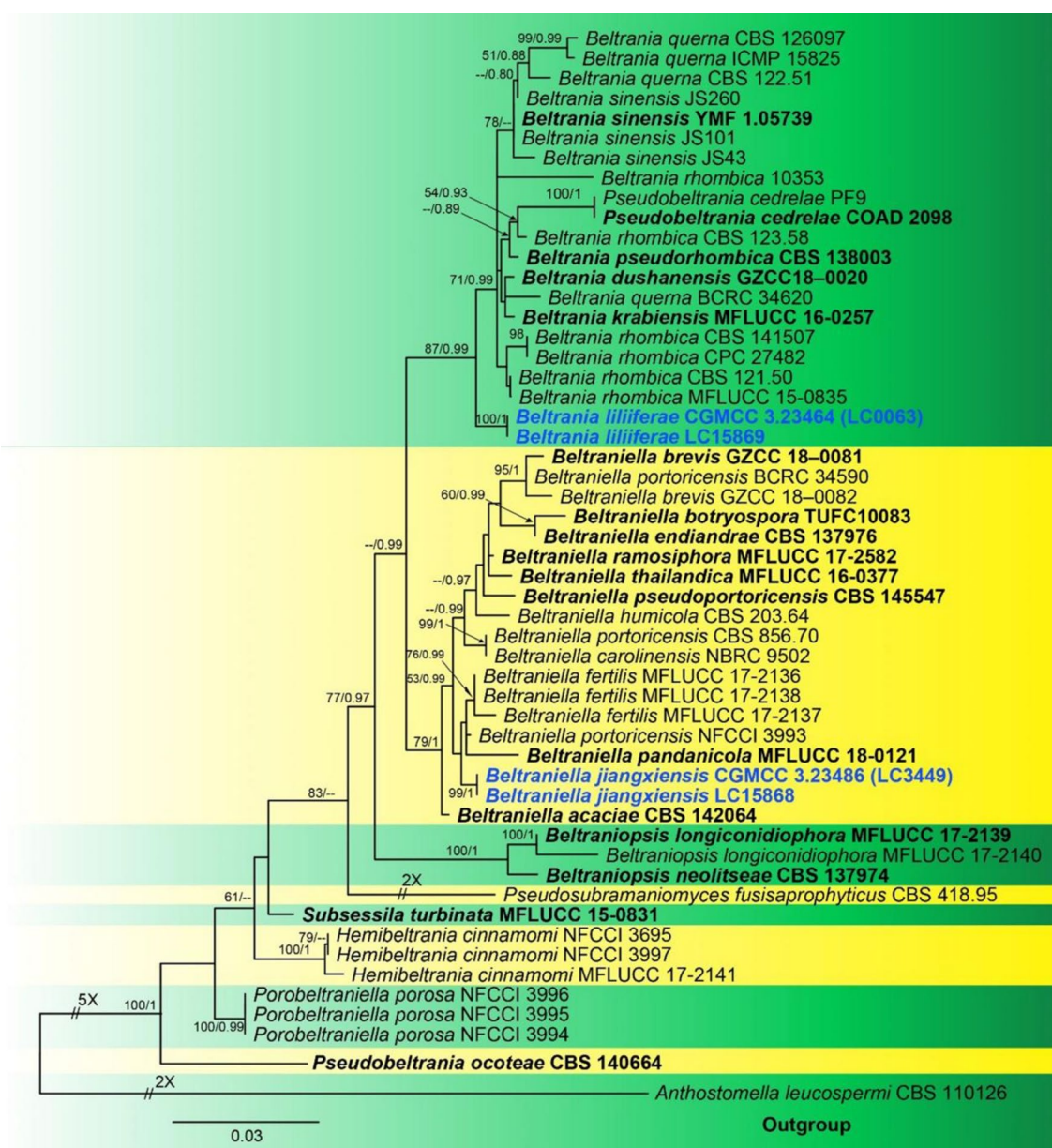
**Culture characteristics:** Colonies on PDA raised, with undulate edge, smooth, grayish green from above, reverse centric circles in grayish green and cream, velutinous, producing olivaceous exudate droplets on aerial mycelia, reaching 71–77 mm in diam after 7 d at 25 °C; on SNA flat, with undulate edge, colorless, sparse aerial mycelia, reaching 36–42 mm diam after 7 d at 25 °C.

**Material examined:** Thailand, on dead leaves of *Magnolia liliifera*, 2010, Anonymous (HMAS 352088, **holotype**), ex-holotype living culture, CGMCC 3.23464 = LC0063. Thailand, on dead leaves of *Magnolia liliifera*, 2010, Anonymous, living culture, LC15869.

**GenBank numbers:** CGMCC 3.23464: ITS = OP022176, LSU = OP022172; LC15869: ITS = OP022177, LSU = OP022173.

**Notes:** Based on phylogenetic analysis of combined LSU and ITS sequence data, two isolates of *Beltrania liliiferae* grouped together and formed a distinct clade closely related to *B. rhombica* (Fig. 31). However, it differs from the latter by having longer setae (155–207  $\mu$ m vs. 103–167  $\mu$ m), larger





**Fig. 31** Phylogenetic tree generated from Maximum likelihood analysis (RAxML) based on combined ITS and LSU sequence data of Beltraniaceae. Fifty-three strains are included in the combined analyses which comprised 1373 characters (547 characters for ITS and 820 characters for LSU) after alignment. *Anthostomella leucospermi* (CBS 110126) was used as the outgroup taxon. The best scoring RAxML tree with a final likelihood value of -4929.358117 is presented. The matrix had 335 distinct alignment patterns, with 11.74% of undetermined characters or gaps. Estimated base frequencies were as follows:

A=0.2705, C=0.2648, G=0.2173, T=0.2474; substitution rates: AC=0.6116, AG=3.9808, AT=1.0000, CG=0.6116, CT=1.9749, GT=1.0000; gamma distribution shape parameter  $\alpha$ =0.4680. Bootstrap support values for ML equal to or greater than 50% are given above the nodes (left side). Bayesian posterior probabilities (BYPP) equal to or greater than 0.80 are given above the nodes (right side). Ex-type strains are in bold and newly generated sequences are in blue

conidiophores [37–91(–380)  $\times$  4–7.5  $\mu$ m vs. 22.5–46  $\times$  2–4.5  $\mu$ m and wider conidia (8.5–10 vs. 6–8.5  $\mu$ m, Lin et al. 2017). *Beltrania rhombica* lacks type material; therefore, to ensure better designation of the species, recollecting on *Citrus limon* in Italy is required.

### *Beltraniella* Subram.

**Notes:** *Beltraniella* was established with *B. odinae* as the type species, found on dead leaves of *Odina woderi* in India. The genus is characterized by setiform conidiophores and polyblastic, sympodial, denticulate conidiogenous cells, acroporeogenous, turbinate or biconic conidia



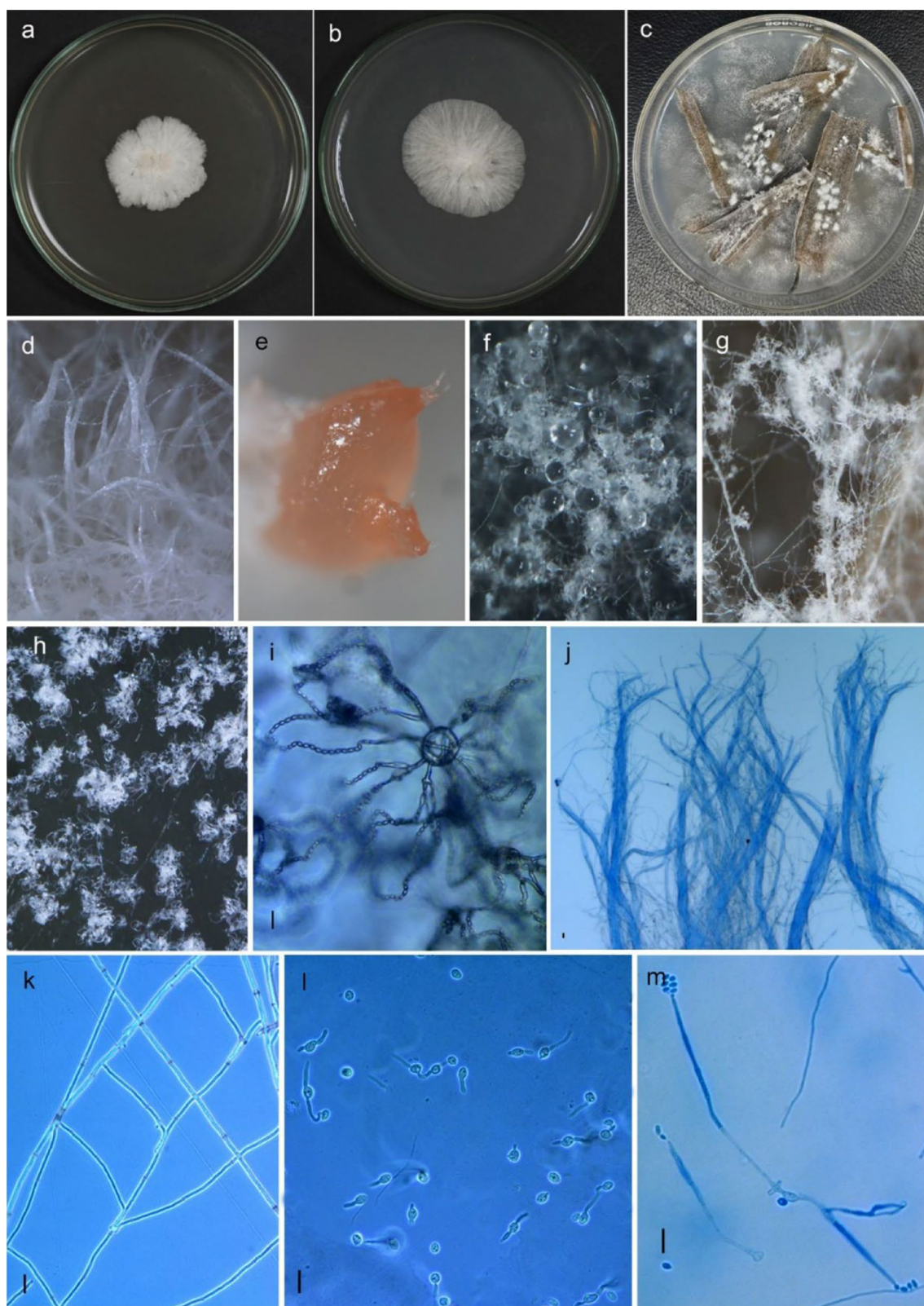
**Fig. 32** *Beltraniella jiangxiensis* (HMAS 352097, holotype). **a–d** Upper and reverse views of cultures on PDA and SNA after 1 week of inoculation, respectively. **e** Conidiophores and setae on pine needle

on SNA. **f–j** Setae, conidiophores and conidiogenous cells. **k–m** Conidiophores and conidiogenous cells. **n** Separating cells. **o** Conidia. Scale bars: 5  $\mu$ m

with a distinct hyaline transverse band at the equatorial zone (Subramanian 1952). There are 31 epithets listed in Index Fungorum (2022).

*Beltraniella jiangxiensis* P. Razaghi, M. Raza & L. Cai, *sp. nov.*





*Index Fungorum* number: IF 900338; *Facesoffungi* number: FoF 12674; Fig. 32

*Etymology*: The name refers to the location it was collected.

*Holotype*: HMAS 352097.



**Fig. 33** *Synnemellisia punensis* (NFCCI 5166, **holotype**). **a, b** Colony morphology on PDA (front view). **c** colony morphology on grass leaf media. **d** Stereomicroscopic surface view of colony grown on PDA with hyphal bundles forming synnemata. **e** Stereomicroscopic surface view of colony grown on PCA with pale orange exudate. **f** Stereomicroscopic surface view of colony grown on grass leaf media with watery exudate. **g, h** Whitish puffy mass of sporodochia. **i** Anastomoses with phialides bearing long chains of conidia. **j** parallel hyphal bundles of hyphae forming synnemata. **k** anastomosed hyphae. **l** bipolar germination in spores (showing arrow). **m** Germinating conidia directly producing phialide with conidia (showing arrow). Scale bars: **i–m** = 10 µm

*Setae* numerous, erect, arising from radially lobed basal cells, straight or flexuous, unbranched, single or in small groups, thick-walled, coarsely verrucose, olivaceous brown, paler towards apex, 81–304 µm long, 5–8.5 µm wide, tapering to a pointed apex, up to 16-septate, arising from a dark brown, swollen, radially lobed basal cell, 11–22 µm in diameter. *Conidiophores* macronematous, short, simple or branched at apical regions, 3–6 septate, reduced to conidiogenous cells, verrucose, thin-walled, swollen at the base, subhyaline to pale olivaceous, arising from basal cells of setae or from separate, 36–65 × 4–7 µm. *Conidiogenous cells* polyblastic, integrated, determinate, terminal, geniculate, denticulate, cylindrical, oblong, hyaline to subhyaline, smooth, 9–19 × 4–6 µm (av. = 12.62 ± 3.27 × 4.68 ± 0.59 µm). *Separating cells* obclavate, thin-walled, smooth, hyaline to subhyaline, 1-denticulate at each end, 8–11 × 3.5–5 µm (av. = 9.91 ± 0.89 × 3.95 ± 0.47 µm). *Conidia* arise directly from conidiogenous cells or from separating cells, aggregated, acrogenous, simple, dry, straight, sometimes verrucose, thin-walled turbinate to pyriform, rostrate to pointed at proximal end, truncate at distal end, hyaline to subhyaline without a hyaline transverse band, 20–24 × 5.5–7.5 µm (av. = 22.12 ± 1.25 × 6.55 ± 0.64 µm). **Sexual morph:** Undetermined.

**Culture characteristics:** Colonies on PDA raised with concave edge, with undulate edge, dense, colony cream from above and reverse, *velutinous*, sterile, reaching 55–57 mm diam after 7 d at 25 °C; on SNA dome shaped, with rhizoid edge, white, reaching 53–60 mm diam after 7 d at 25 °C.

**Material examined:** China, Jiangxi Province, Ganzhou, Fengshan, on *Camellia sinensis*, August 2013, Y. Zhang (HMAS 352097, **holotype**), ex-holotype living culture, CGMCC 3.23486 = LC3449. China, Jiangxi Province, Ganzhou, on leaves of *Camellia sinensis*, August 2013, Y. Zhang, living culture, LC15868.

**GeneBank numbers:** CGMCC 3.23486: ITS = OP022178, LSU = OP022174; LC15868: ITS = OP022179, LSU = OP022175.

**Notes:** Two isolates of *Beltraniella jiangxiensis* formed a well-supported and distinct clade on the ML tree generated from ITS and LSU sequences (Fig. 31), closely related to *B. pandanicola*, *B. portoricensis* and *B. fertilis*. Morphologically, our novel species is distinguished from the most

closely related species, *B. pandanicola* isolated from *Pandanus* sp. in Thailand (Tibpromma et al. 2018) by producing more septate (16 µm × 2–4 µm) and relatively longer setae (81–304 µm vs. 114–200 µm), longer conidiophores (36–65 µm vs. 20–42 µm) and longer conidiogenous cells (9–19 µm vs. 6–10 µm).

### *Hypocreales* Lindau.

**Notes:** The order *Hypocreales* was established by Lindau (1897) and is the monophyletic order under the subclass *Hypocreomycetidae*. *Hypocreales* contains a wide range of economical important fungi from plant pathogens to bio-control agents (Rossman 1996). Most of the members of this order are found in temperate or tropical and subtropical regions (Pöldmaa 2011). This order accommodates ten families, *Bionectriaceae*, *Clavicipitaceae*, *Cordycipitaceae*, *Flammocladiaceae*, *Hypocreaceae*, *Nectriaceae*, *Niessliaceae*, *Ophiocordycipitaceae*, *Stachybotriaceae* and *Tilachlidiaceae*.

### *Bionectriaceae* Samuels & Rossman.

**Notes:** *Bionectriaceae* is the monophyletic family within order *Hypocreales* introduced by Rossman et al. (1999) to accommodate 26 genera. The genera of *Bionectriaceae* are perpetuating in soil, dead wood and as endophytes in tropical and subtropical areas (Huanraluek et al. 2020). As per recent classification, this family contains 39 genera with *Bionectria* as the type genus (Rossman et al. 2001; Maharachchikumbura et al. 2015). This family is characterized by white, yellow, orange to tan colored uniloculate, perithecial or sometimes cleistothecial ascomata (Rossman et al. 1999).

### *Synnemellisia* N.K. Rao, Manohar. & Goos.

**Notes:** *Synnemellisia* was proposed by Rao et al. (1989). The genus is characterized by synnematous conidiomata with conidiogenous cells at their tips. The conidia are holoblastic, usually single, hyaline, lanceolate and aseptate. This is one of the smallest genera of *Bionectriaceae* family and contains only four species according to Index Fungorum records (<http://indexfungorum.org/Names/Names.asp>).

***Synnemellisia punensis*** K. S. Pawar, P. N. Singh, S. K. Singh, **sp. nov.**

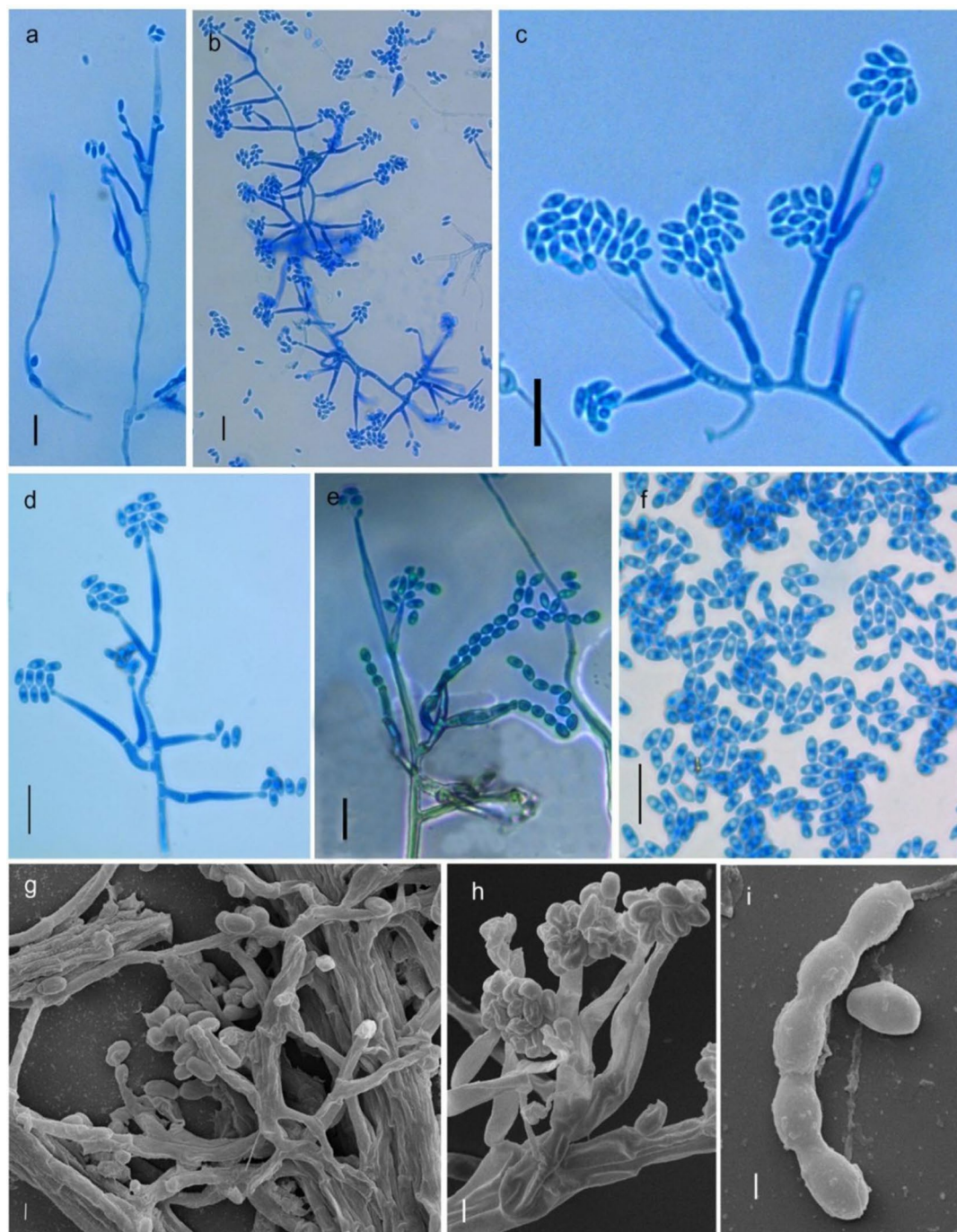
**Index Fungorum number:** IF900322; **Facesoffungi number:** FoF10810; Figs. 33, 34

**Etymology:** specific epithet '*punensis*' refers to name Pune (a district of Maharashtra state).

**Holotype:** NFCCI 5166.

**Colour code follows:** Methuen Handbook of Colour (Kornerup and Wanscher 1978).

Isolated in vitro from the leaf litter. **Asexual morph:** *Synnemata* produced in the form of aggregated mass of parallel bundles hyphae, hyaline. *Vegetative hyphae*



**Fig. 34** *Synnemellisia punensis* (NFCCI 5166, holotype). **a, b** Conidiophores with phialides bearing conidia. **c** Conidiophores with phialides bearing conidia (in higher magnification). **d** Conidiophores with phialides bearing chevron/zipper like arrangement of conidia (showing arrow). **e** Conidiophores, phialides with chains of conidia.

**f** Numerous conidia. **g** SEM images of branched conidiophores, phialides and conidia. **h** Conidiophore with primary and secondary metulae bearing phialides and conidia. **i** Chain of conidia. Scale bars: **a–f** = 10 μm, **g, h** = 2 μm, **i** = 1 μm

aggregated in loose parallel bundles, rope like, branched to unbranched, anastomoses, smooth walled, thin and thick, hyaline, up to 3 μm wide. *Setae* and *hyphopodia* absent. *Chlamydospores* absent. *Conidiophores* arising from superficial hyphae, forming floccose sporodochia, unbranched to

branched, branching unilateral to bilateral verticillate, hyaline, smooth walled,  $9.68\text{--}127.7 \times 1.97\text{--}2.77$  μm. *Conidiogenous cells* polyblastic and polyphialidic, smooth walled, hyaline,  $4.71\text{--}35.91 \times 1.35\text{--}3.46$  μm. *Phialides* solitary or in group of 2–4, sometimes directly produced from

superficial hyphae, cylindrical, attenuated, smooth walled. *Metulae* 1–2, primary metulae solitary, spatulate, variable in size ( $8.59\text{--}10.27 \times 1.05\text{--}1.83\text{ }\mu\text{m}$ ), secondary metulae paired ( $6.98 \times 2.12\text{ }\mu\text{m}$ ),  $8.29\text{--}25.36 \times 1.35\text{--}3.58\text{ }\mu\text{m}$ . *Conidia* produced in long chain from polyblastic and polyphialidic conidiogenous cell, sometimes conidia accumulated in the form of chevron or zipper like, produced in loose mass on the tip of phialides, oval to broadly ovoid, allantoid to fusoid, base broader, sometimes base rarely tapered, base truncate, tip obtuse, aseptate, smooth walled, 1–2 guttulate, smooth walled, hilum unthickened, hyaline,  $2.22\text{--}6.43 \times 1.2\text{--}4\text{ }\mu\text{m}$  ( $\bar{x} = 3.84 \times 2.17\text{ }\mu\text{m}$ ,  $n = 30$ ). **Sexual morph:** Undetermined.

**Culture characteristics:** on semi-synthetic agar medium PDA white (6A1) to orange white (6A2), reaching 3.0 cm diam. in 5 days at 25 °C, forming synnemata, margin irregular, reverse wrinkled, pale orange (5A3); on PCA (Potato Carrot Agar) white (6A1), reverse yellowish white (4A2), reaching 3.7 cm diam. in 5 days at 25 °C, rarely forming dome like synnemata with pale orange (5A3) exudate. No sporulation on PDA and PCA but abundantly sporulating on grass leaf agar.

**Material examined:** India, Maharashtra, Pune District, from leaf litter, 1 October 2020, K.S. Pawar, NFCCI 5166 (**holotype**), ex-type living culture, National Fungal Culture Collection of India, WDCM 932.

**GenBank numbers:** ITS = ON059361, LSU = ON059433.

**Notes:** *Synnemellisia punensis* is morphologically distinct from allied species of *Synnemellisia*. The conidia of *S. hyalospora* are solitary, slightly curved,  $40\text{--}52\text{ }\mu\text{m}$  long,  $4.2\text{--}5\text{ }\mu\text{m}$  wide at the middle, and  $1\text{--}1.4\text{ }\mu\text{m}$  wide at the base (Rao et al. 1989). The conidia of type species *S. aurantia* (COAD 2070) are aggregated on a cushion-like head, navicular to fusiform,  $23\text{--}30$  long and  $7\text{--}9\text{ }\mu\text{m}$  wide, apex subacute, base obtuse to subtruncate, aseptate, guttulate, subhyaline and smooth. (Crous et al. 2016). In present taxon *S. punensis* (NFCCI 5166), the conidia are produced from polyblastic, polyphialidic conidiogenous cells, ovoid, aseptate  $2.22\text{--}6.43\text{ }\mu\text{m}$  long and  $1.2\text{--}4\text{ }\mu\text{m}$  wide. Thus, *S. punensis* morphologically different in having much smaller shape and dimension of conidia as compared to the conidial dimension of *S. hyalospora* and *S. aurantia*. In addition, the conidia in new taxon produced in long chains and in loose aggregated mass, also forming zipper or chevron like pattern. Tan et al. (2021) described both the taxa based only on sequencing and phylogenetic analysis. Hence, morphological features of *S. urenae* (BRIP 71675) and *S. acacia* (BRIP 71652) are missing and hence cannot be compared.

Phylogenetic analysis of ITS and LSU sequence data specifies that *S. punensis* (NFCCI 5166), is a new species in *Bionectriaceae*, which is dissimilar from other known species of *Synnemellisia* (Fig. 35). Based on megablast analysis, ITS sequence of *Synnemellisia punensis* (NFCCI 5166)

showed 94% (541/574) identity and 13 gaps (2%) with ex-type strain of *Synnemellisia aurantia* (COAD 2070), 96% (544/569) identity and 6 gaps (1%) with ex-type strain *Synnemellisia urenae* (BRIP 71675), and 95% (543/572) identity and 10 gaps (1%) with *Synnemellisia acacia* (BRIP 71652). Sequence data of *Synnemellisia hyalospora* is not available in the literature. Based on morphological and phylogenetic analysis, *Synnemellisia punensis* (NFCCI 5166) is proposed as novel species with strong ultrafast bootstrap (96%).

**Cordycipitaceae** Kreisel ex G.H. Sung, J.M. Sung, Hywel-Jones & Spatafora.

**Notes:** Species in the *Cordycipitaceae* have two phenotypes; teleomorph and anamorph. Among them, the main characteristics of the teleomorph are brightly colored, fleshy stromata and filiform ascospores (Sung et al. 2007). Asexual forms are more diverse, e.g. the insect host was covered in powdery conidia, with synnema emerging from specific parts of the host (Mongkolsamrit et al. 2018). Currently, *Cordycipitaceae* is composed of 16 genera, with *Cordyceps* as the type genus (Sung et al. 2007; Kepler et al. 2017; Mongkolsamrit et al. 2018; Thanakitpipattana et al. 2020; Wang et al. 2020a; Chen et al. 2021a). Furthermore, species in the *Cordycipitaceae* have important roles in food (*Cordyceps militaris*, Wen et al. 2014, 2016), medicine (*Cordyceps cicadae*, Zha et al. 2018, 2019) and biocontrol (*Beauveria bassiana*, Biryola et al. 2022; *Beauveria pseudobassiana*, Villamizar et al. 2020).

**Akanthomyces** Lebert.

**Notes:** *Akanthomyces* was introduced by Lebert (1858) based on the type species *Akanthomyces aculeatus*. *Akanthomyces* is usually parasitic in spiders and moth (Chen et al. 2019a; Aini et al. 2020), but also attacks Hemiptera, Coleoptera and Orthoptera (Hodge et al. 2003; Kepler et al. 2017; Mongkolsamrit et al. 2018; Chen et al. 2020a; Nishi et al. 2022). Based on morphological and phylogenetic analyses, *Insecticola*, *Lecanicillium* and *Torrubiella*, are all basionyms of *Akanthomyces* (Samson and Evans 1974; Kepler et al. 2017). Now, this genus has more than 31 species (Index Fungorum, <http://www.indexfungorum.org/Names/Names.asp>, 19th September 2022).

**Akanthomyces xixiuensis** X. C. Peng & T. C. Wen, *sp. nov.*

**Index Fungorum number:** IF900124; **Facesofungi number:** FoF 13898; **Figs.** 36, 37

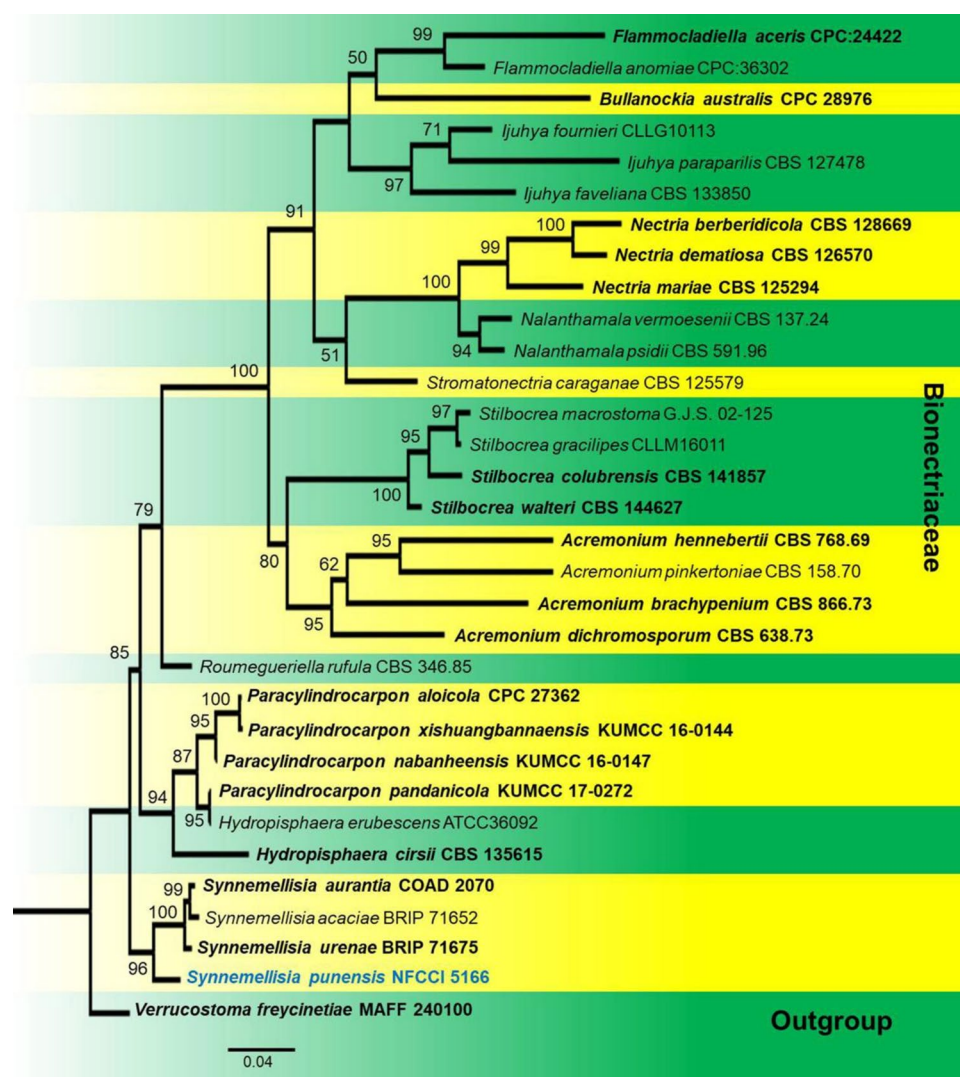
**Etymology:** *xixiuensis* (Lat.) referring to the collecting site “Xixiu District”.

**Holotype:** HKAS 125851.

**Asexual morph:** The host is ca. 14 mm long, moth (Lepidoptera). Several synnemata arising from adult of insect host, cylindrical, yellowish,  $2\text{--}6.5\text{ mm}$  long and  $0.2\text{--}0.7\text{ mm}$  wide. *Phialides*  $6\text{--}27 \times 2\text{--}4\text{ }\mu\text{m}$  ( $\bar{x} = 12.4 \times 3.0\text{ }\mu\text{m}$ ,  $n = 15$ ),



**Fig. 35** Phylogenetic tree of *Synnemellisia punensis* (NFCCI 5166) inferred from Maximum-Likelihood analysis based on combined sequence data of ITS, LSU. *Verrucostoma freycinetiae* MAFF 240100 was used as outgroup. The analysis involved 32 nucleotide sequences. Evolutionary analyses were conducted in IQ-TREE multicore version 1.6.11 (Nguyen et al. 2015) by the Maximum-Likelihood method using the best suitable model (TNe+I+G4 model). Ex-type strains are in bold and newly generated sequence is in blue. One-thousand bootstrap replicates were analyzed to get ultrafast bootstrap values, and the values above 50% were represented on nodes in the tree



cylindrical to ellipsoidal with papillate end. *Conidia* smooth-walled, fusoid to ovoid,  $3.5\text{--}5.6 \times 2.2\text{--}3.2\text{ }\mu\text{m}$  ( $\bar{x}=4.3 \times 2.6\text{ }\mu\text{m}$ ,  $n=15$ ).

**Culture characteristics:** Colonies on PDA, attaining a diameter of 17–23 mm within 14 d at 20 °C, dense, cottony, yellowish to white, reverse pale yellow. Mycelium smooth, branched, hyaline, 0.7–4.8  $\mu\text{m}$  diam. Conidia and reproductive structures not observed.

**Habitat and distribution:** The new species grow on the pine needle litter of mixed forest, and is currently only found in China.

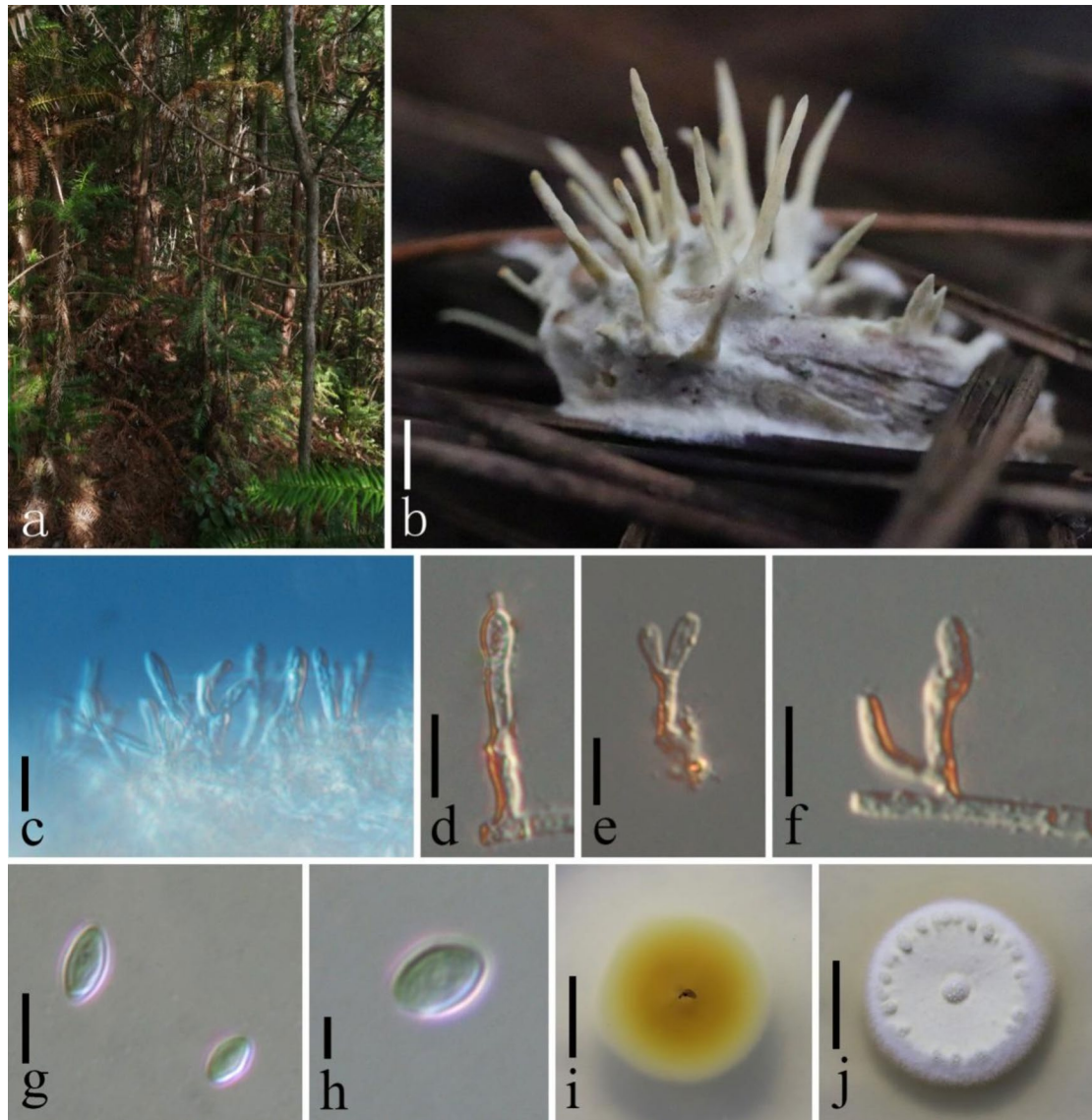
**Material examined:** China, Guizhou Province, Xixiu District, 26°09'13.38" N, 106°05'13.19" E, 1293 m alt., on moth (*Lepidoptera*), 17 August 2021, X. C. Peng, XX21081764 (HKAS 125851, holotype); ex-type living culture XX21081764).

**GenBank numbers:** HKAS 125851: ITS = OP693461; SSU = OP693479; LSU = OP693481; TEF = OP838888; RPB1 = OP838890; RPB2 = OP838892. XX21081764:

ITS = OP693460; SSU = OP693478; LSU = OP693480; TEF = OP838887; RPB1 = OP838889; RPB2 = OP838891.

**Notes:** *Akanthomyces xixiuensis* is characterized by gregarious synnemate with tapering gradually toward the apex, unbranched, obclavate, and yellowish. Two samples of *Akanthomyces xixiuensis* group together with strong statistical support (100/1), and form a separate clade at the basal portion of the *Akanthomyces* lineage. *Akanthomyces xixiuensis* is morphological similar to *A. aculeatus*, *A. pyralidarum*, and *A. tortricidarum*, and the host is *Lepidoptera*. However, the new species differs from *Akanthomyces aculeatus* in having shorter and wider synnemate, and fusoid conidia (Mains 1950), *Akanthomyces tortricidarum* has two kinds of structures of the synnemate, phialides, and conidia (Aini et al. 2020), while the asexual state of the *Akanthomyces pyralidarum* is undetermined (Aini et al. 2020).

**Nectriaceae** Tul. & C. Tul.



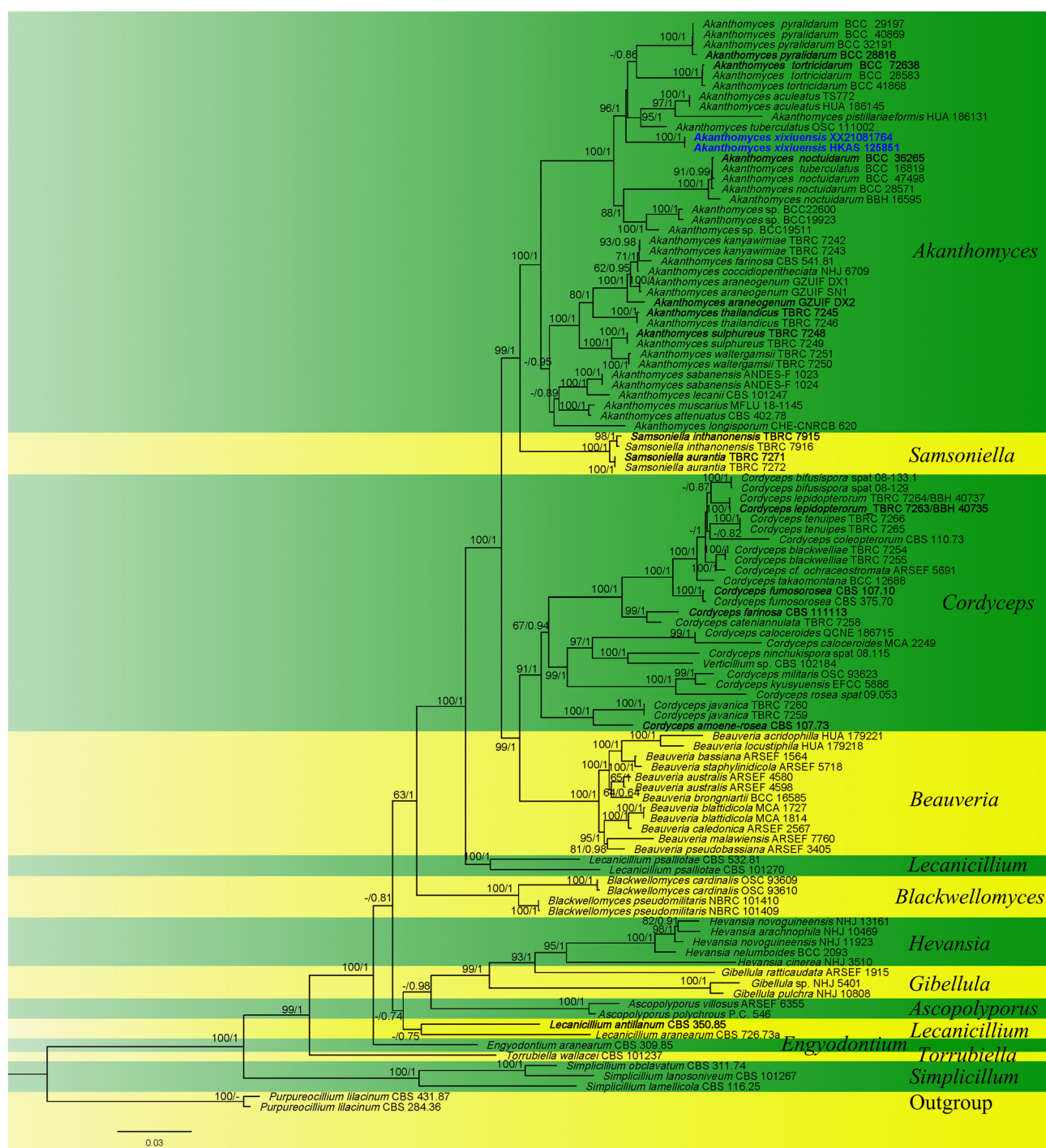
**Fig. 36** *Akanthomyces xixiuensis* (HKAS 125851, **holotype**) **a** Habitat. **b** Fungus on the host. **c–f** Phialides from synnema. **g, h** Conidia. **i, j** Culture on PDA, lower surface (**i**) and upper surface (**j**). Scale bars: **b**=2 mm, **c–f**=10 µm, **g**=5 µm, **h**=2 µm, **i, j**=1 cm

*Notes:* *Nectriaceae*, typified by *Nectria*, was introduced by Tulasne and Tulasne (1865). Wijayawardene et al. (2022) accepted 70 genera under *Nectriaceae* wherein members have worldwide distribution with various lifestyles as saprobes, endophytes, or pathogens of wide-ranging host species (Rossman et al. 1999; Lombard et al. 2015). Sexual morphs of *Nectriaceae* are characterized by uniloculate, white, yellow, orange-red or purple ascomata that change colour in KOH while asexual morphs are mainly hyphomycetous with phialidic conidiogenous cells producing amero-sporous to phragmo-sporous conidia (Lombard et al. 2015; Hyde et al. 2020b). The latest treatment and updated accounts of *Nectriaceae* by Perera et al. (2023) is followed in this paper.

***Paracremonium*** L. Lombard & Crous.

*Notes:* Lombard et al. (2015) introduced *Paracremonium* based on different strains previously treated as *Acremonium recifei* with formation of sterile coils from which conidiophores radiate with inconspicuously swollen septa in the hyphae. Ten species are currently accepted under *Paracremonium* [*P. apiculatum*, *P. bendijkiorum*, *P. binnewijzendii*, *P. contagium*, *P. ellipsoideum*, *P. inflatum* (type species), *P. lepidopterorum*, *P. moubasherii*, *P. pembeum* and *P. variiforme*] isolated from various sources (i.e., soil, water, sewage and *Homo sapiens*) (Lombard et al. 2015; Lynch et al. 2016; Crous et al. 2017, 2021a; Zhang et al. 2017a, 2021a; Al-Bedak 2019; Ming et al. 2021). Zhang et al. (2021a) noted that the sterile coil as a distinguishing feature of

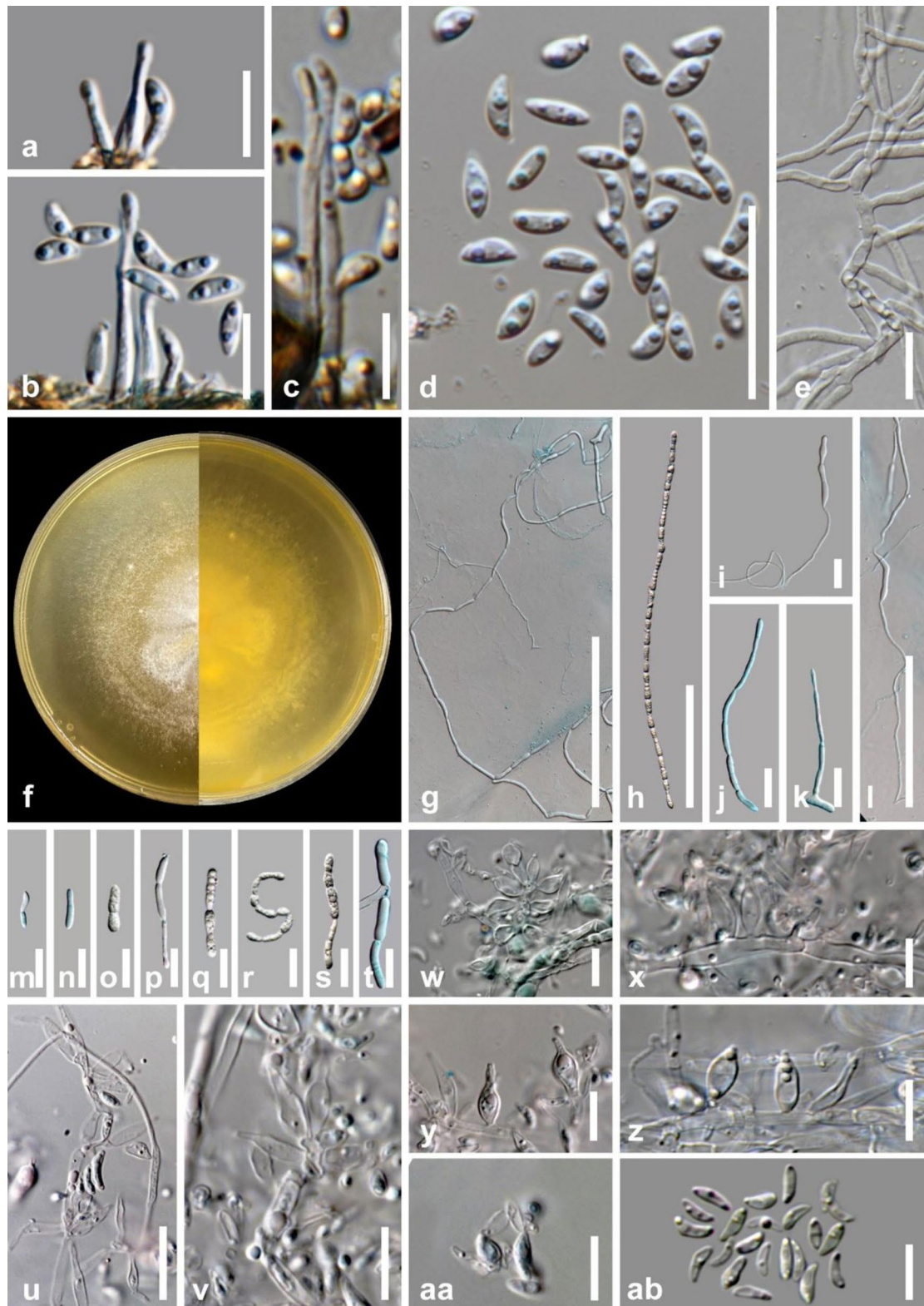




**Fig. 37** Phylogram generated from maximum likelihood analysis based on combined ITS, SSU, LSU, TEF, RPB1 and RPB2 sequence data representing *Cordycipitaceae* in *Hypocreales*. One hundred and four strains are included in the combined analyses which comprised 4633 characters (519 for ITS, 947 for SSU, 774 for LSU, 877 for TEF, 678 for RPB1 and 840 for RPB2) after alignment. *Purpureocillium lilacinum* CBS 431.87 and *Purpureocillium lilacinum* CBS 284.36 in Ophiocordycipitaceae were used as the outgroup taxa. The best scoring RAXML tree with a final likelihood value of  $-44,136.925268$  is presented. Estimated base frequencies were as

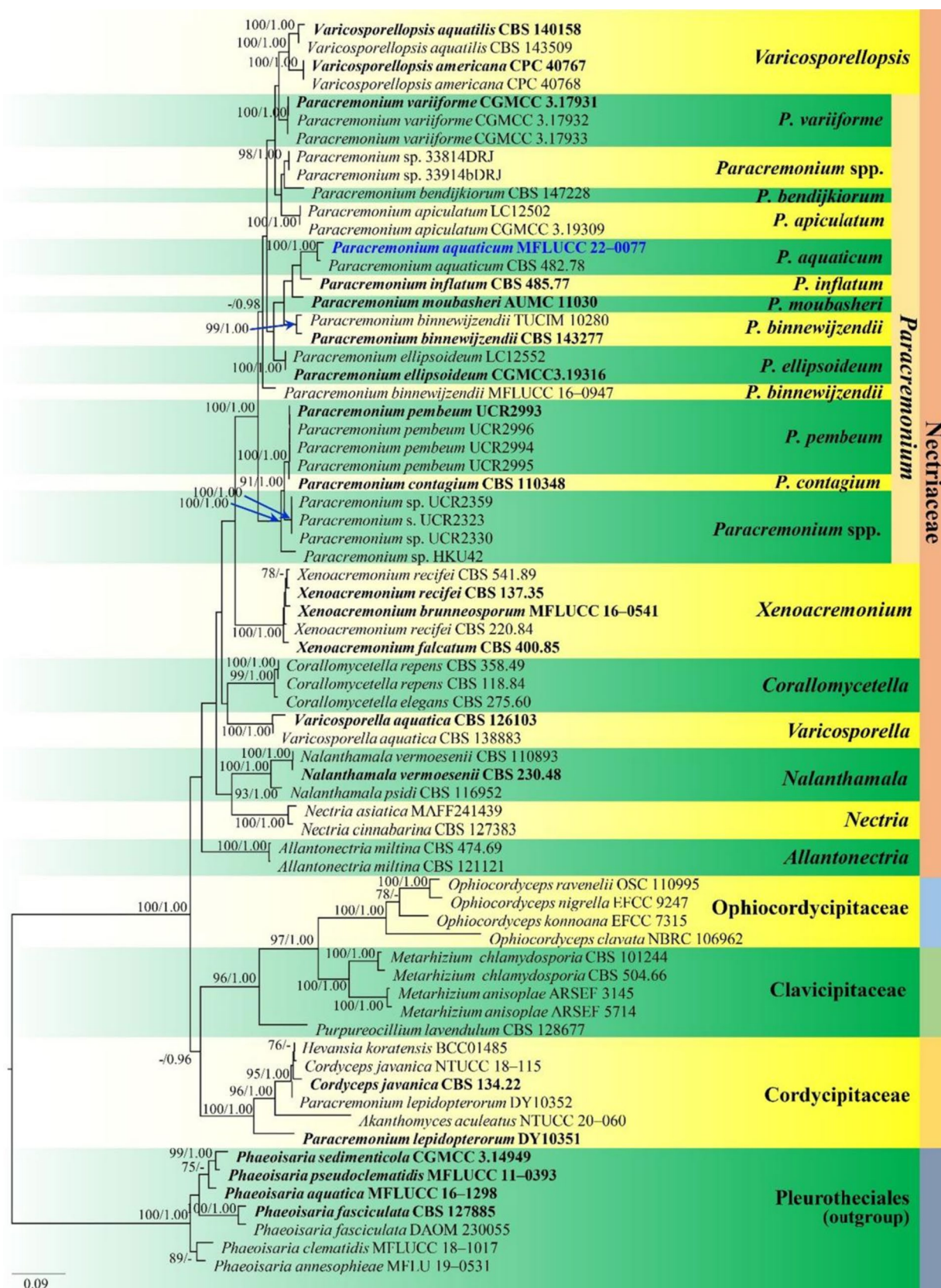
follows: A=0.244444, C=0.269605, G=0.267391, T=0.218561; substitution rates: AC=1.445523, AG=3.809695, AT=0.889234, CG=0.984428, CT=8.185559, GT=1.000000; gamma distribution shape parameter  $\alpha=0.543314$ . Bootstrap support values for ML equal to or greater than 60 are given above the nodes (left side). Bayesian posterior probabilities (BYPP) equal to or greater than 0.7 are given above the nodes (right side). Bold black dots mean support for the two analyses were 100 and 1. Ex-type strains are in bold and newly generated sequences are in blue





**Fig. 38** *Paracremonium aquaticum* (MFLU 22-0120, holotype). **a, c** Conidiophores and conidia. **d** Conidia. **e** Germinated conidium. **f** Colonies on MEA from surface and in reverse. **g–ab** Sporulation on MEA. **g–t** Various moniliform hyphal elements. **m–t** Chla-

mydospores. **w–aa** Conidiophores, conidiogenous cells, and conidia. **ab** Conidia Scale bars: **a–c** = 50 μm, **d, e, i–k, m–t** = 20 μm, **g, h, l** = 100 μm, **w–ab** = 10 μm





**Fig. 39** Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, RPB2, TEF1- $\alpha$ , and TUB2 sequence data representing Nectriaceae (Hypocreales) and closely related families. Seventy-eight strains are included in the combined analyses which comprised 3663 characters (ITS: 499, LSU: 817, RPB2: 1037, TEF1- $\alpha$ : 714, TUB2: 596) after alignment. Seven *Phaeoisaria* species (*P. annesophieae* MFLU 19-0531; *P. aquatica* MFLUCC 16-1298; *P. clematidis* MFLUCC 18-1017; *P. fasciculata* CBS 127885, DAOM 230055; *P. pseudoclematidis* MFLUCC 11-0393; *P. sedimenticola* CGMCC 3.14949) in Pleurotheciaceae (Pleurotheciales) were used as the outgroup taxa. The best scoring RAxML tree with a final likelihood value of -30,486.223016 is presented. The matrix had 1831 distinct alignment patterns, with 38.42% of undetermined characters or gaps. Estimated base frequencies were as follows: A=0.230840, C=0.279253, G=0.276292, T=0.213616; substitution rates: AC=1.237490, AG=2.611546, AT=1.138497, CG=0.936411, CT=6.064431, GT=1.000000; gamma distribution shape parameter  $\alpha$ =0.282744. Bootstrap support values for ML equal to or greater than 75% are given above the nodes (left side). Bayesian posterior probabilities (BYPP) equal to or greater than 0.95 are given above the nodes (right side). Ex-type strains are in bold and newly generated sequences are in blue

*Paracremonium* is no longer significant in characterizing this genus to other acremonium-like genera.

***Paracremonium aquaticum*** M.S. Calabon, E.B.G. Jones & K.D. Hyde, *sp. nov.*

*Index Fungorum number*: IF 559840; *Facesoffungi number*: FoF 05445; *Fig. 38*

*Etymology*: “aquaticum” in reference to the aquatic habitat.

*Holotype*: MFLU 22-0120.

**Sexual morph**: Undetermined. **Asexual morph**: Hyphomycetous. *Saprobic* on submerged decaying wood from a freshwater habitat. *Colonies* on natural substrate effuse, greyish white, velvety. *Mycelium* immersed, composed of hyaline to pale brown, branched, septate hyphae. *Conidiophores* 18–30  $\times$  1.4–2.4  $\mu$ m ( $\bar{x}$ =23.8  $\times$  1.8  $\mu$ m,  $n$ =15), erect, subcylindrical, unbranched, hyaline, smooth. *Conidiogenous cells* terminal, elongate-ampulliform, tapering towards apex, with prominent periclinal thickening and inconspicuous collarette, hyaline, smooth. *Conidia* 4.5–8.5  $\times$  2.0–3.0  $\mu$ m ( $\bar{x}$ =6.3  $\times$  2.5  $\mu$ m,  $n$ =50), formed in heads at apex of conidiogenous cells, aseptate, ellipsoidal to fusiform, acute at both ends, smooth, slightly to strongly curved, with two large guttules. *Chlamydospores* not observed.

*Culture characteristics*: *Conidia* germinating on malt extract agar (MEA) and producing germ tubes at both ends within 24 h. *Colonies* growing on MEA, circular, with flat surface, margin entire, reaching 40–45 mm in 4 weeks at 25 °C, powdery, from above pale yellow to white from edge to center, from white to pale yellow from edge to center. *Hyphae* 2–5.5  $\mu$ m wide, septate, hyaline, mostly smooth, thick-walled, moniliform, abundant. *Conidiophores* erect, simple or mostly branched, septate, bearing whorls of 2–4 conidiogenous cells. *Conidiogenous cells* 8–15  $\times$  1.5–6.0  $\mu$ m ( $\bar{x}$ =11.2  $\times$  3.6  $\mu$ m,

$n$ =20), terminal or lateral, straight, flask-shaped, tapering towards apex, hyaline, with prominent periclinal thickening and inconspicuous collarette, 1.5–2.0  $\mu$ m in diam. *Conidia* 2.5–8.5  $\times$  1.5–3  $\mu$ m ( $\bar{x}$ =5.8  $\times$  2.4  $\mu$ m,  $n$ =50), unicellular, hyaline, ellipsoidal to fusiform, smooth-walled, with slightly apiculate base, slightly curved, guttulate. *Chlamydospores* hyaline, formed intercalary in chains or solitary, smooth, thin-walled, ellipsoidal to mostly cylindrical, guttulate.

*Habitat and distribution*: *Paracremonium aquaticum* was observed from submerged decaying wood in stream, and is currently only found in Thailand.

*Material examined*: Thailand, Chiang Mai Province, Mushroom Research Center, on submerged wood in an artificial lake, 13 September 2019, M.S. Calabon, MRC67 (MFLU 22-0120, **holotype**), ex-type living culture, MFLUCC 22-0077.

*GenBank numbers*: ITS=OP216410, LSU=OP216405, RPB2 = OP251199, TEF1- $\alpha$  = OP251195, TUB2=OP251200.

*Notes*: Multi-locus phylogenetic analysis showed that *Paracremonium aquaticum* MFLUCC22-0077 shared the same subclade with the type species *P. inflatum* CBS 485.77 (Fig. 39). *Paracremonium aquaticum* MFLUCC 22-0077 differs from *P. inflatum* in having flask-shaped conidiogenous cells with larger conidia (2.5–8.5  $\times$  1.5–3  $\mu$ m vs. 5–6  $\times$  1–2  $\mu$ m). In pairwise nucleotide comparisons of *P. aquaticum* with the type strain of *P. inflatum* CBS 124513, there is a nucleotide difference of 2.51% (14/558 bp) in ITS, 4.70% (25/532 bp) in TEF1- $\alpha$ , 8.37% (72/860 bp) in RPB2 and 3.15% (11/349 bp) in TUB2 genes. Another strain of *P. inflatum* CBS 482.78, is a sister taxon to *P. aquaticum* (Fig. 39), but pairwise nucleotide comparison showed 0.89% (5 bp) in ITS (of 564 nucleotides altogether), 1.16% (10 bp) in RPB2 (of 862 nucleotides altogether) and 0.37% (2 bp) in TEF1- $\alpha$  (of 533 nucleotides altogether). Morphological comparison is not possible between *P. inflatum* CBS 482.78 and *P. aquaticum* because the former does not have morphological data. As the strain *P. inflatum* CBS 482.78 forms a sister taxon to *P. aquaticum*, we rename this strain as *P. aquaticum* CBS 482.78. *Paracremonium contagium* also clustered with strains of *P. pembeum* but with inclusions of three more additional loci (calmodulin, histone H3-like and actin) in a separate phylogenetic analysis of *Paracremonium* species (data not shown), *P. contagium* has a distinct lineage basal to *P. pembeum* strains. Phylogenetic analysis also shows that two strains of *P. lepidopterorum* DY10351 and DY10352, a species isolated from an insect pupa in China (Ming et al. 2021), did not cluster within the *Paracremonium* clade, but forms a strongly supported clade with members of *Cordycipitaceae* (Fig. 39). A wider taxon sampling of taxa under *Cordycipitaceae* will help establish the phylogenetic placement of *P. lepidopterorum* within this family. *Paracremonium aquaticum* from freshwater habitats in Thailand is the third



freshwater species of *Paracremonium*, with *P. binnewijzendii* recorded from submerged wood and *P. variiforme* from cave water, both from China (Zhang et al. 2017a; Luo et al. 2019).

**Microascales** Luttr. ex Benny & R.K. Benj.

**Notes:** Benny and Kimbrough (1980) established the order *Microascales* to accommodate three families: *Chadefaudiellaceae*, *Microascaceae* and *Pithoascaceae*. Later, it was expanded to include another four families: *Ceratomyctidaceae*, *Gondwanamycetaceae*, *Halosphaeriaceae* and *Graphiaceae* (Réblová et al. 2011; Maharachchikumbura et al. 2016). The order currently has seven families and 110 genera (Hyde et al. 2020b).

**Halosphaeriaceae** E. Müll. & Arx ex Kohlm.

**Notes:** *Halosphaeriaceae* is the largest family of the order *Microascales* introduced by Müller and von Arx (Kohlmeyer 1972) with *Halosphaeria appendiculata* as the type species. The family currently comprises 167 species in 64 genera (Jones et al. 2017, 2019; Nourel-Din et al. 2022). *Halosphaeriaceae* genera are aquatic with most of them described from marine habitats and usually possess a pseudoparenchymatous centrum that break up into catenophyses, mostly with deliquescing asci and appendaged ascospores.

**Ascoglobospora** Abdel-Wahab, **gen. nov.**

**Index Fungorum number:** IF 559818; **Facesoffungi number:** FoF 12719;

**Etymology:** Named after the globose-shaped asci of the fungus.

**Saprobic** on decaying driftwood. **Sexual morph:** *Ascomata* globose to subglobose, erumpent to superficial, membranous, hyaline to light-brown, ostiolate, papillate, surrounded by septate hyphae. *Neck* hyaline to light-brown in color, cylindrical, periphysate. *Peridium* one-layered, hyaline, forming *textura-angularis*, cell layers consists of elongated, thick-walled, polygonal hyaline cells. *Catenophyses* present. *Asci* eight-spored, subglobose, thin-walled, deliquesce early, without an apical apparatus. *Ascospores* ellipsoidal, with rounded ends, multiseriate, one-septate, not constricted at the septum, hyaline, thick-walled, with bipolar, hamate, apical appendages. *Appendages* extend beyond the median septa, uncoil in water to form long filaments. **Asexual morph:** unknown.

**Type species:** *Ascoglobospora marina* Abdel-Wahab.

**Notes:** Undescribed marine ascomycete with early deliquescing subglobose asci with uncoiling polar appendages to the ascospores was recorded from driftwood collected from a rocky beach at Umikaze Park, Yokohama, Japan and listed as *Aniptodera* sp. (MF966) in Abdel-Wahab (2011). Molecular phylogenetic analyses of the combined SSU and LSU rDNA placed the new taxon with *Aniptosporopsis lignatilis* in all the analyses performed with high statistical support (100 ML/100 MP/100 BYPP, Fig. 40). Other taxa

with polar uncoiling appendages in the clade include: *Aniptodera chesapeakeensis*, *A. aquibella* and *Ascoglobospora marina* cannot be placed in the genus *Aniptosporopsis* because it has an early deliquescing asci that are subglobose in shape, thin-walled and without an apical apparatus. *Aniptosporopsis lignatilis* has clavate asci with a flattened thickened tip, with apical pore, plasmalemma retraction, pedunculate, persistent, with active spore release (Hyde 1992; Jones et al. 2017). A comparison of the 572 nucleotides of the D1/D2 region of the LSU rDNA of *Ascoglobospora marina* and *Aniptosporopsis lignatilis* shows 30 base pair differences (6%), which justifies the erection of a new genus. The pairwise distance of the partial 28S rDNA of genera in the *Halosphaeriaceae* generally ranges between 3 and 9% (Jones et al. 2017).

**Ascoglobospora marina** Abdel-Wahab, **sp. nov.**

**Index Fungorum number:** IF 559819; **Facesoffungi number:** FoF 12718; Fig. 41

**Etymology:** Named after the marine habitat of the fungus.

**Holotype:** CBS H-23855.

**Saprobic** on decaying driftwood. **Sexual morph:** *Hyphae* 2–3 µm in diam, light-brown, septate. *Ascomata* 110–180 µm in diam., globose to subglobose, erumpent to superficial, membranous, hyaline to light-brown, ostiolate, papillate, surrounded by septate hyphae. *Neck* 22–45 µm long, 18–21 µm wide hyaline to light-brown in color, cylindrical, periphysate. *Peridium* 15–24 µm thick, one-layered, hyaline, forming *textura-angularis*, consists of 9–12 cell layers of elongated, thick-walled, polygonal hyaline cells, the first outer layer is hyaline to light-brown in color. *Catenophyses* present. *Asci* 42–48 × 32–37 µm, eight-spored, subglobose, thin-walled, deliquesce early, without an apical apparatus. *Ascospores* 22–30 × 8–9 µm ( $\bar{x}$  = 26.3 × 8.2 µm, n = 50), ellipsoidal, with rounded ends, multiseriate, one-septate, not constricted at the septum, hyaline, thick-walled (0.5–0.7 µm), with bipolar, hamate, apical appendages. *Appendages* 15–20 µm long extend beyond the median septa, uncoil in water to form long filaments. **Asexual morph:** unknown.

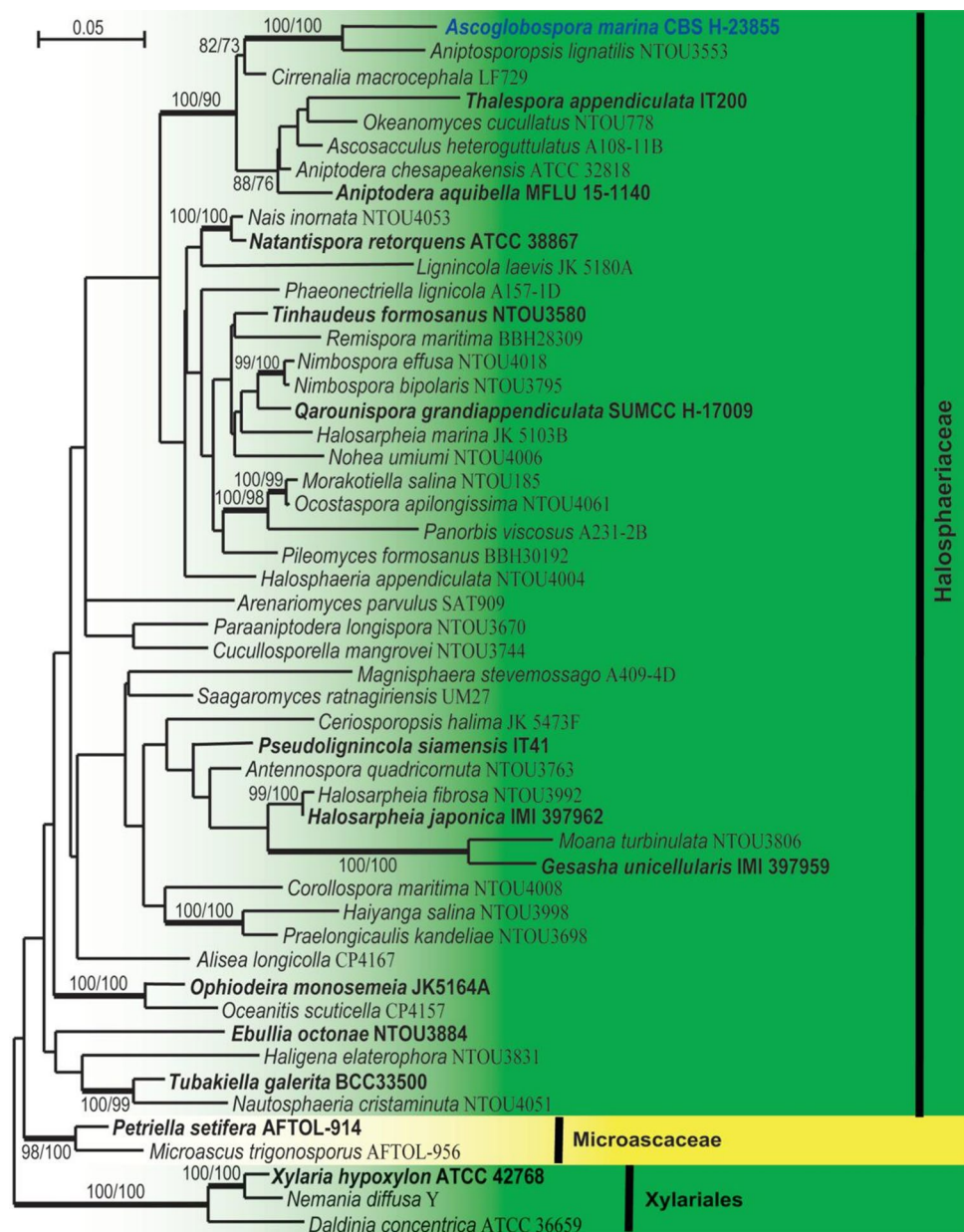
**Culture characteristics:** Single spore isolates of *Ascoglobospora marina* growing on PDA are light brown with tufts of aerial mycelium, reaching a 20–25 mm radius after one month at 25 °C. No sporulation structure was observed.

**Material examined:** Japan, Yokohama, Umikaze Park, 35° 16' 36" N, 139° 41' 02" E, on decaying driftwood, 12 October 2007, M.A. Abdel-Wahab, CBS-H-23855 (**holotype**), ex-type living culture, NBRC 105278.

**GenBank numbers:** CBS-H-23855: ITS = OP150939, SSU = OP151088.

**Notes:** *Ascoglobospora marina* differs from *Aniptosporopsis lignatilis* by having globose, early deliquescing, thin-walled asci without apical apparatus, smaller ascospore dimensions that are ellipsoidal with rounded ends. The latter

**Fig. 40** Phylogenetic relationship of *Ascoglobospora marina* with related genera in Halosphaeriaceae based on the nucleotide sequences of the combined SSU and LSU rDNA. The maximum likelihood (ML) tree was constructed in RAXMLGUI v. 2.0.8 (Silvestro & Michalak 2012) using the GTR + GAMMA substitution model with 1000 bootstrap replicates. The best RAXML tree with a final likelihood value of  $-12,686.5456$  is presented. The maximum parsimonious data set of the combined genes consisted of 51 taxa with 3 representatives of Xylariales used as outgroup. The combined dataset includes 1662 total characters, of which 1004 were constant, 280 parsimony-uninformative and 378 parsimony-informative. The parsimony analyses of the data matrix yielded 4 equally most parsimonious trees with a tree length of 2082 steps (CI=0.4539, RI=0.5734, RC=0.2602). Phylogenetic trees obtained from ML, maximum parsimony (MP) and Bayesian inference posterior probabilities (BYPP) were similar in topology. Bootstrap support on the nodes represents ML and MP  $\geq 70\%$ . Branches with a BYPP of  $\geq 95\%$  are in bold. The new taxon, *Ascoglobospora marina* in blue bold and type strains are in bold



species has clavate, persistent asci, with a thickened plate, plasmalemma retraction, apical pore and active spore dispersal. Ascospores in *A. lignatilis* are fusiform with acute apices and larger than ascospores of *A. marina* (Hyde 1992; Jones et al. 2017).

#### *Pleurotheciales* Réblová & Seifert.

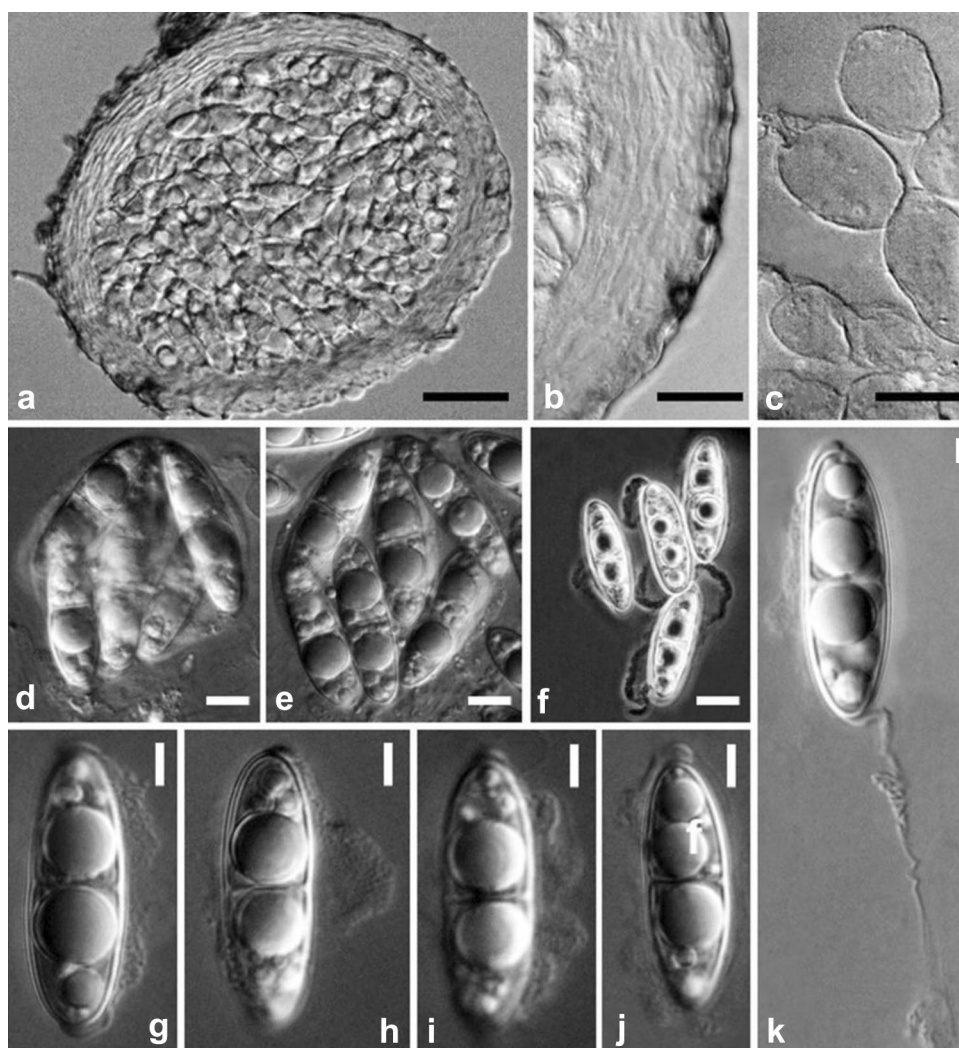
**Notes:** *Pleurotheciales* was established by Réblová et al. (2016) based on the type family *Pleurotheciaceae*. Hongsan et al. (2017) reported that *Pleurotheciales* clustered with *Conioscyphales*, *Fuscosporellales* and *Savoryellales* in a monophyletic clade within Sordariomycetes. Hence, they transferred *Pleurotheciales* to a newly introduced subclass *Savoryellomycetidae* based on molecular evidence and

divergence time (Hongsan et al. 2017). This treatment was confirmed and acknowledged by Dayarathne et al. (2019) and Hyde et al. (2020a).

#### *Pleurotheciaceae* Réblová & Seifert.

**Notes:** The family *Pleurotheciaceae* was established by Réblová et al. (2016) with *Pleurothecium* as the type genus. Currently, there are 13 genera in this family, viz. *Adelosphaeria*, *Anapleurothecium*, *Coleodictyospora*, *Dematiopyriforma*, *Helicoascotaiwania*, *Melanotrigonum*, *Neomonodictys*, *Phaeoisaria*, *Phragmocephala*, *Pleurotheciella*, *Pleurothecium*, *Saprodesmium* and *Sterigmatobotrys* (Bao et al. 2022). It should be noted that some species of *Pleurotheciaceae* were

**Fig. 41** *Ascoglobospora marina* (CBS H-23855, holotype). **a** Vertical section of ascoma. **b** Magnified part of the peridium. **c** Catenophyses. **d, e** Asci at different stages of maturity. **f–k** Various shaped ascospores with various stages of appendages uncoiling. Scale bars: **a** = 25  $\mu$ m, **b–f** = 10  $\mu$ m, **g–k** = 5  $\mu$ m



identified as opportunistic human pathogens (Réblová et al. 2012, 2016; Luo et al. 2019; Hyde et al. 2020a).

#### *Pleurothecium* Höhn.

**Notes:** *Pleurothecium* was introduced by Höhnelt (1919) with *P. recurvatum* ( $\equiv$  *Acrothecium recurvatum*) as the type species. *Pleurothecium* is a holomorphic genus, and there are currently 12 species, of which only two species, viz. *P. recurvatum* and *P. semifecundum*, have sexual morphs (Réblová et al. 2012). The asexual morph of *Pleurothecium* is characterized by having distinct brown conidiophores, polyblastic, sympodially denticulate conidiogenous cells, and solitary, unicellular or septate, cylindrical, ellipsoidal, fusiform or clavate conidia (Réblová et al. 2012; Luo et al. 2019). In addition, most species of *Pleurothecium* are reported as saprobes from freshwater or terrestrial habitats in Australia, Brunei, China and Seychelles (Tsui et al. 2001; Luo et al. 2019; Shen et al. 2022).

#### *Pleurothecium aseptatum* J. Ma & Y.Z. Lu, *sp. nov.*

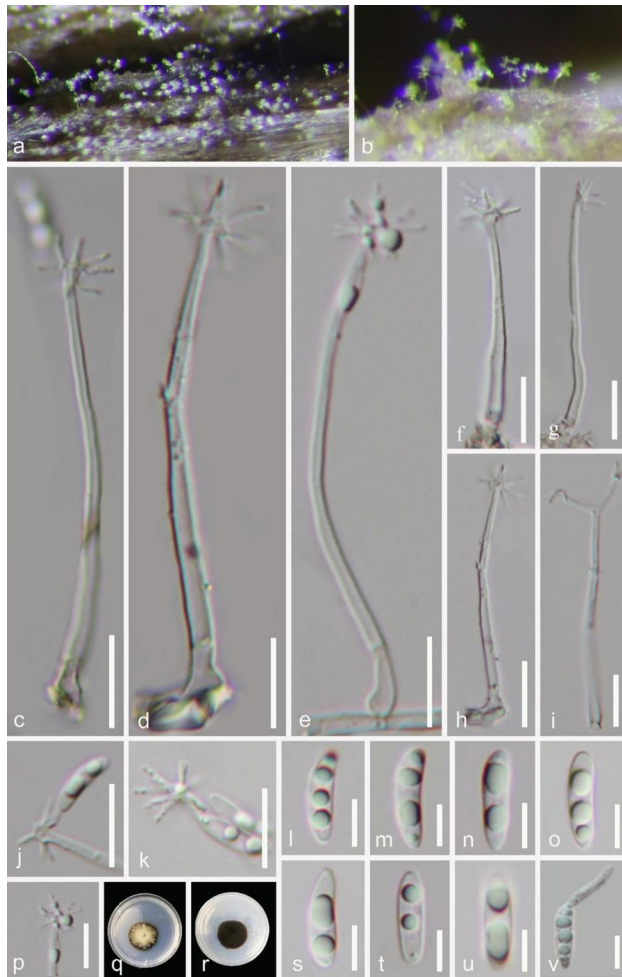
**Index Fungorum number:** IF 900172, **Facesoffungi number:** FoF 13907; **Fig. 42**

**Etymology:** referring to the aseptate conidia.

**Holotype:** GZAAS 22–2019.

**Saprobic** on submerged decaying wood. **Sexual morph:** undetermined. **Asexual morph:** **Colonies** on the substratum superficial, effuse, gregarious, white. **Mycelium** composed of partly immersed, partly superficial, hyaline, septate, branched hyphae, with a little of glistening conidia. **Conidiophores** macronematous, mononematous, erect, cylindrical, mostly unbranched, a few branched, 46–59  $\mu$ m long ( $\bar{x}$  = 53  $\mu$ m,  $n$  = 15), 1.5–2.5  $\mu$ m wide ( $\bar{x}$  = 2  $\mu$ m,  $n$  = 15), tapering to 0.8–1.3  $\mu$ m wide near apex, 0–1-septate, sometimes reduced to conidiogenous cells, hyaline, smooth-walled. **Conidiogenous cells** polyblastic, integrated, terminal, sympodial, cylindrical, 41–53  $\mu$ m, denticulate, hyaline; denticles cylindrical, long, narrow, 3–5  $\times$  0.6–0.8  $\mu$ m ( $\bar{x}$  = 4  $\times$  0.7  $\mu$ m,  $n$  = 20). **Conidia** solitary, acrogenous, subcylindrical, slightly curved, 8.5–10  $\mu$ m  $\times$  2–3  $\mu$ m ( $\bar{x}$  = 9.5  $\times$  2.5  $\mu$ m,  $n$  = 30),





**Fig. 42** *Pleurothecium aseptatum* (GZAAS 22–2019, **holotype**). **a, b** Colonies on dead wood. **c–i** Conidiophores and conidiogenous cells. **j, k, p** Conidiogenous cells bearing conidia. **l–o, s–u** Conidia. **v** Germinated conidia. **q, r** Colony on PDA from above and below. Scale bars: **c–k, p, v** = 10  $\mu$ m, **l–o, s–u** = 5  $\mu$ m

rounded at the apex, obtuse and tapering towards base, aseptate, with 2–4 large guttules, hyaline, smooth-walled.

**Culture characteristics:** Conidia germinating on water agar and germ tubes produced from conidia within 8 h. Colonies growing on PDA, circular, with flat surface, edge entire, reaching 45 mm in 30 days at 25 °C, pale brown to brown.

**Material examined:** China, Guizhou Province, Qian-dongnan Miao and Dong Autonomous Prefecture, Tianzhu County, on decaying wood in a freshwater stream, 16 January 2021, Jian Ma, TZX8 (GZAAS 22–2019, **holotype**), ex-type living culture, GZCC 22–2019.

**GenBank numbers:** LSU = OQ002372, ITS = OQ002375.

**Notes:** Phylogenetically, *Pleurothecium aseptatum* is clustered within *Pleurothecium* and formed a basal clade to *P. recurvatum* and *P. semifecundum* (Fig. 43). Morphologically, *P. aseptatum* differs from *P. recurvatum* and *P.*

*Semifecundum* by having hyaline conidiophores and aseptate conidia, while *P. recurvatum* and *P. semifecundum* having 3-septate conidia and brown conidiophores (Réblová et al. 2012; Luo et al. 2019). Furthermore, the denticles of conidiogenous cells in *P. aseptatum* are rather long, while *P. recurvatum* and *P. semifecundum* having tiny denticles (Réblová et al. 2012; Luo et al. 2019).

## Sordariomycetes, genus *incertae sedis*

### *Pleurotheciella* Réblová, Seifert & J. Fourn.

**Notes:** *Pleurotheciella* was introduced by Réblová et al. (2012) with *P. rivularia* as the type species. The asexual morph of *Pleurotheciella* is characterized by having hyaline or brown, mononematous or synnematus conidiophores, integrated, polyblastic, sympodially denticulate conidiogenous cells, and hyaline, unicellular or septate, ellipsoidal, obovoid, clavate, lunate or subballantoid conidia (Réblová et al. 2012; Luo et al. 2019). Currently, 15 species are included in the genus, with 14 species from freshwater habitats and only one species from dead branches of *Malus* (Luo et al. 2019; Shi et al. 2021).

### *Pleurotheciella hyalospora* J. Ma & Y.Z. Lu, *sp. nov.*

**Index Fungorum number:** IF 900171; **Facesoffungi number:** FoF 13906; **Fig. 44**

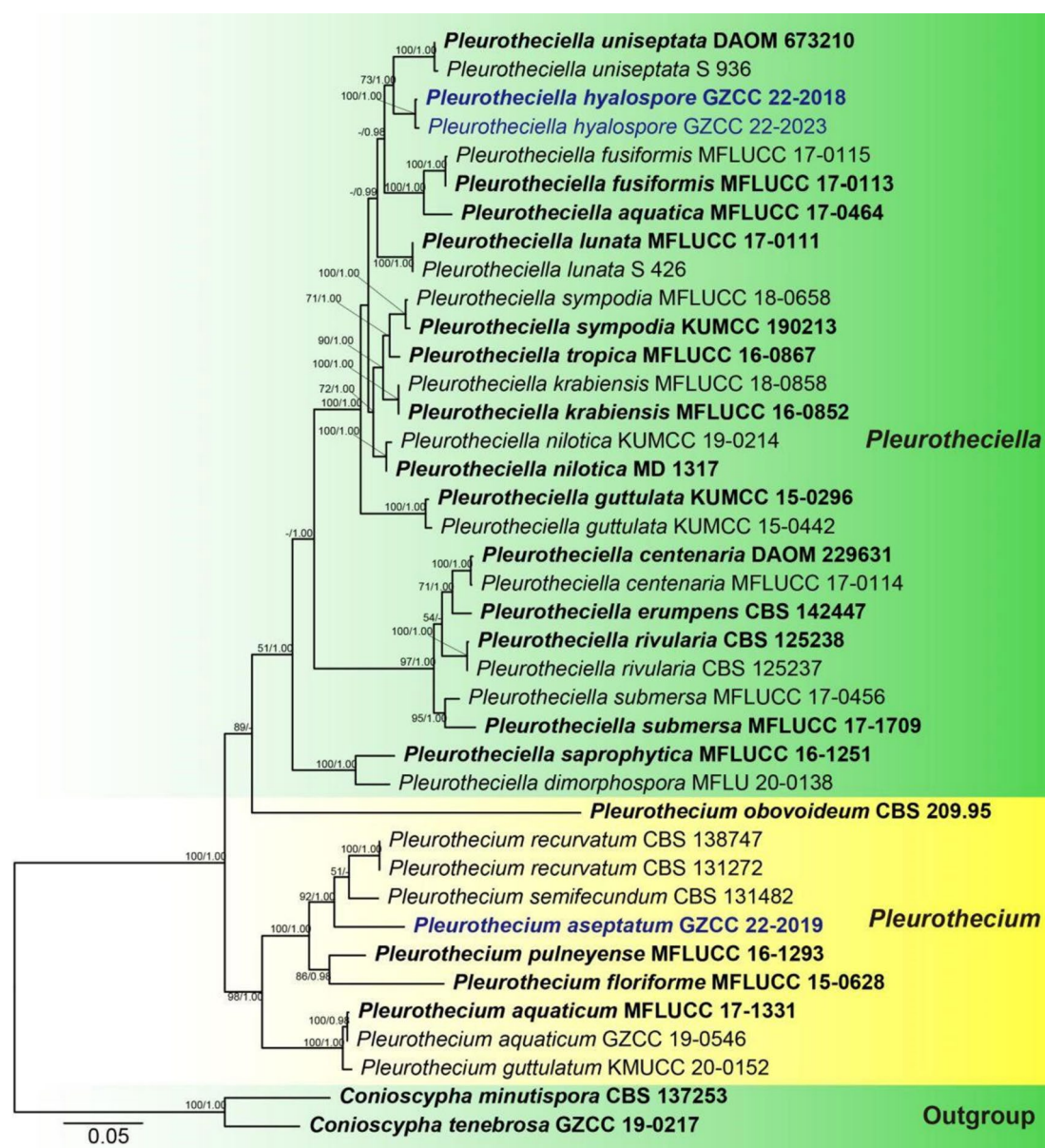
**Etymology:** “*hyalospora*” referring to the hyaline conidia.

**Holotype:** GZAAS 22–2018.

**Saprobic** on decaying wood. **Sexual morph:** undetermined. Asexual morph: **Colonies** on the substratum superficial, effuse, gregarious, white. **Mycelium** composed of partly immersed, partly superficial, hyaline to pale brown, septate, branched hyphae, with a little of glistening conidia. **Conidiophores** macronematous, mononematous, unbranched, straight or flexuous, cylindrical, 73–100  $\times$  3.5–5  $\mu$ m ( $\bar{x}$  = 88  $\times$  4  $\mu$ m,  $n$  = 20), dark brown at the base, hyaline to pale brown toward the apex, smooth-walled. **Conidiogenous cells** polyblastic, terminal, cylindrical, 17–30  $\times$  3–4  $\mu$ m ( $\bar{x}$  = 25  $\times$  3.5  $\mu$ m,  $n$  = 20), with denticles, pale brown near base, hyaline towards apex, smooth-walled. **Conidia** solitary, acropleurogenous, fusoid or clavate, slightly curved, rounded at the apex, obtuse and tapering towards base, 11–20  $\times$  3–5.5  $\mu$ m ( $\bar{x}$  = 16  $\times$  4.5  $\mu$ m,  $n$  = 30), hyaline, 1-septate, often with 1–3 guttules in each cell, smooth-walled.

**Culture characteristics:** Conidia germinating on water agar and germ tubes produced from conidia within 8 h. Colonies growing on PDA, circular, with flat surface and filiform margin, reaching 35 mm in 30 days at 25 °C, brown in center, pale brown at the entire margin.

**Material examined:** China, Guizhou Province, Guiyang City, Xiaochehe Park, on decaying wood in a forest, 29 March 2020, Jian Ma, XCH20 (GZAAS 22–2018,



**Fig. 43** Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, SSU and *rpb2* sequence data representing the species of pleurotheciaceae. Thirty-nine taxa were included in the combined analyses, which comprised 3393 characters (ITS: 621, LSU: 870, SSU=986, *rpb2*=916) after alignment. Boot-

strap support values for ML equal to or greater than 50% and BYPP equal to or greater than 0.95 are given above the nodes. *Conioscypha minutispora* (CBS 137253) and *C. tenebrosa* (GZCC 19-0217) were used as the outgroup taxa. The newly-generated strain is shown in blue and bold. Ex-type strains are indicated by black and bold

**holotype**), ex-type living culture, GZCC 22–2018; Guizhou Province, Longli County, on decaying wood submerged in a freshwater stream, 3 December 2020, Jian Ma, LLSZ2 (GZAAS 22–2023), living culture, GZCC 22–2023.

**GenBank numbers:** GZCC 22–2018: LSU = OQ002371, ITS = OQ002374, SSU = OQ002377, RPB2 = OP999221; GZCC 22–2023: LSU = OQ002370, ITS = OQ002373, SSU = OQ002376, RPB2 = OP999220.

**Notes:** The proposed new species viz. *Pleurotheciella hyalospora* is morphologically similar to *P. uniseptata*

in conidiophores and conidia, but it can be recognized from *P. uniseptata* by having smaller conidiophores ( $73\text{--}100 \times 3.5\text{--}5\text{ }\mu\text{m}$  vs.  $100\text{--}150 \times 4.5\text{--}5\text{ }\mu\text{m}$ ). Besides, the conidia of *P. hyalospora* are slightly curved, while *P. uniseptata* is characterized by straight conidia (Réblová et al. 2016). Phylogenetically, *P. hyalospora* forms a sister clade to *P. uniseptata* and the phylogenetic tree showed that they are distinct species (Fig. 43).



**Fig. 44** *Pleurotheciella hyalospora* (GZAAS 22–2018, **holotype**). **a, b** Colonies on decaying wood. **c, d** Conidiophores. **e–h** conidiogenous cells with attached conidia. **i** Germinated conidia. **j–m** Conidia. **n, o** Colony on PDA from above and below. Scale bars: **c–m** = 10  $\mu$ m



**Basidiomycota** R.T. Moore.

*Notes:* For the latest updated account of Basidiomycota see Zhao et al. (2017).

**Agaricomycetes** Doweld.

*Notes:* For the latest treatments and updated accounts of Agaricomycetes see Hibbett et al. (2014) and Zhao et al. (2017).

**Agaricales** Underw.

*Notes:* *Agaricales* is the largest order of Agaricomycetes with 17,291 species in 508 genera (He et al. 2019). There is no morphological synapomorphy that unites this order. Although they are dominated by pileate-stipitate forms with lamellate hymenophores, this order also includes many other forms such as false truffles, puffballs, bird-nest fungi, resupinate, coral-loid, cyphelloid, and pileate with poroid hymenophores. On

the other hand, the pileate-stipitate traditional morphology is not exclusive to *Agaricales* (Hibbett et al. 2014).

**Agaricaceae** Chevall.

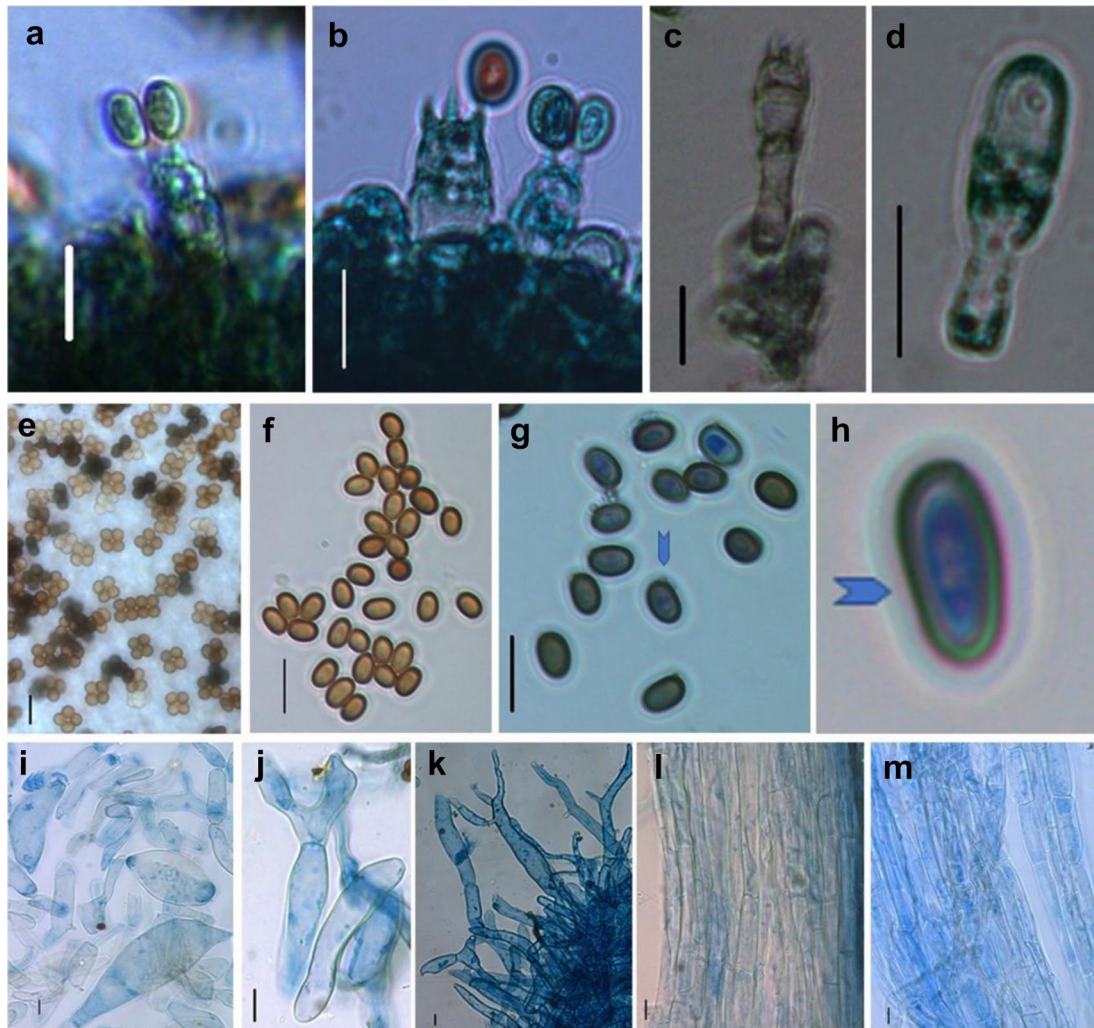
*Notes:* The family *Agaricaceae* was established by Chevallier (1826). It is named after the type genus *Agaricus*, originally confined by Linnaeus (1753). For the latest treatments and updated accounts of *Agaricaceae* see Zhao et al. (2016b), Zhou et al. (2016a) and Hyde et al. (2017).

**Agaricus** L.

*Notes:* The genus *Agaricus* was established by Linnaeus (1753). *Agaricus* is characterized by having a fleshy cap or pileus, from the underside of which grow a number of radiating plates or gills, on which are produced the naked chocolate-brown spores. Members of *Agaricus* have a stipe, which elevates it above the object on which the mushroom grows,

**Fig. 45** *Agaricus agharkarii* (AMH10341, **holotype**). **a** Basidiomes habitat. **b, c** Surface view of growing basidiomes. **d–f** Gill view with attached stipe and disintegrated annulus. **f** A complete gill view. **h** Spore print





**Fig. 46** *Agaricus agharkarii* (AMH10341, **holotype**). **a** A basidium with attached basidiospores on sterigmata. **b** Basidia with basidiospores and cheilocystidia on lateral side. **c** A basidium with sterigmata. **d** A clavate cheilocystidium. **e** Numerous basidiospores arranged in tetrad manner (photographs taken from surface of gill).

**f, g** Numerous basidiospores (arrow showing slightly tapered basal end). **h** An elongated basidiospore with thickened wall (showing arrow). **i–k** Pileocystidia (pileal tissues). **l–m** Stipitipellis (stipe tissues arranged in parallel manner). Scale bars: **a–m** = 10 µm

or substrate, and a partial veil, which protects the developing gills and later forms a ring or annulus on the stalk. The latest treatments and updated accounts of *Agaricus* follow Karunarathna et al. (2016), Zhao et al. (2016b) and Zhou et al. (2016a).

***Agaricus agharkarii*** P.N. Singh, S.K. Singh, S. Rana & A.C. Lagashetti, *sp. nov.*

*Index Fungorum* number: IF 559727; *Facesoffungi* number: FoF11794; Figs. 45, 46, 47

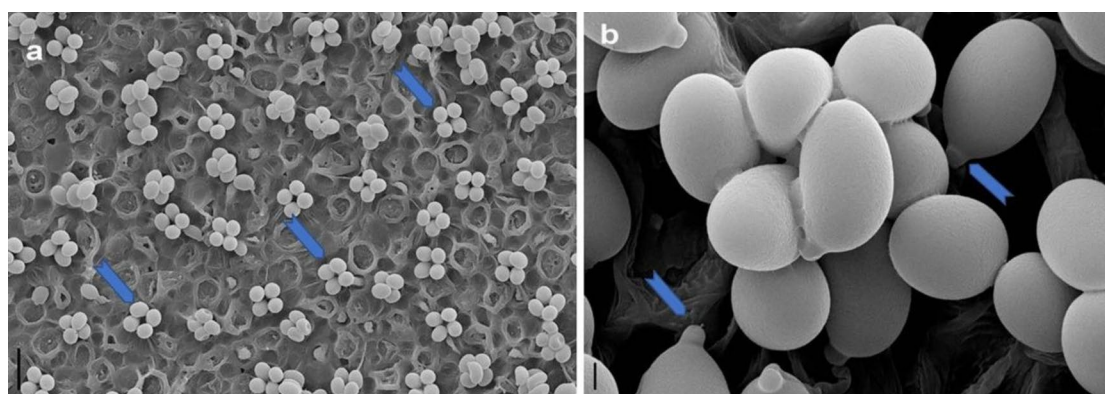
*Etymology*: species named ‘*agharkarii*’ in the surname of Professor Shankar Puroshattam Agharkar, founder Director of Agharkar Research Institute.

*Holotype*: AMH 10341.

*Colour code follows*: Methuen Handbook of Colour (Kornerup and Wanscher 1978).

*Basidiomes* solitary or in groups of 2–4, variable in size, agaricoid, stipitate. *Pileus* 80–110 mm in diam, broadly umbonate, broadly ovate when young, 8 mm thick at the disk, fleshy, convex to plano-convex, when mature the pileus becomes upwards, surface dry, squamulose, color rufescent to greyish brown (8F3) when young, paraboloid when young, surface dry with greyish brown spots (8F3) when mature, margin entire, nonappendiculate. *Lamellae* free, regular, become dark brown with age (6F8); *lamellulae* present in 1–3 tiers, 8–10 mm broad, wavy, greyish brown (8F3). *Stipe* 70–96 × 20–22 mm, compact, attenuated towards length, base slightly bulbous with white (1A1) mycelial threads, fragile, greyish brown (8F3), surface dry,





**Fig. 47** SEM images of *Agaricus agharkarii* (AMH10341, **holotype**). **a** tetrad basidiospores (showing arrow). **b** Basidiospores in higher magnifications (arrow showing protruberant hilum). Scale bars: **a** = 10 µm, **b** = 1 µm

after cutting or touching with finger becomes dark brown (7F5). *Volva* absent. *Annulus* present, drooping or skirt like, membranous covering around the stipe, with double edged margin, white (1A1) to light brown (5D8). *Volva* absent. *Spore print* dark brown (7F5). *Odour* mushroomy. *Taste* not recorded. *Context* thick and fleshy, spongy, whitish (1A1) in pileus and pithy in stipe. *Macrochemical reactions*; negative in Schäffer's reaction, no reaction with Ammonia and Potassium hydroxide.

*Basidia* 21.80–36.10 × 3.5–9.55 µm, clavate to narrowly cylindrical, subhyaline to light olivaceous, pigmented, smooth walled, variable in size, frequently tetrasporic. *Sterigmata* straight to curved sometimes resembles like an incisor canine, hyaline smooth walled, up to 3.52 × 1.90 µm. *Basidiospores* 5.15–9.19 × 3.92–5.67 µm ( $\bar{x}$  = 6.55 × 4.70 µm,  $n$  = 30),  $Q_m$  = 1.43,  $Q$  = 1.11–1.94, oval, ellipsoid to oblong, sometimes slightly tapered towards base with one or two guttulate, dark olivaceous brown, smooth walled, wall thickened and darkened (up to 0.85 µm thick). *Hilum* protruberant. *Lamellar surface* fertile, made-up of basidia, cystidia, and marginal cell. *Cheilocystidia* pedicellate, ampulliform to narrowly clavate, apex rounded, non-fertile, base narrow, subhyaline to light olivaceous, smooth walled, wall thickened and darkened, 19.75–42.47 × 7–8.12 µm. *Pileocystidia* hyphoid, fusoid, unbranched to branched, smooth walled, hyaline, up to 45.5–230 × 13–35 µm. *Subhymenium* 22.5–25 µm thick, composed of globose to oval cells, 6.9–18.65 × 6.55–15.25 µm, light olivaceous, *Hymenial trama* hyphoid, upto 113.35 µm wide, composed of parallel to interwoven thick and thin hyphae, subhyaline to light olivaceous, with distant septation in hyphae, branched, variable in dimensions. *Pileipellis* (pileus trama) dark brown, interwoven, hyphae septate, up to 34.80 µm in diam, branched, pigmented, light olivaceous. *Clamp connections* absent. *Stipitipellis* hyphal, arranged in parallel bundles of hyphae, irregularly septate, subhyaline to light olivaceous, cells irregular, variable in dimensions, 20.38–26.75 µm wide.

*Materials examined*: INDIA, Maharashtra, Pune District, on garden soil, 9 July 2021, P.N. Singh, AMH10341 (**holotype**).

*Host and habitat*: Solitary or in groups, free living in botanical garden under *Albizia* tree.

*GenBank numbers*: ITS = MZ198899, LSU = MZ198900.

*Notes*: In the present taxon, the basidiomes are medium to large sized, squamulose with off-white linings with greyish brown pileus that have negative reaction with Schäffer's test. There is no reaction with KOH and Ammonia on the flesh of fruiting body. The stipe base is white with swollen base and mild mushroomy odour. The pileipellis hyphae are hyphoid and variable in shape and size (10.5–34.80 µm in diam). The presence of cheilocystidia in the present taxon is a key feature of the *A. sect. Flocculenti* under the *A. subg. Pseudochitonina* (Zhao et al. 2011; He et al. 2018). Morphologically, new taxon, *Agaricus agharkarii* is different from its related taxa in having a larger convex pileus with broader lamellae as compared to *A. erectosquamosus* and *A. pallidobrunneus* (Zhao et al. 2016b). The length of cheilocystidia in *A. agharkarii* is comparatively larger than in *A. erectosquamosus* and *A. pallidobrunneus*. In addition to this, the dimension of basidiomes and basidiospores is apparently larger compared to *A. erectosquamosus* and *A. pallidobrunneus* (Table 1).

ITS and LSU sequence comparison has revealed that the sequences of the new species *Agaricus agharkarii* differ at 33 positions in ITS and 10 positions in LSU. Beside this, one deletion and five insertions (four of 1 bp and one of 3 bp) were observed in ITS sequence of the present taxon. The position of the present taxon within *Agaricus* sect. *Flocculenti* was further confirmed by molecular phylogeny based on combined ITS and LSU rDNA data. Phylogenetic analysis based on combined ITS and LSU sequence data indicates that *Agaricus agharkarii* (AMH 10341) is a new species of *A. sec. Flocculenti*, which is different from the other known species of *A. sec. Flocculenti*. The present taxon forms a



**Table 1** Morphotaxonomic comparative features of *Agaricus agharkarii* sp. nov. with allied taxa

Taxon name	Pileus	Lamellae	Stipe	Basidia	Basidiospores	Cheilocystidia
<i>Agaricus agharkarii</i> sp. nov.	80–110 mm in diam, convex	Free, 13 mm broad	70–96 × 20–22 mm, attenuated towards length, compact	21.80–36.10 × 3.5–9.55 µm, clavate to narrowly cylindrical, subhyaline to light olivaceous	5.15–9.19 × 4.22–5.65 µm, dark olivaceous brown, oval, ellipsoid to oblong, thick-walled	19.75–42.47 × 7–8.12 µm, ampulliform to narrowly clavate, subhyaline to light olivaceous
<i>Agaricus erectosquamosus</i> (Zhao et al. 2016b)	40–50 mm in diam, 5 mm thick at the disk, convex to plane	Free, 5 mm broad	45 × 5 mm, cylindrical to slightly clavate, hollow	15–22 × 6.5–7.5 µm, clavate to broadly clavate, hyaline	6.6–7.6 × 4.1–5 µm, brown, ellipsoid to oblong, thick-walled	18–30 × 9–16.5 µm, globose to pyriform or sphaeropedunculate, hyaline
<i>Agaricus pallidobrunneus</i> (Zhao et al. 2016b)	105 mm in diam, 7 mm thick at the disk, convex to plane	Free, 11 mm broad	110 × 13–20 mm, cylindrical and widening towards base, slightly clavate, hollow	16–3 × 6–9 µm, clavate to broadly clavate, hyaline	6.1–7.8 × 3.5–5.2 µm, brown, ellipsoid to oblong, thick-walled	17–35 × 11–21 µm, pyriform, globose to ellipsoid, hyaline

distinct clade from other species of the *A. sec. Flocculenti* (*A. erectosquamosus* and *A. pallidobrunneus*) with a moderately supported ultrafast bootstrap value of 85% (Fig. 48).

On megablast analysis, ITS sequence of *Agaricus agharkarii* showed 95% (654/691) identity and 8 gaps (1%) with *Agaricus erectosquamosus* SDBR-NK0080 and *Agaricus erectosquamosus* SDBR-CJ0032, 95% (653/690) identity and 8 gaps (1%) with *Agaricus pallidobrunneus* SDBR-NK0368, 94% (642/684) identity and 6 gaps (0%) with *Agaricus sparsisquamosus* PU320, 94% (641/684) identity and 6 gaps (0%) with *Agaricus sparsisquamosus* PU256, 93% (640/685) identity and 8 gaps (1%) with *Agaricus sparsisquamosus* PU320, and 94% (641/684) identity and 9 gaps (1%) with *Agaricus sparsisquamosus* PU320.

The distinct morphology compared to other species of *A. sec. Flocculenti* (*A. erectosquamosus* and *A. pallidobrunneus*), as well as the phylogenetic analysis, clearly establishes *Agaricus agharkarii* as a novel species.

***Agaricus allostipitatus*** E. Tarafder, A.K. Dutta & K. Acharya, *sp. nov.*

*Mycobank number*: MB 843678; *Facesoffungi number*: FoF 10832; Figs. 49, 50

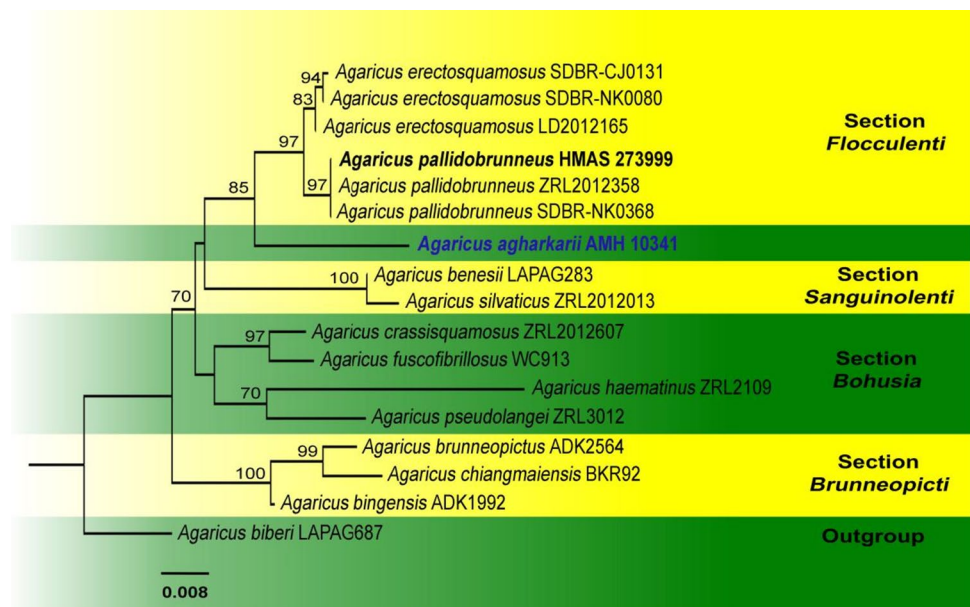
*Etymology*: The epithet “*allostipitatus*” refers to an entirely white coloured stipe.

*Holotype*: CAL 1871.

*Pileus* 12–60 mm in diam., convex when young, becoming broadly convex to plano-convex on maturity, overall white (1A1), rarely with slight light brown (6D5-6) patches especially at the center, smooth, margin incurved, associated with traces of partial veilar remnants, often rimose; context ca. 4 mm thick at the centre, gradually thinner towards margin (up to 1 mm), white (1A1). *Lamellae* 4–6 mm broad, free, crowded with two series of lamellulae, light pinkish (14A2) when young, becoming brown (7F4) to dark chocolate brown (6F4) on maturity, edge even, concolorous. *Stipe* 25–70 × 5–7 mm, central, cylindrical with slightly broader at base (up to 10 mm), rarely tapered toward base, slightly curved, smooth, sometimes slightly fibrillose at the apex, entirely white, basal portion turning brownish orange (6C4–5) on bruising; context narrowly hollow, white. *Annulus* supramedian, entire, simple, persistent, rarely fragile and remains at traces on the stipe surface, upper side brown, smooth, lower side white, fibrillose. *Odour* mushroomy.

*Basidiospores* (6.5–)7.4–8.5(–9.7) × (4.4–)5.3–5.9(–6.5) µm ( $X_{mr} = 7.9–8.2 \times 5.4–5.8$  µm,  $X_{mm} = 8.1 \pm 0.9 \times 5.6 \pm 0.5$  µm,  $Q_{mr} = 1.41–1.45$ ,  $Q_{mm} = 1.43 \pm 0.1$ ,  $n = 60$  spores,  $s = 2$  specimens), ellipsoid, brown to dark brown, smooth, thick-walled. *Basidia* 22–32 × 8–10 µm, clavate, hyaline, thin-walled, 4-spored; sterigmata 1–3 µm long, hyaline. *Basidioles* 14–25 × 5–7.5 µm, clavate, hyaline, thin-walled. *Cheilocystidia* 11–21 × 6–10 µm, pyriform to ovoid, smooth, thin-walled. *Pleurocystidia* absent. *Pileipellis* a cutis, composed of hyphae

**Fig. 48** Phylogenetic tree of *Agaricus agharkarii* (AMH 10341) by Maximum-Likelihood method based on combined sequence data of ITS and LSU. *Agaricus biberi* LAPAG687 was used as an outgroup. The analysis involved 17 nucleotide sequences. Evolutionary analyses were conducted in IQ-TREE multicore version 1.6.11 (Nguyen et al. 2015) by the Maximum-Likelihood method using the best suitable model (TPM3u + F + R2 model). One-thousand bootstrap replicates were analysed to get ultrafast bootstrap values, and the values above 50% were represented on nodes in the tree



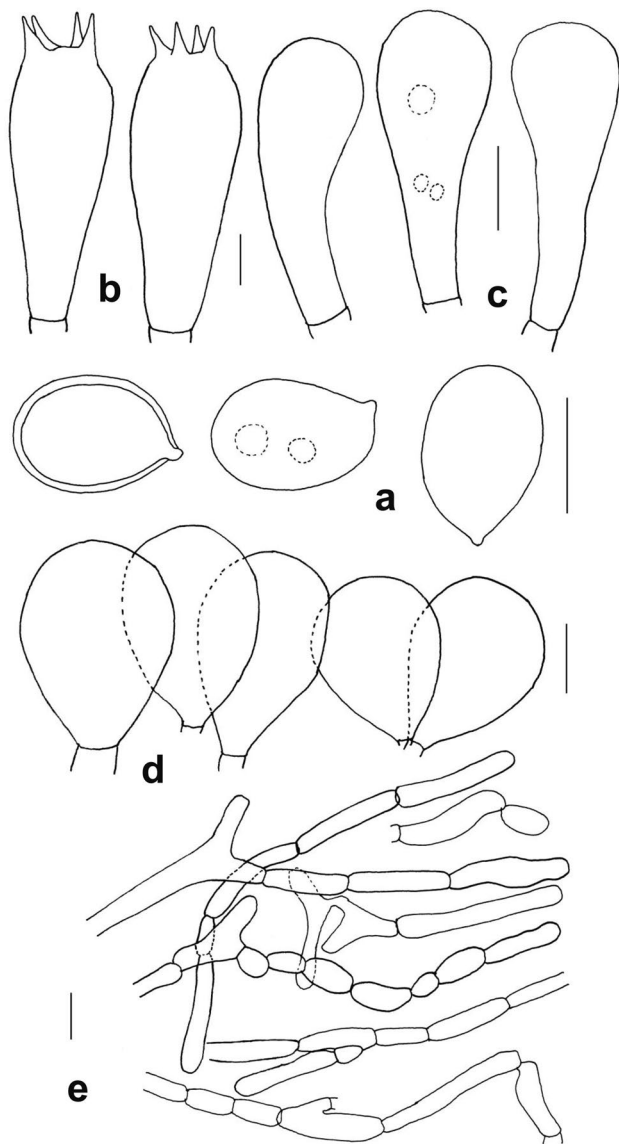
**Fig. 49** *Agaricus albostipitatus* (CAL 1871, holotype). **a** Immature stage of the basidiomes showing stipe context and lamellae colouration. **b** Basidiomes showing pileus surface feature. **c** Basidiomes

showing developing stages and gradual maturity of the lamellae. **d** Mature basidiomes showing lamellae colouration and annulus features. Scale bars: **a–d** = 20 mm

measuring 5–7  $\mu$ m broad, cylindrical, smooth constricted at the septa, branched, hyaline, thin-walled. *Stipitipellis* hyphae 5–7  $\mu$ m broad, unbranched, cylindrical, hyaline, thin-walled. *Annulus* hyphae 5–7  $\mu$ m broad, hyaline, thin-walled.

**Chemistry:** KOH reaction negative on pileus and stipe surface. Schaffer's reaction negative on pileus surface.





**Fig. 50** *Agaricus allostipitatus* (CAL 1871, **holotype**). **a** Basidiospores. **b** Basidia. **c** Basidioles. **d** Cheilocystidia. **e** Pileipellis hyphae. Scale bars: **a–d** = 5  $\mu$ m, **e** = 10  $\mu$ m

**Habitat and distribution:** The new species grows on humus mixed soil in a grassy field, and is currently only found in India.

**Material examined:** India, West Bengal, Nadia district, Village Chandirampur, 22°59'54.48" N, 88°31'43.3" E, 9.0 m alt., on humus mixed soil, 1 May 2020, E. Tarafder, ENTJ 01/2020 (CAL 1871, **holotype**); West Bengal, Village Chandirampur, 22°59'54.5"N, 88°31'42.92"E, 9.0 m alt., on humus mixed soil, 9 May 2020, E. Tarafder, CUH AM688.

**GenBank numbers:** CAL 1871: ITS = OM654932, LSU = OM677382; CUH AM688: ITS = OM654933, LSU = OM677383.

**Notes:** *Agaricus allostipitatus* is characterized by its entirely white, smooth pileus, crowded lamellae with two series of lamellulae, a cylindrical stipe with slightly broader base coloured white all over that turning brownish orange on bruising, a supramedian annulus with smooth, brown upper side and fibrillose, white lower side, ellipsoid basidiospores measuring  $7.9\text{--}8.2 \times 5.4\text{--}5.8 \mu\text{m}$ , and pyriform to ovoid cheilocystidia ( $11\text{--}21 \times 6\text{--}10 \mu\text{m}$ ).

Considering the overall morphological features and phylogenetic analyses (Figs. 51 and 52), *Agaricus allostipitatus* appears related to *A. argyropotamicus* and *A. inilleasper*. However, *A. argyropotamicus* differs from *A. allostipitatus* by its smaller basidiospores ( $5.5\text{--}7.5 \times 4.3\text{--}5.4 \mu\text{m}$ ) and almost indistinguishable cheilocystidia (Kerrigan 2016; Liu et al. 2020). *Agaricus inilleasper* has fused pileus margin with the stipe, and ellipsoid to subglobose, somewhat differently sized basidiospores measuring  $6.0\text{--}8.0 \times 5.0\text{--}7.0 \mu\text{m}$  (Lebel and Syme 2012) compared to *A. allostipitatus*.

In the phylogenetic analyses (Figs. 51 and 52), the newly described taxon, *Agaricus allostipitatus*, clustered together with well-represented members of the sect. *Agaricus* of subg. *Agaricus* confirming its position within that section and subgenus. In the ITS sequence based phylogenetic tree (Fig. 51), two newly generated sequences of *A. allostipitatus* (CUH AM688 and CAL 1871) cluster together with five unnamed sequences of *Agaricus* species (ZRL2010103, LD201247, F2272, ZRL2010102 and ZRL2010010) with strong statistical support values (99% BS, 1.00 PP), suggesting all of them to be the morphotype of the same taxon. However, other than the sequence data, no other morphological features were associated with those sequences in any published literature for comparison of those specimens with the newly described species.

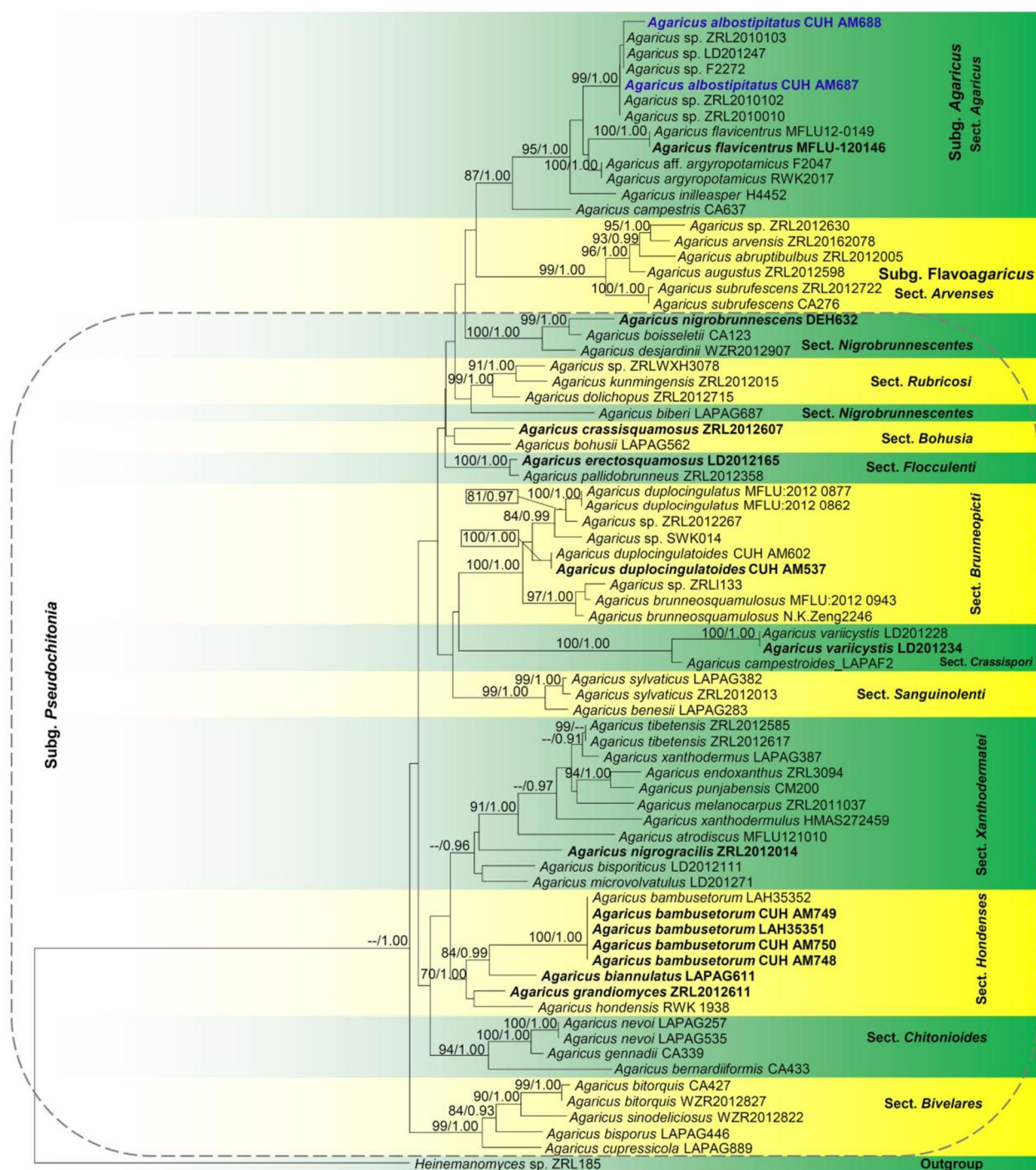
Among the five unnamed *Agaricus* species (ZRL2010103, LD201247, F2272, ZRL2010102 and ZRL2010010), the LSU sequence data of only *Agaricus* sp. ZRL2010010 was available in the NCBI GenBank nucleotide database. However, in the phylogenetic tree constructed using the LSU sequences (Fig. 52), the sequence deposited after the name *Agaricus* sp. ZRL2010010 cluster in a different clade with the members of *Agaricus* subg. *Flavoagaricus*, which suggests that the sequence might have been mistakenly named after *Agaricus* sp. ZRL2010010.

***Agaricus bambusetorum*** H. Bashir & Niazi, in Bashir, Chen, Jabeen, Ullah, Khan, Rehman Khan Niazi, Zhang, Khalid, Parra & Callac, Scientific Reports 11(no. 12905): 9 (2021).

**Index Fungorum number:** IF 828314; **Facesoffungi number:** FoF 10833; Figs. 53, 54

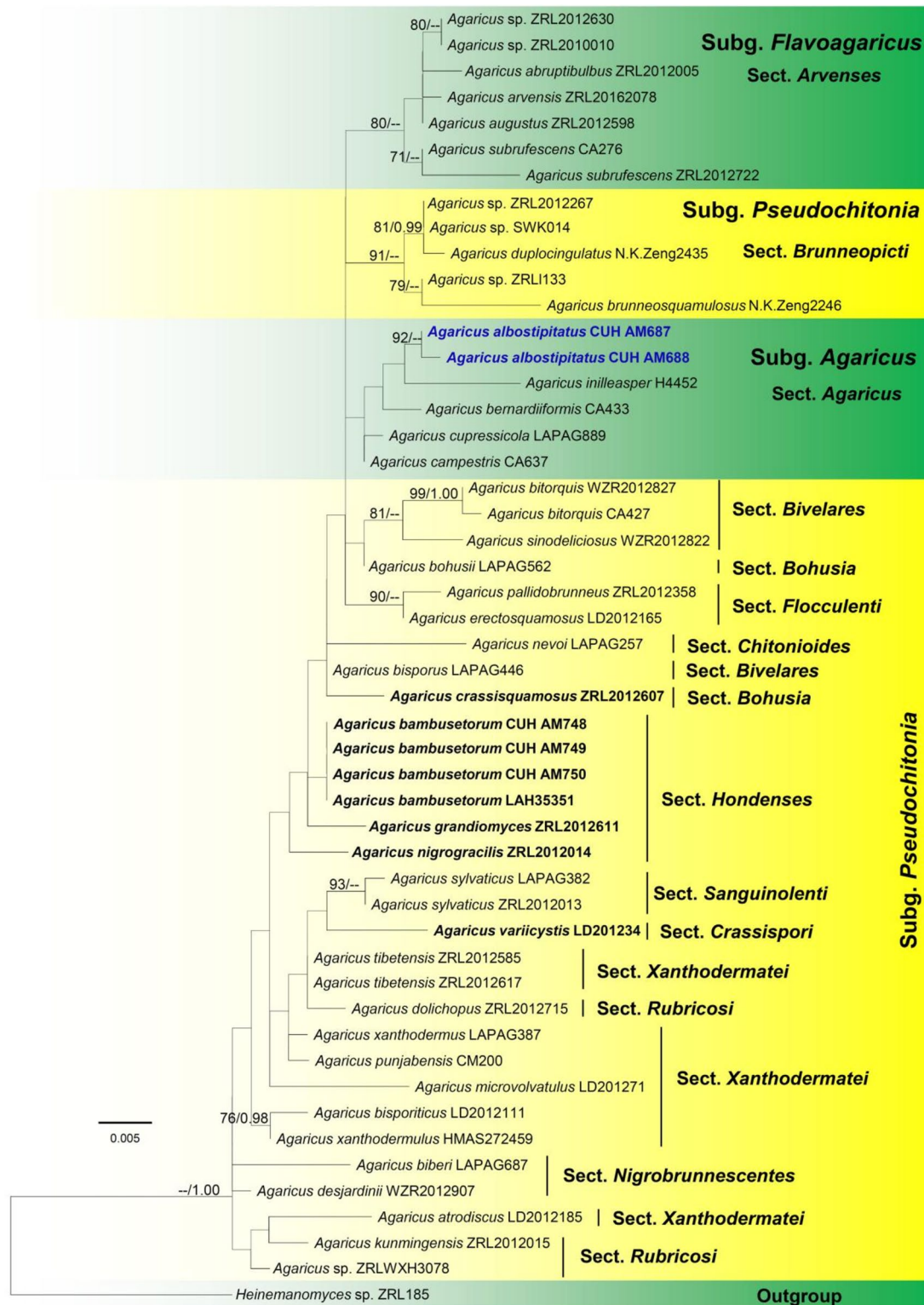
**Pileus** 44–95 mm in diam., convex when young, becoming broadly convex to applanate with a slight central depression, surface smooth, white (1A1), reddish brown (8D8,





**Fig. 51** Phylogram generated from maximum likelihood analysis based on ITS sequence data. Seventy-four vouchers are included in the ITS analyses which comprised 703 characters after alignment. *Heinemanomyces* sp. ZRL185 was used as the outgroup taxa. The best scoring RAxML tree with a final likelihood value of  $-5901.668865$  is presented. The matrix had 364 distinct alignment patterns, with 7.57% of undetermined characters or gaps. Estimated base frequencies were as follows: A=0.227109, C=0.202541, G=0.237172, T=0.333179; substitution rates: AC=0.869861,

AG=4.823902, AT=0.890497, CG=0.397316, CT=5.110861, GT=1.000000; gamma distribution shape parameter  $\alpha=0.764408$ . Bootstrap support values for ML equal to or greater than 70% are given above the nodes (left side of '/'). Bayesian posterior probabilities (BYPP) equal to or greater than 0.90 are given above the nodes (right side of '/'). Ex-type specimens are in black bold and the sequences of the newly described taxa for the present study are placed in blue font to highlight its phylogenetic position in the tree. Voucher numbers for all of the sequences are indicated in the tree



**Fig. 52** Phylogram generated from maximum likelihood analysis based on LSU sequence data. Fifty vouchers are included in the LSU analyses which comprised 598 characters after alignment. *Heinemanomyces* sp. ZRL185 was used as the outgroup taxa. The best scoring RAxML tree with a final likelihood value of -1645.607832 is presented. The matrix had 96 distinct alignment patterns, with 0.84% of undetermined characters or gaps. Estimated base frequencies were as follows: A=0.257065, C=0.195979, G=0.302519, T=0.244438; substitution rates: AC=0.614943,

AG=6.869678, AT=2.033440, CG=0.301621, CT=17.053330, GT=1.000000; gamma distribution shape parameter  $\alpha=0.748655$ . Bootstrap support values for ML equal to or greater than 70% are given above the nodes (left side of '/'). Bayesian posterior probabilities (BYPP) equal to or greater than 0.90 are given above the nodes (right side of '/'). Ex-type specimens are in black bold and the sequences of the newly described taxa for the present study are placed in blue font to highlight its phylogenetic position in the tree. Voucher numbers for all of the sequences are indicated in the tree

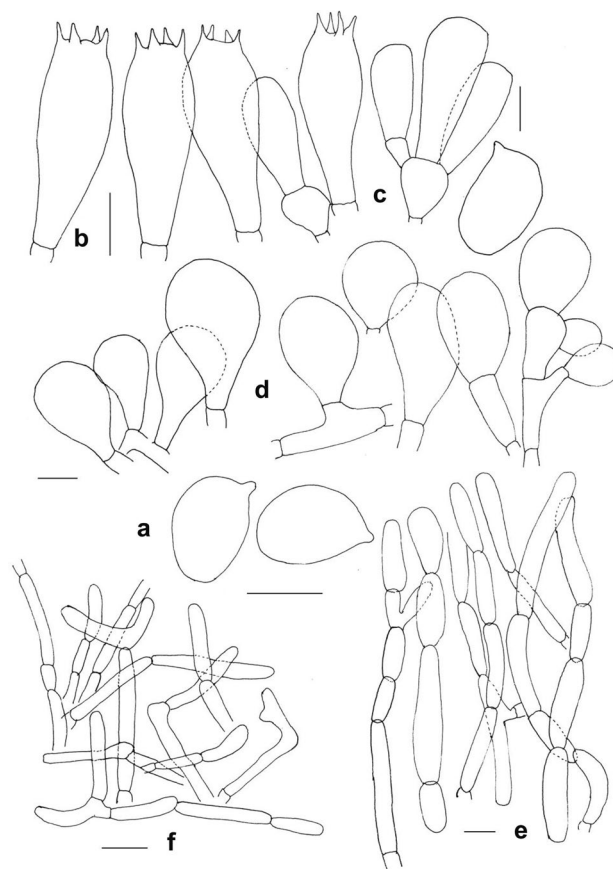




**Fig. 53** *Agaricus bambusetorum* (CAL 1872, holotype). **a** Field photographs of the immature stage of the basidiomes showing pileus surface, lamellae colouration, and annulus features. **b** Mature basidiomes showing lamellae colouration and annulus features. Scale bars: 20 mm

9D-E8) on bruising, margin split radially; context white (1A1), gradually discoloring to light-yellow when cut. *Lamellae* 5–6 mm broad, free, crowded with up to two series of lamellulae, pinkish to pinkish-brown when young, dark brown (6F6) on maturity, edge entire, concolorous. *Stipe* 32–96 × 6–12 mm, cylindrical with slightly bulbous base (up to 15 mm), curved at the base, surface smooth, white, immediately turning brown on brushing. *Annulus* superous, simple, pendant, membranous, thin, smooth in both sides, fragile, white (1A1). *Odour* pleasant, mushroomy.

*Basidiospores* (5.9–)7.4–8.5(–8.8) × (3.5–)4.4–5.6(–5.9)  $\mu\text{m}$  ( $X_{\text{mr}} = 6.9\text{--}8.3 \times 4.5\text{--}5.3$   $\mu\text{m}$ ,  $X_{\text{mm}} = 7.8 \pm 0.9 \times 5.0 \pm 0.6$   $\mu\text{m}$ ,  $Q_{\text{mr}} = 1.5\text{--}1.6$ ,  $Q_{\text{mm}} = 1.56 \pm 0.1$ ,  $n = 41$  spores,  $s = 3$  specimens), ellipsoid, brown to dark brown when viewed with KOH, smooth, with a prominent apiculus measuring 0.8–1.5  $\mu\text{m}$  long. *Basidia* 15–22 × 5.5–7.5  $\mu\text{m}$ , clavate to broadly clavate, hyaline, 4-spored, sterigmata 1.5–2.5  $\mu\text{m}$  long. *Basidioles* 12–17 × 4–6  $\mu\text{m}$ , clavate, hyaline, thin-walled. *Cheilocystidia* 13–37 × 5–17  $\mu\text{m}$ , pyriform to ovoid or



**Fig. 54** *Agaricus bambusetorum*. **a** Basidiospores. **b** Basidia. **c** Basidioles. **d** Cheilocystidia. **e** Pileipellis hyphae. **f** Annulus hyphae. Scale bars: **a–c** = 5  $\mu\text{m}$ , **d** = 10  $\mu\text{m}$ , **e** = 5  $\mu\text{m}$ , **f** = 15  $\mu\text{m}$

broadly clavate, thin-walled, simple septate at the base, basal cells 10–15 × 3.5–5  $\mu\text{m}$ , cylindrical. *Pleurocystidia* absent. *Pileipellis* a cutis, composed of hyphae measuring 4.5–7  $\mu\text{m}$  broad, branched, frequently septate, wider at middle, constricted at the septa, elements 5–12  $\mu\text{m}$  broad with round apices. *Stipitipellis* hyphae 5–8.5  $\mu\text{m}$  broad, cylindrical, parallel, hyaline, smooth, branched, thin-walled. *Annulus* hyphae 4–7  $\mu\text{m}$  broad, cylindrical, short branched, hyaline, smooth, thin-walled.

**Chemistry:** KOH reaction positive, pileus surface pastel yellow (1A4) to light yellow (1A5) when fresh, greyish yellow (4C5) on dry specimen; greenish yellow (1A6–7, 1B6–7) on stipe surface; and light yellow (1A5) on lamellae surface. Schäffer's reaction negative on dry specimen.

**Habitat and distribution:** The species grows solitary to scattered on leaf litter mixed soil in the roadside vegetation covered by *Phoenix dactylifera* and is currently found in Pakistan and India.

**Material examined:** India, West Bengal, South 24-parganas district, Mathurapur, 22°7'7.24" N, 88°23'34.43" E, alt. 8.0 m asl., on leaf litter mixed soil, 4 August 2019, E. Tarafder, CAL 1872 (**new record for India**); Mathurapur,



22°7'10.25" N, 88°23'28.78" E, alt. 10.0 m asl., on leaf litter mixed soil, 7 August 2019, E. Tarafder, CUH AM749 (**new record**); East Midnapur District, Narayangarh, Datan, Jenkapur, 21°53'50.01" N, 87°22'56.45" E, alt. 17.0 m asl., on leaf litter mixed soil, 11 August 2019, A. K. Dutta, CUH AM750 (**new record for India**).

**GenBank numbers:** CAL 1872: ITS = OM278635, LSU = ON171824; CUH AM749: ITS = OM278636, LSU = ON171824; CUH AM750: ITS = OM278638, LSU = OM677380.

**Notes:** *Agaricus bambusetorum* was originally described from Pakistan (Bashir et al. 2021) in habitat dominated by bamboo forests. However, in case of the present collection, the specimen was collected growing on leaf litter mixed soil in the roadside vegetation covered by *Phoenix dactylifera*. Besides, the cheilocystidia of the present collection shows slightly longer in size compared to the Pakistani collection. In the phylogenetic analyses (Figs. 51 and 52), three newly generated sequences from the Indian collections clustered together with sequences deposited from Pakistan, suggesting all of them to be the morphotypes of the same taxon.

Among morphologically related taxa, *Agaricus bianulatus* has a pileus coloured dull to brownish-ochre with ochraceous to brownish-pink scales on its surface, and globose or pyriform to sphaeropedunculate cheilocystidia

(Parra et al. 2011). *Agaricus hondensis* differs from *A. bambusetorum* by its larger pileus, phenolic odor, smaller basidiospores ( $3.4\text{--}5.7 \times 3.0\text{--}3.5 \mu\text{m}$ ), and considerably smaller ( $10\text{--}15 \times 10\text{--}15 \mu\text{m}$ ), subglobose cheilocystidia (Kerrigan 2016).

#### *Leucocoprinus* Pat.

**Notes:** The genus *Leucocoprinus* has been accepted by Singer (1986) with *L. cepistipes* as the type species. This genus is characterized by a pluteoid habit, convex to umbonate pileus with floccose pulverulent squamules, a striate-sulcate margin, a very thin context, free lamellae, and the absence of colour changes with ammonia vapour, a central stipe with bulbous-clavate base and annulus, and a white to pale pink spore-print (Singer 1986; Vellinga 2001; Wartchow et al. 2008). The *Leucocoprinus* species is widely distributed in tropical, subtropical and temperate areas throughout the world as saprobes (Kirk 2008). According to Singer (1986), this genus occupies a position intermediate between *Macrolepiota* and *Leucoagaricus*. The generally small-sized basidiomes and the absence of clamp-connections differentiate *Leucocoprinus* from *Macrolepiota*, while it can be distinguished from *Leucoagaricus* by the fragile coprinoid basidiomes, the plicate-sulcate-striate pileal margin, large cheilocystidia, and the presence of

**Fig. 55** *Leucocoprinus cretaeus* (SDBR-CMUNK0559). **a** Basidiomes. **b** Basidiospores. **c** Basidia. **d** Cheilocystidia. Scale bars: **a** = 50 mm, **b–d** = 10  $\mu\text{m}$



pseudoparaphyses (pavement cells) in the hymenium (Singer 1986). Currently, there are 100 accepted species of *Leucocoprinus* in the Index Fungorum (2022).

***Leucocoprinus cretaceus*** (Bull.) Locq., Bull. mens. Soc. linn. Soc. Bot. Lyon 14: 93 (1945).

*Index Fungorum number*: IF287726; *Facesoffungi number*: FoF3137; Fig. 55

*Pileus* 30–90 mm in diameter, at first ovoid then convex to broadly conical, umbonate in maturity, white (1A1), covered by easily removed, granular floccose, white (1A1) to yellowish white (1A2) squamules, conical to pyramidal on the umbo; margin entire, sulcate. *Lamellae* distantly free, rather broad, thin; white, edge slightly fimbriate, white (1A1). *Stipe* 50–80 × 4 mm, broad at apex, gradually enlarged downward to a broadly clavate to somewhat fusiform 6–14 mm broad base; sometimes coarsely farinose to slightly flocculose-farinose below annulus, subfarinose above; white (1A1) to yellowish white (1A2). *Annulus* white, very soft, rather flaring, median to superior. *Spore print* white.

*Basidiospores* 7–11 × 5–8 µm,  $Q = 1.31–1.47$  ( $n = 50$ ), dextrinoid, ellipsoid to amygdaliform, thick-walled, with an apical germ pore covered with a hyaline lens. *Basidia* 16–24 × 8–12 µm, pyriform to clavate with a bulbous base, hyaline, thin-walled, bearing four sterigmata, 1.0–3.0 µm long, surrounded by 4 pseudoparaphyses. *Pseudoparaphyses* 10–13 × 7–10 µm, sphaeropedunculate to broadly clavate to pyriform, very broad point of attachment. *Pleurocystidia* absent. *Cheilocystidia* 25–65 × 6.5–18 µm, thin-walled, hyaline, subcylindrical to narrowly fusiform to slightly narrowly lageniform, mucronate, rarely obtuse, moderately pedicellate. *Pileipellis* made up of hyaline hyphae with smooth walls and cylindric terminal elements with excrescences, branched in different shapes (H, T and Y), 24–45 × 7.5–15 µm. *Stipitipellis* a cutis of narrowly cylindrical, 2–7 µm broad hyphae. *Clamp connections* absent.

*Habit and distribution*: Solitary to gregarious, on decomposed wood. Known from Argentina, Brazil, Europe, North America, Sri Lanka and Thailand (Candusso and Lanzoni 1990; Birkebak 2010; Ferreira and Cortez 2012; Niveiro et al. 2012; Tipbromma 2017; this study).

*Material examined*: Thailand, Chiang Mai Province, Muang District, Chiang Mai University, 18°48'14"N 98°57'14"E, elevation 331 m, solitary to gregarious on decomposed wood, 27 July 2019, J. Kumla and N. Suwannarach, SDBR-CMUNK0559 (**new record for Thailand**); Sukhothai Province, Si Satchanalai National Park, Natural trail; 17°55'12"N 99°48'44"E, elevation 277 m, solitary to gregarious on decomposed wood, 23 August 2020, N. Wannathes, J. Kumla, N. Suwannarach and S. Khuna, SDBR-CMUNW1461 (**new record for Thailand**).

*GenBank numbers*: SDBR-CMUNK0559: ITS = OP503474; SDBR-CMUNW1461: ITS = OP503476.

*Notes*: *Leucocoprinus cretaceus* is easily recognized by its fleshy white basidiomes covered by floccose squamules that are easily removed when touched and by a fusoid stipe inflated toward the base. Phylogenetic analysis indicated that *L. cretaceus* forms monophyletic clade and clearly separated from other species of *Leucocoprinus* (Fig. 56). Morphologically, this species is related to *L. squamulosus* and *L. cepistipes*. *Leucocoprinus cretaceus* differs from *L. squamulosus* by its which lacks an annulus and an inflated stipe base (Dennis 1952; Wartchow et al. 2008). *Leucocoprinus cepistipes* separate from *L. cretaceus* based on the ochraceous to pale brown squamules covering the pileus surface (Candusso and Lanzoni 1990; Wartchow et al. 2008; Rother and Silveira 2009).

### **Cortinariaceae** R. Heim ex Pouzar.

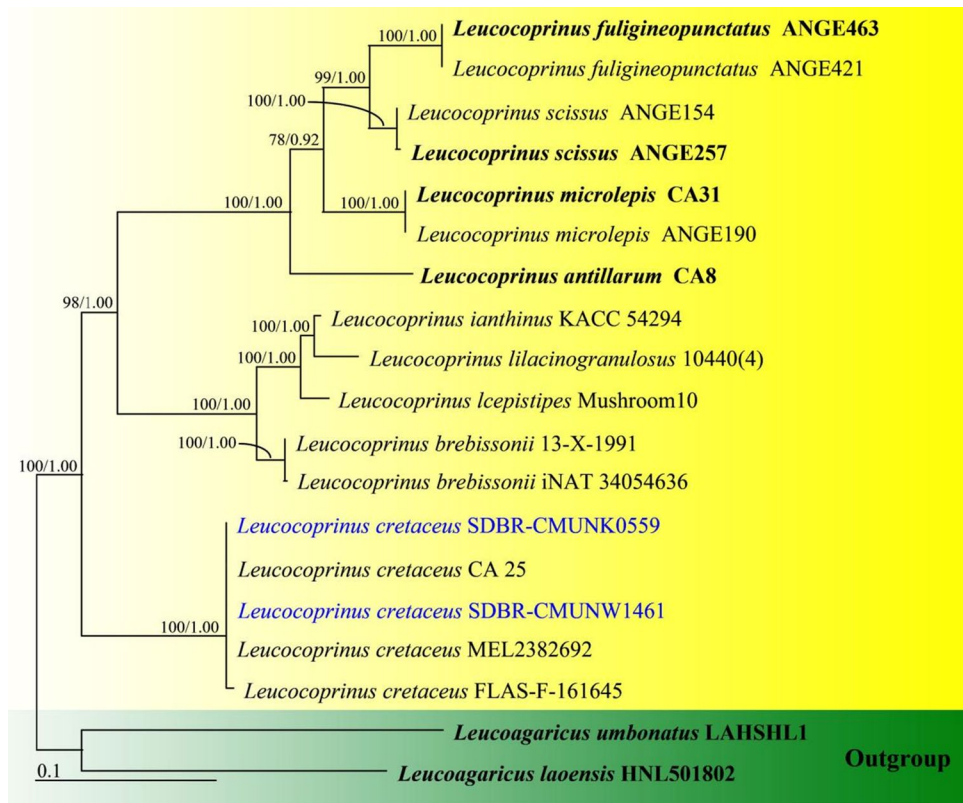
*Notes*: *Cortinariaceae* typified by *Cortinarius violaceus* belongs to *Agaricales*. It is a large family with a worldwide distribution (Liimatainen et al. 2022). The basidiomes range from small to large size and from agaricoid to sequestrate form. Species of the group are characterized by a cobweb-like partial veil (cortina), ornamented basidiospores and a cinnamon brown spore print. They are important ectomycorrhizal fungi forming associations with different trees and shrubs: *Fagaceae*, *Salicaceae*, *Caesalpiniaceae*, *Cistaceae*, *Dipterocarpaceae*, *Myrtaceae*, *Rhamnaceae*, *Rosaceae* and *Pinaceae*, as well as some herbaceous plants in the *Cyperaceae* and *Polygonaceae*. The classification of the group was recently revised by Liimatainen et al. (2022) and the family was divided into ten genera: *Aureonarius*, *Austrocortinarius*, *Calonarius*, *Cortinarius*, *Cystinarius*, *Hygronarius*, *Mystinarius*, *Phlegmacium*, *Thaxterogaster* and *Volvanarius*.

### **Calonarius** Niskanen & Liimat.

*Notes*: This species-rich genus with an estimated around 200 species is only known from the Northern Hemisphere. The species are predominantly calcicolous or calciphilous, many are rare with narrow ecological preferences and thus are included in national red lists in several countries. Typical for the members of this genus are medium- to large-sized, pileocarpic, often brightly coloured basidiomes with a more or less, usually distinctly marginated bulb at the base of the stipe. The pileus is viscid to glutinous, and the stipe is dry. The basidiospores are amygdaloid to citriform and coarsely verrucose, and the pileipellis is simplex. Part of the species have a positive KOH-reaction. The genus includes three subgenera: *Calonarius*, *Calochroi* and *Fulvi* (Liimatainen et al. 2022).

### **Calonarius caesiofulvus** Niskanen, Liimat. & M. E. Sm., *sp. nov.*

*Index Fungorum number*: IF 900300; *Facesoffungi number*: FoF 14857; Figs. 57a, 58a, 59



**Fig. 56** Phylogenetic tree derived from maximum likelihood analysis of ITS gene of 19 sequences and the aligned dataset was comprised of 787 characters including gap. The average standard deviation of the split frequencies of the BI analysis was 0.00563. A best scoring RAxML tree was established with a final ML optimization likelihood value of -3057.9735. The matrix had 296 distinct alignment patterns with 13.97% undetermined characters or gaps. Estimated base frequencies were found to be: A=0.2280, C=0.2242, G=0.2429, T=0.3047; substitution rates AC=0.4870, AG=4.0084, AT=1.4356,

CG=0.2018, CT=3.7781, GT=1.0000. *Leucoagaricus laeensis* HNL501802 and *Leucoagaricus umbonatus* LAHSHL1 were used as outgroup. Numbers above branches are the bootstrap statistics percentages (left) and Bayesian posterior probabilities (right). Branches with bootstrap values  $\geq 70\%$  and  $PP \geq 0.90$  are shown at each branch. The bar represents 0.1 substitutions per nucleotide position. Type strains are in bold. The newly generated sequences are indicated in blue

**Etymology:** The name refers to the colours of the basidiomes.

**Holotype:** K-M 001434088.

**Pileus** 4–10 cm in diam., at first hemispherical, then low convex to almost plane with a long-incurved margin, innately fibrillose, at first pale greyish purple, becoming yellow on the margin and brown in centre, viscid. **Lamellae** crowded, yellow. **Stipe** 4–7 cm long, 1–2 cm thick at the apex, marginate bulbous, pale yellow, covered up to halfway by a bluish purple universal veil. **Context** in pileus white to very pale yellow, in stipe, and especially at the base of the stipe, yellow. **Universal veil** bluish purple. **Mycelium** white to yellow. **Odour** not recorded. **Basidiospores**  $9.5\text{--}11 \times 5\text{--}5.5 \mu\text{m}$ , narrowly amygdaloid-citriform, moderately to strongly coarsely verrucose. Some basidia with brownish purplish-red granulate contents in 5% KOH. **ITS sequence** (GenBank ON843392, **ex holotype**) distinct from other members of *Calonarius* and with 97% similarity to the closest known species *C. alcalinophilus*.

**Habitat and distribution:** In deciduous forests with *Fagaceae* and so far known from Florida, USA.

**Material examined:** USA. Florida, Gainesville, University of Florida campus, under oak, 12 January 2015, coll. Richard Kneal, T. Niskanen 14–167, K-M 001434088 (**holotype** in K-M; isotype in H); Gainesville, Rock Creek Neighborhood, under oaks and pines, 10 January 2017, coll. Matthew E. Smith, MES-2020, FLAS-F-60313 (FLAS).

**GenBank numbers:** TN14-167: ITS=ON843392; FLAS-F-60313: ITS=MF074799.

**Notes:** The species can be recognized by the combination of yellow lamellae, pale yellow stipe, initially greyish purple pileus and narrowly amygdaloid-citriform,  $9.5\text{--}11 \times 5\text{--}5.5 \mu\text{m}$  basidiospores. It belongs to *Calonarius* subgenus *Fulvi* section *Fulvi*.

***Calonarius nobilis*** Niskanen & Liimat., *sp. nov.*

**Index Fungorum number:** IF900301; **Facesoffungi number:** FoF 14858; Figs. 57b, 58b, 59





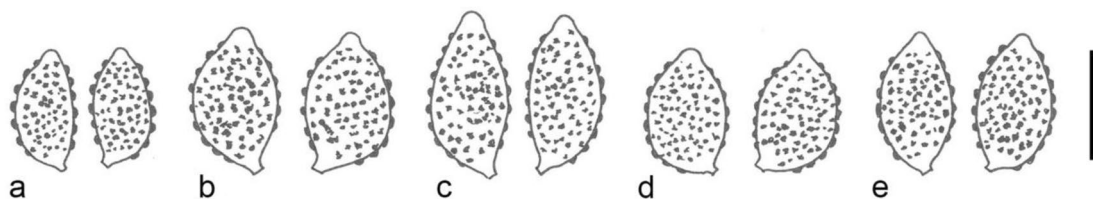
**Fig. 57** Basidiomes of the species of the genus *Calonarius*. **a** *Calonarius caesiofulvus* (K-M 001434088, **holotype**). **b** *Calonarius nobilis* (K-M 001434089, **holotype**). **c** *Calonarius pacificus* (K-M

001434090, **holotype**). **d** *Calonarius pulcher* (K-M 001434092, **holotype**). **e** *Calonarius subcorrosus* (K-M 001434093, **holotype**). Photographs: **a** Matthew E. Smith, **b–e** Kare Liimatainen

**Etymology:** The species is rare and included in the red list e.g. in Sweden, thus the name *nobilis* meaning nobel, distinct.

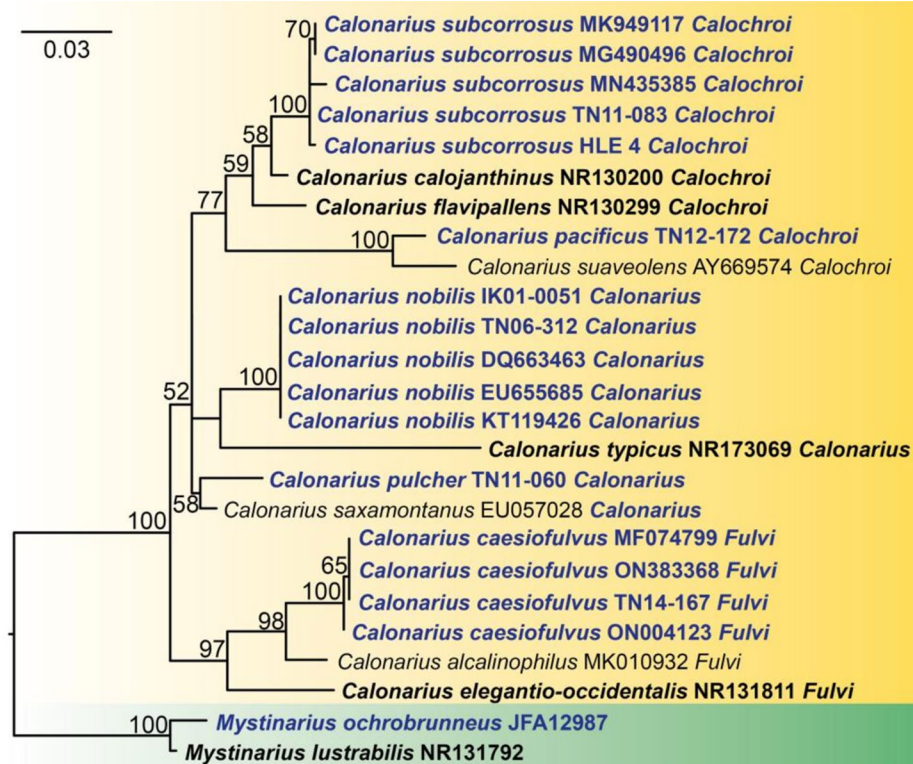
**Holotype:** K-M 001434089.

**Pileus** 3–8 cm in diam, at first hemispherical, then low convex to almost plane, at first greenish yellow, soon



**Fig. 58** Basidiospores of the species of the genus *Calonarius*. **a** *Calonarius caesiofulvus* (K-M 001434088, **holotype**). **b** *Calonarius nobilis* (K-M 001434089, **holotype**). **c** *Calonarius pacificus* (K-M

001434090, **holotype**). **d** *Calonarius pulcher* (K-M 001434092, **holotype**). **e** *Calonarius subcorrosus* (K-M 001434093, **holotype**). Drawings: Tuula Niskanen. Scale bars: 10  $\mu$ m



**Fig. 59** The best scoring RAxML tree of the genera *Calonarius* and *Mystinarius* based on the ITS region. Related sequences were retrieved from GenBank. Twenty-five specimens were included in the analysis of the ITS region which comprises 663 characters after alignment. The tree is rooted with *Mystinarius*. Estimated base frequencies were: A=0.246760, C=0.199165, G=0.201141, T=0.352933; substitution rates AC=0.954938, AG=3.189949, AT=1.426518,

CG=0.990207, CT=5.977045, GT=1.000000, gamma distribution shape parameter  $\alpha=0.312392$ . Maximum likelihood bootstrap values higher than 50% are given at the nodes. The holotype specimens retrieved from the GenBank are in bold and black. The new species are in bold and blue. The subgenus of the species is indicated after the collection/GenBank no. of each specimen

greenish yellow brown, viscid. *Lamellae* crowded, greenish yellow. *Stipe* 4–7 cm long, 1–2 cm thick at the apex, with a marginate bulb, greenish yellow with some purplish tint. *Context* in most parts with white with a purplish tint, except in the bulb and cortex bright greenish yellow. *Universal veil* greenish yellow, on the margin of the bulb. *Mycelium* white to yellow. *Odour* slightly yeast-like. *KOH-reaction* on pileus, on context of the base of the stipe, and mycelium red. *Basidiospores* (11.5–)12–13.5(–14)  $\times$  8–9  $\mu$ m, broadly citriform, moderately coarsely verrucose. Some *basidia* with dark brownish purplish-red contents. *ITS sequence* (GenBank ON843393, **ex holotype**) distinct from other members of *Calonarius* and with 96% similarity to the closest known species.

**Habitat and distribution:** In coniferous forests on calcareous ground and so far known from Europe: Estonia, Finland, France, Germany and Spain.

**Material examined:** Estonia, Hiiumaa, Pühalepa, NE of Suuremõisa, Vahtrepa, Kallaste pank, dryish to damp grass-herb *Picea* forest with *Pinus*, *Corylus*, *Betula*, *Populus tremula* and deciduous bushes under the precipice,

17 September 2001, T. Niskanen, I. Kytövuori 01-0051 (H). FINLAND, Ahvenanmaa, Jomala, Önningsby, N of Södervik, mesic (to moist) spruce (*Picea abies*) forest with some *Pinus sylvestris* and *Betula* on calcareous ground, 27 October 2006, K. Liimatainen, T. Niskanen 06–312, 001434089 (**holotype** in K-M; isotype in H).

**GenBank numbers:** IK01-0051: ITS=ON843432; TN06-312: ITS=ON843393.

**Notes:** Typical characters for *Calonarius nobilis* are the greenish yellow colours in pileus, lamellae, stipe and universal veil combined with a purplish tint on stipe and context of the pileus and stipe, at least when young. The spores are broadly citriform and large. The species belongs to *C. subgenus Calonarius* and has previously been called *C. cedretorum* in the Nordic countries.

***Calonarius pacificus*** Niskanen, Liimat. & Bojantchev, *sp. nov.*

**Index Fungorum number:** IF 900302; **Facesoffungi number:** FoF 14859; Figs. 57c, 58c, 59



**Etymology:** The species was first found in California, a state in the Western United States by the Pacific Ocean.

**Holotype:** K-M 001434090.

**Pileus** 5–9 cm in diam, at first hemispherical, then low convex to almost plane, can be quite purplish when young but becoming more and more ochre brown with age, with small, dark yellowish brown patches in the centre, glutinous. **Lamellae** crowded, pale brownish purple when young, becoming somewhat darker brown and losing the purple tint when old. **Stipe** 6–10 cm long, 1–2 cm thick at the apex, up to 4.5 cm at the base, with a marginate bulb, completely purple or upper part of the stipe purple when young, later very pale ochre brown. **Context** in pileus at first purple/white marbled hygrophanous, becoming pale yellow with age and on exposure, in the stipe or apex of the stipe purple/white, at the base of the stipe brownish ochre/white marbled hygrophanous. **Mycelium** white with yellowish brown patches. **Universal veil** not recorded. **Odour** indistinct. **Basidiospores** 12.5–14.5 × 6.5–7.5 µm, amygdaloid-citriiform to citriiform, moderately, coarsely verrucose. Part of the **basidia** with pale yellowish contents. **ITS sequence** (GenBank ON843394, **ex holotype**) distinct from other members of *Calonarius* and with 97% similarity to the closest known species *C. suaveolens*.

**Habitat and distribution:** In oak forests and so far known from California, USA.

**Material examined:** USA, California, Humboldt Co., Willow Creek, camping site, live oak forest, 30 November 2012, K. Liimatainen, J. Olsson, T. Niskanen 12–172, 001434090 (**holotype** in K-M; isotype in H); Santa Cruz Co., Scotts Valley, NAMA Foray site 12, 15 December 2012, K. Liimatainen, T. Niskanen 12–332, 001434091 (K-M).

**GenBank number:** ITS = ON843394.

**Notes:** Characteristic for *Calonarius pacificus* are the purple colours in all parts of basidiomes, at least when young, large basidiospores and habitat with oaks in Western North America. The morphology supports its placement in the *C.* subgenus *Calochroi* as a sister species to European *C. suaveolens*, although the placement of *C. suaveolens* in the *C.* subgenus *Calochroi* was not always been well supported by the previous phylogenetic studies (Frøslev et al. 2007; Liimatainen et al. 2022).

***Calonarius pulcher*** Niskanen, Liimat., & Bojantchev, *sp. nov.*

**Index Fungorum number:** IF 900303; **Facesoffungi number:** FoF 14860; Figs. 57d, 58d, 59

**Etymology:** The epithet *pulcher* means beautiful, noble.

**Holotype:** K-M 001434092.

**Pileus** 8–12 cm in diam, at first hemispherical, then low convex, reddish brown, edge purple when young, yellow when old. **Lamellae** crowded, at first pale brownish grey, later pale brown. **Stipe** 6–8 cm long, 2–3 cm thick at the

apex, up to 5 cm at the base, with a marginate bulb, yellowish white, sometimes with a purple tint when young, base becoming reddish brown when handled. **Context** in pileus and lower part of the stipe yellow, at the upper part of stipe white, with a purplish tint at least when young. **Universal veil** yellow, at the margin of the bulb. **Mycelium** white (to yellow). **Odour** indistinct or very faintly aniseed. **Basidiospores** 10.5–12 × 6.5–7.5 µm, broadly citriiform, moderately to strongly, coarsely verrucose. Some **basidia** with brownish purplish-red granulose contents in 5% KOH. **ITS sequence** (GenBank ON843396, **ex holotype**) distinct from other members of *Calonarius* and with 97% similarity to the closest known species *C. saxamontanus*.

**Habitat and distribution:** In coniferous forests on calcareous ground and so far known from Alaska, USA.

**Material examined:** USA, Alaska, Fairbanks, Ballaine Lake trails, NE of University campus, *Picea* dominated forest with some *Betula*, *Populus*, *Salix* and *Alnus*, on rich ground, 14 August 2011, K. Liimatainen, T. Niskanen 11-060, 001434092 (**holotype** in K-M; isotype in H).

**GenBank number:** ITS = ON843396.

**Notes:** *Calonarius pulcher* has pale brownish grey lamellae when young, purple tints occur in the pileus and stipe at least when young, and the basidiospores are broadly citriiform and rather large. The pileus is reddish brown with a purple edge when young and yellow when old. The species belongs to *Calonarius* subgenus *Calonarius*.

***Calonarius subcorrosus*** Niskanen & Liimat., *sp. nov.*

**Index Fungorum number:** IF 900304; **Facesoffungi number:** FoF 14861; Figs. 57e, 58e, 59

**Etymology:** The species is close to *C. calojanthinus* (*C. corrosus* ss auct.).

**Holotype:** K-M 001434093.

**Pileus** 3–6 cm in diam, hemispherical, then low convex to almost plane, ochre brown from the centre with small brownish spots, paler and more yellowish towards the margin, margin bright citrus yellow, somewhat viscid. **Lamellae** crowded, very pale brownish grey when young, later brown. **Stipe** 4–6 cm long, 1.3–1.7 cm thick at the apex, up to 2.5 cm at the base, with a marginate bulb, white with a very faint, yellow tint. **Context** white. **Universal veil** not recorded. **Mycelium** white. **Odour** indistinct. **Basidiospores** 10.5–12 × 6–7 µm, amygdaloid-citriiform to citriiform, moderately to strongly, coarsely verrucose. **Basidia** hyaline, with hyaline oil drops. **ITS sequence** (GenBank ON843397, **ex holotype**) distinct from other members of *Calonarius* and with 98% similarity to the closest known species, *C. calojanthinus* (*C. corrosus* ss auct.).

**Habitat and distribution:** In coniferous forests on calcareous ground and so far known from China and North America, Alaska, Arizona and Mexico.



**Material examined:** Mexico, Veracruz, Cofre de Perote, coniferous forest, 1965, H. L. Evans no. 4 (K(M)). USA, Alaska, Fairbanks, trails at the NW side of the campus, at the end of Yukon Road (trail starting from parking place), *Picea* dominated forest with some *Betula*, *Populus* and *Alnus*, on rich ground, 15 August 2011, K. Liimatainen, T. Niskanen 11-083, 001434093 (**holotype** in K-M; isotype in H).

**GenBank numbers:** HLE 4: ITS = ON843431; TN11-083: ITS = ON843397.

**Notes:** Typical characters for the species are the lack of purplish tints in the basidiomes, ochre brown pileus with a bright yellow margin, white stipe with a very faint yellow

tint, and white context. The species belongs to the *C.* subgenus *Calochroi*. The North American-European sister species *C. calojanthinus* (*C. corrosus* ss auct.) has pale ochraceous to cream-coloured pileus.

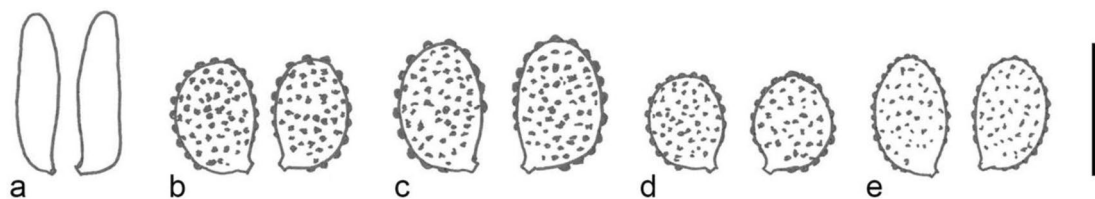
***Cortinarius* (Pers.) Gray.**

**Notes:** This is the most species-rich genus of the family with an estimated over 2000 species and a worldwide distribution. The species are characterized by mainly stipitocarpic development and a pileipellis duplex with a more or less developed hypoderm. The basidiomes range from very small to large size and from dry to glutinous contexture.



**Fig. 60** Basidiomes of the species of the genera *Cortinarius*, *Hygronarius* and *Mystinarium*. **a** *Cortinarius flaureifolius* (K-M 001434094, **holotype**). **b** *Cortinarius floridaensis* (K-M 001434095, **holotype**). **c** *Cortinarius subiodes* (K-M 001434108, **holotype**). **d**

*Hygronarius californicus* (K-M 001434114, **holotype**). **e** *Mystinarium ochrobrunneus* (CR 4064459, **holotype**). Photographs: **a** Matthew E. Smith, **b–d** Kare Liimatainen, **e** Joseph F Ammirati



**Fig. 61** Basidiospores of the species of the genera *Cortinarius*, *Hygronarius* and *Mystinarius*. **a** *Cortinarius flaureifolius* (K-M 001434094, **holotype**). **b** *Cortinarius floridaensis* (K-M 001434095, **holotype**). **c** *Cortinarius subiodes* (K-M 001434108, **holotype**). **d**

*Hygronarius californicus* (K-M 001434114, **holotype**). **e** *Mystinarius ochrobrunneus* (CR 4064459, **holotype**). Drawings: Tuula Niskanen. Scale bars: 10  $\mu$ m

Majority of species have brown colours in their basidiomes, but some species also have purple, red, yellow, orange, green or black colours. Eleven subgenera are recognized: *Cortinarius*, *Camphorati*, *Dermocybe*, *Illumini*, *Infracti*, *Iodolentes*, *Leprocyebe*, *Myxadium*, *Orellani*, *Paramyxadium* and *Telamonia* (Liimatainen et al. 2020, 2022).

***Cortinarius flaureifolius*** Niskanen, Liimat. & M. E. Sm., *sp. nov.*

*Index Fungorum number*: IF 900305; *Facesoffungi number*: FoF 14862; Figs. 60a, 61a, 62

*Etymology*: Derived from the name of the sister species *Cortinarius aureifolius* and the location Florida.

*Holotype*: K-M 001434094.

*Pileus* 1.5–3.5 cm in diam, convex to plane, tomentose fibrillose, brown. *Lamellae* medium spaced, at first yellow, later brown. *Stipe* 2–4 cm long, up to 0.4 cm thick at the apex, cylindrical, at first pale greyish white silky fibrillose, later pale yellowish to ochre brown. *Context* not recorded. *Universal veil* ochre (brown), quite sparse. *Mycelium* not recorded. *Odour* indistinct. *Basidiospores* 11–13  $\times$  3.5–4  $\mu$ m, boletoid, almost smooth. *Basidia* hyaline. *ITS sequence* (GenBank ON843398, **ex holotype**) distinct from other members of *C.* subgen. *Dermocybe* and with 92% similarity to the closest known species *C. aureifolius*.

*Habitat and distribution*: With *Pinus* on sandy soil and so far only known from Florida, USA.

*Material examined*: USA, Florida, Melrose, Ordway-Swisher Reserve, in sandy soil with mostly pines but some oaks, 1 December 2014, M. E. Smith, MES811, 001434094 (**holotype** in K-M; isotype in FLAS).

*GenBank number*: ITS = ON843398.

*Notes*: In the field the species looks like a representative of *Cortinarius* sect. *Dermocybe* or an *Inocybe*. The species is easy to recognize by the narrow, boletoid basidiospores. The sister species *C. aureifolius* has yellow orange to ochraceous orange lamellae when young. For an unambiguous identification ITS sequence is recommended.

***Cortinarius floridaensis*** Niskanen, Liimat. & M. E. Sm., *sp. nov.*

*Index Fungorum number*: IF 900306; *Facesoffungi number*: FoF 14863; Figs. 60b, 61b, 62

*Etymology*: The species was first found from Florida, USA.

*Holotype*: K-M 001434095.

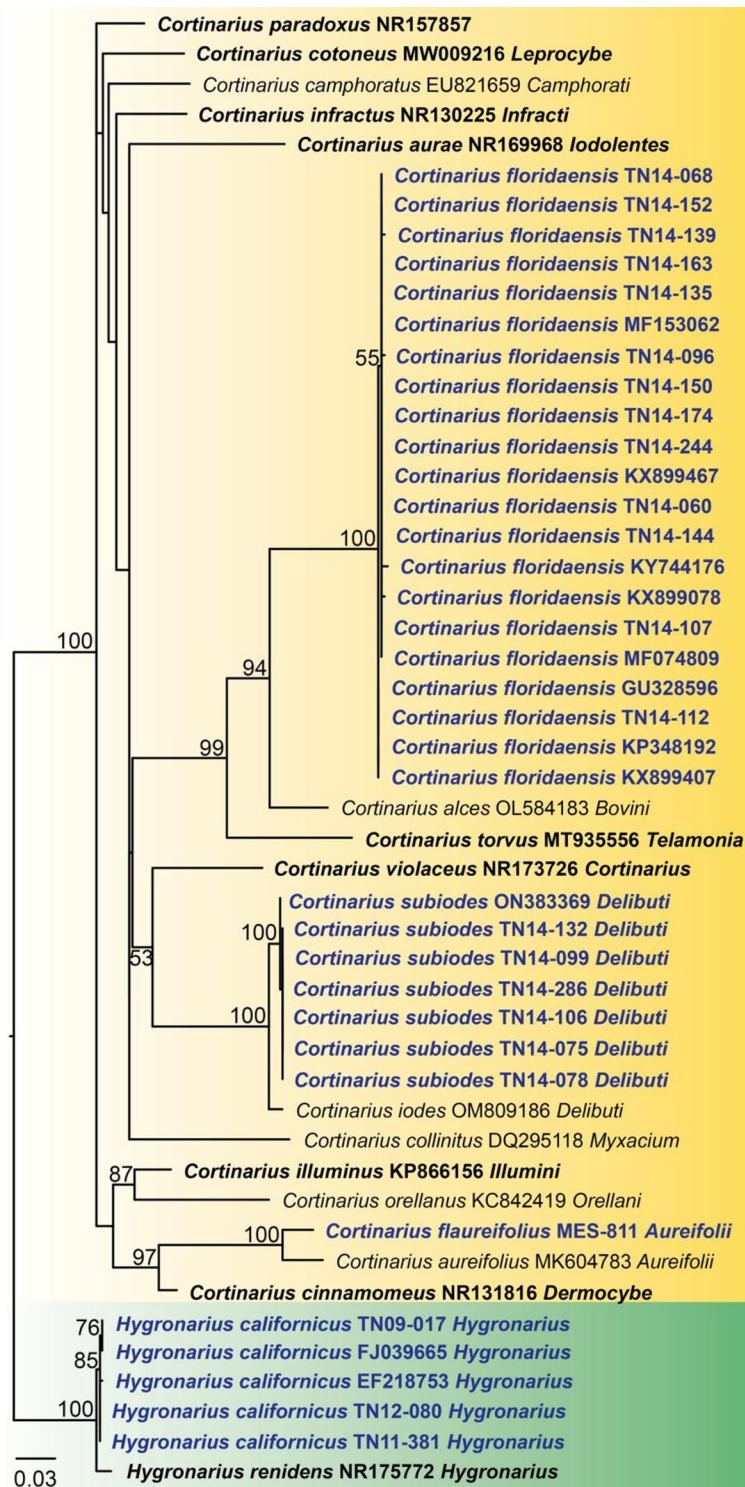
*Pileus* 1.5–5.5 cm in diam, at first hemispherical, then low convex to almost plane, often with a quite low and broad umbo, distinctly innately fibrillose, greyish brown when young, later more olive yellow brown, hygrophanous. *Lamellae* medium spaced, brown to dark brown. *Stipe* 2.5–5.5 cm long, 0.5–0.8 cm thick at the apex, cylindrical to clavate, blue at the apex, greyish white fibrillose lower down, becoming pale yellowish brown with age. *Context* in pileus brown, in stipe apex pale greyish brown, in the rest of the stipe brown. *Universal veil* ochraceous yellow to ochraceous brown, forming a thin sock or some bands on the lower half of the stipe. *Mycelium* white. *Odour* raphanoid. *Basidiospores* 8–9  $\times$  5.5–6  $\mu$ m, broadly obovoidly ellipsoid, rather strongly verrucose. *Basidia* hyaline, some with pale brownish-yellow contents in 5% KOH. *ITS sequence* (GenBank ON843399, **ex holotype**) distinct from other members of *C.* subgen. *Telamonia* and with 90% similarity to the closest known species *C. alces*.

*Habitat and distribution*: In mixed forests with *Fagaceae* and so far known from Eastern USA: Florida, Massachusetts, Michigan and Tennessee.

*Material examined*: USA, Florida, Wakulla Co., Crawfordville, 306 Wakulla Beach Road, under *Pinus*, mixed deciduous and *Pinus* forest with some *Quercus virginiana*, *Magnolia grandiflora* and sweetgum, sandy soil, on calcareous bedrock, 24 December 2014, K. Liimatainen, T. Niskanen 14-060, 001434096 (K-M). *loc. cit.* 27 December 2014, K. Liimatainen, T. Niskanen 14-096, 001434097 (K-M). *loc. cit.* 30 December 2014, K. Liimatainen, T. Niskanen 14-112, 001434098 (K-M). Tallahassee Co., Lake Talquin State Forest, by the road 267, Bear Creek Educational forest, *Fagus*, *Carpinus*, *Castanea*, *Pinus*, laurel oak, live oak, white oak, on sandy soil, 25 December 2014, K. Liimatainen, T. Niskanen 14-068, 001434099 (K-M). *loc. cit.* mostly evergreen oaks, 29 December 2014, K. Liimatainen, T. Niskanen



**Fig. 62** The best scoring RAXML tree of the genera *Cortinarius* and *Hygronarius* based on the ITS region. Related sequences were retrieved from GenBank. Forty-nine specimens were included in the analysis of the ITS region which comprises 732 characters after alignment. The tree is rooted with *Hygronarius*. Estimated base frequencies were: A=0.242037, C=0.200516, G=0.214242, T=0.343206; substitution rates AC=1.323688, AG=3.480113, AT=1.611311, CG=0.756641, CT=4.952595, GT=1.000000, gamma distribution shape parameter  $\alpha$ =0.362036. Maximum likelihood bootstrap values higher than 50% are given at the nodes. The holotype specimens retrieved from the GenBank are in bold and black. The new species are in bold and blue. The section of the species is indicated after the collection/GenBank no. of each specimen



14–107, 001434100 (K-M). Gainesville, Sweetwater, Eastern trail, Xeric oak forest with some pines, 9 January 2015, K. Liimatainen, T. Niskanen 14–135, 001434101 (K-M). High Springs, O'Leno State Park, Xeric oak forest with pine hammock, 11 January 2015, K. Liimatainen, T.

Niskanen 14–139, 001434102 (K-M). *loc. cit.* 11 January 2015, K. Liimatainen, T. Niskanen 14–144, 001434103 (K-M). *loc. cit.* 11 January 2015, K. Liimatainen, T. Niskanen 14–150, 001434104 (K-M). *loc. cit.* 11 January 2015, K. Liimatainen, T. Niskanen 14–152, 001434105



(K-M). *loc. cit.* 11 January 2015, K. Liimatainen, T. Niskanen 14–163, 001434106 (K-M). Columbia Co., River Rise State Park, laurel oak, live oak, *Pinus*, *Magnolia*, sweetgum, 13 January 2015, K. Liimatainen, T. Niskanen 14–174, 001434095 (**holotype** in K-M; isotype in H). Paynes Prairie Preserve State Park, parking place in east side of the road at Puggy Road junction, Park-like oak spp. dominated forest, 14 January 2015, K. Liimatainen, T. Niskanen 14–244, 001434107 (K-M).

**GenBank numbers:** TN14-174: ITS = ON843399; TN14-060: ITS = ON843400; TN14-096: ITS = ON843401; TN14-112: ITS = ON843402; TN14-068: ITS = ON843403; TN14-107: ITS = ON843404; TN14-135: ITS = ON843405; TN14-139: ITS = ON843406; TN14-144: ITS = ON843407; TN14-150: ITS = ON843408; TN14-152: ITS = ON843409; TN14-163: ITS = ON843410; TN14-224: ITS = ON843411.

**Notes:** Although a brown species of *C.* subgenus *Telamonia*, *C. floridaensis* has a combination of characters that make it rather easy to identify. It is a medium-sized species with an innately fibrillose, olive yellow brown pileus, the apex of the stipe is blue, the universal veil is ochraceous yellow to ochraceous brown, and the smell is raphanoid. The systematic position of the species in the subgenus was not resolved, but the species is most reminiscent of those in sections *Brunneotincti*, *Valgi* and *Bovini*.

***Cortinarius subiodes*** Niskanen, Liimat. & M. E. Sm., *sp. nov.*

**Index Fungorum number:** IF 900307; **Facesoffungi number:** FoF 14864; Figs. 60c, 61c, 62

**Holotype:** K-M 001434108.

**Etymology:** The name refers to affinity with *Cortinarius iodes*.

**Pileus** 3–7.5 cm in diam, at first hemispherical, then low convex to almost plane, greyish blue to purple, and becoming pale yellow from the centre with age, innately fibrillose, somewhat slimy. **Lamellae** subcrowded to medium spaced, greyish blue when young, later greyish brown. **Stipe** 2–4.5 cm long, 0.7–1.5 cm thick at the apex, more or less marginate bulbous, white fibrillose. **Context** faint greyish or yellowish white with bluish tints. **Universal veil** glutinous, blue, forming a sock-like sheet or some belts at the bottom of stipe. **Mycelium** white. **Odour** in lamellae sweet. **Basidiospores** 9.5–10.5 × 6–6.5 µm, ellipsoid, moderately verrucose. **Basidia** hyaline. **ITS sequence** (GenBank ON843412, **ex holotype**) distinct from other members of *Cortinarius* and with 98% similarity to the closest known species *C. iodes*.

**Habitat and distribution:** In mixed forest (oaks and *Pinus*) and so far known from Florida, USA.

**Material examined:** USA, Florida, Franklin Co., by the bridge, when entering to Franklin Co., boat ramp place, young oak-dominated forest with some *Pinus*, 26 December

2014, K. Liimatainen, T. Niskanen 14-075, 001434110 (K-M). Wakulla Co., Crawfordville, 306 Wakulla Beach Road, under *Pinus*, mixed deciduous and *Pinus* forest with some *Quercus virginiana*, *Magnolia grandiflora* and sweetgum, sandy soil, on calcareous bedrock, 27 December 2014, K. Liimatainen, T. Niskanen 14-078, 001434111 (K-M). Otter Lake Road, young evergreen oak and *Pinus* forest, on sandy soil, 28 December 2014, K. Liimatainen, T. Niskanen 14-099, 001434112 (K-M). Tallahassee Co., Lake Talquin State Forest, by the road 267, Bear Creek Educational forest, mostly evergreen oaks, 29 December 2014, K. Liimatainen, T. Niskanen 14–106, 001434113 (K-M). Alachua Co., Gainesville, Sweetwater Preserve, Eastern trail, Xeric oak forest with some pines, 9 January 2015, K. Liimatainen, T. Niskanen 14–132, 001434109 (K-M). *loc. cit.* 15 January 2015, K. Liimatainen, T. Niskanen 14–286, 001434108 (**holotype** in K-M; isotype in H).

**GenBank numbers:** TN14-286: ITS = ON843412; TN14-132: ITS = ON843413; TN14-075: ITS = ON843414; TN14-078: ITS = ON843415; TN14-099: ITS = ON843416; TN14-106: ITS = ON843417.

**Notes:** *Cortinarius subiodes* is easy to spot in the field due to its bright greyish blue to purple colours. The pileus and universal veil are slimy and the basidiospores are ellipsoid. The species belongs to *C.* cf. subgenus *Camphorati*, section *Delibuti*. The sister species *C. iodes* can be distinguished by relatively longer, cylindrical to slightly clavate stipe.

***Hygronarius*** Niskanen & Liimat.

**Notes:** This small genus with bihemispheric distribution has an estimated 10 species including small- to medium-sized, stipitocarpic, agaricoid (telamonioid) species with brownish colours. The stipe is dry and the pileus is dry or viscid and hygrophanous. The basidiospores are subglobose or ellipsoid and the pileipellis is duplex with a more or less developed hypoderm. Two subgenera, *Hygronarius* and *Vincisi* are recognized (Liimatainen et al. 2022).

***Hygronarius californicus*** Niskanen, Liimat., Bojantchev & Ammirati, *sp. nov.*

**Index Fungorum number:** IF 900308; **Facesoffungi number:** FoF 14865; Figs. 60d, 61d, 62

**Etymology:** The species was first found from California, USA.

**Holotype:** K-M 001434114.

**Pileus** 1.5–3.5 cm in diam, at first hemispherical, then low convex to almost plane, sometimes with a broad and low umbo, red brown, strongly hygrophanous. **Lamellae** medium spaced, pale brown. **Stipe** 4–6 cm long, 0.5–1.0 cm thick at the apex, cylindrical, yellowish brown to ochre brown fibrillose. **Context** yellow brown to red brown. **Universal veil** and **cortina** absent. **Mycelium** white. **Odour** indistinct. **Basidiospores** 6.5–7.5 × 5–5.5(–5.7) µm, somewhat

obovoid-subglobose to very broadly obovoid-ellipsoid, moderately to almost strongly verrucose. *ITS sequence* (GenBank ON843418, **ex holotype**) distinct from other members of *Hygronarius* and with 98% similarity to the closest known species *H. renidens*.

**Habitat and distribution:** In mixed coniferous forests and so far known from North America: Alberta, British Columbia, California, Oregon and Washington.

**Material examined:** Canada, Alberta, Hinton, 05 September 2011, T. Niskanen 11–381, 001434115 (K-M). USA, California, Mendocino Co, Jackson Demonstration State Forest, crossing of the roads 408 and 409, mixed conifer dominated forest (*Tsuga*), 17 November 2012, T. Niskanen 12-080, 001434114 (**holotype** in K-M; isotype in H). Oregon, Detroit, Breitenbush, surroundings of the Breitenbush Hot Springs Retreat & Conference centre, mixed coniferous forest of *Tsuga heterophylla* and *Pseudotsuga mentziesi* with some *Castanopsis chrysophylla*, 12 October 2007, K. Liimatainen, T. Niskanen 07–482, 001434116 (K-M). Washington, Mount Baker, Easy Pass trailhead, coniferous forest (*Tsuga heterophylla*, *Abies* and some *Picea engelmannii*), 28 September 2009, K. Liimatainen, T. Niskanen 09-017, 001434117 (K-M).

**GenBank numbers:** TN12-080: ITS = ON843418; TN11-381: ITS = ON843419; TN07-482: ITS = ON843420; TN09-017: ITS = ON843421.

**Notes:** *Hygronarius californicus* is characterised by the red brown pileus, absence of universal veil, and small, obovoid-subglobose to very broadly obovoid-ellipsoid basidiospores. The spores are slightly longer than those in the North American-European sister species *H. renidens* ( $6\text{--}7 \times 5\text{--}5.5 \mu\text{m}$ ), but for an unambiguous identification an ITS sequence is needed. *Hygronarius californicus* belongs to the *H.* subgen. *Hygronarius*.

### ***Mystinarius* Niskanen & Liimat.**

**Notes:** The species of this small (< 5 species), bihemispheric genus have medium-sized, stipitocarpic, agaricoid (myxacioid/phlegmacioid) basidiomes with a yellow to reddish brown, somewhat viscid to almost dry pileus, and a white to yellow, dry or very slightly viscid stipe. The basidiospores are medium-sized and the pileipellis is duplex (Liimatainen et al. 2022).

***Mystinarius ochrobrunneus* Ammirati, Halling, Niskanen & Liimat., sp. nov.**

**Index Fungorum number:** IF 900309; **Facesoffungi number:** FoF 14866; Figs. 60e, 61e

**Etymology:** Named for the general coloration of the basidiomes.

**Holotype:** CR 4064459.

**Pileus** 2.5–4 cm in diam, campanulate to obtuse-umbonate, rarely plano-umbonate, margin often irregular,

1/3–1/2 pellucid striate, orange yellow brown to orange brown or reddish brown, margin ochraceous brown to light ochraceous tawny with darker brown striations or more orange ochraceous brown, edge sometimes very pale, viscid.

**Lamellae** crowded to subcrowded, adnexed, bright ochraceous brown, pallid to whitish in places. **Stipe** 7–9 cm long, 0.4–0.6 cm thick at the apex, up to 1.3 cm at the base, clavate-bulbous, at first white then yellowish, colour often watery, viscid at mid-stipe when young. **Context** to 3–4 mm on disc, very thin over lamellae, watery and  $\pm$  concolorous (watery brown), in stipe hollow, cortex white to watery white, in hollow ochraceous to pale watery yellowish. **Universal veil** white, forming thin patches on the stipe. **Mycelium** white. **Odour** fungoid. **Taste** of gluten and context bitter. **Basidiospores**  $8\text{--}9 \times 5\text{--}5.5 \mu\text{m}$ , amygdaloid to somewhat ellipsoid, finely verrucose. *ITS sequence* (GenBank ON843422, **ex holotype**) distinct from *M. lustrabilis* with 98% similarity.

**Habitat and distribution:** In *Quercus* spp. forests and so far known from Costa Rica.

**Material examined:** Costa Rica, San José, Pérez Zeledón, Paramo, R.F. Los Santos, San Gerardo de Dota, Albergue de Montaña Savegre, 2200–2500 m, *Quercus* spp. gregarious in deep leaf litter, 7 June 2004, J. F. Ammirati, 4064459 (**holotype** in CR; isotypes in NY & K).

**GenBank number:** ITS = ON843422.

**Notes:** *Mystinarius ochrobrunneus* is a rather small and fragile species with bitter taste, viscid orange brown pileus, white, somewhat viscid stipe when young, and amygdaloid to somewhat ellipsoid basidiospores. The sister species *M. lustrabilis* occurs in Europe. Morphologically the species also resembles those of *Thaxterogaster* sect. *Vibratiles*.

### ***Phlegmacium* (Fr.) Wünsche.**

**Notes:** This predominantly Northern Hemispheric genus is estimated to include around 200 species. Basidiomes are medium- to large-sized, rarely small. Typical for the species are a dry stipe and viscid to glutinous pileus, or if dry, then the KOH reaction in the context of the pileus is usually yellow. Most species have a pileipellis duplex with a more or less developed hypoderm but the species of the subgenus *Cyanicium* and some lineages of *P.* subgen. *Phlegmacium* have a simplex pileipellis. The genus includes four subgenera: *Phlegmacium*, *Bulbopodium*, *Carbonella* and *Cyanicium* (Liimatainen et al. 2022).

***Phlegmacium fennicum* Kekki, Kytöv., Niskanen & Liimat., sp. nov.**

**Index Fungorum number:** IF 900310; **Facesoffungi number:** FoF 14867; Figs. 63a, 64a, 65

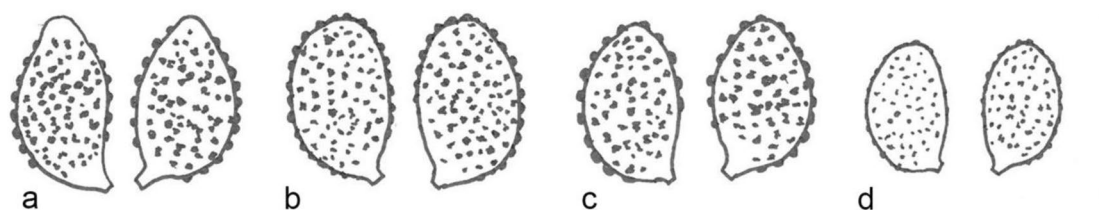
**Etymology:** The species has thus far only been found from Finland.

**Holotype:** K-M 001434119.



**Fig. 63** Basidiomes of the species of the genera *Phlegmacium* and *Thaxterogaster*. **a** *Phlegmacium fennicum* (K-M 001434119, **holotype**). **b** *Phlegmacium pallidocaeruleum* (K-M 001434120, **holotype**).

**c** *Thaxterogaster americanoporphyropus* (K-M 001434121, **holotype**). **d** *Thaxterogaster obscurovibratilis* (K-M 001434124, **holotype**). Photographs: **a** Tapio Kekki, **b–d** Kare Liimatainen



**Fig. 64** Basidiospores of the species of the genera *Phlegmacium* and *Thaxterogaster*. **a** *Phlegmacium fennicum* (K-M 001434119, **holotype**). **b** *Phlegmacium pallidocaeruleum* (K-M 001434120, **holotype**).

**c** *Thaxterogaster americanoporphyropus* (K-M 001434121, **holotype**). **d** *Thaxterogaster obscurovibratilis* (K-M 001434124, **holotype**). Drawings: Tuula Niskanen. Scale bars: 10  $\mu$ m

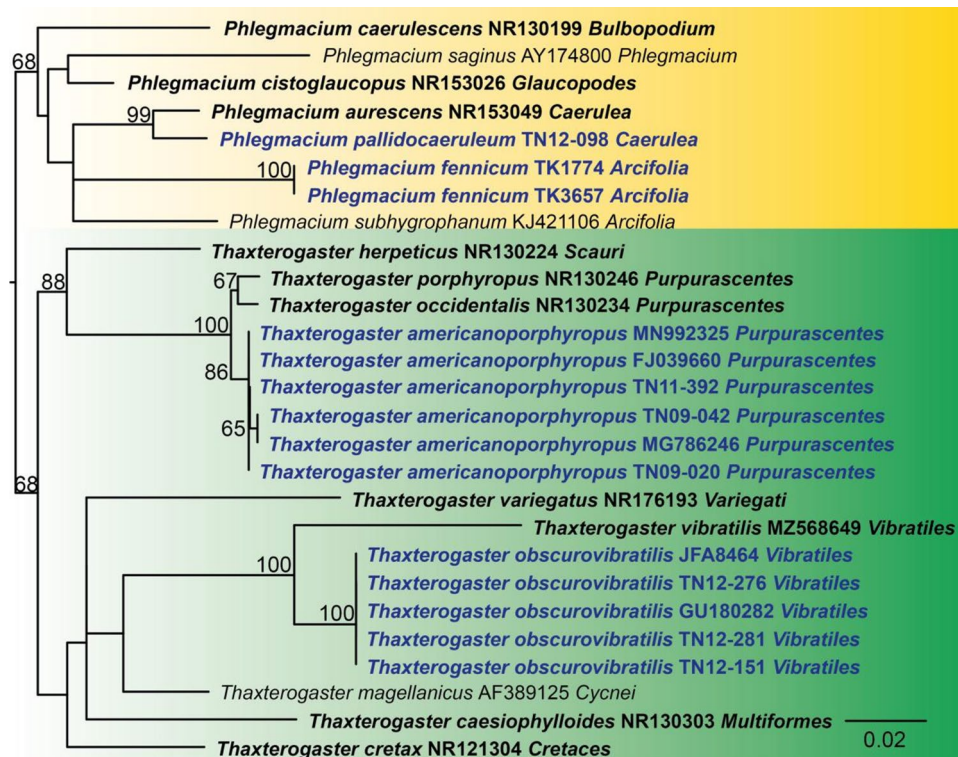
*Pileus* 4.5–7 cm in diam, at first hemispherical, then low convex to almost plane, yellowish brown with brown fibrils, with hygrophanous streaks. *Lamellae* subcrowded, pale brown to pale greyish brown when young, brown when old. *Stipe* 6–8 cm long, 1–1.5 cm thick at the apex, up to 3 cm at base, bulbous with a somewhat marginate to more rarely rounded bulb, at first very pale yellowish brown, later pale yellowish brown, fibrillose. *Context* pale yellowish brown. *Universal veil* pale brown, at the margin of the bulb. *Mycelium* white. *Odour* indistinct. *Taste* somewhat bitter. *KOH reaction* in pileus, in the context of bulb and in bulbipellis negative. *Basidiospores* (8.5–)9–10(–10.5)  $\times$  5–6(–6.5)  $\mu$ m,

amygdaloid-citriform to citriform, coarsely verrucose. *ITS sequence* (GenBank ON843423, **ex holotype**) distinct from other members of *Phlegmacium* and with 92% similarity to the closest known species.

*Habitat and distribution*: In *Picea abies* forest on calcareous ground and so far known only from Finland.

*Material examined*: Finland, Perä-Pohjanmaa, Keminmaa, Kallinkangas, W part, herb-rich *Picea abies* forest on calcareous ground, 28 June 2015, T. Kekki 1774, 215553 (TUR). *loc. cit.*, 25 June 2019, T. Kekki 3657, 001434119 (**holotype** in K-M; isotype in OULU).





**Fig. 65** The best scoring RAxML tree of the genera *Phlegmacium* and *Thaxterogaster* based on the ITS region. Related sequences were retrieved from GenBank. Twenty-six specimens were included in the analysis of the ITS region which comprises 671 characters after alignment. The tree is rooted with *Thaxterogaster*. Estimated base frequencies were: A=0.246332, C=0.202234, G=0.200934, T=0.350500; substitution rates AC=1.534815, AG=3.904253, AT=1.485681,

CG=0.452034, CT=6.187457, GT=1.000000, gamma distribution shape parameter  $\alpha$ =0.257017. Maximum likelihood bootstrap values higher than 50% are given at the nodes. The holotype specimens retrieved from the GenBank are in bold and black. The new species are in bold and blue. The section of the species is indicated after the collection/GenBank no. of each specimen

*GenBank numbers*: TK1774: ITS = ON843434; TK3657: ITS = ON843423.

*Notes*: *Phlegmacium fennicum* is a precocious species producing basidiomes already in June. It can be recognized by the combination of yellowish brown basidiomes without bluish tints, amygdaloid-citriform to citriform, coarsely verrucose basidiospores and habitat with *Picea* on calcareous ground. It belongs to the *P.* subgenus *Bulbopodium* sect. *Arcifolia*. The two other known species of the section, *P. arcifolium* and *P. subhygrophanum*, occur with *Fagus* in Europe.

***Phlegmacium pallidocaeruleum*** Niskanen Liimat. & Bojantchev, *sp. nov.*

*Index Fungorum number*: IF 900311; *Facesoffungi number*: FoF 14868; Figs. 63b, 64b, 65

*Etymology*: Named for the general coloration of the basidiomes.

*Holotype*: K-M 001434120.

*Pileus* 4.5–7.5 cm in diam, at first hemispherical, then low convex to almost plane, innately fibrillose, ochraceous in the middle, silvery bluish grey towards margin, ochraceous part enlarging with age, viscid, somewhat hygrophanous striate.

*Lamellae* subcrowded to crowded, bluish grey, adnexed to adnate. *Stipe* 5–9 cm long, 1–2 cm thick at the apex, up to 3 cm at the base, with a rounded bulb, at first pale greyish blue, later more whitish, becoming brownish ochraceous when handled or gaining brownish ochraceous spots with age. *Context* when young bluish white marbled hygrophanous in the pileus and upper part of the stipe, white at the lower part of the stipe, when old white or yellowish white in the pileus and the base of stipe, greyish blue at the apex of stipe. *Universal veil* white at the very base of the stipe/bulb. *Mycelium* white, often forming strands. *Odour* indistinct. *Basidiospores* 8.5–10 × 5–6  $\mu$ m, obovoidly ellipsoid, moderately verrucose, somewhat more strongly at the apex. *Basidia* hyaline in 5% KOH. *ITS sequence* (GenBank ON843424, **ex holotype**) distinct from other members of *Phlegmacium* and with 98% similarity to the closest known species *P. aureum*.

*Habitat and distribution*: In mixed coniferous forests and so far known from California, USA.

*Material examined*: USA, California, Mendocino Co., Caspar, Caspar cemetery, mixed conifer dominated forest with *Tsuga*, *Abies* and *Picea*, 22 November 2012, K.

Liimatainen, T. Niskanen 12-098, 001434120 (**holotype** in K-M; isotype in H).

*GenBank number*: ITS = ON843424.

*Notes*: *Phlegmacium pallidocaeruleum* is a typical member of the *P.* sect. *Caerulea*. It has pallid blue colours, the pileus is innately fibrillose and becoming more ochraceous from the centre with age, and the basidiospores are ellipsoid. The sister species *P. aurescens*, currently known from Washington, USA, has less bluish basidiomes and longer (10–11 × 5.5–6.5 µm) basidiospores.

### *Thaxterogaster* Singer.

*Notes*: The centre of the diversity of this genus is in the Southern Hemisphere and it is estimated to include around 200 species. The size of the basidiomes ranges from small to large and varies in coloration from white, ochraceous, greenish, brown to purple. Typical characters for all agaricoid species, however, are a pileipellis duplex and a negative or, more rarely, red KOH reaction. Several lineages of this genus have a honey-like or sweet smell in the context, otherwise known only in *Cortinarius* subgen. *Myxacium*. The development of basidiomes ranges from stipitocarpic to pileocarpic type. Six subgenera are currently recognized: *Thaxterogaster*, *Cretaces*, *Multiformes*, *Riederorum*, *Scauri* and *Variegati* (Liimatainen et al. 2022).

*Thaxterogaster americanoporphyropus* Niskanen, Liimat. & Ammirati, *sp. nov.*

*Index Fungorum number*: IF 900312; *Facesoffungi number*: FoF 14869; Figs. 63c, 64c, 65

*Etymology*: The species is known from North America and is reminiscent of *T. porphyropus*.

*Holotype*: K-M 001434121.

*Pileus* 4–8 cm in diam, at first hemispherical, then low convex, pale silvery grey to ochraceous, viscid-sticky to glutinous. *Lamellae* medium spaced, at first purplish grey, pale brown with age, becoming strongly purple when touched. *Stipe* 5–8 cm long, 0.8–1.3 cm thick at the apex, up to 2 cm at the base, clavate, whitish grey, with more or less purplish tints, especially when young, becoming strongly purple when touched. *Context* completely purple or only in parts of the pileus, cortex and at the base of the stipe, and then other parts white. *Universal veil* white, sparse. *Mycelium* white. *Odour* at the base of the stipe honey-like. *Basidiospores* 8.5–9.5 × 5–6 µm, amygdaloid to obovoidly amygdaloid-ellipsoid, strongly verrucose. *Basidia* hyaline in 5% KOH. *ITS sequence* (GenBank ON843425, ex holotype) distinct from other members of *T.* subgen. *Scauri* sect. *Purpurascens* and with 98.5% similarity to the closest known species, *T. porphyropus* and *T. occidentalis*.

*Habitat and distribution*: In mixed coniferous forests and so far known from North America: Alberta, British Columbia, Quebec and Washington.

*Material examined*: Canada, Alberta, Hinton, 5 September 2011, K. Liimatainen, T. Niskanen 11–392, 001434123 (K-M). USA, Washington, Mount Baker, Easy Pass trailhead, coniferous forest with *Tsuga heterophylla*, *Abies* and some *Picea engelmannii*, 28 September 2009, K. Liimatainen, T. Niskanen 09-020, 001434122 (K-M). Snohomish Co., Barlow past, Mount Baker-Snoqualmie national forest, mixed coniferous forest with mainly *Tsuga heterophylla* and some *Pseudotsuga mentziesi* and *Abies amabilis*, 3 October 2009, K. Liimatainen, T. Niskanen 09-042, 001434121 (**holotype** in K-M; isotype in H).

*GenBank numbers*: TN09-042: ITS = ON843425; TN09-020: ITS = ON843426; TN11-392: ITS = ON843427.

*Notes*: In the field the species looks like *T. porphyropus* and also their basidiospores are similar. Thus far, *T. porphyropus* is not known from the Western side of the Rocky Mountains and there the default identification would be *T. americanoporphyropus*. In the east side an ITS sequence is needed for unambiguous identification. The closely related *C. occidentalis* differs by having purple basidiomes and somewhat smaller (7–9 × 4.5–5.5 µm), slightly to moderately verrucose basidiospores.

*Thaxterogaster obscurovibratilis* Niskanen, Liimat. & Ammirati, *sp. nov.*

*Index Fungorum number*: IF 900313; *Facesoffungi number*: FoF 14870; Figs. 63d, 64d, 65

*Etymology*: The species belongs to *Thaxterogaster* sect. *Vibratiles* and has a darker pileus than other species of the section.

*Holotype*: K-M 001434124.

*Pileus* 2.5–5 cm in diam, at first hemispherical, later low convex to almost plain, sometimes with an umbo, dark reddish brown to pale yellowish brown, viscid to glutinous. *Lamellae* crowded, very pale greyish brown. *Stipe* 4–6 cm long, 0.4–0.8 cm thick at the apex, up to 1.5 cm at the base, clavate to rarely almost bulbous with a tapered base, almost dry, whitish silky fibrillose. *Context* dark brown to brown in the pileus, white at the apex of the stipe, pale yellow towards the base. *Universal veil* white, sparse. *Mycelium* white. *Taste* very bitter on the pileus. *Odour* in lamellae and context more or less raphanoid. *Basidiospores* 6.5–7.5 × 4.5–5 µm, ellipsoid to amygdaloid-ellipsoid, almost smooth to very finely verrucose. *Basidia* hyaline, with hyaline oil drops. *Lamellar trama hyphae* hyaline with oil drops in 5% KOH. *ITS sequence* (GenBank ON843428, ex holotype) distinct from other members of *Thaxterogaster* and with 93% similarity to the closest known species *T. vibratilis*.

*Habitat and distribution*: In mixed forests and so far known from USA: California and Washington.

*Material examined*: USA, California, Humboldt Co., Big Lagoon, trail starting from the school, spruce forest with moss cover, 3 December 2012, J. Olsson & K.



Liimatainen, T. Niskanen 12–225, 001434127 (K-M); Mendocino Co., Jackson State Forest, S of the crossing of roads 408 and 409 by road 720, mixed forest (*Lithocarpus* and *Pseudotsuga*), 26 November 2012, K. Liimatainen, T. Niskanen 12–151, 001434126 (K-M). Close to 408 road, *Pseudotsuga* and *Lithocarpus*, 8 December 2012, K. Liimatainen, T. Niskanen 12–276, 001434125 (K-M). *loc. cit.*, K. Liimatainen, T. Niskanen 12–281, 001434124 (**holotype** in K-M; isotype in H). Washington, Gray's Harbor County, Ocean Shores, caespitose to gregarious under *Tsuga heterophylla*, 17 December 1979, M. McCaw, J. F. Ammirati 8464 (WTU).

**GenBank numbers:** TN12-151: ITS = ON843430; TN12-276: ITS = ON843429; TN12-281: ITS = ON843428; JFA8464: ITS = ON843433.

**Notes:** A unique looking species in the *Thaxterogaster* sect. *Vibratiles* due to the dark colour of the pileus and thus easy to distinguish from the other members of the section. Otherwise, the species has the typical characters of the section: basidiomes are rather small, pileus is viscid to glutinous, stipe is white and somewhat viscid to almost dry, and the spores are small, amygdaloid-ellipsoid and finely verrucose.

#### *Cystostereaceae* Jülich.

**Notes:** *Cystostereaceae* was established by Jülich (1981) with *Cystostereum* as the type genus. Additional six genera, viz. *Crustomyces*, *Cystidiodontia*, *Parvobasidium*, *Parvodontia* and *Rigidotubus* are also accepted in this family (Larsson 2007a; Song et al. 2018c). Moreover, one new genus is described below as *Tenuimyces* in *Cystostereaceae*.

#### *Crustomyces* Jülich.

**Notes:** *Crustomyces* was erected by Jülich (1978) with *C. subabruptus* as the type species. Five species were described worldwide (Jülich 1978; Hjortstam 1987a, 1987b, 1995). *Crustomyces* is morphologically circumscribed by smooth to odontoid hymenophore, a dimitic hyphal system, and the presence of gloecystidia (Jülich 1978; Bernicchia and Gorjón 2010).

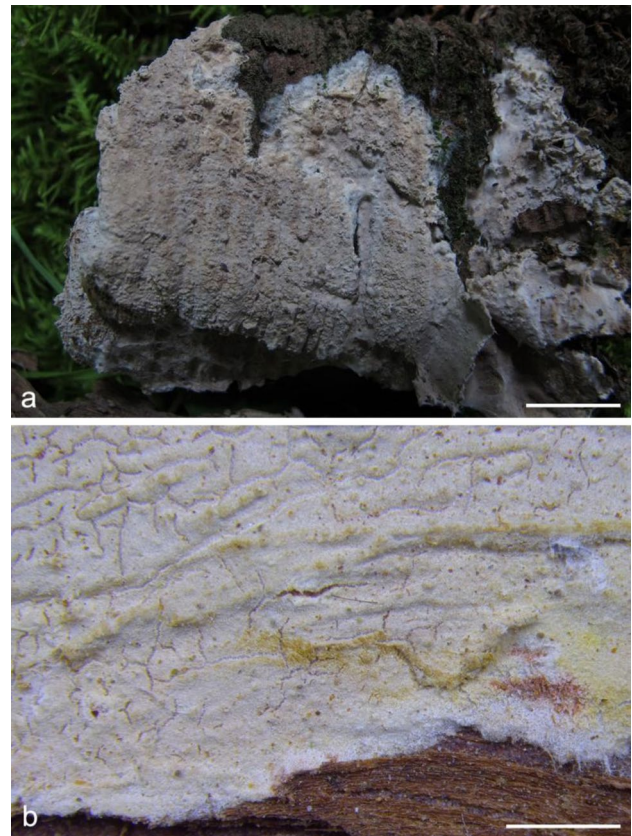
#### *Crustomyces juniperi* S.L. Liu & L.W. Zhou, *sp. nov.*

**Index Fungorum number:** IF 901033; **Facesoffungi number:** FoF 14803; Figs. 66, 67

**Etymology:** *juniperi* (Lat.) referring to inhabiting *Juniperus przewalskii*.

**Holotype:** LWZ 20180905–5 (HMAS).

**Diagnosis:** Differing from *Crustomyces heteromorphus* by its thin-walled gloecystidia with an apical rounded bulb and relatively larger basidiospores (Hallenberg 1980).



**Fig. 66** Basidiomes of *Crustomyces juniperi* (LWZ 20180905–5, **holotype**). Scale bars: **a** = 1 cm, **b** = 1 mm

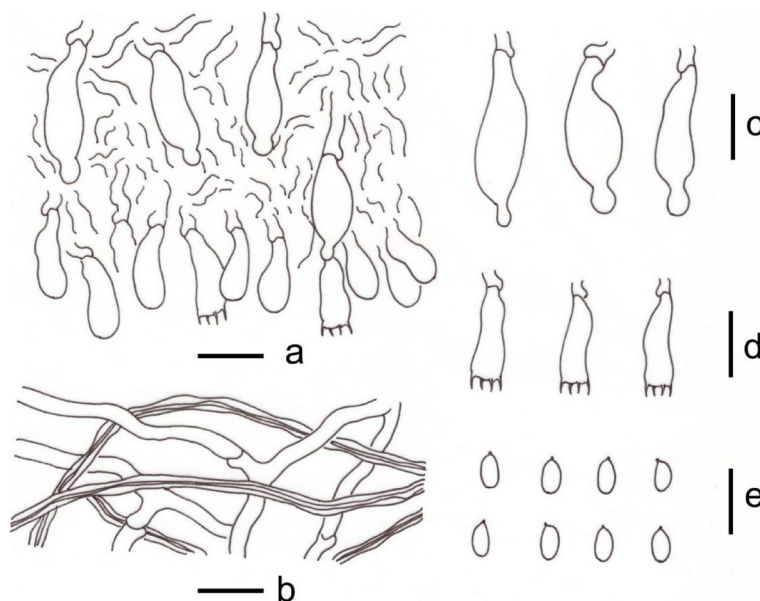
**Basidiomes** resupinate, effused, adnate, crustaceous, up to 8 cm long, 4 cm wide, 200  $\mu$ m thick. **Hymenophore** smooth with scattered tubercles, olivaceous buff when fresh, concolorous when dry, cracked. **Margin** white, thinning out as byssoid, 2 mm wide.

**Hyphal system** dimitic; **generative hyphae** with clamp connections, hyaline, thin-walled, moderately branched in subiculum, 2–3  $\mu$ m in diam; **skeletal hyphae** hyaline, unbranched or occasionally unbranched, with a narrow to wide lumen, 1.5–2  $\mu$ m in diam; **tissues** becoming a clay-buff colour in KOH. **Gloecystidia** numerous, with an empty content, thin-walled, clavate, with an apical rounded bulb, 20–30  $\times$  5–7  $\mu$ m. **Dendrohyphidia** absent. **Basidia** subclavate, 4-sterigmate, basal clamp present, 12–18  $\times$  4.5–6  $\mu$ m. **Basidiospores** ellipsoid to subcylindrical, hyaline, smooth, thin-walled, IKI–, CB–, (4–)4.5–5.2(–5.5)  $\times$  2.2–3(–3.3)  $\mu$ m, L = 4.9  $\mu$ m, W = 2.7  $\mu$ m, Q = 1.8–1.9 (n = 90/3).

**Material examined:** China, Qinghai Province, Menyuan Hui Autonomous County, Qilian Mountains National Nature Reserve, Xianmi Forest Farm, Sigou, on base of living *Juniperus przewalskii*, 9 September 2018, L.W. Zhou,



**Fig. 67** Microscopic structures of *Crustomyces juniperi* (LWZ 20180905–5, **holotype**). **a** A vertical section of basidiomes. **b** Hyphae from subiculum. **c** Cystidia. **d** Basidia. **e** Basidiospores. Scale bars: 10  $\mu$ m



LWZ 20180905–5 (HMAS, **Holotype**), LWZ 20180905–3 (HMAS), LWZ 20180905–4 (HMAS).

**GenBank numbers:** LWZ 20180905–5: ITS = OR557241, LSU = OR527267; LWZ 20180905–3: ITS = OR557242, LSU = OR527268; LWZ 20180905–3: ITS = OR557243, LSU = OR527269.

**Notes:** *Crustomyces juniperi* is nested within the *Crustomyces* clade from a phylogenetic perspective (Fig. 68). Morphologically, *C. juniperi* resembles *C. indecorus* by olivaceous buff hymenophore and similar basidiospores; however, the latter species differs in lack of apical schizopapilla on gloeocystidia and presence of dendrohyphidia (Hjortstam 1987b).

***Crustomyces scytinostromoides*** S.L. Liu & L.W. Zhou, *sp. nov.*

**Index Fungorum number:** IF 901046; **Facesoffungi number:** FoF 14804; **Figs.** 69, 70

**Etymology:** *scytinostromoides* (Lat.) referring to the similarity to the genus *Scytinostroma*.

**Holotype:** LWZ 20190808-14b (HMAS).

**Diagnosis:** Differing from *C. subabruptus* by the dominance of skeletal hyphae in subhymenium and subiculum (Eriksson and Ryvarden 1975; Jülich 1979).

**Basidiomes** resupinate, effused, adnate, at first ceraceous, with age crustaceous, up to 15 cm long, 5 cm wide, 200  $\mu$ m thick. **Hymenophore** smooth with scattered tubercles, whitish to cream when fresh, cream to buff when dry, not cracked. **Margin** white, thinning out as byssoid, 1 mm wide.

**Hyphal system** dimitic; **generative hyphae** with clamp connections, hyaline, thin-walled, 2–3  $\mu$ m in diam; **skeletal hyphae** dominant in subhymenium and subiculum, hyaline to yellowish, unbranched, 1.5–2.5  $\mu$ m in diam; **tissues**

becoming a clay-buff colour in KOH. **Gloeocystidia** numerous, thin-walled, clavate, sometimes with an apical rounded bulb, 20–30  $\times$  5–7  $\mu$ m. **Dendrohyphidia** numerous, hyaline. **Basidia**, **basidioles** and **basidiospores** not seen.

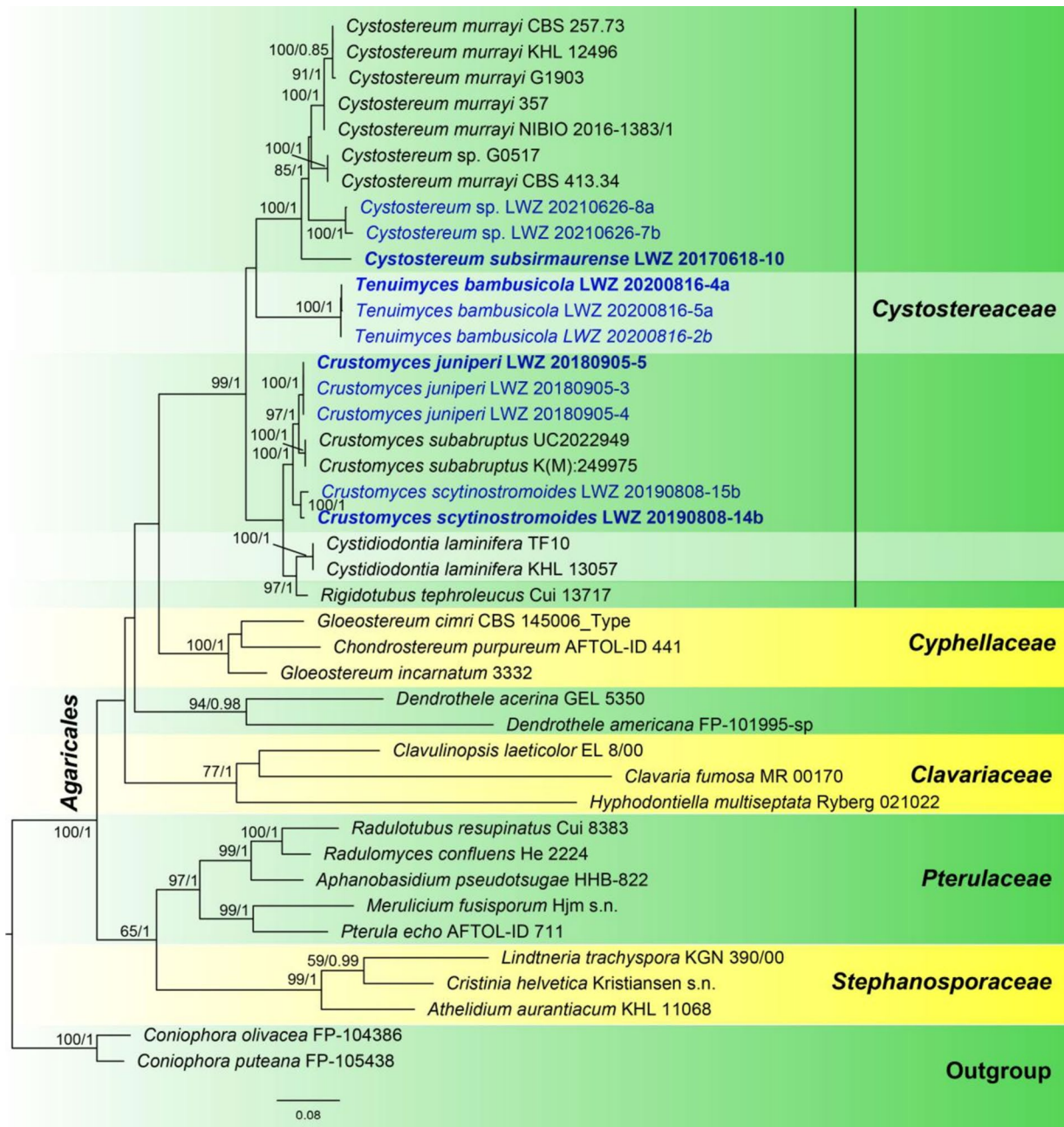
**Material examined:** China, Sichuan Province, Ganzi Tibetan Autonomous Prefecture, Jiulong County, Wuxuhai Scenic Spot, on fallen branch of angiosperm, 8 August 2019, L.W. Zhou, LWZ 20190808-14b (HMAS, **Holotype**), LWZ 20190807-15b (HMAS).

**GenBank numbers:** LWZ 20190808-14b: ITS = OR557244, LSU = OR527270; LWZ 20190807-15b: ITS = OR557245, LSU = OR527271.

**Notes:** *Crustomyces scytinostromoides* has a close phylogenetic relationship with other species of *Crustomyces* (Fig. 68). Morphologically, *C. scytinostromoides* has smooth hymenophore, a dimitic hyphal system, and the presence of gloeocystidia, which makes it fit with the concept of *Crustomyces*. However, the tubercles scattered on smooth hymenophore and the presence of skeletal hyphae in both subhymenium and subiculum make *C. scytinostromoides* distinct from other species in this genus. Although both specimens of *C. scytinostromoides* are sterile, the above-mentioned unique morphological characters are acceptable for describing a new species, like previous publications (Tchoumi et al. 2020; Yu et al. 2021).

***Cystostereum*** Pouzar.

**Notes:** *Cystostereum*, a genus of corticioid fungi in the family *Cystostereaceae*, contains nine species. Species in the *Cystostereum* have a dimitic hyphal system with very scarce light-colored skeletal hyphae, numerous vesicular gloeocystidia, and inamyloid basidiospores (Pouzar 1959; Bernicchia and Gorjón 2010; Kaur et al. 2019).



**Fig. 68** Phylogeny generated by the maximum likelihood algorithm based on combined ITS and nLSU regions is presented along with the bootstrap values and the Bayesian posterior probabilities above 50% and 0.8, respectively, at the nodes. Holotypes are in bold and

the newly generated sequences are in blue. *Coniophora olivacea* FP-104386 and *C. puteana* FP-105438 were selected as the outgroup taxa

***Cystostereum subsirmaurens* S.L. Liu & L.W. Zhou, *sp. nov.***

*Index Fungorum* number: IF 901050; *Facesoffungi* number: FoF 14805; Figs. 71, 72

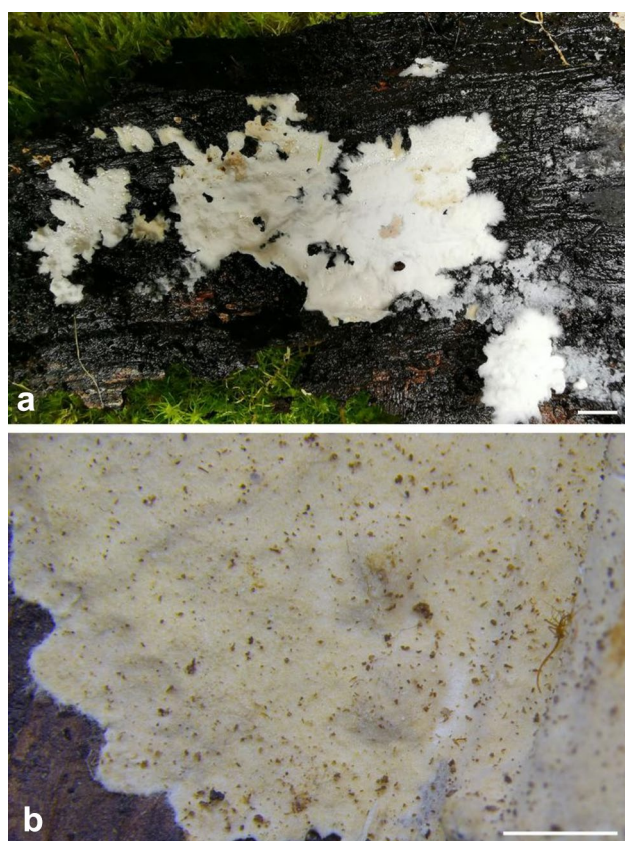
*Etymology*: *subsirmaurens* (Lat.) referring to the similarity to *Cystostereum sirmaurens*.

*Holotype*: LWZ 20170618–10 (HMAS).

*Diagnosis*: Differing from *C. sirmaurens* in thick-walled, wider cystidia (Kaur et al. 2019).

*Basidiomes* annual, resupinate, effused, adnate, corky to hard and brittle, up to 20 cm long, 4 cm wide, 200 µm thick. *Hymenophore* smooth, with minute scattered tubercles, white when fresh, becoming yellowish white to orange white on drying. *Margin* thinning or indeterminate, concolorous or paler.





**Fig. 69** Basidiomes of *Crustomyces scytinostromoides* (LWZ 20190808-14b, **holotype**). Scale bars: **a** = 1 cm, **b** = 1 mm

*Hyphal system* dimitic; *generative hyphae* with clamp connections, hyaline, thin-walled, 2–3  $\mu\text{m}$  in diam; *skeletal hyphae* subhyaline, unbranched, 1–1.5  $\mu\text{m}$  in diam. *Cystidia* subglobose to clavate, generally with an obtuse apex, thick-walled, with a basal clamp connection, embedded in hymenium and subhymenium, 30–50  $\times$  7–15  $\mu\text{m}$ . *Basidia* subclavate, 4-sterigmate, with a basal clamp connection,

15–20  $\times$  5–6  $\mu\text{m}$ . *Basidiospores* ellipsoid to subcylindrical, hyaline, smooth, thin-walled, IKI–, CB–, 3.5–4  $\times$  2.6–3  $\mu\text{m}$ ,  $L = 3.7 \mu\text{m}$ ,  $W = 2.8 \mu\text{m}$ ,  $Q = 1.3$  ( $n = 30/1$ ).

*Material examined*: China, Yunnan Province, Xishuangbanna Dai Autonomous Prefecture, Jinghong, Mengla County, Xishuangbanna National Park of Tropical Rainforests, on fallen branch of angiosperm, 18 June 2017, L.W. Zhou, LWZ 20170618–10 (HMAS, **Holotype**).

*GenBank numbers*: ITS = OR557246, LSU = OR527272.

*Notes*: *Cystostereum subsirmaurens* is nested within the *Cystostereum* clade from a phylogenetic perspective (Fig. 68). Morphologically, this species is recognized by smooth hymenophore with minute scattered tubercles, which makes it similar to *C. sirmaurens*. However, *C. sirmaurens* differs in slightly thick-walled, narrower cystidia (7–8.5  $\mu\text{m}$  in width, Kaur et al. 2019).

***Tenuimyces* S.L. Liu & L.W. Zhou, *gen. nov.***

*Index Fungorum number*: IF 901051; *Facesoffungi number*: FoF 14801.

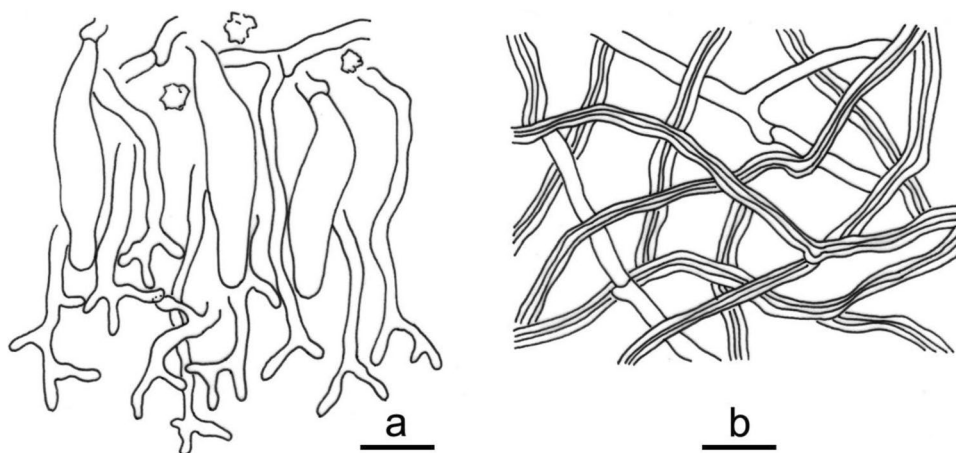
*Etymology*: *Tenuimyces* (Lat.) referring to thin basidiomes.

*Diagnosis*: Distinguished from other genera in *Cystostereaceae* by extremely thin basidiomes, a monomitic hyphal system, the presence of cystidioles and hyphidia, and aculeate, slightly thick-walled basidiospores.

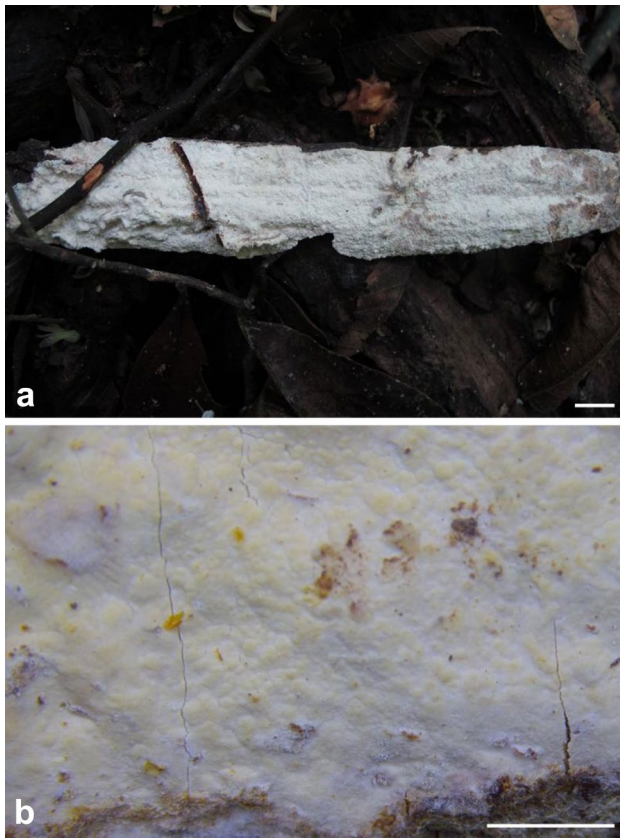
*Basidiomes* annual, resupinate, effused, thin, up to 50  $\mu\text{m}$  thick in section. *Hymenophore* smooth, white to cream. *Margin* thinning or indeterminate, concolorous or paler. *Hyphal system* monomitic; *generative hyphae* with clamp connections, hyaline, thin-walled. *Cystidioles* and *hyphidia* present. *Basidia* subclavate, 4-sterigmate. *Basidiospores* broadly ellipsoid, hyaline, aculeate, slightly thick-walled, IKI–, CB–.

*Type species*: *Tenuimyces bambusicola* S.L. Liu & L.W. Zhou.

**Fig. 70** Microscopic structures of *Crustomyces scytinostromoides* (LWZ 20190808-14b, **holotype**). **a** A vertical section of basidiomes. **b** Hyphae from subiculum. Scale bars: 10  $\mu\text{m}$







**Fig. 71** Basidiomes of *Cystostereum subsirmaurens* (LWZ 20170618–10, **holotype**). Scale bars: a = 1 cm, b = 1 mm

**Notes:** Three corticioid specimens from Southwest China form a distinct lineage with strong support within *Cystostereaceae* in phylogenetic analysis (Fig. 68). Morphologically, these three specimens have smooth hymenophore, a monomitic hyphal system, aculeate, slightly thick-walled basidiospores that are distinguished from known genera in *Cystostereaceae* (Song et al. 2018c). Therefore, a new genus *Tenuimyces* is described on the basis of these three specimens.

***Tenuimyces bambusicola* S.L. Liu & L.W. Zhou, *sp. nov.***

**Index Fungorum number:** IF 901052; **Facesoffungi number:** FoF 14806; **Figs.** 73, 74

**Etymology:** *bambusicola* (Lat.) referring to the growth on bamboo.

**Holotype:** LWZ 20200816-4a (HMAS).

**Diagnosis:** Characterized by cream, extremely thin basidiomes, and aculeate basidiospores.

**Basidiomes** annual, resupinate, effused, thin, up to 50  $\mu\text{m}$  thick in section. **Hymenophore** smooth, white to cream when fresh, concolorous when dry, cracked. **Margin** thinning or indeterminate, concolorous or paler.

**Hyphal system** monomitic; **generative hyphae** with clamps, hyaline, thin-walled, 1.5–2  $\mu\text{m}$  in diam; tissues

darkening in KOH. **Cystidioles** subfusiform, rare in the hymenium, thin-walled, with a basal clamp connection, 30–50  $\times$  7–15  $\mu\text{m}$ . **Hyphidia** rare, branched or unbranched. **Basidia** subclavate, 4-sterigmate, with a basal clamp connection, 15–20  $\times$  5–6  $\mu\text{m}$ . **Basidiospores** broadly ellipsoid, hyaline, aculeate, slightly thick-walled, IKI–, CB–, 3.5–4  $\times$  2.6–3  $\mu\text{m}$ ,  $L = 3.7 \mu\text{m}$ ,  $W = 2.8 \mu\text{m}$ ,  $Q = 1.3$  ( $n = 90/3$ ).

**Material examined:** China, Sichuan Province, Leshan, Mabian Yi Autonomous County, Dafengding National Nature Reserve, on dead bamboo, 16 August 2020, L.W. Zhou, LWZ 20200816-4a (HMAS, **Holotype**), LWZ 20200816-5a (HMAS), LWZ 20200816-2b (HMAS).

**GenBank numbers:** LWZ 20200816-4a: ITS = OR557247, LSU = OR527273; LWZ 20200816-5a: ITS = OR557249, LSU = OR527274; LWZ 20200816-2b: ITS = OR557248, LSU = OR527275.

**Notes:** *Tenuimyces bambusicola* is characterized by white to cream basidiomes with smooth hymenophore, subfusiform cystidioles, slightly thick-walled, aculeate basidiospores, and the growth on bamboo.

## Incertae sedis

***Henningsomyces* Kuntze.**

*Henningsomyces*, typified by *H. candidus*, is characterized by annual hymenophores consisting of sparse or gregarious tubes, a monomitic hyphae system usually bearing both clamp connections and simple septa, the absence of cystidia, and globose to subglobose basidiospores (Wei and Qin 2009).

***Henningsomyces hengduanensis* S.L. Liu & L.W. Zhou, *sp. nov.***

**Index Fungorum number:** IF 901053; **Facesoffungi number:** FoF 14807; **Figs.** 75, 76

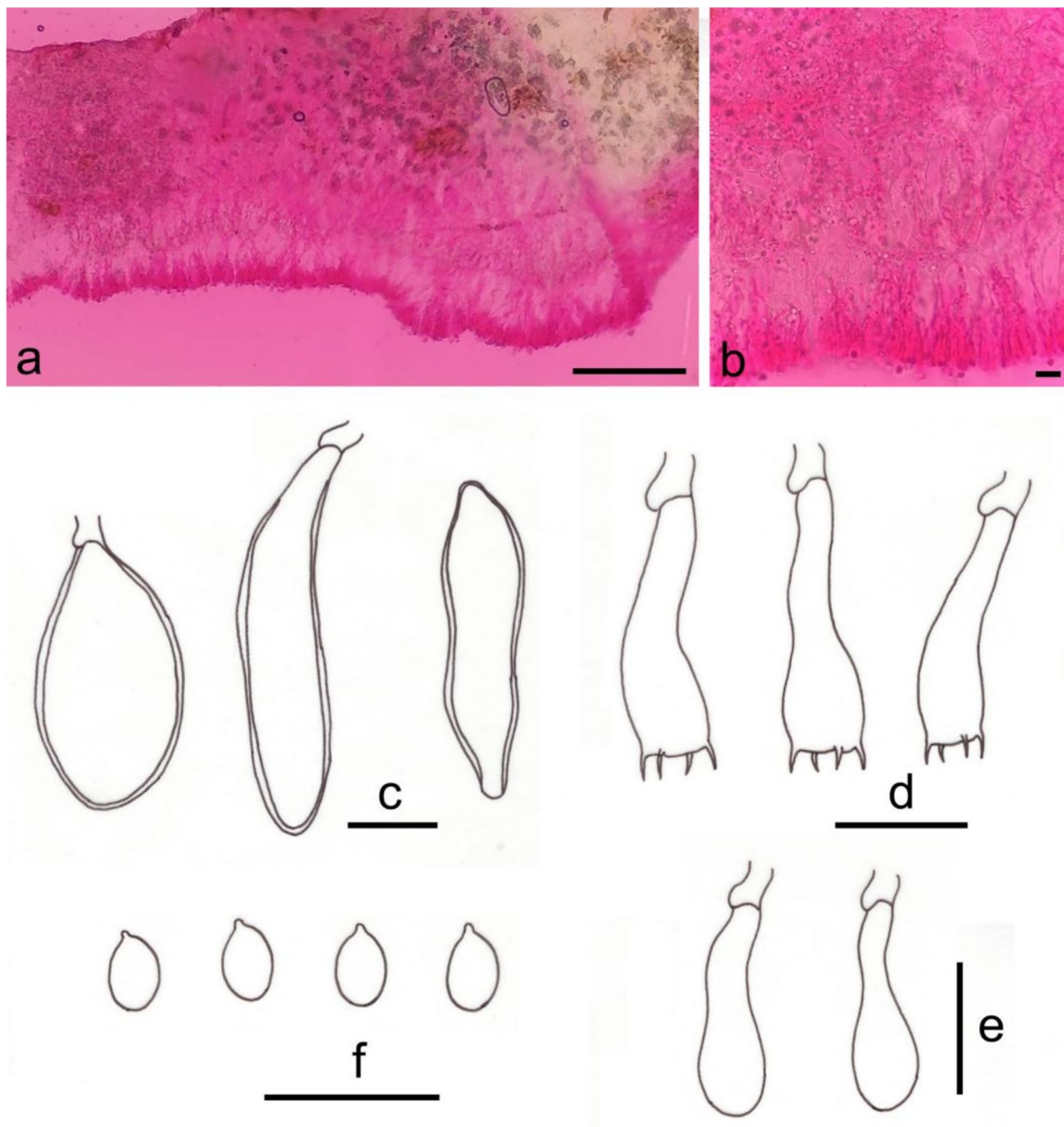
**Etymology:** *hengduanensis* (Lat.) referring to the type locality Hengduan Mountains.

**Holotype:** LWZ 20190807-11b (HMAS).

**Diagnosis:** Differing from *Henningsomyces minimus* in smaller tubes and smaller basidiospores (Wei and Qin 2009).

**Basidiomes** annual, soft when fresh, becoming a little chalky when drying, without odour or taste, white when fresh, turned cream when bruised or drying, consisting of tiny tubes. **Tubes** densely aggregated, each 0.2–0.3 mm long, 0.07–0.1 mm in diam. **Subiculum** absent.

**Hyphal system** monomitic; **generative hyphae** bearing both clamp connections and simple septa; **tramal hyphae** in tubes hyaline, smooth, thin-walled, often branched, winding, more or less tightly parallel along the tubes, 1.5–2  $\mu\text{m}$



**Fig. 72** Microscopic structures of *Cystostereum subsirmaurense* (LWZ 20170618–10, **holotype**). **a–b** A vertical section of basidiomes. **c** Cystidia. **d** Basidia. **e** Basidioles. **f** Basidiospores. Scale bars: **a** = 100  $\mu$ m, **b–f** = 10  $\mu$ m

in diam; *hyphae* at tube margin finely branched. *Cystidia* absent. *Basidia* broadly clavate, with four sterigmata and a basal clamp connection,  $15\text{--}20 \times 6\text{--}8\text{ }\mu\text{m}$ . *Basidiospores* subglobose, hyaline, thin-walled, smooth, IKI–, CB–,  $5\text{--}6 \times (4\text{--})4.5\text{--}5\text{ }\mu\text{m}$ ,  $L = 5.5\text{ }\mu\text{m}$ ,  $W = 4.7\text{ }\mu\text{m}$ ,  $Q = 1.2$  ( $n = 60/2$ ).

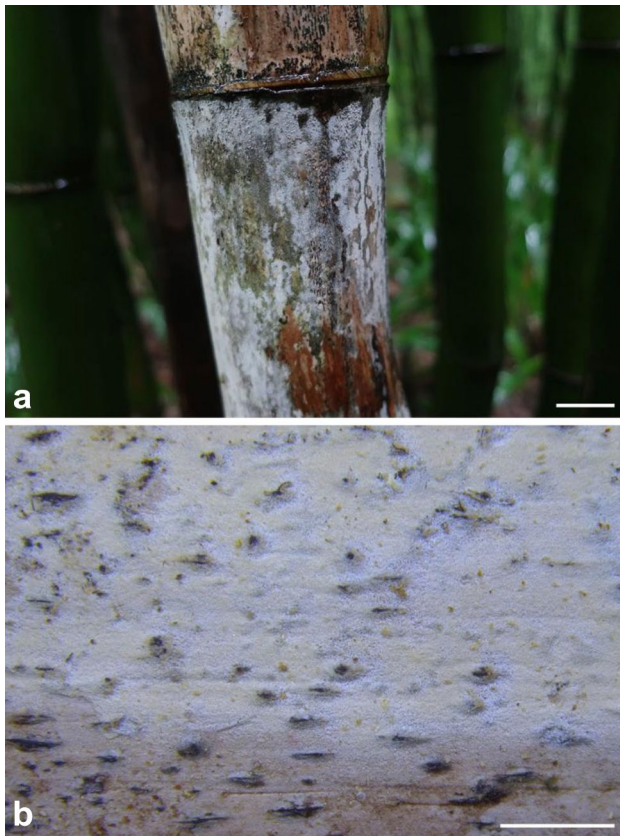
**Material examined:** China, Sichuan Province, Ganzi Tibetan Autonomous Prefecture, Jiulong County, Wahuishan Nature Reserve, on fallen trunk of *Abies*, 7 August 2019, L.W. Zhou, LWZ 20190807-11b (HMAS, **Holotype**); *ibid.*,

on fallen trunk of *Abies*, 7 August 2019, L.W. Zhou, LWZ 20190807-22b (HMAS).

**GenBank numbers:** LWZ 20190807-11b: ITS=OR557250, LSU=OR527276; LWZ 20190807-22b: ITS=OR557251, LSU=OR527277.

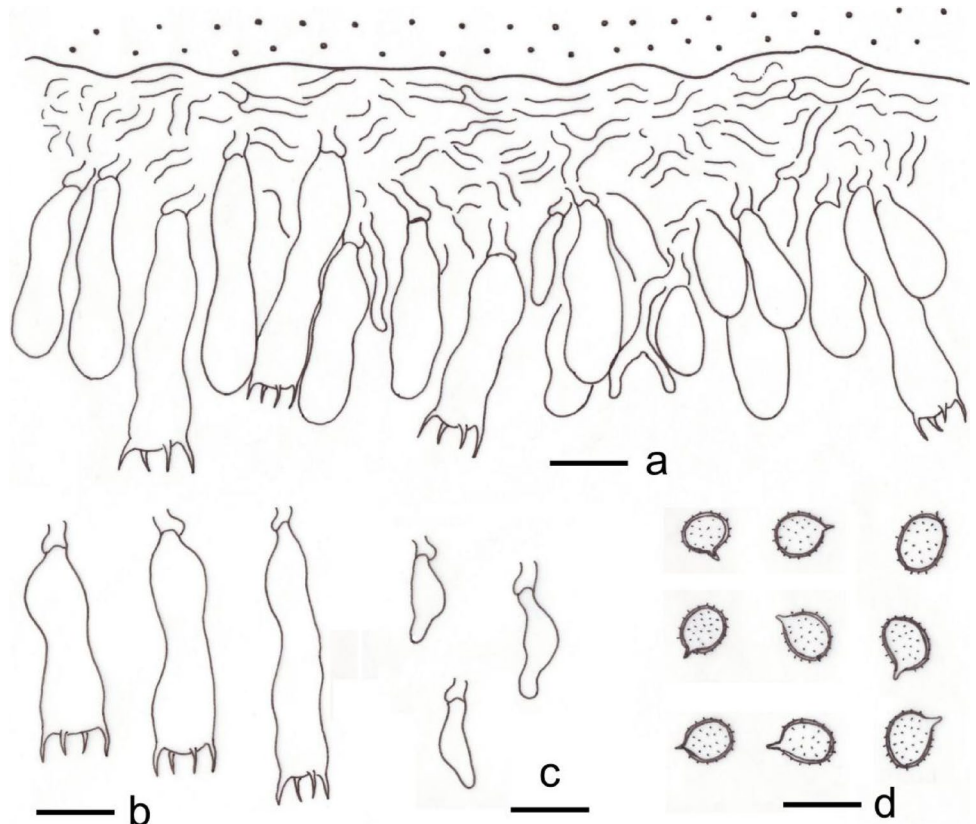
**Notes:** *Henningsomyces hengduanensis* has typical morphological characters of this genus, and falls within the clade of *Henningsomyces* as a distinct lineage (Fig. 77). Morphologically, *H. hengduanensis* resembles *H. candidus*, *H. leptus* and *H. minimus* by the absence of subiculum, but differs





**Fig. 73** Basidiomes of *Tenuimyces bambusicola* (LWZ 20200816-4a, **holotype**). Scale bars: a = 1 cm, b = 1 mm

**Fig. 74** Microscopic structures of *Tenuimyces bambusicola* (LWZ 20200816-4a, **holotype**). **a** A vertical section of basidiomes. **b** Basidia. **c** Cystidioles. **d** Basidiospores. Scale bars: 10  $\mu$ m



mainly in its smaller tubes (0.5–1 mm in length and about 0.2 mm in diam in *H. candidus*, 1.2–1.8 mm in length and 0.1–0.15 mm in diam in *H. leptus*, and up to 0.5 mm in length and 0.1 mm in diam in *H. minimus*; Wei and Qin 2009).

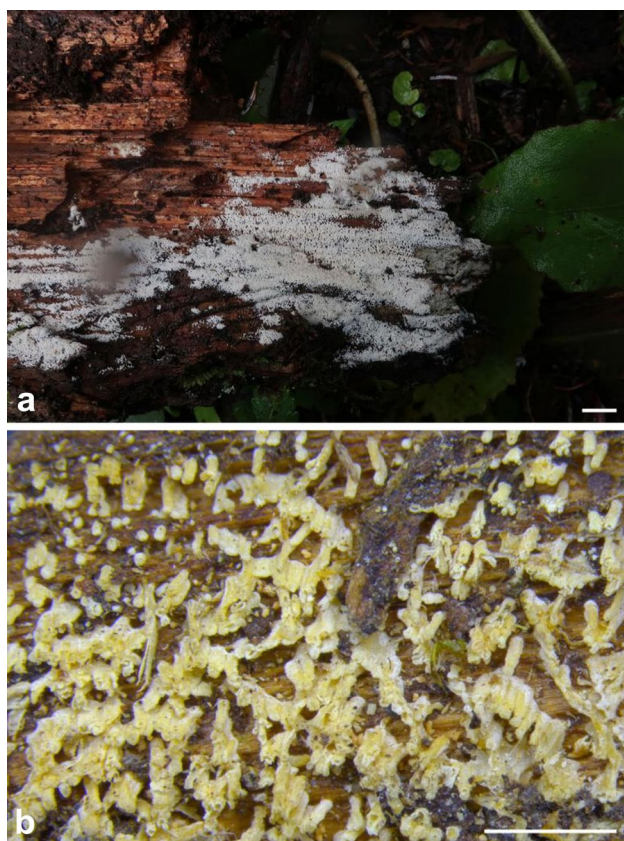
#### *Lyophyllaceae* Jülich.

*Notes:* *Lyophyllaceae* was circumscribed by Jülich (1981) and *Lyophyllum* is the generic type. Currently, *Lyophyllaceae* contains 19 genera based on molecular phylogenetic analyses (He et al. 2019; Wijayawardena et al. 2022).

#### *Calocybella* Vizzini, Consiglio & Setti.

*Notes:* The genus *Calocybella* (*Lyophyllaceae*, *Agaricales*) was circumscribed by Vizzini et al. (2015) with *C. pudica* as the type species. *Calocybella* is saprotrophic and distributed in Europe, Dominican Republic and India (Vizzini et al. 2015, 2017; Latha et al. 2016, 2020; Corriol et al. 2017). Species of *Calocybella* are characterized by collybioid or slenderly tricholomatoid basidiomes, a cutis- or a trichoderm-type pileipellis, and clamped hyphae (Vizzini et al. 2015, 2017; Latha et al. 2016). Currently, there are eight accepted species of *Calocybella* in the Index Fungorum (2022).





**Fig. 75** Basidiomes of *Henningsomyces hengduanensis* (LWZ 20190807-11b, **holotype**). Scale bars: **a** = 1 cm, **b** = 1 mm

*Calocybella sribuabanensis* N. Suwannarach, J. Kumla and S. Lumyong, *sp. nov.*

*Index Fungorum* number: IF559933; *Facesoffungi* number: FoF 12909; Fig. 78

*Etymology*: “sribuabanensis” referring to Sri Bua Ban Subdistrict where holotype was found.

*Holotype*: SDBR-CMUNK0910.

*Basidiomes* small, collybioid. *Pileus* 10–25 mm broad, convex or hemispherical when young, becoming campanulate and finally plano-convex with a small indistinct umbo; surface initially reddish brown (7E7) to brown (7E8) except at the margin which is grayish orange (5B6), not striate, somewhat granulose all over; margin initially incurved, becoming decurved to somewhat straight with age, slightly wavy or somewhat lobate. *Lamellae* emarginate with a small decurrent tooth, moderately crowded, initially grayish yellow (4B6), becoming light yellow (4A5) at maturity, up to 3 mm wide, with lamellulae of 3–6 lengths; edge finely torn, concolorous with the sides. *Stipe* 20–32 × 3–4 mm, central, terete or slightly compressed, equal or slightly tapering towards the base, stuffed; light yellow (4A4) to grayish yellow (4B5), appressed-fibrillose all over; base slightly enlarged, whitish. *Context* up to 2 mm thick at the center of the pileus, light yellow (4A4). *Odor* not distinctive.

*Basidiospores* 5–8 × 3–5 µm,  $Q = 1.33$ –2.00,  $Q_m = 1.65$ , ellipsoid to oblong-ellipsoid, with a fine verrucose ornamentation, hyaline, thin- to slightly thick-walled, acyanophilous, inamyloid. *Basidia* 22–25 × 7–8 µm, clavate or rarely pedicellate-clavate, hyaline, thin-walled, 4-spored, rarely 2-spored; sterigmata up to 6 µm long. *Lamella-edge* fertile. *Pleurocystidia* and *cheilocystidia* absent. *Lamellar trama* subregular to almost regular; hyphae 3–6 µm wide, hyaline, thin-walled, not discoloring in KOH, inamyloid. *Pileus trama* interwoven; hyphae 4–10 µm wide, with a pale yellowish brown wall pigment which is darker towards the pileipellis, thin-walled, not discoloring in KOH, inamyloid. *Pileipellis* a cutis; hyphae 3–5 µm wide, with a pale yellow wall pigment, thin-walled, slightly gelatinized. *Stipitipellis* a cutis composed of narrow, interwoven hyphae coated with a resinous material; hyphae 3–7 µm wide, with a pale yellow wall pigment which is paler towards the stipe base, thin-walled. *Caulocystidia* absent. *Clamp connections* observed on all hyphae.

*Habitat and distribution*: Solitary to gregarious on soil. Known only from Thailand.

*Material examined*: Thailand, Lamphun Province, Sri Bua Ban Subdistrict, Chiang Mai University Haripunchai Campus, 18°32'18"N 99°7'2"E, elevation 368 m, solitary to gregarious on soil, 16 August 2020, J. Kumla and N. Suwannarach, SDBR-CMUNK0910 (**holotype**); 18°32'19"N 99°7'4"E, elevation 371 m, solitary to gregarious on soil, 19 August 2022, J. Kumla and N. Suwannarach, SDBR-CMUNK1783.

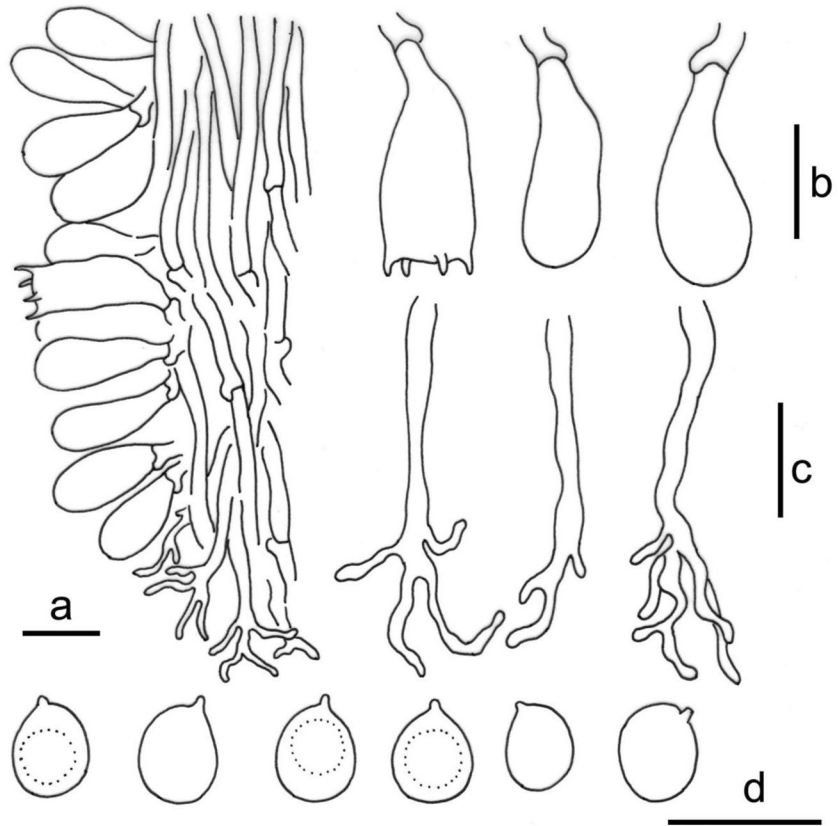
*GenBank numbers*: SDBR-CMUNK0910: ITS = OP503445; SDBR-CMUNK1783: OP503940.

*Notes*: Phylogenetic analysis of the ITS sequence confirmed that *C. sribuabanensis* stands within the genus *Calocybella* and clearly separate from the other *Calocybella* species (Fig. 79). This is the first record of the genus *Calocybella* from Thailand. Morphologically, *C. sribuabanensis* is similar to *C. goethei*; however, *C. goethei* has a longer stipe (30–45 × 3–5 mm) than *C. sribuabanensis* (20–32 × 3–4 mm, Crous et al. 2021b). A phylogenetic tree showed that *C. sribuabanensis* and *C. goethei* formed distinct species. *Calocybella sribuabanensis* forms a sister taxon to *C. dicholamellata* known from India with high support value (100% BS and 1.00 PP, Latha et al. 2020). However, the latter species is distinct by its brownish yellow pileus and narrower size of basidia (20–25 × 5–7 µm, Latha et al. 2020). An ITS sequence of *C. sribuabanensis* exhibit 97.68% similarity with both sequences of the *C. dicholamellata* CAL1242 (**holotype**) and DKP522.

#### *Marasmiaceae* Roze ex Kühner.

*Notes*: Kühner (1980) established *Marasmiaceae* with the type genus *Marasmius* and with a combination of three tribes viz. *Marasmiaceae*, *Collybieae* and *Myceneae* of *Tricholomataceae* in the classification of Singer (1986). Molecular phylogeny has revealed that *Marasmiaceae* is monophyletic,

**Fig. 76** Microscopic structures of *Henningsomyces hengduanensis* (LWZ 20190807–11, **holotype**). **a** A vertical section of basidiomes. **b** Basidia and basidioles. **c** Hyphae from tube margin. **d** Basidiospores. Scale bars: 10  $\mu$ m



and comprises 10 genera (*Amyloflagellula*, *Brunneocortium*, *Campanella*, *Chaetocalathus*, *Crinipellis*, *Hymenogloea*, *Marasmius*, *Moniliophthora*, *Neocampanella* and *Tetrapyrgos*) with more than 750 species (Matheny et al. 2006; He et al. 2019; Wijayawardene et al. 2020). *Marasmiaceae* is a lineage mainly integrated by white-spored agaricoid fungi with small, membranous and toughness pileus, and saprophytes on wood and leaf-litter or occasionally biotrophs (*Moniliophthora*).

#### *Crinipellis* Pat.

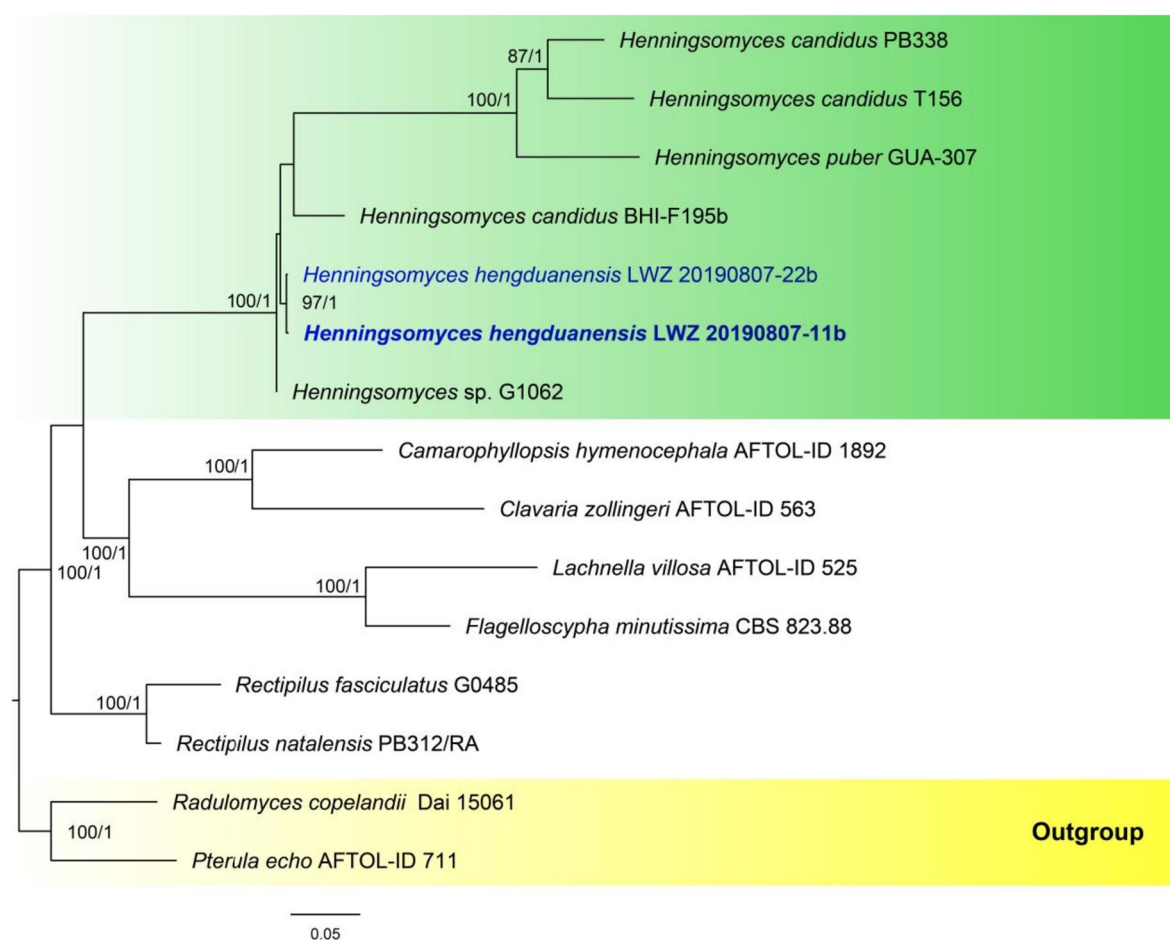
**Notes:** The genus *Crinipellis* (*Marasmiaceae*, *Agaricales*) was established by Patouillard (1900) with *C. scabella* (syn. *Agaricus stipitarius* and *C. stipitaria*) as the type species (Singer 1943). This genus is characterized by a presence of thick-walled, dextrinoid, hair-like terminal cells in the pileipellis (Kerekes and Desjardin 2009). The *Crinipellis* species has been recognized both saprotrophic and parasitic species (Singer 1943; Aime and Phillips-Mora 2005; Kerekes and Desjardin 2009). This genus comprises over 150 species and is considered to have a worldwide distribution (Kirk et al. 2008; Antonín et al. 2009; Kerekes and Desjardin 2009; Antonín and Noodeloos 2010; Antonín 2012).

*Crinipellis trichialis* (Lév.) Pat. ex Antonín, Ryoo & H.D. Shin, Mycotaxon 108: 432 (2009).

**Index Fungorum number:** IF 543142; **Facesoffungi number:** FoF 12910; **Fig. 80**

**Pileus** 5–18 mm in diameter, hemispherical to convex-cylindrical when young, becoming convex to plano-convex or applanate with age, disc with a tuft of scales forming a small papilla, with concentric zones of erect fibrils or scales around the disc, margin fibrillose; papilla and central zone dark brown (6F6–7F8), middle zone brown (6F6–7F8), margin brownish yellow (5C5–5C8). **Context** < 1 mm thick, white. **Lamellae** adnexed to free, close to crowded with 2–4 series of lamellulae, white to pale yellowish white (3A1–3A2). **Stipe** 5–25 × 0.5–1.5 mm, central, cylindrical, equal with an enlarged base, tough, pliant, fibrillose to hairy overall, insititious, brown to dark brown. **Rhizomorphs** absent.

**Basidiospores** 6–11 × 5–8  $\mu$ m,  $Q = 1.0$ –2.0 ( $n = 50$ ), ellipsoid, smooth, hyaline, inamyloid, thin-walled. **Basidia** 18–35(–40) × 6–8  $\mu$ m, clavate, 4-spored. **Pleurocystidia** 30–60 × 6–10  $\mu$ m, clavate, hyaline, inamyloid, thick-walled. **Cheilocystidia** 20–32 × 5–10  $\mu$ m, clavate, simple or a majority with 1–4 apical appendages, hyaline, inamyloid, thin-walled. **Pileipellis** a cutis, 5–6  $\mu$ m in diam, hyaline, inamyloid, with spiral encrustations, giving rise to terminal hairs with basal clamp connections. **Hairs** 50–460 × 2–5  $\mu$ m diam,



**Fig. 77** Phylogeny generated by the maximum likelihood algorithm based on combined ITS and nLSU regions is presented along with the bootstrap values and the Bayesian posterior probabilities above 50% and 0.8, respectively, at the nodes. Holotypes are in bold and

the newly generated sequences are in blue. *Radulomyces copelandii* Dai 15061 and *Pterula echo* AFTOL-ID 711 were selected as the out-group taxa

cylindrical, apex rounded to acute, with secondary septations, thick-walled, dextrinoid, yellowish-brown to greenish brown in KOH. *Stipitipellis* composed of repent cortical hyphae and terminal hairs; cortical hyphae 1–3 µm in diam, cylindrical, dextrinoid, light yellow brown to green in KOH; medullary hyphae 3–5 µm in diam, cylindrical, strongly dextrinoid, hyaline; terminal hairs 100–325 × 7.5–10 µm, cylindrical, apices acute, with secondary septations, dextrinoid, yellowish brown to greenish brown in KOH. *Clamp connections* present.

**Habitat and distribution:** Solitary to gregarious, on decomposing wood and sticks (mostly found in bamboo). Known from Brazil, Indonesia, Malaysia, Thailand and Venezuela (Kerekes and Desjardin 2009; This study).

**Material examined:** Thailand, Lamphun Province, Sri Bua Ban subdistrict, Chiang Mai University Haripunchai Campus, 18°31'59"N 99°7'46"E, elevation 401 m, solitary to gregarious on decaying wood, 16 August 2020, J. Kumla

and N. Suwannarach, SDBR-CMUNK0900 (**new record for Thailand**).

**GenBank number:** ITS=OP503450 (SDBR-CMUNK0900).

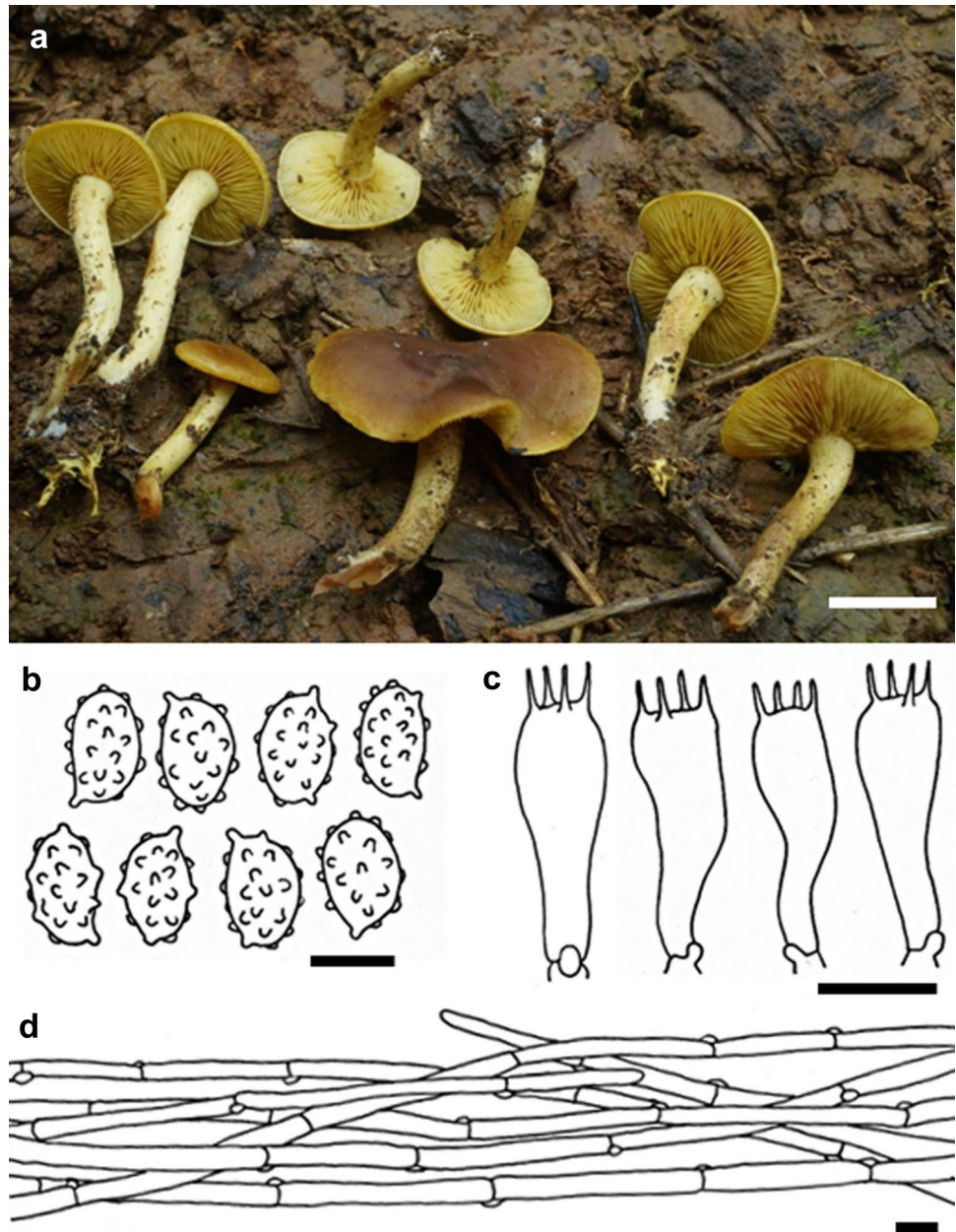
**Notes:** Phylogenetic analysis indicated that *Crinipellis trichialis* separated from sister taxon *C. scabella* and *C. rhizomaticola* (Fig. 81). *Crinipellis scabella* differs from *C. trichialis* by negative KOH reaction (Singer 1943). The narrower size of basidiospores in *C. rhizomaticola* (8.5–10 × 4–5.25 µm, Antonín et al. 2009) clearly distinguishes it from *C. trichialis* (6–11 × 5–8 µm).

#### **Marasmius** Fr.

**Notes:** *Marasmius* is a saprotrophic fungus that decomposes leaves or wood debris and distributes throughout the world. *Marasmius* contains more than 1000 species and is known as polyphyletic genus (Owings and Desjardin 1997; Wannathes et al. 2009). This genus was first divided into 12 sections by Singer, but some of them have been reclassified into several genera with the introduction of molecular



**Fig. 78** *Calocybella sribuabensis* (SDBR-CMUNK0910, holotype). **a** Basidiomes. **b** Basidiospores. **c** Basidia. **d**. Pileipellis hyphae. Scale bars: **a** = 10 mm, **b**, **d** = 5  $\mu$ m, **c** = 10  $\mu$ m



analysis. *Marasmius* is restricted to include only seven sections: *Globules*, *Hygrometrici*, *Scotophysini*, *Leveilleani*, *Marasmius*, *Neosessiles* and *Sicci*. Among them, *Marasmius* section *Marasmius*, sect. *Sicci*, and sect. *Globulares* formed a strongly supported lineage, and this clade was designated as *Marasmius sensu stricto* (Owings and Desjardin 1997; Wilson and Desjardin 2005).

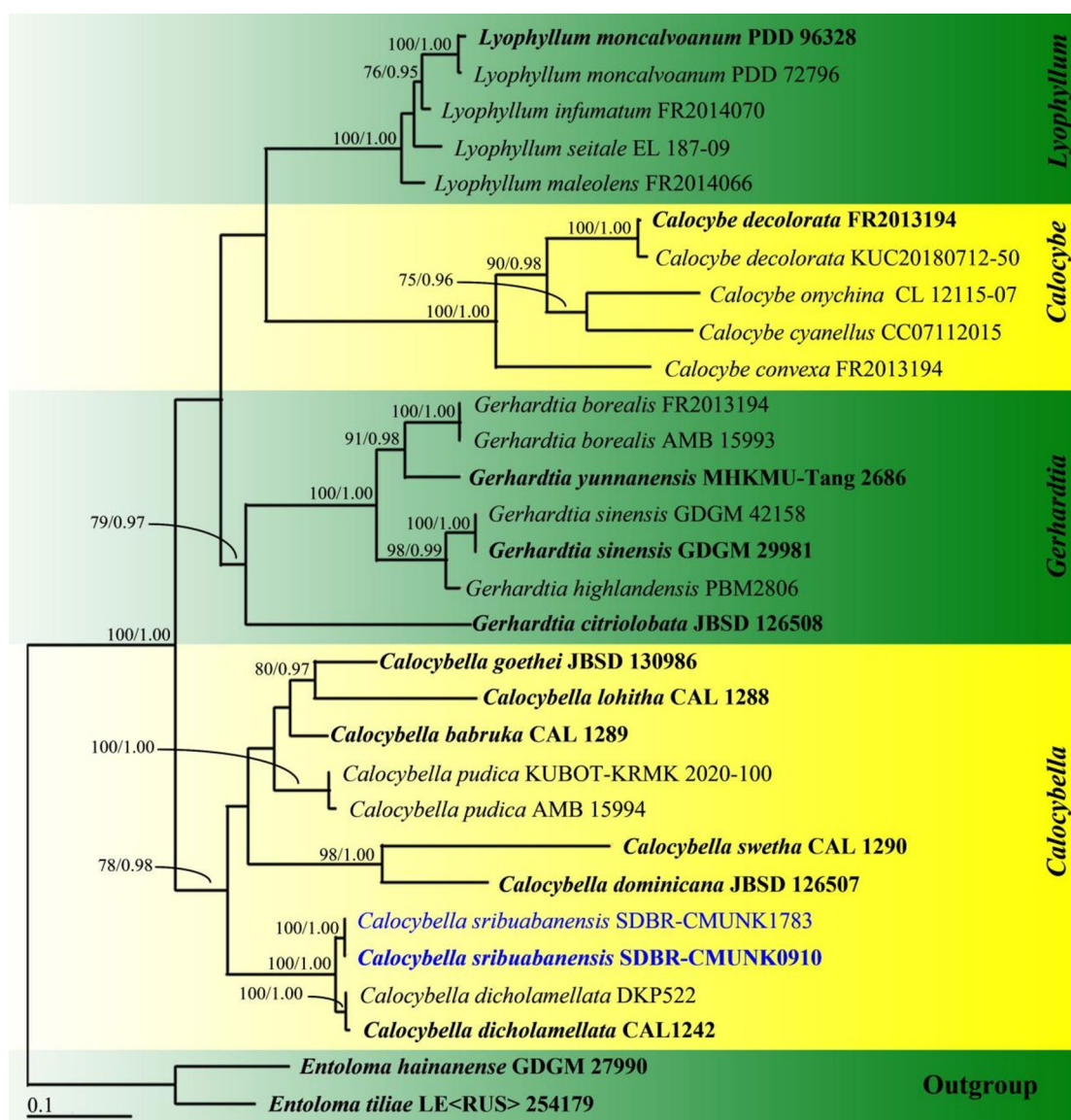
***Marasmius centrocinnameus* J.S. Kim & Y.W. Lim, *sp. nov.***

*Index Fungorum* number: IF900042; *Facesoffungi* number: FoF 13254; Fig. 82

*Etymology*: ‘*centrocinnameus*’ refers to the cinnamon (bright brown) colored center of pileus.

*Holotype*: SFC20180704-02.

*Pileus* 12–67 mm in diam, convex to campanulate when young, becoming plano-convex to uplifted when old, sometimes slightly depressed in or near the center, rugulose, glabrous, hygrophanous, greyish orange (5B5) to brown (6E6) when moist, yellowish white (3A2) to greyish yellow (4B6), margin white to yellowish white (3A2 to 4A2). *Lamellae* adnexed, distant ( $L = 12\text{--}22$ ), with 1–3 series of lamellulae, white to yellowish white (3A2 to 4A2), concolorous with margin. *Stipe* 30–110  $\times$  11–50 mm, central, cylindrical, greyish yellow (4B4) to orange white (5A2) toward apex,



**Fig. 79** Phylogenetic tree derived from maximum likelihood analysis of ITS gene of 30 sequences and the aligned dataset was comprised of 804 characters including gap. The average standard deviation of the split frequencies of the BI analysis was 0.00893. A best scoring RAxML tree was established with a final ML optimization likelihood value of -6247.2241. The matrix had 511 distinct alignment patterns with 18.35% undetermined characters or gaps. Estimated base frequencies were found to be: A=0.2542, C=0.2004, G=0.2186, T=0.3266; substitution rates AC=1.5589, AG=4.1460,

AT=1.7968, CG=0.7747, CT=5.1818, GT=1.0000. *Entoloma hainanense* GDGM 27990 and *E. tiliae* LE<RUS> 254179 were used as outgroup. Numbers above branches are the bootstrap statistics percentages (left) and Bayesian posterior probabilities (right). Branches with bootstrap values  $\geq 70\%$  and PP  $\geq 0.90$  are shown at each branch. The bar represents 0.1 substitutions per nucleotide position. Type strains are in bold. The newly generated sequences are indicated in blue

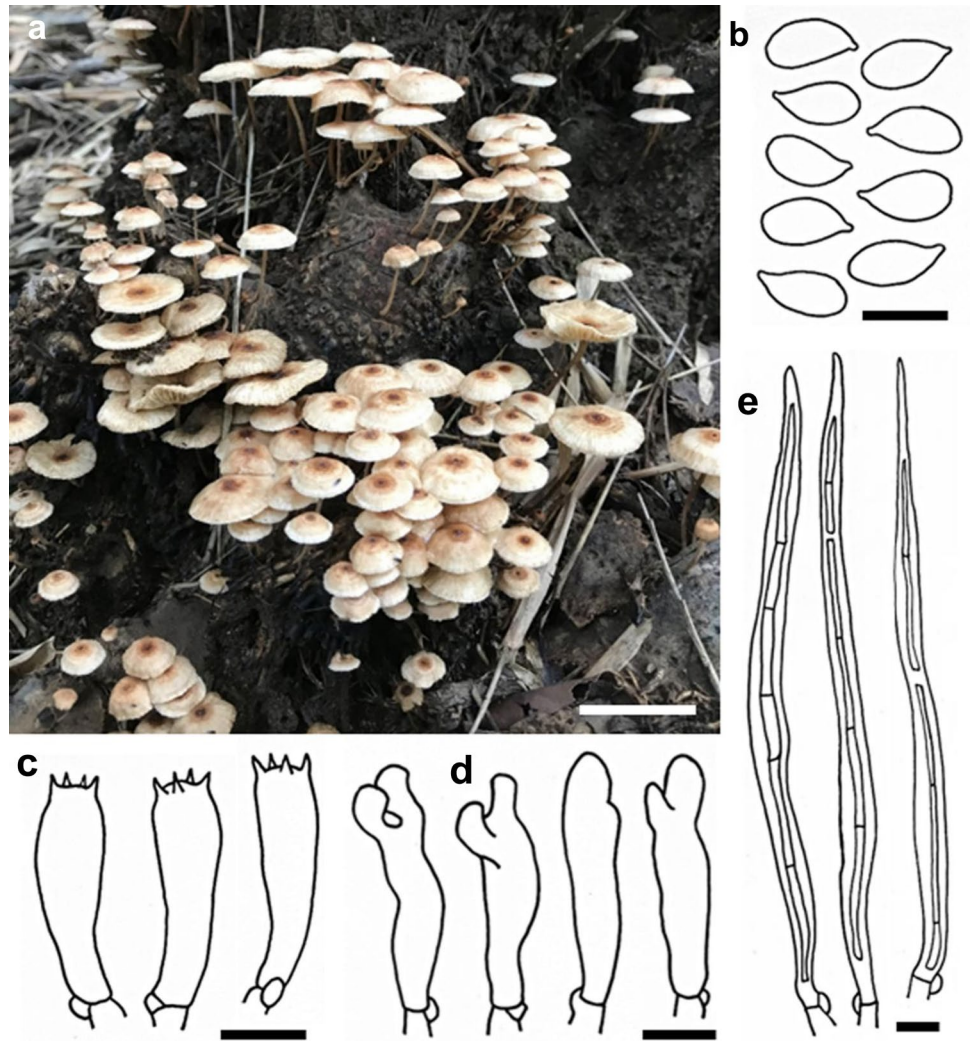
brownish orange (5C4) to light brown (6D5) towards the base, non-insititious, with whitish basal mycelium.

**Basidiospores** (5.8–)6.1–8(–8.7)  $\times$  3.4–4.6(–5.1)  $\mu\text{m}$  ( $\bar{x}$  = 7.1  $\times$  4  $\mu\text{m}$ , n/s = 30), Q = 1.3–2.1 ( $\bar{x}$  = 1.78), asymmetrical, ellipsoid to oblong, hyaline, inamyloid, thin-walled, sometimes with oil drops. **Basidia** (29–)31.2–38.8(–42)  $\times$  5.4–7.3  $\mu\text{m}$ , cylindrical, clavate. **Basidioles** 20–37  $\times$  3.3–7  $\mu\text{m}$ , cylindrical, fusoid, clavate, hyaline,

thin-walled. **Pleurocystidia** absent. **Cheilocystidia** (18–)20–32.5(–37)  $\times$  (5.5–)6–9.9(–11)  $\mu\text{m}$ , (broadly) clavate, obovoid, hyaline, thin- to slightly thick-walled. **Tramal hyphae** formed by cylindrical or sometimes inflated, thin walled, hyaline, up to 12  $\mu\text{m}$  wide. **Pileipellis** a hymeniderm composed of cells 13.5–26  $\times$  7–17  $\mu\text{m}$ , broadly clavate to sphaeropedunculate, vesiculate, thin- to slightly thick-walled, smooth, yellowish white (1A2) in KOH. **Stipe tramal hyphae** 3–7(–7.6)  $\mu\text{m}$



**Fig. 80** *Crinipellis trichialis* (SDBR-CMUNK0900). **a** Basidiomes. **b** Basidiospores. **c** Basidia. **d** Cheilocystidia. **e** Pileipellis hairs. Scale bars: **a** = 10 mm, **b–e** = 10  $\mu$ m



broad, cylindrical, hyaline, moderately dextrinoid, slightly thick-walled. *Caulocystidia* (13–)14.5–38(–41)  $\times$  (4.5–)5.2–8.5(–9.3)  $\mu$ m, abundant, cylindrical to clavate, fusoid, branched, hyaline, inamyloid, thin-walled. *Clamp connections* present in all tissues.

**Material examined:** Republic of Korea, Jeollanam-do, Wando-gun, cedar Recreation Forest, 34°20'47.4"N 126°40'14.4"E, on leaf litter dominated with pine needles, 4 July 2018, Young Woon Lim, SFC20180704-02 (**holotype**); Jeju island, Jeolmul Natural Recreation Forest, 33°26'22.7"N 126°37'34.7"E, on leaf litter, 3 July 2014, Jae Young Park (SFC20140703-03); Incheon, Ganghwa-gun, Manisan, 37°36'41.8"N 126°26'05.4"E, on leaf litter in a mixed forest dominated with *Carpinus laxiflora*, 16 July 2015, Jae Young Park, SFC20150716-07; Incheon, Ongjin-gun, Jangbongdo, 37°32'20.7"N 126°20'12.0"E, on leaf litter of broadleaf tree, 26 July 2016, Nam Kyu Kim, SFC20160726-33.

**Habitat:** On litter in a mixed forest of conifer and broad-leaf trees.

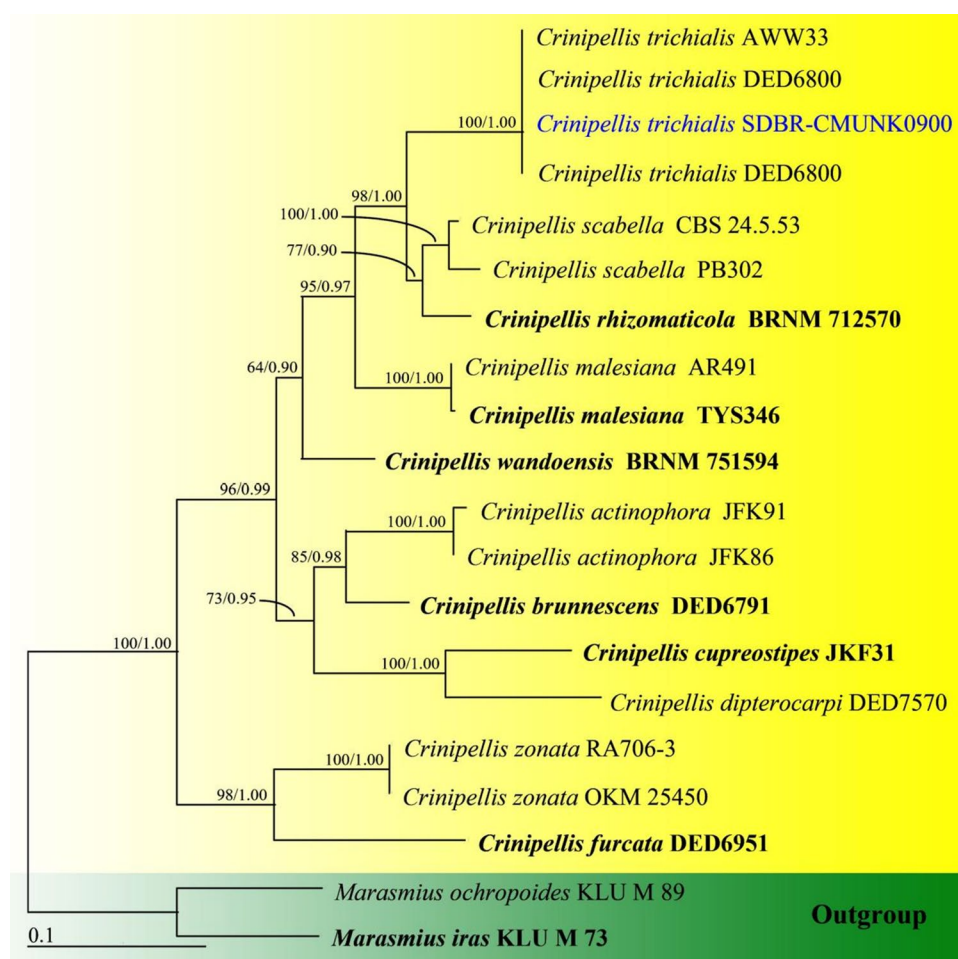
**GenBank numbers:** SFC20180704-02: ITS = OP730947; SFC20140703-03: ITS = OP730948; SFC20150716-07: ITS = OP730949; SFC20160726-33: ITS = OP730946.

**Notes:** The diagnostic characteristics of *Marasmius centrocinnaeomeus* are convex to plano-convex and brownish pileus, adnexed and distant lamellae, central, cylindrical, greyish yellow to light brown colored, non-insititious stipe that becomes brownish toward the base, ellipsoid to oblong basidiospores, (broadly) clavate to obovoid cheilocystidia, and a hymeniderm pileipellis composed of broadly clavate to sphaeropenduculate cells. *Marasmius maximus* is morphologically similar species and phylogenetically close species to *M. centrocinnaeomeus* (Fig. 83). However, *Marasmius maximus* differs from *M. centrocinnaeomeus* by shorter stipe with a darker brownish base, larger basidiospores, and bigger caulocystidia (Hongo 1962; Antonín et al. 2010).

***Marasmius ferrugineodiscus*** J.S. Kim & Y.W. Lim, *sp. nov.*

**Index Fungorum number:** IF900041; **Facesoffungi number:** FoF 13255; Fig. 84





**Fig. 81** Phylogenetic tree derived from maximum likelihood analysis of ITS gene of 20 sequences and the aligned dataset was comprised of 782 characters including gap. The average standard deviation of the split frequencies of the BI analysis was 0.00637. A best scoring RAxML tree was established with a final ML optimization likelihood value of -3314.6448. The matrix had 347 distinct alignment patterns with 18.53% undetermined characters or gaps. Estimated base frequencies were found to be: A=0.2579, C=0.1949, G=0.2212, T=0.3258; substitution rates AC=1.0835, AG=3.5775,

AT=1.5611, CG=0.3860, CT=4.5691, GT=1.0000. *Marasmius iras* KLU M 73 and *Marasmius ochropoides* KLU M 89 were used as outgroup. Numbers above branches are the bootstrap statistics percentages (left) and Bayesian posterior probabilities (right). Branches with bootstrap values  $\geq 70\%$  and  $PP \geq 0.90$  are shown at each branch. The bar represents 0.1 substitutions per nucleotide position. Type strains are in bold. The newly generated sequences are indicated in blue

**Etymology:** ‘*ferrugineodiscus*’ refers to the light brown color of the center of the pileus.

**Holotype:** SFC20160714-57.

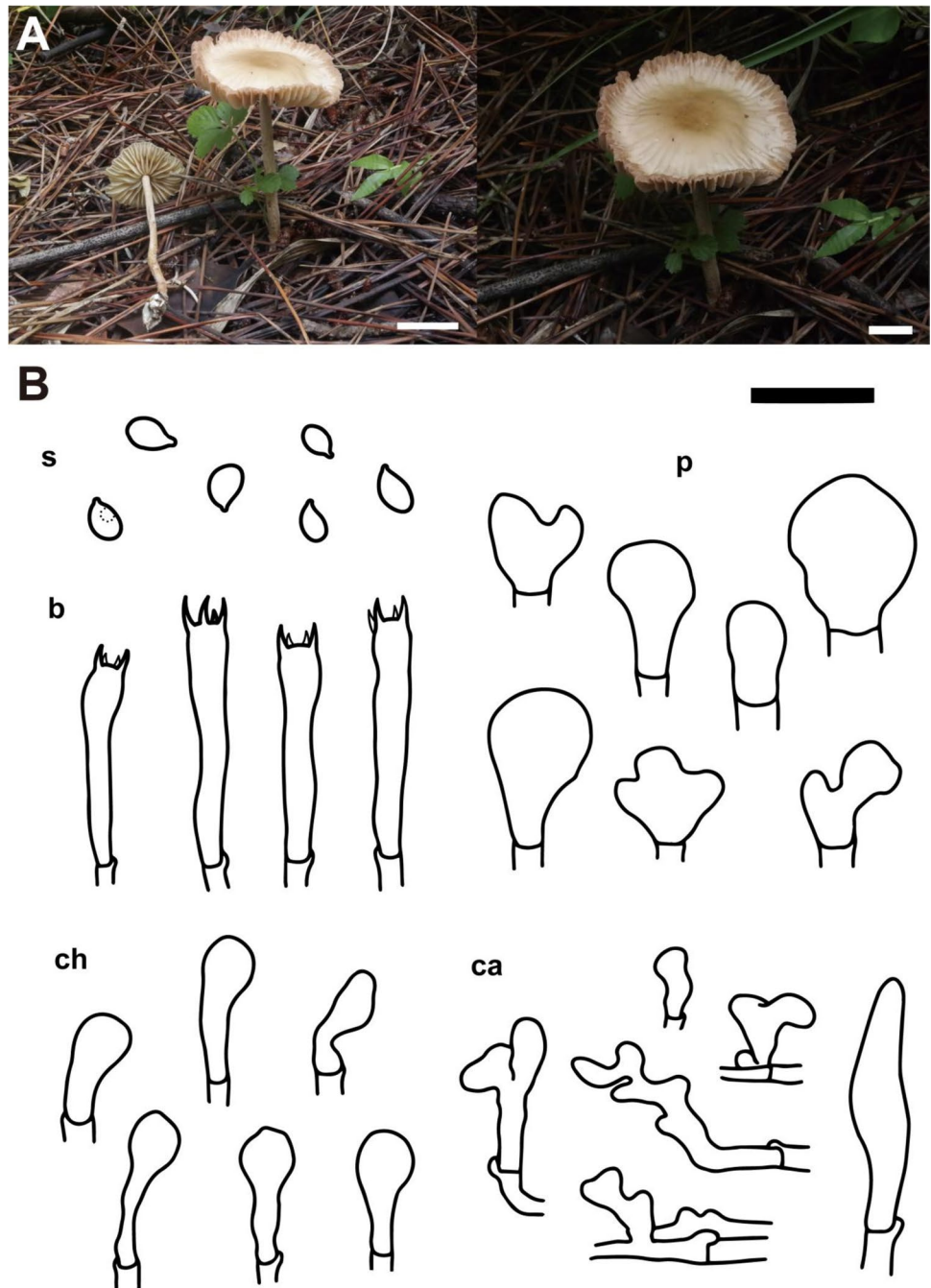
**Pileus** 15–30 mm in diam, convex when young, becoming plano-convex to undulate when old, sometimes slightly depressed in center, wrinkled, glabrous, orange grey (5B2), greyish orange (5B5) to light brown (6D4), margin yellowish grey (4B2) to greyish orange (5B3), hygrophanous. **Lamellae** adnexed to sinuate, subdistant (L=20–32), with 2–4 series of lamellulae, white with concolorous edge. **Stipe** 23–68 × 1.3–3 mm, central, cylindrical, hollow, brownish orange (5B4), grayish brown (5D3) to brownish orange (6C3) towards base, yellowish grey (4A2) to orange grey

(5B2) towards apex, non-insititious, with whitish basal mycelium.

**Basidiospores** 5.4–7.8 (–8.4) × 2.7–4 (–4.5)  $\mu\text{m}$  ( $\bar{x}$  = 6.7 × 3.5  $\mu\text{m}$ , n/s = 30), Q = 1.6–2.6 ( $\bar{x}$  = 1.98), oblong to amygdaliform, hyaline, inamyloid, thin-walled, with oil drops. **Basidia** 26.3–30.8 × 3.5–6  $\mu\text{m}$ , cylindrical, (narrowly) clavate. **Basidioles** 19.2–29.4 × 2.8–5.6 (–6)  $\mu\text{m}$ , cylindrical, fusoid to narrowly clavate, hyaline, thin-walled. **Pleurocystidia** absent. **Cheilocystidia** 16–27 × (5.4–)5.7–12.6  $\mu\text{m}$ , variable in shape, (broadly) clavate, pyriform, obovoid, branched, hyaline. **Tramal hyphae** formed by cylindrical, slightly thick-walled, hyaline, up to 12  $\mu\text{m}$  wide cells. **Pileipellis** a hymeniderm composed of cells 15.6–22.3 × 8.7–17.5  $\mu\text{m}$ , ellipsoid, (broadly) clavate,

**Fig. 82** Basidiomes and microscopic drawings of *Marasmius centrocinnamomeus* (SFC201807014-02, **holotype**).

**A** Field pictures of the basidiomes, **B** Drawings of the microscopic features. Abbreviations: **s** Basidiospores, **b** Basidia, **ch** Cheilocystidia, **p** pileipellis cells, **ca** Caulocystidia. Scale bars: **A** = 1 cm, **B** = 20  $\mu$ m



obovoid, vesiculate, thin-walled, smooth, yellowish white (1A2) in KOH. *Stipe tramal hyphae* 3.5–9.2(–11)  $\mu$ m broad, cylindrical to fusoid, hyaline, strongly dextrinoid, slightly thick-walled. *Caulocystidia* 20–42  $\times$  5.5–12  $\mu$ m, sometimes clustered, cylindrical to clavate, hyaline, inamyloid, slightly thin-walled. *Clamp connections* present in all tissues.

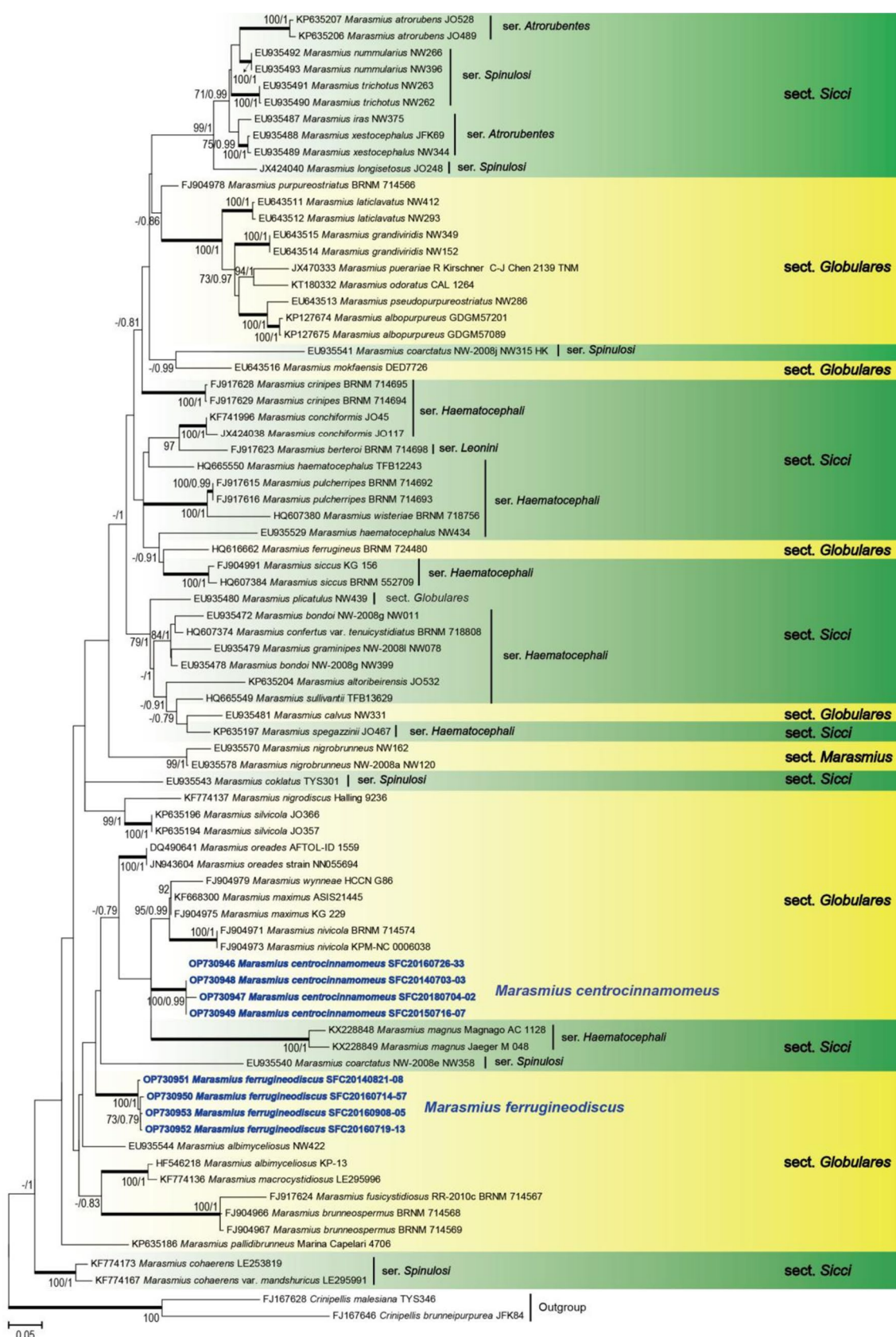
**Material examined:** Republic of Korea, Gyeongsangbuk-do, Ulleung-gun, Ulleung-eup, 37°30'44.4"N 130°54'31.1"E, on the decomposed branch, 14 July 2016, Jae Young Park, SFC20160714-57 (**holotype**); Seoul, Gwanak-gu, Seoul National University, 37°27'51.8"N 126°57'08.0"E, on leaf

litter, 21 August 2014, Jae Young Park, SFC20140821-08; Incheon, Ongjin-gun, Yeongheung-myeon, 37°15'25.0"N 126°27'37.1"E, on leaf litter, 19 July 2016, Nam Kyu Kim, SFC20160719-13.

**GenBank numbers:** SFC20160714-57: ITS = OP730950; SFC20140821-08: ITS = OP730951; SFC20160719-13: ITS = OP730952.

**Habitat:** On litter of leaves and branches in a mixed forest of conifer and broadleaf trees.

**Notes:** *Marasmius ferrugineodiscus* is characterized by a convex to undulate pileus which is orange grey to light



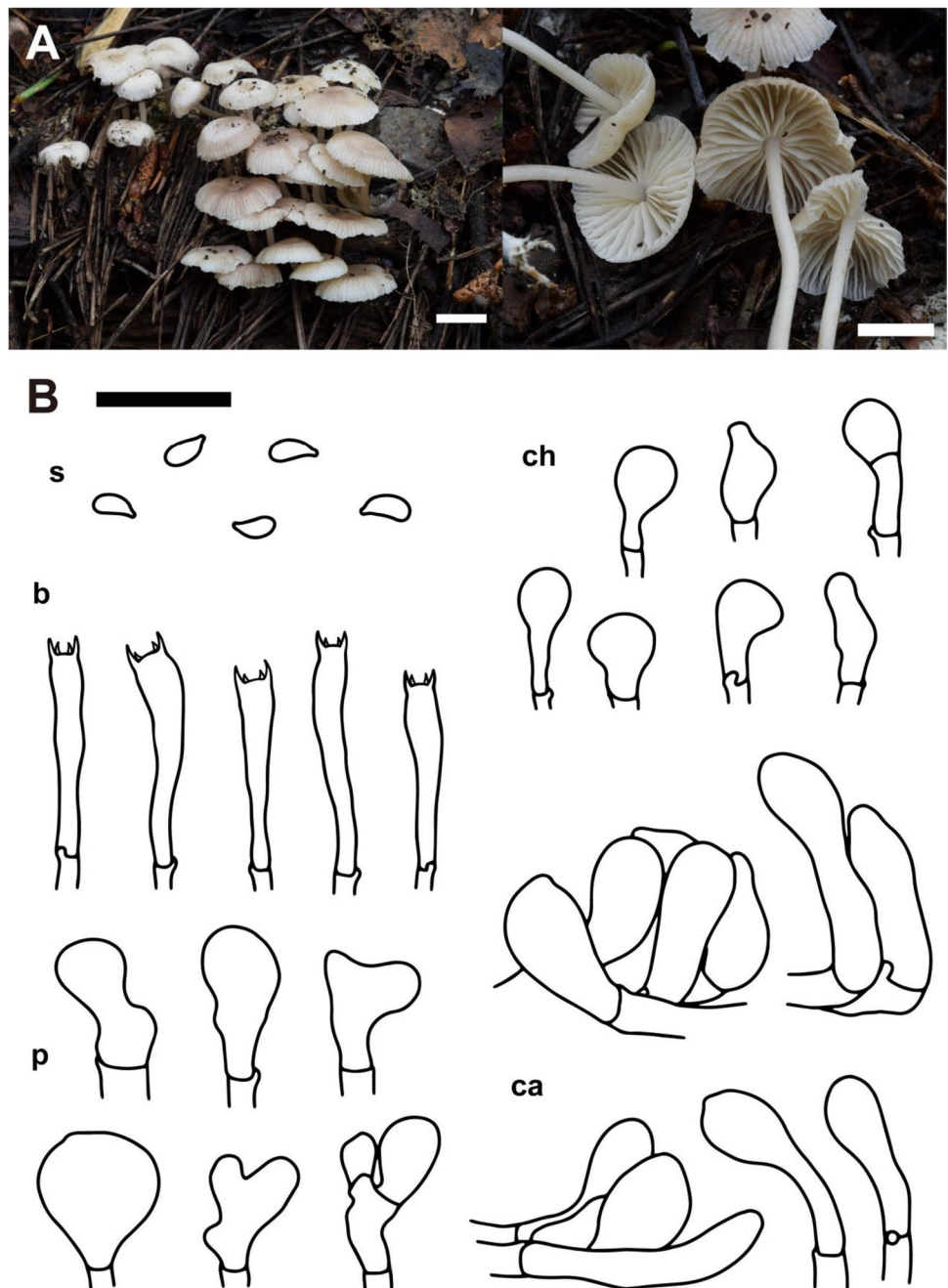


**Fig. 83** Phylogenetic tree conducted from maximum likelihood analysis based on ITS sequence data of *Marasmius* species with Bayesian Information Criterion values. Related sequences are mostly taken from Oliveira et al. (2020). A total of 49 *Marasmius* and two *Crinipellis* species as outgroup taxa are included in the phylogenetic analysis. *Crinipellis malesiana* and *Crinipellis brunneipurpurea* are used as the outgroup taxa. Support values at the nodes consist of BS over 70 and PP over 0.95. The nodes with 100 BS are represented as thicker stems. The sequences obtained in this work are indicated in blue

brown colored center but gets whiter as it goes to margin, subdistant and adnexed lamellae, central and cylindrical

stipe, oblong to amygdaliform basidiospores, (broadly) clavate to pyriform cheilocystidia, and a hymeniderm formed pileipellis composed of clavate, obovoid, vesiculate cells. These characteristics place this species under sect. *Globulares*. The macromorphological characteristics of this species are similar to *Marasmius wynneae*. *Marasmius wynneae* has more whitish and greyish pileus when comparing with *M. ferrugineodiscus*. *Marasmius ferrugineodiscus* is phylogenetically close to *Marasmius albimyceliosus* (Fig. 83). However, *M. albimyceliosus* can be distinguished from *M. ferrugineodiscus* by pale cream pileus, fewer lamellae, and the lack of caulocystidia (Wannathes et al. 2009).

**Fig. 84** Basidiomes and microscopic drawings of *Marasmius ferrugineodiscus* (SFC20160714-57, **holotype**). **A** Field pictures of the basidiomes, **B** Drawings of the microscopic features. Abbreviations: **s** Basidiospores, **b** Basidia, **ch** Cheilocystidia, **p** pileipellis cells, **ca** Caulocystidia. Scale bars: **A** = 1 cm, **B** = 20  $\mu$ m



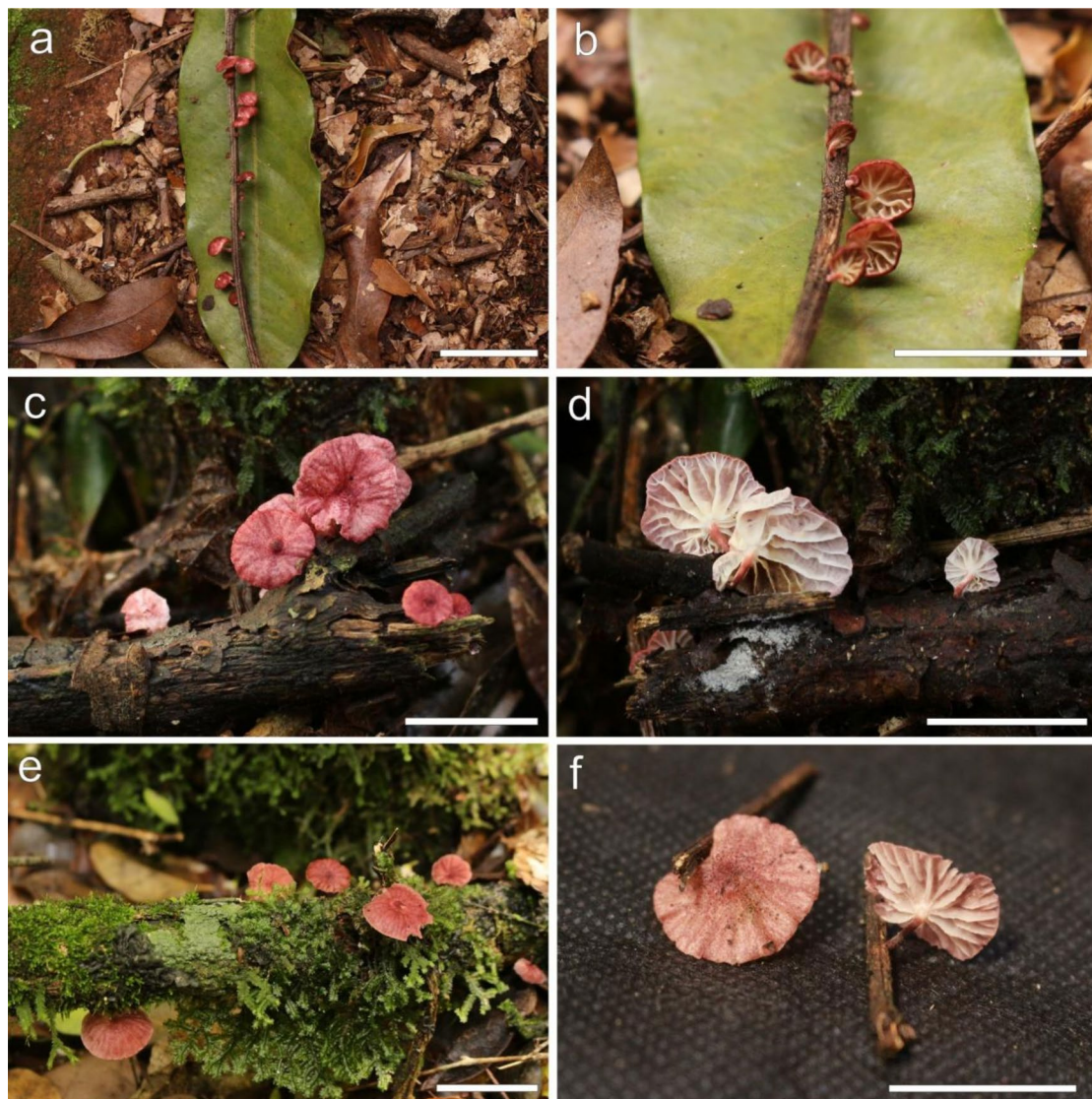
***Moniliophthora*** H.C. Evans, Stalpers, Samson & Benny.

**Notes:** *Moniliophthora* was described by Evans et al. (1978) as an *incertae sedis*, monotypic genus of basidiomycetes, with *M. roreri*, a parasitic fungus of *T. cacao*, as the type (Niveiro et al. 2020). Later, based on phylogenetic studies, Aime and Phillips-Mora (2005) placed *M. roreri* within *Marasmiaceae* (*Agaricales*), and included *M. perniciosa* (= *M. Crinipellis*) in *Moniliophthora*. The authors speculated that other *Crinipellis* species, especially those currently placed in section *Iopodinae*, would be found to belong to *Moniliophthora* (Aime and Phillips-Mora 2005). The primary morphological diagnostic characters that separate *Crinipellis* and *Moniliophthora* are pliant vs. stiff (*Crinipellis*) stipes, and a tendency toward production of pink to orange pigments in the basidiome that do not change to green or olive when

treated with KOH or NaOH (*Moniliophthora*). Additionally, many *Moniliophthora* species appear to have a biotrophic habit, including important pathogens of tropical crops such as cocoa (*Theobroma cacao*), while those of *Crinipellis* are primarily saprotrophic (Niveiro et al. 2020). Ten species of *Moniliophthora* are currently known (Evans et al. 1978; Aime and Phillips-Mora 2005; Arruda et al. 2005; Kerekes and Desjardin 2009; Kropp and Albee-Scott 2012; Antonín et al. 2014; Lisboa et al. 2020; Niveiro et al. 2020; Izhar et al. 2022).

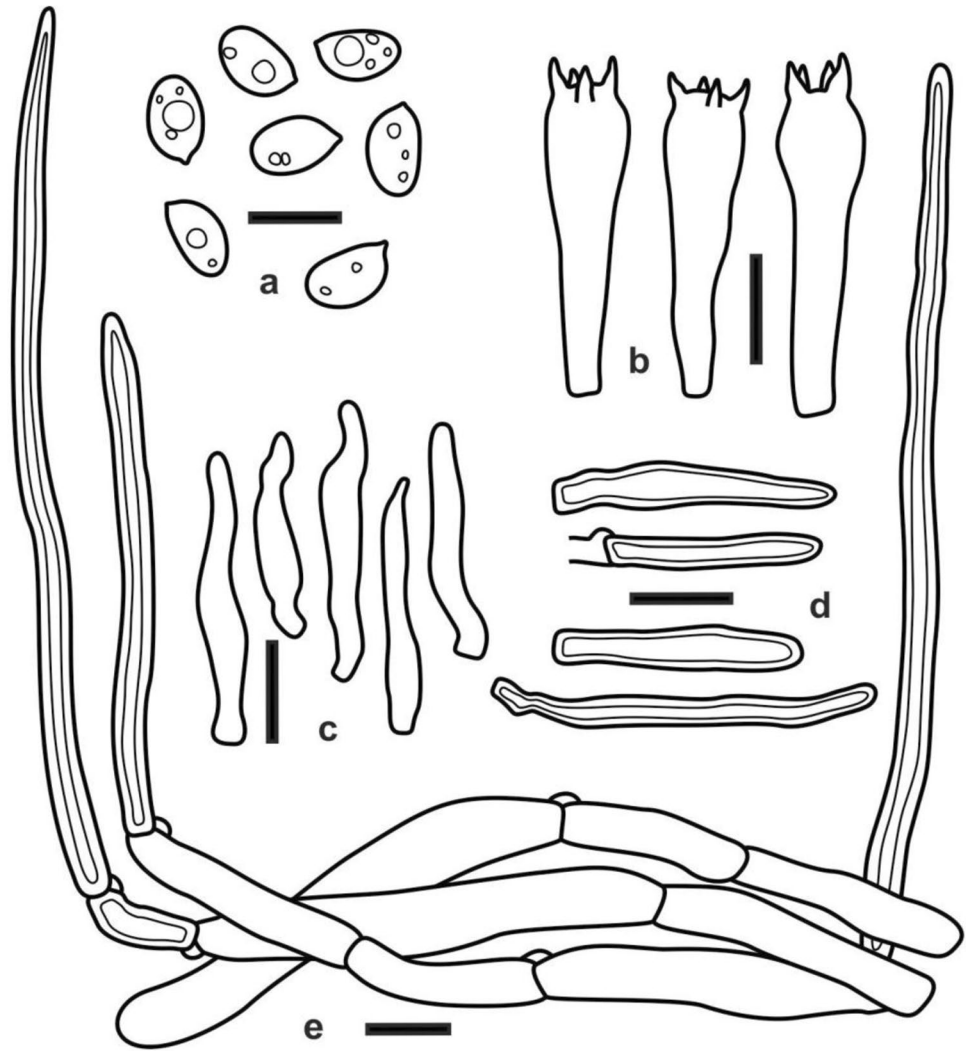
***Moniliophthora atlantica*** N. A. Ramirez & Niveiro, *sp. nov.*

**Index Fungorum number:** IF555944; **Facesoffungi number:** FoF 10838; Figs. 85, 86



**Fig. 85** *Moniliophthora atlantica*, general aspect, lamellae and stipe. **a, b** TC17-2-7 (holotype). **c, d** OS18-2-5. **e** TC19-2-1. **f** IG16-3-11. Scale bars: 20 mm

**Fig. 86** *Moniliophthora atlantica* microscopic characters. **A** Basidiospores. **B** Basidia. **C** Cheilocystidia. **D** Caulocystidia. **E** Pileipellis elements. Scale bars: 10  $\mu$ m



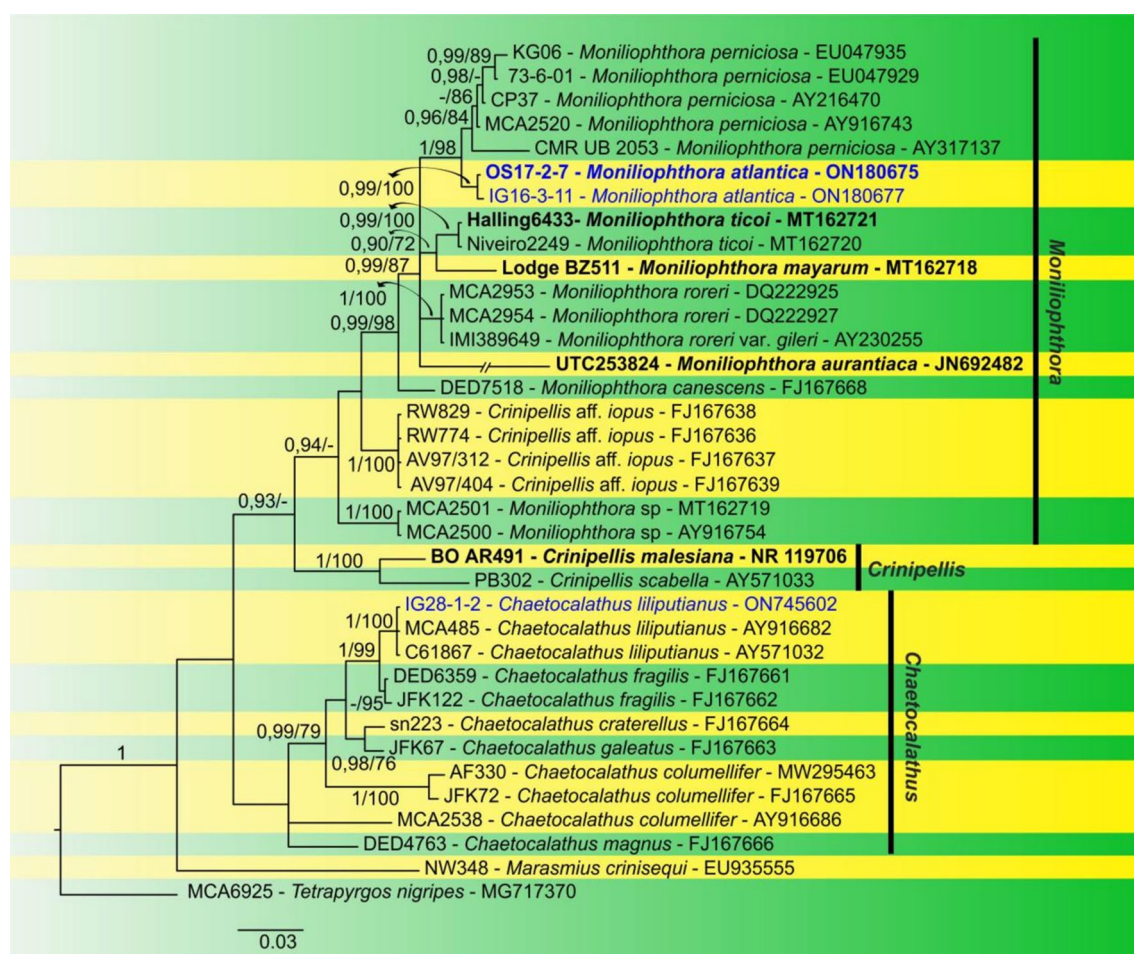
**Etymology:** referring to the ecoregion where the species was collected, the Atlantic Forest.

**Holotype:** OS17-2-7 (CTES 0568284).

**Pileus** 3–20 mm in diam, circular, convex to broadly convex when mature, some subumbonated, slightly depressed at center, surface pale red (7A3-8A3), pastel red (7A4-8A4), dull red (8B4-8C4) to greyish red (8B5-8C5), usually darker near the center, reddish brown (8D7-8E6-7); surface fibrillose to pubescent, dry, opaque, not hygrophanous, sulcate-striate; margin incurved to plane. **Context** thin (< 1 mm), membranaceous, yellowish white (1A2), odor and taste not tested. **Lamellae** free to slightly adnexed, subdistant, regular, sometimes furcate towards the margin and with intervenose, lamellulae in 2–3 series, yellowish white (1A2) to pale yellow (1A3), smooth margin, concolorous with sides. **Stipe** 2–12 × 0.8–2 mm, central, sometimes slightly lateral, cylindrical, equal or slightly thinner towards the middle, hollow, insititious, apex concolorous with lamellae, yellowish white (4A2), turning pale orange (6A4-6B4) towards the middle

of the stipe, darkening towards the base, reddish brown (9E6-7) to dark brown (9F6-8), surface fibrillose, pubescent under lens, more distinctive toward the base. Spore-print not observed, presumably yellowish white (1A2). KOH and NaOH reactions on pileus surface negative. **Basidiospores** (7–)8.2–11.1 × 4.5–6.2 (–7.2)  $\mu$ m,  $\bar{x}$  = 9.4 ± 0.77 × 5.6 ± 0.4 5  $\mu$ m, Q = 1.4–2.1, Qx = 1.7 ± 0.12, n = 25, N = 2, ellipsoidal to oblong, amygdaliform in lateral view, with a slight suprahilar depression, thin-walled, smooth, hyaline, inamyloid, without germ-pore. **Basidia** 34.7–50 × 7.5–9  $\mu$ m, clavate to narrowly clavate, 4-spored, thin-walled. **Basidioles** 22.2–34 × 4–7.7  $\mu$ m, clavate, thin-walled, abundant. **Pleurocystidia** absent. **Cheilocystidia** 18–33.2 × 2.5–6.4  $\mu$ m, subcylindrical to narrowly clavate, sometimes with a finger-like apical protuberance, rounded apex, thin-walled, hyaline. **Hymenophoral trama** subregular, composed of cylindrical interwoven hyphae, up to 7  $\mu$ m in diam, thin-walled, hyaline. **Pileipellis** a cutis of repent, more or less interwoven cylindrical hyphae, up to 8  $\mu$ m broad, thin-walled, smooth,





**Fig. 87** Bayesian Inference Analysis based on ITS sequences of *Moniliophthora* and related genera. The sequences obtained in this work are indicated in blue, type material in bold. Support values, when present, consist of the posterior probability (PP) followed by the boot-

strap (BS), separated by a /. Only nodes with support above 50% were scored, and support values greater than 0.90/70 are showed (- indicates a lower value)

hyaline, inamyloid, covered by clusters of dextrinoid hairs. *Hairs of the pileus surface* 50–315 × 4–8.5 µm, setiform, acicular, thick-walled, up to 3 µm broad, dextrinoid, sometimes with secondary septa, rounded apex, KOH– (do not turn olive green). *Stipitipellis* a cutis of repent hyphae, up to 8 µm in diam, parallel, elongated, dextrinoid. *Hairs of the stipe surface* 20.1–44.1 × 4.4–8.3 µm, setiform, similar to hairs of the pileus surface, thick-walled, up to 2 µm broad, dextrinoid, more abundant in young specimens. *Clamp connections* presents.

**Habitat and distribution:** Marasmioid, growing on small freshly fallen branches of unidentified dicots and stems of living lianas. In Misiones Province, Argentina.

**Material examined:** Argentina, Misiones, San Ignacio, Osunún Private Reserve, 27°17'09.3" S, 055°34'03.6" O, 206 m asl, on recently fallen branches, 30 September 2018, on recently fallen branches leg. Ramirez N. et al., OS17-2–7 (CTES 0568284, **holotype**), OS18-2–5 (CTES); *ibid.*,

Teyú Cuaré Provincial Park, 27°17'05.5" S, 055°35'21.1" O, 177 m asl, on living liana, 1 October 2018, leg. Ramirez N. et al., TC19-2–1 (CTES); Iguazú, Iguazú National Park, 25°43'29.2" S, 054°28'08.6" O, 239 m asl, 2 October 2018, leg. Ramirez N. et al., IG16-3–11 (CTES); *ibid.*, Palmital, 25°41'19.7" S, 054°28'26.3" O, 186 m asl, 13 October 2017, leg. Ramirez N. et al., IG10-1–1 (CTES).

**GenBank numbers:** OS17-2–7: ITS = ON180675; IG16-3–11: ITS = ON180677.

**Notes:** The matrix included 35 sequences belonging to 20 taxa of *Moniliophthora* and related genera, such as *Crinipellis*, *Chaetocalathus* and *Marasmius*. A *Tetrapyrgos nigripes* sequence was used to root the tree (Kropp and Albee-Scott 2012). The alignment resulted in a total of 602 characters, of which 367 were conserved sites, 235 variables and 150 parsimony-informative. The best substitution models were estimated as TPM2uf + G, K80, and SYM + G for ITS1, 5.8S, and ITS2 respectively.

Since the Maximum Likelihood and Bayesian Inference analysis yielded trees with similar topology, only the latter is shown in which the support values of PP/BS for the compatible nodes between them (Fig. 87). In the phylogeny, two main clades are observed, although without statistical support: *Chaetocalathus*, which groups all species of this genera included, and the clade *MonilophthoralCrinipellis*. Within the latter, *M. atlantica*, the new species proposed here, forms a well-supported clade (0.99/100) as sister group to *M. pernicioso* (1/98).

*Monilophthora atlantica* is characterized by its small to medium sized basidiomes, reddish to violet in color, covered by hairs that preserve their color in contact with KOH. The most closely related species, both morphologically and phylogenetically (Fig. 87), is *M. pernicioso*. Both species share the general appearance and coloration of the basidiomes, but *M. pernicioso* differs in the lageniform and more elongated cheilocystidia ( $35\text{--}50 \times 9\text{--}14\text{ }\mu\text{m}$ ), the shorter basidia ( $31\text{--}32\text{ }\mu\text{m}$ ), and shorter hairs of the pileus surface ( $80\text{--}150\text{ }\mu\text{m}$ , Singer 1976). Another very similar species in terms of coloration is *M. marginata* known from Malaysia, but it is differentiated by its marginate lamellae with a reddish-brown edges (10D6), basidiospores smaller on average ( $\bar{x} = 7.0 \pm 1.0 \times 4.0 \pm 0.6\text{ }\mu\text{m}$ ), shorter basidia ( $35\text{--}36\text{ }\mu\text{m}$ ), and longer stipe hairs ( $60\text{--}150\text{ }\mu\text{m}$ , Kerekes and Desjardin 2009).

*Monilophthora pernicioso* is a widely studied species since it is the cause of the main disease of cocoa (*Theobroma cacao*) called “witches’ broom”, and has been reported in numerous hosts of different families, such as *Malvaceae*, *Malpighiaceae*, *Solanaceae*, *Bixaceae*, *Sapindaceae*, *Asteraceae*, and lianas possibly belonging to the *Bignoniaceae* (Lisboa et al. 2020). These authors observed in the hosts the presence of symptoms caused by the fungus, concluding that there are non-pathogenic life forms (on lianas and *Allophylus edulis*) and pathogenic forms (in the other hosts studied). Considering the absence of symptoms or visible anomalies in the hosts of *M. atlantica* at the time of collection, this species can be classified as non-pathogenic. However, it should be highlighted that a more extensive sampling, with a more detailed study of its hosts and studies including other regions of the genome is considered necessary to define this issue.

#### *Pleurotaceae* Kühner.

*Notes:* *Pleurotaceae* is erected by Kühner (1980) with the type genus *Pleurotus*. The fungi in this family feed on dead wood, nematodes and bacteria, so they can often be seen growing on dead trees and logs. Most of them are directly attached to wood. They often grow in loose or dense clusters (Thorn 2000).

#### *Resupinatus* Nees ex Gray.

*Notes:* *Resupinatus* was established by Gray (1821). Singer (1986) proposed *Hohenbuehelia* and *Resupinatus* belong to the tribe *Resupinateae*, family *Tricholomataceae*. Thorn and Barron (1986) judged *Hohenbuehelia* and *Resupinatus* as different taxonomic levels, arguing that the two genera are fundamentally different: *Hohenbuehelia* possesses nematophagous anamorph and *Resupinatus* is non-nematophagous and lacks a conidial anamorph (Thorn and Barron 1986). Until 2000, further studies by Thorn et al. (2000) based on ribosomal DNA sequences showed that other members of the *Resupinateae*, *Asterotus* and *Resupinatus* are a monophyletic group within family *Tricholomataceae*, distinct from family *Pleurotaceae*, but *Resupinatus* is now a part of the family *Pleurotaceae*. There are 83 records in the Index, of which 55 are valid records, including 7 variants. There is no clear opinion on the division of its subordinates.

#### *Resupinatus porrigens* J.Z. Xu & Yu Li, *sp. nov.*

*Index Fungorum number:* IF 901101; *Fungal names number:* FN 571222; Fig. 88

*Etymology:* “porrigens” refers to the macroscopic morphological features resembling a conch.

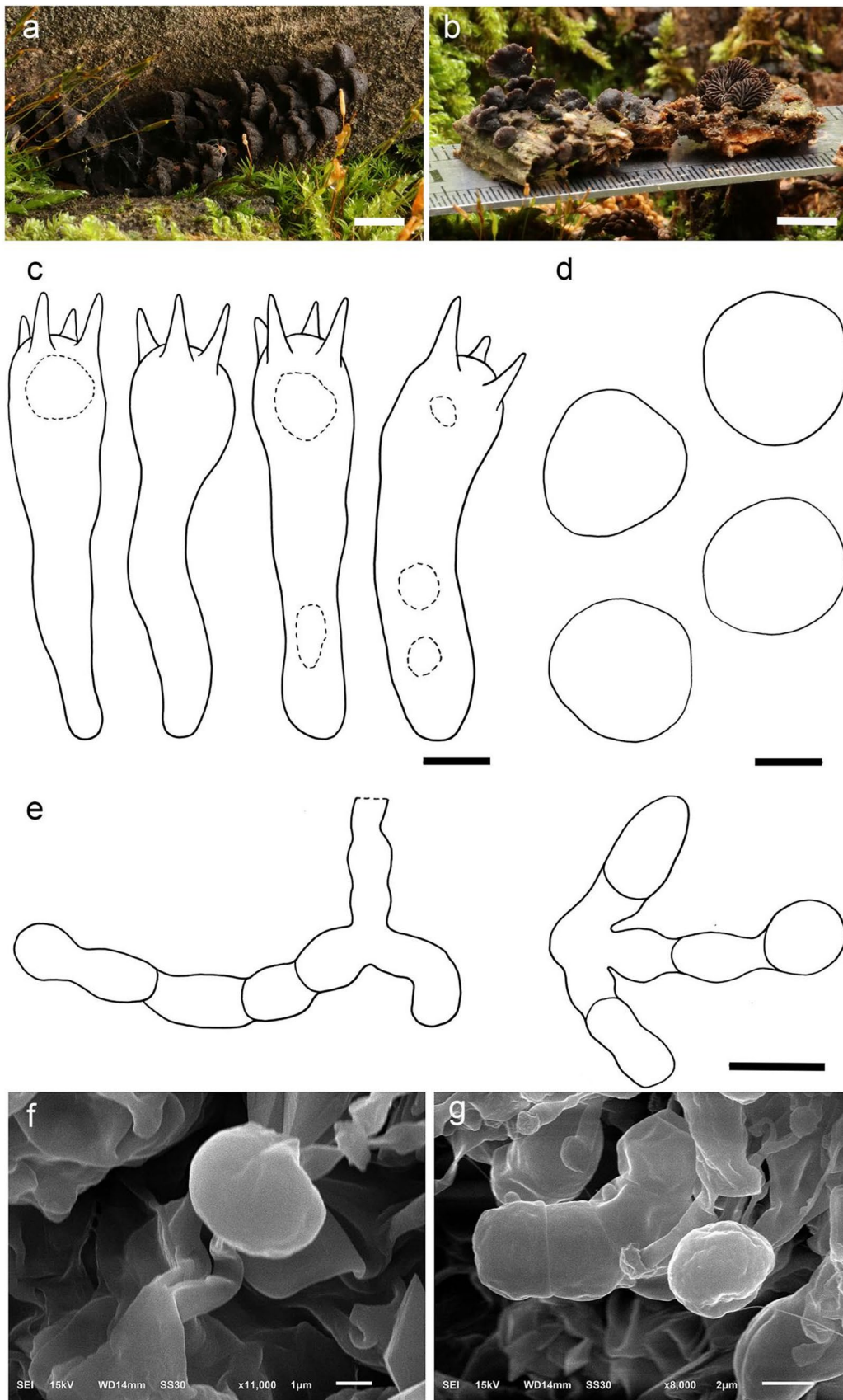
*Holotype:* HMJU 261.

*Basidiomes* small, sessile, mostly lateral or dorsal, fleshy. *Pileus* up to 7 mm in diam, surface beige (7F3), red-brown (8E4) toward the margin, convex, orbicular when young, becoming conchate, flabelliform, discoid when mature, smooth; margin incurved, entire to variously cracked or wavy. *Hymenophore* lamella-like with radiating folds, separated by 4–6 series of lamellulae interconnected, reddish brown (8E5). *Basidiospores* ( $3.8\text{--}4.1\text{--}4.6(-4.9) \times (3.0\text{--})3.3\text{--}4.0(-4.3)\text{ }\mu\text{m}$  ( $\bar{x} = 4.3 \times 3.6\text{ }\mu\text{m}$ ,  $n = 20$ ),  $Q = 1.04\text{--}1.40$ ,  $Q_m = 1.19$ , globose to subglobose, with a small hilar appendage, faint bump, multiguttulate, thin-walled, hyaline. *Basidia* ( $17.2\text{--}19.0\text{--}25.1(-27.4) \times 5.0\text{--}6.9\text{ }\mu\text{m}$  ( $\bar{x} = 22 \times 5.9\text{ }\mu\text{m}$ ,  $n = 20$ ), narrowly clavate, tetrasporic, sterigmata up to  $3.2\text{ }\mu\text{m}$  long, with numerous oil drops. *Cheilocystidia*  $2.1\text{--}4.2\text{ }\mu\text{m}$  wide, clavate to subcoralloid, with 1 or 2 branches, hyaline. Divergent *hymenophoral trama*. *Pileipellis* intricately interwoven layer of hyphae  $1.6\text{--}4.4\text{ }\mu\text{m}$  in diam, thin-walled, compact. *Clamp connections* are present in all hyphae.

*Material examined:* China, Qinghai Province, Halihatu National Forest Park, on the rotting coniferous trunk, 7 August 2018, Jize Xu, HMJU 261 (**holotype**); Qinghai Province, Halihatu National Forest Park, 22 July 2021, HMJU 3836.

*GenBank numbers:* HMJU 261: ITS = OP727724, LSU = OP727807; HMJU 3836: ITS = OP729420, LSU = OP727819.

*Notes:* The main characteristic of *Resupinatus porrigens* is the lateral or dorsal, beige pileus with conchate,



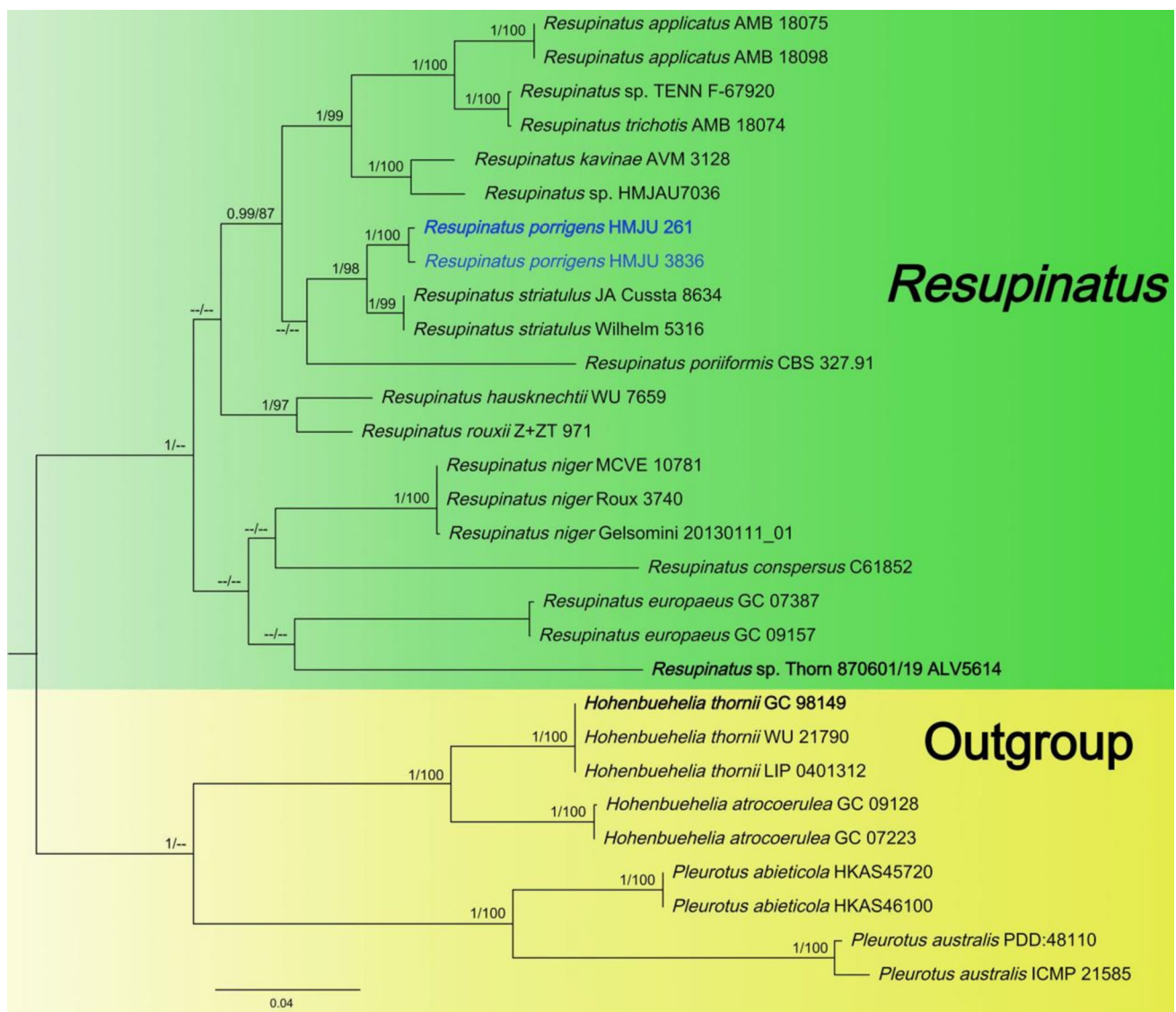


**Fig. 88** *Resupinatus porrigens* (HMJU 261, holotype). **a, b** Habitat and basidiomes **c** Basidia **d** Basidiospores **e** Cheilocystidia **f–g** SEM images of basidiospores. Scale bars: **a, b** 10  $\mu$ m, **c** 5  $\mu$ m, **d** 2  $\mu$ m, **e** 5  $\mu$ m, **f** 1  $\mu$ m, **g** 2  $\mu$ m

flabelliform, discoid, entire to variously cracked or wavy form, and reddish brown hymenium, lamella-like with radiating folds, separated by 4–6 series of lamellulae interconnected. The pileus is beige similar to *Resupinatus merulioides*, but *R. merulioides* is differentiated by taupe and alveolate hymenium (Redhead and Nagasawa 1987). *Resupinatus odoratus* resemblance *R. porrigens* due to cracked edge, but *R. odoratus* has a sticky and striate pileus with a beige and poroid hymenium when young (Bijeesh 2020).

*Resupinatus vinosolidus* is distinguished from *R. porrigens* by lamellulae, but *R. vinosolidus* having the livid vinaceous and floccose pileus with alveolate and livid hymenium (Cooper 2012). *Resupinatus porrigens*, *R. applicatus* and *R. trichotis* are lamella-like of hymenium distributed in China, but *R. porrigens* has thickened lamella, similar to *Cantharellus*, and the relationships were not closed in the phylogenetic analysis tree (Fig. 89).

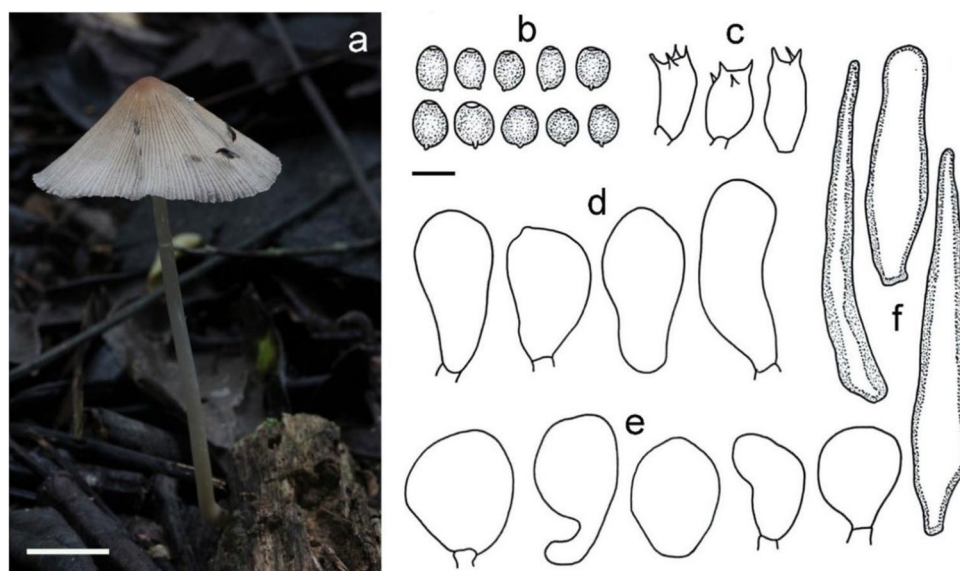
*Resupinatus porrigens* also has many microscopic similarities with other species of the genus *Resupinatus*. *Resupinatus merulioides* shows similarities with *R. porrigens* in the appearance of globose basidiospores; however, *R. merulioides* is differentiated by smooth basidiospores, longer basidia, and clavate to cylindrical cheilocystidia



**Fig. 89** Bayesian and ML phylogenetic trees of *Resupinatus* based on ITS and LSU sequences, nodes were annotated if supported by > 0.95 Bayesian posterior probability (PP) (left) or > 80% ML bootstrap pro-

portions (BP) (right) values. Newly generated sequences are shown in bold black. The ex-types are in bold; the new isolates are in blue

**Fig. 90** *Parasola setulosa* (SDBR-CMUNW1161). **a** Habit and basidiome. **b** Basidiospores. **c** Basidia. **d** Cheilocystidia. **e** Pleurocystidia. **f** Sclerocystidia. Scale bars: **a** = 10 mm, **b–f** = 10  $\mu$ m



(Redhead 1987). *Resupinatus porosus* also has globose basidiospores, but *R. porosus* has clavate-acanthophysoid or coralloid cheilocystidia, often bearing granular to crystalline encrustation (Thorn et al. 2005). *Resupinatus stictoides* shows similarities with *R. porrigens* in the appearance of basidia; however, *R. stictoides* is differentiated by ellipsoid basidiospores and coralloid-diverticulate pileipellis (Nakasone 2008). In phylogenetic analysis, *R. porrigens* has the highest similarity with *R. striatulus*, but it is a clade of its own (Fig. 89).

#### ***Psathyrellaceae*** Vilgalys, Moncalvo & Redhead.

**Notes:** *Psathyrellaceae* was classified from other coprinoid taxa based on molecular phylogenetic data, which circumscribed by *Psathyrella* and *Lacrymaria*, together with related species in the polyphyletic genus *Coprinus* sensu lato that were transferred to the genera *Coprinellus*, *Coprinopsis* or *Parasola* (Redhead et al. 2001). Afterwards, several other genera were included in *Psathyrellaceae* currently comprising 21 accepted genera (Wijayawardena et al. 2022).

#### ***Parasola*** Redhead, Vilgalys & Hopple.

**Notes:** *Parasola* is a genus of coprinoid mushroom that forms a small, umbrella-like, non-deliquescent pilei lacking of veils (Redhead et al. 2001; Nagy et al. 2009). *Parasola plicatilis* is the specific type species (Redhead et al. 2001). The species are common decomposers of leaf-litter, wood and herbivore dung (Schafer 2014), and are distributed worldwide. Species of *Parasola* are divided into section *Auricomi* (the presence of thick-walled, brown sclerocystidia) and section *Parasola* (the absence of thick-walled, brown sclerocystidia, Schafer 2010). There are 48 epithets listed in the Index Fungorum (2022). However, the genus currently has 24 species based on recent taxonomic

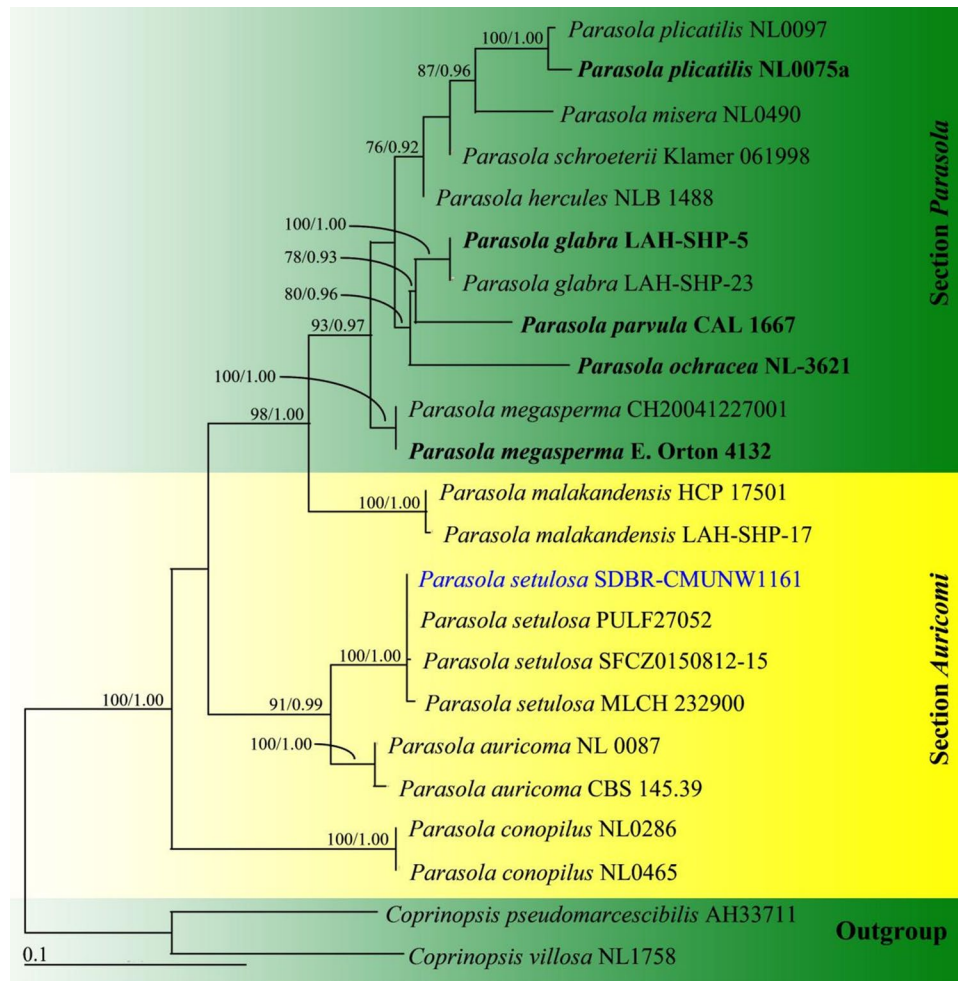
treatments dealing with morphological and molecular studies (Nagy et al. 2010; Schafer 2014; Hussain et al. 2016, 2017, 2018; Szarkándi et al. 2017; Schafer et al. 2022).

***Parasola setulosa*** (Berk. & Broome) Redhead, Vilgalys & Hopple, in Redhead, Vilgalys, Moncalvo, Johnson & Hopple, Taxon 50: 236 (2001).

**Index Fungorum number:** IF474661; **Facesoffungi number:** FoF 12911; **Fig. 90**

**Pileus** 20–30 mm in diam, very thin, conical when young, expanding to broadly conical in age; dull, dry, plicato-striate with minute, erect, brown setules; brownish orange (7C6, 6C4) at center, light brown (7D4) to greyish brown (7D3) fading to orange white (5A2), orange grey (5B2) or brownish grey (5C2) at margin. **Context** very thin, orange grey (5B2). **Lamellae** free to adnate, moderately crowded with 1–2 series of lamellulae, narrow, orange grey (5B2) finally black, not deliquescent. **Stipe** 65–90 × 1.5–2 mm, cylindrical, hollow, central, glabrous, dull, orange grey (5B2).

**Basidiospores** (8–)9–11 × 7–9 × (6–)7–8  $\mu$ m,  $Q = 1.13–1.43$ ,  $q = 1.25 \pm 0.10$  ( $n = 25$ ), lentiform, broadly ovoid to subglobose in frontal view, ellipsoid to broadly ellipsoid in lateral view, smooth, dark brown, moderately thick-walled, germ-pore central, 1.5–2  $\mu$ m wide. **Basidia** 17–22 × 9–11  $\mu$ m, clavate to broadly clavate, with 4 sterigmata, thin-walled, inamyloid. **Lamella-edge** heteromorphous with cheilocystidia. **Cheilocystidia** common, 31–45 × 16–21  $\mu$ m, clavate to broadly clavate, hyaline, inamyloid, thin-walled. **Pleurocystidia** numerous, 26–35 × 13–25  $\mu$ m, pyriform to turbinate, hyaline, inamyloid, thin-walled. **Pileipellis** a non-stratified epithelium of hyaline elements and numerous sclerocystidia, elements 19–40 × 15–23  $\mu$ m, clavate to pyriform, hyaline, inamyloid,



**Fig. 91** Phylogenetic tree derived from maximum likelihood analysis of ITS gene of 23 sequences and the aligned dataset was comprised of 667 characters including gap. The average standard deviation of the split frequencies of the BI analysis was 0.00826. A best scoring RAXML tree was established with a final ML optimization likelihood value of -2987.9897. The matrix had 268 distinct alignment patterns with 9.05% undetermined characters or gaps. Estimated base frequencies were found to be: A=0.2290, C=0.2428, G=0.2255, T=0.3024; substitution rates AC=1.3958, AG=2.6467,

AT=2.2120, CG=0.2505, CT=4.1800, GT=1.0000. *Coprinopsis pseudomarcescibilis* AH33711 HNL501802 and *Coprinopsis villosa* NL1758 were used as outgroup. Numbers above branches are the bootstrap statistics percentages (left) and Bayesian posterior probabilities (right). Branches with bootstrap values  $\geq 70\%$  and PP  $\geq 0.90$  are shown at each branch. The bar represents 0.1 substitutions per nucleotide position. Type strains are in bold. The newly generated sequences are indicated in blue

thin-walled; *sclerocystidia* setoid  $56\text{--}190 \times 14\text{--}19 \mu\text{m}$ , lageniform, cylindrical, brown, thick-walled (up to  $4 \mu\text{m}$ ).

**Habitat and distribution:** Solitary on dead wood or the ground, and known from Sri Lanka, Pakistan and Thailand (Redhead et al. 2001; Szarkándi et al. 2017; This study).

**Material examined:** Thailand, Nakhon Ratchasima Province, Khao Yai National Park, trail to Kong Kaew waterfall,  $14^\circ 26' 22'' \text{N}$ ,  $101^\circ 22' 19'' \text{E}$ , elevation 744 m, 24 September 2018, N. Wannathes, N. Suwannarach, J. Kumla, S. Khuna, P. Lumyong and S. Lumyong, SDBR-CMUNW1161 (**new record for Thailand**).

**GenBank number:** ITS = OP503478.

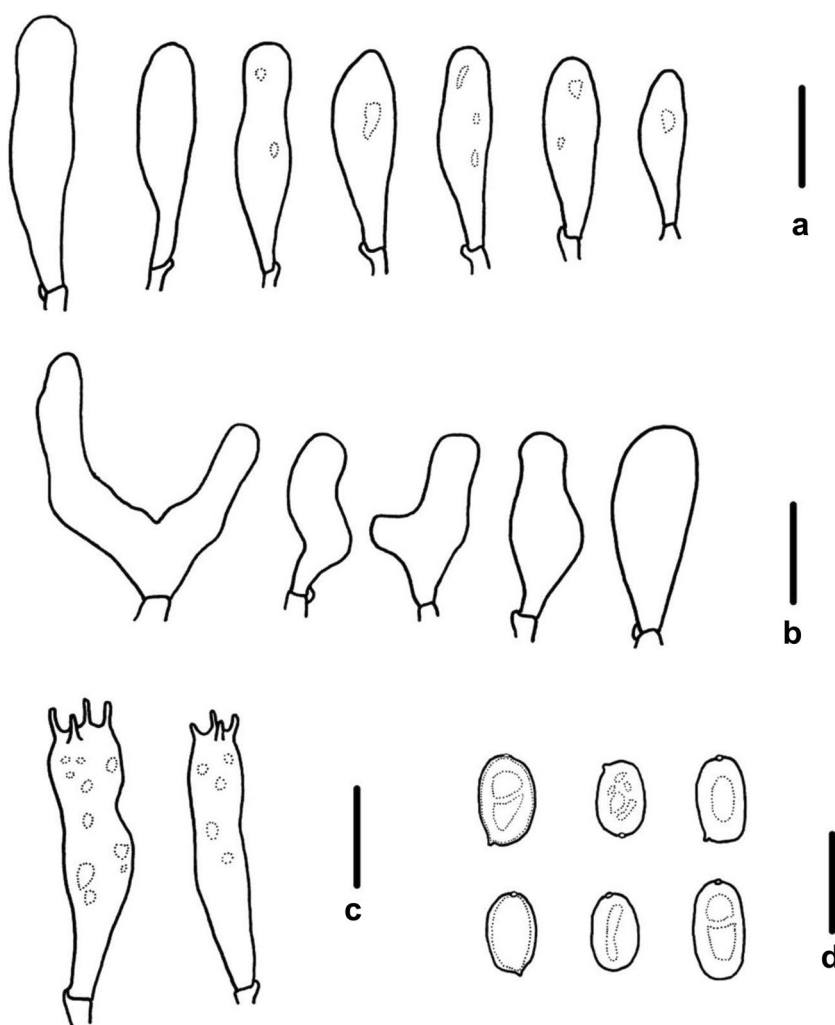
**Notes:** *Parasola setulosa* was classified into *Parasola* section *Auricomi* based on morphological and phylogenetic analysis (Fig. 91). This species is characterized by a small to medium-sized coprinoid basidiomes with light brown to greyish brown, radial plicato-striate pileus, moderately crowded lamella, cylindrical, orange grey stipe, lentiform basidiospores with broadly ovoid to subglobose in frontal view with the size of  $8\text{--}11 \times 7\text{--}9 \times 6\text{--}8 \mu\text{m}$ , and central germ pore. The pileipellis is composed of hyaline *sclerocystidia* with brown thick wall, and presence of cheilo- and pleurocystidia. The Thai specimen matches nicely with the description of type study reported by Nagy et al. (2010) and is in concordance with the note of Pegler





**Fig. 92** Basidiome of *Pholiota betulicola* (HMJAU37328, **holotype**). Photo by T. Bau

**Fig. 93** *Pholiota betulicola*. **A** Pleurocystidia. **B** Cheilocystidia. **C** Basidia. **D** Basidiospores. Scale bars: 10  $\mu$ m. Drawings by E. Tian



(1986). *Parasola setulosa* is morphologically similar to *P. malakandensis*, but differs by forming larger basidiospores ( $13\text{--}18 \times 12.5\text{--}16 \times 10\text{--}13$   $\mu$ m, Hussain et al. 2016).

**Strophariaceae** Singer & A.H. Sm.

**Notes:** The family *Strophariaceae* was established by Overeem in 1927. It is an important group in Basidiomycota. This family accommodates 18 genera and about 1300

species, distributing worldwide (Kirk et al. 2008). There are many edible and medicinal properties in this family, such as *Pholiota nameko*, *P. adiposa*, *Stropharia rugosoannulata* and so on (Dai et al. 2008, 2010).

***Pholiota* (Fr.) P. Kumm.**

**Notes:** *Pholiota* is a widespread agaric genus, containing about 150–155 species worldwide, with most species being found in the north temperate zone (Smith and Hesler 1968; Jacobsson 1990; Holec 2001; Kirk et al. 2008; Noordeloos 2011; Holec et al. 2014). The genus *Pholiota* is mainly characterized by a glabrous or fibrillose to scaly pileus often with yellow and brown tint, a partial veil forming an annulus on the stipe, rusty brown to yellow–brown spore deposit, smooth basidiospores frequently with a germ pore, and often typical chrysocystidia or prominent lageniform pleurocystidia (Smith and Hesler 1968; Jacobsson 1990).

***Pholiota betulicola* T. Bau & E.J. Tian, *sp. nov.***

**Index Fungorum number:** IF559944; **Facesoffungi number:** FoF 12906; **Figs.** 92, 93

**Etymology:** The epithet *betulicola* refers to the tree which this species grows on.

**Holotype:** HMJAU37328.

**Diagnosis:** Differs from other *Pholiota* species by yellowish pileus with light brown minute fibrillose spots, distinct spicy-aromatic content, whitish stipe with brownish longitudinal stripes and basal yellowish tomentum, pleurocystidia buried in hymenium, sometimes sub-rectangle basidiospores, as well as growing on living birch.

**Pileus** 11 cm in diam, convex; surface slightly viscid, with appressed light brown (6D6) minute fibrillose spots; brownish yellow (5C8) at center, becoming yellowish white (1A2) to white towards the margin; the margin irregularly undulate. **Context** thick, firm, yellowish white (2A2), odor distinct spicy-aromatic. **Lamellae** adnexed, broad, close, L = 60–65 mm, I = 3–7 mm, dark blonde (5D4), the edges even. **Stipe** 5 cm long, 1.9 cm thick, central or eccentric, slightly enlarged at the base, hard, solid, smooth and white above the annulus, ground color whitish and with brownish longitudinal stripes and brown fibrillose squamules below the annulus, with yellowish white (1A2) tomentum near the base. **Partial veil** leaving an annular zone. **Spore print** cinnamon brown (6D6).

**Basidiospores** (6.5–)7.5–10 × (3.7–)4.5–5 µm, Q = (1.25–)1.5–2, in face view elliptic, oblong to sub-rectangle, rarely broadly elliptic, in side view elliptic, somewhat inequilateral to slightly reniform, wall smooth and thick, germ pore minute, pale rusty, yellow-brownish to pale brown in KOH, slightly paler in Melzer's reagent. **Basidia** 22–28 × 5–7.5 µm, 4-spored, clavate, hyaline in KOH. **Pleurocystidia** 15–27 × 4.5–5 µm, buried in the hymenium,

clavate to subfusiform, sometimes with refractive and amorphous-granular content, wall thin, smooth, pale tawny to dark yellow brown in KOH. **Cheilocystidia** 17–25 × 5–8 µm, clavate, clavate-irregular to utriform or lageniform to versiform, rarely branched, thin-walled, smooth, content homogeneous, hyaline to pale yellow brown in KOH. **Caulocystidia** not observed. **Gill trama** of parallel hyphae hyaline to yellowish in KOH, walls smooth, thin to thick, 3.5–10 µm in diam. **Pileus cutis** of yellowish brown to cinnamon hyphae 2.5–5 µm in diam, thin-walled, smooth. **Content hyphae** hyaline to yellowish in KOH, cells inflated, smooth, thin-walled, interwoven. **Clamp connections** present in all tissues.

**Habitat:** Solitary at the base of living birch in mixed broadleaf-conifer forest in late summer.

**Materials examined:** China, Jilin Province, Jiaohe, Hongye Valley, elev. 520 m, solitary at the base of living birch in mixed broadleaf-conifer forest, 27 August 2016, Tolgor Bau, HMJAU37328 (**holotype**); Jiaohe, Shansongling, 1 September 2020, Yuhou Zhai, HMJAU37369.

**Genbank numbers:** HMJAU37328: ITS = OP244886, LSU = MN251156, RPB2 = MN329729, TEF1-α = MN311972; HMJAU37369: ITS = OP244887, LSU = OP223414.

**Notes:** This species is readily recognized due to its yellowish pileus with light brown minute fibrillose spots, thick content with distinct spicy-aromatic odor reminding of *Tricholoma matsutake*, whitish stipe with brownish longitudinal stripes and yellowish tomentum at the base, as well as numerous pleurocystidia buried in hymenium and sometimes sub-rectangle basidiospores.

Growing on living trees and the large and robust basidiomes of this species remind one of *Pholiota populnea*. However, the pileus of the latter has no yellow tone and covers with conspicuous floccose or patches scales, and the lack of the pleurocystidia and cylindric-capitate cheilocystidia also makes it different from *P. betulicola*.

In the phylogenetic analysis (Fig. 94), the samples of *Pholiota betulicola* occupied an isolated phylogenetic position apart from the other species of *Pholiota*. Furthermore, in the multiple alignment, this species has a unique insertion of 181 bp.

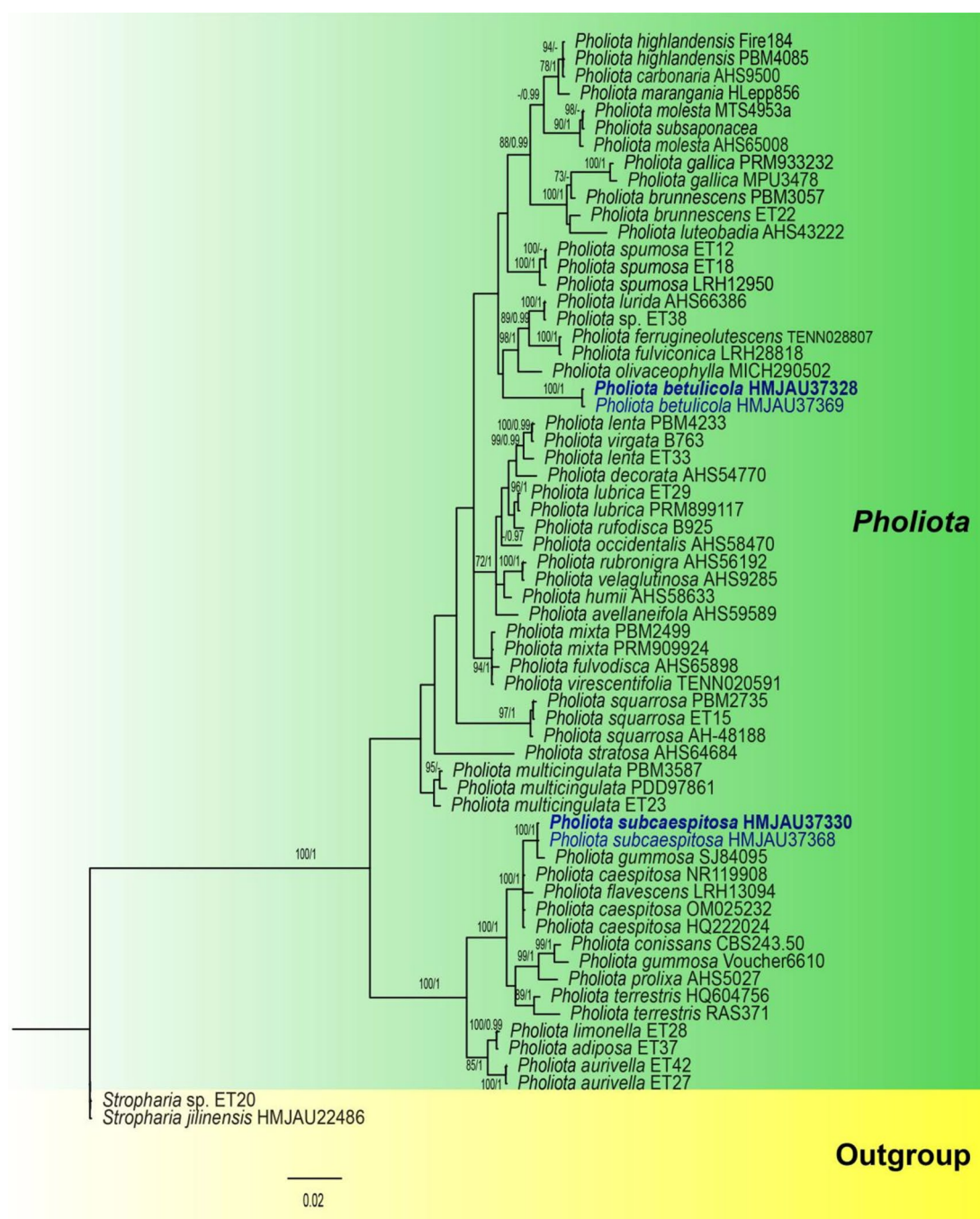
***Pholiota subcaespitosa* E.J. Tian, *sp. nov.***

**Index Fungorum number:** IF559945; **Facesoffungi number:** FoF 12907; **Figs.** 95, 96

**Etymology:** Based on the similarity to *Pholiota caespitosa*.

**Holotype:** HMJAU37330.

**Diagnosis:** Differs from other *Pholiota* species by the pileus with umbonate or depressed disc, slim stipe, brownish to brown fibrillose scales on the surface of pileus and stipe, small basidiospores, pleurocystidia as chrysocystidia, cheilocystidia mainly with two shapes:



**Fig. 94** BI phylogram of *Pholiota* based on data set (ITS + 28S). PPs > 0.95 and bootstrap values > 70% are shown. The new species in this study are in bold and blue. The tree is rooted with the two species of *Stropharia*

fusoid-ventricose and cylindric with subcapitate, the former small and rare with short cells chained at base, the latter often flexuous and at times with branches.

*Pileus* 18–35 mm broad, convex, becoming plane, with obtuse umbo or slightly depressed on the disc in age, with a waved margin at maturity, yellowish white (4A2), fading to near whitish toward margin, light brown (5D4) on the disc, slightly viscid when wet, decorated with brownish

fibrillose scales appressed and often not apparent in age. *Lamellae* adnate to sinuate-uncinate or with a decurrent tooth, light brown to brown, narrow, close, edges even. *Stipe* 40–70 mm long, 2–5 mm thick, equal, solid becoming stuffed to hollow, dingy pallid, becoming light brownish below, naked above, elsewhere with dingy brown fibrils or scales. *Veil* fibrillose, leaving an evanescent ring zone.



**Fig. 95** Basidiomes of *Pholiota subcaespitosa* (HMJAU37330, holotype). Photo by G. Cao



*Spore deposit* brown. *Basidiospores*  $5\text{--}7 \times 3.2\text{--}4\text{ }\mu\text{m}$  ( $Q = 1.5\text{--}2$ ), in face view elliptic, oblong to subovate, in side view slightly inequilateral, wall smooth and thick, germ pore distinct, sometimes making the spore apex somewhat truncate, rust brown (6E8) to light brown (6D8) in KOH, slightly paler in Melzer's reagent. *Basidia*  $20\text{--}24 \times 5.5\text{--}6.5\text{ }\mu\text{m}$ , 4-spored, clavate, hyaline in KOH. *Pleurocystidia* as chrysocystidia,  $30\text{--}42 \times 8\text{--}9.5\text{ }\mu\text{m}$ , sub-fusoid, fusoid-ventricose to clavate-mucronate, with thin and smooth wall, hyaline to yellow brown in KOH, content showing a refractive amorphous inclusion as revived in KOH. *Cheilocystidia*  $20\text{--}67 \times 5\text{--}8\text{ }\mu\text{m}$ , cylindric with subcapitate apex, often flexuous, at times with branches, or fusoid-ventricose, some ventricose with 2–3 short cells chained at base, wall thin, rare slightly thick, hyaline in KOH, rarely yellowish, content homogeneous. *Gill trama* parallel, hyphae  $3\text{--}24\text{ }\mu\text{m}$  diam, thin-walled, hyaline to yellowish brown in KOH. *Pileus hyphae*  $2\text{--}8.6\text{ }\mu\text{m}$  in diam, yellowish to yellowish brown in KOH, wall thin, with spiral incrustations. *Context hyphae*  $3\text{--}10\text{ }\mu\text{m}$  in diam, thin-walled, hyaline in KOH. *Clamps* regularly present.

*Habitat*: Caespitose on hardwood stumps in autumn.

*Materials examined*: China, Jilin Province, Changchun, Saman huanle Valley, Jingyuetan National Forest Park, 10 September 2016, Guangcheng Cao, HMJAU37330 (**holotype**); *ibid.*, 1 September 2012, Enjing Tian, HMJAU37368.

*GenBank numbers*: HMJAU37330: ITS = OP244888, LSU = OP223415; HMJAU37368: ITS = OP244889, LSU = OP223416.

*Notes*: *Pholiota subcaespitosa* is similar to *P. caespitosa* in shape, germ pore and size of basidiospores, the pleurocystidia, and caespitose growth (Smith and Hesler 1968). However, the latter lack cylindric cheilocystidia. In the phylogram (Fig. 94), *P. subcaespitosa* clustered together with *P. caespitosa* and *P. gummosa*. *Pholiota gummosa* has the similar cylindric cheilocystidia with *P. subcaespitosa*, but the former can be easily distinguished by its absence of pleurocystidia (Smith and Hesler 1968).

#### *Atheliales* Jülich.

*Notes*: Sulistyo et al. (2021) recently emended the taxonomic frame of *Atheliales*. For now, five families are accepted in this order, viz. *Atheliaceae*, *Byssocorticaceae*, *Lobuliciaceae*, *Pilodermataceae* and *Tylosporaceae* (Sulistyo et al. 2021).

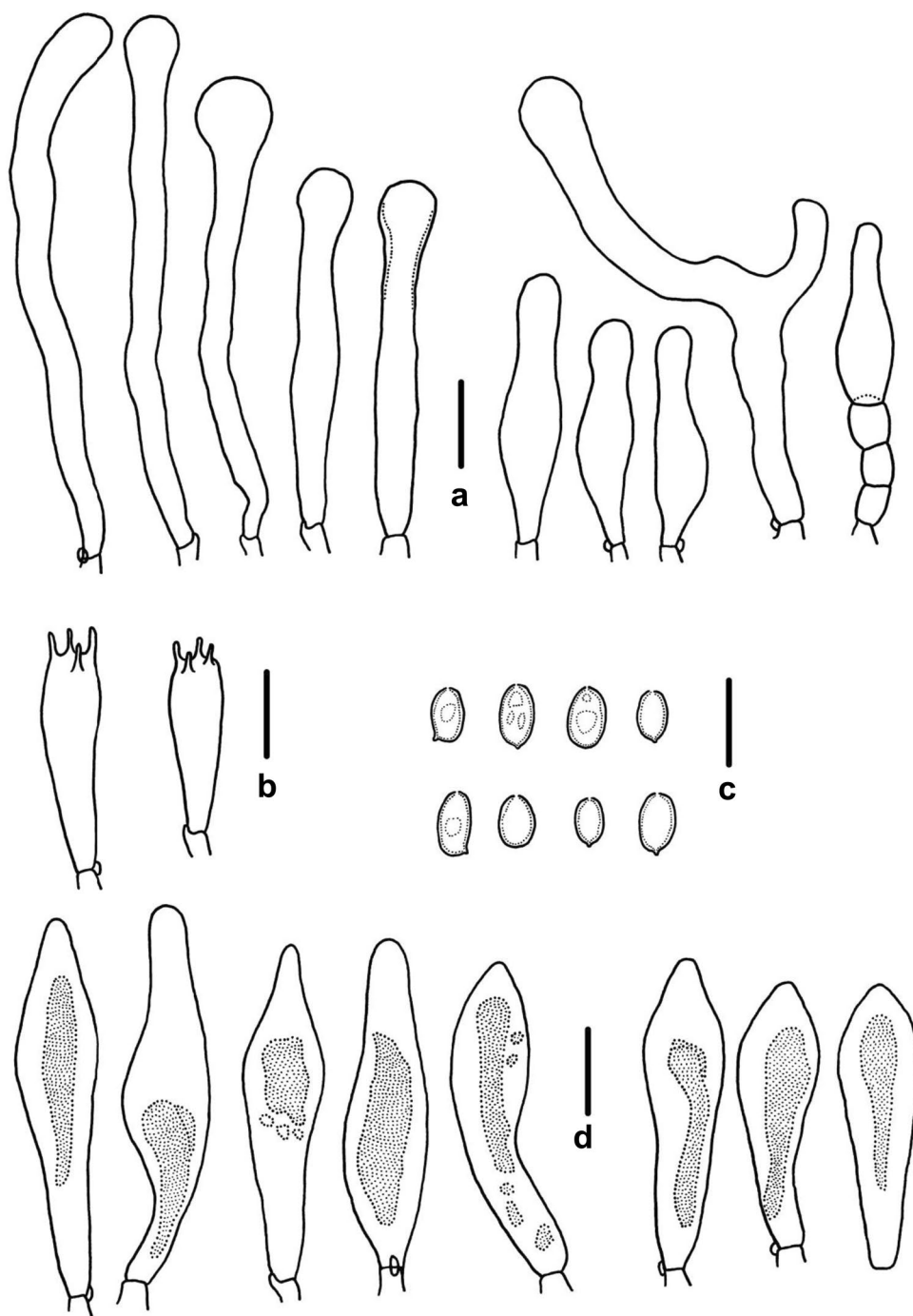
#### *Atheliaceae* Jülich.

*Notes*: *Atheliaceae*, typified by *Athelia*, is a family dominated by saprotrophic taxa (but with one lichenicolous species *Athelia arachnoidea*; Sulistyo et al. 2021). Two genera, viz. *Athelia* and *Fibulomyces* are included in this family (Sulistyo et al. 2021).

#### *Athelia* Pers.

*Notes*: *Athelia* was originally erected by Persoon (1818), and more than one hundred years later *Athelia epiphylla* was designated as the type species of this genus (Donk 1957). *Athelia* is the largest genera in *Atheliales*, with 117 names are recorded in Index Fungorum (18 November 2022). Morphologically, *Athelia* is characterized by thin and pellicular

**Fig. 96** *Pholiota subcaespitosa*. **A** Cheilocystidia. **B** Basidia. **C** Basidiospores. **D** Pleurocystidia. Scale bars: **A–D** = 10  $\mu$ m. Drawings by E. Tian



basidiomes, loosely intertwined subicular hyphae and inamyloid basidiospores (Bernicchia and Gorj3 2010; Maekawa et al. 2020).

***Athelia naviculispora*** S.L. Liu & L.W. Zhou, *sp. nov.*

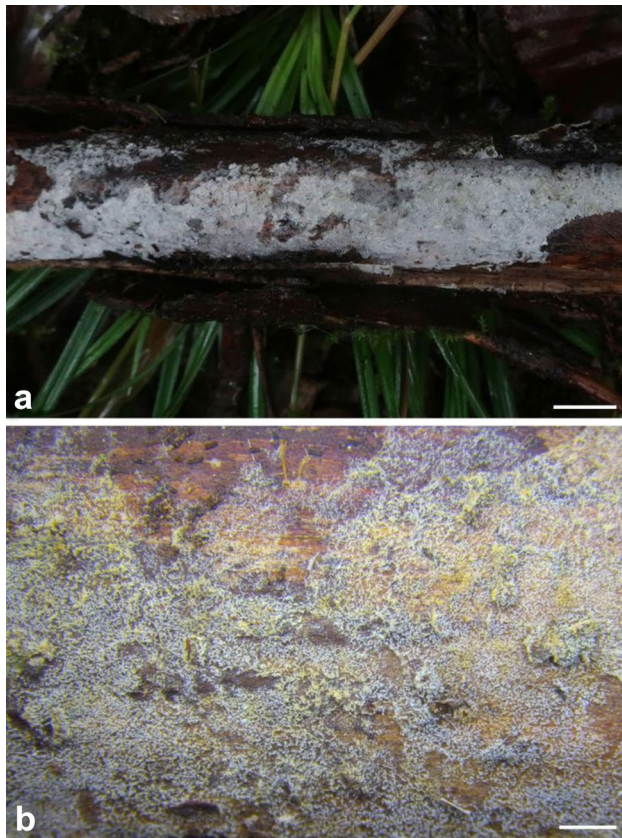
*Index Fungorum* number: IF 901054; *Facesoffungi* number: FoF 14808; Figs. 97, 98

*Etymology*: *naviculispora* (Lat.) referring to the navicular basidiospores.

*Holotype*: LWZ 20200921-21a (HMAS).

*Diagnosis*: Differing from other species of *Athelia* in the absence of cystidia and the presence of navicular to broadly subfusiform basidiospores.

*Basidiomes* resupinate, effused, thin, loosely adnate, athelioid, fragile, up to 10 cm long, 2 cm wide, 100  $\mu$ m thick. *Hymenophore* smooth, reticulate or continuous, grayish white when fresh, pale mouse-grey to olivaceous buff when dry, not cracked. *Margin* thinning out as byssoid, finely fibrillose, white, 0.8 mm wide.



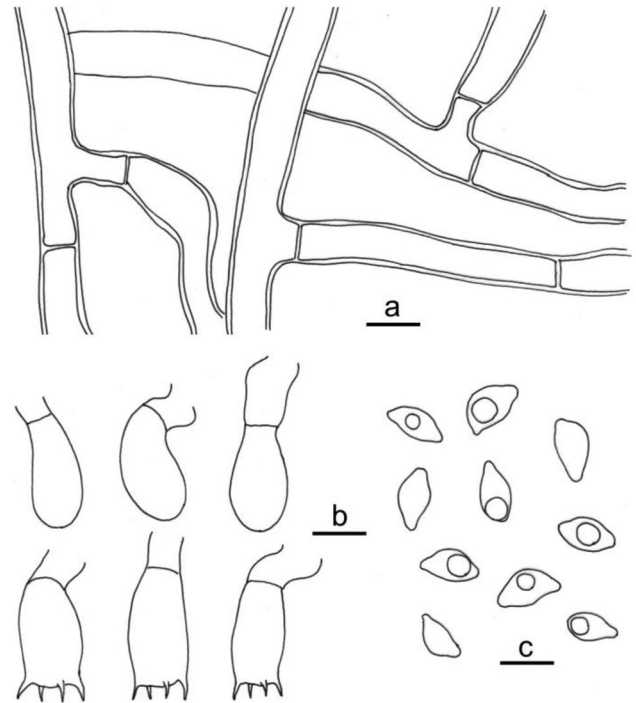
**Fig. 97** Basidiomes of *Athelia naviculisporea* (LWZ 20200921-21a, **holotype**). Scale bars: **a** = 1 cm, **b** = 1 mm

*Hyphal system* monomitic; *generative hyphae* without clamp connections, hyaline, thick-walled, frequently branched at right angles, 6–8 µm in diam. *Cystidia* absent. *Basidia* clavate, 4-sterigmata, simple-septate at the base, 18–22 × 9–13 µm. *Basidiospores* navicular to broadly subfusiform, hyaline, thin to slightly thick-walled, smooth, IKI–, CB–, 9–11 × 5–6 µm, L = 10 µm, W = 5.5 µm, Q = 1.8 (n = 60/2).

*Material examined*: China, Sichuan Province, Liangshan Yi Autonomous Prefecture, Leibo County, Mamize Provincial Nature Reserve, on fallen trunk of angiosperm, 21 September 2020, L.W. Zhou, LWZ 20200921-21a (HMAS, **holotype**); Anhui Province, Jinzhai County, Tianma National Nature Reserve, on fallen trunk of *Pinus*, 12 October 2020, L.W. Zhou, LWZ 20201012–13 (HMAS).

*GenBank numbers*: LWZ 20200921-21a: ITS = OR557252, LSU = OR527278; LWZ 20201012–13: ITS = OR557253.

*Notes*: Phylogenetically, *Athelia naviculisporea* is nested within the core clade of *Athelia* including the generic type *A. epiphylla* (Fig. 99). *Athelia naviculisporea* may be morphologically confused with *A. epiphylla* by grayish



**Fig. 98** Microscopic structures of *Athelia naviculisporea* (LWZ 20200921-21a, **holotype**). **a** Hyphae from subiculum. **b** Basidia and basidioles. **c** Basidiospores. Scale bars: 10 µm

hymenophore and absence of cystidia; however, *A. epiphylla* differs in its cylindrical to ellipsoid basidiospores (Eriksson and Ryvarden 1973; Bernicchia and Gorjón 2010).

#### *Byssocorticiaceae* Jülich.

*Notes*: *Byssocorticiaceae* is originally erected in *Atheliales* by Jülich (1981). Recently, Sulistyo et al. (2021) emended the circumscription of *Byssocorticiaceae* and accepted *Athelopsis*, *Byssocorticium* and *Leptosporomyces* in this family.

#### *Athelopsis* Oberw. ex Parmasto.

*Notes*: *Athelopsis*, typed by *A. glaucina*, is characterized by the pellicular basidiomes, usually with yellowish or green tints and ellipsoid, allantoid to cylindrical basidiospores (Bernicchia and Gorjón 2010; Gorjón et al. 2011). *Athelopsis* is similar to *Athelia* in micromorphology, but differs in its basidia arranged in a compacted layer (Bernicchia and Gorjón 2010; Gorjón et al. 2011).

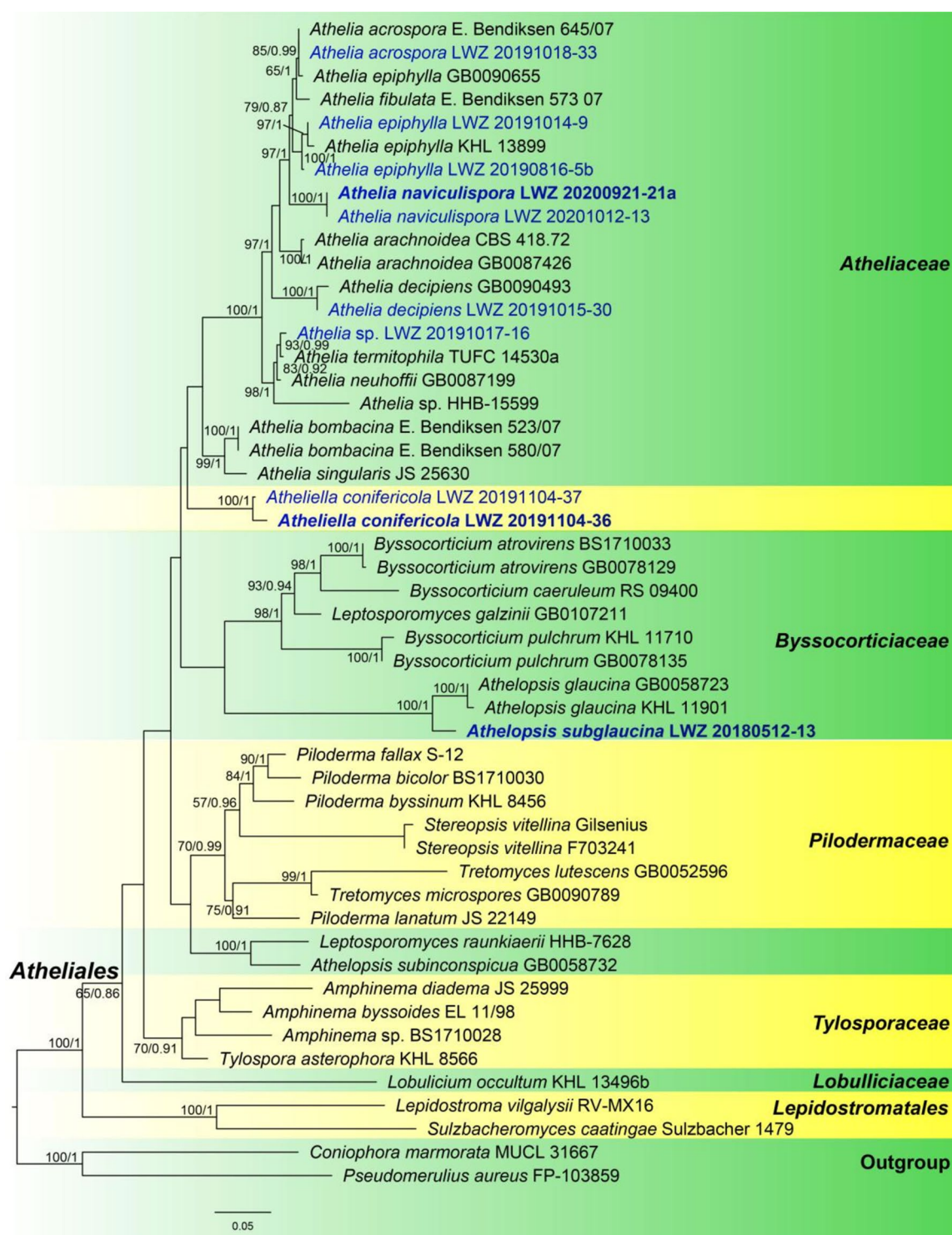
#### *Athelopsis subglaucina* S.L. Liu & L.W. Zhou, *sp. nov.*

*Index Fungorum number*: IF 901055; *Facesoffungi number*: FoF 1480; Figs. 100, 101

*Etymology*: *subglaucina* (Lat.) referring to the similarity to *A. glaucina*.

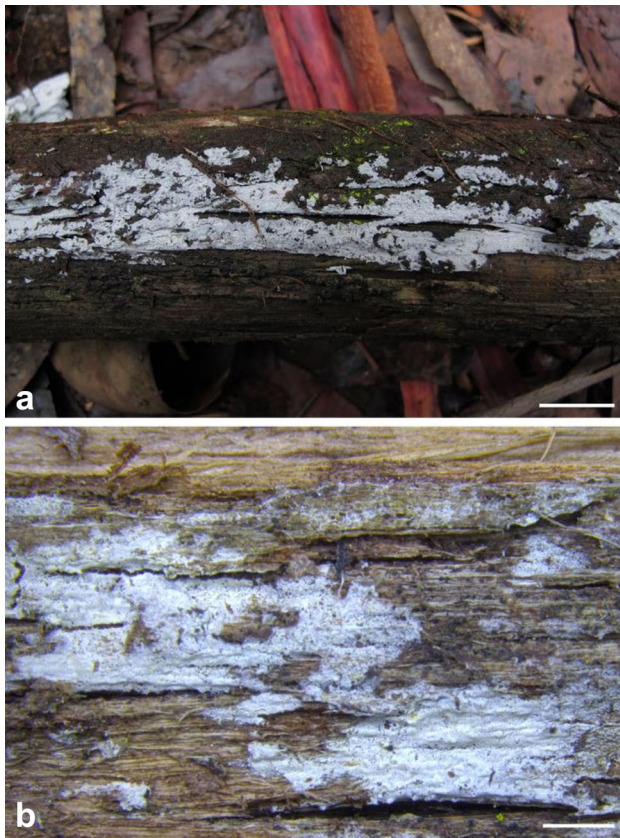
*Holotype*: LWZ 20180512–13 (HMAS).



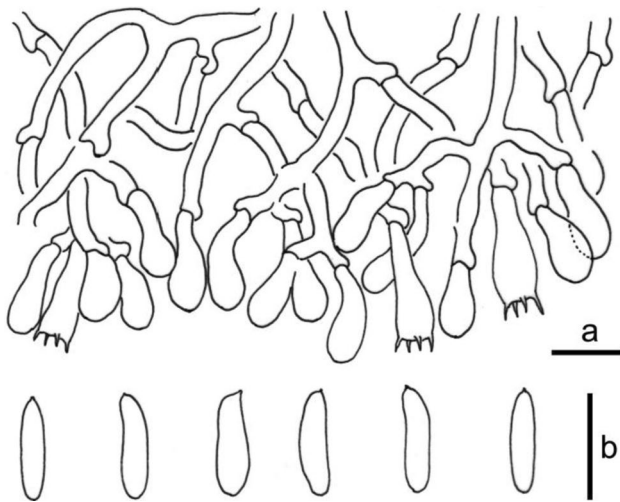


**Fig. 99** Phylogeny generated by the maximum likelihood algorithm based on combined ITS and nLSU regions is presented along with the bootstrap values and the Bayesian posterior probabilities above 50% and 0.8, respectively, at the nodes. *Coniophora marmorata*

MUCL 31667 and *Pseudomerulius aureus* FP-103859 were selected as the outgroup taxa. Holotypes are in bold and the newly generated sequences are in blue



**Fig. 100** Basidiomes of *Athelopsis subglauca* (LWZ 20180512–13, **holotype**). Scale bars: **a** = 1 cm, **b** = 1 mm



**Fig. 101** Microscopic structures of *Athelopsis subglauca* (LWZ 20180512–13, **holotype**). **a** A vertical section of basidiomes. **b** Basidiospores. Scale bars: 10  $\mu$ m

**Diagnosis:** Differing from *A. glauca* in whitish to ash-gray basidiomes and wider basidiospores (Eriksson and Ryvarden 1973; Bernicchia and Gorjón 2010).

*Basidiomes* resupinate, effused, thin, loosely adnate, up to 12 cm long, 3 cm wide, 100  $\mu$ m thick. *Hymenophore* smooth, continuous, whitish to ash-gray when fresh, grayish when dry, not cracked. *Margin* thinning out, concolorous.

*Hyphal system* monomitic; *generative hyphae* with clamp connections, hyaline, thin-walled, frequently branched, 2–3  $\mu$ m. *Cystidia* absent. *Basidia* clavate, 14–16  $\times$  6–7  $\mu$ m, with four sterigmata and a basal clamp connection. *Basidiospores* cylindrical, some narrowed toward the apex, hyaline, thin walled, smooth, IKI–, CB–, 8.5–10  $\times$  2.5–3  $\mu$ m, L = 9  $\mu$ m, W = 2.6  $\mu$ m, Q = 3.5 (n = 30/1).

**Material examined:** Australia, Victoria, Yarra Ranges National Park, Dandenong Ranges Botanic Garden, on fallen branch of *Eucalyptus*, 12 May 2018, L.W. Zhou, LWZ 20180512–13 (HMAS, **holotype**).

**GenBank numbers:** ITS = OR557255, LSU = OR527279.

**Notes:** *Athelopsis subglauca* is morphologically similar to *A. glauca* and these two species have a close phylogenetic relationship (Fig. 99). However, *A. glauca* differs in yellowish basidiomes and narrower basidiospores (2–2.5  $\mu$ m in width; Eriksson and Ryvarden 1973; Bernicchia and Gorjón 2010).

## ***Atheliales*, genus *incertae sedis***

***Atheliella*** S.L. Liu & L.W. Zhou, **gen. nov.**

**Index Fungorum number:** IF 901056; **Facesoffungi number:** FoF 14802;

**Etymology:** *Atheliella* (Lat.) referring to the close relationship with *Athelia*.

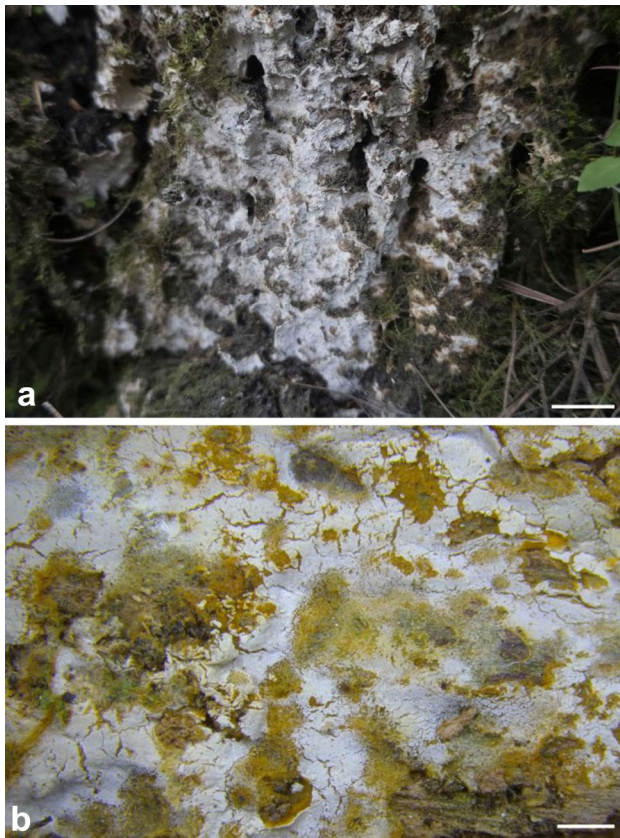
**Diagnosis:** Characterized by the pellicular basidiomes with cracked and peeped out, brownish subiculum, loosely intertwined subicular hyphae, the absence of cystidia, and ellipsoid basidiospores.

*Basidiomes* resupinate, effused, thin, loosely adnate, soft, membranous. *Hymenophore* smooth, continuous, whitish. *Subiculum* cracked, peeped out brownish. *Hyphal system* monomitic; *generative hyphae* with clamp connections. *Cystidia* absent. *Basidia* clavate, with four sterigmata. *Basidiospores* ellipsoid, hyaline, thin-walled, smooth, IKI–, CB–. On wood.

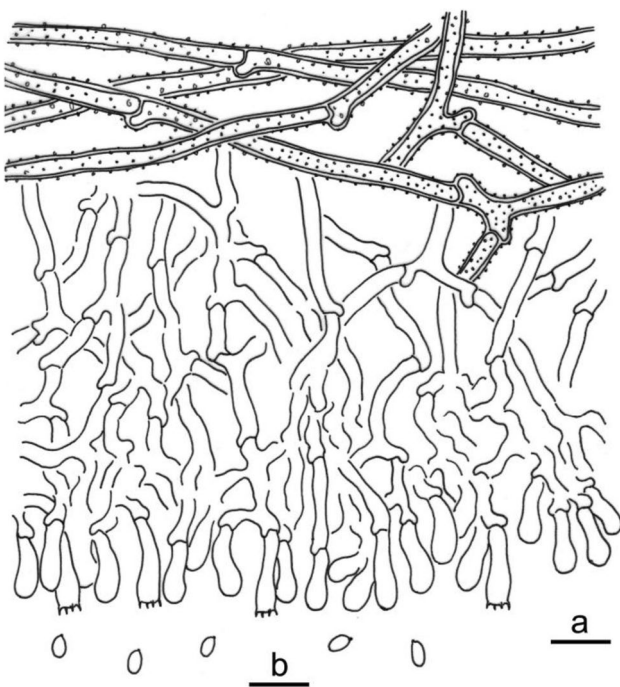
**Type species:** *Atheliella conifericola* S.L. Liu & L.W. Zhou.

**Notes:** *Atheliella* falls into the *Atheliales*, but is separated from any known families and genera (Fig. 99). The family position of this genus needs to be further clarified. *Atheliella* seems to be morphologically related to members of *Atheliaceae*; however, *Atheliella* is distinct by the combination of brownish subiculum and ellipsoid basidiospores (Eriksson and Ryvarden 1973; Bernicchia and Gorjón 2010).





**Fig. 102** Basidiomes of *Atheliella conifericola* (LWZ 20191104–36, **holotype**). Scale bars: **a** = 1 cm, **b** = 1 mm



**Fig. 103** Microscopic structures of *Atheliella conifericola* (LWZ 20191104–36, **holotype**). **a** A vertical section of basidiomes. **b** Basidiospores. Scale bars: 10  $\mu$ m

*Atheliella conifericola* S.L. Liu & L.W. Zhou, *sp. nov.*

*Index Fungorum* number: IF 901057; *Facesoffungi* number: FoF 14810; Figs. 102, 103

*Etymology*: *conifericola* (Lat.) referring to occurrence on conifers.

*Holotype*: LWZ 20191104–36 (HMAS).

*Diagnosis*: Characterized by the pellicular basidiomes with cracked and peeped out, brownish subiculum, loosely intertwined subicular hyphae, the absence of cystidia, and ellipsoid basidiospores.

*Basidiomes* resupinate, effused, thin, loosely adnate, soft, membranous, up to 10 cm long, 5 cm wide, 200  $\mu$ m thick. *Hymenophore* smooth, continuous, whitish, pinkish buff when dry. *Subiculum* cracked, peeped out brownish. *Margin* thinning out, brownish.

*Hyphal system* monomitic; *generative hyphae* with clamp connections; *subicular hyphae* yellowish, thick-walled, moderately branched at right angles, 3  $\mu$ m in diam; *subhymenia hyphae* hyaline, thin-walled, frequently branched. *Cystidia* absent. *Basidia* clavate, with four sterigmata and a basal clamp connection, 14–18  $\times$  3.5–5  $\mu$ m. *Basidiospores* ellipsoid, hyaline, thin-walled, smooth, IKI–, CB–, 3.8–4.2  $\times$  2–2.3  $\mu$ m, L = 4  $\mu$ m, W = 2.2  $\mu$ m, Q = 1.8 (n = 60/2).

*Material examined*: China, Yunnan Province, Dali Bai Autonomous Prefecture, Cangshan Mountain, on stump of *Pinus*, 4 November 2019, L.W. Zhou, LWZ 20191104–36 (HMAS, **holotype**); *ibid.*, on fallen trunk of *Pinus*, 4 November 2019, L.W. Zhou, LWZ 20191104–37 (HMAS).

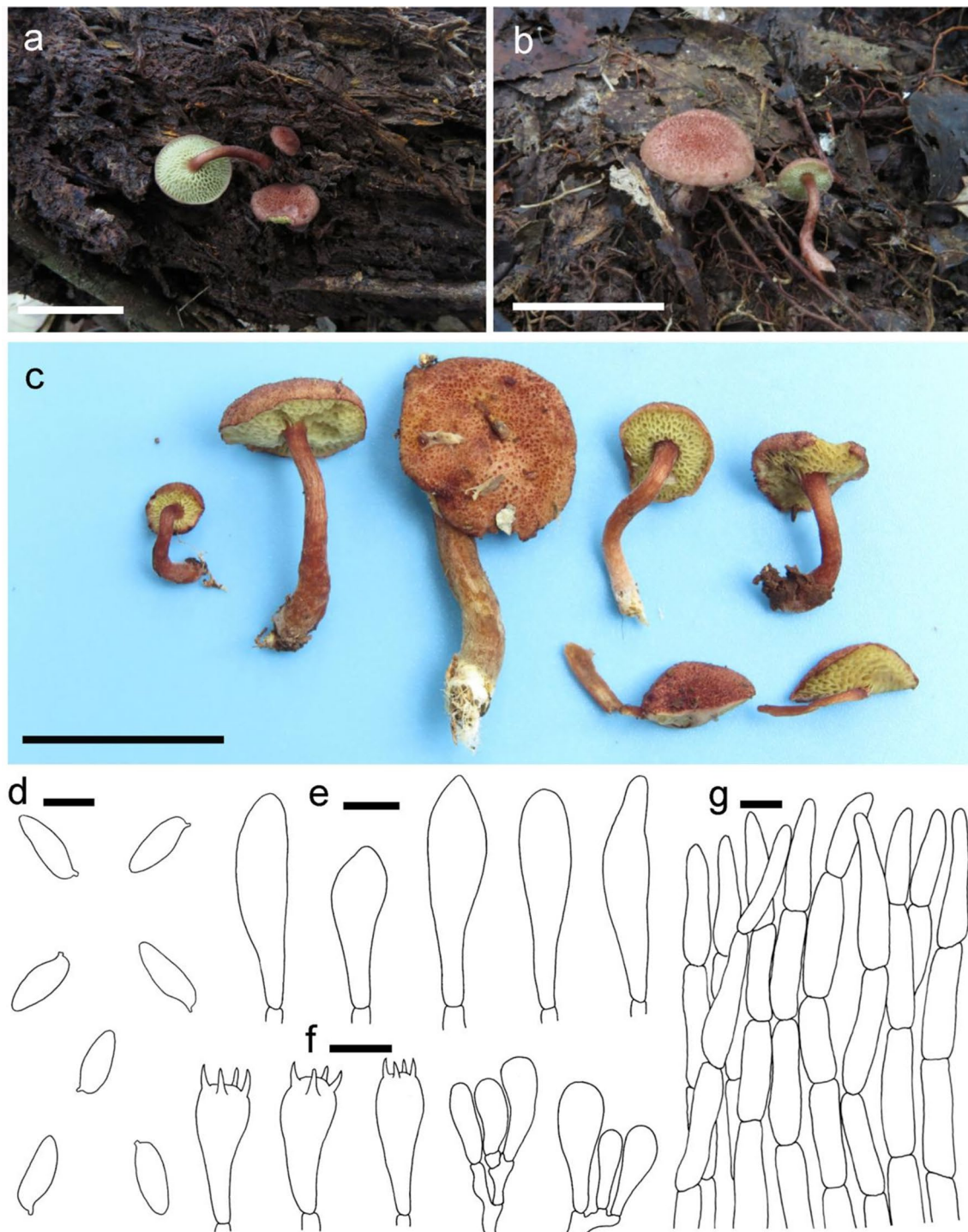
*GenBank numbers*: LWZ 20191104–36: LSU = OR527280; LWZ 20191104–37: ITS = OR557254, LSU = OR527281.

*Notes*: Morphologically, *Atheliella conifericola* resembles *Athelia bombacina* by thin and pellicular basidiomes, loosely intertwined subicular hyphae with encrusted crystals, clamp-connected hyphae, the absence of cystidia, and ellipsoid basidiospores (Eriksson and Ryvarden 1973; Bernicchia and Gorjón 2010). However, *Athelia bombacina* differs in its whitish basidiomes and larger basidiospores (4.5–6  $\times$  2.5–3  $\mu$ m, Eriksson and Ryvarden 1973; 4.5–5.5  $\times$  2.5–3  $\mu$ m, Bernicchia and Gorjón 2010).

**Boletales** E.-J. Gilbert.

*Notes*: *Boletales* was first formally proposed by Gilbert (1931). It is a diverse order that includes stipitate-pileate forms, puffball-like forms, resupinate or crust-like fungi, and polypore-like species (Binder and Hibbett 2006). This order contains five suborders (*Boletineae*, *Sclerodermatineae*, *Suillineae*, *Coniophorineae* and *Tapinellineae*), 16 families, 141 genera, and more than 2000 species (Kirk et al. 2001; Binder and Hibbett 2006; He et al. 2019). Phylogenomic analysis estimates that the *Boletales* lineage arose in the





**Fig. 104** *Aureoboletus minimus* (GDGM44400, holotype). **a–c** Basidiomes. **d** Basidiospores. **e** Cheilocystidia and pleurocystidia. **f** Basidia and basidioles. **g** Pileipellis. Scale bars: **a–c** = 2 cm, **d–f** = 10  $\mu$ m, **g** = 20  $\mu$ m

early Cretaceous period approximately 113 Mya (Watkinson and Eastwood 2012).

***Boletaceae*** Chevall.

*Notes:* *Boletaceae* was introduced by Chevallier (1826) as a family separated from the *Agaricaceae* to accommodate *Boletus*. Species of *Boletaceae* are mainly characterized by stipitate-pileate forms with fleshy context and a tubulate, sometimes lamellate or loculate hymenophore, while few

species in this family are puffball-like fungi (Binder and Hibbett 2006; Kirk et al. 2008; Wu et al. 2014, 2016a). The family contains approximately 92 genera, which are interesting and important in forestry for their mycorrhizal properties and the edibility of many species (Zeng et al. 2013, 2014; Chai et al. 2019; He et al. 2019).

### *Aureoboletus* Pouzar.

**Notes:** *Aureoboletus* (Boletaceae, Basidiomycota) is a relatively small but cosmopolitan genus; species in this genus can be found in tropical, subtropical and temperate regions of different continents, especially rich in Asia and North America (Klofac 2010; Wu et al. 2016a; Zhang et al. 2019). This group of fungi can form ectomycorrhizal symbiosis with an array of ectotrophic plants of the families *Fagaceae*, *Myrtaceae* and *Pinaceae* (Pouzar 1957; Yang et al. 2003; Klofac 2010; Wu et al. 2016a; Zhang et al. 2019). Phylogenetic analyses demonstrated that *Aureoboletus* is a monophyletic group, and about 50 species have been reported worldwide (Klofac 2010; Wu et al. 2016a; Zhang et al. 2019; Wang et al. 2020b).

*Aureoboletus minimus* Ming Zhang, C.Q. Wang & T.H. Li, **sp. nov.**

**Index Fungorum number:** IF 900314; **Facesoffungi number:** FoF 14038; **Fig.** 104

**Etymology:** “*minimus*” refers to the small basidiomes.

**Holotype:** GDGM44400.

**Macroscopic characters:** *Basidiomes* small-sized. *Pileus* 0.8–2 cm wide, obtuse to convex at first, becoming broadly convex to plane in age, fleshy, surface dry or slightly viscid when wet, covered with fibrillose to tomentose squamules, light orange (6A6), pastel red (7A6–9A6) to grayish red (7B5–9B5, 8C5–9C5), usually cracking when mature; *margin* somewhat involute at young, nearly flat when mature, without veil remnants at margin. *Context* 1–2.5 mm thick at stipe, firm and tough in youth, soft when matured, white on the whole, greyish red (10B5–11B5) beneath pileipellis, slightly becoming greyish-pinkish or greyish red (10B5–11B5) when exposed. *Tubes* 2–3 mm deep, distinctly depressed around stipe, yellowish white, yellowish gray to pale yellow (2A2–4A3, 2A3–4A3, 2B2–3B2), often with an olive tint, unchanging when bruised. *Pores* 2–3 per mm, irregular angular, slightly elongated around stipe at maturity, concolorous with tubes, unchanging when bruised. *Stipe* 15–40 × 3–6 mm, central, cylindrical or narrowly clavate, solid, slightly enlarged toward the base, concolorous with pileus, covered with white to yellowish brown fibril or tomentum, with white basal mycelium. *Odour* not distinct. *Taste* mild.

**Microscopic characters:** *Basidiospores* 13–16 × 5–6 µm, ( $\bar{x}$  = 14.5 × 5.4 µm,  $n$  = 20), subfusiform, inequilateral in side view, smooth, yellowish to yellowish brown in 5%

KOH, thin-walled. *Basidia* 25–30 × 7–10 µm, clavate, 4-spored, sterigmata 2–4.5 µm long, yellowish white to hyaline in 5% KOH, without basal clamps. *Pleurocystidia* 32–50 × 10–13 µm, fusiform, thin-walled. *Cheilocystidia* frequent, similar to pleurocystidia in shape and size. *Hymenophoral trama* subparallel, yellowish white to hyaline in 5% KOH, with 4–10 µm broad. *Pileipellis* a trichodermium of erect hyphae 12–22 µm in diam, yellowish white to hyaline in 5% KOH; *terminal cells* 37–70 × 12–22 µm, cylindrical, clavate or nearly fusoid. *Stipitipellis* a layer of repent to suberect branching hyphae 4–8 µm in diam, hyaline in 5% KOH. *Clamp connections* absent in all tissues.

**Habit, habitat and distribution:** Solitary to scattered on soil or decayed wood in broadleaf forest dominated by *Fagaceae* trees. Currently only known from central Vietnam.

**Material examined:** Vietnam, Lam Dong Province, Da Lat, Bi Doup Nui Ba National Park, alt. 1500 m, 15 October 2017, Ming Zhan, GDGM44400 (**holotype**), Tai-Hui Li, GDGM44401.

**GenBank numbers:** GDGM44400: LSU = OP901640, TEF1- $\alpha$  = OP918149, RPB1 = OP918155, RPB2 = OP918152; GDGM44401: LSU = OP901641, TEF1- $\alpha$  = OP918150, RPB1 = OP918156, RPB2 = OP918153.

**Notes:** *Aureoboletus minimus* is characterized by its small basidiomes with a dry and usually cracked pileus densely covered with fibrillose to tomentose squamules, white context slightly changing greyish-pinkish or greyish red when exposed, yellowish gray to pale yellow hymenophore unchanging when bruised, subfusiform and relatively larger basidiospores. The above combination of features makes it easily distinguished from other species in *Aureoboletus*.

Morphologically, *A. minimus* is similar to *A. glutinosus* and *A. tenuis*. However, *A. glutinosus* differs by its strongly glutinous or mucilaginous basidiomes, reddish-brown to greyish-ruby pileus with irregular reticulation and gelatinous veil remnants at margin, and smaller basidiospores 10–13.5 × 4.5–5 µm (Zhang et al. 2019). *Aureoboletus tenuis* differs in having relatively larger basidiomata, glutinous and wrinkled pileus, and smaller basidiospores 11–12 × 4–5 µm (Zhang et al. 2014).

Phylogenetic analyses based on the combined sequence of LSU, TEF1- $\alpha$ , RPB1, RPB2 shown that two specimens of *A. minimus* formed a distinct lineage in *Aureoboletus*, and showed close relationships with *A. auriflammeus*, *A. garciae* and *A. miniatoaurantiacus* but with low support value and larger genetic distance (Fig. 105). In morphology, *A. auriflammeus* and *A. miniatoaurantiacus* can be easily distinguished by their pileus minutely covered with orange yellow, orange to reddish-orange tomentum or powder (Zhang et al. 2019). *Aureoboletus garciae*, recently reported from Mexico, differs in having vivid blue to light blue pileus with some reddish tones, bright yellow





**Fig. 105** Phylogram generated from maximum likelihood analysis based on combined LSU, tef1, rpb1 and rpb2 sequence data of *Aureoboletus*. Bootstrap support values for maximum likelihood greater than 50% are indicated above or below the nodes, and branches with

Bayesian posterior probabilities greater than 0.95 are given in bold. The new species are in blue. The tree is rooted with *Phylloporus imbricatus* HKAS68642 and *Xerocomus subtomentosus* HKAS58865

hymenophore, and smaller basidiospores  $9\text{--}14 \times 4\text{--}5(-6)\ \mu\text{m}$  (Haelewaters et al. 2020).

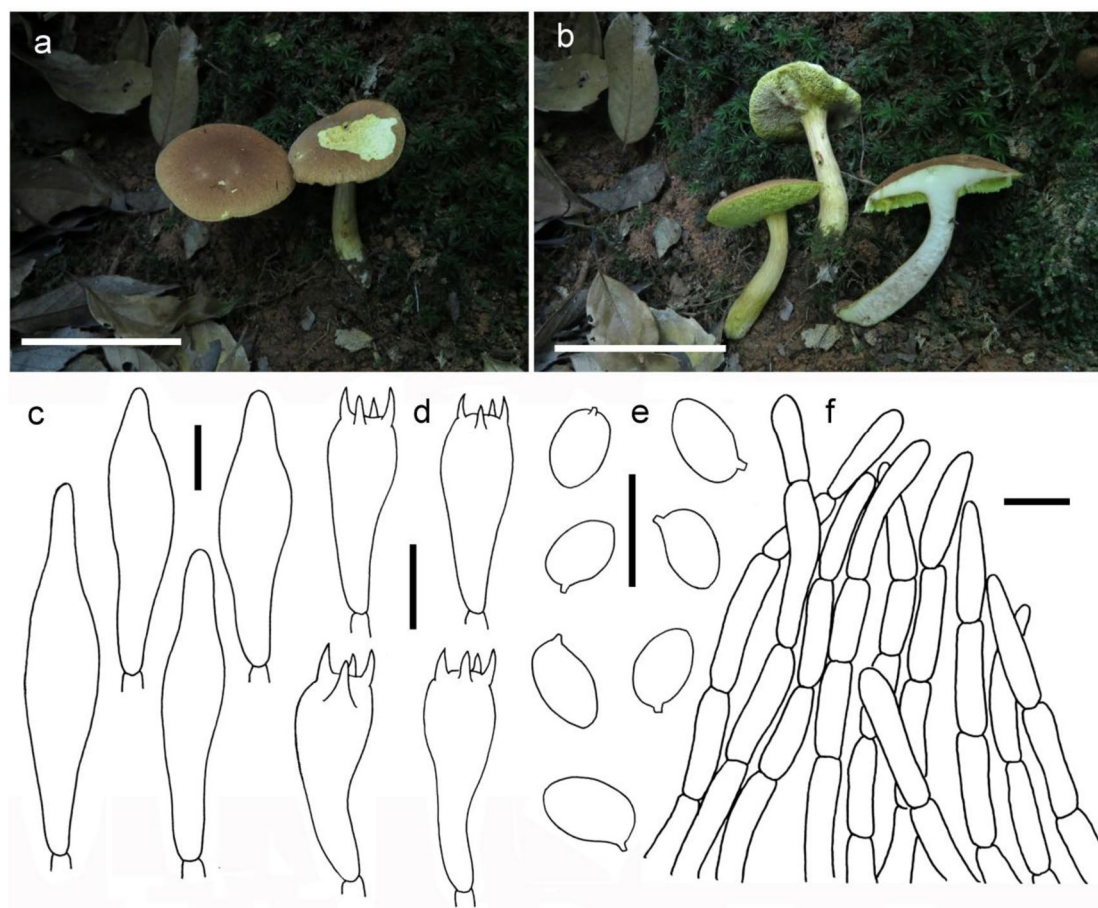
*Aureoboletus nanlingensis* Ming Zhang, C.Q. Wang & T.H. Li, *sp. nov.*

*Index Fungorum* number: IF 900315; *Facesoffungi* number: FoF 14039; Fig. 106

*Etymology*: “nanling” refers to the type locality Nanling National Forest Park.

*Holotype*: GDGM71707.





**Fig. 106** *Aureoboletus nanlingensis* (GDGM71707, holotype). **a, b** Basidiomes. **c** Cheilocystidia. and pleurocystidia. **d** Basidia. **e** Basidiospores. **f** Pileipellis. Scale bars: **a, b** = 5 cm, **c–e** = 10  $\mu$ m, **f** = 20  $\mu$ m

**Macroscopic characters:** *Basidiomes* small-sized. *Pileus* 2–4.5 cm wide, hemispheric when young, becoming convex to nearly plane in age, fleshy, dry, subtomentose, grayish yellow to brownish orange (4C5–7C5), slightly paler toward pileus margin; *margin* thin, slightly incurved when young, becoming nearly straight in age, without veil remnants. *Context* 4–7 mm thick at center, firm and tough in youth, becoming soft, white, unchanging when exposed. *Tubes* 3–6 mm deep, pastel yellow, light yellow, greenish yellow to greyish yellow (1A4–1A2, 2A4–2A5, 1B4–2B4), unchanging when bruised. *Pores* small, 2–3 per mm, somewhat larger around the stipe, circular to angular, concolourous with tubes, unchanging when bruised. *Stipe* 40–60  $\times$  8–10 mm, central, cylindrical or clavate, equal to slightly enlarged downwards, surface dry, yellowish white to pale yellow (1A2–2A2, 1A3–2A3), with obscure fibrous stripes. *Stipe context* white, unchanging or slightly changing greyish red when exposed, especially in the lower part. *Basal mycelium* white. *Odour* none. *Taste* mild.

**Microscopic characters:** *Basidiospores* 7–8.5  $\times$  (4–)4.5–5  $\mu$ m, ( $\bar{x}$  = 7.7  $\times$  4.7  $\mu$ m,  $n$  = 20),

ellipsoidal to broadly ellipsoidal, oblong in ventral view, smooth, yellowish to yellowish brown in 5% KOH, thin-walled. *Basidia* 25–30  $\times$  8–10  $\mu$ m, clavate, 4-spored, sterigmata 3–5  $\mu$ m long, yellowish white to hyaline in 5% KOH, without basal clamps. *Pleurocystidia* 35–60  $\times$  10–13  $\mu$ m, fusiform, thin-walled. *Cheilocystidia* frequent, similar to pleurocystidia in shape and size. *Hymenophoral trama* subparallel, yellowish white to hyaline in 5% KOH, with 4–10  $\mu$ m broad. *Pileipellis* a trichodermium of suberect hyphae 8–15  $\mu$ m in diam, branched, yellowish white to hyaline in 5% KOH; *terminal cells* 40–70  $\times$  8–15  $\mu$ m, cylindrical, clavate or nearly fusoid. *Stipitipellis* a layer of repent hyphae 4–8  $\mu$ m in diam, hyaline in 5% KOH. *Clamp connections* absent in all tissues.

**Habit, habitat and distribution:** Solitary to scattered on soil in broadleaf forest dominated by *Fagaceae* trees. Currently only known from southern China.

**Material examined:** China, Guangdong Province, Shao-guan, Nanxiong Town, Qingzhangshan-Xiaoliukeng Provincial Natural Reserve, alt. 500 m, 16 May 2018, Ming Zhang,



**Fig. 107** Basidiomes of *Hemileccinum duriusculum*. **a–c** EFHAAU2843 (**holotype**). **d** HKAS76664. **e, f** HKAS91279. Scale bars: 2 cm

GDGM71707 (**holotype**); *ibid.*, alt. 580 m, 17 May 2018, Ming Zhang, GDGM44729.

**GenBank numbers:** GDGM71707: LSU = MN204556, RPB1 = MN473174, RPB2 = MN549710; GDGM44729: LSU = OP901643, TEF1- $\alpha$  = OP918151, RPB1 = OP918157, RPB2 = OP918154.

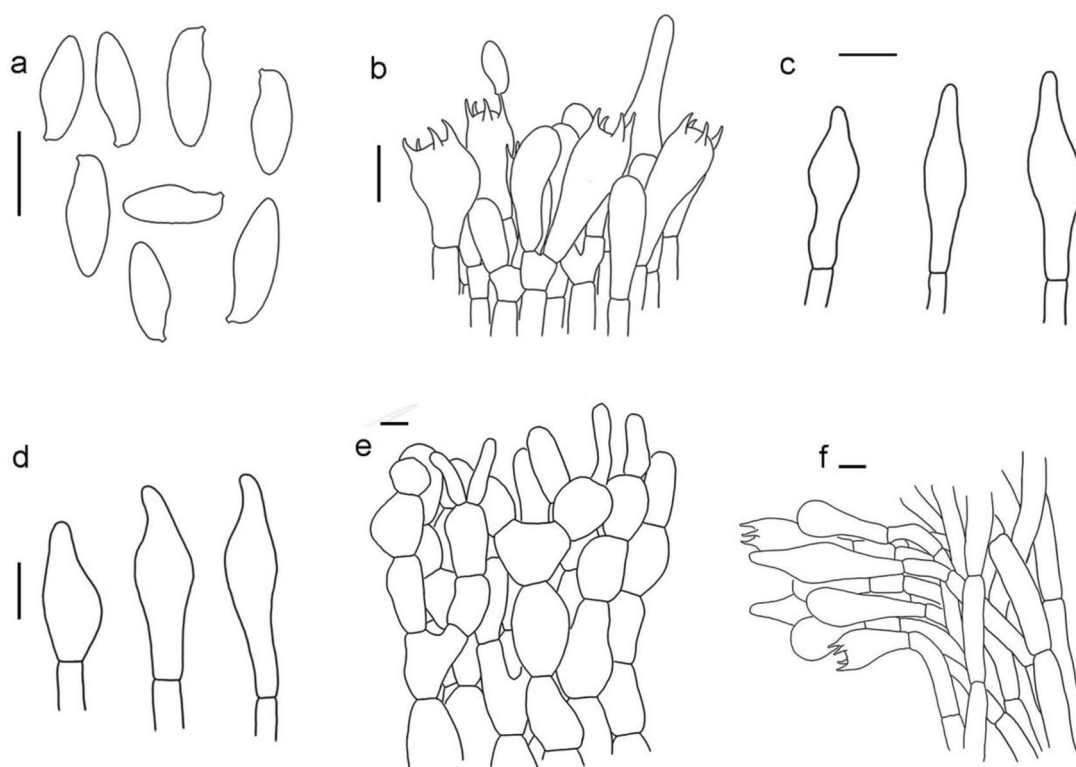
**Notes:** *Aureoboletus nanlingensis* is characterized by its dry, subtomentose and grayish yellow to brownish orange pileus, white context unchanging when exposed, light yellow to greyish yellow hymenophore unchanging when bruised, and ellipsoidal to broadly ellipsoidal basidiospores. The

combination of above features corresponds to the define of “Clade II” of *Aureoboletus* in Zhang et al. (2019).

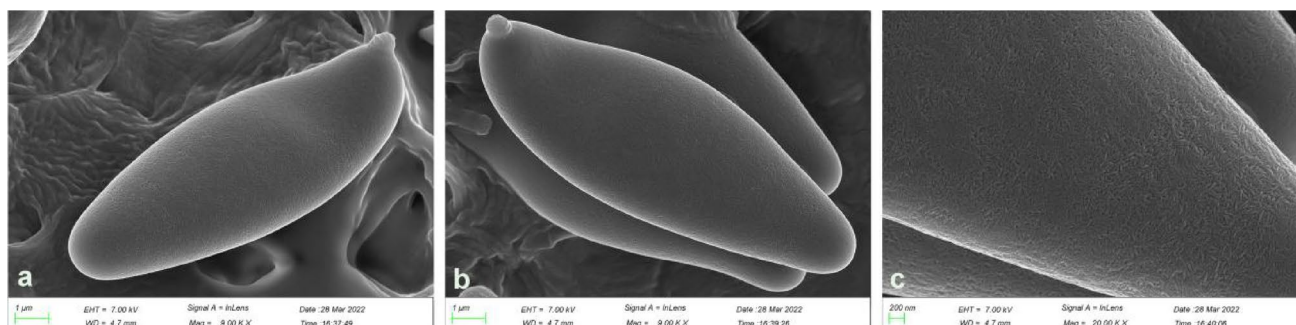
Morphologically, *A. nanlingensis* resembles *A. raphanaceus* and *A. solus*. However, *A. raphanaceus* differs by its yellowish-white to pinkish-white pileus covered with fibrillose to tomentose squamules, radish smell and broader basidiospores  $7.5\text{--}9 \times 5\text{--}6\text{ }\mu\text{m}$  (Zhang et al. 2019); *A. solus* differs by its brownish-yellow to greyish-red pileus, glabrous stipe and larger basidiospores  $(7\text{--})8\text{--}10.5\text{--}(11) \times (4\text{--})4.5\text{--}5\text{ }\mu\text{m}$  (Zhang et al. 2019).

Phylogenetically, *A. nanlingensis* nested well into the “Clade II” of genus *Aureoboletus*, which defined by Zhang





**Fig. 108** Microscopic features of *Hemileccinum duriusculum* (EFHAAU2843, **holotype**). **a** Basidiospores. **b** Hymenium and subhymenium. **c** Cheilocystidia. **d** Pleurocystidia. **e** Pileipellis. **f** Stipitipellis. Scale bars: 10 µm



**Fig. 109** The basidiospores under SEM of *Hemileccinum duriusculum* (EFHAAU2843, **holotype**)

et al. (2019), and closely related to *A. velutipes*. However, the latter differs by its brown orange to reddish-brown pileus, light yellow to pastel yellow stipe covered with obviously fibrillose to tomentose squamules, and larger basidiospores  $10\text{--}13 \times 4\text{--}6.5\text{ }\mu\text{m}$  (Zhang et al. 2019).

### *Hemileccinum* Šutara.

**Notes:** The genus *Hemileccinum* was erected with type species *H. impolitum* (Šutara 2008). Species in this genus can be distinguished by their rugose pileus often covered with inconspicuous subtomentose or pulverulent squamules,

unchanging context and hymenophore when bruised, often yellowish punctate squamules on the stipe surface, fusoid basidiospores ornamented with irregular warts, and hyphoepithelium to subepithelium pileipellis. Currently *Hemileccinum* comprises 15 species (Šutara 2008; Halling et al. 2015; Wu et al. 2016a; Kuo and Ortiz-Santana 2020; Li et al. 2021). Among them, seven species were recorded from China including the new species described below.

***Hemileccinum duriusculum*** Mei-Xiang Li, Zhu L. Yang & G. Wu, *sp. nov.*



*Index Fungorum* number: IF 901102; *Facesoffungi* number: FoF 14841; Figs. 107, 108, 109

*Etymology*: The epithet '*duriusculum*' refers to the wrinkled pileus.

*Holotype*: HKAS 125907.

*Basidiomes* stipitate-pileate, medium-sized to large. *Pileus* up to 9 cm in diam, convex to plano-convex, surface glabrous, but some areas often covered with inconspicuous subtomentose or pulverulent squamules, often strong rugose, light brown to brown (5D5, 6D5–6E5), sometimes much paler with light red tinge, margin and surface ridges lighter in color, dry; *context* yellowish white to pale yellow (1A2–1A3), unchanging when bruised, ca. 10–15 mm thick. *Hymenophoral tubes* concolorous with pores, pale yellow (3A3) to grayish yellow (4B4), unchanging when bruised; *pores* polygonal to roundish, 1.5–2 per mm, *tubes* ca. 13 mm long, unchanging when bruised. *Stipe* 10–13 × 1.2–2.1 cm, subcylindrical, clavate, slightly bulbous at the base, upper part light yellow (4A5), lower part reddish to grayish reddish (5C4–8C5); surface covered with finely granular yellowish to brownish yellowish scales; *context of stipe* cream to pale yellow, unchanging when bruised; *basal mycelium* cream.

*Basidia* 24–35 × 8–12 µm, clavate, thin-walled, 4-spored; sterigmata 4–6 µm long, colorless in KOH. *Basidiospores* [40/2/2] 12–15 × 4–6 µm [ $Q = (2.5\text{--}) 2.6\text{--}2.8 (-3)$ ,  $Q_m = 2.74 \pm 0.17$ ], subfusiform in side view with slight suprahilar depression, subfusoid in ventral view, yellowish to brownish in KOH, smooth under light microscopy, but ornamented with irregularly warts under SEM. *Hymenophoral trama* nearly phylloporoid type with hyphae of the lateral strata touching or almost touching each other with hyphae diverging from the central strand to the subhymenium; *hyphae* subcylindrical to cylindrical, 5–13 µm wide. *Cheilocystidia* 25–49 × 10–14 µm, lanceolate to clavate or ventricose, thin-walled, colorless in KOH. *Pleurocystidia* 33–43 × 8–10 µm, ventricose-subfusiform, with long beak, thin-walled. *Pileipellis* a subepithelium 110–130 µm thick, composed of moniliform hyphal segments 5–30 µm wide, thin-walled, colorless in KOH, with narrowly cylindrical to shortly cystidioid terminal cells 6–23 × 4–20 µm. *Pileal trama* composed of interwoven hyphae 4–24 µm wide. *Stipitipellis* ca. 130 µm thick, hymeniform, with narrowly or broadly clavate terminal cells 11–25 × 7–12 µm. *Caulobasidia* abundant, 16–32 × 9–12 µm, thin-walled. *Stipe trama* composed of parallel hyphae 4–10 µm wide. *Clamp connections* absent in all tissues.

*Habitat and distribution*: Scattered on soil in subtropical forests dominated by *Fagaceae* (*Quercus* spp., *Castanopsis* spp. and *Lithocarpus* spp.). Currently known from eastern, central and northeastern China.

*Material examined*: China, Zhejiang Province, Huzhou, Anji County, 1400 m elev., 21 September 2021, Yan-Jia Hao

2527 (HKAS 125907, **holotype**; EFHAAU2843, isotype). Henan Province, Nanyang, Neixiang County, 600 m elev., 31 July 2010, Xiao-Fei Shi 416 (HKAS76664). Liaoning Province, Anshan, 1980 m elev., 14 August 2015, Jing Li 251 (HKAS91279).

*GenBank numbers*: HKAS 125907: LSU = OQ600185, TEF1- $\alpha$  = OQ718485, RPB1 = OQ750573; HKAS76664: LSU = OQ600186, TEF1- $\alpha$  = OQ718484, RPB1 = OQ750572, RPB2 = OQ718482; HKAS91279: LSU = OQ600187, TEF1- $\alpha$  = OQ718483, RPB1 = OQ750573, RPB2 = OQ718481.

*Notes*: *Hemileccinum duriusculum* is characterized by the yellowish brown to brown wrinkled pileus, context and hymenophore unchanging in color when cut, scaly stipe surface and a subepitheliod pileipellis. Phylogenetically, *Hemileccinum rugosum* is closely related to *H. duriusculum* (Fig. 110). However, *H. rugosum* differs from *H. duriusculum* in its narrower basidiospores (10–12 × 4–5 µm) and the lighter color (light orange to reddish orange) of the pileus (Wu et al. 2016a). Morphologically, *Hemileccinum hortonii* originally described from Illinois, USA is somewhat similar to *H. duriusculum*, but differs from the latter by its narrower basidiospores (12–15 × 3.5–4.5 µm, Smith and Thiers 1971).

### ***Rufoboletus* N.K. Zeng & Zhi Q. Liang, *gen. nov.***

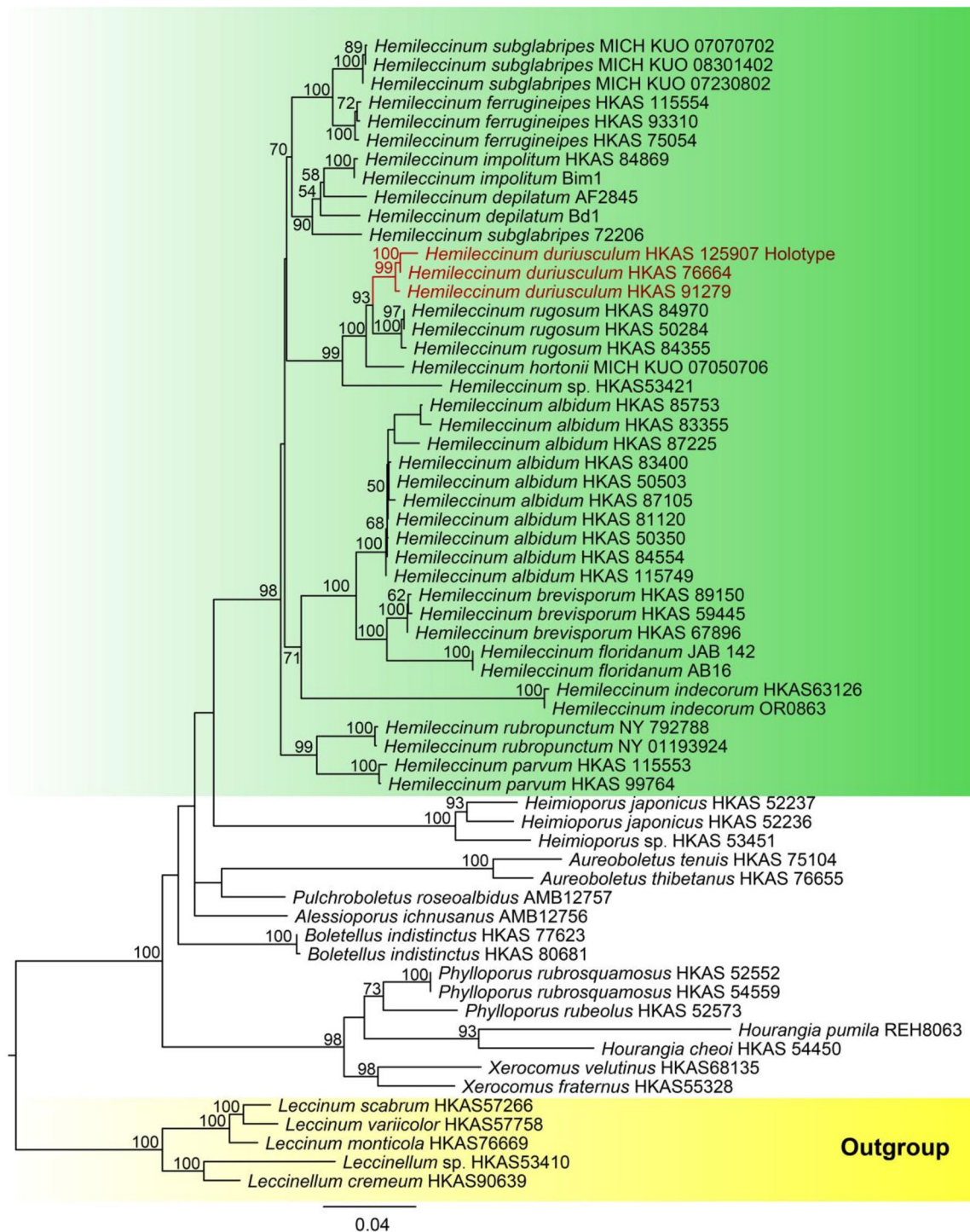
*Index Fungorum* number: IF559490; *Facesoffungi* number: FoF 14856.

*Etymology*: Latin "*rufo*–", meaning the hymenophore and context of the new genus turning red when injured.

*Basidiomes* stipitate-pileate with tubular hymenophore. *Pileus* hemispherical, convex to applanate, surface tomentose; *context* thick, white, changing blue quickly, then turning red and finally black when injured. *Hymenophore* thin, yellow, changing blue quickly, then turning red and finally black when injured. *Stipe* central, subcylindrical; surface without reticulations; *context* white, changing blue quickly, then turning red and finally black when injured. *Basal mycelium* white. *Basidiospores* subfusiform to ellipsoid, smooth. *Pleuro- and cheilocystidia* present. *Pileipellis* a trichoderm. *Clamp connections* absent.

*Type species*: ***Rufoboletus hainanensis*** (N.K. Zeng, Zhi Q. Liang & S. Jiang) N.K. Zeng & Zhi Q. Liang.

*Notes*: *Rufoboletus* is characterized by a large basidiome, a pileus with thick context and thin hymenophore, a blue-red–black color change of hymenophore and context when injured, a stipe without reticulations, and smooth basidiospores. In previous studies, species of *Rufoboletus* was placed into the genus *Butyriboletus* (Liang et al. 2016; Chai et al. 2019). However, species of *Butyriboletus* has a blue (without red) color change of hymenophore and context when injured, and a stipe with obvious reticulations. The thick context and thin hymenophore characterized by *Rufoboletus* are also reminiscent of the genus *Baorangia*;

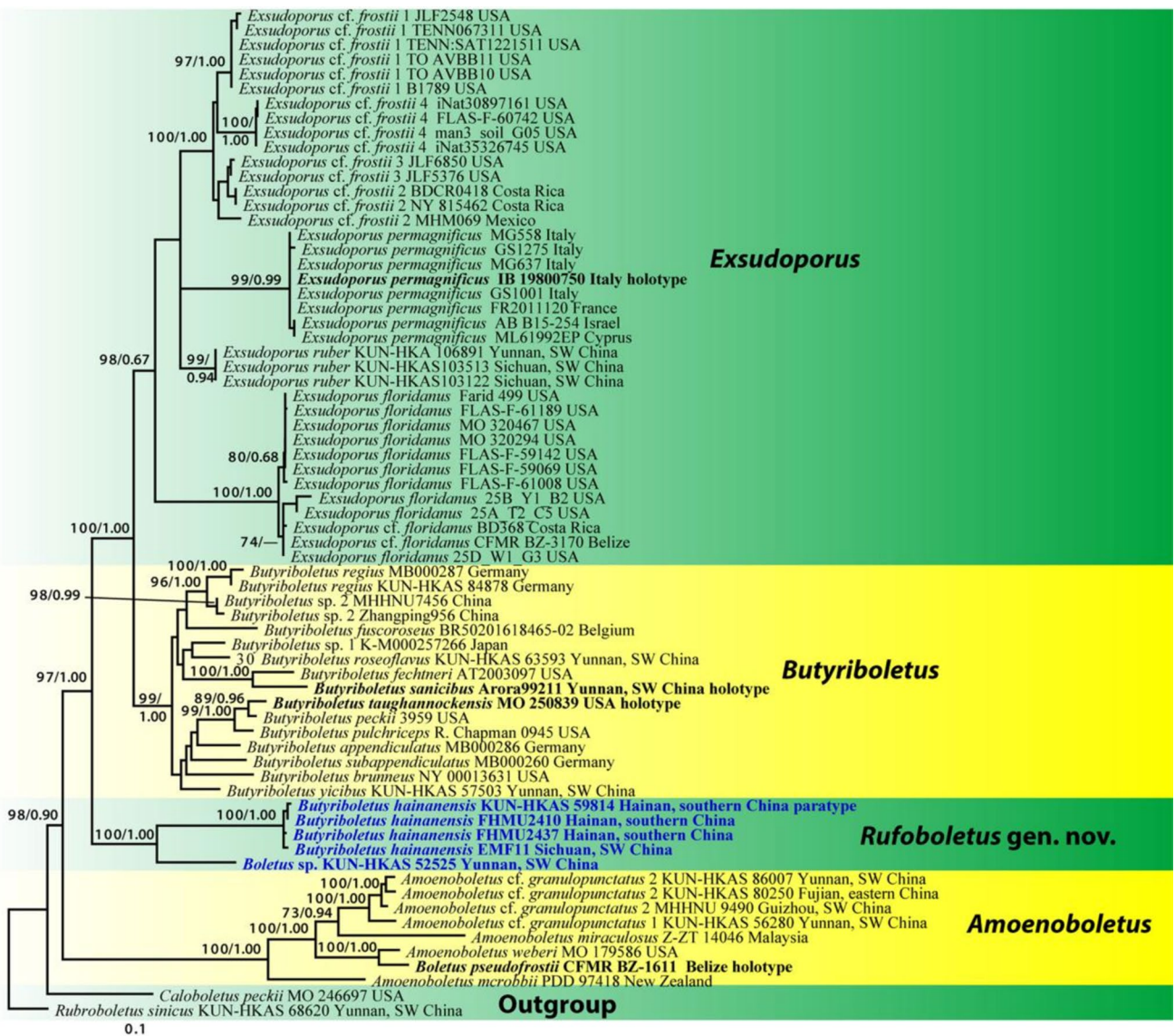


**Fig. 110** The phylogenetic analysis of *Hemileccinum* based on nrLSU, TEF1, RPB1 and RPB2 sequences using maximum likelihood method. The new species was labelled in red. Bootstrap values ( $\geq 50$ ) were shown on the branches

however, species of *Baorangia* has a blue (without red) color change of hymenophore and context when injured, and a stipe usually with reticulations (Wu et al. 2016b; Zhang et al. 2021b).

Phylogenetically, the type species of *Rufoboletus*, viz. *B. hainanensis* and *Boletus* sp. (KUN-HKAS 52525) formed an independent generic clade (Fig. 111), which was labeled as “hainanensis clade” by Biketova et al. (2022) and also supported by the phylogenetic analyses of Gelardi et al. (2015),





**Fig. 111** Phylogenetic placement of *Rufoboletus* inferred from a four-locus (28S, ITS, *TEF1*, and *RPB2*) dataset using RAxML. BS  $\geq$  50% and PP  $\geq$  0.95 are indicated above or below the branches as RAxML BS/PP

Liang et al. (2016), Fu et al. (2022) and Wang et al. (2022a, b).

***Rufoboletus hainanensis*** (N.K. Zeng, Zhi Q. Liang & S. Jiang) N.K. Zeng & Zhi Q. Liang, *comb. nov.*

≡ *Butyriboletus hainanensis* N.K. Zeng, Zhi Q. Liang & S. Jiang, in Liang, An, Jiang, Su & Zeng, *Phytotaxa* 267(4): 257 (2016).

*Index Fungorum* number: IF559491; *Facesoffungi* number: FoF 14871; Figs. 112, 113

*Basidia* 32–38 × 8–9  $\mu$ m clavate, colorless to yellowish in KOH, thin-walled, four-spored; sterigmata 4–6  $\mu$ m long. *Basidiospores* [66/3/2] (6.5–)7–9 × 4–5  $\mu$ m, Q = (1.4–)1.5–2.13, Qm = 1.81 ± 0.18, subfusiform to

ellipsoid, slightly thick-walled (up to 0.8  $\mu$ m), olive brown to yellowish brown in KOH, smooth. *Hymenophoral trama* boletoid. *Cheilocystidia* 32–52 × 5–8  $\mu$ m, abundant, subfusiform or fusiform, thin- to slightly thick-walled (up to 0.5  $\mu$ m), sometimes with yellowish brown contents, without encrustations. *Pleurocystidia* 38–70 × 8–12  $\mu$ m, abundant, fusiform or subfusiform, thin- to slightly thick-walled (up to 0.5  $\mu$ m), sometimes with brown or golden brown contents, without encrustations. *Pileipellis* an intricate trichodermal type, 110–160  $\mu$ m thick, composed of colorless, pale yellowish brown to yellowish brown in KOH, thin- to slightly thick-walled (up to 0.5  $\mu$ m) hyphae 3–9  $\mu$ m broad; *terminal cells* 28–44 × 4–11  $\mu$ m, narrowly clavate or subcylindrical, with obtuse apex. *Pileus trama* composed of thin- to slightly





**Fig. 112** *Rufoboletus hainanensis*. **a** from FHMU2394. **b** from FHMU2410. **c** from HKAS 59815. **d** from HKAS 59816, holotype. **e** from HKAS 59814, paratype. Photos by N.K. Zeng

thick-walled (up to 0.5  $\mu\text{m}$ ) hyphae 3–9  $\mu\text{m}$  broad. *Stipitipellis* a trichoderm-like structure 90–160  $\mu\text{m}$  thick, composed of thin- to slightly thick-walled (up to 0.5  $\mu\text{m}$ ) hyphae with narrowly or broadly clavate, subfusiform or fusiform terminal cells (14–30  $\times$  6–10  $\mu\text{m}$ ). *Stipe trama* composed of cylindrical, thin to slightly thick-walled (up to 0.5  $\mu\text{m}$ ), *parallel hyphae* 4–10  $\mu\text{m}$  broad. *Clamp connections* absent in all tissues.

**Materials examined:** China, Hainan Province, Yinggeling of Hainan Tropical Rainforest National Park, elev. 850 m, 26 July 2009, N.K. Zeng334 (KUN-HKAS 59816, **holotype**), N.K. Zeng332 (KUN-HKAS 59814, paratype), N.K. Zeng333 (KUN-HKAS 59815), 16 June 2013, N.K. Zeng1197 (FHMU2410), 31 July 2015, N.K. Zeng2418 (FHMU2437).

**GenBank numbers:** KUN-HKAS 59814: ITS = KU317762, LSU = KF112336, TEF1- $\alpha$  = KF112199; FHMU2410: ITS = KU961653, LSU = KU961651, RPB2 = KU961658; FHMU2437: ITS = KU961654, LSU = KU961652, TEF1- $\alpha$  = KU961656, RPB2 = KX453856.

**Notes:** *Rufoboletus hainanensis* was firstly described from Hainan, tropical China. The description of macrostructures has been provided by Liang et al. (2016); the microstructures have been reexamined in the present study.

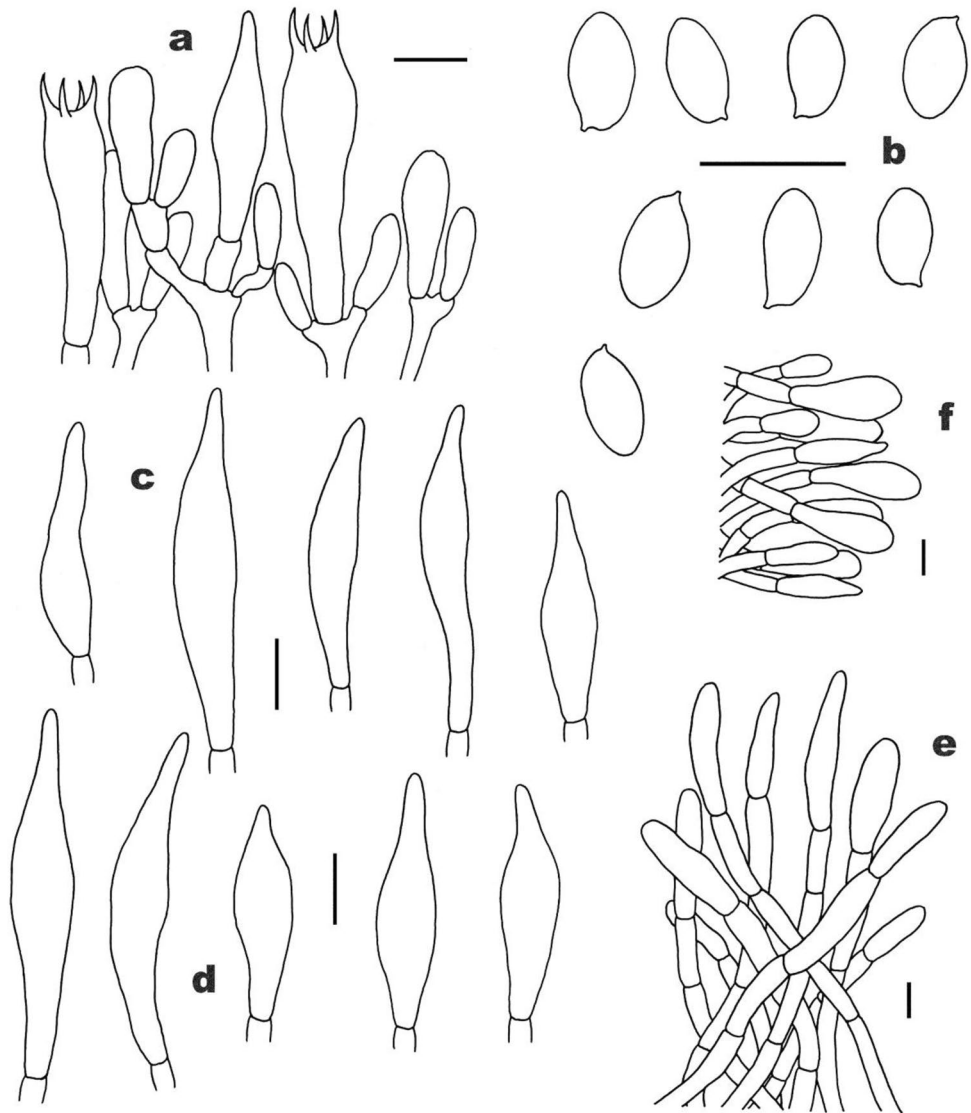
### *Cantharellales* Gäum.

**Notes:** *Cantharellales* with *Cantharellaceae* as the type family is a morphologically diverse fungal order in Agaricomycetes. Although less than 300 species are known in this order (Kirk et al. 2008), these species may have corticioid, stipitate or coralloid basidiomes with smooth, hydroid, poroid or veined hymenophores (Hibbett et al. 2014). The most striking morphological character of *Cantharellales* is the dominant presence of two, five, six or eight sterigmata in basidia, instead of four sterigmata present in other orders of Agaricomycetes (Hibbett et al. 2014). Moncalvo et al. (2006) performed the first comprehensive phylogenetic analyses of *Cantharellales* (the cantharelloid clade) with the help of multiloci. Later, Veldre et al. (2013) recognized four families, viz. *Botryobasidiaceae*, *Ceratobasidiaceae*, *Hydnaceae* (synonym of *Cantharellaceae*) and *Tulasnellaceae* in *Cantharellales*, while later *Botryobasidiaceae*, *Clavulinaceae* and *Hydnaceae* accepted in this order by Zhao et al. (2017). Nevertheless, the taxonomic frame of *Cantharellales* still needs to be further explored with more samples.

### *Botryobasidiaceae* Jülich.

**Notes:** *Botryobasidiaceae* was originally erected to accommodate *Botryobasidium* (Jülich 1981). Phylogenetically, besides *Botryobasidium*, *Botryohypochnus* is also

**Fig. 113** Microscopic features of *Rufoboletus hainanensis* (FHMU2410). **a** Basidia and pleurocystidium. **b** Basidiospores. **c** Cheilocystidia. **d** Pleurocystidia. **e** Pileipellis. **f** Stipitipellis. Scale bars: 10  $\mu$ m. Drawings by Y.X. Han



included in the well-supported *Botryobasidiaceae* clade, which is a sister to *Ceratobasidiaceae*, *Hydnaceae* and *Tulasnellaceae* (Larsson 2007a; Cao et al. 2021).

***Botryobasidium* Donk.**

**Notes:** *Botryobasidium*, typified by *B. subcoronatum*, is a saprobic genus in *Cantharellales*, and characterized by discontinuous, arachnoid to porulose basidiomes and short, subcylindrical basidia usually with 6–8 sterigmata (Bernicchia and Gorjón 2010; Bernicchia et al. 2010). *Botryobasidium* was protected over *Acladium*, *Allescheriella*, *Alysidium*, *Haplotrichum*, *Physospora*, and *Sporocephalum* (Stalpers et al. 2021).

***Botryobasidium coniferarum* S.L. Liu & L.W. Zhou, *sp. nov.***

**Index Fungorum number:** IF 901058; **Facesoffungi number:** FoF 14811; Figs. 114, 115

**Etymology:** *coniferarum* (Lat.) referring to occurrence on conifers.

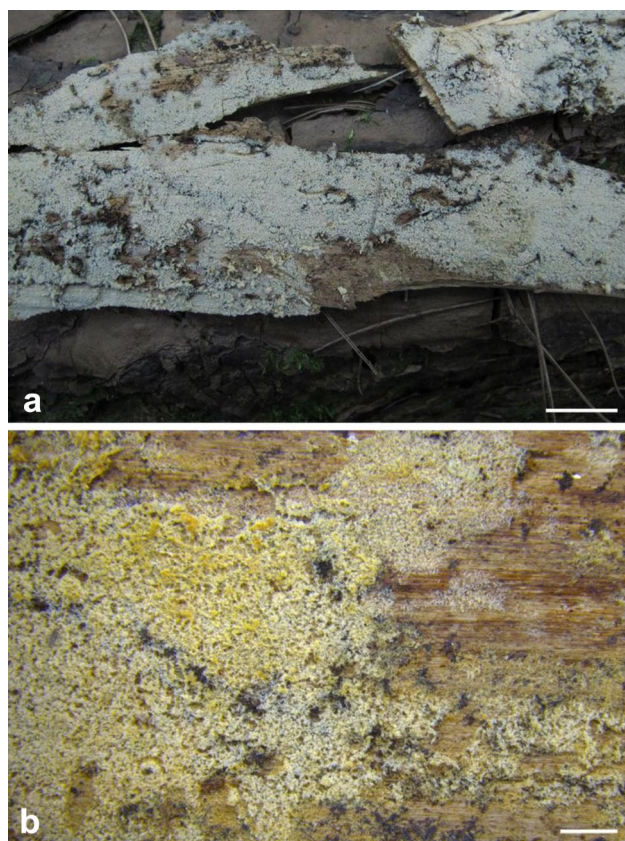
**Holotype:** LWZ 20210928–3 (HMAS).

**Diagnosis:** Differing from *Botryobasidium conspersum* in thick-walled hyphae in subiculum (Bernicchia and Gorjón 2010).

**Basidiomes** resupinate, thin, separable, up to 15 cm long, 6 cm wide, 150  $\mu$ m thick. **Hymenophore** smooth, arachnoid, whitish to cream when fresh, honey-yellow to olivaceous buff when dry, not cracked. **Margin** white, thinning out as byssoid, finely fibrillose, 0.5 mm wide.

**Hyphal system** monomitic; **generative hyphae** without clamp connections; **subhymenial hyphae** hyaline, thin-walled, 6–8  $\mu$ m in diam; **basal hyphae** hyaline to yellowish, thick-walled, frequently branched at right angles, 6–10  $\mu$ m in diam.





**Fig. 114** Basidiomes of *Botryobasidium coniferarum* (LWZ 20210928–3, **holotype**). Scale bars: **a** = 1 cm, **b** = 1 mm

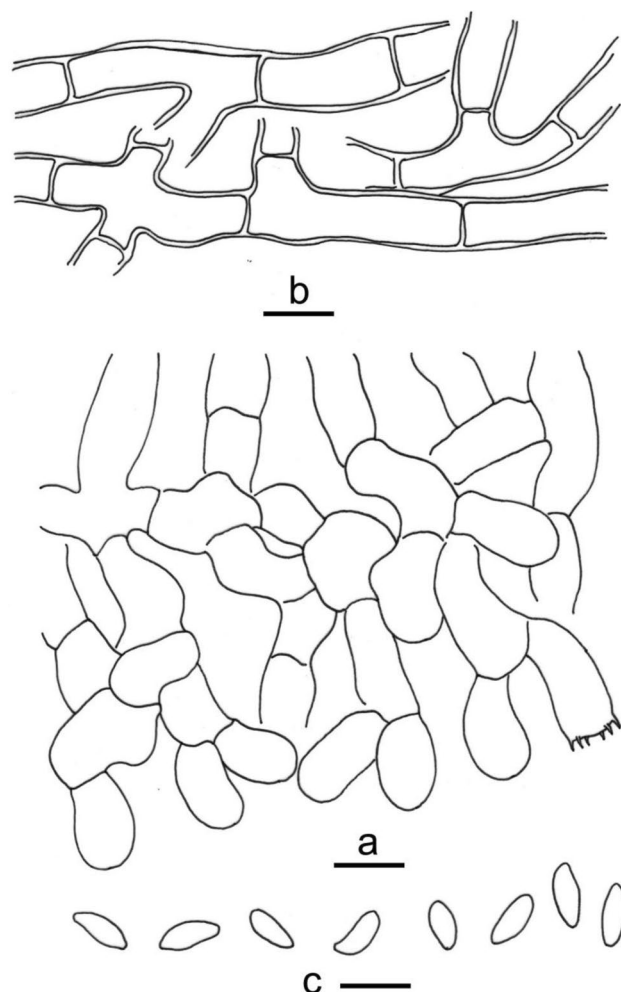
*Cystidia* absent. *Basidia* subcylindrical,  $16\text{--}20 \times 7\text{--}9\text{ }\mu\text{m}$ , 6-sterigmata, simple-septate at the base. *Basidiospores* navicular, hyaline, thin-walled, smooth, IKI–, CB–,  $7\text{--}8 \times 3\text{--}3.5\text{ }\mu\text{m}$ ,  $L = 7.5\text{ }\mu\text{m}$ ,  $W = 3.3\text{ }\mu\text{m}$ ,  $Q = 2.3$  ( $n = 60/2$ ).

*Anamorph* not found.

**Material examined:** China, Guizhou Province, Jiulong County, Wuxuhai Scenic Spot, on fallen branch of *Pinus*, 28 September 2019, L.W. Zhou, LWZ 20210928–3 (HMAS, **holotype**); *ibid.*, on fallen branch of *Pinus*, 28 September 2019, L.W. Zhou, LWZ 20210928–4 (HMAS); Sichuan Province, Xichang, Luoishan Scenic Spot, on fallen branch of gymnosperm, 11 August 2019, L.W. Zhou, LWZ 20190811–36a (HMAS). VIETNAM, Da Lat, Bidoup Nui Ba National Park, on fallen branch of *Pinus*, 16 October 2017, L.W. Zhou, LWZ 20171016–5 (HMAS), LWZ 20171016–15 (HMAS).

**GenBank numbers:** LWZ20171016-5: ITS = OR557261; LSU = OR527285; LWZ20171016-15: ITS = OR557262; LSU = OR527286; LWZ20190811-36a: LSU = OR527284; LWZ 20210928-3: ITS = OR557259; LSU = OR527282; LWZ LWZ 20210928-3: ITS = OR557260; LSU = OR527283.

**Notes:** Besides differing from the most phylogenetic close (Fig. 116) and morphological similar species



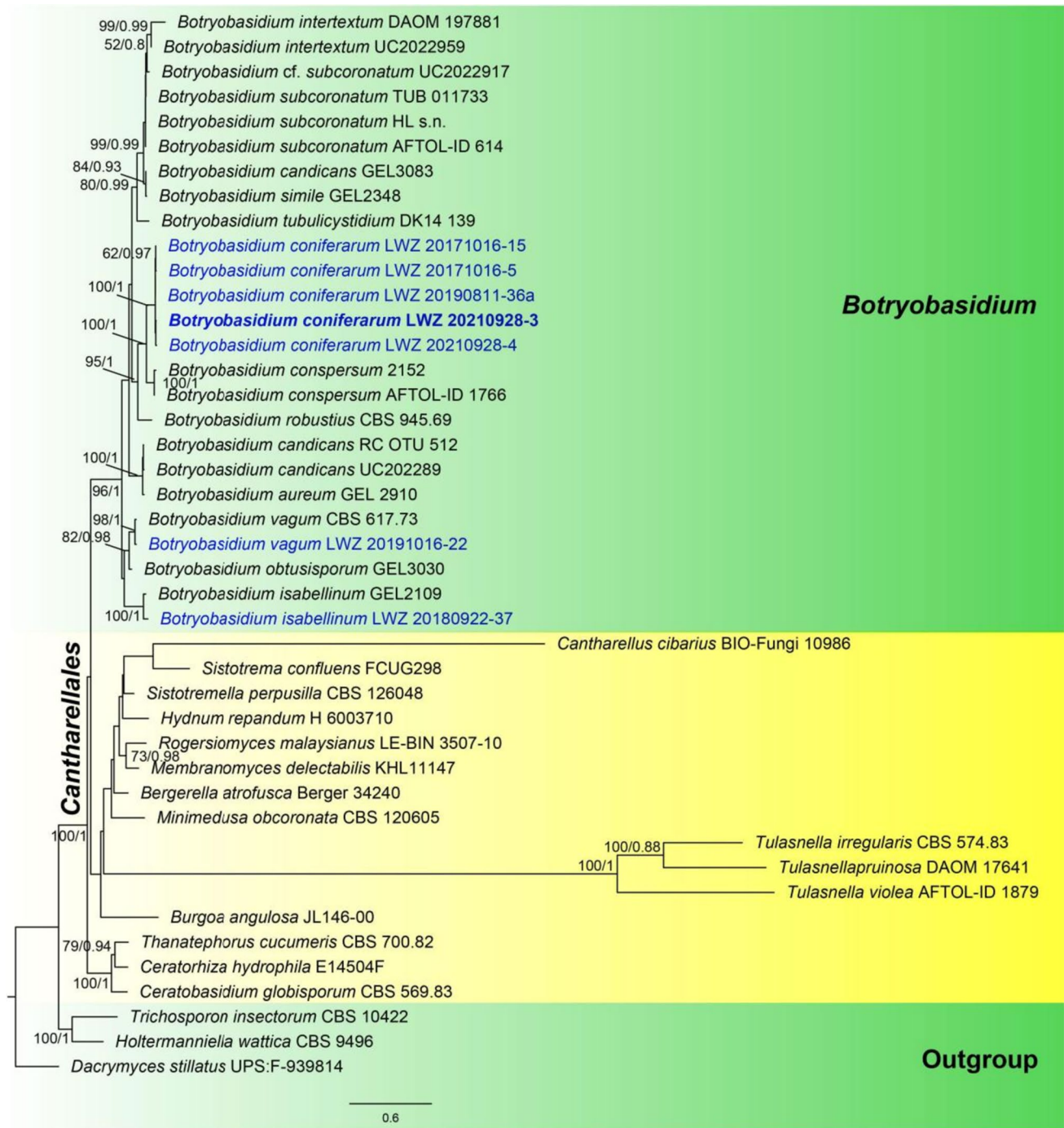
**Fig. 115** Microscopic structures of *Botryobasidium coniferarum* (LWZ 20210928–3, **holotype**). **a** A vertical section of basidiomes. **b** Hyphae from subiculum. **c** Basidiospores. Scale bars: 10  $\mu\text{m}$

*Botryobasidium conspersum* in thick-walled subicular hyphae (Bernicchia and Gorjón 2010), *B. coniferarum* also resemble *Botryobasidium chilense* and *B. yutajense*. However, *B. chilense*, originally described from Chile and New Zealand, is separated by broadly rounded basidiospores with a lateral and prominent basal apiculus at the base (Holubová-Jechová 1980) and *B. yutajense* differs in its shorter basidiospores ( $6\text{--}7\text{ }\mu\text{m}$  in length, Ryvarden et al. 2005).

#### *Gomphales* Jülich.

**Notes:** The order *Gomphales* consists 633 described species in three families and 18 genera (González-Ávila et al. 2017; He et al. 2022). They are abundantly reported from the temperate zones of Northern Hemisphere (Kirk et al. 2008) with a very sparse reports from tropical and subtropical zones (Corner 1966; Petersen 1971; Kirk et al. 2008; González-Ávila et al. 2017). The gomphoid fungi shows great





**Fig. 116** Phylogeny generated by the maximum likelihood algorithm based on combined ITS and nLSU regions is presented along with the bootstrap values and the Bayesian posterior probabilities above 50%

and 0.8, respectively, at the nodes. Holotype is in bold and the newly generated sequences are in blue. *Dacrymyces stillatus* UPS:F-939814 was selected as the outgroup taxon

variations in basidiomal morphologies, from hypogeous or epigeous, stalked ramarioid or clavarioid to cantharelloid-gomphoid, resupinate, odontoid, to sequestrate form (Giachini et al. 2010; González-Ávila et al. 2020). Here, we follow the phylogenetic treatment of *Gomphales* by Giachini et al. (2010).

### *Gomphaceae* Donk.

**Notes:** The family *Gomphaceae* was proposed by Donk (1961) in the order *Aphylophorales* to incorporate macroscopically heterogeneous fungi, which differs in their hymenial constrictions (Giachini 2004). He included the resupinate-odontoid genera *Kavinia* and *Ramaricium*, the stalked

clavarioid genera *Lentaria* and *Ramaria*, the stalked hydroid genus *Beenakia*, the stipitate agaricoid genus *Gloeocantharellus*, and the pileate genera *Chloroneuron* and *Gomphus* in his familial classification (Giachini 2010). Later, members of the family *Gomphaceae* were divided into several smaller families and placed in a new order *Gomphales* (Jülich 1981). Giachini (2004) reviewed the generic concepts in the family *Gomphaceae* and recombined the species of *Gomphus* sensu lato into *Gloeocantharellus*, *Gomphus* sensu stricto, *Phaeoclavulina* and *Turbinellus* (Giachini et al. 2010). Currently the family *Gomphaceae* consists 14 genera. They are *Araeocoryne*, *Ceratellopsis*, *Delentaria*, *Destuntzia*, *Gautieria*, *Gloeocantharellus*, *Gomphus*, *Phaeoclavulina*, *Protogautieria*, *Pseudogomphus*, *Ramaria*, *Ramaricium*, *Terenodon* and *Turbinellus* (Kirk et al. 2008; Index Fungorum 2022).

### *Gomphus* Pers.

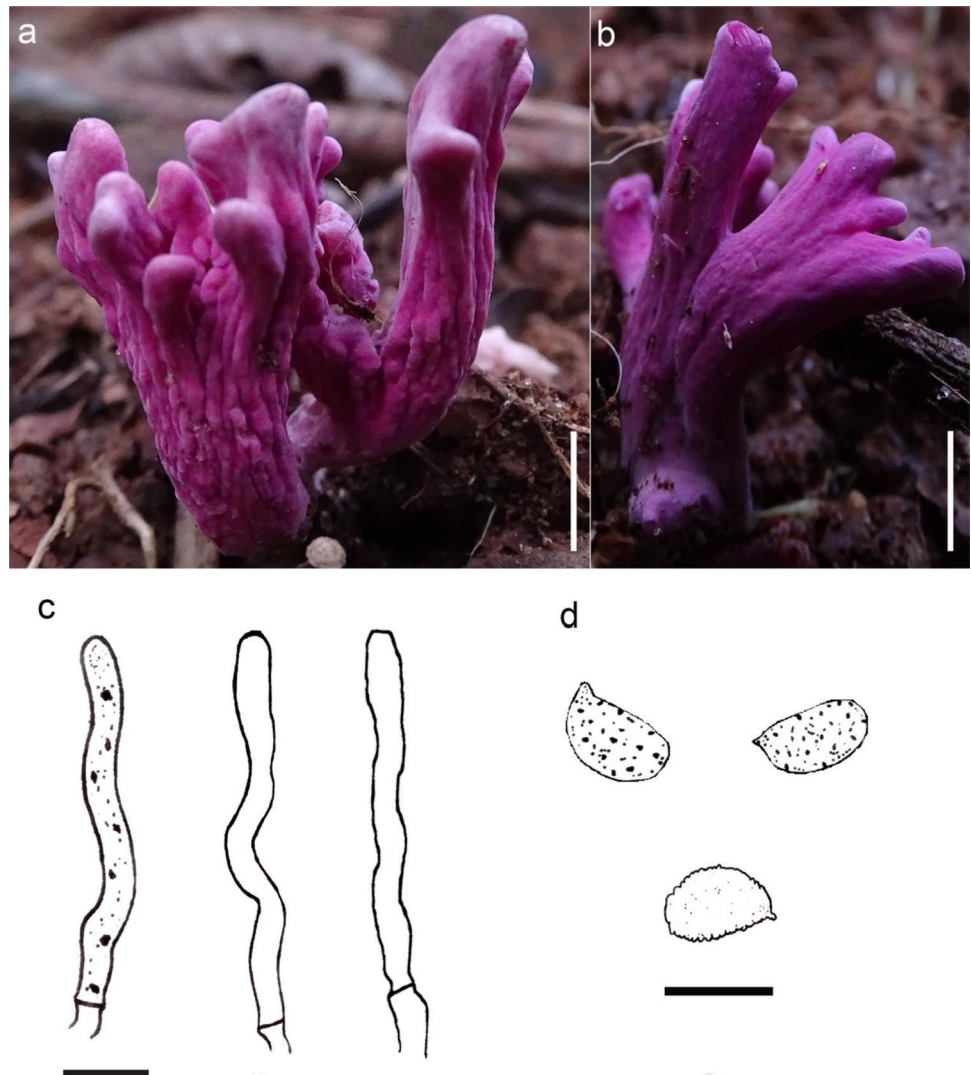
**Notes:** The genus *Gomphus* sensu lato was proposed by Persoon (1796) to include the species with wrinkled hymenia

and verrucose spore in the cantharelloid-gomphoid clade (Giachini and Castellano 2011; Giachini 2004). The genus currently comprises 16 described species (Index Fungorum 2022). No species was assigned in the genus *Gomphus*, when it was introduced to generic level. Later, it was Gray (1821) who described *Gomphus clavatus* as the type species for the genus *Gomphus* (Giachini and Castellano 2011). Lacks of distinctive morphological characters make it difficult in the taxonomic identification of the genus *Gomphus*. According to the latest classification by Giachini and Castellano (2011) for *Gomphus* sensu lato (*Gomphus* sensu stricto, *Gloeocantharellus*, *Phaeoclavulina* and *Turbinellus*), *Gomphus* sensu stricto is the only genus with strictly violet, lavender-brown, or milky-coffee colored hymenia.

***Gomphus zamorinorum*** Krishnapriya K. & T.K.A. Kumar, *sp. nov.*

**Mycobank number:** MB 844405; **Facesoffungi number:** FoF 11792; **Fig. 117**

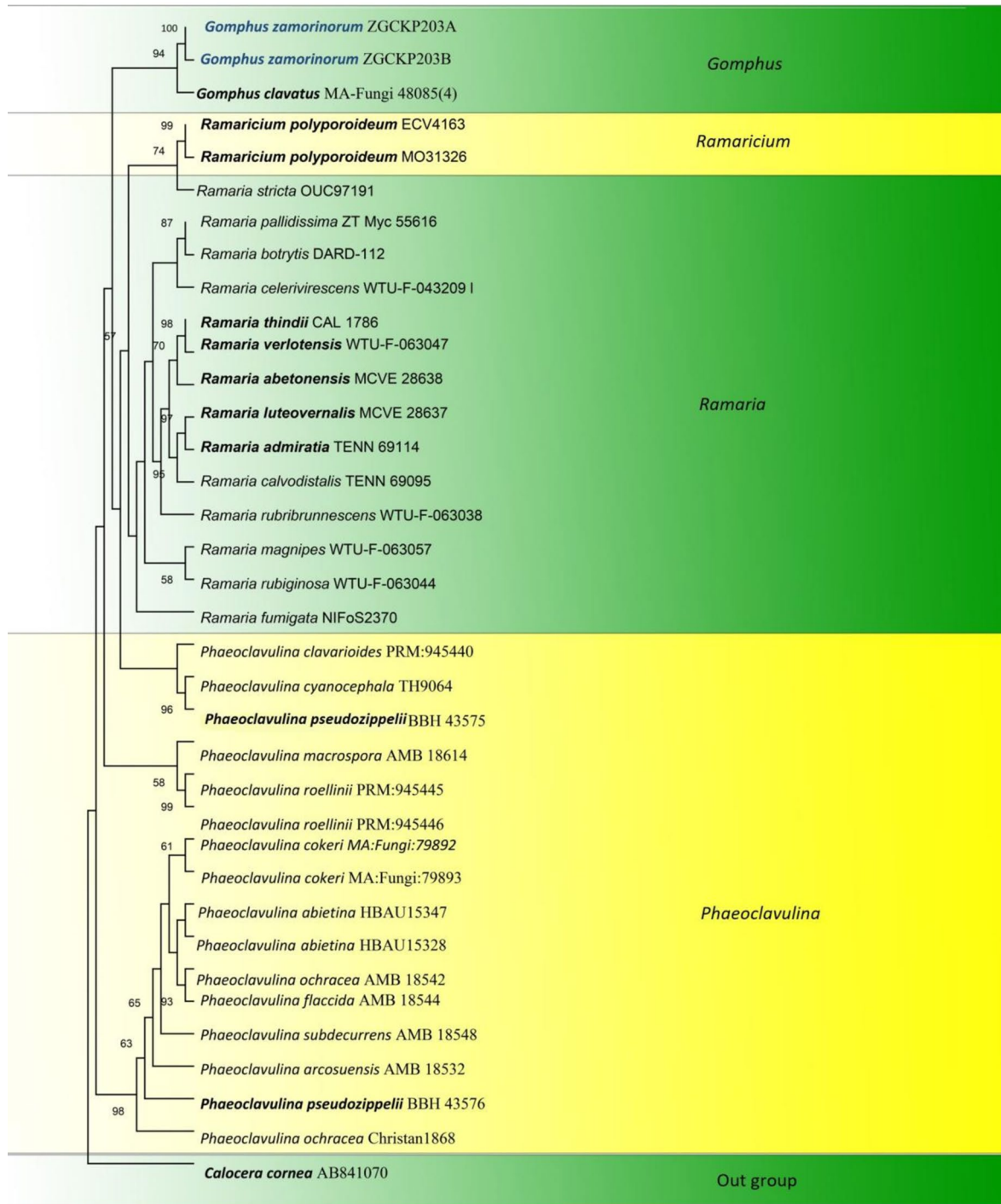
**Fig. 117** *Gomphus zamorinorum* (ZGCKP203A, **holotype**). **a, b** Basidiomes. **c** Hymenial cystidia. **d** Basidiospores. Scale bars: **a, b** = 10 mm, **c** = 10  $\mu$ m, **d** = 7  $\mu$ m



**Etymology:** In honour of the Zamorins, the hereditary monarchs (1124 CE – 1806 CE) of the kingdom of Kozhikode that was an important trading port on the south-western coast of India (South Malabar).

**Holotype:** ZGCKP203A.

*Basidiomes* gregarious, growing as a cluster, two to three basidiomes in a cluster, 30 to 40 mm long, 6 to 10 mm wide at the apex, not differentiated into stipe and pileus. *Young basidiomes* cylindrical, arising from a thick rhizomorph like structure, branched (2–3) towards the apex, branches 5 to



**Fig. 118** Phylogram generated from maximum likelihood analysis based on ITS sequence data showing the placement of *Gomphus zamorinorum*. This analysis involved 36 nucleotide sequences. There was a total of 837 positions in the final dataset. *Calocera cornea*

was taken as the out-group. The tree with the highest log likelihood (– 17,846.00) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Type strains are in blue and newly generated sequences are in blue



6 mm thick, branching irregular, apex pyxidate, round or obtuse, not acute, glabrous to fibrillose. *Mature basidiomes* becoming partially lobed downwards, branched upwards, round, with broad hymenial folds or wrinkles, ellipsoid in cross section, solid, fleshy, fragile, bright violet fruitbody, with a purplish tint towards the apex, no color change on drying, odour pleasant. Positive reaction in  $\text{FeCl}_3$ .

*Basidiospores*  $6\text{--}7 \times 4\text{--}5 \text{ }\mu\text{m}$  ( $Q = 1.2\text{--}1.7 \text{ }\mu\text{m}$ ;  $Q_m = 1.4 \text{ }\mu\text{m}$ ), phaseoliform in side view, oblong in front view, with guttulate contents (uniguttulate), verrucose, thin to thick-walled, hyaline, apiculus prominent (up to  $1 \text{ }\mu\text{m}$  long), in some hilar appendage protruded up to  $6\text{--}7 \text{ }\mu\text{m}$  long, inamyloid, cyanophilic in cotton blue. *Basidia*  $25\text{--}50 \times 4\text{--}7 \text{ }\mu\text{m}$ , uniguttulate to agguttulate, cylindrical to clavate, not smooth, incrustations present on the basidia, sterigmata 2–4 (up to  $4\text{--}7 \text{ }\mu\text{m}$  long), cyanophilic. *Hymenial cystidia*  $21\text{--}60 \times 5\text{--}6 \text{ }\mu\text{m}$ , cylindrical to flexuose, projecting from the hymenium, thin-walled, inamyloid, pileocystidia absent. *Hymenium*  $80\text{--}110 \text{ }\mu\text{m}$  wide. *Subhymenium* not distinguishable. *Context* composed of interwoven, irregularly arranged, encrusted, and agglutinated hyphae, hyphal constrictions present, septate,  $4\text{--}8 \text{ }\mu\text{m}$  wide, blackish in group, gleophorous hyphae present, in some bulged at the septal portion (up to  $11 \text{ }\mu\text{m}$ ), thin walled, cyanophilic, inamyloid. *Hyphal clamp-connections* absent.

*Habitat*: In gregarious clusters among leaf litters on soil.

*Material examined*: India, Kerala State, Wayanad District, Banasura sagar dam site area ( $11.6942^\circ \text{ N}$ ,  $75.9081^\circ \text{ E}$ ), 29 September 2019, Krishnapriya K., ZGCKP203A (**holotype**), KP203B (isotype).

*GenBank numbers*: ZGCKP203A: ITS = ON732852; KP203B: ITS = ON732853.

*Notes*: In ITS based phylogenetic analysis, *Gomphus zamorinorum* settled in the *Gomphus* clade, sister to *Gomphus clavatus* (Fig. 118). *Gomphus zamorinorum* is characterised by its deep violet basidiomes with wrinkled hymenophore, branched, comparatively smaller basidiospores and basidia, presence of hymenial cystidia, presence of gleophorous hyphae, generative hyphae with ampulliform swelling and absence of clamp connections. *Gomphus zamorinorum* is similar to *G. clavatus* macroscopically in having the wrinkled hymenophore with deep violet colour (Giachini et al. 2012). However, *G. zamorinorum* differs from the latter morphologically, with its branched basidiomes, smaller basidiospore and basidia, absence of pileocystidia, presence of gleophorous hyphae and absence of clamp-connections. Besides this, hyphal encrustations are observed in *G. zamorinorum*, which is absent in the latter.

### *Hymenochaetales* Oberw.

*Notes*: *Hymenochaetales* is one of the largest orders of the class Agaricomycetes. Oberwinkler (1977) included the characters of xanthochoroid polypores in *Série des Igniaries* (Patouillard 1900), the concept of subfamily



**Fig. 119** Basidiomes of *Kneiffiella pseudoabdita* (LWZ 20210624-6b, **holotype**)

*Hymenochaetoidae* (Donk 1948) of *Hymenochaetales* and raised to the order *Hymenochaetales*. Micromorphological features of *Hymenochaetales* varies widely from resupinate, effused-reflexed, imbricate, pileate, stipitate, coral-like to spathulate pilei with smooth, poroid, hydroid or lamellate hymenophore. Microscopically, mono, mono-di, di or trimitic hyphal system, absence of clamp connections, and globose to cylindrical, smooth to finely ornamented basidiospores, with or without sterile elements such as cystidioles and setae are the distinct characteristic features.

### *Chaetoporellaceae* Jülich.

*Notes*: *Chaetoporellaceae* was introduced with *Chaetoporellus* as the type genus (Jülich 1981). However, due to the conservation of *Hyphodontia* against its synonyms *Chaetoporellus* and some other genera (Eriksson et al. 1982; Gams 1993; Langer et al. 1996), the family name *Chaetoporellaceae* has long been in oblivion. Recently, Wang et al. (2021a) revealed that *Chaetoporellus* is a later synonym of *Kneiffiella* and both genera occupy a distinct lineage in *Hymenochaetales*; therefore, *Chaetoporellaceae* was reinstated as a monotypic family.

### *Kneiffiella* P. Karst.

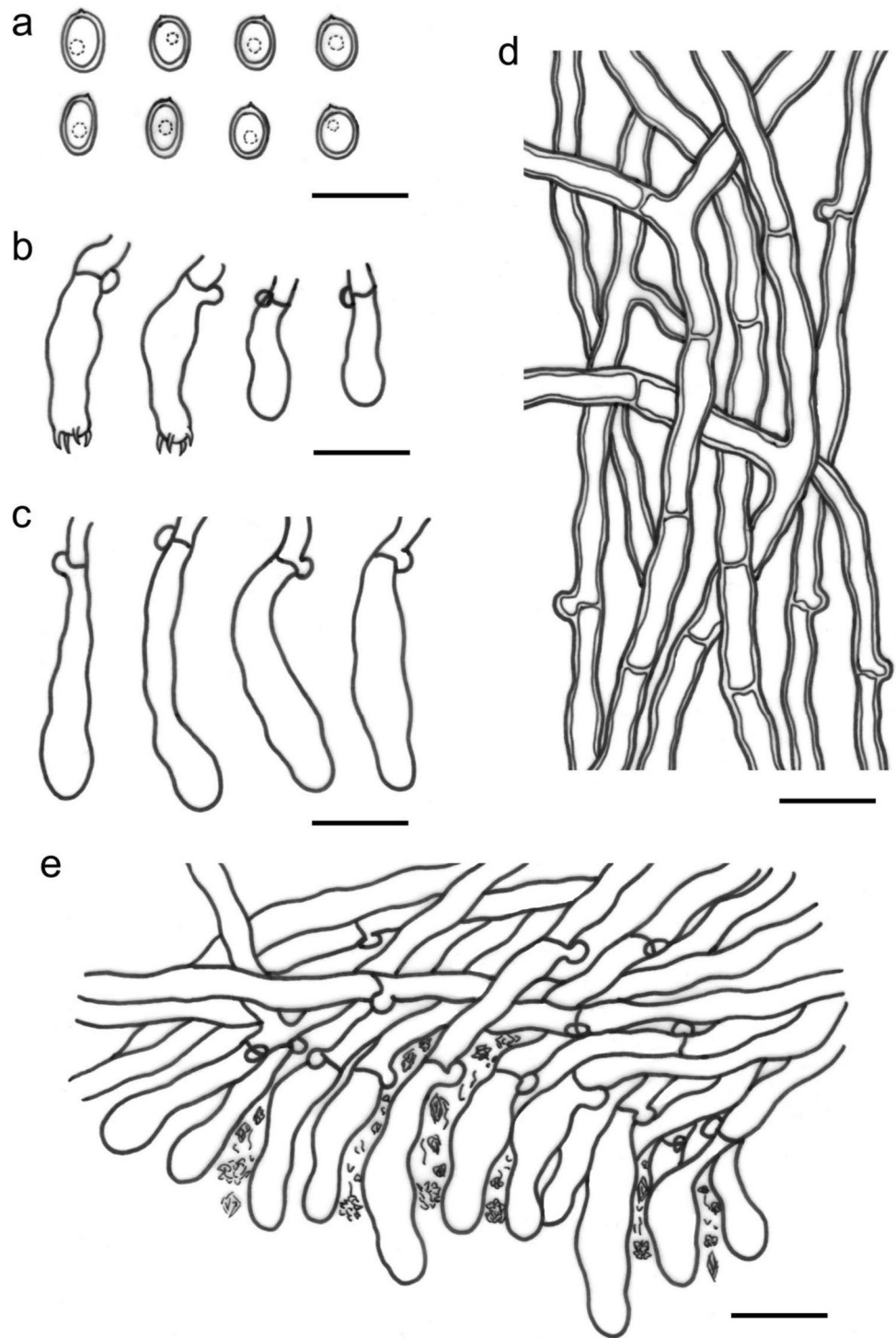
*Notes*: *Kneiffiella* is a prior synonym over *Chaetoporellus* and thus represents the single accepted genus in *Chaetoporellaceae* (Wang et al. 2021a). See Wang et al. (2021a) for the latest comprehensive summarization of *Kneiffiella*.

### *Kneiffiella pseudoabdita* Xue W. Wang & L.W. Zhou, *sp. nov.*

*Index Fungorum number*: IF900289; *Facesoffungi number*: FoF 14052; Figs. 119, 120

*Etymology*: *pseudoabdita* (Lat.) referring to the similarity to *Kneiffiella abdita*.

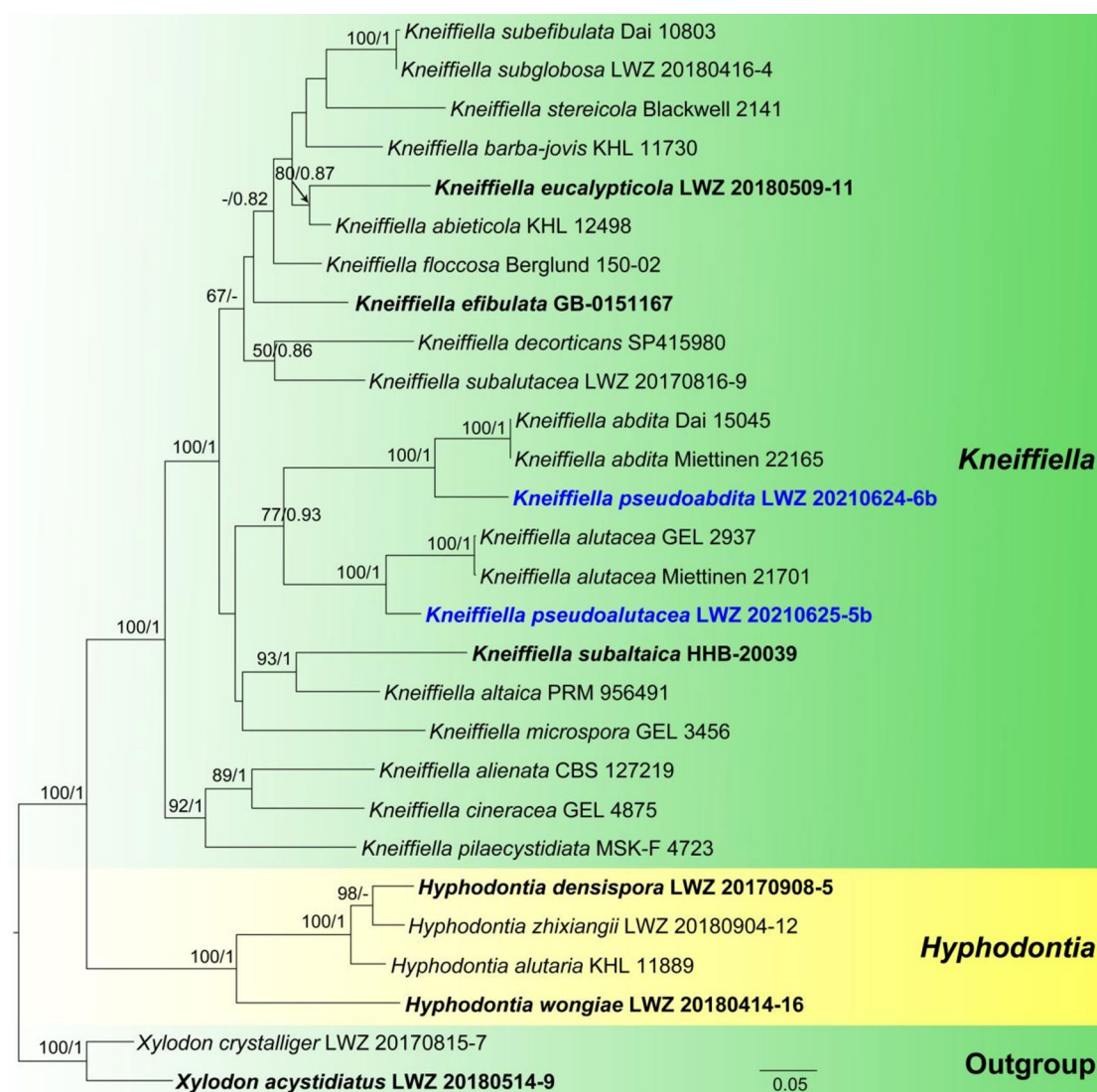
**Fig. 120** Microscopic structures of *Kneiffiella pseudoabdita* (LWZ 20210624-6b, **holotype**). **a** Basidiospores. **b** Basidia and basidioles. **c** Cystidia. **d** Tramal hyphae. **e** Section in hymenium. Scale bars: **a–e** = 10  $\mu$ m



*Holotype*: LWZ 20210624-6b (HMAS).

*Diagnosis*: Characterized by annual, resupinate, adnate basidiomes, poroid hymenophore, the presence of two types of generative hyphae, subcylindrical to subclavate cystidia, clavate basidia, and ellipsoid, thick-walled basidiospores.

*Basidiomes* annual, resupinate, adnate, cracked and brittle when dry, without odour. *Hymenophore* poroid with angular and variable pores, buff to buff-yellow. *Margin* thinning out, paler than hymenial surface, indeterminate, sometimes pruinose.



**Fig. 121** Phylogram generated by the maximum likelihood algorithm based on combined nLSU and ITS sequence data is presented along with the bootstrap values and the Bayesian posterior probabilities

above 50% and 0.8, respectively, at the nodes. Type specimens are in bold and the isolates of new species characterized are in blue



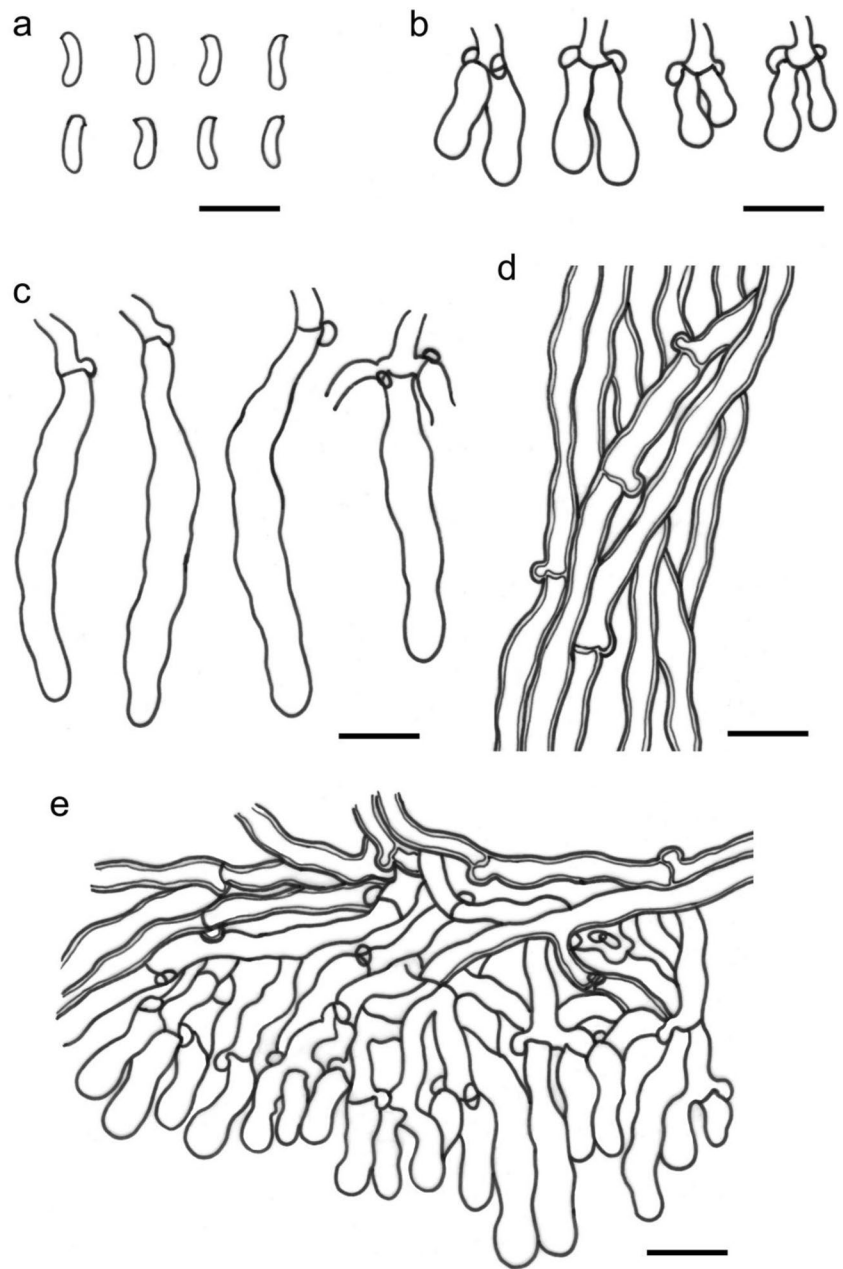
**Fig. 122** Basidiomes of *Kneiffiella pseudoalutacea* (LWZ 20210625-5b, holotype)

*Hyphal system* monomitic; two types of generative hyphae: 1) with clamp connections, hyaline, dichotomous branching, interwoven, slightly thick-walled, 2.5–3.5  $\mu\text{m}$  in diam; 2) simple septate, brown, slightly thick-walled with a wide lumen, usually dichotomous branching, interwoven, 3–4  $\mu\text{m}$  in diam. *Cystidia* subcylindrical to subclavate, 25–45  $\times$  4.5–5.5  $\mu\text{m}$ . *Basidia* clavate, 16.5–20  $\times$  4.5–5.5  $\mu\text{m}$ , with four sterigmata and a basal clamp; *basidioles* similar in shape to basidia, but smaller. *Basidiospores* narrowly to broadly ellipsoid, with a small oily drop, hyaline, smooth, thick-walled, IKI–, CB–, (5.2–)5.3–6.4(–6.5)  $\times$  (3.1–)3.2–4.3(–4.4)  $\mu\text{m}$ ,  $L = 5.76 \mu\text{m}$ ,  $W = 3.81 \mu\text{m}$ ,  $Q = 1.51$  (30/1).

*Material examined*: China, Jiangxi Province, Jiujiang, Lushan Mountain, on fallen trunk of *Pinus*, 24 June 2021, L.W. Zhou, LWZ 20210624-6b (HMAS, **holotype**).



**Fig. 123** Microscopic structures of *Kneiffiella pseudoalutacea* (LWZ 20210625-5b, **holotype**). **a** Basidiospores. **b** Basidia and basidioles. **c** Cystidia. **d** Tramal hyphae. **e** Section in hymenium. Scale bars: **a–e** = 10  $\mu$ m



*GenBank numbers*: ITS = OQ540894; LSU = OQ540852.

*Notes*: *Kneiffiella pseudoabditata* is distinct in this genus by the presence of two types of generative hyphae. Phylogenetically, *Kneiffiella pseudoabditata* groups with *K. abdita* (Fig. 121). These two species share similar poroid hymenophore, tubular cystidia and clavate basidia; however, *K. abdita* differs in its narrowly allantoid basidiospores ( $3\text{--}4 \times 0.5\text{--}1\text{ }\mu\text{m}$ , Wang et al. 2021a). *Kneiffiella pilae-cystidiata* resembles *K. pseudoabditata* by sharing ellipsoid basidiospores, but differs in having odontoid hymenophore and capitate cystidia (Eriksson and Ryvarden 1976). Moreover, *K. pilae-cystidiata* grows on decayed wood of *Salix* and

*Populus* (Eriksson and Ryvarden 1976), while *K. dimitica* was found on *Pinus*.

***Kneiffiella pseudoalutacea*** Xue W. Wang & L.W. Zhou, *sp. nov.*

*Index Fungorum number*: IF900290; *Facesoffungi number*: FoF 14053; Figs. 122, 123

*Etymology*: pseudoalutacea (Lat.) referring to the similarity to *Kneiffiella alutacea*.

*Holotype*: LWZ 20210625-5b (HMAS).

*Diagnosis*: Characterized by annual, resupinate, adnate basidiomes, smooth to slightly tuberculate, lime to cream hymenophore, a monomitic hyphal system, subcylindrical

cystidia, subclavate basidia and narrowly allantoid basidiospores.

*Basidiomes* annual, resupinate, adnate, membranous, cracked and brittle when dry, without odour. *Hymenophore* smooth to slightly tuberculate, lime to cream. *Margin* concolorous with subiculum, thinning out, indeterminate.

*Hyphal system* monomitic; generative hyphae in trama with clamp connections, hyaline, slightly thick-walled with a wide lumen, parallel, 3.5–4.5 µm in diam; generative hyphae in subhymenium with clamp connections, hyaline, thin-walled to slightly thick-walled with a wide lumen, usually dichotomous branching, 3–4 µm in diam. *Cystidia* subcylindrical, smooth, thin-walled, 35–50 × 5.5–6 µm, projecting up to 10 µm beyond the hymenial surface. *Basidia* subclavate with a median constriction, 12–15 × 4–4.7 µm, with a clamp connection at the base; *basidioles* similar in shape to basidia, but smaller. *Basidiospores* narrowly allantoid, hyaline, smooth, thin-walled, IKI–, CB–, (6–)6.1–6.8(–7) × 1.3–2.2(–2.3) µm, L = 6.38 µm, W = 1.78 µm, Q = 3.58 (30/1).

*Material examined*: China, Jiangxi Province, Jiujiang, Lushan Mountains, on fallen branch of gymnosperm, 25 June 2021, L.W. Zhou, LWZ 20210625-5b (HMAS, **holotype**).

*GenBank numbers*: ITS = OQ540895; LSU = OQ540853.

*Notes*: *Kneiffiella pseudoalutacea* is phylogenetically close to *K. alutacea* (Fig. 121). Morphologically, these two species share a monomitic hyphal system, thin-walled cylindrical to subcylindrical cystidia, subclavate basidia and allantoid basidiospores; however, *K. alutacea* differs in the presence of creamish white to ochraceous, odontoid to coralloid hymenophore and longer cystidia (50–75 µm in length, Eriksson and Ryvarden 1976).

### *Hymenochaetaceae* Donk.

*Notes*: *Hymenochaetaceae* proposed by Donk (1948), are white rot saprophytes or parasites causing wood decaying in Angiosperms and Gymnosperms. They are characterized by annual to perennial, yellow to brownish basidiomes with a xanthochroic reaction to KOH, smooth, poroid or corticioid hymenophore with microscopic features such as monomitic, mono-dimitic or dimitic hyphal system, clampless generative hyphae, presence or absence of cystidioles and setae with thin to thick walled, hyaline to brown, globose to cylindrical basidiospores (Ryvarden 1991; Dai 2010).

Fiasson and Niemela (1984), studied the morphological, cultural, chemical, and nuclear behavioural of *Phellinus* and *Inonotus* complex and raised *Fomitiporia*, *Fulviformes*, *Fuscoporia*, *Ochroporus*, *Phellinidium*, *Phellinus* s.s. and *Porodaedalea* from *Phellinus* s.l.; *Inonotus* s.s., *Inocutis* and *Inonotopsis* from *Inonotus* s.l. Góes-Neto et al. (2000) proposed 12 genera namely, *Aurificaria*, *Clavariachaete*, *Coltricia*, *Coltriciella*, *Cyclomyces*, *Hydnochaete*,



**Fig. 124** Basidiomes of *Fulvoderma microporum* (LWZ 20210626-12b, **holotype**)

*Hymenochaetaeae*, *Inonotus*, *Phellinus*, *Phylloporia*, *Pyrrhoderma* and *Stiptochaete* under this family. Dai (2010) studied 170 Hymenochaetoid fungi and grouped into 23 genera. Subsequently, several new genera, like *Coniferiporia*, *Cylindrosporus*, *Fulvoderma*, *Sanghuangporus* and *Tropicoporus* (Zhou 2015; Zhou et al. 2016b, c, 2018) were introduced in this family. Recently, Wu et al. (2022a) revised the systematics of 672 poroid hymenochaetoid fungi, and classified them under 34 genera.

### *Fulvoderma* L.W. Zhou & Y.C. Dai.

*Notes*: *Fulvoderma* typified by *F. australe* was segregated from *Pyrrhoderma* to accommodate the generic type and another species *F. scaurum* (Zhou et al. 2018). *Fulvoderma* is characterized by the combination of sessile to stipitate basidiomes, the absence of any setal materials, and hyaline, thin-walled basidiospores within *Hymenochaetaceae* (Zhou et al. 2018).

### *Fulvoderma microporum* Xue W. Wang & L.W. Zhou, *sp. nov.*

*Index Fungorum number*: IF900291; *Facesoffungi number*: FoF 14054; Figs. 124, 125

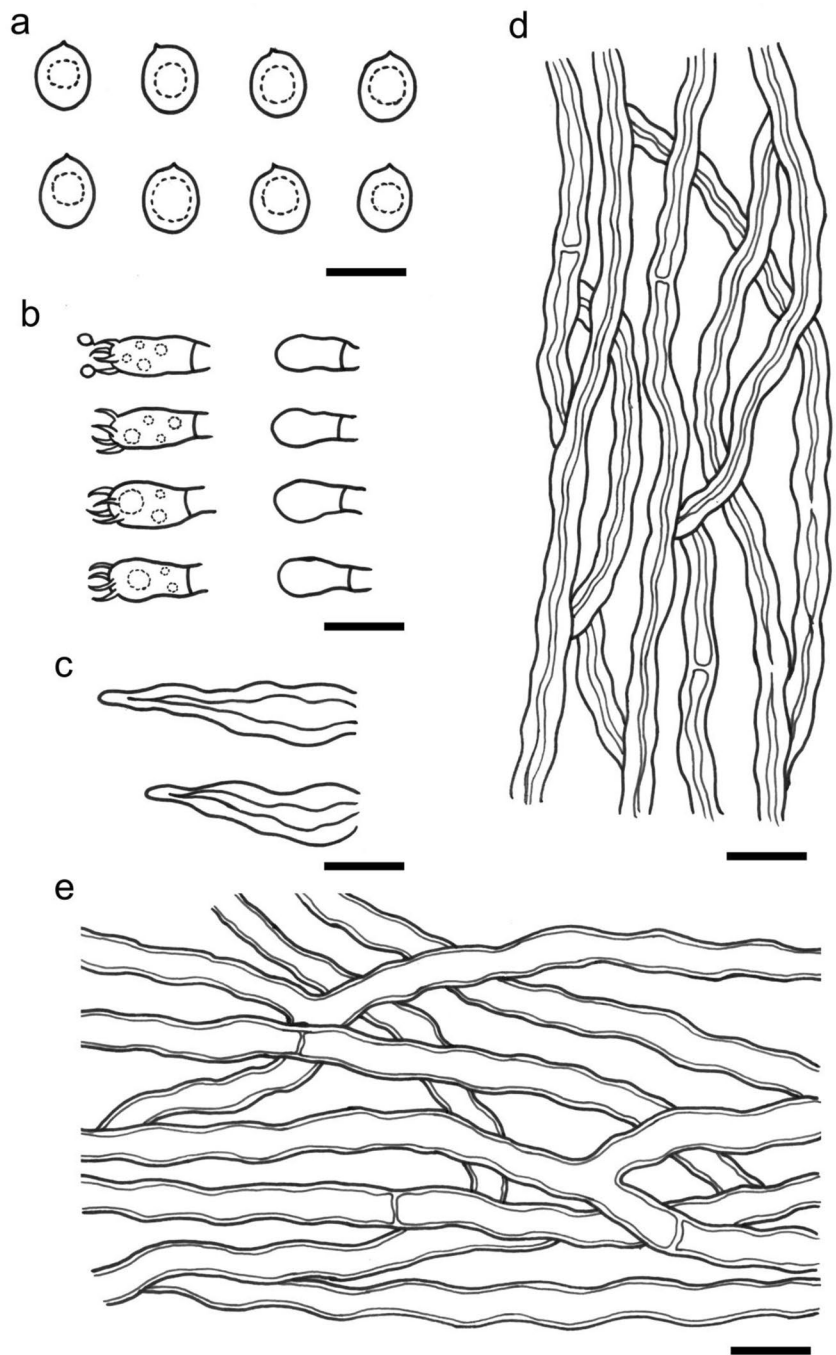
*Etymology*: microporum (Lat.) referring to the small pores.

*Holotype*: LWZ 20210626-12b (HMAS).

*Diagnosis*: Characterized by fulvous to snuff brown pileal surface, umber pore surface, small, circular pores, the absence of cystidia and cystidioles, and small, broadly ellipsoid to globose basidiospores.

*Basidiomes* annual, laterally stipitate, solitary or imbricate, without odor or taste when fresh, hard corky. *Pilei* projecting up to 7 cm long, 8 cm wide and 1 cm thick at base. *Pileal surface* fulvous to snuff brown, distinctly concentrically zonate, tuberculate and warty; margin acute, colour consistent with pileal surface, wavy. *Pore surface* umber,

**Fig. 125** Microscopic structures of *Fulvoderma microporum* (LWZ 20210626-12b, **holotype**). **a** Basidiospores. **b** Basidia and basidioles. **c** Hymenial setae. **d** Hyphae from context. **e** Hyphae from trama. Scale bars: **a** = 5  $\mu$ m, **b**–**e** = 10  $\mu$ m

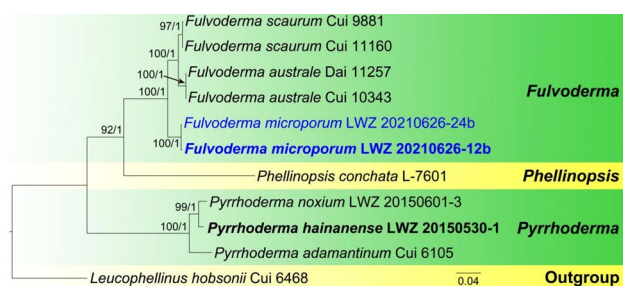


glancing; sterile margin cinnamon-buff, up to 5 mm wide; pores mostly circular, 7–8 per mm; *dissepiments* thin, entire. *Context* honey-yellow, hard corky, up to 7 mm thick. *Tubes* clay-buff, hard corky, up to 3 mm long. *Stipe* up to 3 cm long and 2.5 cm in diam.

*Hyphal system* monomitic; generative hyphae simple septate; tissue xanthochroic. *Contextual hyphae* pale yellowish to yellowish, thick-walled with a wide lumen, rarely branched, simple septate, interwoven, 5–6  $\mu$ m in diam. *Tramal hyphae* hyaline, pale yellowish to yellowish,

thick-walled with a narrow lumen, unbranched, simple septate, interwoven, 3–4  $\mu$ m in diam. *Hymenial setae* dark brown, thick-walled with a narrow lumen, ventricose and apex sharp, 20–35  $\times$  7–7.5  $\mu$ m. *Cystidia and cystidioles* absent. *Basidia* barrel-shaped to subclavate, simple septate with four sterigmata, 10  $\times$  5–6  $\mu$ m; *basidioles* in shape similar to basidia but slightly smaller. *Basidiospores* broadly ellipsoid to globose, with a big guttule, hyaline, thin-walled, IKI–, CB–, 4–4.5(–5)  $\times$  3–3.5  $\mu$ m,  $L = 4.25 \mu$ m,  $W = 3.25 \mu$ m,  $Q = 1.29–1.31$  ( $n = 60/2$ ).





**Fig. 126** Phylogram generated by the maximum likelihood algorithm based on combined nLSU and ITS sequence data is presented along with the bootstrap values and the Bayesian posterior probabilities above 50% and 0.8, respectively, at the nodes. Type specimens are in bold and the isolates of new species characterized are in blue

**Material examined:** China, Jiangxi Province, Jiujiang, Bailudong Academy, ground under gymnosperm, 26 June 2021, L.W. Zhou, LWZ 20210626-12b (HMAS, **holotype**); *ibid.*, LWZ 20210626-24b (HMAS).

**GenBank numbers:** LWZ 20210626-12b: ITS = OQ540896; LSU = OQ540854; LWZ 20210626-24b: ITS = OQ540897; LSU = OQ540855.

**Notes:** *Fulvoderma microporum* resembles the other two species of *Fulvoderma*, *F. australe* and *F. scaurum*, for their annual, sessile to laterally stipitate, solitary or imbricate basidiomes and yellowish brown pileal surface. However, *F. australe* has larger angular pores (5–6 per mm) and basidiospores ( $4.5\text{--}5.5 \times 4\text{--}4.5\ \mu\text{m}$ ), and *F. scaurum* is also distinct by larger pores (4–5 per mm) and basidiospores ( $5\text{--}6 \times 4\text{--}4.6\ \mu\text{m}$ , Zhou et al. 2018). Moreover, *F. microporum* occupies a distinct lineage from *F. australe* and *F. scaurum* within *Fulvoderma* (Fig. 126).

### ***Tropicoporus*** L.W. Zhou, Y.C. Dai & Sheng H. Wu.

**Notes:** Based on molecular systematics and microscopical illustrations, Zhou et al. (2016c) proposed *Tropicoporus* as a new genus along with seven new combinations from the *Inonotus linteus* complex. *Tropicoporus* accommodates species with annual to perennial, resupinate, effused-reflexed to pileate brown, dark greyish to black pilei, velutinate, hispid, tomentose with glabrous to radially (un)cracked pileal surface. Context vary from homogeneous to duplex with or without black line. Microscopically, a dimitic or mono-dimitic hyphal system with simple septate generative hyphae, presence or absence of cystidioles, presence of hymenial setae with smooth, fairly thick walled to thick walled, yellowish, subglobose to ellipsoid basidiospores are characteristic features (Zhou et al. 2016c; Wu et al. 2022a).

Later, *T. boehmeriae* (Wu et al. 2015), *T. stratificans* (Coelho et al. 2016), *T. drechleri* (Salvador-Montoya et al. 2018), *T. texanus* (Brown et al. 2020), *T. flabellatus* and *T. nullisetus* (Lima et al. 2022) were added to the genus

*Tropicoporus*. Wu et al. (2022a, b) described seven new species viz., *T. angustisulcatus*, *T. hainanicus*, *T. lineatus*, *T. minus*, *T. ravidus*, *T. substratificans* and *T. tenuis* with 24 new combinations. Of known species of *Tropicoporus*, *T. nullisetus* was reported without setae (Lima et al. 2022).

***Tropicoporus natarajaniae*** M. Kaliyaperumal, S. Gunaseelan, K. Kezo, Xue W. Wang & L.W. Zhou, **sp. nov.**

**Index Fungorum number:** IF559816; **Facesoffungi number:** FoF 12715; Figs. 127, 128

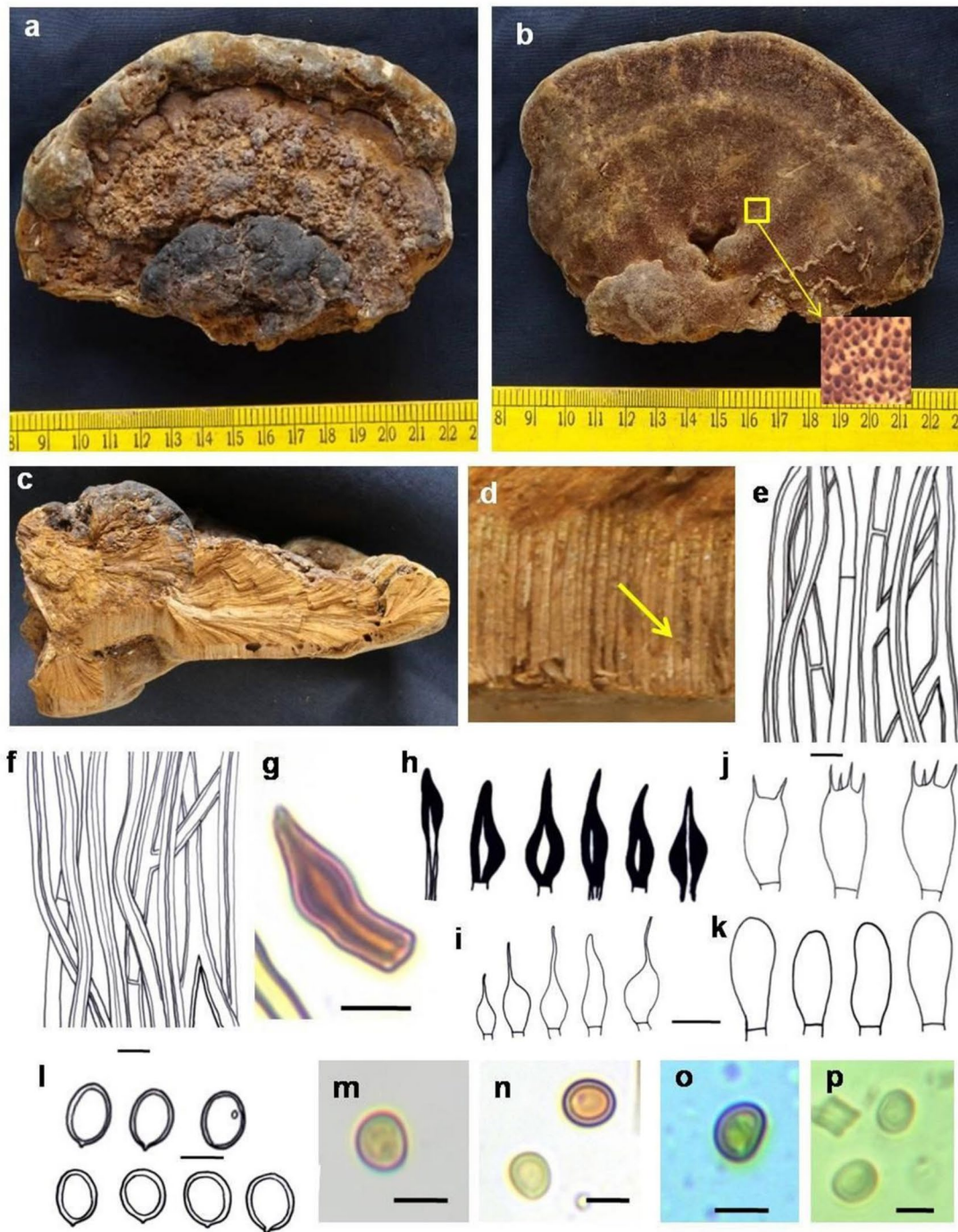
**Etymology:** The species epithet “*natarajaniae*” referring to the Indian mycologist, Krishnamoorthy Natarajan, for his contributions to the Indian mycology especially on taxonomic studies in Agaricomycetes.

**Holotype:** MUBL4020.

**Diagnosis:** *Tropicoporus natarajaniae* is characterized by velutinate to abundantly tuberculae or warted pilear, uncracked pilear surface, on maturity becoming greyish brown with few cracks only near attachment, obtuse, velutinate margin and stratified tube with mono-dimitic hyphal system, presence of cystidioles and setae with broadly ellipsoid to subglobose basidiospores.

**Basidiomes** perennial, solitary, pileate, sessile, light in weight, hard when dry. **Pileus** dimidiate, applanate, with no distinct crust, projecting up to 5.4 cm, 6.6 cm wide and 3.6 cm thick near the attachment. **Pilear surface** on first pubescent to velutinate, smooth with few tuberculae or warts in young basidiomes, uncracked, azonate, yellowish brown (5E5, 5F8) to brown (6E8), on maturation pilei becoming velutinate with abundant tuberculate or warts on the surface, becoming greyish brown (6F3) with few cracks near attachment. **Margin** entire, obtuse, yellowish brown (5F8). **Pore surface** brown (6E6) to dark brown (6F6). **Pores** round to angular, regular, 5–7 per mm. **Dissepiments** entire, thick. **Context** duplex with no blackline, up to 1.5 cm, light brown (6D8) to brown (6E7). **Tubes** 0.7 cm in length, indistinctly stratified, each stratum up to 3 mm, brown (6E8).

**Hyphal system** monomitic in the context and dimitic in the tubes, tissue darkening with KOH without swelling. **Context generative hyphae**, thin to thick walled, hyaline to golden yellow, simple septate, rarely branched, 2–5  $\mu\text{m}$  in diam. **Tramal generative hyphae** dominant, thin to thick walled, hyaline to pale yellow, septate, occasionally branched, 2–4.8  $\mu\text{m}$  in diam. **Skeletal hyphae** thick-walled with narrow to wide lumen, yellowish brown, aseptate, unbranched, 2–4.5  $\mu\text{m}$  in diam. **Hymenial setae** dark brown, thick-walled, ventricose to subulate with a sharp to blunt tips,  $6\text{--}18.7 \times 4.3\text{--}5.3\ \mu\text{m}$ . **Cystidia** absent. **Cystidioles** hyaline, thin-walled, ventricose to fusoid with elongated tapering apical portion,  $4.8\text{--}27 \times 3.8\text{--}6\ \mu\text{m}$ . **Basidia** clavate to subclavate,  $6\text{--}18 \times 3.8\text{--}6.2\ \mu\text{m}$ , with four sterigmata and a simple septum at the base. **Basidioles** clavate,  $4.8\text{--}16 \times 3.5\text{--}6\ \mu\text{m}$ . **Basidiospores** broadly ellipsoid to



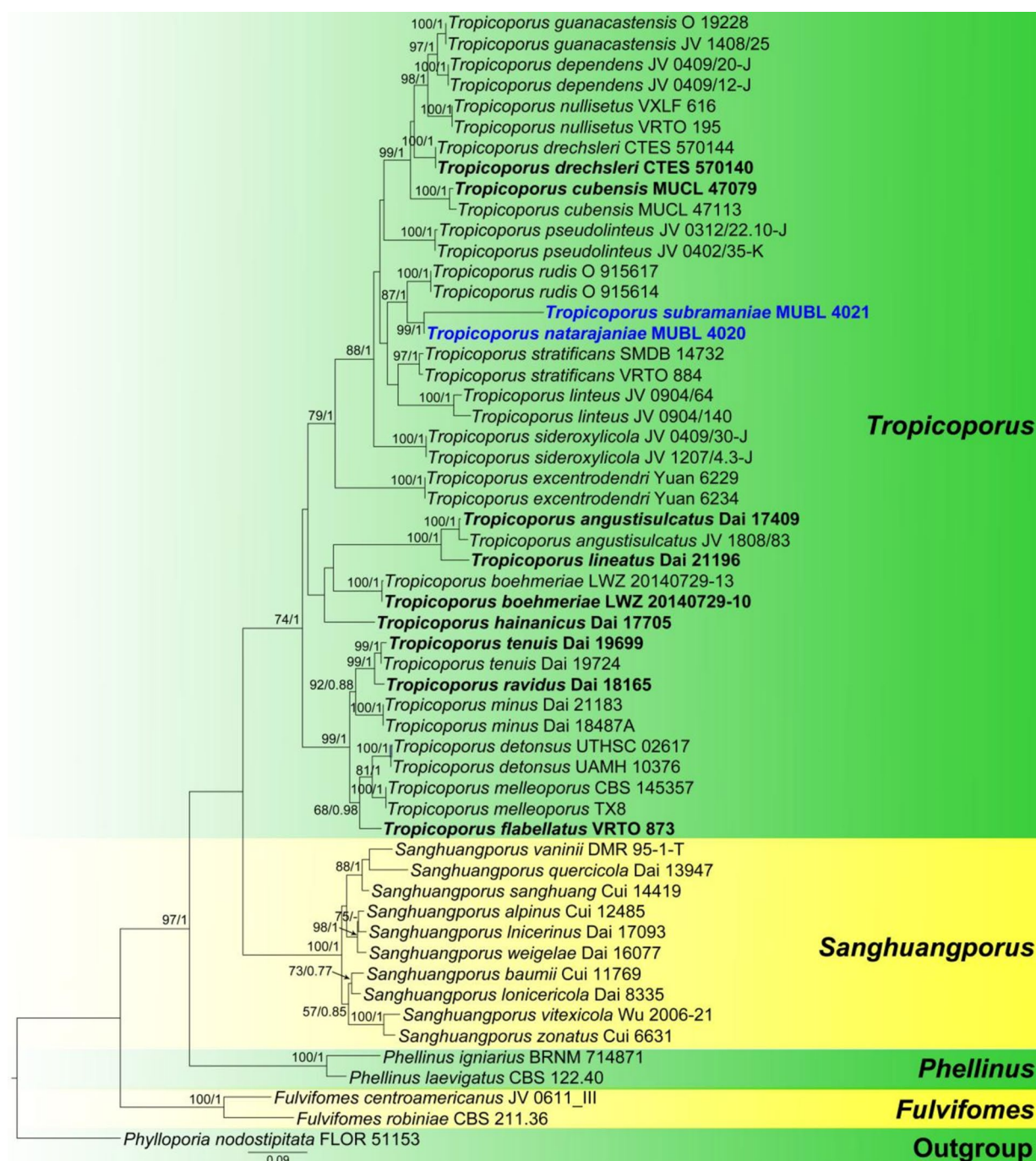
**Fig. 127** Morphological characters of *Tropicoporus natarajaniae*. **a** Basidiomes (**Holotype**). **b** Pore surface. **c** Cross-section of basidiome with obtuse margin. **d** Indistinctly stratified tube layer. **e** Contextual hyphae. **f** Tramal hyphae. **g–h** Hymenial setae. **i** Cystidioles.

**j** Basidia. **k** Basidioles. **l–p** Basidiospores: **l** Basidiospore. **m** Basidiospore in water. **n** Basidiospore in KOH. **o** Basidiospore in cotton blue. **p** Basidiospore in Melzer's reagent. Scale bars: **e–p** = 5  $\mu$ m

subglobose, pale yellow in water, turning golden yellow to brown in KOH, fairly thick walled to thick-walled, smooth, inamyloid, nondextrinoid, acyanophilous, (4.6–) 5–6 (–6.5)  $\times$  (4.1–) 4.6–4.9 (–5.2)  $\mu$ m ( $n = 50/1$ ),  $Q = 1.1$  ( $Q$  range 1.05–1.3).

**Material examined:** India, Tamil Nadu, Thiruvannamalai district, Sathanur, Pennaiyar river, 12° 08'00.34"N, 78° 56'48.63"E, on living angiosperm tree (*Albizia amara*), 03 February 2018, Sugantha Gunaseelan, MUBL4020 (**holotype**).





**Fig. 128** Phylogram generated by the maximum likelihood algorithm based on combined nLSU and ITS sequence data is presented along with the bootstrap values and the Bayesian posterior probabilities

GenBank number: ITS = OP003881.

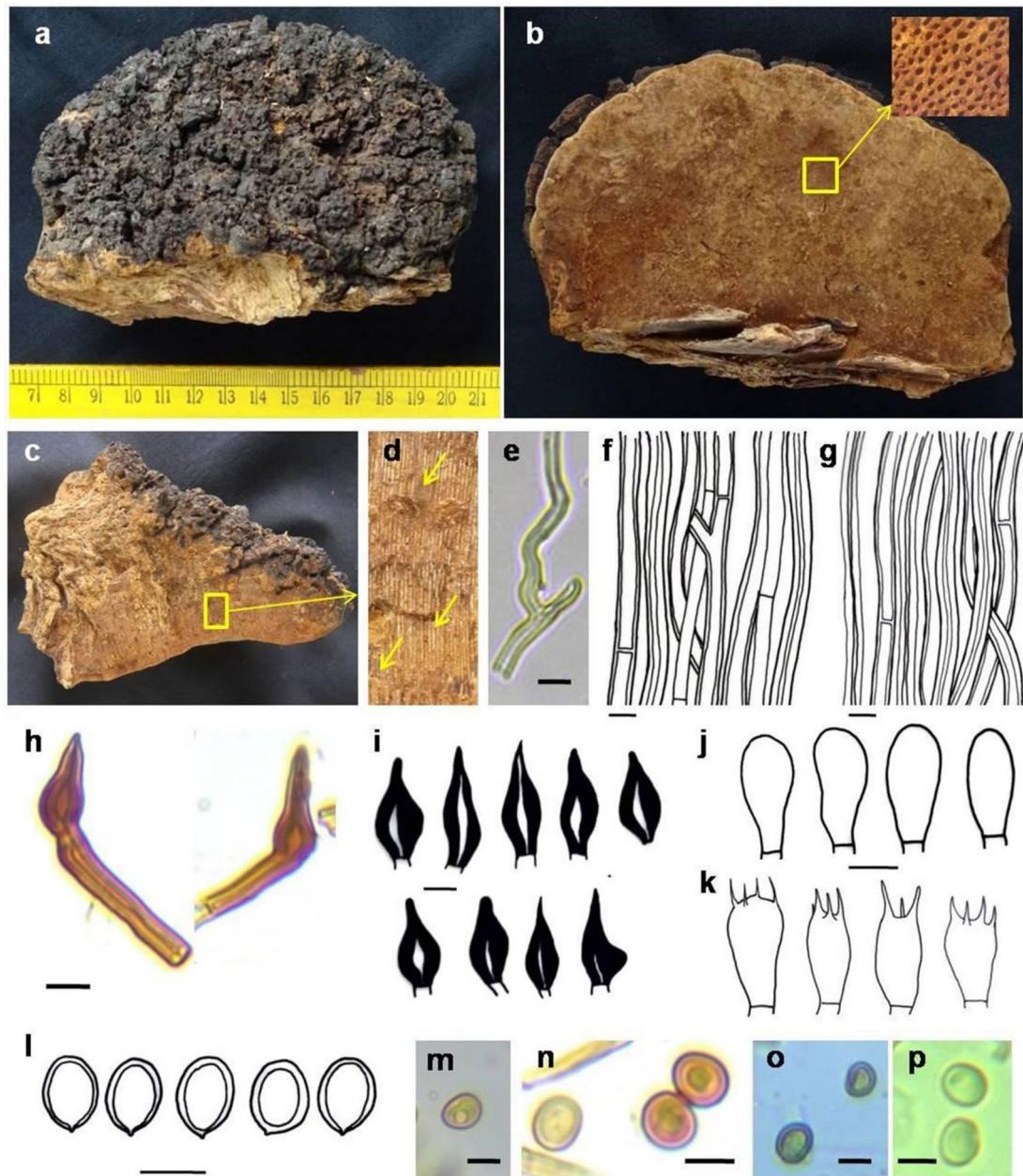
**Notes:** *Tropicoporus natarajaniae* is characterized by pileate basidiomes with a mono-dimitic hyphal system, while other *Tropicoporus* species such as *T. boehmeriae*, *T. hainanicus*, *T. minus*, *T. ravidus*, *T. stratificans*, *T. tenuis* and *T. texanus* are reported to be resupinate with a dimitic hyphal system (Wu et al. 2015, 2022a, b; Coelho et al. 2016;

above 50% and 0.8, respectively, at the nodes. Type specimens are in bold and the isolates of new species characterized are in blue

Brown et al. 2020). Absence of setae makes *T. nullisetus* (Lima et al. 2022) distinct from other reported *Tropicoporus* species.

*Tropicoporus angustisulcatus*, *T. excentrodendri*, *T. lineatus* and *T. substratificans* (Wu et al. 2022a, b) have a dimitic hyphal system and larger pores (Zhou et al. 2016c; Wu et al. 2022a, b), when compared with *T. natarajaniae* that





**Fig. 129** Microscopic structures of *Tropicoporus subramaniae*. **a** Basidiomes (**Holotype**). **b** Pore surface. **c** Cross-section of basidiome. **d** Stratified tube layer. **e** branched generative hyphae from context. **f** Contextual hyphae. **g** Tramal hyphae. **h–j** Hymenial setae. **k**

Basidioles. **l** Basidia. **m–q** Basidiospores: **m** Basidiopore in water. **n** Basidiopore in KOH. **o** Basidiopore in cotton blue. **p** Basidiopore in Melzer's reagent. Scale bars: **e–p** = 5  $\mu$ m

has a mono-dimitic hyphal system and smaller pores (5–7 per mm).

*Tropicoporus guanacastensis* (Zhou et al. 2016c) is similar to *T. natarajaniae* in sharing a mono-dimitic hyphal system, stratified tube layer and presence of ventricose setae but differs from later in radially cracked, concentrically zonate and sulcate basidiomes, small pores (7–8 per mm), absence of cystidioles and ellipsoidal spores. While our Indian collection has pilei with abundant warts, large pores (5–7 per

mm), presence of cystidioles and broadly ellipsoid to sub-globose spores.

*Tropicoporus flabellatus* (Lima et al. 2022) and *T. natarajaniae* shows significant variations in basidiomes characters and microscopical features, the former have radially folded pilear surface with projections, velutinate to black and brown concentric zones, acute margin with smaller pores (7–9 per mm), absence of cystidioles and ellipsoidal basidiospores, whereas *T. natarajaniae* have abundant warts without any

black or brown zones, obtuse margin with large pores (5–7 per mm), presence of cystidioles and broadly ellipsoid to subglobose basidiospores.

*Tropicoporus drechsleri* (Salvador-Montoya et al. 2018), similar with *T. natarajaniae* in a mono-dimitic hyphal system, presences of setae and cystidioles, yet *T. drechsleri* differs widely with pilear and basidiospores characters such as concentrically sulcate, radially deeply cracked pilei with broadly ellipsoid to ellipsoid basidiospores, while *T. natarajaniae* has frequently warted pilear surface, with few cracks near attachment and broadly ellipsoid to subglobose basidiospores.

***Tropicoporus subramaniae*** S. Gunaseelan, M. Kaliyaperumal, K. Kezo, Xue W. Wang & L.W. Zhou., *sp. nov.*

*Index Fungorum*: IF559817; *Facesoffungi* number: FoF 12714; Figs. 129

*Etymology*: The species epithet “*subramaniae*” referring to the Indian mycologist C. V. Subramanian, for his contributions to the fungal taxonomic studies in India.

*Holotype*: MUBL4021.

*Diagnosis*: *Tropicoporus subramaniae* is characterized by sulcate, deeply rimose, irregularly cracked pilear surface, acute margin, homogenous context and stratified tube with monomitic context and dimitic hyphal system in trama, absence of cystidioles and presence of setae and broadly ellipsoid to subglobose basidiospores.

*Basidiomes* perennial, solitary, pileate, sessile, woody hard, light in weight when dry. *Pileus* dimidiate, applanate, unguulate, projecting up to 9.3 cm, 13.7 cm wide and 6.4 cm thick near the attachment. *Pilear surface* glabrous to sulcate, deeply rimose with irregular cracks, with crust, brownish grey (6F2), greyish brown (6E3) to almost black. *Margin* entire, acute, golden brown (5D7) to brownish grey (6F2). *Pore surface* brown (6E7). *Pores* round to angular, regular, 4–6 per mm. *Dissepiments* entire, thick. *Context* homogenous, up to 0.5 cm, light brown (6D8) to brown (6E8). *Tube layer* up to 3.7 cm, stratified, each strata up to 0.4 cm thick.

*Hyphal system* monomitic in the context and dimitic in the tubes, tissue darkening with KOH without swelling; *Context generative hyphae*, thin- to thick-walled, hyaline to golden yellow, simple septate, rarely branched, 2–5.2 µm in diam. *Trama generative hyphae*, dominant, thin to thick-walled, hyaline to pale yellow, septate, occasionally branched, 2–4.2 µm in diam. *Skeletal hyphae*, thick-walled with narrow to wide lumen, yellowish brown, aseptate, unbranched, 2–4 µm in diam. *Hymenial setae* dark brown, thick-walled, ventricose to subulate with a sharp to blunt tips, 12–28 × 4.5–8 µm. *Cystidia and cystidioles* absent. *Basidia* clavate to sub clavate, 8–18.2 × 3.8–6.2 µm, with four sterigmata and a simple septum at the base. *Basidioles* clavate, 5–16.5 × 3–5.8 µm. *Basidiospores* broadly ellipsoid to subglobose, pale yellow to golden yellow in water, turning

brown in KOH, thick-walled, smooth, inamyloid, nondextrinoid, acyanophilous, (5–)5.3–6.3(–6.7) × (4.5–)4.8–5(–5.2) µm (n = 50/1), Q = 1.2 (Q range 1.1–1.5).

*Material examined*: India, Tamil Nadu, Thiruvannamalai district, Sathanur, Pennaiyar river, 12° 08'00.34"N, 78° 56'48.63"E, on living angiosperm tree (*Albizia amara*), 3 February 2018, Sugantha Gunaseelan, MUBL4021 (**holotype**).

*GenBank* number: ITS = OP003882.

*Notes*: *Tropicoporus subramaniae*, has a mono-dimitic hyphal system, and deeply and irregularly cracked basidiomes; however, *T. angustisulcatus*, *T. excentrodendri*, *T. lineatus* and *T. substratificans* (Zhou et al. 2016c; Wu et al. 2022a, b), differs from our Indian collection in having a dimitic hyphal system and uncracked basidiomes.

Despite sharing a mono-dimitic hyphal system and absence of cystidioles, *Tropicoporus flabellatus* differs from *T. subramaniae* by having velutinate to black and brown zones in pilear surface, uncracked basidiomes with smaller pores (7–9 per mm), duplex context with black line and ellipsoidal spores (4.5–5 × 3.5–4 µm), whereas *T. subramaniae* has sulcate, deeply cracked pilei with larger pores (4–6 per mm), homogenous context and broadly ellipsoid to subglobose basidiospores (5–6.7 × 4.5–5 µm).

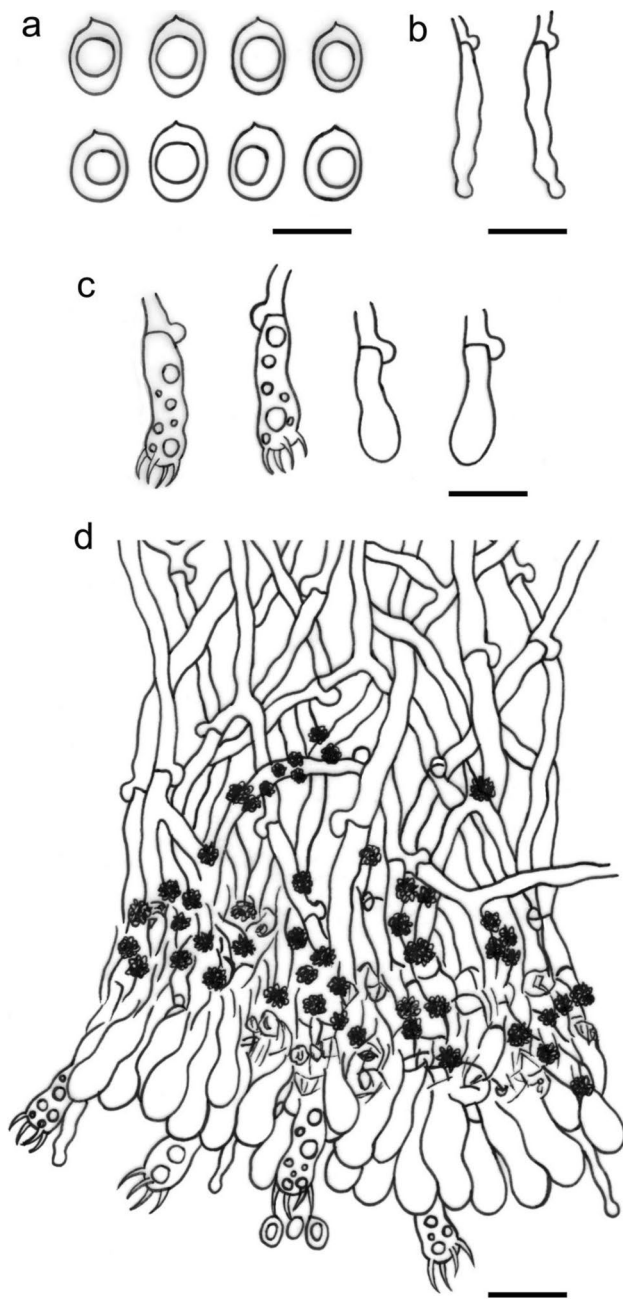
*Tropicoporus guanacastensis* and *T. subramaniae* are similar in having sulcate, cracked basidiomes, stratified tube, a mono-dimitic hyphal system, absence of cystidioles and presence of ventricose setae, but the former differs in smaller pores (7–8 per mm) and ellipsoidal spores (Zhou et al. 2016c), while our Indian species have comparatively larger pores (4–6 per mm) and broadly ellipsoid to subglobose spores.

*Tropicoporus subramaniae* and *T. drechsleri* (Salvador-Montoya et al. 2018), shares concentrically sulcate deeply cracked pilei with a mono-dimitic hyphal system, larger pores (< 6 per mm), but the South American species



**Fig. 130** Basidiomes of *Lyomyces austro-occidentalis* (LWZ 20190816-40a, **holotype**)





**Fig. 131** Microscopic structures of *Lyomyces austro-occidentalis* (LWZ 20190816-40a, **holotype**). **a** Basidiospores. **b** Cystidia. **c** Basidia and basidioles. **d** A vertical section of hymenium. Scale bars: 10  $\mu$ m

varies with indistinctly stratified tube layer, presence of cystidioles and broadly ellipsoid to ellipsoid basidiospores ( $4\text{--}5.5 \times 3\text{--}4.5 \mu\text{m}$ ), while *T. subramaniae* have stratified tramal layer without cystidioles and broadly ellipsoid to subglobose basidiospores ( $5\text{--}6.7 \times 4.5\text{--}5 \mu\text{m}$ ).

*Tropicoporus boehmeriae*, *T. hainanicus*, *T. minus*, *T. ravidus*, *T. stratificans*, *T. tenuis* and *T. texanus* are having resupinate basidiomes with a dimittic hyphal system (Coelho

et al. 2016; Brown et al. 2020; Wu et al. 2022a, b), whereas *T. subramaniae* could be easily distinguished by its pileate basidiomes and a mono-dimittic hyphal system.

### *Schizoporaceae* Jülich.

**Notes:** *Schizoporaceae* with *Schizopora* as the type genus was introduced by Jülich (1981). Similar to *Chaetoporellaceae*, due to *Schizopora* being against by the conservation of *Hyphodontia*, the family name *Schizoporaceae* has long been ignored, until that Wang et al. (2021a) reinstated *Schizoporaceae* to accommodate *Fasciodontia*, *Lyomyces* and *Xylodon* (a prior synonym over *Schizopora*).

### *Lyomyces* P. Karst.

**Notes:** *Lyomyces* typified by *L. serus* is a well supported monophyletic genus. See Wang et al. (2021a) for the latest comprehensive summarization of *Lyomyces*.

### *Lyomyces austro-occidentalis* Xue W. Wang & L.W. Zhou, *sp. nov.*

**Index Fungorum number:** IF900292; **Facesoffungi number:** FoF 14055; Figs. 130, 131

**Etymology:** *austro-occidentalis* (Lat.) referring to the distribution of this species in Southwest China.

**Holotype:** LWZ 20190816-40a (HMAS).

**Diagnosis:** Characterized by annual, resupinate, adnate basidiomes, smooth, white to cream hymenophore, a monomittic hyphae system with encrusted subhymenial hyphae, capitulate cystidia, clavate basidia, and ellipsoid basidiospores.

**Basidiomes** annual, resupinate, adnate, cracked and brittle when dry, without odour. **Hymenophore** smooth, white to cream colored. **Margin** concolorous with or slightly paler than subiculum, abrupt.

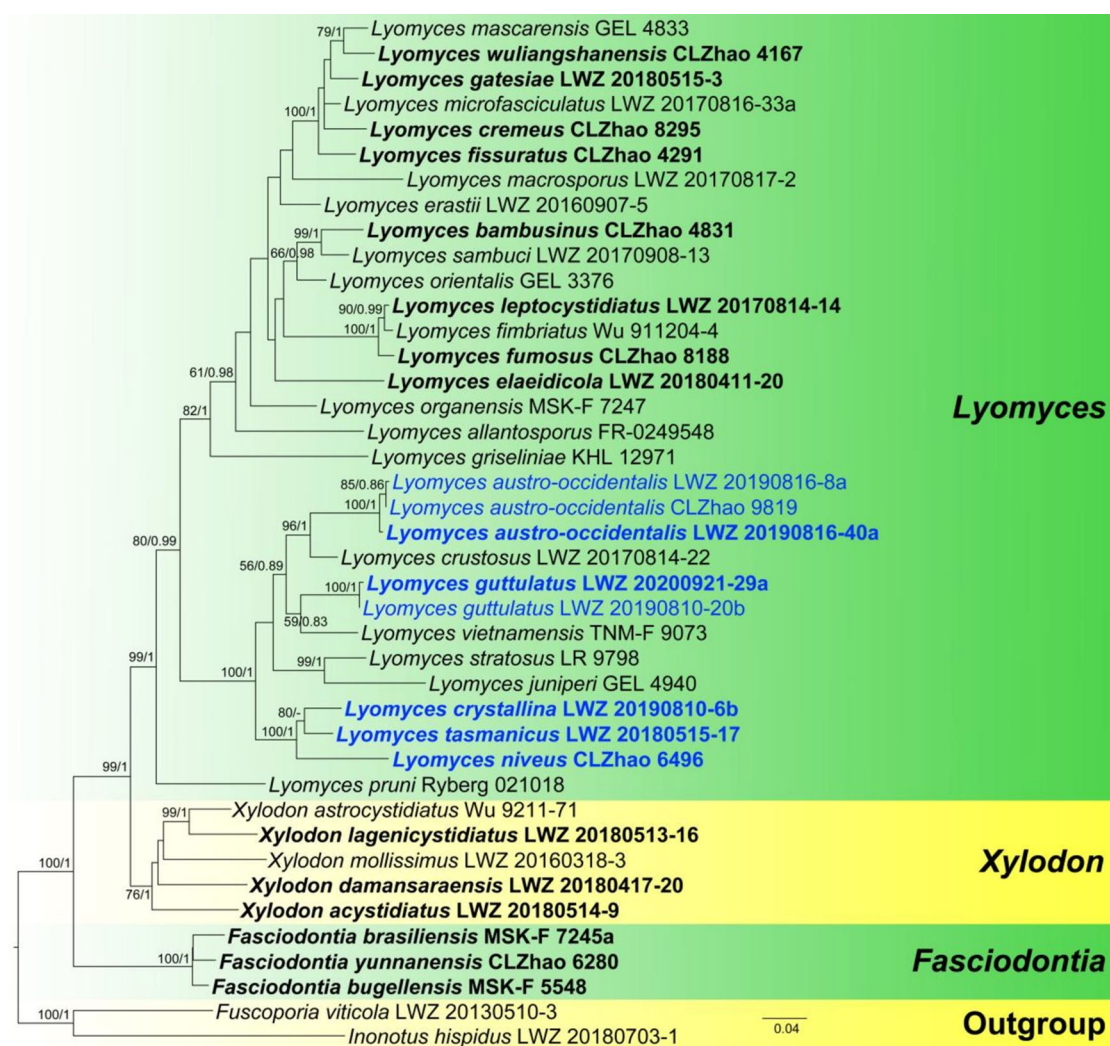
**Hyphal system** monomittic; generative hyphae with clamp connections, hyaline, dichotomous branching, interwoven, thin-walled,  $2\text{--}3.5 \mu\text{m}$  in diam, subhymenial hyphae usually with encrustation. **Cystidia** capitulate, ca.  $20 \times 3 \mu\text{m}$ . **Basidia** clavate,  $15\text{--}20 \times 5\text{--}5.5 \mu\text{m}$ , with four sterigmata ca.  $3\text{--}4 \mu\text{m}$  long and a clamp connection at the base; **basidioles** similar in shape to basidia, but smaller. **Basidiospores** ellipsoid, with a large oily drop, hyaline, smooth, thin-walled, IKI–, slightly CB+,  $4.2\text{--}5.2 \times 3.1\text{--}3.5 \mu\text{m}$ ,  $L = 4.63 \mu\text{m}$ ,  $W = 3.27 \mu\text{m}$ ,  $Q = 1.39\text{--}1.44$  (60/2).

**Material examined:** China, Sichuan Province, Leshan, Ebian Yi Autonomous County, Heizhugou National Forest Park, on fallen branch of angiosperm, 16 August 2019, L.W. Zhou, LWZ 20190816-40a (HMAS, **holotype**), LWZ 20190816-8a (HMAS).

**GenBank numbers:** LWZ 20190816-8a: LSU=OQ540856; LWZ 20190816-40a: LSU=OQ540857.

**Notes:** Phylogenetically, *Lyomyces austro-occidentalis* and *L. ochraceoalbus* (CLZhao 9819) are nested within a





**Fig. 132** Phylogram generated by the maximum likelihood algorithm based on combined nLSU and ITS sequence data is presented along with the bootstrap values and the Bayesian posterior probabilities

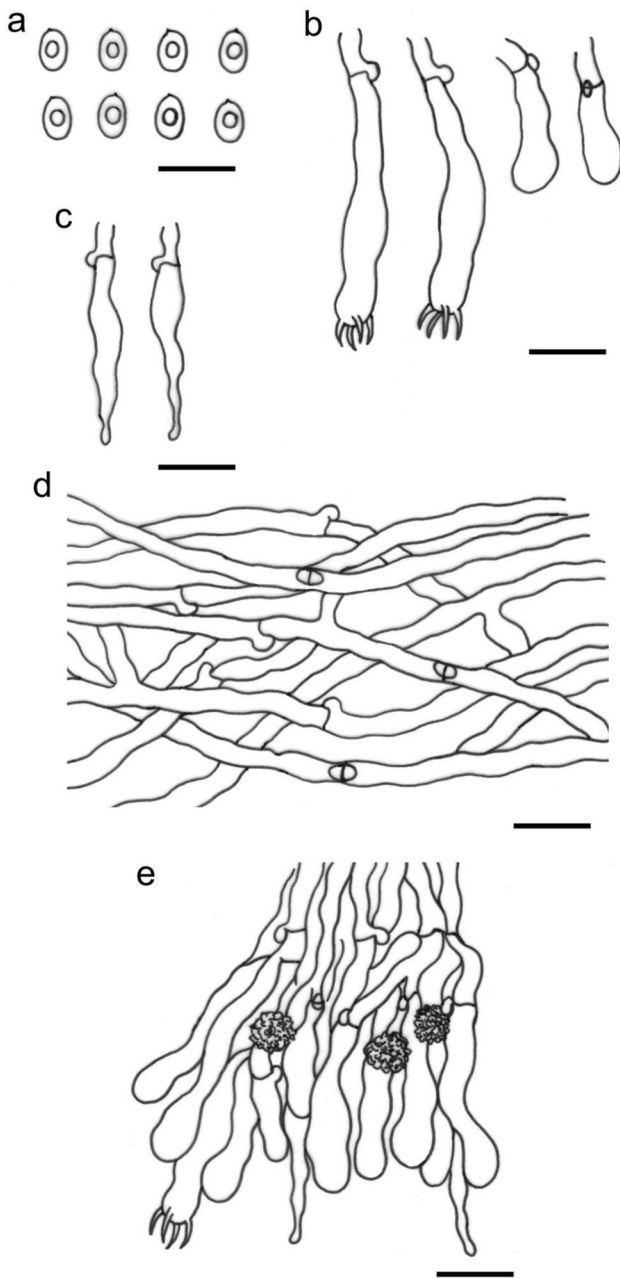
above 50% and 0.8, respectively, at the nodes. Type specimens are in bold and the isolates of new species characterized are in blue

single clade (Fig. 132). Morphologically, *L. austro-occidentalis* is highly similar to the original description of *L. ochraceoalbus* in Luo et al. (2021). Therefore, these two names indeed represent the same species. Unfortunately, Luo et al. (2021) did not effectively published the name *L. ochraceoalbus* according to Art. 40.7 of the International Code of Nomenclature for algae, fungi, and plants (Turland et al. 2018). Here, we redescribed this species as *L. austro-occidentalis*.

*Lyomyces crustosus* and *L. austro-occidentalis* have a close phylogenetic relationship (Fig. 132), and share white to cream colored hymenophoral surface; however, *L. crustosus* differs in grandinioid to odontoid hymenophore, narrowly ellipsoid to cylindrical, sometimes slightly allantoid, longer basidiospores (5–7  $\mu$ m in length, Langer 1994). *Lyomyces juniperi* resembles *L. austro-occidentalis*



**Fig. 133** Basidiomes of *Lyomyces crystallina* (LWZ 20190810-6b, holotype)



**Fig. 134** Microscopic structures of *Lyomyces crystallina* (LWZ 20190810-6b, **holotype**). **a** Basidiospores. **b** Basidia and basidioles. **c** Cystidia. **d** Hyphae from subiculum. **e** A vertical section of hymenium. Scale bars: 10 µm

by smooth, white to cream hymenophore and ellipsoid basidiospores, but *L. juniperi* is differentiated by its subulate cystidia and suburniform basidia (Langer 1994).

*Lyomyces crystallina* Xue W. Wang & L.W. Zhou, *sp. nov.*

*Index Fungorum* number: IF900296; *Facesoffungi* number: FoF 14059; Figs. 133, 134



**Fig. 135** Basidiomes of *Lyomyces guttulatus* (LWZ 20200921-29a, **holotype**)

*Etymology*: *crystallina* (Lat.) referring to crystalline materials covering generative hyphae.

*Holotype*: LWZ 20190810-6b (HMAS).

*Diagnosis*: Characterized by annual, resupinate, adnate basidiomes, smooth to slightly grandinoid, cream to pale buff hymenophore, fusoid cystidia with subulate apex, subcylindrical basidia, and narrowly ellipsoid to oblong basidiospores.

*Basidiomes* annual, resupinate, adnate, cracked and brittle when dry, without odour. *Hymenophore* smooth to slightly grandinoid, cream to pale buff. *Margin* concolorous with subiculum, abrupt.

*Hyphal system* monomitic; *generative hyphae* with clamp connections, hyaline, dichotomous branching, interwoven, thin-walled, 2.5–3.5 µm in diam, encrusted with coarse crystalline materials throughout the hymenium. *Cystidia* fusoid with subulate apex, 20–25 × 3.5–4 µm. *Basidia* subcylindrical and constricted, with four sterigmata and a clamp connection at the base, 30–35 × 5–5.5 µm; *basidioles* subclavate, 13–20 × 4.5–5.5 µm. *Basidiospores* narrowly ellipsoid to oblong, usually with an oily drop, hyaline, smooth, thin-walled, IKI–, CB–, (5–)5.1–5.6(–5.7) × 3.1–3.4(–3.5) µm, *L* = 5.32 µm, *W* = 3.26 µm, *Q* = 1.63 (30/1).

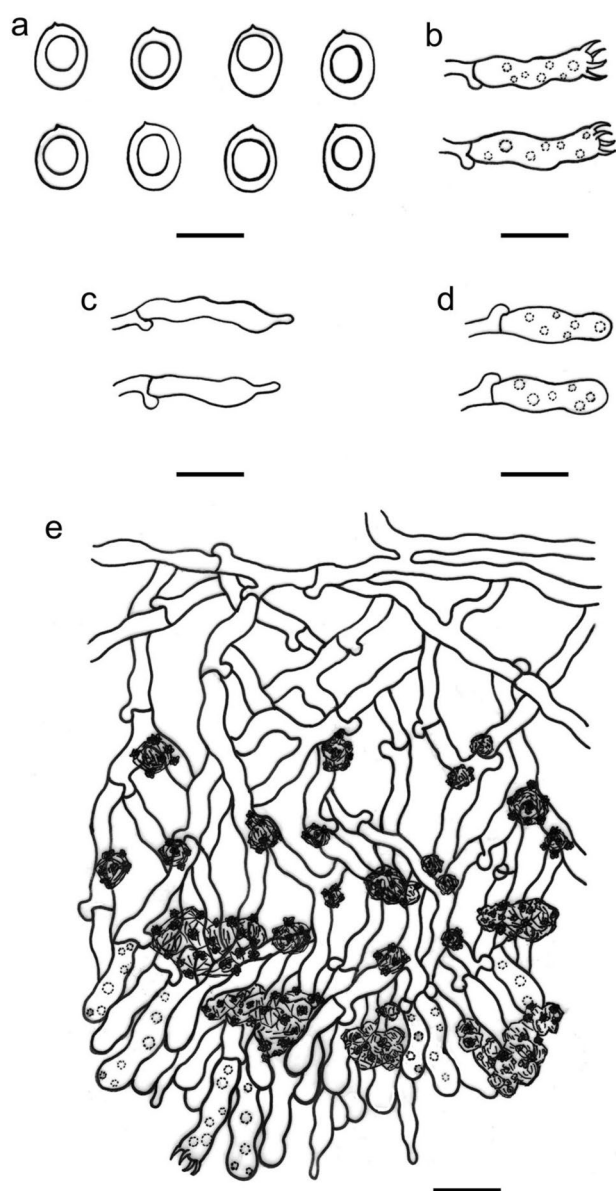
*Materials examined*: China, Sichuan Province, Ganzi Tibetan Autonomous Prefecture, Jiulong County, on fallen branch of angiosperm, 10 August 2019, L.W. Zhou, LWZ 20190810-6b (HMAS, **holotype**).

*GenBank* number: ITS = OQ540901.

*Notes*: *Lyomyces juniperi* resembles *L. crystallina* for sharing annual, resupinate, adnate basidiomes, slightly grandinoid hymenophore, fusoid cystidia with subulate apex, and ellipsoid basidiospores; however, *L. juniperi* differs in its larger basidiospores (5–6.5 × 3.5–4 µm, Langer 1994).

*Lyomyces guttulatus* Xue W. Wang & L.W. Zhou, *sp. nov.*





**Fig. 136** Microscopic structures of *Lyomyces guttulatus* (LWZ 20200921-29a, **holotype**). **a** Basidiospores. **b** Basidia. **c** Cystidia. **d** Basidioles. **e** Section in hymenium. Scale bars: **a** = 5  $\mu$ m, **b–e** = 10  $\mu$ m

*Index Fungorum* number: IF900294; *Facesoffungi* number: FoF 14057; Figs. 135, 136

*Etymology*: guttulatus (Lat.) referring to the numerous oil-like globules on basidia.

*Holotype*: LWZ 20200921-29a (HMAS).

*Diagnosis*: Characterized by annual, resupinate, adnate basidiomes, smooth to slightly grandinioid hymenophore, crystalline hyphae, tapering cystidia, subclavate to cylindrical basidia with numerous oil-like globules and broadly ellipsoid basidiospores.

*Basidiomes* annual, resupinate, adnate, cracked and brittle when dry, without odour. *Hymenophore* smooth to slightly

grandinioid, lime to cream colored. *Margin* concolorous with subiculum, abrupt.

*Hyphal system* monomitic; generative hyphae with numerous clamp connections, hyaline, dichotomous branching, interwoven, thin-walled. *Subhymenial hyphae* frequently encrusted by crystals, 2.5–4.5  $\mu$ m in diam. *Tapering cystidia* colourless, smooth, thin-walled, ca. 20  $\times$  3  $\mu$ m. *Basidia* subclavate to cylindrical, with numerous oil-like globules, ca. 20  $\times$  4  $\mu$ m, with four sterigmata and a basal clamp connection; *basidioles* abundant, similar in shape to basidia, but slightly smaller. *Basidiospores* broadly ellipsoid, with a large oily drop, hyaline, smooth, thin-walled, IKI–, slightly CB +, 4–6  $\times$  3–4  $\mu$ m,  $L = 4.98 \mu$ m,  $W = 3.47 \mu$ m,  $Q = 1.43–1.44$  (60/2).

*Material examined*: China, Sichuan Province, Liangshan Yi Autonomous Prefecture, Leibo County, Mamize Nature Reserve, on fallen trunk of *Picea*, 21 September 2020, L.W. Zhou, LWZ 20200921-29a (HMAS, **holotype**). China, Sichuan Province, Yaan, Shimian County, Hongba Nature Reserve, on fallen branch of angiosperm, 10 August 2019, L.W. Zhou, LWZ 20190810-20b (HMAS).

*GenBank* numbers: LWZ 20190810-20b: ITS = OQ540898; LSU = OQ540858; LWZ 20200921-29a: ITS = OQ540899; LSU = OQ540859.

*Notes*: *Lyomyces niveus* and *L. sambuci* resembles *L. guttulatus* by having resupinate basidiomes, light colored hymenophore and crystalline hyphae. However, *L. niveus* differs from *L. guttulatus* in having capitate, fusiform cystidia and barreled basidia (Luo et al. 2021), while *L. sambuci* differs in its capitate cystidia (Langer 1994).

*Lyomyces niveus* C.L. Zhao ex L.W. Zhou & Xue W. Wang, *sp. nov.*

*Index Fungorum* number: IF900293; *Facesoffungi* number: FoF 14056.

Based on *Lyomyces niveus* C.L. Zhao, in Luo, Chen & Zhao, *Nordic J Bot.*(e03414): 7 (2021), invalid name, not effectively published.

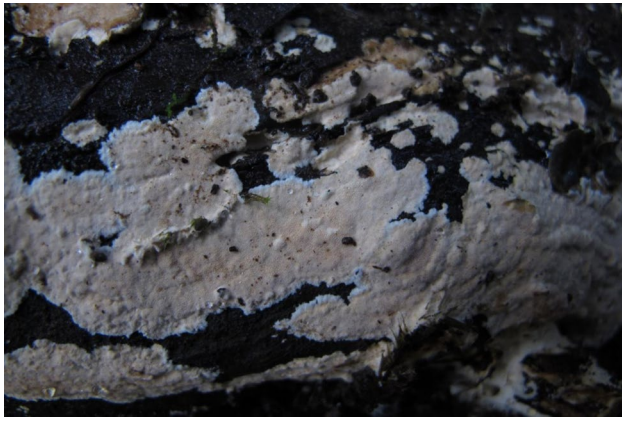
*Holotype*: CLZhao 6496 (SWFC).

*Basidiomes* annual, resupinate, subcoriaceous when fresh, becoming pruinose upon drying, up to 20 cm long and 3.5 cm wide, 50–130  $\mu$ m thick. *Hymenial surface* smooth, white when fresh, turning white to pale buff upon drying. *Margin* indistinct, white.

*Hyphal system* monomitic; generative hyphae with clamp connections, colorless, thin-walled, frequently branched; subhymenium with moderately encrusted crystals, 1.5–4.0  $\mu$ m in diameter; IKI–, CB–; tissues unchanged in KOH.

*Cystidia* of two types: 1) capitate cystidia colorless, thin-walled, smooth, 12.5–20.5  $\times$  4.5–5.0  $\mu$ m; 2) fusiform cystidia colorless, thin-walled, smooth, 12.5–22.0  $\times$  3.0–5.0  $\mu$ m; *cystidioles* absent. *Basidia* barreled, with 4 sterigmata and a





**Fig. 137** Basidiomes of *Lyomyces tasmanicus* (LWZ 20180515–17, holotype)

basal clamp connection,  $9.5\text{--}15.0 \times 3.5\text{--}5.5\ \mu\text{m}$ ; *basidioles* abundant, in shape similar to basidia, but slightly smaller.

*Basidiospores* broadly ellipsoid, colorless, thin-walled, smooth, IKI–, cyanophilous, with a single oil-like globule,  $(3.0\text{--})3.5\text{--}5.0(\text{--}6.5) \times (2.5\text{--})3.0\text{--}4.0(\text{--}5.0)\ \mu\text{m}$ ,  $L = 4.45\ \mu\text{m}$ ,  $W = 3.31\ \mu\text{m}$ ,  $Q = 1.28\text{--}1.46$  ( $n = 150/5$ ).

*Material examined*: China, Yunnan Province, Yuxi, Xinning County, Mopanshan National Forestry Park,  $101^\circ 57'\text{E}$ ,  $23^\circ 57'\text{N}$ , 2185 m a.s.l., on the trunk of *Pinus armandii*, leg. 19 January 2018, C.L. Zhao, CLZhao 6496 (SWFC, holotype).

*GenBank numbers*: CLZhao 6496: ITS = MZ262545, LSU = MZ262530.

*Notes*: *Lyomyces niveus* was published with a detailed description and phylogenetic analyses inferred from combined ITS and nLSU regions (Luo et al. 2021). However, it was indicated that the holotype (CLZhao 6496) was deposited at two separated herbaria (SWFC and HKAS, Luo et al. 2021), which is contrary to Art. 40.7 of the International Code of Nomenclature for algae, fungi, and plants (Turland et al. 2018). The current phylogeny (Fig. 132) confirms the phylogenetic conclusion of Luo et al. (2021), and thus we validate *L. niveus* here by reproducing the original description and selecting the piece of CLZhao 6496 at SWFC as the holotype. Then, the other piece of CLZhao 6496 at HKAS should be the isotype.

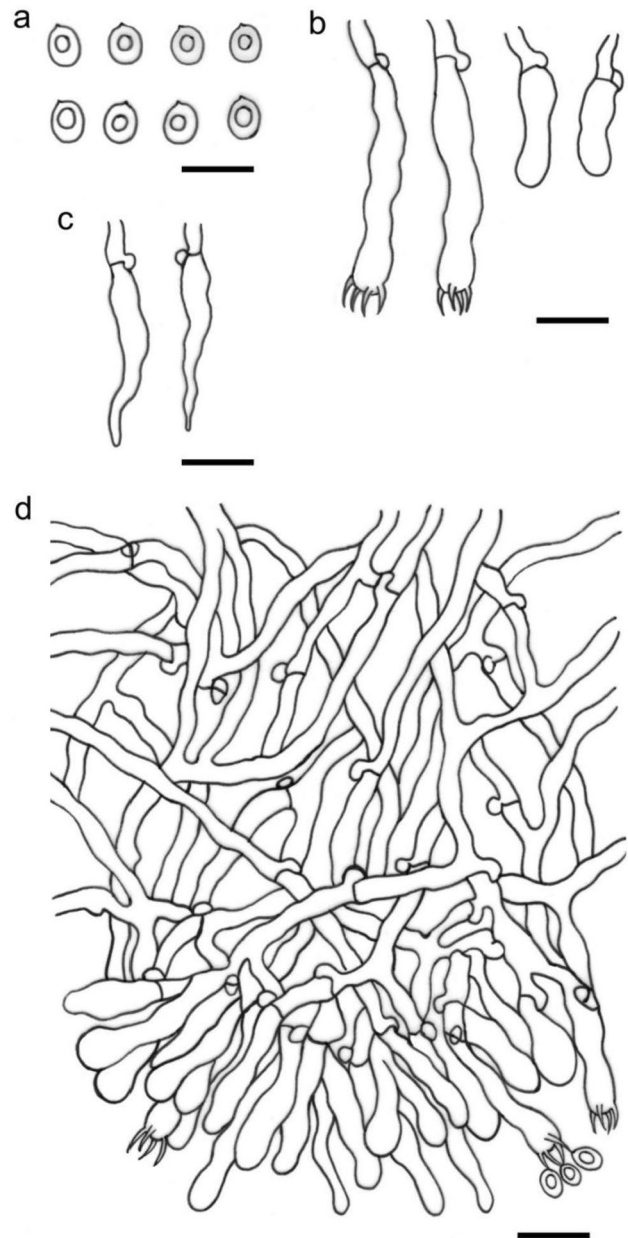
***Lyomyces tasmanicus*** Xue W. Wang & L.W. Zhou, *sp. nov.*

*Index Fungorum* number: IF900295; *Facesoffungi* number: FoF 14058; Figs. 137, 138

*Etymology*: tasmanicus (Lat.) referring to the type locality Tasmania.

*Holotype*: LWZ 20180515–17 (HMAS).

*Diagnosis*: Characterized by annual, resupinate, adnate basidiomes, smooth, white to cream hymenophore, fusoid



**Fig. 138** Microscopic structures of *Lyomyces tasmanicus* (LWZ 20180515–17, holotype). **a** Basidiospores. **b** Basidia. **c** Cystidia. **d** Basidioles. **e** Section through a basidiome. Scale bars: **a** =  $5\ \mu\text{m}$ , **b–e** =  $10\ \mu\text{m}$

cystidia with subulate apex, subcylindrical basidia, and broadly ellipsoid basidiospores.

*Basidiomes* annual, resupinate, adnate, cracked and brittle when dry, without odour. *Hymenophore* smooth, white to cream. *Margin* concolorous with subiculum, abrupt.

*Hyphal system* monomitic; *generative hyphae* with clamp connections, hyaline, dichotomous branching, interwoven, thin-walled,  $2\text{--}3.5\ \mu\text{m}$  in diam, without encrustation. *Cystidia* fusoid with tapering apex,  $25\text{--}30 \times 3.5\text{--}4\ \mu\text{m}$ . *Basidia* subcylindrical and constricted, with four sterigmata and a



**Fig. 139** Basidiomes of *Xylodon muchuanensis* (LWZ 20200819-2b, holotype)

clamp connection at the base,  $32\text{--}35 \times 4.5\text{--}6\text{ }\mu\text{m}$ ; *basidioles* subclavate to suburniform,  $13\text{--}20 \times 4.5\text{--}5.5\text{ }\mu\text{m}$ . *Basidiospores* broadly ellipsoid, usually with an oily drop, hyaline, smooth, thin-walled, IKI–, CB–,  $5\text{--}5.4(-5.5) \times 4\text{--}4.7(-4.8)\text{ }\mu\text{m}$ ,  $L = 5.25\text{ }\mu\text{m}$ ,  $W = 4.36\text{ }\mu\text{m}$ ,  $Q = 1.20$  (30/1).

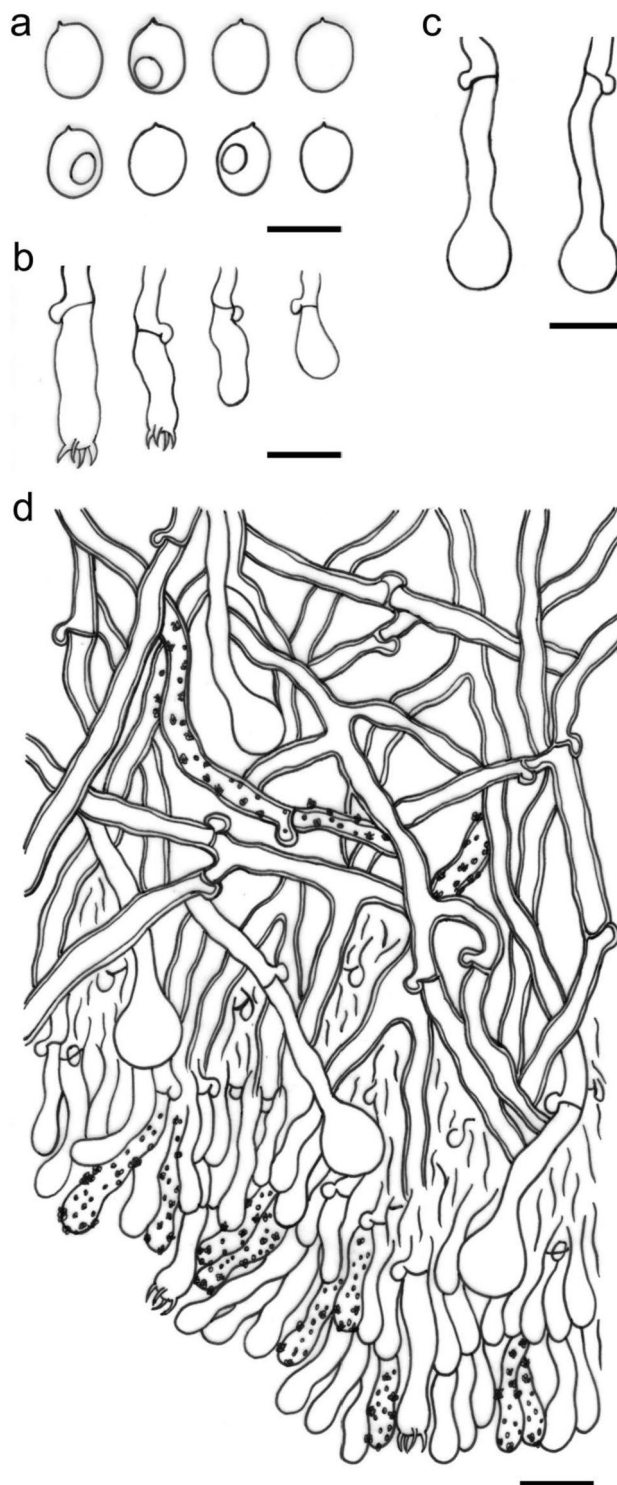
**Material examined:** Australia, Tasmania, Tahune Adventures, The look-in look-out, on fallen twig of angiosperm, 15 May 2018, L.W. Zhou, LWZ 20180515–17 (HMAS, holotype).

**GenBank number:** ITS = OQ540900, LSU = OQ540860.

**Notes:** *Lyomyces tasmanicus* has a close relationship with *L. crystallina* from a phylogenetic perspective (Fig. 132). These two new species also have similar morphological characters, except that *L. crystallina* has encrusted generative hyphae and narrower basidiospores ( $3.1\text{--}3.4\text{ }\mu\text{m}$ ). *Lyomyces organensis* resembles *L. tasmanicus* for sharing annual, resupinate, adnate basidiomes and fusoid cystidia. However, *L. organensis* differs in its crystalline hyphal system, and ellipsoid to narrowly ellipsoid, thin- to slightly thick-walled, narrower basidiospores ( $2.5\text{--}3.5\text{ }\mu\text{m}$  in width, Yurchenko et al. 2017). *Lyomyces bambusinus* is also similar to *L. tasmanicus* by its annual, resupinate, adnate basidiomes, white to cream hymenophore, and fusoid cystidia, but it differs in the presence of capitate cystidia, thick-walled basidiospores and the growth on bamboo (Chen and Zhao 2020).

***Xylodon* (Pers.) Gray.**

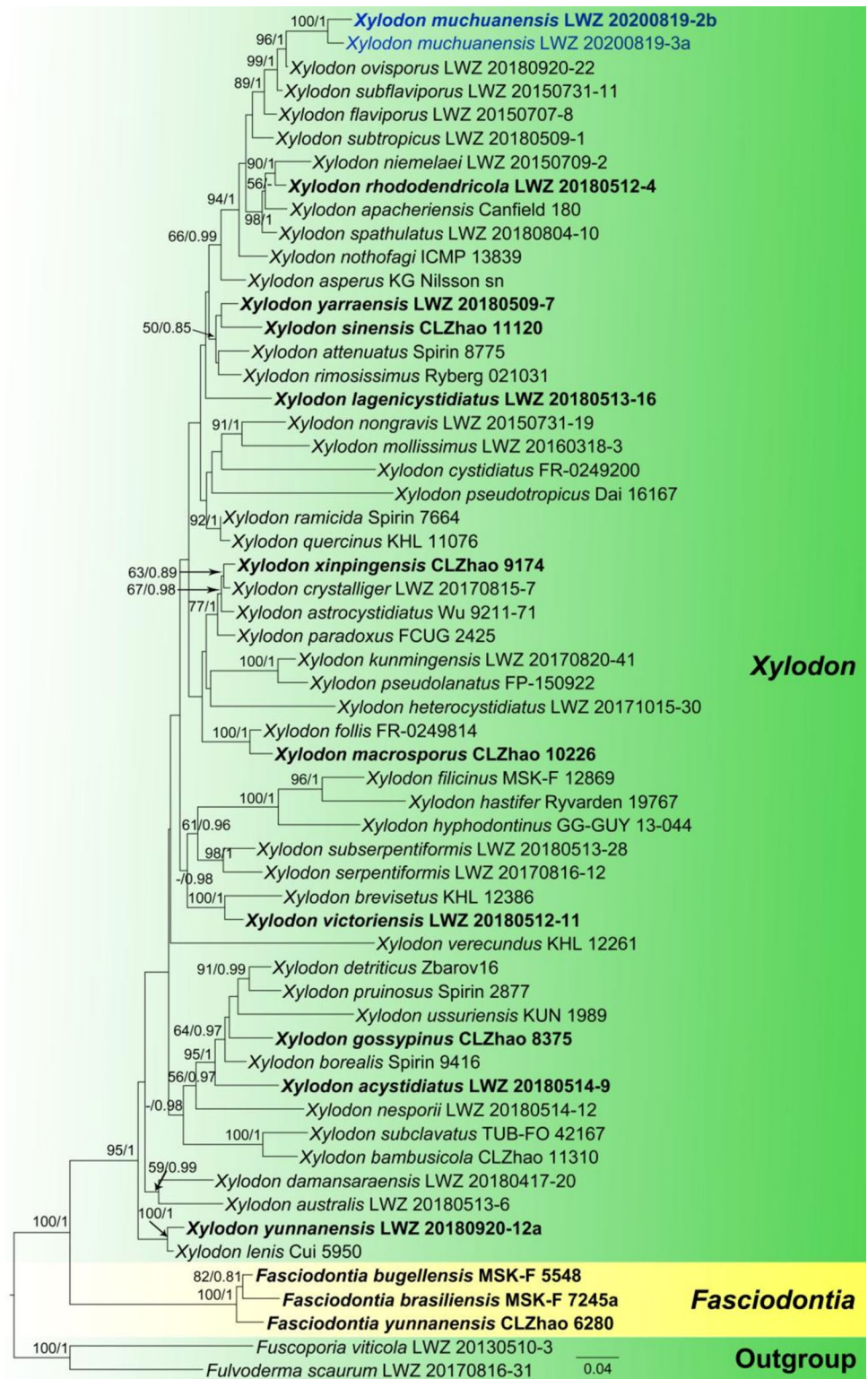
**Notes:** *Xylodon* typified by *X. quercinus* is a well supported monophyletic genus and has a priority over *Schizopora* the type genus of *Schizoporaceae*. See Wang et al. (2021a) for the latest comprehensive summarization of *Xylodon*.



**Fig. 140** Microscopic structures of *Xylodon muchuanensis* (LWZ 20200819-2b, holotype). **a** Basidiospores **b** Basidia **c** Cystidia **d** Basidioles **e** Section through a basidiomes. Scale bars: **a** =  $5\text{ }\mu\text{m}$ , **b–e** =  $10\text{ }\mu\text{m}$



**Fig. 141** Phylogram generated by the maximum likelihood algorithm based on combined nLSU and ITS sequence data is presented along with the bootstrap values and the Bayesian posterior probabilities above 50% and 0.8, respectively, at the nodes. Type specimens are in bold and the isolates of new species characterized are in blue



***Xylodon muchuanensis*** Xue W. Wang & L.W. Zhou, *sp. nov.*

*Index Fungorum* number: IF900297; *Facesoffungi* number: FoF 14060; Figs. 139, 140

*Etymology*: muchuanensis (Lat.) referring to the type locality Muchuan County, Sichuan Province, China.

*Holotype*: LWZ 20200819-2b (HMAS).

*Diagnosis*: Characterized by annual, resupinate, adnate basidiomes, poroid, cream to buff hymenophore,





**Fig. 142** Basidiomes of *Ginnsia laricicola* (LWZ 20180830–9, holotype)

a monomitic hyphal system, the presence of capitate cystidia, clavate to subcylindrical basidia, and broadly ellipsoid basidiospores.

*Basidiomes* annual, resupinate, adnate, cracked and brittle when dry. *Hymenophore* poroid, cream to buff at young part and cinnamon-buff at old part. *Margin* concolorous or slightly paler than subiculum, abrupt.

*Hyphal system* monomitic; *generative hyphae* with clamp connections, hyaline, dichotomous branching, interwoven, slightly thick-walled, 3.5–4.5  $\mu\text{m}$  in diam, occasionally with encrustation. *Capitate cystidia* embedded in hymenium, ca.  $30 \times 3.5 \mu\text{m}$ , with a round swollen top, about 7.5–8.5  $\mu\text{m}$  in diam. *Basidia* clavate to subcylindrical,  $15\text{--}20 \times 4\text{--}5 \mu\text{m}$ , with four sterigmata and a clamp connection at the base; *basidioles* similar in shape to basidia but smaller. *Basidiospores* broadly ellipsoid, with an oily drop, hyaline, smooth, thin-walled, IKI–, slightly CB+,  $(4.1\text{--})4.2\text{--}5.2\text{--}(5.3) \times 3.1\text{--}3.6 \mu\text{m}$ ,  $L = 4.46 \mu\text{m}$ ,  $W = 3.32 \mu\text{m}$ ,  $Q = 1.33\text{--}1.36$  (60/2).

*Material examined*: China, Sichuan Province, Leshan, Muchuan County, on fallen branch of angiosperm, 19 August 2020, L.W. Zhou, LWZ 20200819-2b (HMAS, **holotype**); *ibid.*, on fallen trunk of angiosperm, 19 August 2020, L.W. Zhou, LWZ 20200819-3a (HMAS).

*GenBank numbers*: LWZ 20200819-2b: ITS = OQ540902; LSU = OQ540861; LWZ 20200819-3a: ITS = OQ540903; LSU = OQ540862.

*Notes*: Phylogenetically, *Xylodon muchuanensis* groups with several other poroid species of *Xylodon* (Fig. 141). Of these species, *X. muchuanensis* is most similar to *X. taiwanianus* by sharing poroid hymenophore and ellipsoid basidiospores; however, *Xylodon taiwanianus* differs from *X. muchuanensis* by its suburniform basidia and the presence of resinous matter on the top of capitate cystidia (Wu 2001).

## *Hymenochaetales*, genus *incertae sedis*

*Ginnsia* Sheng H. Wu & Hallenb.

*Notes*: *Ginnsia* typified by *G. viticola* is a monotypic genus segregated from *Phanerochaete* (Wu et al. 2010a). The placement of *G. viticola* in *Hymenochaetales* was supported by phylogenetic analyses (Wu et al. 2010a; Ghobad-Nejhad et al. 2015).

*Ginnsia laricicola* Xue W. Wang & L.W. Zhou, *sp. nov.*

*Index Fungorum* number: IF900285; *Facesoffungi* number: FoF 14049; Figs. 142, 143

*Etymology*: *laricicola* (Lat.) referring to the host genus *Larix*.

*Holotype*: LWZ 20180830–9 (HMAS).

*Diagnosis*: Characterized by annual resupinate basidiomes, byssoid to fibrillose subiculum, cinnamon to yellowish brown hymenophore, a monomitic hyphal system with densely encrusted subicular hyphae, cylindrical cystidia, clavate basidia, and ellipsoid to broadly ellipsoid basidiospores.

*Basidiomes* resupinate, annual, flaking easily off subiculum when dry. *Subiculum* byssoid to fibrillose. *Hymenophore* smooth, cinnamon to yellowish brown; *margin* abrupt, concolorous with subiculum.

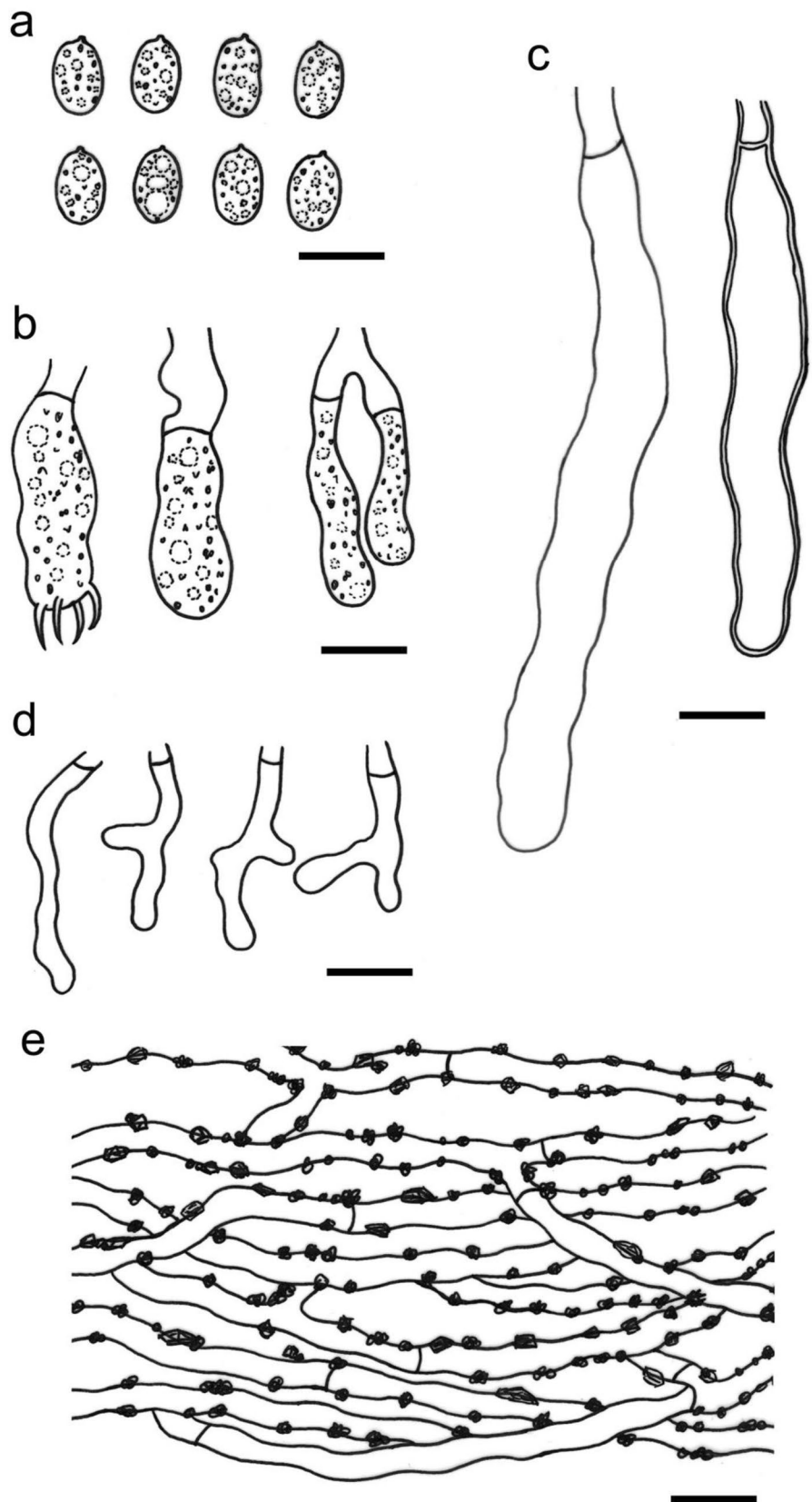
*Hyphal system* monomitic; *generative hyphae* hyaline, thin-walled, simple septate. *Subicular hyphae* hyaline, thin-walled, frequently branched, simple septate, interwoven, densely encrusted, 3.5–4  $\mu\text{m}$  in diam. *Subhymenium* thin, poorly delimited from context. *Cystidia* cylindrical with obtuse apex, thin- to slightly thick-walled,  $60\text{--}90 \times 9\text{--}10 \mu\text{m}$ . *Basidia* clavate with stalked bases, thin-walled, simple septate with four sterigmata, guttulate,  $20\text{--}30 \times 8.5\text{--}9.5 \mu\text{m}$ ; *basidioles* in shape similar to basidia but slightly smaller. *Hyphidia* hyaline, thin-walled, smooth, usually branched, 2.5–3.5  $\mu\text{m}$  in diam. *Basidiospores* ellipsoid to broadly ellipsoid, with blunt apex, hyaline, thin-walled, guttulate, IKI–, CB–,  $(8.5\text{--})9\text{--}9.5 \times 5\text{--}6 \mu\text{m}$ ,  $L = 9.29 \mu\text{m}$ ,  $W = 5.52 \mu\text{m}$ ,  $Q = 1.66\text{--}1.68$  ( $n = 90/3$ ).

*Material examined*: China, Shaanxi Province, Baoji, Mei County, Taibai Mountain, on stump of *Larix*, 30 August 2018, L.W. Zhou, LWZ 20180830–9 (HMAS, **holotype**); *ibid.*, LWZ 20180830–5 (HMAS), LWZ 20180830–6 (HMAS).

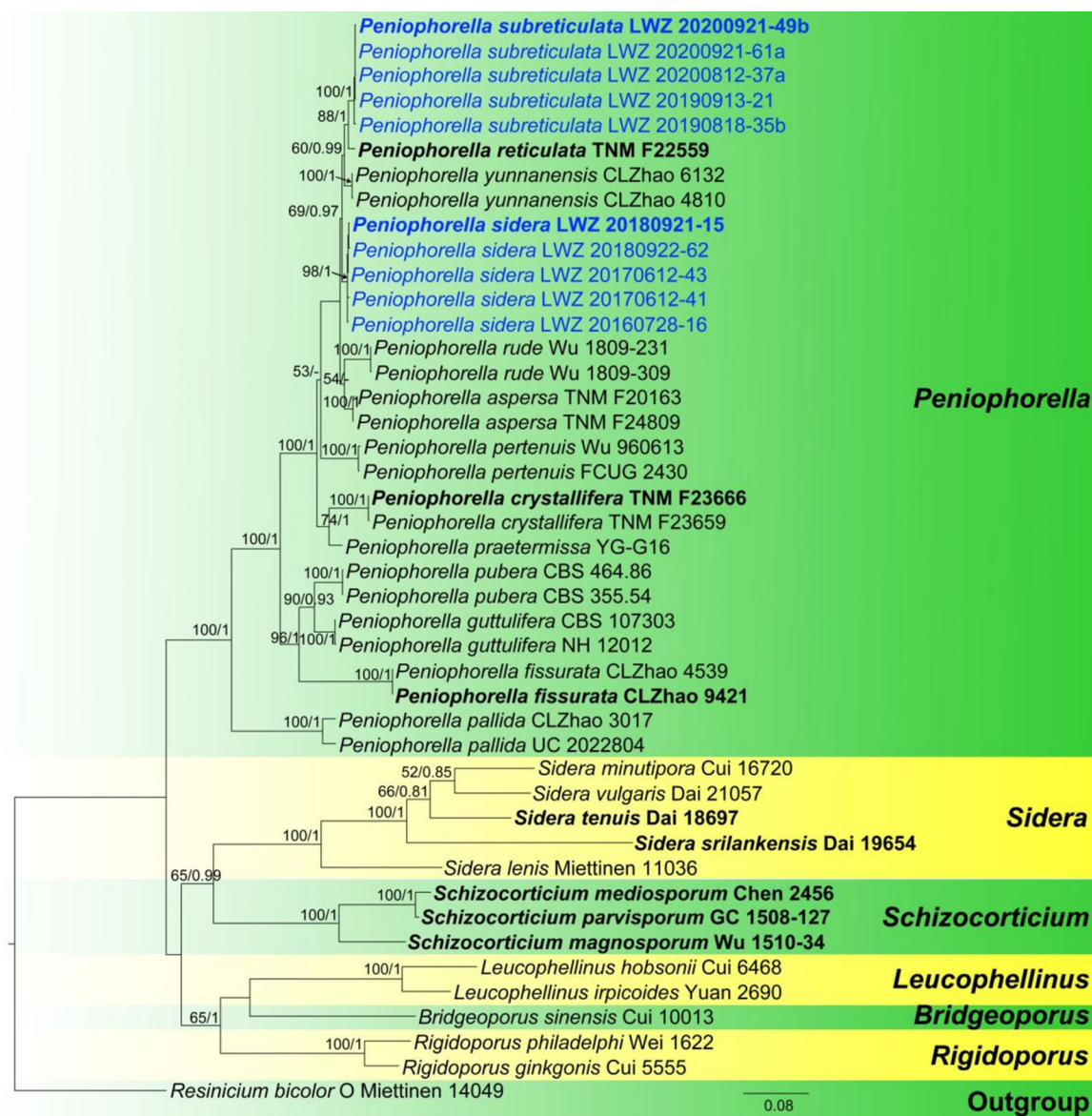
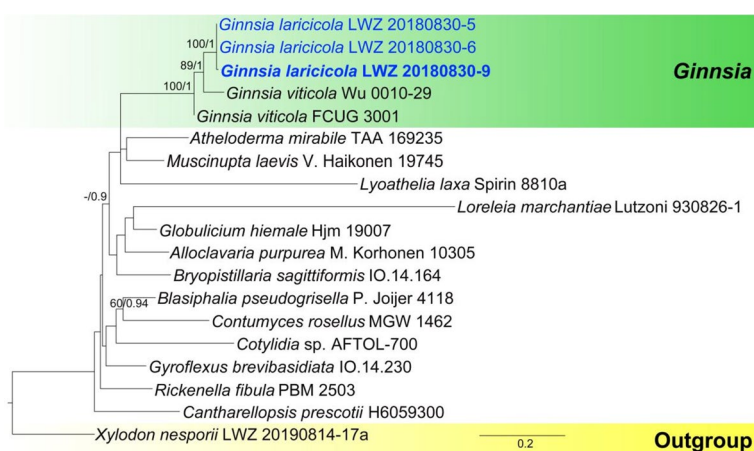
*GenBank numbers*: LWZ 20180830–5: ITS = OQ540881; LSU = OQ540842; LWZ 20180830–6: ITS = OQ540882; LSU = OQ540843; LWZ 20180830–9: ITS = OQ540883; LSU = OQ540844.

*Notes*: *Ginnsia laricicola* resembles the generic type *G. viticola*; however, *G. viticola* differs in its slightly longer cystidia (60–125  $\mu\text{m}$ ) and basidia (25–50  $\mu\text{m}$ , Burdsall 1985). Moreover, *G. laricicola* was only found on *Larix*,

**Fig. 143** Microscopic structures of *Ginnsia laricicola* (LWZ 20180830–9, **holotype**). **a** Basidiospores. **b** Basidia and basidioles. **c** Cystidia. **d** Hyphidia. **e** Subicular hyphae. Scale bars: **a–e** = 10  $\mu$ m



**Fig. 144** Phylogram generated by the maximum likelihood algorithm based on combined nLSU and ITS sequence data is presented along with the bootstrap values and the Bayesian posterior probabilities above 50% and 0.8, respectively, at the nodes. Type specimens are in bold and the isolates of new species characterized are in blue



**Fig. 145** Phylogram generated by the maximum likelihood algorithm based on combined nLSU and ITS sequence data is presented along with the bootstrap values and the Bayesian posterior probabilities

above 50% and 0.8, respectively, at the nodes. Type specimens are in bold and the isolates of new species characterized are in blue





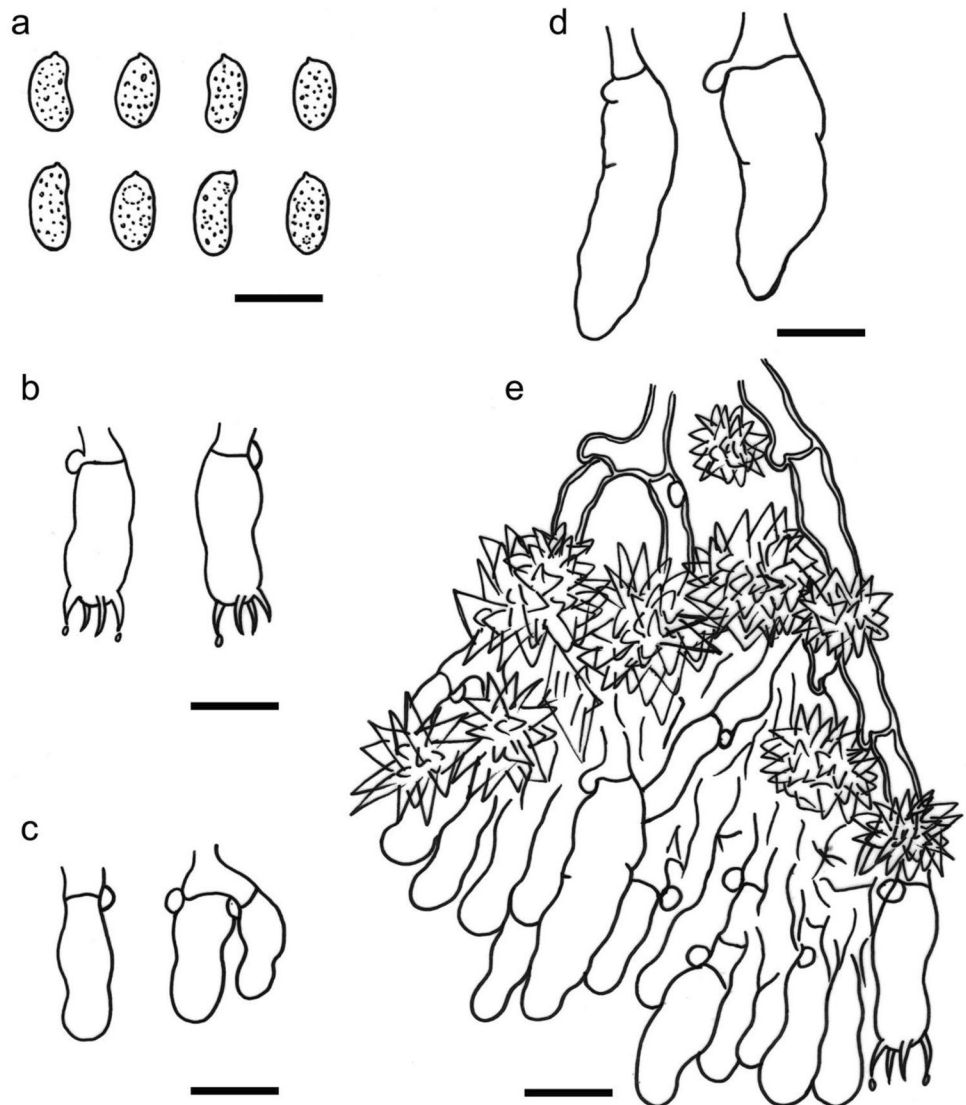
**Fig. 146** Basidiomes of *Peniophorella sidera* (LWZ 20180921–15, holotype)

while *G. viticola* has a wider host range. Phylogenetically, two vouchers labeled as *G. viticola* are separated from each other (Fig. 144), which indicates that the concept of *G. viticola* may be a species complex and needs to be further clarified.

***Peniophorella* P. Karst.**

**Notes:** *Peniophorella* typified by *P. pubera* was introduced as a monotypic genus (Karsten 1889). After a long time of oblivion, Larsson (2007b) reinstated the independency of *Peniophorella* from *Hyphoderma* in *Hymenochaetales*. Since then, the known species number of *Peniophorella* has been improved to about 30 (Yurchenko et al. 2020). Although several papers placed *Peniophorella* in *Rickenellaceae* (He et al. 2019; Olariaga et al. 2020), its taxonomic position at the family level in *Hymenochaetales* needs to be further clarified with more comprehensive phylogenetic analyses,

**Fig. 147** Microscopic structures of *Peniophorella sidera* (LWZ 20180921–15, holotype). **a** Basidiospores. **b** Basidia. **c** basidioles. **d** Leptocystidia. **e** Section through hymenium. Scale bars: **a–e** = 10  $\mu$ m





**Fig. 148** Basidiomes of *Peniophorella subreticulata* (LWZ 20200921-49b, **holotype**)

which is beyond the the current scope of phylogenetic analysis (Fig. 145).

***Peniophorella sidera*** Xue W. Wang & L.W. Zhou, *sp. nov.*

*Index Fungorum* number: IF900287; *Facesoffungi* number: FoF 14051; Figs. 146, 147

*Etymology*: *sidera* (Lat.) referring to the star-like crystals covering subhymenial hyphae.

*Holotype*: LWZ 20180921-15 (HMAS).

*Diagnosis*: Characterized by annual, resupinate basidiomes, grandinioid, white to cream hymenophore, a monomitic hyphal system, star-like crystals, fusoid to subcylindrical cystidia, urniform basidia, and ellipsoid to subcylindrical basidiospores.

*Basidiomes* annual, resupinate, adnate, ceraceous, without odour or taste when fresh, becoming cracked upon drying. *Hymenophore* grandinioid, white to cream, margin abrupt.

*Hyphal system* monomitic; *generative hyphae* with clamp connections, hyaline. *Subicular hyphae* thin- to slightly thick-walled, smooth, 4.5–5 µm in diam. *Subhymenial hyphae* thin- to slightly thick-walled, strongly encrusted with star-like crystals, moderately branched, 4–5.5 µm in diam. *Cystidia* scattered, embedded in hymenium, fusoid to subcylindrical, somewhat constricted, smooth, thin-walled, 30–35 × 9–12 µm. *Basidia* urniform, thin-walled, smooth, with four sterigmata and a basal clamp connection, 17–18 × 7.5–8.5 µm; *basidioles* in shape similar to basidia but slightly smaller. *Basidiospores* ellipsoid to subcylindrical, with flat or slightly concave adaxial side, thin-walled, IKI–, CB–, (7.5–)8.2–10 (–10.2) × (4–)4.1–5.1 (–5.3) µm, L = 8.95 µm, W = 4.55 µm, Q = 1.95–1.98 (n = 150/5).

*Material examined*: China, Yunnan Province, Baoshan, Gaoligong Mountains National Nature Reserve, Baihua Ridge, on fallen branch of angiosperm, 21 September 2018, L.W. Zhou, LWZ 20180921-15 (HMAS, **holotype**); *ibid.*,

on fallen twig of *Pinus*, 22 September 2018, L.W. Zhou, LWZ 20180922-62 (HMAS); Hainan Province, Bawangling National Nature Reserve, on fallen branch of angiosperm, 12 June 2017, L.W. Zhou, LWZ 20170612-41 (HMAS); *ibid.*, on fallen twig of angiosperm, 12 June 2017, L.W. Zhou, LWZ 20170612-43 (HMAS); Hunan Province, Yizhang County, Mangshan National Nature Reserve, on fallen branch of angiosperm, 28 July 2016, L.W. Zhou, LWZ 20160728-16 (HMAS).

*GenBank numbers*: LWZ 20180921-15: ITS = OQ540892; LSU = OQ540850; LWZ 20180922-62: ITS = OQ540893; LSU = OQ540851; LWZ 20170612-41: ITS = OQ540890; LSU = OQ540848; LWZ 20170612-43: ITS = OQ540891; LSU = OQ540849; LWZ 20160728-16: ITS = OQ540889.

*Notes*: *Peniophorella sidera* is distinct from other species of *Peniophorella* by the subicular hyphae encrusted by star-like. *Peniophorella reticulata* is similar to *P. sidera* by the presence of peg-like hyphal structures, smooth, immersed cystidia, and the absence of stephanocysts and echinocysts; however, *P. reticulata* differs in its wider basidiospores (5–6 µm in width, Yurchenko et al. 2020). *Peniophorella rude* resembles *P. sidera* by similar hymenophoral configuration, but differs in the presence of stephanocysts and wider basidiospores (6 µm in width, Larsson 2007b).

***Peniophorella subreticulata*** Xue W. Wang & L.W. Zhou, *sp. nov.*

*Index Fungorum* number: IF900288; *Facesoffungi* number: FoF 14050; Figs. 148, 149

*Etymology*: *subreticulata* (Lat.) referring to the similarity to *P. reticulata*.

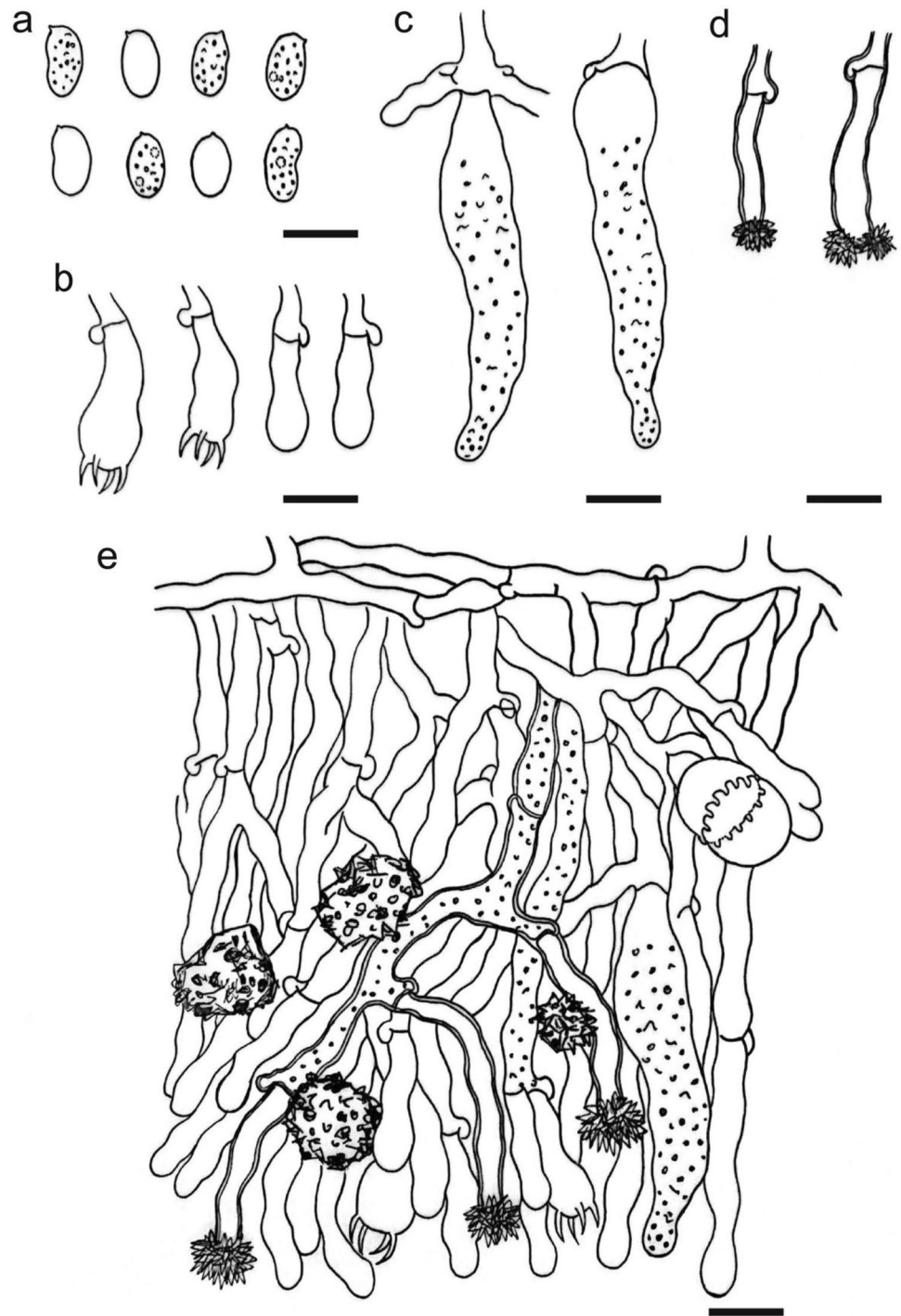
*Holotype*: LWZ 20200921-49b (HMAS).

*Diagnosis*: Characterized by annual, resupinate, basidiomes, grandinioid to odontoid, white to cream hymenophore, a monomitic hyphal system, embedded, fusoid to subcylindrical leptocystidia and subcylindrical asterocystidia, the presence of stephanocysts, and ellipsoid to oblong basidiospores.

*Basidiomes* annual, resupinate, adnate, ceraceous, without odour or taste when fresh, becoming cracked upon drying. *Hymenophore* grandinioid to odontoid, white to cream when fresh, turn to cream upon drying, *margin* abrupt.

*Hyphal system* monomitic; *generative hyphae* with clamp connections, hyaline. *Subicular hyphae* thin-walled, 4–5 µm in diam. *Subhymenial hyphae* thin- to slightly thick-walled, occasionally encrusted with granules, moderately branched, 4.5–5.5 µm in diam. *Stephanocysts* present in subhymenium. *Cystidia* two types: 1) leptocystidia scattered, embedded in subhymenium and hymenium, fusoid to subcylindrical, thin-walled, often with granules on the surface, 45–50 × 9–10 µm; 2) asterocystidia subcylindrical, thick-walled, 15–35 × 4–5.5 µm. Large solitary or aggregated

**Fig. 149** Microscopic structures of *Peniophorella subreticulata* (LWZ 20200921-49b, **holotype**). **a** Basidiospores **b** Basidia and basidioles **c** Leptocystidia **d** Hyphidia **e** Section through a basidiomes. Scale bars: **a–e** = 10  $\mu$ m



crystals occurring in lower subhymenium and between hyphae in peg-like projections. *Basidia* clavate, thin-walled, smooth, with four sterigmata and a basal clamp connection,  $15\text{--}20 \times 7.5\text{--}8\text{ }\mu\text{m}$ ; *basidioles* in shape similar to basidia but slightly smaller. *Basidiospores* narrowly ellipsoid to oblong with flat or slightly concave adaxial side, thin-walled, IKI–, CB–,  $(7.5\text{--})7.8\text{--}9.3(\text{--}10.3) \times 3.8\text{--}4.7(\text{--}5.1)\text{ }\mu\text{m}$ ,  $L=8.51\text{ }\mu\text{m}$ ,  $W=4.33\text{ }\mu\text{m}$ ,  $Q=1.95\text{--}1.99$  ( $n=90/3$ ).

*Material examined*: China, Sichuan Province, Liangshan Yi Autonomous Prefecture, Leibo County, Mamize Nature Reserve, on fallen branch of gymnosperm, 21 September 2020, L.W. Zhou, LWZ 20200921-49b (HMAS, **holotype**); *ibid.*, on fallen trunk of *Picea*, 21 September 2020, L.W. Zhou, LWZ 20200921-61a (HMAS); Liangshan Yi autonomous prefecture, Meigu County, Dafengding National Nature Reserve, on fallen branch of *Cryptomeria fortunei*,





**Fig. 150** Basidiomes of *Meruliopsis crystallina* (LWZ 20190726–28, holotype)

18 August 2019, L.W. Zhou, LWZ 20190818–35b (HMAS); Ganzi Tibetan Autonomous Prefecture, Jiulong County, Wuxuhai Scenic Spot, on fallen trunk of *Picea*, 13 September 2019, L.W. Zhou, LWZ 20190913–21 (HMAS); *ibid.*, on fallen branch of *Picea*, 12 August 2020, L.W. Zhou, LWZ 20200812–37a (HMAS).

**GenBank numbers:** LWZ 20200921–49b: ITS = OQ540884; LSU = OQ540845; LWZ 20200921–61a: ITS = OQ540885; 20190818–35b: ITS = OQ540887; LWZ 20190913–21: ITS = OQ540888; LSU = OQ540847; LWZ 20200812–37a: ITS = OQ540886; LSU = OQ540846.

**Notes:** *Peniophorella reticulata* phylogenetically groups with *P. subreticulata*. Morphologically, *P. reticulata* differs in wider basidiospores (5–6 µm in width,  $Q = 1.5–1.7$ ), and the absence of stephanocysts and asterocystidia (Yurchenko et al. 2020).

### **Polyporales** Gäum.

**Notes:** *Polyporales* is a large order of poroid to irpicoid to dentate, sometimes lamellate macro-fungi having roughly 1800 species under 216 genera and 13 families described worldwide (Kirk et al. 2008). Binder et al. (2005, 2013) divided *Polyporales* into four major clades based on molecular phylogenetic studies such as core polyporoid clade, phlebioid clade, *Antrodia* clade and residual polyporoid clade. Some genera have uncertain positions in this order at the family level. Most of the genera are polyphyletic. Therefore, it is necessary to construct a phylogenetic tree to systematically show the position of the taxa of *Polyporales*. The latest updated accounts of *Polyporales* in Phookamsak et al. (2019) and Wijayawardene et al. (2020).

### **Irpicaceae** Spirin & Zmitr.

**Notes:** *Irpicaceae* introduced by Spirin (2003) with *Irpex* as the type genus is one of the three families of the phlebioid clade accommodating wood-inhabiting fungi in *Polyporales*

(Justo et al. 2017). Chen et al. (2021b) updated the taxonomic circumscription of *Irpicaceae* from both morphological and phylogenetic perspective, and accepted 13 genera in this family. Species diversity in *Irpicaceae* was further explored recently by Li et al. (2022).

### **Meruliopsis** Bondartsev.

**Notes:** *Meruliopsis* typified by *M. taxicola* has long been considered to be a synonym of *Gloeoporus* (Ryvarden and Gilbertson 1993), but molecular phylogeny supported *Meruliopsis* as an independent genus (Justo et al. 2017). Chen et al. (2020b) redelimited the taxonomic concept of *Meruliopsis* according to phylogenetic analyses. *Meruliopsis* is characterized by resupinate to effused-reflexed basidiomes with meruloid to poroid hymenophore, a monomitic hyphal system with simple septate generative hyphae, and ellipsoid to cylindrical, or cylindrical to allantoid basidiospores (Chen et al. 2020b).

### **Meruliopsis crystallina** Xue W. Wang & L.W. Zhou, *sp. nov.*

**Index Fungorum number:** IF900298; **Facesoffungi number:** FoF 14061; Figs. 150, 151

**Etymology:** *crystallina* (Lat.) referring to the rhombic crystals in subicular hyphae.

**Holotype:** LWZ 20190726–28 (HMAS).

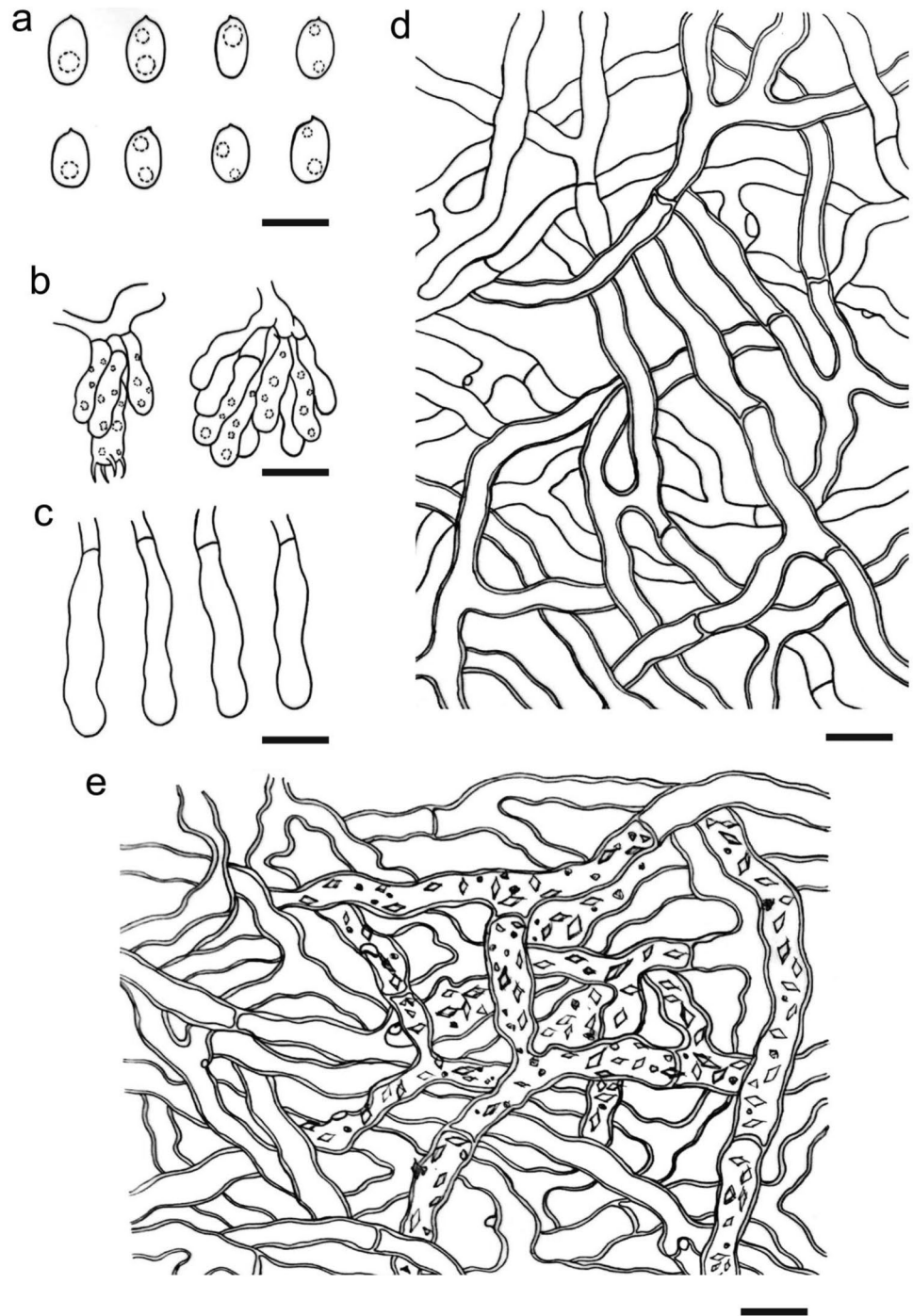
**Diagnosis:** Characterized by white to cream basidiomes, a monomitic hyphal system with strongly rhombic crystallized subicular hyphae, presence of leptocystidia, cylindrical to clavate basidia with numerous oily drops, and ellipsoid basidiospores.

**Basidiomes** annual, resupinate, effuse, adnate, membranaceous. **Pore surface** white to cream when dry; **pores** 4–5 per mm, round; **tubes** up to 65 µm deep, concolorous with pore surface; **dissepiments** up to 80 µm thick, entire, with continuous hymenium; **margin** slightly paler than pore surface, thinning out.

**Hyphal system** monomitic; **generative hyphae** simple septate. **Subicular hyphae** hyaline, thick-walled, strongly dichotomous branched, interwoven, strongly encrusted with rhombic crystals, 3.5–6.5 µm in diam. **Tramal hyphae** hyaline, slightly thick- to thick-walled, strongly dichotomous branched, interwoven, 3.5–5.5 µm in diam. **Leptocystidia** cylindrical, hyaline, projecting from hymenium, 25–30 × 4.5–5.5 µm. **Basidia** cylindrical to clavate, 4-sterigmata, with numerous oily drops, without clamp connection, 15–20 × 4–5 µm; **basidioles** in shape similar to basidia but slightly smaller. **Basidiospores** ellipsoid, hyaline, thin-walled, smooth, IKI–, CB+, usually with one or two oily drops, (3.7–)3.8–4.5 × (1.9–)2.0–2.3(–2.5) µm,  $L = 4.15$  µm,  $W = 2.17$  µm,  $Q = 1.90–1.92$  ( $n = 120/4$ ).

**Material examined:** China, Beijing, Yanqing County, Songshan National Forest Park, on fallen trunk of *Pinus*, 26

**Fig. 151** Microscopic structures of *Meruliopsis crystallina* (LWZ 20190726–28, **holotype**). **a** Basidiospores. **b** Basidia and basidioles. **c** Leptocystidia. **d** Hyphae from subiculum. **e** Hyphae from trama. Scale bars: **a**=5  $\mu$ m, **b–e**=10  $\mu$ m

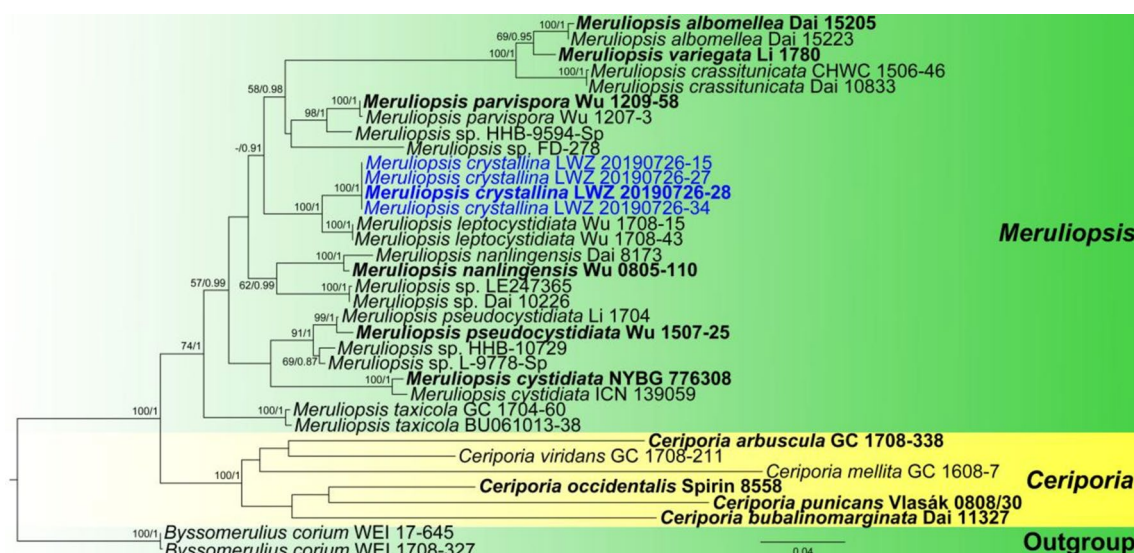


July 2019, L.W. Zhou, LWZ 20190726–28 (HMAS, **holotype**), LWZ 20190726–15 (HMAS), LWZ 20190726–27 (HMAS); *ibid.*, on fallen branch of angiosperm, 26 July 2019, L.W. Zhou, LWZ 20190726–34 (HMAS).

*GenBank numbers*: LWZ 20190726–15: ITS=OQ540904, LSU=OQ540863; LWZ 20190726–27: ITS=OQ540905, LSU=OQ540864; LWZ 20190726–28: ITS=OQ540906, LSU=OQ540865; LWZ 20190726–34: ITS=OQ540907, LSU=OQ540866.

*Notes*: Phylogenetically, *Meruliopsis crystallina* is closely related to *M. leptocystidiata* (Fig. 152). These two species share white to cream pore surface, strongly encrusted subicular hyphae and the presence of leptocystidia. However, *M. leptocystidiata* differs by smaller basidiospores ( $3\text{--}4 \times 1.5\text{--}2 \mu\text{m}$ ) and the absence of oily drops in basidia (Chen et al. 2020b).





**Fig. 152** Phylogram generated by the maximum likelihood algorithm based on combined nLSU and ITS sequence data is presented along with the bootstrap values and the Bayesian posterior probabilities

above 50% and 0.8, respectively, at the nodes. Type specimens are in bold and the isolates of new species characterized are in blue



**Fig. 153** Basidiomes of *Wolfiporiella macrospora* (LWZ 20170821–7, holotype). Scale bars: a = 1 cm, b = 1 mm

### *Laetiporaceae* Jülich.

**Notes:** *Laetiporaceae* was established by Jülich (1981) with *Laetiporus* as the type genus. *Laetiporaceae* belongs to the *antrodia* clade within the *Polyporales*, and accommodates species that cause a brown rot (Liu et al. 2022a). Five genera, viz. *Kusaghioporia*, *Laetiporus*, *Macrohyporia*, *Wolfiporiella* and *Wolfiporiopsis* are included in *Laetiporaceae* (Liu et al. 2022a). *Laetiporaceae* is closely related to *Phaeolaceae* (Liu et al. 2022a), and the later family includes some important pathogens on conifer trees (Yuan et al. 2022).

### *Wolfiporiella* B.K. Cui & Shun Liu.

**Notes:** *Wolfiporiella* with *Wolfiporia dilatohypha* as type species was separated from *Wolfiporia* because of its smaller pores (Liu et al. 2022a).

### *Wolfiporiella macrospora* X.H. Ji, L.W. Zhou & S.L. Liu, *sp. nov.*

**Index Fungorum number:** IF 901059; **Facesoffungi number:** FoF 14812; Figs. 153, 154

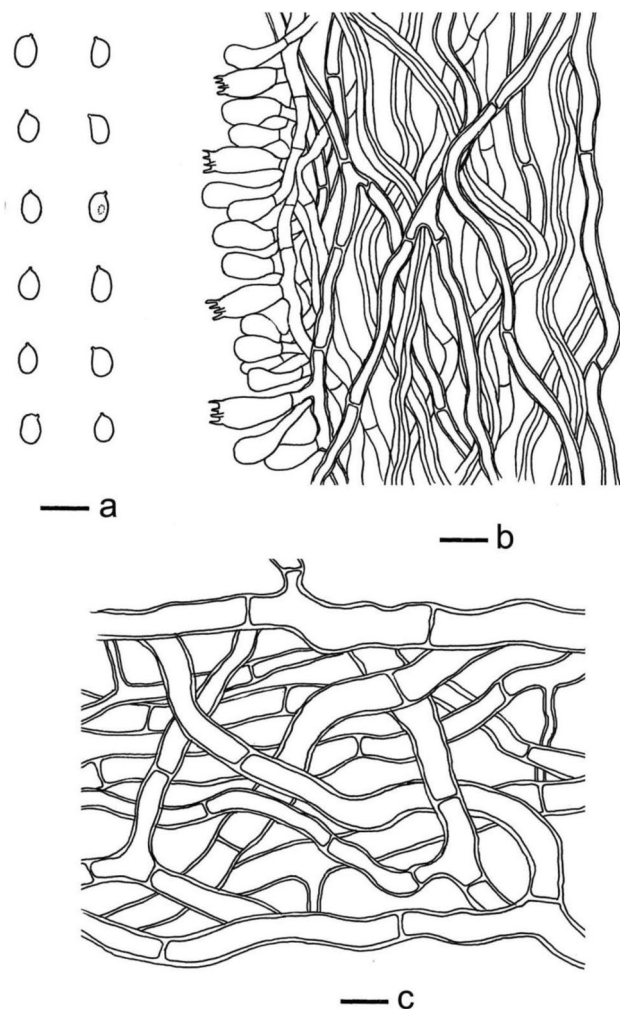
**Etymology:** *macrospora* (Lat.) referring to the large basidiospores.

**Holotype:** LWZ 20170821–7 (HMAS).

**Diagnosis:** Differing from other species of *Wolfiporiella* by having large basidiospores.

**Basidiomes** annual, resupinate, soft to juicy when fresh, without odour or taste, becoming fragile, light in weight when dry, up to 15 cm long, 12 cm wide and 5 mm thick. **Pore surface** buff yellow when fresh, white when bruised, buff to pinkish buff when dry; **sterile margin** distinct, buff, up to 5 mm wide; pores round to angular, 4–6 per mm;





**Fig. 154** Microscopic structures of *Wolfiporiella macrospora* (LWZ 20170821–7, **holotype**). **a** Basidiospores. **b** A vertical section of basidiomes. **c** Hyphae from subiculum. Scale bars: 10  $\mu$ m

dissepiments thin, lacerate. *Context* vinaceous buff, corky, very thin, up to 2 mm thick. *Tubes* concolourous with the pore surface, fragile, up to 2 mm long.

*Hyphal system* dimitic in trama, monomitic in context; generative hyphae simple septate; skeletal hyphae dominant; IKI–, CB–. *Generative hyphae in context* hyaline, fairly thick-walled with a large lumen, frequently branched, simple septate, agglutinated, 6–11  $\mu$ m in diam. *Generative hyphae in tube* hyaline, thin- to slightly thick-walled, frequently branched, simple septate, 3.5–5  $\mu$ m in diam; *skeletal hyphae* frequent, pale yellow, thick-walled with a narrow lumen, unbranched, aseptate, interwoven, 4–6  $\mu$ m in diam. *Basidia* broadly clavate to barrel-shaped with four sterigmata and a basal simple septum, 13–15  $\times$  5–7  $\mu$ m; *basidioles* similar to basidia in shape, but smaller. *Basidiospores* ellipsoid, hyaline, thin-walled, smooth, IKI–, CB+, 5–6.1(–7)  $\times$  (3.4–)3.6–4.1  $\mu$ m, L = 5.7  $\mu$ m, W = 3.8  $\mu$ m, Q = 1.5 (n = 60/2).

**Material examined:** China, Hubei Province, Danjiangkou County, Wudangshan Scenic Area, on base of dead angiosperm, 21 August 2017, L.W. Zhou, LWZ 20170821–7 (HMAS, **holotype**); *ibid.*, on stump of angiosperm, 21 August 2017, L.W. Zhou, LWZ 20170821–8 (HMAS).

**GenBank numbers:** LWZ 20170821–7: ITS = OR557256, LSU = OR527287; LWZ 20170821–8: ITS = OR557257, LSU = OR527288.

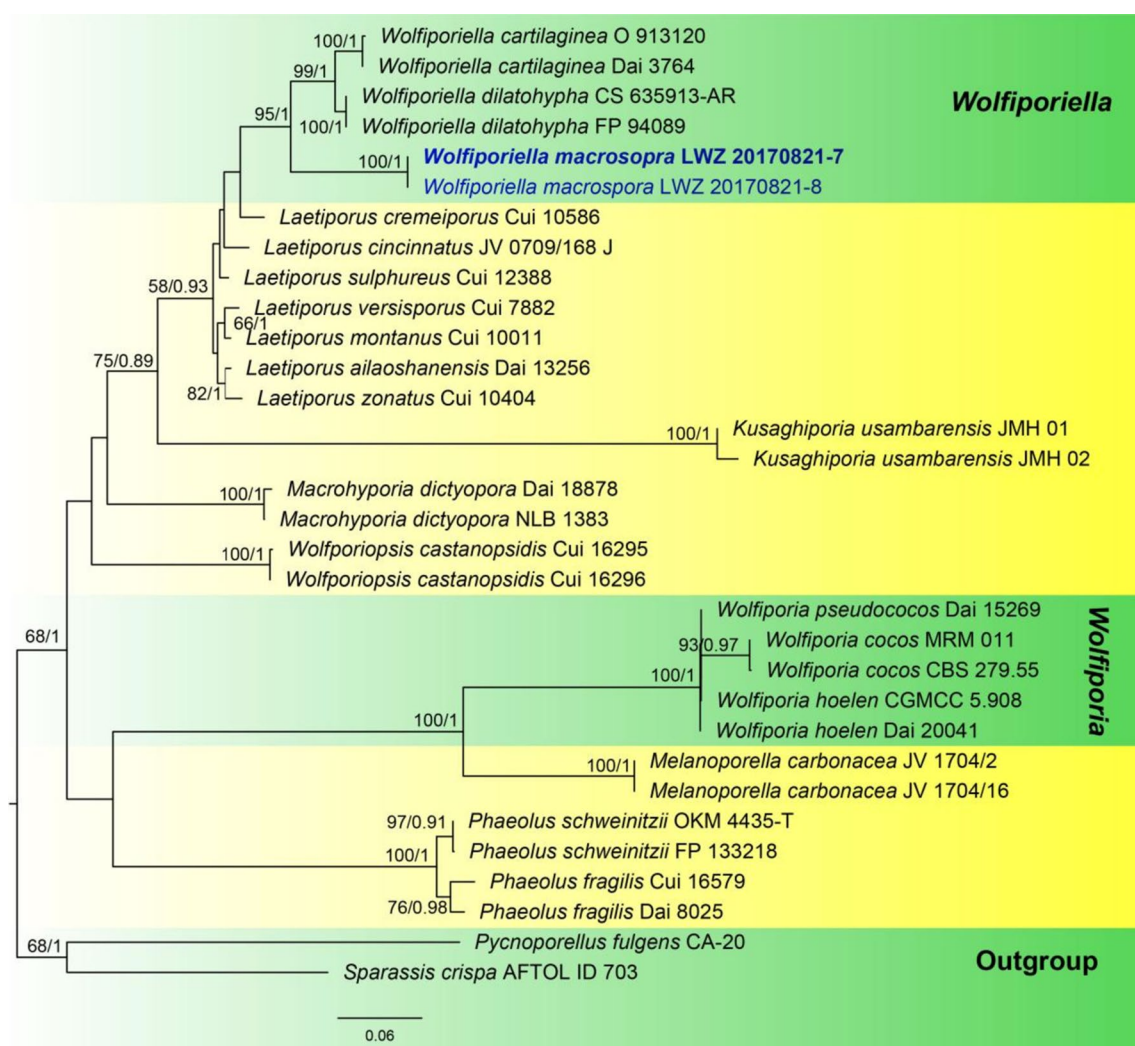
**Notes:** Phylogenetically, *Wolfiporiella macrospora* falls within the clade of *Wolfiporiella* and has a close relationship with *Wolfiporiella cartilaginea* and *W. dilatohypha* (Fig. 155). Morphologically, the latter two species differ by smaller basidiospores (3.2–4.5  $\times$  2.2–3  $\mu$ m in *W. cartilaginea*, Ryvarden et al. 1986; 3.8–4.7  $\times$  2.9–3.1  $\mu$ m in *W. dilatohypha*, Dai et al. 2011).

#### **Meruliaceae** Rea.

**Notes:** Species belonging to the family *Meruliaceae*, generally possess waxy appearance when dry; a monomitic type of hyphal system, rarely dimitic and tightly interwoven; hyphae with or without clamp-connection; thin walled, hyaline, smooth basidiospores; mostly presence or sometimes absence of cystidia; and causing white-rot symptoms (Justo et al. 2017).

#### **Metuloidea** G. Cunn.

**Notes:** The genus *Metuloidea* belonging to the family *Meruliaceae* having distinctive characteristic features like pileate basidiomes, brownish coloured, corky to somewhat waxy with a sweet smell when fresh, and entire margins; poroid or hydroid hymenophore; a dimitic type of hyphal system, generative hyphae clamped, strongly branched yellowish skeletal hyphae; variable shaped cystidia, thin- to thick-walled, usually with lumen and apically encrusted with crystals, fusoid-ventricose to clavate; thin-walled septocystidia (*M. reniforme*) and ellipsoid to cylindrical shaped basidiospores (Westphalen et al. 2021). *Steccherinum*, the largest genus in the family *Steccherinaceae*, is microscopically characterized by the presence of thick-walled skeletal cystidia, a dimitic type of hyphal system and clamped generative hyphae. Mainly, *Steccherinum* included only hydroid species, but the phylogenetic studies showed that different types of hymenophore present in this genus, and it also includes poroid species (Miettinen et al. 2012; Miettinen and Ryvarden 2016; Westphalen et al. 2018). With the addition of molecular data, some authors used broad treatments of the *Steccherinaceae* and consequently some genera were transferred to the *Meruliaceae* (Larsson 2007a; Zmitrovich 2018). Some species, such as *Steccherinum murashkinskyi* previously belonged to the genus *Steccherinum*; however, phylogenetic studies showed that these species do not belong to *Steccherinum*, and they have been transferred to the genus, *Metuloidea*. About six species of *Metuloidea* are known till



**Fig. 155** Phylogeny generated by the maximum likelihood algorithm based on combined ITS and nLSU regions is presented along with the bootstrap values and the Bayesian posterior probabilities above 50%

and 0.8, respectively, at the nodes. *Pycnoporellus fulgens* CA-20 and *Sparassis crispa* AFTOL ID 703 were selected as the outgroup taxa. Holotypes are in bold and the newly generated sequences are in blue

date (Miettinen and Ryvarden 2016; Westphalen et al. 2021). Of them, the type species is *Metuloidea tawa* (Westphalen et al. 2021).

***Metuloidea imbricata*** R. Saha, A.K. Dutta & K. Acharya, *sp. nov.*

*Index Fungorum* number: IF559643; *Facesoffungi* number: FoF 11346; Figs. 156, 157

*Etymology*: The specific epithet ‘*imbricata*’ means overlapping or closely put together, referring to the growth habits of the basidiomes.

*Holotype*: CUH AM338.

*Basidiomes* annual, sessile, imbricate, pileate. *Pileus* 30–50 × 23–40 mm in diam, 5–13 mm thick at base, coriaceous, glabrous, concentrically zonate, even, reddish white (8A2) when fresh, becoming greyish orange (5B3) on

drying. *Margin* distinct, even to slightly wavy, 0.7–2 mm thick, white (1A1) when fresh, greyish orange (5B3) on drying. *Context* fibrillose, greyish orange (5B3) on drying, 0.5–2 mm thick at base. *Hymenophore* hydroid; *spine* 1–5 mm long, conical, dense, reddish grey (8B2) when fresh, brownish orange (7C3) to brown (7E4) on drying, 4–5 per mm. *Odour* sweet. *Taste* unknown.

*Hyphal system* dimitic. *Context generative hyphae* coralloid, solid, sometimes sklerified, 2.9–5.3 µm broad, clamped, thin- to thick-walled; *skeletal hyphae* 3.9–6.7 µm broad, hyaline, unbranched, thick-walled. *Spine hyphae* dimitic, parallel; *skeletal hyphae* 3.3–6.7 µm broad, thick-walled with narrow lumen, unbranched, hyaline, (–) ve in cotton blue; *generative hyphae* 1.3–3.3 µm broad, thin-walled, hyaline, branched. *Skeletocystidia* 3.9–6.7 µm broad, sub-ventricose, hyaline, epically encrusted, deeply rooted,

**Fig. 156** *Metuloidea imbricata* (CUH AM338, **holotype**). **a–d** Field pictures of the basidiomes. Scale bars: **a–d** = 10 mm



thick-walled. *Septocystidia* 3.5–6  $\mu\text{m}$  broad, apex clavate to subclavate, thick-walled with adventitious septa, hyaline, smooth. *Basidia* 9.9–16.7  $\times$  2.9–3.8  $\mu\text{m}$  in diam, clavate, hyaline, thin-walled, 4-sterigmatic with basal clamps, CB –. *Basidiospores* thin-walled, ellipsoid to elongate, hyaline, (2.9–)3.37–4.0  $\times$  (1.3–)1.88–3.4  $\mu\text{m}$ ,  $Q = 1.1$ –2.5,  $Q_m = 1.90$ , inamyloid, non-dextrinoid, CB –.

**Habitat and distribution:** The new species grows on the dead wooden logs of unknown angiosperm and is currently only found in India.

**Material examined:** India, West Bengal, Jalpaiguri District, Apalchand forest, 26.8648°N, 88.7421°E, elevation 151 m alt., on dead wooden logs of unknown angiosperm, 13 October 2017, R. Saha, K. Acharya, CUH AM338 (**holotype**), on dead wooden logs of unknown angiosperm, 14 October 2017, R. Saha, K. Acharya, CUH AM773.

**GenBank numbers:** CUH AM338: ITS = ON227062, LSU = ON227059; CUH AM773: ITS = ON227063, LSU = ON227064.

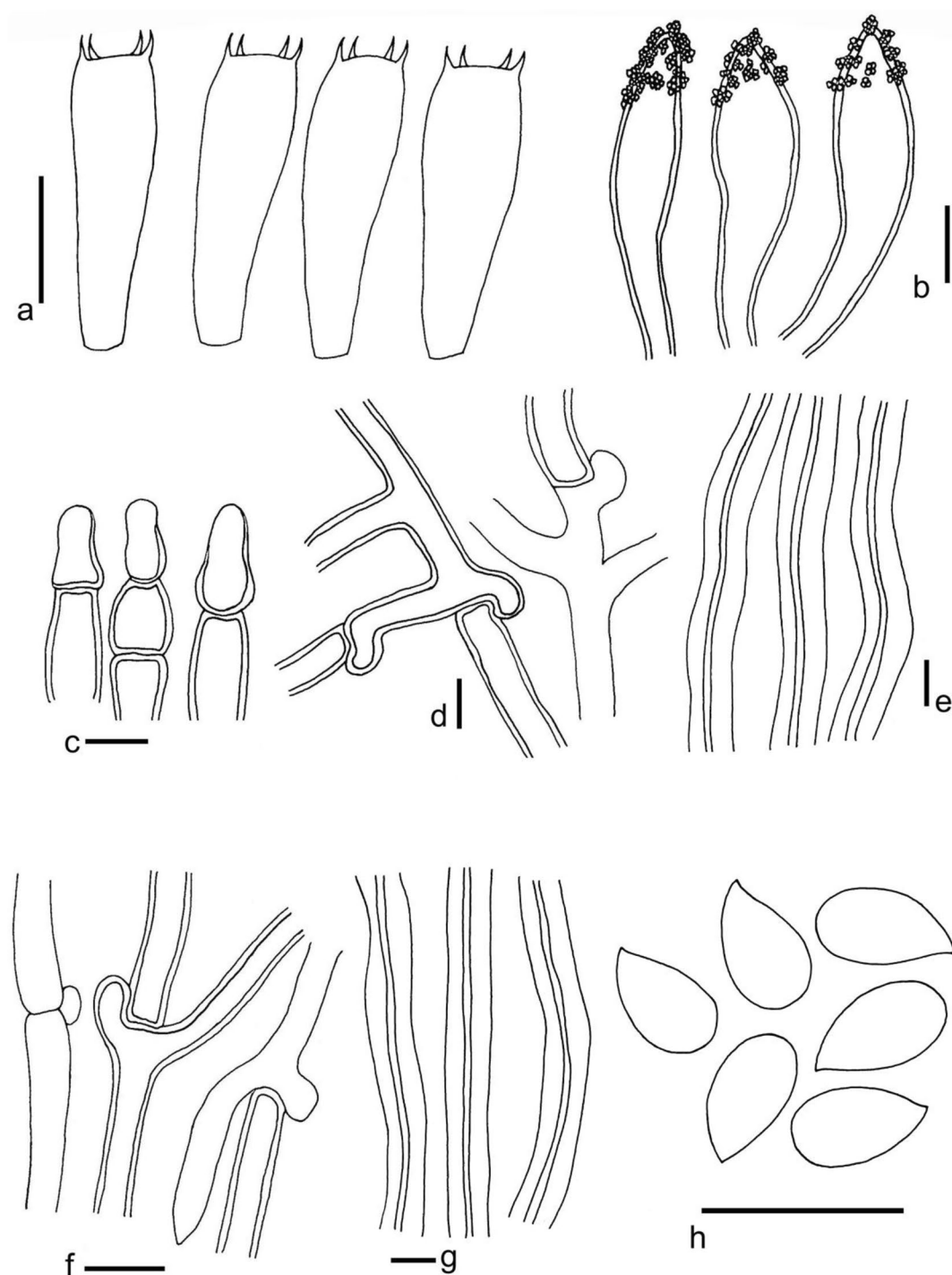
**Notes:** Characteristic features of *Metuloidea imbricata* include pileate, imbricate, sessile basidiomes smelled sweetish, reddish grey coloured, hydroid hymenophore consisting of conical spines; presence of a dimitic hyphal system with clamped generative hyphae, and thick-walled, unbranched skeletal hyphae reacting (–) ve in cotton blue; epically encrusted, deeply rooted, thick-walled, subventricose skeletal cystidia; often with septocystidia and ellipsoid to elongate basidiospores measuring 2.9–4.0  $\times$  1.3–3.4  $\mu\text{m}$ .

Among similar taxa, *Metuloidea cinnamomea* differs from *Metuloidea imbricata* by the presence of poroid hymenophore; sub-cylindrical basidiospores, less than 2  $\mu\text{m}$

wide and lack of any smell (Miettinen and Ryvarden 2016). *Metuloidea tawa* differs by having solitary, conchate, applanate, or effused-reflexed, occasionally resupinate basidiomes, pileus upper surface azonate, coarsely strigose, hairs adpressed to radiately arranged, hymenophore poroid, pores angular or round, hyphal system trimitic and basidiospores elliptical, up to 2  $\mu\text{m}$  wide (Cunningham 1965). *Metuloidea rhinocephala* differs by having a strong smell in herbarium sample; basidiomes solitary, effused-reflexed, pileus upper surface hairy; hymenophore poroid; generative hyphae simple septate and basidiospores globose to obovate, 4–4.5  $\mu\text{m}$  in diam (Miettinen and Ryvarden 2016). *Metuloidea fragrans* differs by having annual, pileate, sessile, more rarely effused reflexed, poroid basidiomes with a strong scent of coumarin, trimitic type of hyphal system and ovoid basidiospores measuring 3–4  $\times$  2–3  $\mu\text{m}$  (David and Tortic 1986). *Metuloidea reniformis* differs by having deep brown coloured basidiomes with pleasant, coumarin-like smell and yellowish skeletal hyphae (Westphalen et al. 2021).

In the phylogenetic tree, *Metuloidea imbricata* appears to be close to *Steccherinum* cf. *murashkinskyi* (96% MLBS, 0.99 BYPP; Figs. 158 and 159). However, details of *Steccherinum* cf. *murashkinskyi* cannot be verified because of lacking any morphological details in the form of published literature. *Metuloidea murashkinskyi* differs from *Metuloidea imbricata* by having pileate to decurrent to resupinate basidiomes, cap surface tomentose, cinnamon brown; hymenophore hydroid, sometimes irpicoid or poroid; spicy odour; context hyphae monomitic with thick walled sklerified generative hyphae and spine hyphae dimitic; skeletal hyphae of spine (+) ve in cotton blue and basidiospores



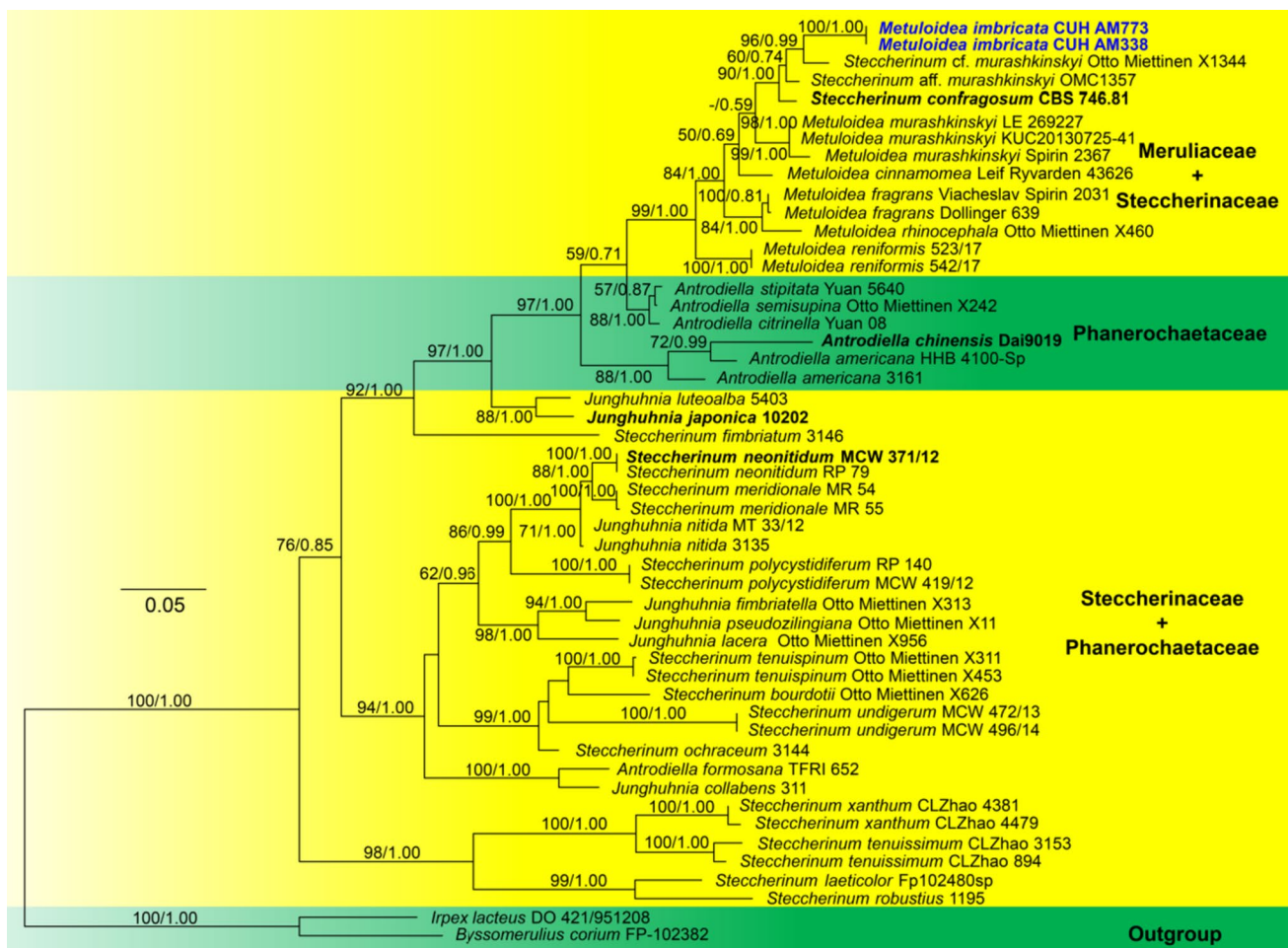


**Fig. 157** *Metuloidea imbricata* (CUH AM338, **holotype**). **a** Basidia. **b** skeletocystidia. **c** septocystidia. **d** generative hyphae of context. **e** skeletal hyphae of context. **f** generative hyphae of spine. **g** skeletal hyphae of spine. **h** basidiospores. Scale bars: **a–h** = 5  $\mu$ m

short-cylindrical (Spirin et al. 2007). *Steccherinum confragosum* differs by the presence of clavate to lageniform cystidia, and absence of septocystidia (Geesteranus and Lanquetin 1975).

**Polyporaceae** Fr. ex Corda.

**Notes:** Corda (1839) proposed the family *Polyporaceae* with characters such as smooth, hyaline, thin-walled, typically cylindrical, non-amyloid, non-dextrinoid spores and usually lack of true hymenial cystidia, and since then these



**Fig. 158** Phylogenetic analyses were based on data set of nrDNA ITS sequences. Reference sequences were selected from relevant literature (Westphalen et al. 2021; Wu et al. 2021), BLAST searches (Altschul et al. 1997) and data retrieved from GenBank (Clark et al. 2016). Two sequences of the genus *Byssomerulius* and *Irpex*, were chosen as the outgroup for rooting purpose (Wu et al. 2021). ClustalX2 (Thompson et al. 1997) with the use of default settings, and finally the alignment was upgraded wherever needed using MEGA v. 7.0 (Kumar et al. 2016) for manual adjustments. For maximum likelihood (ML) analyses, the statistically best fit models of nucleotide substitution using Cyber Infrastructure for Phylogenetic Research (CIPRES) web portal (<https://www.phylo.org/portal2/>) were determined by jModeltest 2.1.6 (Darriba et al. 2012) on XSEDE (Miller et al. 2010). Based on the Bayesian information criterion (BIC), the GTR+I+G (13,859.931977) model chosen as the most suitable model for the

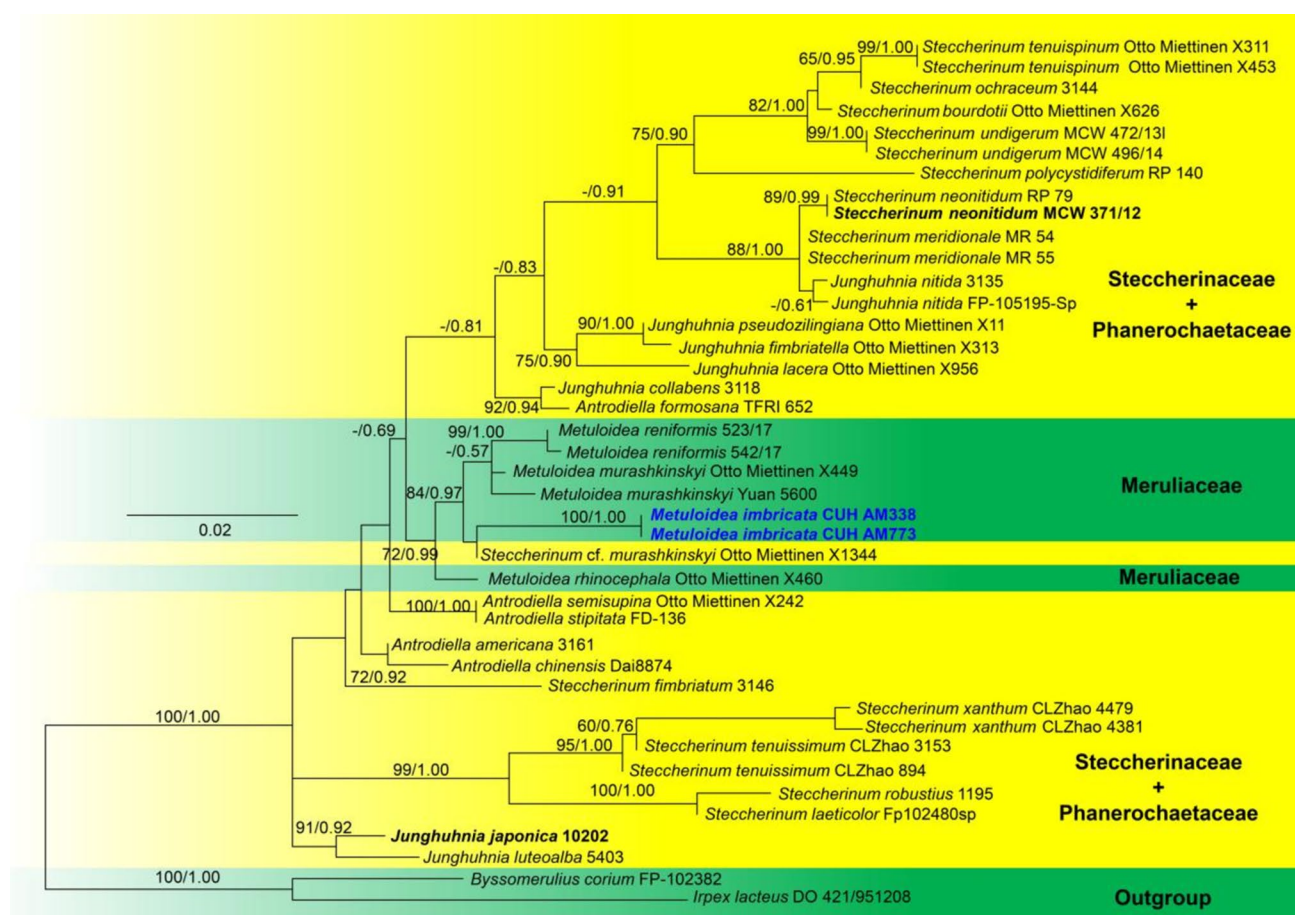
alignment. Maximum Likelihood analysis was performed using RAxML-HP2 ver. 8.2.12 (Stamatakis 2006) with bootstrap statistics worked out from 1000 rapid bootstrap replicates on the CIPRES NSF XSEDE resource. Bayesian inference (BI) of the phylogeny was worked out with the application of MrBayes v.3.2.2 (Ronquist et al. 2012) using the selected model operating Markov chain Monte Carlo (MCMC) analyses (Geyer 1991). Bayesian analyses extended to a standard deviation of split frequencies of 0.003 after  $10^6$  generations. After 25% preliminary burn in (Hall 2004), MrBayes was used to figure out the remaining trees' 50% majority rule consensus phylogram to enumerate the PPs (posterior probabilities) of the groups. MLBS and PP values over 50% and 0.50 are displayed in the resulting phylogenetic tree. The newly described species are represented in blue bold font to highlight its position in the phylogenetic tree

characters have been widely used in the identification and taxonomy of polyporoid fungi. Ryvarden (1991) classified the family *Polyporaceae* into 11 groups, using hyphal types as the main criterion. He grouped 16 genera of fungi mostly with a trimitic hyphal system and white rotting habit, viz. *Cerrena*, *Corioloopsis*, *Cryptoporus*, *Daedaleopsis*, *Datroina*, *Earliella*, *Elmerina*, *Fomitella*, *Hexagonia*, *Lenzites*, *Megasporoporia*, *Microporus*, *Mollicarpus*, *Pycnoporus*, *Trametes* and *Trichaptum* into the *Trametes* group. A recent

monograph of the family on the Chinese species was published and 217 species are described by Cui et al. (2019), and more new species are described from China very recently (Zhou et al. 2021; Mao et al. 2023). At present, MycoBank has recorded 187 genera as of 6 August, 2022.

***Megasporoporia*** Ryvarden & J.E. Wright.

*Notes:* *Megasporoporia* was established by Ryvarden et al. (1982) based on *Poria setulosa*. The genus is



**Fig. 159** Phylogenetic analyses were based on data set of nrDNA LSU sequences. Reference sequences were selected from relevant literature (Westphalen et al. 2021; Wu et al. 2021), BLAST searches (Altschul et al. 1997) and data retrieved from GenBank (Clark et al. 2016). Two sequences of the genus *Byssomerulius* and *Irpex*, were chosen as the outgroup for rooting purpose (Wu et al. 2021). ClustalX2 (Thompson et al. 1997) with the use of default settings, and finally the alignment was upgraded wherever needed using MEGA v. 7.0 (Kumar et al. 2016) for manual adjustments. For maximum likelihood (ML) analyses, the statistically best fit models of nucleotide substitution using Cyber Infrastructure for Phylogenetic Research (CIPRES) web portal (<https://www.phylo.org/porta12/>) were determined by jModeltest 2.1.6 (Darriba et al. 2012) on XSEDE (Miller et al. 2010). Based on the Bayesian information criterion (BIC), the GTR + I + G (5329.291785) model chosen as the most

suitable model for the alignment. Maximum Likelihood analysis was performed using RAxML-HPC2 ver. 8.2.12 (Stamatakis 2006) with bootstrap statistics worked out from 1000 rapid bootstrap replicates on the CIPRES NSF XSEDE resource. Bayesian inference (BI) of the phylogeny was worked out with the application of MrBayes v.3.2.2 (Ronquist et al. 2012) using the selected model operating Markov chain Monte Carlo (MCMC) analyses (Geyer 1991). Bayesian analyses extended to a standard deviation of split frequencies of 0.006 after 106 generations. After 25% preliminary burn in (Hall 2004), MrBayes was used to figure out the remaining trees' 50% majority rule consensus phylogram to enumerate the PPs (posterior probabilities) of the groups. MLBS and PP values over 50% and 0.50 are displayed in the resulting phylogenetic tree. The newly described species are exhibited in blue bold font to highlight its position in the phylogenetic tree

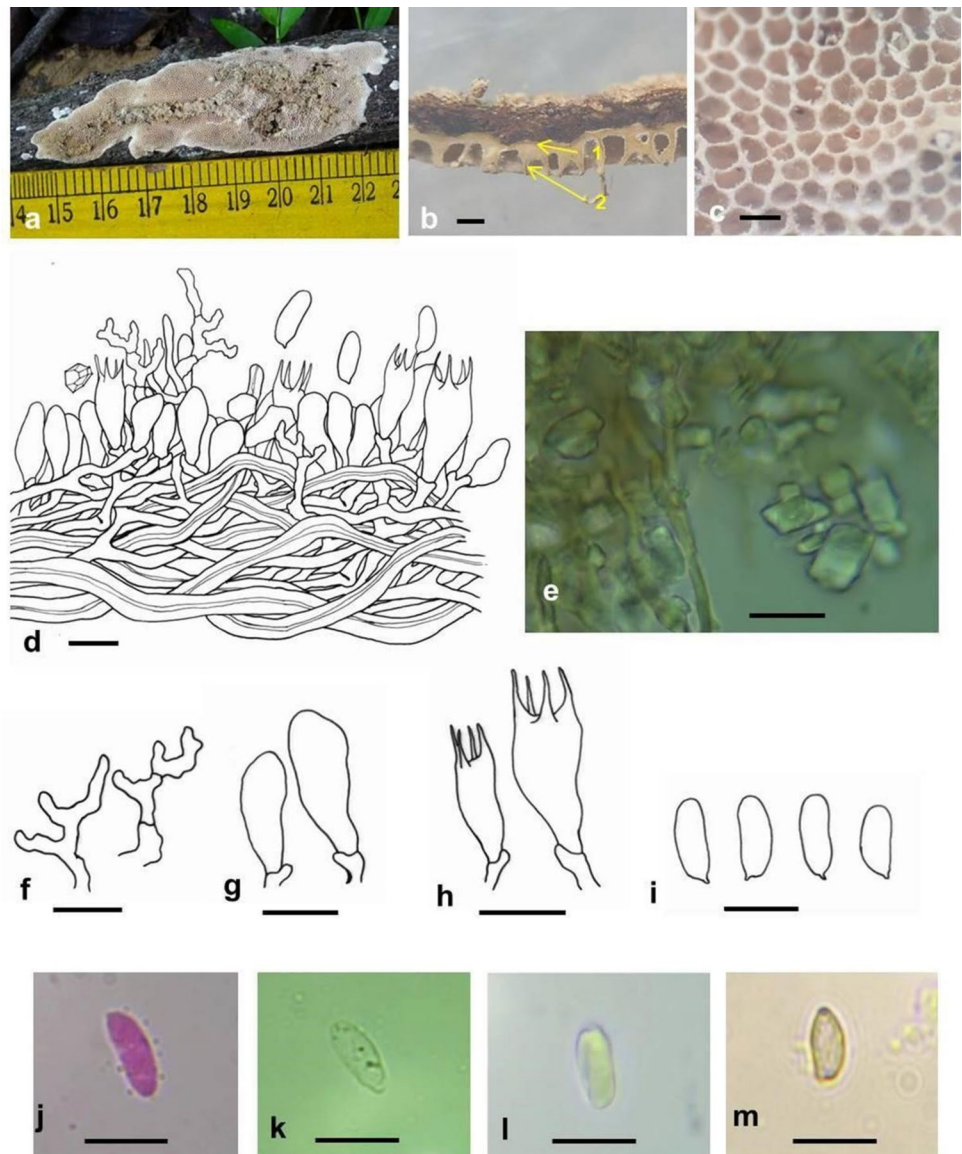
characterized by resupinate basidiomes, large basidiospores, a dimitic to trimitic hyphal structure with clamped generative hyphae and dextrinoid skeletal hyphae, presence of rhomboid or bipyramidal crystals, dendrohyphidia, hyphal pegs, presence or absence of cystidioles/cystidia, and causing a white rot mostly on fallen angiosperm branches or twigs (Ryvarden et al. 1982; Dai and Li 2002; Dai and Wu 2004; Zhou and Dai 2008; Du and Cui 2009; Wang et al. 2022c). At present MycoBank has recorded 16 species under this genus as of 23 July, 2022. However, in the recent years, some of the species listed under *Megasporoporia* has

been grouped under different genera such as *Megasporia cavernulosa*, *Jorgewrightia cystidiolophora*, *Jorgewrightia ellipsoidea*, *Megasporia hexagonoides*, *Jorgewrightia major*, *Jorgewrightia violacea*, *Megasporia mexicana*, *Grammothele quercina*, *Mariorajchenbergia rhododendri* and *Mariorajchenbergia subcavernulosa* (Li and Cui 2013; Yuan et al. 2017; Lira et al. 2021).

***Megasporoporia tamilnaduensis*** K. Kezo, M. Kaliyaperumal, S. Gunaseelan, Xue W. Wang & L.W. Zhou., *sp. nov.*



**Fig. 160** Microscopic structures of *Megasporoporia tamilnaduensis* (MUBL4022, holotype). **a** Basidiomes. **b1** Duplex Context. **b2** Tube layer. **c** Pore surface. **d** Cross section of hymenium. **e** Crystals. **f** Dendrohyphidia. **g** Basidioles. **h** Basidia. **i** Basidiospores. **j** Phloxine. **k** Water. **l** Cotton blue. **m** Melzer. Scale bars: **b**, **c** = 1 mm, **d–m** = 10  $\mu$ m



*Index Fungorum*: IF559790; *Facesoffungi* number: FoF 12713; Figs. 160, 161

*Etymology*: “*tamilnaduensis*” refers to the place of collection.

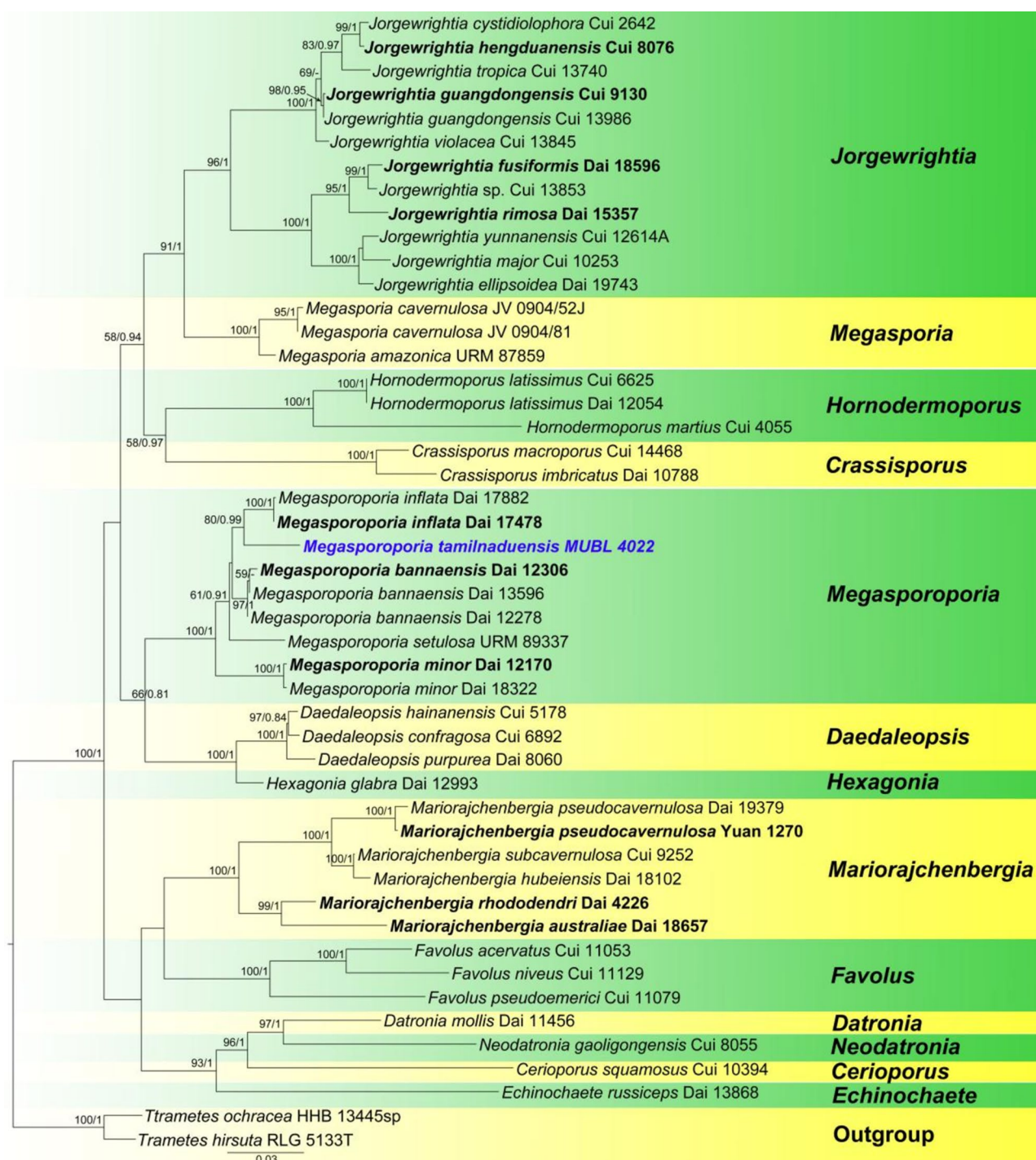
*Holotype*: MUBL4022.

*Diagnosis*: Basidiomes annual, resupinate with white to brownish grey pore surface and duplex context, a dimitic hyphal system with clamped generative hyphae, presence of dendrohyphidia and tetrahedric to polyhedric crystals in the hymenium, absence of cystidia and cystidioles and cylindrical, hyaline, thin-walled basidiospores.

*Basidiomes* annual, resupinate, without odor or flavor when fresh, becoming corky upon drying, up to 9 cm long, 2.5 cm wide and 1.5 mm thick at the centre. *Margin* white (5A1) when fresh becoming yellowish white (4A2) on drying, up to 0.5 mm wide. *Pore surface* reddish white (7A2)

when fresh to brownish grey (6C3) on drying; *pores* round to angular, 1–2 per mm; *dissepiments* thin. *Context* duplex without black line, yellowish white (4A2) towards substrate, white (5A1) towards the tube, up to 0.5 mm thick. *Tubes* concolorous with the pore surface, up to 1 mm long.

*Hyphal system* dimitic, skeletal hyphae dominant in context, while in trama generative hyphae. *Context generative hyphae* thin- to thick-walled, hyaline, clamped septate, branched, 2–3  $\mu$ m in diam, CB +, IKI–; *skeletal hyphae* thick-walled with narrow lumen, unbranched, aseptate, 2.5–6.2  $\mu$ m in diam, CB +, IKI–. *Trama generative hyphae* thin-walled, hyaline, clamped septate, branched, 1.8–2.5  $\mu$ m in diam, CB +, IKI–; *skeletal hyphae* thick-walled with narrow lumen, aseptate, unbranched, 2.5–6  $\mu$ m in diam, CB +, IKI–. Abundant tetrahedric to polyhedric *crystals* present in the hymenium.



**Fig. 161** Phylogram generated by the maximum likelihood algorithm based on combined nLSU and ITS sequence data is presented along with the bootstrap values and the Bayesian posterior probabilities

above 50% and 0.8, respectively, at the nodes. Type specimens are in bold and the isolates of new species characterized are in blue

*Cystidia* and *Cystidioles* absent. *Dendrohyphidia* present, 1.8–2.7 µm in diam. *Basidioles* clavate, 14–20 × 7–7.8 µm. *Basidia* clavate, with four sterigmata, 16–24.2 × 7–8.2 µm. *Basidiospores* cylindrical, hyaline, thin-walled, smooth,

IKI–, CB–, (9.5–)9.7–11.5(–12) × (3.3–)3.5–4(–4.2) µm, Q = 2.85 (n = 30/2).

**Material examined:** India, Tamil Nadu, Thiruvannamalai district, 12°29'15.4"N, 78°55'01.8"E, on dead wood, 14 November, 2019, Kezhocuyi Kezo, MUBL4022



**Fig. 162** *Laxitextum subrubrum* (CUH AM774, **holotype**). **a, b** Field pictures of the basidiomes. **c** SEM image of basidiospore. Scale bars: **a–d** = 5 mm, **c** = 1  $\mu$ m



(**holotype**). INDIA, Tamil Nadu, Thiruvannamalai district, Jawadhu hills, Nallapathur Reserve Forest, 12°32'49.9"N, 78°54'05.9"E, on dead wood, 14 January 2020, Kezhocuyi Kezo, KSM-NP7.

*GenBank numbers*: ITS = ON249127, LSU = ON254196.

*Notes*: *Megasporoporia tamilnaduensis* (MUBL4022) shares similarities with *M. bannaensis* (Li and Cui 2013) by annual, resupinate basidiomes and pores size (1–2 per mm). However, the former differs by the presence of dendrohyphidia and smaller basidiospore size (9.5–12  $\times$  3.3–4.2  $\mu$ m). The spore size of *M. tamilnaduensis* and *M. inflata* are similar; however, the latter has smaller pore size (2–3 per mm) and lacks dendrohyphidia (Wang et al. 2021b). Our Indian species shares similar pore size with *M. setulosa* but the latter varies by having larger basidiospore (10–14  $\times$  4.2–5.7  $\mu$ m) and absence of dendrohyphidia (Lira

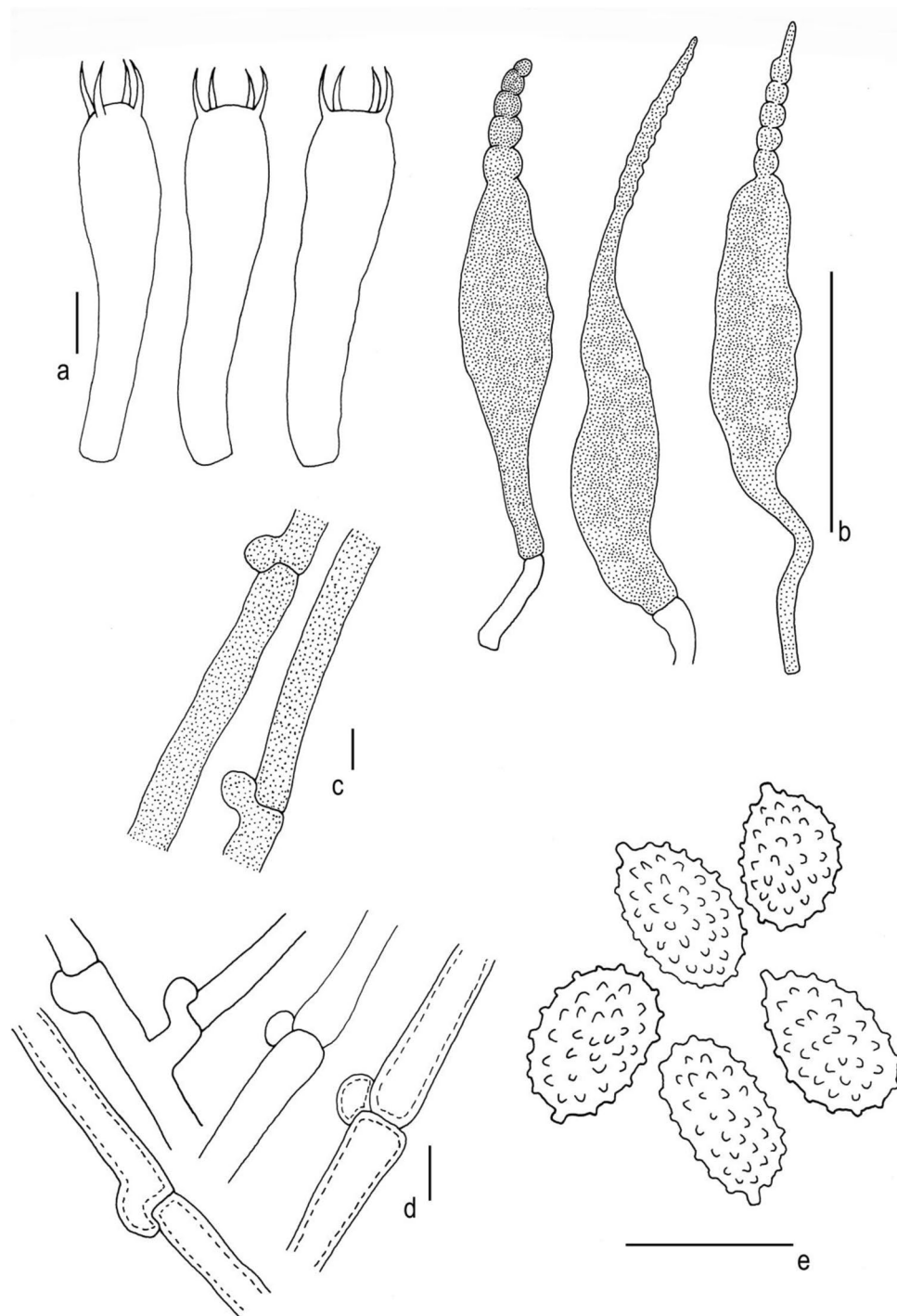
et al. 2021). *Megasporoporia tamilnaduensis* share similar basidiospore and pore size with *M. neosetula*, but the latter varies in the absence of dendrohyphidia and homogenous context (Lira et al. 2021). *Megasporoporia minuta* varies from *M. tamilnaduensis* by small pores (6–8 per mm), narrowly ovoid basidiospores, and lack of hyphal pegs, dendrohyphidia and tetrahedric or polyhedric crystals (Zhou and Dai 2008).

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

*Notes*: *Russulales* is well-supported clade in Agaricomycetes. About 10 families, 99 genera and 4436 species had been reported in this order according to the latest overview of Basidiomycota (He et al. 2019; Wu et al. 2020). A large number of studies were focused on the taxonomy and phylogeny of *Russulales* taxa in last ten years. A total of 13



**Fig. 163** *Laxitextum subrubrum* (CUH AM774, **holotype**). **a** Basidia. **b** gloeocystidia. **c** Oleiferous hyphae. **d** generative hyphae. **e** basidiospores. Scale bars: **a–e** = 5  $\mu$ m



new genera have been proposed in the order in this period (Audet 2010; Wu et al. 2010b; Zhou and Dai 2013; Larsson 2014; Ryvarden and Tutka 2014; Chen et al. 2016; Liu et al. 2017b). The genus/family-level classification of *Russulales* are continuously provided (Miller et al. 2006; Hibbett et al. 2007; Zhao et al. 2017; He et al. 2019). In addition, a certain number of edible and medicinal and pathogenic species are

the members of *Russulales* (Dai and Yang 2008; Li et al. 2015d; Yuan et al. 2021).

#### ***Hericiaceae* Donk.**

**Notes:** Species belonging to the family *Hericiaceae* generally having resupinate, effused-reflexed to pileate, membranous to fleshy basidiomes; smooth, odontoid to toothed hymenophore; white or pallid, fleshy to membranous

context; a monomitic type of hyphal system with thin- to thick-walled, clamped hyphae; presence of gloeocystidia; clavate, 4-sterigmate basidia; and globose, ovoid to ellipsoid, smooth to echinulate, amyloid basidiospores (Sharma 2012).

### *Laxitextum* Lentz.

**Notes:** The genus *Laxitextum* includes three species (retrieved from [www.mycobank.org](http://www.mycobank.org), 20 April 2022) till date having distinctive characteristic features like resupinate to subpileate basidiomes; brown, tomentose, zonate pileus upper surface; white when fresh, smooth hymenial surface; a monomitic type of hyphal system with thin-walled, clamped generative hyphae; numerous, subulate gloeocystidia; and subglobose to ellipsoid, echinulate and amyloid basidiospores (Lee and Jung 2006). The type species of *Laxitextum* is *L. bicolor* (Lee and Jung 2006).

### *Laxitextum subrubrum* R. Saha, A.K. Dutta & K. Acharya, *sp. nov.*

**Index Fungorum number:** IF559644; **Facesoffungi Number:** FoF 11347; **Figs.** 162, 163

**Etymology:** Named after sub- (Latin)= under, almost, and rubrum (Latin)= red, referring to the reddish or dull red colouration of the pileus.

**Holotype:** CUH AM774.

**Basidiomes** pileate, sessile, soft-spongy when fresh and brittle on drying, 10–30 mm long, 5–20 mm wide and up to 1–2 mm thick. **Pileus** upper surface uneven, slightly zonate, velutinous, dull red (9C4). **Margin** thin, wavy, brownish orange (7C3). **Hymenophore** smooth, white (1A1), cracked on drying. **Context** soft, thin, dull red (9C3).

**Hyphal system** monomitic, generative hyphae 2.9–5.9 µm wide, hyaline, thin- to thick-walled, clamped. **Oleiferous hyphae** 3.5–6.5 µm wide. **Gloeocystidia** 102–156 × 8.5–15 µm, lanceolate, sometimes apex moniliform, pale orange (5A3), filled with oily substance. **Basidia** 23.5–38 × 5.5–9 µm, narrowly clavate, hyaline, thin-walled, 4-sterigmate, with basal clamp. **Basidiospores** (3.5–)4.74–5.9 × (2.9–)3.06–3.5 µm, Q = 1.2–2, Q<sub>m</sub> = 1.54, thin-walled, hyaline, ellipsoid, apiculate, finely echinulate, strongly amyloid in Melzer's reagent.

**Habitat and distribution:** The new species grows on dead wood of unknown angiosperm, and is currently only found in India.

**Material examined:** India, West Bengal, Jalpaiguri District, Moraghat range, Khuttimari, 26.4728°N, 88.5957°E, elevation 144 m alt., on dead wooden logs of unknown angiosperm, 7 October 2018, R. Saha & K. Acharya, CUH AM774 (**holotype**), 8 October 2018, R. Saha, K. Acharya, CUH AM775.

**GenBank numbers:** CUH AM774: ITS = ON227060, LSU = ON226874; CUH AM775: ITS = ON227061, LSU = ON227065.

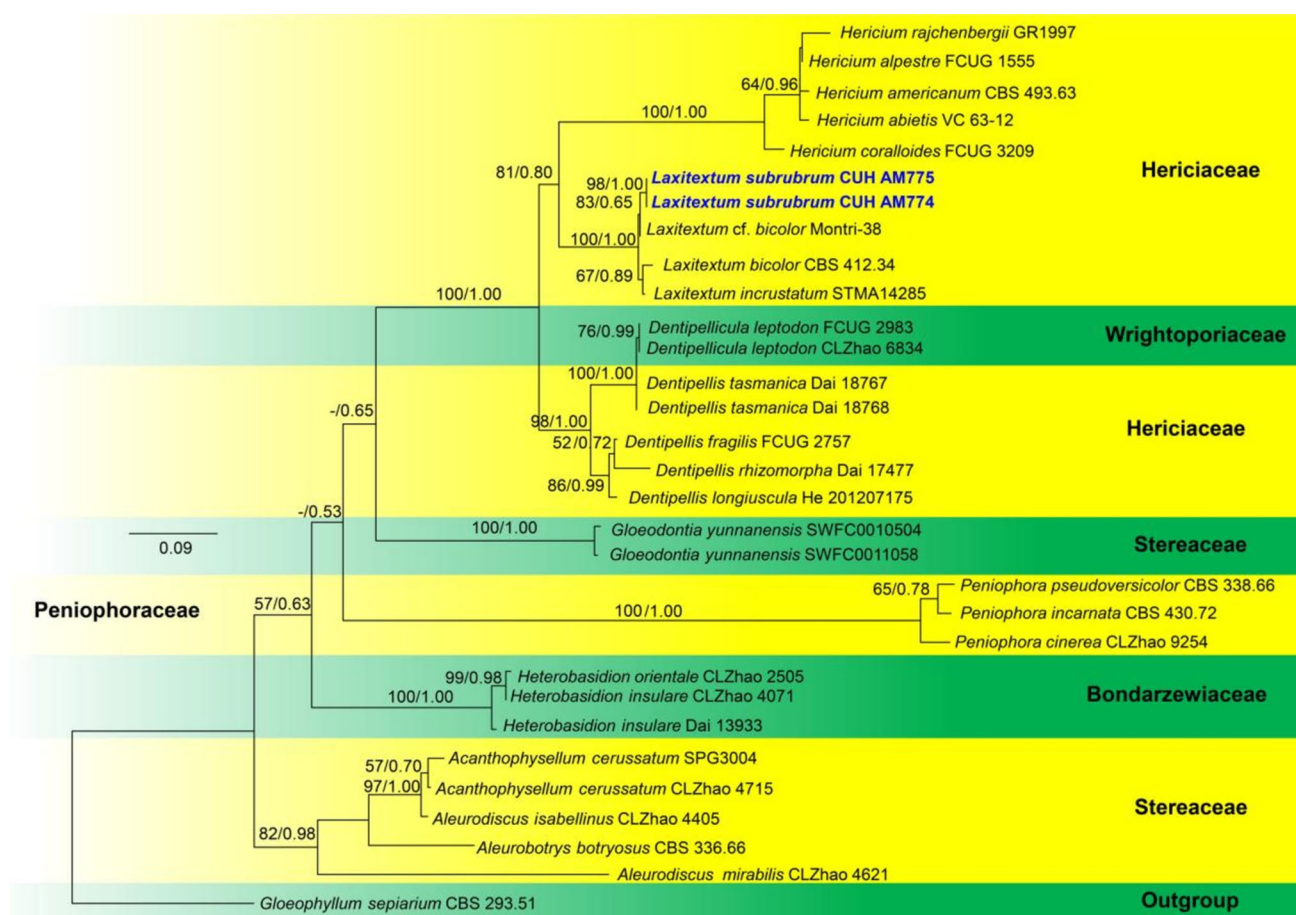
**Notes:** Characteristic features of the present specimens include pileate, sessile basidiomes with slightly zonate, velutinous, dull red upper surface; brownish orange margin, smooth, white hymenophore; dull red context; presence of a monomitic hyphal system with clamped generative hyphae; lanceolate, pale orange gloeocystidia, apex sometimes moniliform; narrowly clavate, hyaline, thin-walled, 4-sterigmate basidia; and thin-walled, hyaline, ellipsoid, apiculate, finely echinulate, strongly amyloid in Melzer's reagent basidiospores measuring 3.5–5.9 × 2.9–3.5 µm.

Among similar taxa, *Laxitextum bicolor* differs by having resupinate to effused-reflexed basidiomes; brown coloured and finely tomentose pileus upper surface with appressed hyphal hairs (Lentz 1955). *Laxitextum incrustatum* differs by the presence of resupinate and widely effused basidiomes; white to pallid, cottony to matted tomentose margin; tubular gloeocystidia, sometimes with a bulbous swelling near base and hyphidia (Hjortstam and Ryvarden 1981). *Laxitextum lutescens* differs by having resupinate to distinctly reflexed basidiomes; deep yellow to pale brown velutinous, azonate pileus upper surface; cream-yellowish to straw coloured hymenium with a light purple-brown tint (Hjortstam and Ryvarden 1981).

In the phylogenetic tree, *Laxitextum subrubrum* appears to be close to *Laxitextum* cf. *bicolor* (83% MLBS, 0.65 BYPP; Figs. 164 and 165). However, details of *Laxitextum* cf. *bicolor* cannot be verified because of lacking any morphological details in the form of published literature.

### *Russulaceae* Lotsy.

**Notes:** The family was typified by *Russula* (Persoon 1796), and its concept was originally described to accommodate the genera that have granular flesh, thick gills, spiny spores with amyloid ornamentations, and sphaerocytes in context (Lotsy 1907). Subsequently, the members of *Russulaceae* have been revised for several times, and this family has been reclassified as the development of molecular phylogeny (Hibbett and Thorn 2001; Larsson and Larsson 2003). Recently, systematic studies on the taxonomy and phylogeny of some sequestrate genera of *Russulaceae* have been reported. The phylogenetic results showed that the russuloid genera nested with the non-sequestrate *Russulaceae* members (Calonge and Martín 2000; Lebel and Tonkin 2007; Buyck et al. 2010). Although Buyck et al. (2018) presented systematic analyses of *Russulaceae* at subgenus level based on sequences from LSU, TEF1-α, mtSSU, RPB1 and RPB2 genes, geographically comprehensive studies on this family are still lacking. Further analyses of *Russulaceae* are still needed in the future.



**Fig. 164** Phylogenetic analyses were based on data set of nrDNA ITS sequences. Reference sequences were selected from relevant literature (He and Zhao 2022; Hofstetter et al. 2019), BLAST searches (Altschul et al. 1997) and data retrieved from GenBank (Clark et al. 2016). Two sequences of the genus *Gloeophyllum*, was chosen as the outgroup for rooting purpose (He and Zhao 2022). ClustalX2 (Thompson et al. 1997) with the use of default settings, and finally the alignment was upgraded wherever needed using MEGA v. 7.0 (Kumar et al. 2016) for manual adjustments. For maximum likelihood (ML) analyses, the statistically best fit models of nucleotide substitution using Cyber Infrastructure for Phylogenetic Research (CIPRES) web portal (<https://www.phylo.org/portal2/>) were determined by jModeltest 2.1.6 (Darriba et al. 2012) on XSEDE (Miller et al. 2010). Based on the Bayesian information criterion (BIC), the GTR+I+G (10,768.817815) model chosen as the most suitable model for the

alignment. Maximum Likelihood analysis was performed using RAxML-HPC2 ver. 8.2.12 (Stamatakis 2006) with bootstrap statistics worked out from 1000 rapid bootstrap replicates on the CIPRES NSF XSEDE resource. Bayesian inference (BI) of the phylogeny was worked out with the application of MrBayes v.3.2.2 (Ronquist et al. 2012) using the selected model operating Markov chain Monte Carlo (MCMC) analyses (Geyer 1991). Bayesian analyses extended to a standard deviation of split frequencies of 0.002 after 106 generations. After 25% preliminary burn in (Hall 2004), MrBayes was used to figure out the remaining trees' 50% majority rule consensus phylogram to enumerate the PPs (posterior probabilities) of the groups. MLBS and PP values over 50% and 0.50 are displayed in the resulting phylogenetic tree. The newly described species are exhibited in black bold font to highlight its position in the phylogenetic tree

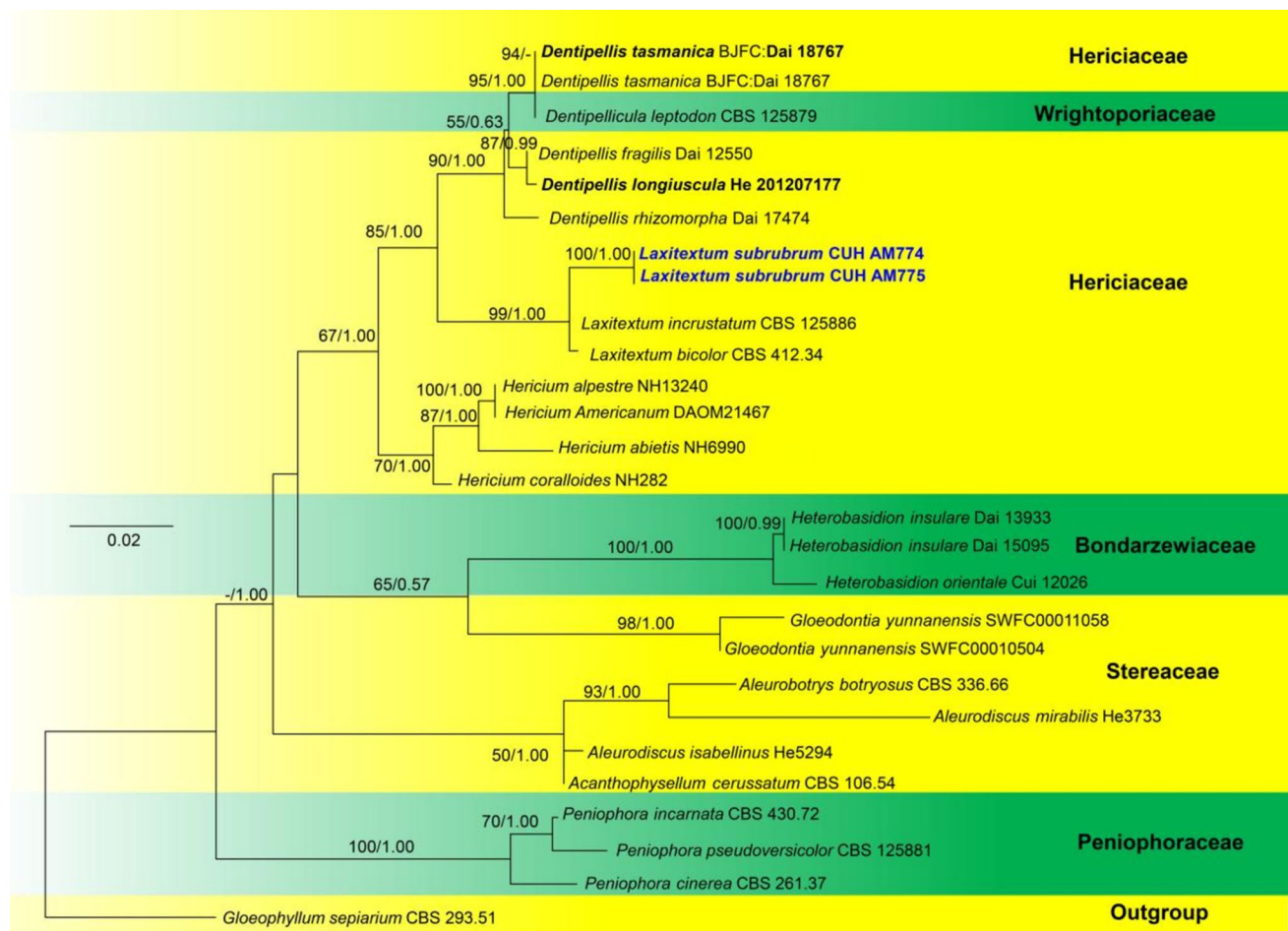
### *Russula* Pers.

**Notes:** *Russula* is a large, world-wide distributed genus growing in many types of forest ecosystem from tropical broad-leaved forest to subalpine coniferous forest (Li 2014; Li et al. 2015a, d; Looney et al. 2016). The genus is characterized by absence of veils or rings on stipes, brittle lamellae and context caused by the presence of sphaerocysts, and lacks of latex secretion when basidiomes are injured (Romagnesi 1985; Sarnari 1998). China has become one of the main sources of new species of *Russula* in recent ten years (Li et al. 2011, 2012, 2013a, b, 2015b, c, 2016, 2018a,

b, 2020; Ariyawansa et al. 2015; Zhao et al. 2015; Sang et al. 2016; Das et al. 2017; Jiang et al. 2017; Tibpromma et al. 2017; Zhang et al. 2017b; Li and Deng 2018; Song et al. 2018a, b, 2019; Caboň et al. 2019; Chen et al. 2019b; Wang et al. 2019a; Yuan et al. 2019; Buyck et al. 2020; Rossi et al. 2020; Wu et al. 2022b). Specific delimitation, DNA barcode selection and population genetics of *Russula* species have also been analysed (Li et al. 2010, 2019; Cao et al. 2013; Kleine et al. 2013; Looney 2015; Wang et al. 2015).

***Russula albocarpa* G.J. Li & Chun Y. Deng, *nom. nov.***





**Fig. 165** Phylogenetic analyses were based on data set of nrDNA LSU sequences. Reference sequences were selected from relevant literature (He and Zhao 2022; Hofstetter et al. 2019), BLAST searches (Altschul et al. 1997) and data retrieved from GenBank (Clark et al. 2016). Two sequences of the genus *Gloeophyllum*, was chosen as the outgroup for rooting purpose (He and Zhao 2022). ClustalX2 (Thompson et al. 1997) with the use of default settings, and finally the alignment was upgraded wherever needed using MEGA v. 7.0 (Kumar et al. 2016) for manual adjustments. For maximum likelihood (ML) analyses, the statistically best fit models of nucleotide substitution using Cyber Infrastructure for Phylogenetic Research (CIPRES) web portal (<https://www.phylo.org/portal2/>) were determined by jModeltest 2.1.6 (Darriba et al. 2012) on XSEDE (Miller et al. 2010). Based on the Bayesian information criterion (BIC), the GTR+I+G (5221.325866) model chosen as the most suitable model for the align-

ment. Maximum Likelihood analysis was performed using RAXML-HPC2 ver. 8.2.12 (Stamatakis 2006) with bootstrap statistics worked out from 1000 rapid bootstrap replicates on the CIPRES NSF XSEDE resource. Bayesian inference (BI) of the phylogeny was worked out with the application of MrBayes v.3.2.2 (Ronquist et al. 2012) using the selected model operating Markov chain Monte Carlo (MCMC) analyses (Geyer 1991). Bayesian analyses extended to a standard deviation of split frequencies of 0.002 after 106 generations. After 25% preliminary burn in (Hall 2004), MrBayes was used to figure out the remaining trees' 50% majority rule consensus phylogram to enumerate the PPs (posterior probabilities) of the groups. MLBS and PP values over 50% and 0.50 are displayed in the resulting phylogenetic tree. The newly described species are exhibited in black bold font to highlight its position in the phylogenetic tree

*Fungal Names Number*: FN 570688; *Facesoffungi number*: FoF 14524.

= *Russula leucocarpa* G.J. Li & Chun Y. Deng, Mycosystema 39(4): 624, 2020. *nom. illeg.*

*Etymology*: Referring to the white color of basidiomes.

*Holotype*: HGAS-MF 009910.

*Notes*: The name *Russula leucocarpa* G.J. Li & Chun Y. Deng (Li et al. 2020) is an illegitimate later homonym of *Russula leucocarpa* (T. Lebel) T. Lebel (Lebel 2017).

Thus a new name *Russula albocarpa* is proposed herein as a replacement of *R. leucocarpa* G.J. Li & Chun Y. Deng.

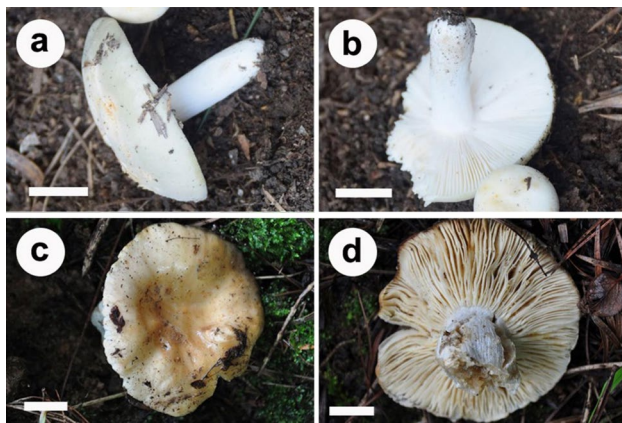
*Russula chlorina* G.J. Li & Chun Y. Deng, *sp. nov.*

*Fungal Names Number*: FN 570737; *Facesoffungi number*: FoF 14523; Figs. 166a, b, 167, 168a

*Etymology*: Referring to the pale yellowish green pileus.

*Holotype*: HBAU 15024.

*Basidiomes* small to medium sized. *Pileus* 29–37 mm in diam, first hemispheric, then convex, plane when mature, not depressed at center, a tinge of pale green centrally



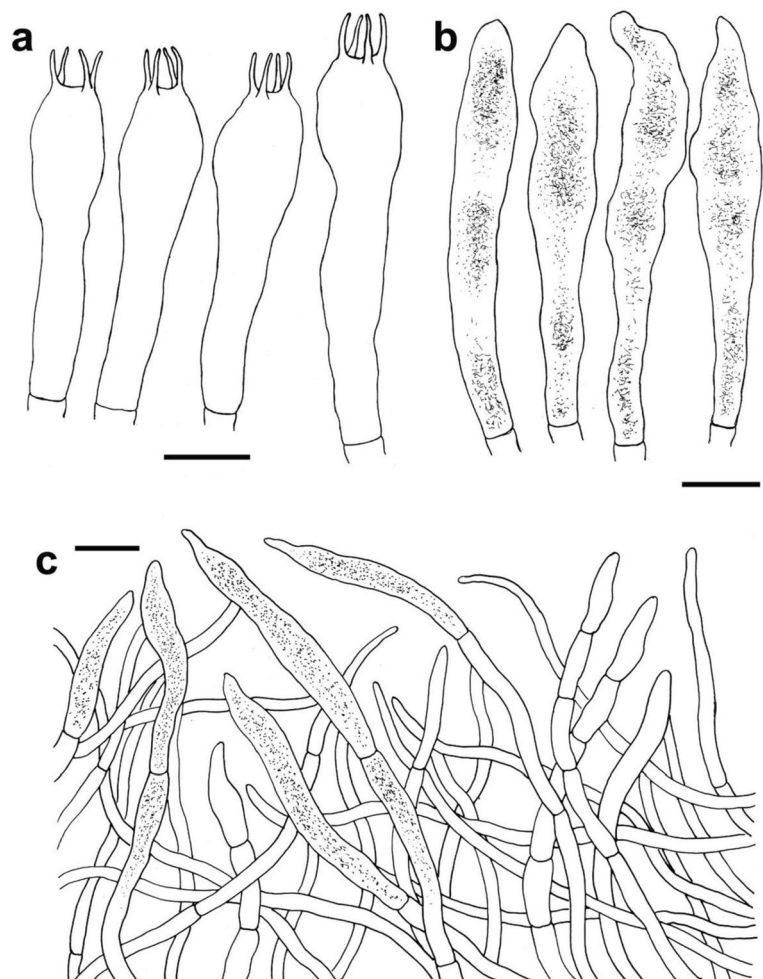
**Fig. 166** Basidiomes of new *Russula* species (**holotypes**). **a, b** *Russula chlorina*. **c, d** *R. luteocarpa*. Scale bars: **a–d** = 10 mm

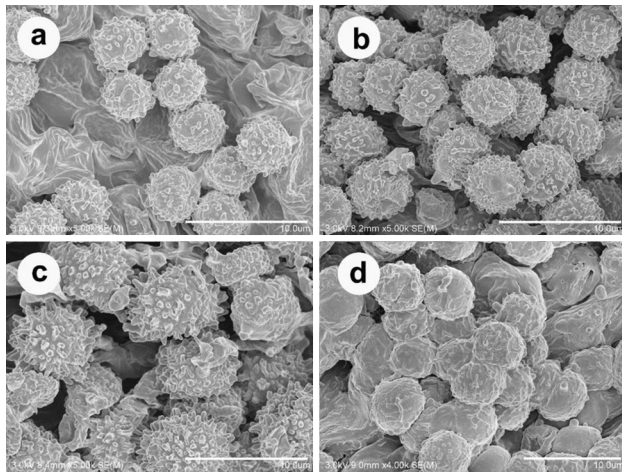
intermixed with yellow, light green (DDE5D9, E3E8DC), to pale yellowish green (B5CF61, BFD833), sometimes faded to a paler yellowish tinge (F1F2F1, EFEFDF), sometimes intermixed with yellowish ocher tinge (91672C, D8AC59), smooth, dull, slightly viscid when wet; margin not striate,

not cracked, peeling 1/4–1/3 from the edge, sometimes entirely faded to pale yellow (F1E5BE, EFEFDF). *Lamellae* adnate, 2–3 mm in height, 17–20 pieces per centimeter at edge, often forked near the stipes, Intervined, white (FFFFFF), unchanging when injured, *lamellulae* absent. *Stipes* 26–38 × 8–12 mm, central, cylindrical, rugulose longitudinally, white (FFFFFF), turning pale ocher (F1E5BE, F4EAE0) when bruised, smooth, dull, not viscid when wet, slightly tapered downward the base, first stuffed, hollow when old, annulus absent. *Context* 2 mm thick at pileus center, white (FFFFFF), unchanging, taste mild, smell indistinct. *Spore print* white to pale cream (Romagnesi Ib–IIa).

*Basidiospores* [150/3/3] (5.3–)5.6–6.9(–7.3) × (4.6–)4.9–5.9 μm,  $Q = 1.07–1.28$  (1.31),  $Q = 1.19 \pm 0.09$ ), hyaline, subglobose to broad ellipsoid, rarely globose and ellipsoid, ornamentations amyloid, up to 0.7 μm in height, composed of warts and short ridges interconnected as incomplete network, certain amount of isolated warts and short crests also exist, suprahilar area plage indistinct and inamyloid. *Basidia* 33–44 × 6–10 μm, subcylindrical, subclavate to clavate, rarely cylindrical, four-spored, projecting 5–20 μm beyond hymenium, hyaline, sterigmata 5–7 μm long. *Hymenial*

**Fig. 167** Microscopic structures of *Russula chlorina* (HBAU 15024, **holotype**). **a** Basidia. **b** Hymenial cystidia. **c** Suprapellis of pileipellis. Scale bars: **a–c** = 10 μm





**Fig. 168** Basidiospores of new *Russula* species (**holotypes**). **a** *Russula chlorina*. **b** *R. chrysea*. **c** *R. cruenta*. **d** *R. luteocarpa*. Scale bars: **a–d** = 10 µm

*cystidia* infrequent,  $58\text{--}77 \times 8\text{--}14$  µm, fusiform to clavate, sometimes ventricose towards the apex, contents crystal, unevenly distributed, blackish grey in sulfovanillin (SV), apex obtuse, rarely subacute. *Pileipellis* two layered, vaguely delimited from the spherocytes in context; *epipellis* a trichoderm, ca. 50–100 µm deep, hyphae erect, oblique to repent, hyaline, mostly 2–4 µm wide, rarely 5–7 µm; *terminal cells* fusiform, subulate to bayonet-shaped, attenuate towards the apex; *pileocystidia* abundant, 5–8 µm wide, rarely septate, cylindrical, narrowing towards the apex, contents crystal, unevenly distributed, blackish in SV; *subpellis* composed of somewhat gelatinized, densely interweaved, branched and septate, hyaline hyphae 2–5 µm wide, rarely intermixed with spherocytes 15–25 µm.

**Habitat:** Single or scattered in coniferous and broad-leaved intermixed forest.

**Material examined:** China, Guizhou Province, Yinjiang County, Chanxi Township, Fengxiangping Nature Reserve, in broad-leaved forest, 31 July 2019, Lu-Yao Shi, Guo-Jie Li 20190156 (HBAU 15024, **holotype**).

**GenBank number:** ITS = MT505888.

**Notes:** The new species *Russula chlorina* clusters with *R. grisea*, *R. ionochlora*, *R. subalpinogrisea* and an undescribed *Russula* specimen from Papua New Guinea (TU 110491) in phylogenetic analysis (Fig. 169). The morphological differences between *R. chlorina* and the other three known species are as follows: *R. grisea* differs by its violet, bluish, rarely greenish pileus, lilac shade on stipes, cream spore print (IIc), larger basidiospores ( $6.4\text{--}8.5 \times 5.4\text{--}6.5$  µm), and longer hymenial cystidia ( $6.4\text{--}8.5 \times 5.4\text{--}6.5$  µm) with lower warts up to 0.5 µm; *R. ionochlora* can be distinguished by its larger basidiospores ( $6.4\text{--}8 \times 4.7\text{--}6$  µm), inflated subapical cells, and bayonet shaped terminal cells in pileipellis (Sarnari

1998); *R. subalpinogrisea* is separated by its strongly viscous pileus, larger basidiospores ( $6.16\text{--}9.45 \times 5.85\text{--}8.38$  µm), longer basidia  $47\text{--}59 \times 10.5\text{--}13.5$  µm, narrower pileocystidia 4.8–5.2 µm wide, and a habitat of subalpine mixed forest (Das et al. 2018).

***Russula chrysea* G.J. Li & Chun Y. Deng, *sp. nov.***

**Fungal Names Number:** FN 570739; **Facesoffungi number:** FoF 14521; Figs. 168b, 170a, b, 171

**Etymology:** Referring to the pale yellowish tinge of pileus.

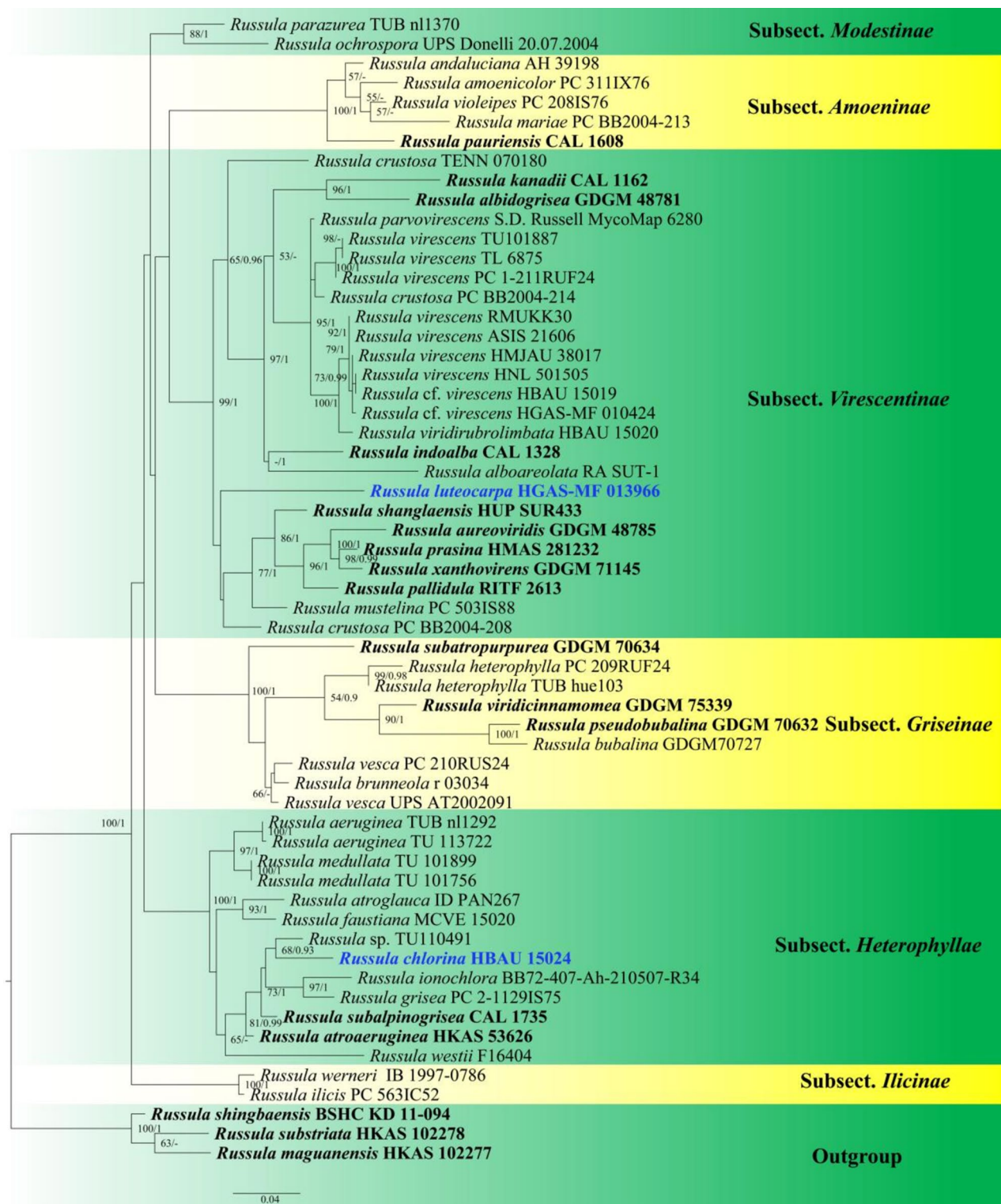
**Holotype:** HBAU 15023.

**Basidiomes** small to medium sized. **Pileus** 26–35 mm in diam, hemisphere to plano-convex, rarely applanate, a tinge of pale greenish yellow (E2E3A7, E3ECA6), sometimes faded to slight yellow tinge (EFEFDF, F5EED3), smooth, glabrous, not viscid when wet; *margin* not striate, not cracked, peeling 1/5–1/4 from the edge. **Lamellae** adnate, 2–3 mm in height, 16–20 pieces per centimeter at edge, sometimes forked near the stipes, interveined, white (FFFFFF), pale cream (F4EAE0) when mature, unchanging when bruised, lamellulae not observed. **Stipes** 25–33 × 5–11 mm, central to subcentral, cylindrical, slightly ventricose downward the base, rugulose longitudinally, white (FFFFFF), unchanging or slightly turning pale ocher (B78B5F, B6855A) when injured, smooth, dull, not viscid when wet, stuffed when young, hollow after mature, annulus absent. **Context** 1–3 mm thick at pileus center, white (FFFFFF), unchanging or turning pale yellow (F0E1BF, ECD6A3) when bruised, taste mild, smell indistinct. **Spore print** cream to pale ocher (Romagnesi IIc–IId).

**Basidiospores** [150/3/3]  $5.6\text{--}7.2$  (–7.6) × (4.3–) 4.6–6 µm,  $Q = 1.05\text{--}1.27$  (1.36),  $Q = 1.18 \pm 0.08$ , hyaline, subglobose to broad ellipsoid, rarely ellipsoid, ornamentations amyloid, up to 1 µm in height, composed of long ridges interconnected as complete reticulum, mixed up with a few isolated warts and short crests, suprahilar area plage distinct and amyloid. **Basidia** 34–52 × 9–12 µm, clavate to subclavate, rarely subcylindrical, four-spored, projecting 10–30 µm beyond hymenium, hyaline, sterigmata 4–7 µm long. **Hymenial cystidia** infrequent,  $56\text{--}71 \times 8\text{--}9$  µm, fusiform to subclavate, sometimes clavate, contents granulate, sparse, unchanging or slightly grey in SV, apex obtuse, rarely subacute. **Pileipellis** two layered, not clearly distinguished from the context; *epipellis* a trichoderm, ca. 30–70 µm deep; *terminal cells* hyaline, cylindrical, rarely branched, often 3–5 µm wide, seldom up to 8 µm; *primordial hyphae* abundant, septate, 5–8 µm wide, surface with acido-resistant incrustations; *pileocystidia* absent; *subpellis* composed of somewhat gelatinized, densely interlaced, rarely branched and septate, hyaline hyphae 3–6 µm wide.

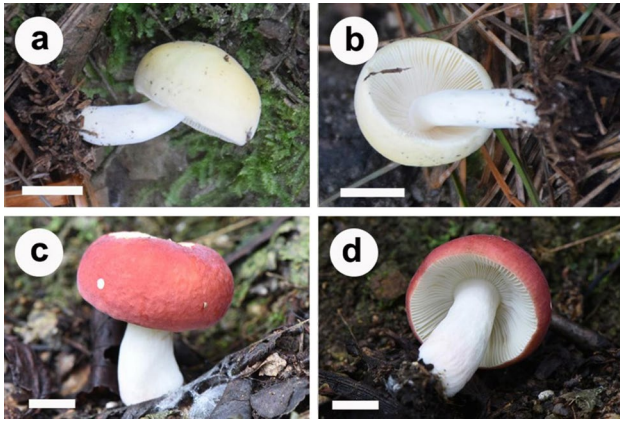
**Habitat:** Single or scattered in coniferous and broad-leaved intermixed forest.





**Fig. 169** Maximum likelihood tree illustrating the phylogeny of *Russula chlorina* and *R. luteocarpa* (holotype) with related species in *R. sect. Heterophyllae* based on ITS sequences. Branches are labeled with maximum likelihood bootstrap higher than 50%, and Bayesian

posterior probabilities more than 0.9 respectively. Sequences of *R. sect. Substriatinae* were used as outgroup to root trees. The new isolates are in bold



**Fig. 170** Basidiomes of new *Russula* species (**holotypes**). **a, b** *Russula chrysea*. **c, d** *R. cruenta*. Scale bars: **a–d** = 10 mm

**Material examined:** China, Guizhou Province, Yinjiang County, Chanxi Township, Fengxiangping Nature Reserve, in broad-leaved forest, 31 July 2019, 16 June 2014, Guo-Jie Li, Lu-Yao Shi 20190155 (HBAU 15023, **holotype**).

**GenBank number:** ITS = MT505890.

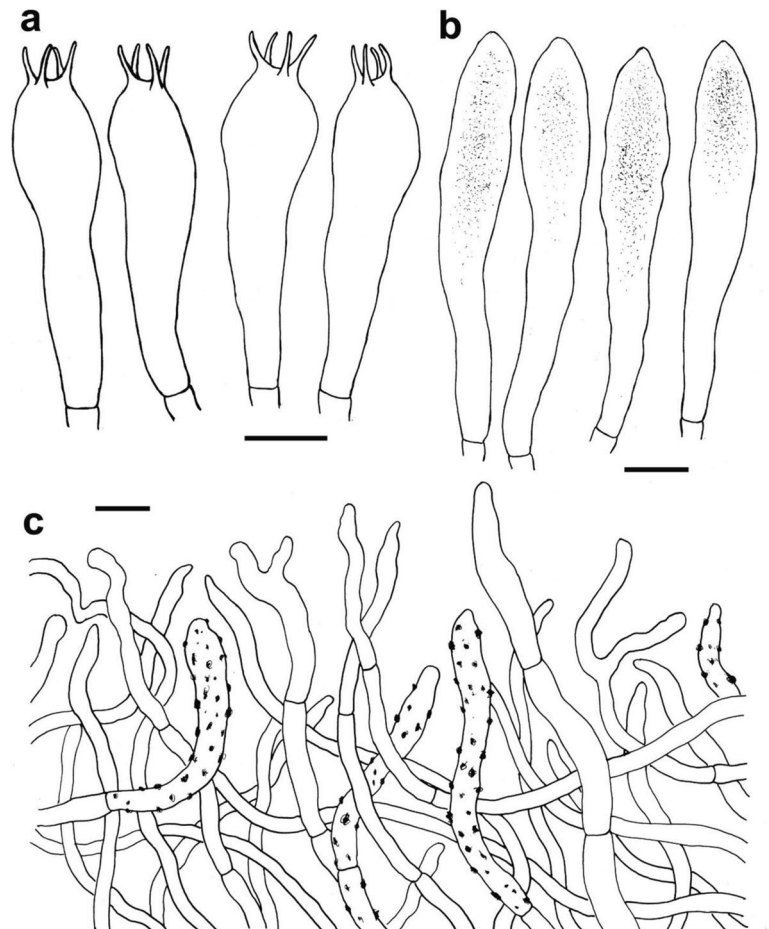
**Notes:** *Russula chrysea* forms an independent clade with two unidentified samples from Japan in phylogenetic analyses (Fig. 172). This clade has a close relationship with members of *Russula* section *Amethystinae*. The yellowish-capped species of this section, *R. helios*, *R. ochracea*, *R. postiana* and *R. risigallina* are different from *R. chrysea* in following morphological characters: *R. helios* has larger basidiospores ( $8\text{--}9.5 \times 6.3\text{--}7.8\ \mu\text{m}$ ) and narrower primordial hyphae  $3\text{--}4\ \mu\text{m}$  in diam; *R. ochracea* can be distinguished its thick and flashy pileus and larger basidiospores ( $7\text{--}9.2 \times 5.3\text{--}7.2\ \mu\text{m}$ ) with isolated warts; *R. postiana* is differentiated in having greenish yellow tinged pileus, larger basidiospores ( $8\text{--}11 \times 8.7\ \mu\text{m}$ ), and longer and wider hymenial cystidia ( $70\text{--}85 \times 10\text{--}12\ \mu\text{m}$ ); *R. risigallina* differs in often reddish tinged pileus, context smell of old fruit, larger basidiospores ( $7\text{--}9 \times 5.8\text{--}6.7\ \mu\text{m}$ ) with ornamentation composed of mostly isolated warts (Romagnesi 1985; Sarnari 2005).

***Russula cruenta* G.J. Li & Chun Y. Deng, *sp. nov.***

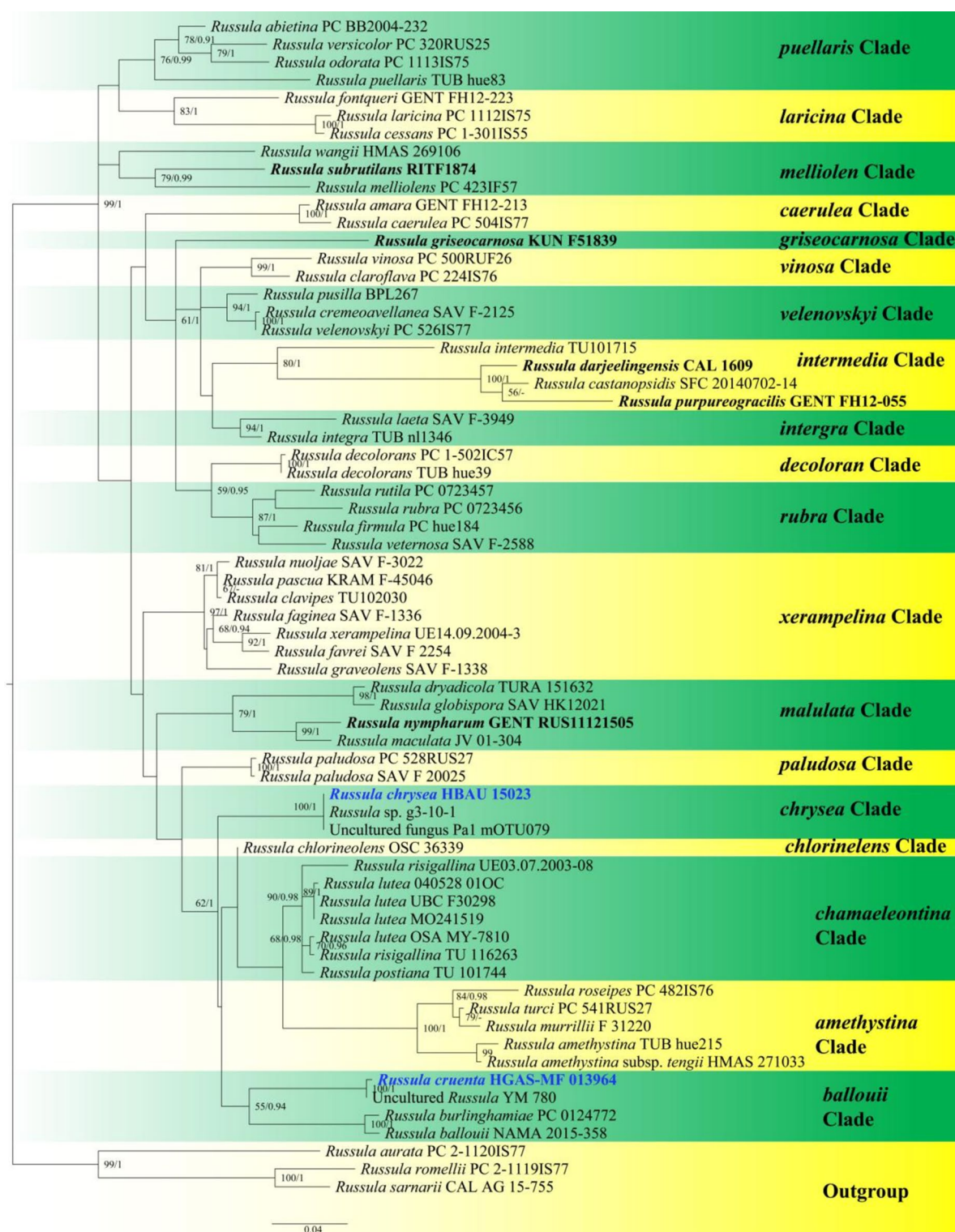
**Fungal Names Number:** FN 570740; **Facesoffungi number:** FoF 14522; Figs. 168c, 170c, d, 173

**Etymology:** Referring to the reddish tinge of pileus.

**Fig. 171** Microscopic structures of *Russula chrysea* (HBAU 15023, **holotype**). **a** Basidia. **b** Hymenial cystidia. **c** Suprapellis of pileipellis. Scale bars: **a–c** = 10  $\mu\text{m}$





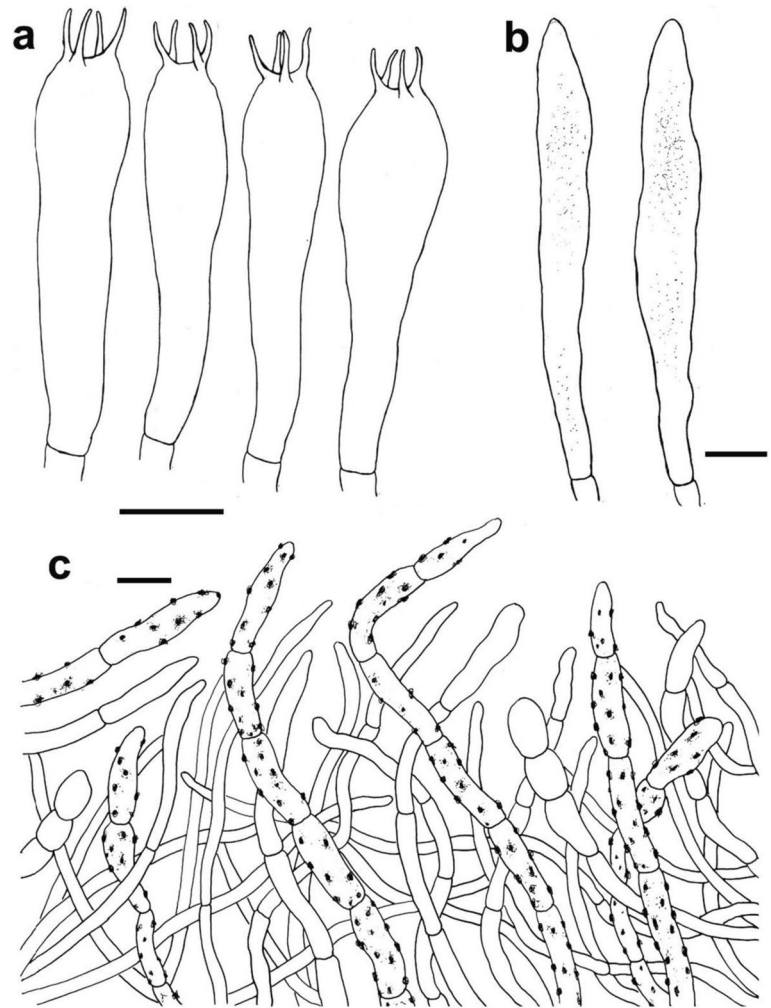


**Fig. 172** Maximum likelihood tree illustrating the phylogeny of *Russula chrysea* and *R. cruenta* (holotypes) with related species in “crown clades” as illustrated in Looney et al. (2016) based on ITS sequences. Branches are labeled with maximum likelihood bootstrap

higher than 50%, and Bayesian posterior probabilities more than 0.9 respectively. Sequences of *R. sect. Auratinae* were used as outgroup to root trees. The new isolates are in bold



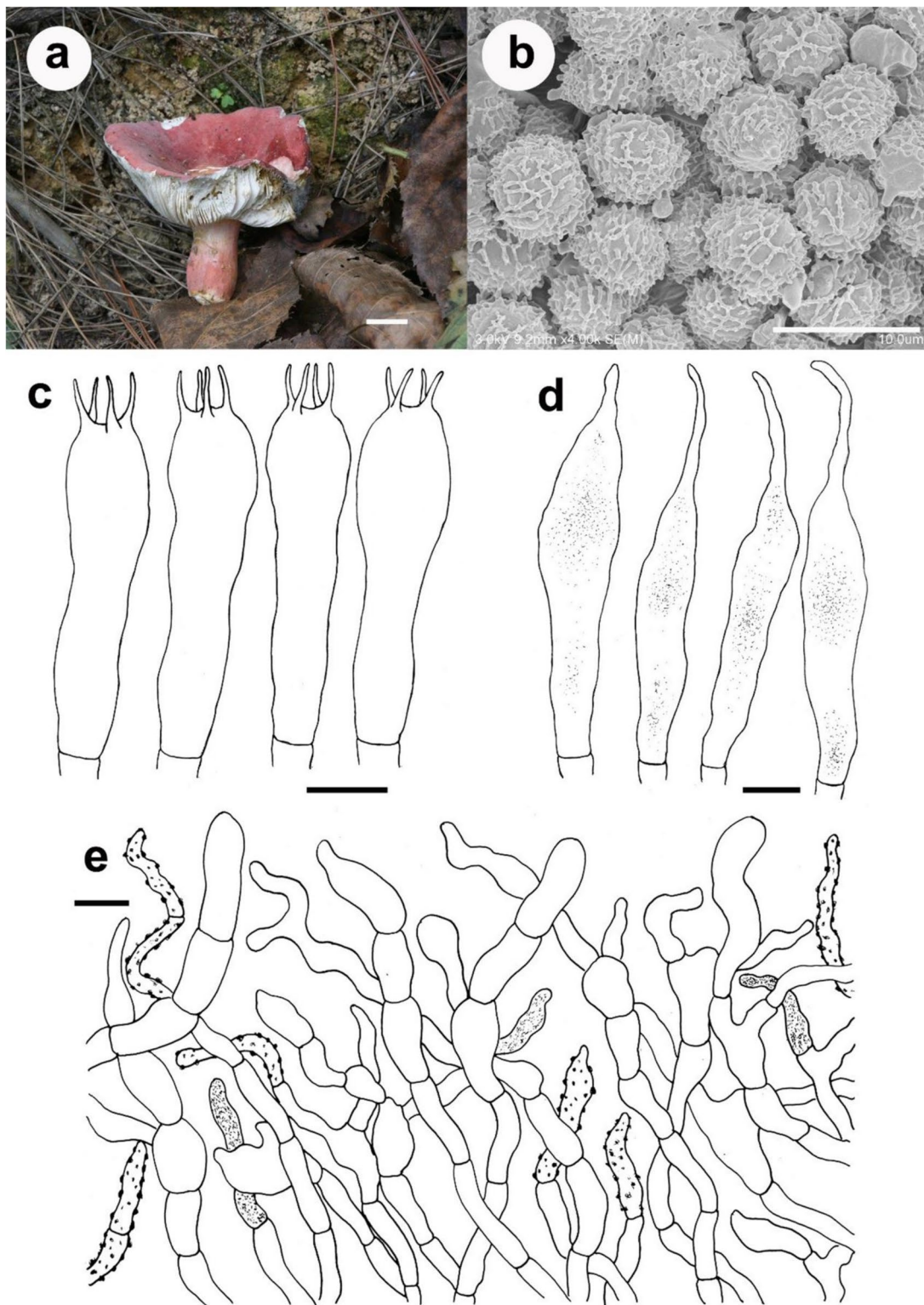
**Fig. 173** Microscopic structures of *Russula cruenta* (HGAS-MF 013964, **holotype**). **a** Basidia. **b** Hymenial cystidia. **c** Suprapellis of pileipellis. Scale bars: **a–c** = 10  $\mu$ m



*Holotype*: HGAS-MF 013964.

*Basidiomes* small to medium sized. *Pileus* 29–38 mm in diam, hemispheric when young, then convex, expanded when old, a tinge of brightly red (D66467, CB3145), often faded to a paler orange reddish tinge (F4512C, E9693D) towards the margin, smooth, glabrous, slightly viscid when wet; *margin* not striate, rarely cracked, exfoliated in small patches, peeling 1/3–1/2 from the edge. *Lamellae* adnate, 3–4 mm in height, 13–16 pieces per centimeter at edge, not forked, interveined, white (FFFFFF), pale cream (F4EAE0) when mature, unchanging when bruised, *lamellulae* not observed. *Stipes* 29–48  $\times$  10–13 mm, central to subcentral, cylindrical, rugulose longitudinally, white (FFFFFF), partly pale pink (F1ACB0, EEB0AE), unchanging when bruised, smooth, not viscid when wet, slightly ventricose downward the base, first stuffed, hollow when mature, annulus absent. *Context* 2 mm thick at pileus center, white (FFFFFF), unchanging when injured, taste mild to slightly acrid, smell indistinct to fruity. *Spore print* cream to pale ocher (Romagnesi IIc–IId).

*Basidiospores* [150/3/3] (6.6–) 7–5.9 (–10.3)  $\times$  (5.4–) 5.9–8.5 (–9.1)  $\mu$ m,  $Q = 1.00$ –1.34 (1.42),  $Q = 1.17 \pm 0.07$ , hyaline, subglobose, broad ellipsoid to ellipsoid, rarely globose, ornamentations amyloid, up to 1.2  $\mu$ m in height, composed of isolated warts rarely connected as short crests, not forming reticulum, suprahilar area plage distinct but inamyloid. *Basidia* 34–53  $\times$  10–12 (–15)  $\mu$ m, cylindrical, subcylindrical to subclavate, rarely clavate four-spored, projecting 10–20  $\mu$ m beyond hymenium, hyaline, sterigmata 4–6  $\mu$ m long. *Hymenial cystidia* scarce, 60–70  $\times$  8–10  $\mu$ m, fusiform to subclavate, sometimes subfusiform or clavate, contents sparsely distributed, granulate, greyish in SV, apex obtuse to subacute. *Pileipellis* two layered, not clearly delimited from the spherocytes in context; *epipellis* trichoderm, ca. 30–60  $\mu$ m deep, erect to ascending, rarely horizontal; *terminal cells* hyaline, sometimes inflated, 5–10  $\mu$ m wide; *primordial hyphae* abundant, 5–8  $\mu$ m wide, septate, surface with acido-resistant incrustations; *pileocystidia* absent; *subpelleis* composed of somewhat gelatinized, densely interlaced, rarely branched and septate, hyaline hyphae 3–6  $\mu$ m wide.



**Fig. 174** Microscopic structures of *Russula haematina* (HGAS-MF 013965, **holotype**). **a** Basidiomes. **b** Basidiospores. **c** Basidia. **d** Hymenial cystidia. **e** Suprapellis of pileipellis. Scale bars: **a** = 10 mm, **b–e** = 10  $\mu$ m

*Stipitipellis* a cutis, composed of parallel hyaline hyphae 3–5 µm wide.

**Habitat:** Single or scattered in coniferous and broad-leaved intermixed forest.

**Material examined:** China, Guizhou Province, Songtao County, in coniferous and broad-leaved intermixed forest, 20 October 2017, HGAS-MF 013964 (**holotype**).

**GenBank number:** ITS = MT505893.

**Notes:** The new species *Russula cruenta* clusters with an unknown *Russula* sample from Japan (Fig. 172). The *Cruenta* clade loosely groups with another clade which is composed of two North American species *R. ballouii* and *R. burlinghamiae* (Fig. 172). These two species can be distinguished from *R. cruenta* by their yellowish tinged pileus with fractured pigment patches. *Russula ballouii* also differs in basidiospore ornamentations forming incomplete reticulum (Peck 1913; Buyck et al. 2003). *Russula cruenta* is also morphologically similar to two reddish-capped species: one is the newly described Asian *R. clavatohyphata* from India, and the other is the North American species *R. luteobasis*. *Russula clavatohyphata* differs in having rare lamellulae at pileus margin, pink to pale red stipe, and appendages up to 30 µm long at the hymenial cystidium apex (Wang et al. 2019b). *Russula luteobasis* can be differentiated in its yellowish turning pileus, low basidiospore ornamentations 0.1–0.3 µm without isolated warts, and hymenial cystidium apex mainly with 4–10 µm long appendage (Adamčík et al. 2018).

***Russula haematina*** G.J. Li & Chun Y. Deng, *sp. nov.*

**Fungal Names Number:** FN 570741; *Facesoffungi* number: FoF 14527; Fig. 174

**Etymology:** Referring to the brightly red pileus.

**Holotype:** HGAS-MF 013965.

**Basidiomes** medium sized. **Pileus** 35–48 mm in diam, first plano-hemisphere, then convex, flat when mature, a tinge of brightly red (B82928, C52242), often intermixed with pinkish red tinge (F87B90, F58FA3), sometimes faded to a pinkish yellow tinge (FCC1A2, FED1B0) at center, smooth, dull, slightly viscid when wet; **margin** not striate, rarely cracked, peeling about 1/3 from the edge. **Lamellae** adnate, 2–4 mm in height, 12–16 pieces per centimeter at edge, not forked, interveined, white (FFFFFF), unchanging when bruised, lamellulae not observed. **Stipes** 31–43 × 10–14 mm, central to subcentral, cylindrical, rugulose longitudinally, pale pinkish red (E08087, F496A1), partly white (FFFFFF), turning pale ocher (B49B57, 9A7C37) when injured and old, smooth, dull, not viscid when wet, gradually attenuate downward the base, first stuffed, hollow when old, annulus absent. **Context** 3–4 mm thick at pileus center, white (FFFFFF), turning pale ochreous yellow (BC8B1F, DBB960) when bruised and old, taste mild, smell indistinct. **Spore print** pale cream (Romagnesi IIa–IIb).

**Basidiospores** [150/3/3] (6.3–) 6.6–8.4 (–8.8) × (5.3–) 5.7–7.7 (–8.2) µm,  $Q = 1.01–1.27$ ,  $Q = 1.13 \pm 0.06$ , hyaline, subglobose to broad ellipsoid, rarely globose, ornamentations amyloid, up to 0.7 µm in height, composed of long ridges interconnected as complete reticulum, isolated warts and short crests absent, suprahilar area plage distinct and amyloid. **Basidia** 31–42 × 10–12 µm, subcylindrical to subclavate, rarely clavate, four-spored, projecting 10–20 µm beyond hymenium, hyaline, sterigmata 5–7 µm long. **Hymenial cystidia** rare, 65–90 × 12–14 µm, fusiform, unchanging or slightly greyish in SV, apex constricted, mostly forming an elongate appendage. **Pileipellis** two layered, not clearly delimited from the spherocytes in context; **epipellis** a trichoderm, ca. 30–70 µm thick, hyphae erect to oblique, often branched, hyaline; **terminal cells** cylindrical to flexuous, 5–10 µm wide, often with a capitate or mucronate apex, rarely containing granulate contents slightly greyish in SV, subapical cells sometimes protruding, irregular, 7–14 µm wide; **primordial** abundant, hyphae 3–6 µm wide, cylindrical, surface with acido-resistant incrustations; **subpellis** composed of somewhat gelatinized, loosely interwoven, rarely branched and septate, hyaline hyphae 3–7 µm wide, rarely intermixed with spherocytes 10–25 µm in diam.

**Habitat:** Single or scattered in coniferous and broad-leaved intermixed forest.

**Material examined:** China, Guizhou Province, Guiyang, Yunyan District, Qianlingshan Park, in coniferous and broad-leaved forest, 1 September 2019, Chun-Ying Deng 2018–48 (HGAS-MF 013965, **holotype**).

**GenBank number:** ITS = MT505891.

**Notes:** Phylogenetically, in *Russula* sect. *Roseinae* (Fig. 175), the new species *Russula haematina* forms a clade with specimens of *Rosa* clade. The other members of the clade can be distinguished from *R. haematina* as follows: *R. amarissima* has violaceous purple to cigar brown pileus, bitter taste of context, narrower basidia 8–10 µm wide, and longer hymenial cystidia up to 115 µm long; *R. rosea* has longer hymenial cystidia with obtuse apex and narrower epipellis hyphae 3.2–4.5 µm wide (Romagnesi 1985; Sarnari 2005). There are two species, *R. guangxiensis* and *R. hakkae* of *R. sect. Roseinae* which were described from South China. These two species also have brightly red pileus. *Russula guangxiensis* can be differentiated from *R. haematina* by its white stipe, mild tasted context, smaller basidiospores (5.9–6.9 × 4.9–6.1 µm), and shorter and narrower hymenial cystidia (55–63 × 7–12 µm); *R. hakkae* differs in the ornamentations of basidiospores composed of dense and isolated warts (0.9–1.2 µm in height), longer and wider basidia, and round to subacute, often shortly appendiculate to subcapitate apex of hymenial cystidia (40–50 × 10–15 µm, Ariyawansa et al. 2015).

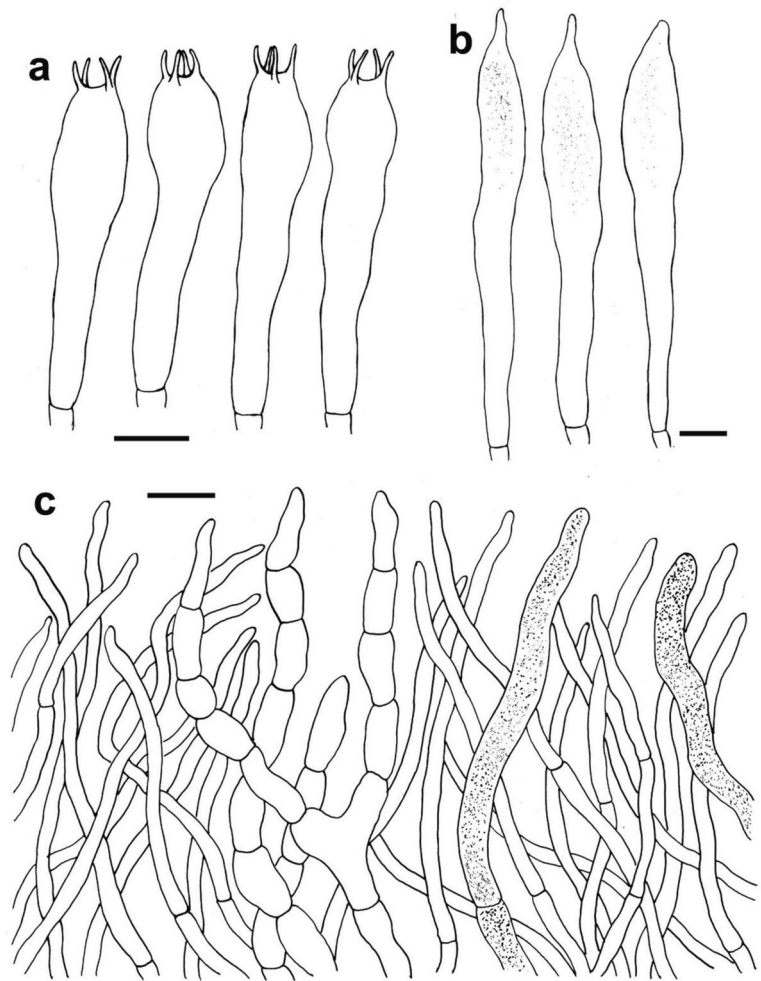


terior probabilities more than 0.9 respectively. Sequences of *R. sect. Lilaceinae* were used as outgroup to root trees. The new isolates are in bold

*Basidiomes* medium sized. *Pileus* 37–48 mm in diam, first plano-hemisphere to convex, turning applanate to slightly depressed at center when mature, ochrous tinged, brownish yellow (947563, B0876D) to dark yellow (BC9C69, D1A14A), faded to a pale yellow tinge (F1DE9C, F9E397) towards the margin, smooth, glabrous, somewhat sticky when wet; *margin* not striate to slightly striate, seldom

cracked, peeling 1/3–1/2 from the edge. *Lamellae* adnate, 3–4 mm in height, 14–18 pieces per centimeter at edge, often forked near the stipes, interveined, white (FFFFFFF) when young, cream (F1DDCF, F0D8C3) when mature, unchanging when bruised, *lamellulae* not observed. *Stipes* 42–56 × 10–14 mm, central to subcentral, cylindrical, rugulose longitudinally, white (FFFFFFF), slowly turning pale ocher (B88E4D, B48834) when bruised, smooth, dull, not viscid when wet, slightly attenuate downward the base, first stuffed, hollow when old, *annulus* absent. *Context* 2–3 mm thick at pileus center, slightly turning white (FFFFFFF), pale ocher (BD7B27, D5A372) when injured, taste mild, smell indistinct. *Spore print* cream (Romagnesi IIc–IID).

**Fig. 176** Microscopic structures of *Russula luteocarpa* (HGAS-MF 013966, **holotype**). **a** Basidia. **b** Hymenial cystidia. **c** Suprapellis of pileipellis. Scale bars: **a–c** = 10  $\mu$ m



*Basidiospores* [150/3/3] (4.8–)5.1–7.1 (–7.4)  $\times$  (4.1–)4.4–6.6 (–7.1)  $\mu$ m,  $Q = 1.02$ –1.31 (1.36),  $Q = 1.18 \pm 0.07$ , hyaline, subglobose to broad ellipsoid, rarely globose and ellipsoid, ornamentations amyloid, up to 0.5  $\mu$ m in height, composed of long ridges interconnected as nearly complete reticulum, often intermixed with rare isolated warts, suprahilar area plage indistinct and inamyloid. *Basidia* 32–44  $\times$  7–10  $\mu$ m, cylindrical, subcylindrical to subclavate, rarely clavate four-spored, projecting 10–20  $\mu$ m beyond hymenium, hyaline, sterigmata 4–6  $\mu$ m long. *Hymenial cystidia* 61–76  $\times$  11–14  $\mu$ m, fusiform to cylindrical, sometimes subclavate, contents granulate, sparse, weakly greyish in SV, apex lanceolate, sometimes subacute. *Pileipellis* two layered, indistinctly delimited from the spherocytes in context; *epipellis* a trichoderm, ca. 100–150  $\mu$ m thick, hyphae erect to ascending, rarely branched, cylindrical, hyaline, 2–4  $\mu$ m wide, rarely septate, some hyphae inflated to 5–7  $\mu$ m, multi-septate; *terminal cells* attenuated towards the apex; *pileocystidia* rare, 6–8  $\mu$ m wide, cylindrical to clavate, often with an obtuse apex, contents dense, granulate, blackish in SV; *subpellis* composed of somewhat gelatinized, densely

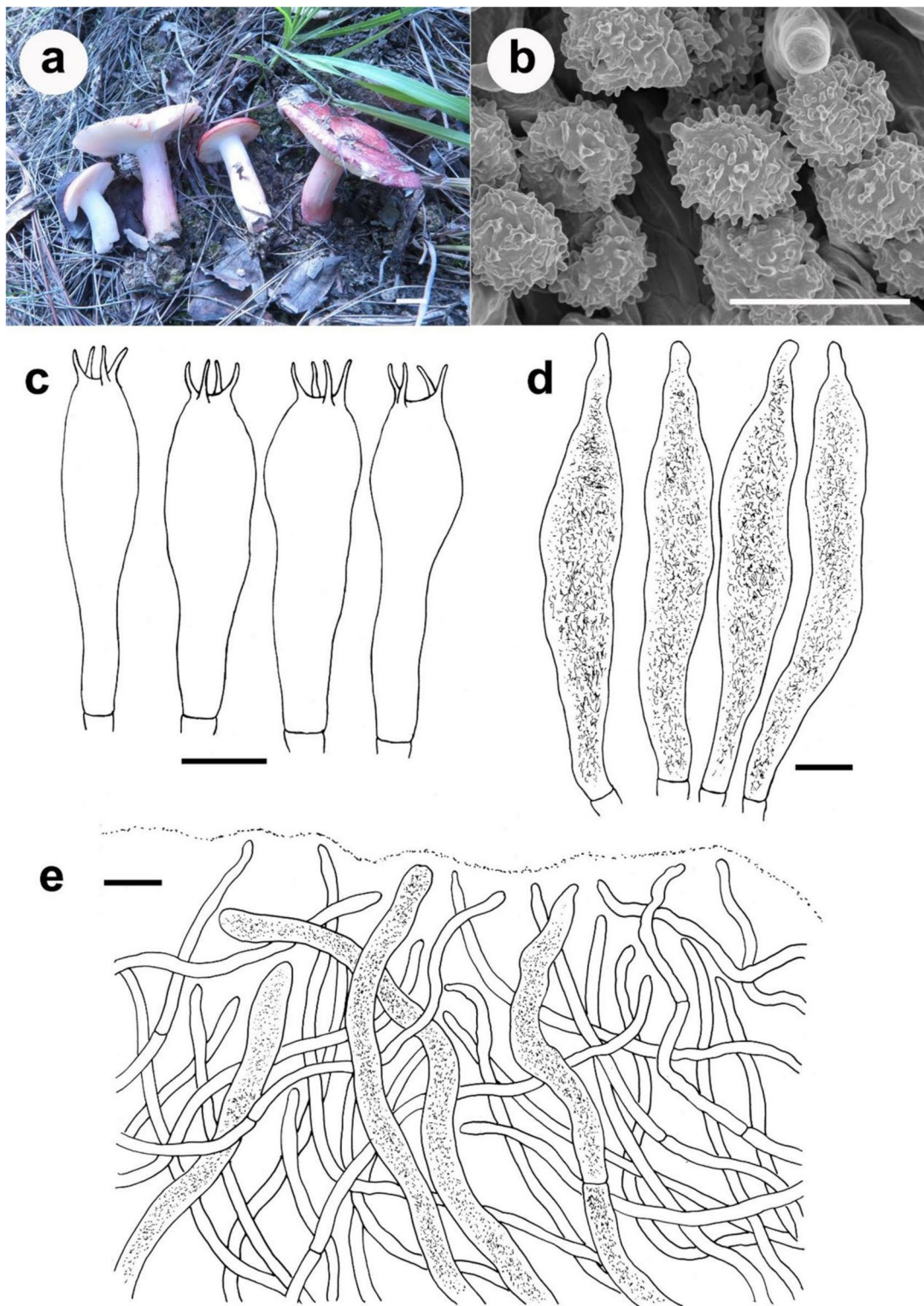
interlaced, rarely branched and septate, hyaline hyphae 3–6  $\mu$ m wide.

*Habitat*: Single or scattered in coniferous and broad-leaved intermixed forest.

*Material examined*: China, Guizhou Province, Weining County, Caohai Nature Reserve, in coniferous and broad-leaved intermixed forest, 4 August 2016, Chun-Ying Deng CH2016080404 (HGAS-MF 013966, **holotype**).

*GenBank number*: ITS = MT505889.

*Notes*: Topologically, *Russula luteocarpa* lies in the clade of *Russula* subsect. *Heterophyllae*, but the phylogenetic position of this new species in this subsection is still not clear (Fig. 168). Future multi-gene phylogenetic analyses are needed to clarify the concrete relationships between *R. luteocarpa* and the other species of this subsection. The viscid yellowish, not furfuraceous or areolate pileus of *R. luteocarpa* is unique in *R.* subsect. *Heterophyllae*, but is reminiscent of *R.* section *Ingratae*. However, members of that section are different from *R. luteocarpa*, because they often have strongly striate pileus margin and acid context taste.



**Fig. 177** Microscopic structures of *Russula sanguinolenta* (HGAS-MF 013963, **holotype**). **a** Basidiomes. **b** Basidiospores. **c** Basidia. **d** Hymenial cystidia. **e** Suprapellis of pileipellis. Scale bars: **a** = 10 mm, **b–e** = 10  $\mu$ m



***Russula sanguinolenta*** G.J. Li & Chun Y. Deng, *sp. nov.*

*Fungal Names Number*: FN 570742; *Facesoffungi number*: FoF 14525; Fig. 177

*Etymology*: Referring to the brightly reddish tinge of pileus.

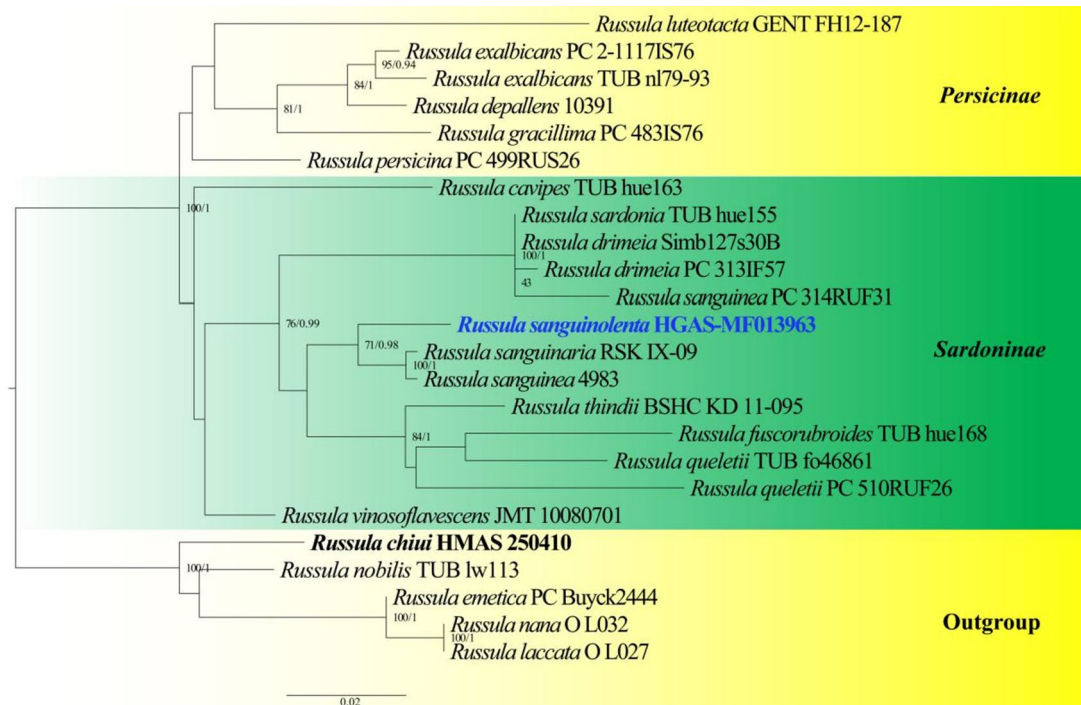
*Holotype*: HGAS-MF 013963.

*Basidiomes* small to medium sized. *Pileus* 29–57 mm in diam., first hemispheric, then convex, applanate when mature, a tinge of brightly red (9B2335, BC243C), often partly faded to a paler pinkish red tinge (EC5D73, EC5D73) at center, rarely turning pale orange pink (EEB0AE, FEA188) to white (FFFFFF) smooth, glabrous, slightly viscid when wet; *margin* slightly striate, rarely cracked, peeling 1/4–1/2 from the edge. *Lamellae* adnate, 2–4 mm in height, 11–18 pieces per centimeter at edge, rarely forked near the stipes, interveined, white (FFFFFF) first, pale cream (F4EAE0) when mature, unchanging when bruised, lamellulae not observed. *Stipes* 29–48 × 10–13 mm, central to subcentral, cylindrical, rugulose longitudinally, pale pink (E08087, FABC B1), rarely faded to white (FFFFFF), a darker pale pinkish red tinge (ED5656, FA7268) near the base, unchanging when injured, smooth, dull, not viscid when wet, slightly tapered downward the base, first stuffed, hollow when mature, annulus absent. *Context* 3–4 mm thick at pileus center, white (FFFFFF),

unchanging, taste acrid, smell indistinct. *Spore print* cream to pale ocher (Romagnesi IIc–IId).

*Basidiospores* [150/3/3] (5.6–) 6.1–8 (–8.5) × (4.7–) 5–6.8 (–7.1) μm,  $Q = (1.00–)1.05–1.37(–1.41)$ ,  $Q = 1.21 \pm 0.09$ , hyaline, subglobose to broad ellipsoid, rarely globose and ellipsoid, ornamentations amyloid, up to 1 μm in height, composed of short crests interconnected as incomplete network, intermixed with a few isolated warts, suprahilar area plage indistinct but amyloid. *Basidia* 34–43 × 9–13 μm, clavate to subclavate, rarely cylindrical, four-spored, projecting 15–25 μm beyond hymenium, hyaline, sterigmata 5–6 μm long. *Hymenial cystidia* abundant, 57–99 × 10–16 μm, fusiform, sometimes clavate, ventricose towards the apex, contents crystal, densely distributed, blackish in SV, apex contracted. *Pileipellis* two layered, distinctly delimited from the spherocytes in context; *epipellis* an ixotrichoderm, ca. 100–150 μm thick, hyphae hyaline, ascending to erect, rarely septate, 2–4 μm wide; *terminal cells* cylindrical, tapering towards the apex; *pileocystidia* abundant, cylindrical to subclavate, 6–9 μm wide, contents granulate, dense, blackish in SV, apex obtuse, sometimes tapering; *subpellis* a cutis, hyphae repent, slightly gelatinized, densely interweaved, rarely branched, septate, hyaline, 3–6 μm wide.

*Habitat*: Scattered in coniferous forest.



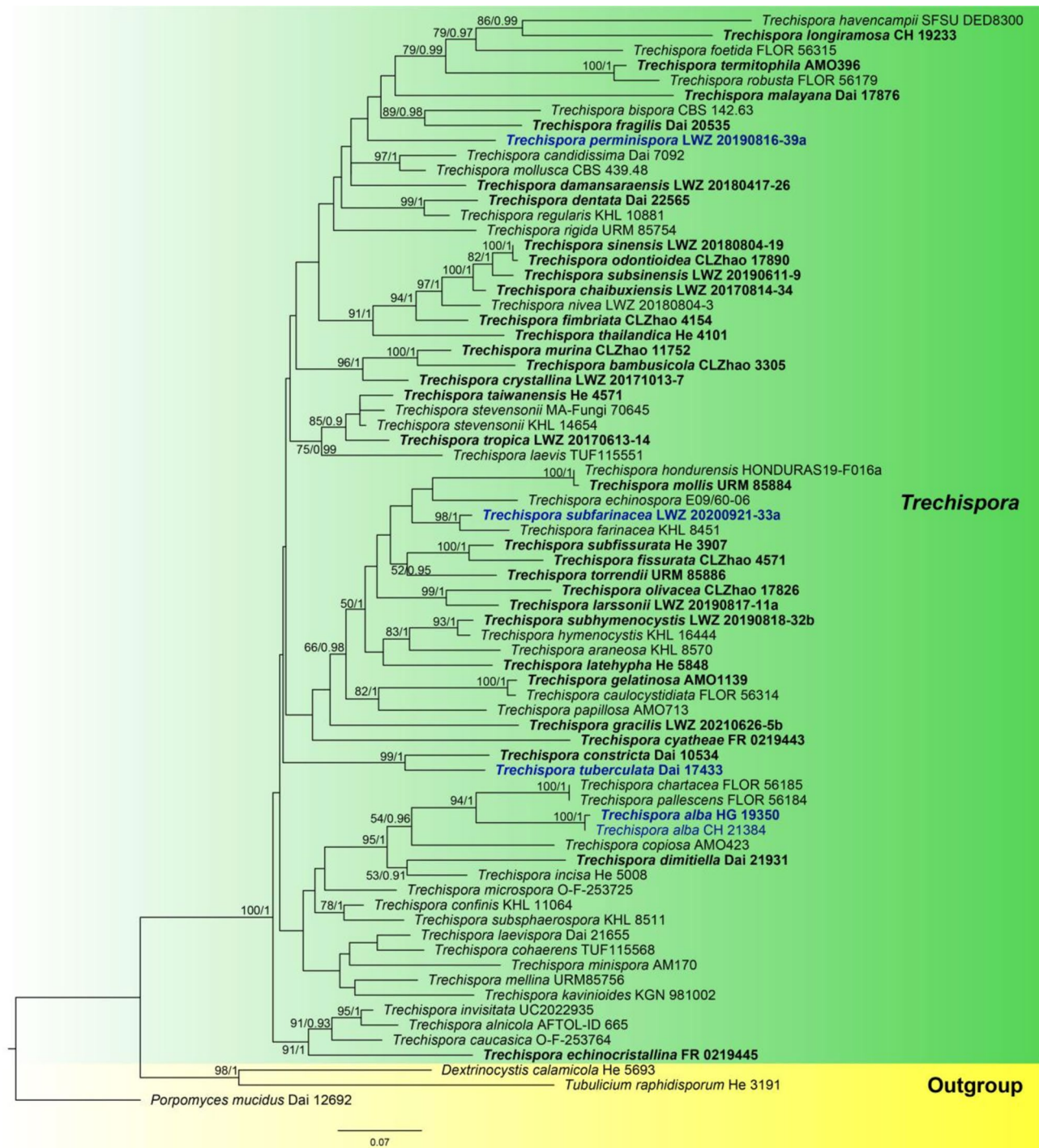
**Fig. 178** Maximum likelihood tree illustrating the phylogeny of *Russula sanguinolenta* (**holotype**) with related species in *R.* sect. *Persicinae* and *R.* sect. *Sardoninae* based on ITS sequences. Branches are labeled with maximum likelihood bootstrap higher than 50%,

and Bayesian posterior probabilities more than 0.9 respectively. Sequences of *R.* sect. *Emeticinae* were used as outgroup to root trees. The new isolates are in bold

**Material examined:** China, Guizhou Province, Guiyang, Huaxi District, Fengbaoyun Village, in coniferous forest, 1 July 2017, Chun-Ying Deng 2017–131 (HGAS-MF 013963, **holotype**).

**GenBank number:** ITS = MT505892.

**Notes:** A combination of brightly red pileus, pinkish tinged stipe, cream to ochre spore print, and a habitat of coniferous forest indicates this new specie close to *Russula*



**Fig. 179** Phylogeny generated by the maximum likelihood algorithm based on combined ITS and nLSU regions is presented along with the bootstrap values and the Bayesian posterior probabilities above 50% and 0.8, respectively, at the nodes. *Dextrinocystis calamicola*

He 5693, *Porpomyces mucidus* Dai 12692 and *Tubulicium raphidisporum* He 3191 were selected as the outgroup taxa. Holotypes are in bold and the newly generated sequences are in blue

*sanguinea*. This affinity is also supported in phylogenetic analyses (Fig. 178). The *R. sanguinolenta* group includes *R. sanguinea* and *R. sanguinaria*. *Russula sanguinea* differs from *R. sanguinolenta* by its subdecurrent lamellae, larger basidiospores ( $7.2\text{--}9.6 \times 6.3\text{--}7.4\text{ }\mu\text{m}$ ) with lower ornamentations up to  $0.8\text{ }\mu\text{m}$ , longer basidia ( $40\text{--}54 \times 9\text{--}12\text{ }\mu\text{m}$ ), and wider hymenial cystidia up to  $16\text{ }\mu\text{m}$  (Sarnari 1998). *Russula sanguinaria* is distinguished from *R. sanguinolenta* by its yellowish turing pileus and larger basidiospores ( $7.5\text{--}9 \times 6.5\text{--}7.5\text{ }\mu\text{m}$ , Rauschert 1989). The other two closely related species are *R. helodes* and *R. renidens*. *Russula helodes* is distinguished by distinctly greyish context, basidiospores up to  $10.5\text{ }\mu\text{m}$  in diam with ornamentations of a complete network, and a habitat of *Sphagnum* environment. *Russula renidens* differs in its shiny to glazer pileus, abundant lamellulae in pileus margin, larger basidiospores ( $7.5\text{--}9 \times 6.5\text{--}7.5\text{ }\mu\text{m}$ ), and narrower hymenial cystidia up to  $11\text{ }\mu\text{m}$  wide (Sarnari 1998).

#### *Trechisporales* K.H. Larss.

**Notes:** *Trechisporales* was erected by Hibbett et al. (2007) to replace its equivalent order namer *Hydnodontaes*, due to that the type genus *Trechispora* has a priority over the synonym *Hydnodon* and is the speciose genus in this order. Recently, Liu et al. (2022b) reduced the circumscription of *Trechisporales* by segregating *Sertulicium* and *Sistotremastrum* to a new order. Phylogenetically, *Trechisporales* is a well supported order, accommodating a single family *Hydnodontaceae*.

#### *Hydnodontaceae* Jülich.

**Notes:** *Hydnodontaceae* was erected by Jülich (1981) with *Hydnodon* as the type genus that is a later synonym of *Trechispora* (Ryvarden 2002). For now, 12 genera are accepted in this family (Liu et al. 2022b).

#### *Trechispora* P. Karst.

**Notes:** The genus *Trechispora* was erected by Karsten (1980) with *T. onusta* as the type species. The main morphological character that defines the genus is remarkable ampullate hyphal septa, and in addition, most species in this genus have ellipsoid, ornamented basidiospores (Liu et al. 2022b). A total of 90 species have been previously recorded all over the world (Liu et al. 2022b; Luo and Zhao 2022b). Here, four additional new lineages revealed from the phylogenetic analysis (Fig. 179) are described as new species.

#### *Trechispora alba* S.L. Liu, G. He & L.W. Zhou, *sp. nov.*

**Index Fungorum number:** IF 901060; **Facesoffungi number:** FoF 14813; **Figs.** 180, 181, 182

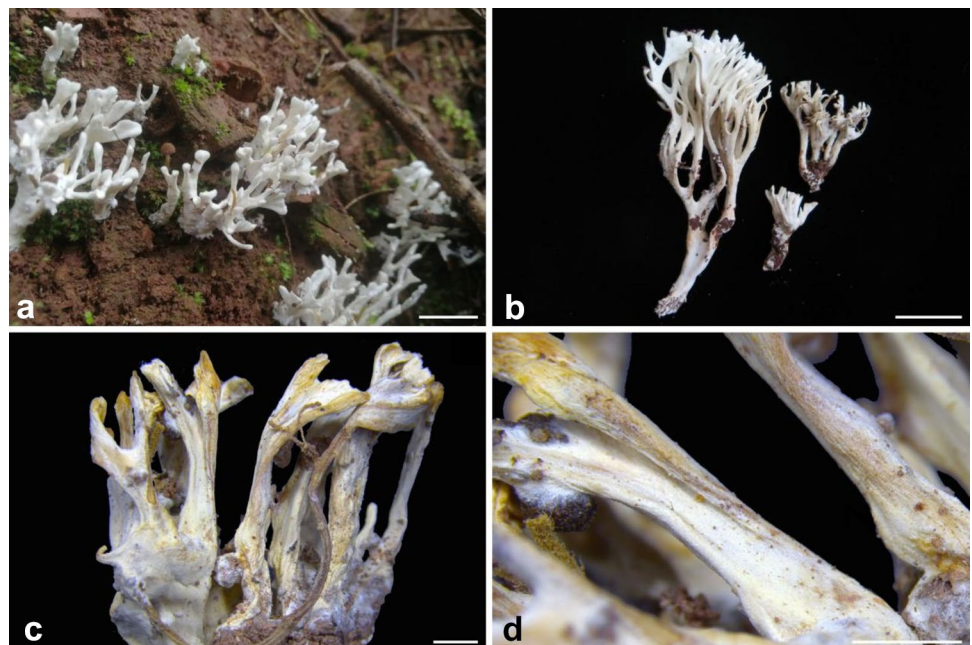
**Etymology:** *alba* (Lat.) referring to the white colour of basidiomes.

**Holotype:** HG 19350 (HMAS).

**Diagnosis:** Differing from *Trechispora pallescens* in slightly wider basidiospores (de Meiras-Ottoni et al. 2021).

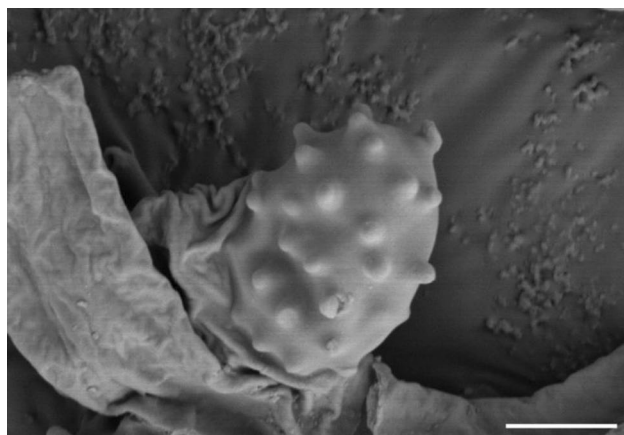
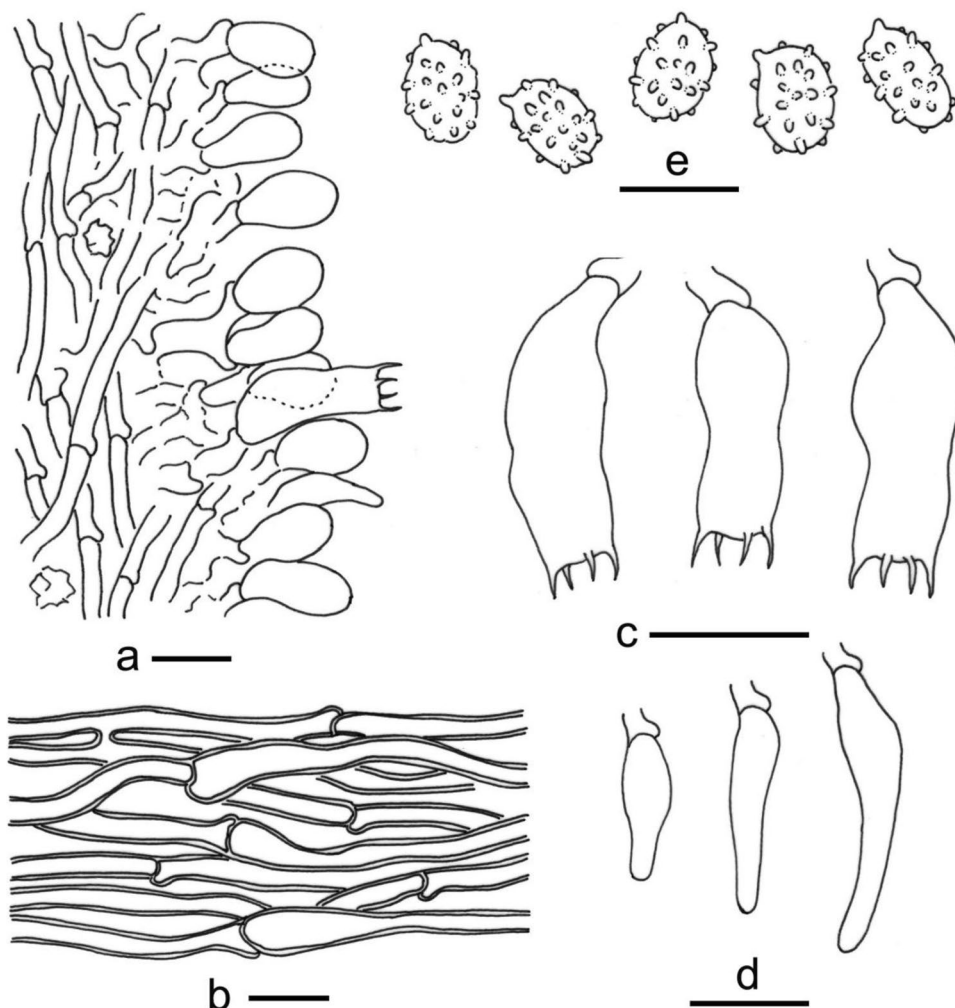
**Basidiomes** annual, clavarioid, solitary or in small groups, densely branched, moderately open, fleshy consistency, white when fresh, cream to curry-yellow when dry, 2–8 cm high. **Branches** polychotomous, axils V-shaped, somewhat palmately branched, slightly flattened, 2–5 mm wide, occasionally flattened to 10 mm, tips subacute to blunt. **Stipe** white to cream, 5–15  $\times$  2–3 mm.

**Fig. 180** Basidiomes of *Trechispora alba* (HG 19350, holotype). Scale bars: **a** = 1 cm, **b** = 1 mm





**Fig. 181** Microscopic structures of *Trechispora alba* (HG 19350, **holotype**). **a** A vertical section of basidiomes. **b** Hyphae from subiculum. **c** Basidia. **d** Cystidia. **e** Basidiospores. Scale bars: 10  $\mu$ m



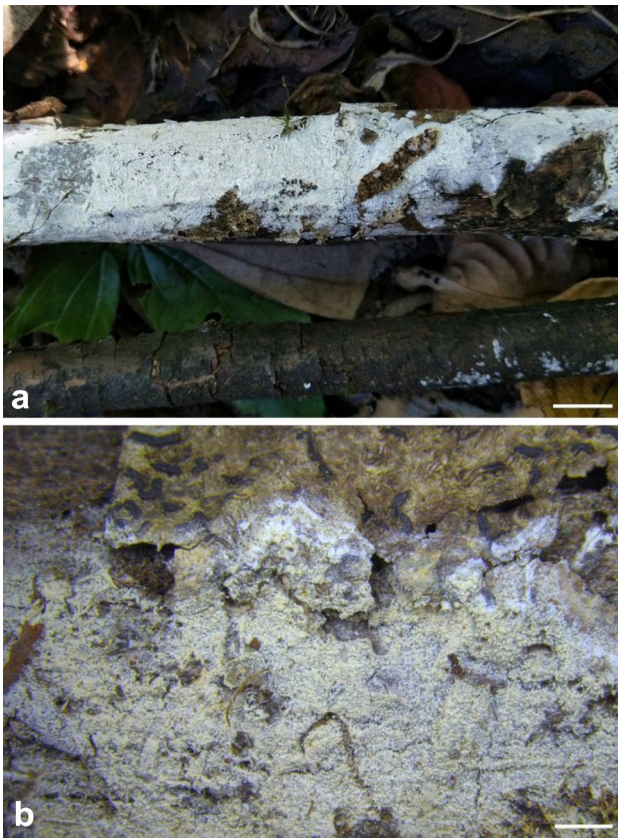
**Fig. 182** Scanning electron micrograph of basidiospores of *Trechispora alba* (HG 19350, **holotype**). Scale bars: 2  $\mu$ m

*Hyphal system* monomitic; *generative hyphae* with clamp connections. *Subicular hyphae* hyaline, thick-walled, cylindrical, moderately branched and septate, subparallel,

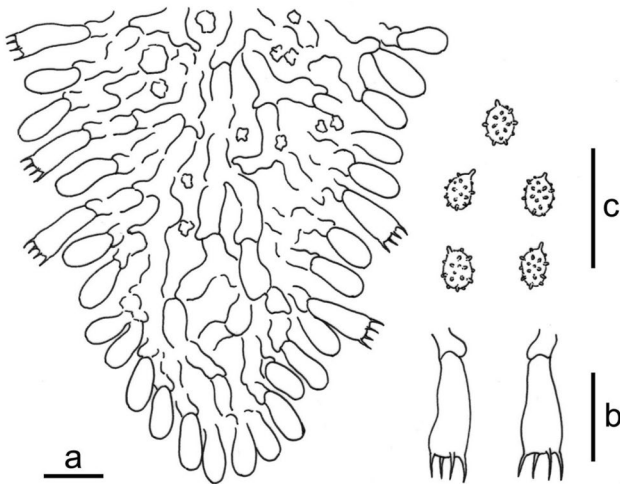
2–3.5  $\mu$ m in diam; *ampullate septa* usually present in the hyphae at the base of the stipe, up to 6–7  $\mu$ m wide. *Subhyphal hyphae* short-celled and wide, 2–3.5  $\mu$ m in diam, much branched. *Basidia* suburniform to subclavate, hyaline, thin-walled, with four sterigmata and a basal clamp connection, agglutinated, 20–26  $\times$  5–8  $\mu$ m; *basidioles* in shape similar to basidia, but slightly smaller. *Basidiospores* ellipsoid, hyaline, thin-walled, aculeate, IKI–, CB–, 5–7(–7.5)  $\times$  (3.3–)3.5–5(–5.5)  $\mu$ m, L = 5.7  $\mu$ m, W = 4.1  $\mu$ m, Q = 1.4 (n = 60/2).

*Material examined*: China, Yunnan Province, Xishuangbanna Dai Autonomous Prefecture, Mengla County, on ground, 30 July 2019, G. He and Y. Chen, HG 19350 (HMAS, **holotype**); Yunnan Province, Honghe Hani and Yi Autonomous Prefecture, Honghe County, Dayangjie Township, on ground, 22 August 2021, J.W. Guo, CH 21384 (HMAS).

*GenBank numbers*: HG 19350: ITS = OM523516; CH 21384: ITS = OR557258.

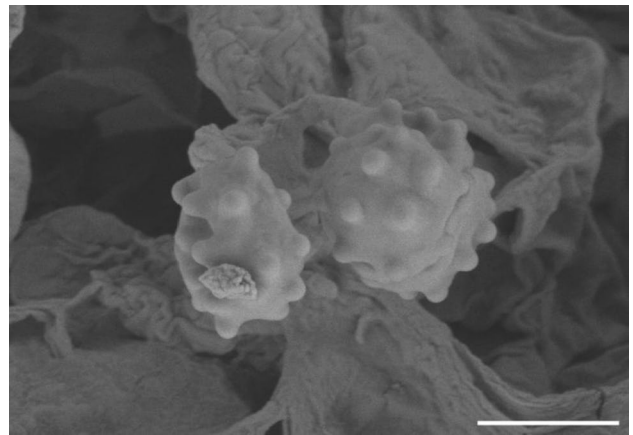


**Fig. 183** Basidiomes of *Trechispora perminispora* (LWZ 20190816-39a, **holotype**). Scale bars: **a** = 1 cm, **b** = 1 mm



**Fig. 184** Microscopic structures of *Trechispora perminispora* (LWZ 20190816-39a, **holotype**). **a** A vertical section of basidiomes. **b** Basidia. **c** Basidiospores. Scale bars: 10  $\mu$ m

**Notes:** *Trechispora alba* is similar to *T. caulocystidiatus* and *T. gelatinosa* by white to yellowish white basidiomes when fresh and the presence of cystidial structures. However, *T. caulocystidiatus* differs from *T. alba* in the presence of reddish-brown apices on basidiomes, caulocystidial hairs in



**Fig. 185** Scanning electron micrograph of basidiospores of *Trechispora perminispora* (LWZ 20190816-39a, **holotype**). Scale bars: 2  $\mu$ m

stipitipellis and smaller basidiospores ( $3.5\text{--}4.5 \times 3\text{--}3.5 \mu\text{m}$ , Furtado et al. 2021); *T. gelatinosa* differs in its dull yellow to brownish orange basidiomes when dried and smaller basidiospores ( $3.2\text{--}4.5 \times 2.5\text{--}3.5 \mu\text{m}$ , de Meiras-Otoni et al. 2021).

***Trechispora perminispora*** S.L. Liu & L.W. Zhou, *sp. nov.*

*Index Fungorum* number: IF 901061; *Facesoffungi* number: FoF 14814; Figs. 183, 184, 185

**Etymology:** *perminispora* (Lat.) referring to very small basidiospores.

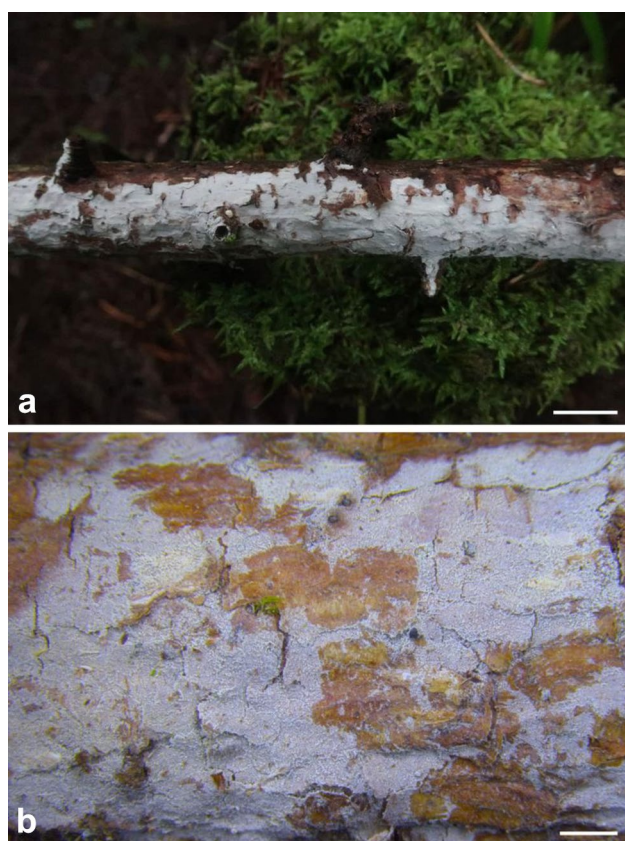
**Holotype:** LWZ 20190816-39a (HMAS).

**Diagnosis:** Differing from other species of *Trechispora* in the smallest basidiospores.

**Basidiomes** annual, resupinate, effused, thin, soft and fragile, easily separated from substrates, up to 15 cm long, 3 cm wide. **Subiculum** too thin to be seen. **Hymenophore** grandinioid with numerous small aculei, white to cream when fresh, cream to buff when dry. **Margin** white, slightly fimbriate, up to 0.5 mm wide.

**Hyphal system** monomitic; **generative hyphae** with clamp connections. **Tramal hyphae** distinct, hyaline, thin-walled, frequently branched, smooth, interwoven,  $3\text{--}3.5 \mu\text{m}$  in diam. **Cystidia** absent. **Crystals** aggregated, rhomboidal flakes. **Basidia** cylindrical with a slight median constriction, hyaline, thin-walled, with four sterigmata and a basal clamp connection,  $9\text{--}12 \times 4\text{--}4.5 \mu\text{m}$ ; **basidioles** in shape similar to basidia, but slightly smaller. **Basidiospores** ellipsoid, hyaline, slightly thick-walled, verrucose, IKI–, CB–,  $(2.5\text{--})2.6\text{--}3(\text{--}3.2) \times 1.8\text{--}2.1(\text{--}2.3) \mu\text{m}$ ,  $L = 2.8 \mu\text{m}$ ,  $W = 2 \mu\text{m}$ ,  $Q = 1.4$  ( $n = 30/1$ ).

**Material examined:** China, Sichuan Province, Ebian Yi Autonomous County, Heizhugou National Nature Reserve, on fallen branch of angiosperm, 16 August 2019, L.W. Zhou, LWZ 20190816-39a (HMAS, **holotype**).



**Fig. 186** Basidiomes of *Trechispora subfarinacea* (LWZ 20200921-33a, **holotype**). Scale bars: **a** = 1 cm, **b** = 1 mm

*GenBank numbers*: ITS = OM523525, LSU = OM339329.

*Notes*: In *Trechispora*, basidiospores are mostly more than 3.5  $\mu\text{m}$  in length and 2.5  $\mu\text{m}$  in width. Two species, viz. *Trechispora microspora* and *T. minispora*, have smaller basidiospores than these sizes (Larsson 1996; de Meiras-Ottoni 2021). However, even in comparison with these two

species, *T. perminispora* has smaller basidiospores, which make it distinguished in this genus.

*Trechispora subfarinacea* S.L. Liu & L.W. Zhou, *sp. nov.*

*Index Fungorum number*: IF 901062; *Facesoffungi number*: FoF 14815; Figs. 186, 187, 188

*Etymology*: *subfarinacea* (Lat.) referring to the morphological similarity and phylogenetic kinship to *Trechispora farinacea*.

*Holotype*: LWZ 20200921-33a (HMAS).

*Diagnosis*: Differing from *T. farinacea* in smooth hymenophore and smaller basidiospores (Larsson 1995).

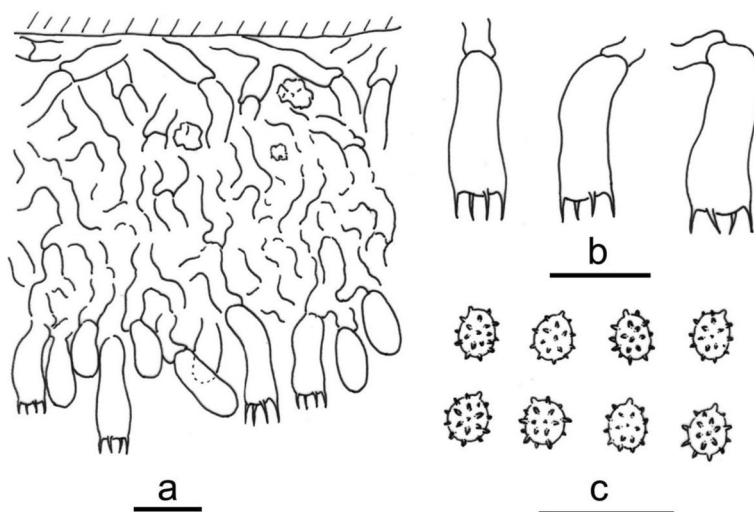
*Basidiomes* annual, resupinate, effused, thin, soft, easily separated from substrates, up to 20 cm long, 2 cm wide, 50–80  $\mu\text{m}$  thick. *Hymenophore* smooth, arachnoid, white when fresh, ash-grey to pale mouse-gray when dry, not cracked. *Margin* white, thinning out as byssoid, 0.2 mm wide.

*Hyphal system* monomitic; *generative hyphae* with clamp connections. *Subicular hyphae* long-celled, hyaline, thin-walled, frequently branched and septate, interwoven, 3–4  $\mu\text{m}$  in diam, ampullate septa up to 5  $\mu\text{m}$  wide. *Subhymenium* composed of indistinct generative hyphae, much branched. *Cystidia* absent. *Crystals* rare, aggregated, rhomboidal flakes. *Basidia* cylindrical with a slight median constriction, hyaline, thin-walled, with four sterigmata and a basal clamp connection, 10–15  $\times$  5–6  $\mu\text{m}$ ; *basidioles* in shape similar to basidia, but slightly smaller. *Basidiospores* subglobose, hyaline, thick-walled, verrucose, IKI–, CB–, 3–3.5(–3.7)  $\times$  2.8–3(–3.1)  $\mu\text{m}$ , L = 3.2  $\mu\text{m}$ , W = 2.9  $\mu\text{m}$ , Q = 1.1 (n = 30/1).

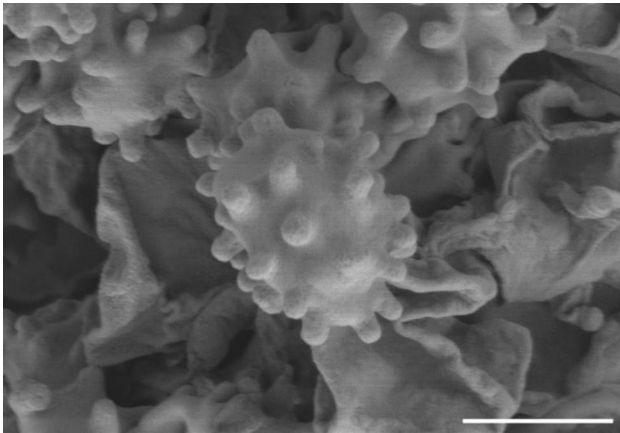
*Material examined*: China, Sichuan Province, Liangshan Yi Autonomous Prefecture, Leibo County, Mamize Nature Reserve, on fallen branch of *Picea*, 21 September 2020, L.W. Zhou, LWZ 20200921-33a (HMAS, **holotype**).

*GenBank numbers*: ITS = OM523528, LSU = OM339331.

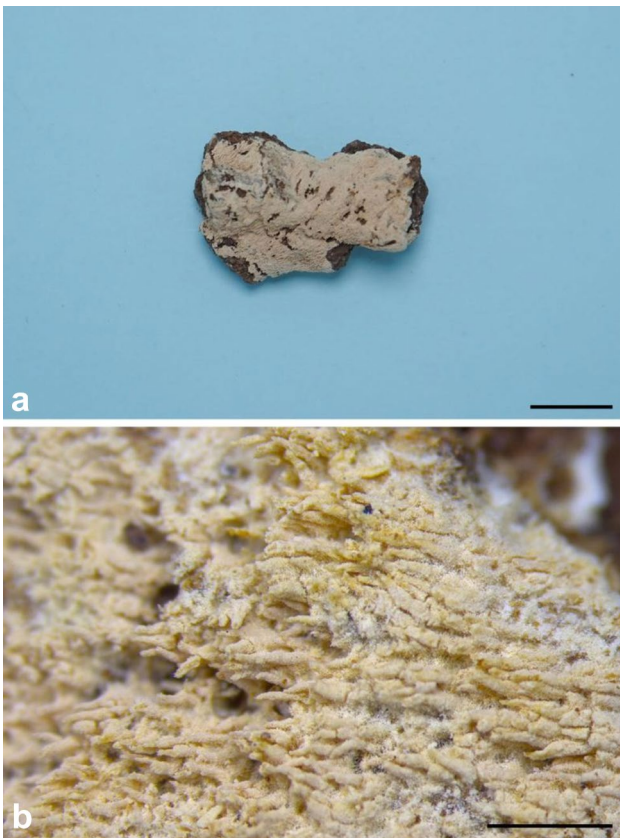
**Fig. 187** Microscopic structures of *Trechispora subfarinacea* (LWZ 20200921-33a, **holotype**). **a** A vertical section of basidiomes. **b** Basidia. **c** Basidiospores. Scale bars: 10  $\mu\text{m}$





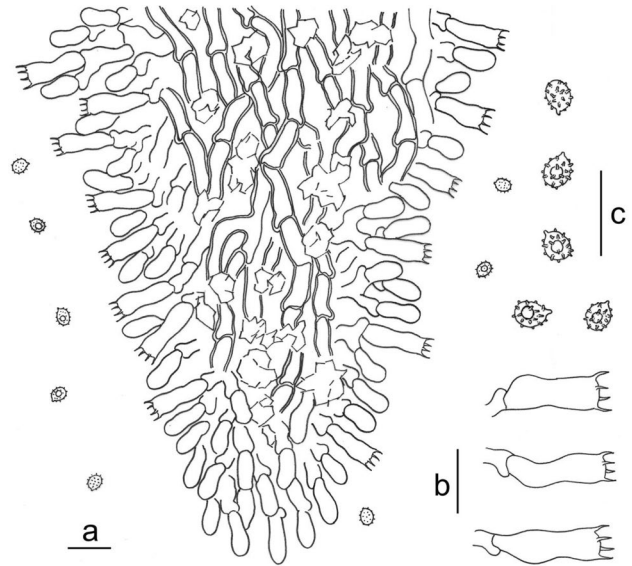


**Fig. 188** Scanning electron micrograph of basidiospores of *Trechispora tuberculata* (LWZ 20200921-33a, **holotype**). Scale bars: 2  $\mu$ m

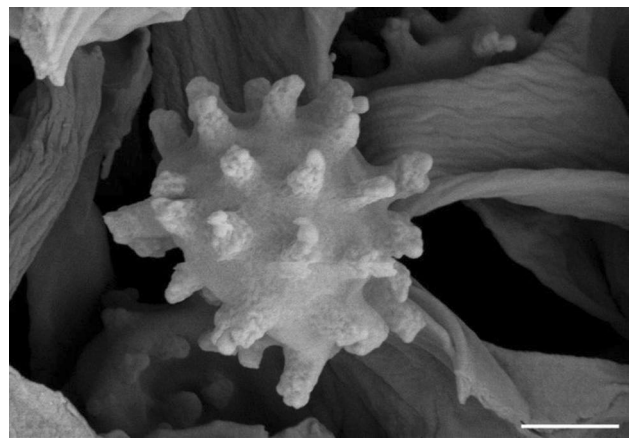


**Fig. 189** Basidiomes of *Trechispora tuberculata* (Dai 17433, **holotype**). Scale bars: **a** = 1 cm, **b** = 1 mm

*Notes:* *Trechispora gracilis* is quite similar to *T. subfari-nacea* by thin basidiomes and smooth hymenophore, but differs in cream to light ash-grey hymenophore when fresh and slightly smaller basidiospores ( $2.8\text{--}3.2 \times 2.3\text{--}2.8\text{ }\mu\text{m}$ , Liu et al. 2022b).



**Fig. 190** Microscopic structures of *Trechispora tuberculata* (Dai 17433, **holotype**). **a** A vertical section of basidiomes. **b** Basidia. **c** Basidiospores. Scale bars: 10  $\mu$ m



**Fig. 191** Scanning electron micrograph of basidiospores of *Trechispora tuberculata* (Dai 17433, **holotype**). Scale bars: 2  $\mu$ m

***Trechispora tuberculata* S.L. Liu & L.W. Zhou, *sp. nov.***

*Index Fungorum* number: IF 901063; *Facesoffungi* number: FoF 14816; Figs. 189, 190, 191

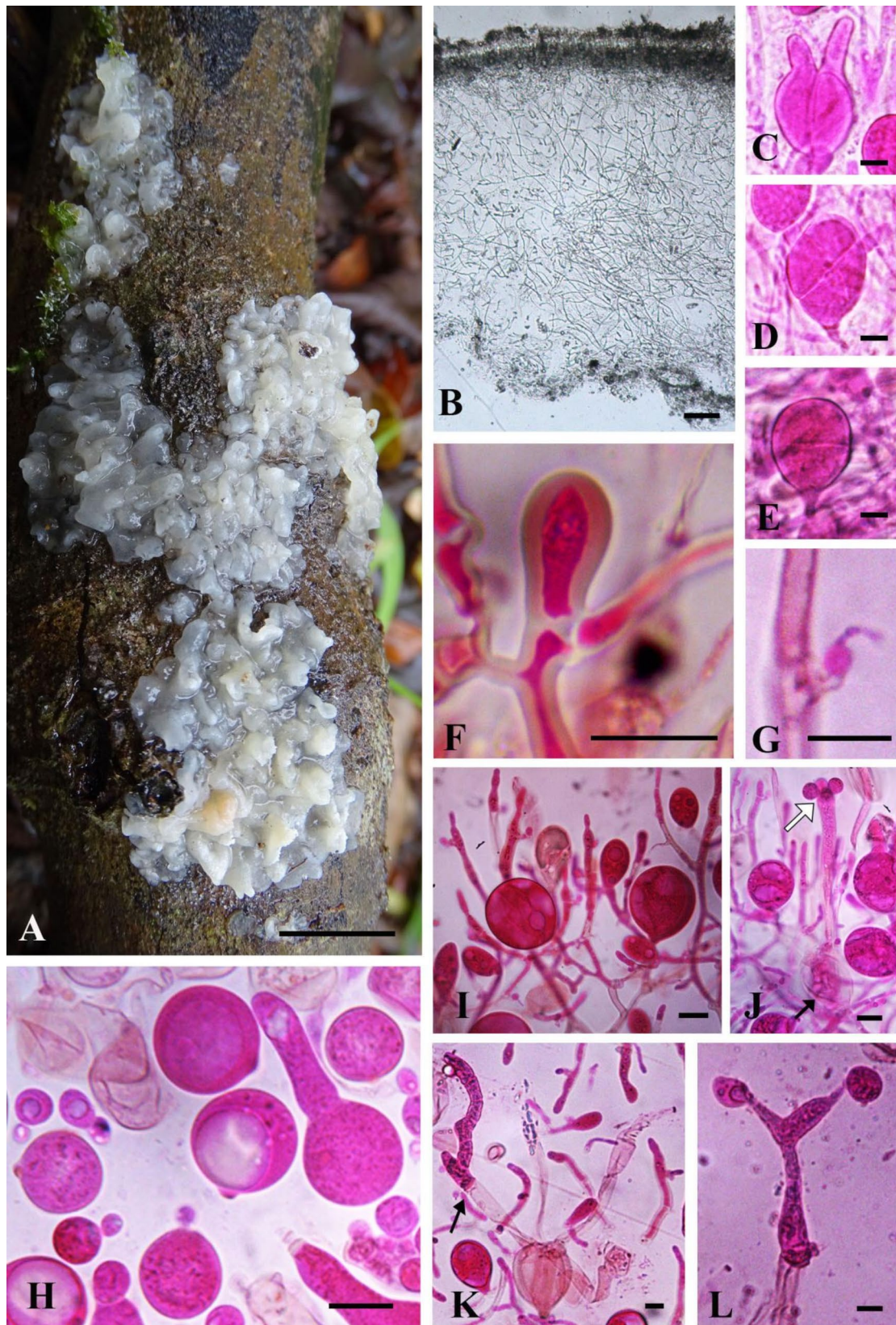
*Etymology:* *tuberculata* (Lat.) referring to tubercles on spines of basidiospores.

*Holotype:* BJFC024964.

*Diagnosis:* Differing from other species of *Trechispora* by having numerous tubercles on spines of basidiospores.

*Basidiomes* annual, resupinate, effused, thin, soft, easily separated from substrates, up to 4 cm long, 3 cm wide. *Hymenophore* hydroid with numerous, small aculei, straw-yellow to bluish grey when dry. *Margin* undifferentiated.

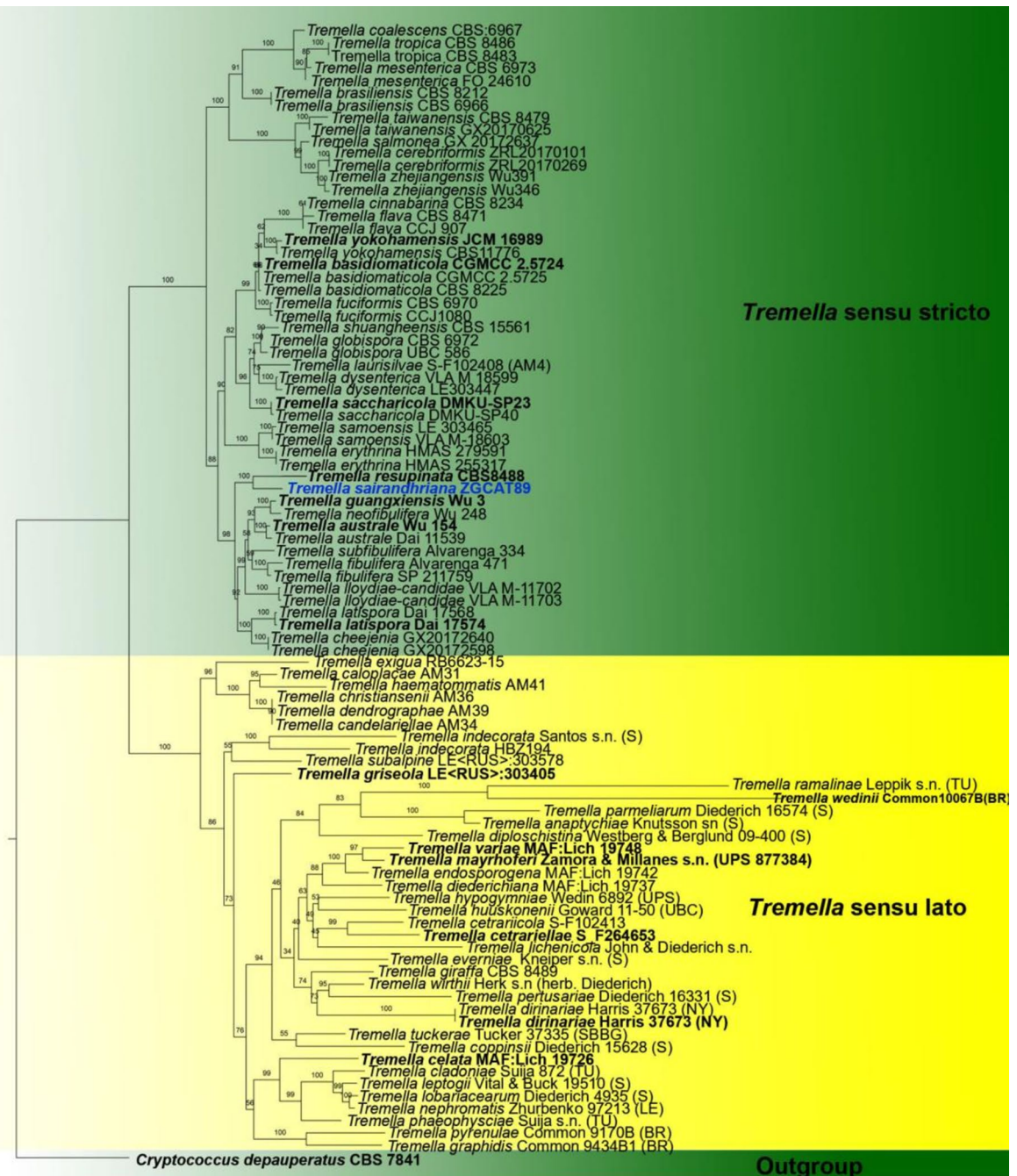






◀**Fig. 192** *Tremella sairandhrana* (ZGCAT89, holotype). **A** Basidiomes. **B** Cross section in water. **C–E** Different septations in mature basidia. **F** Vesicle. **G** Haustoria. **H** Basidiospores, budding, and germination via germ tube. **I** Hyphidia with basidia of different developmental stages. **J** Collapsed basidia (Black Arrow) and conidia from its sterigmata (White Arrow). **K** Septate sterigmata (Black Arrow). **L** Bifurcating sterigmata bearing basidiospores. Scale bars: **A** = 10 mm, **B** = 30 µm, **C–L** = 10 µm

Hyphal system monomitic; generative hyphae with clamp connections. Subicular hyphae hyaline, thick-walled, moderately branched and septate, subparallel, 3–5 µm in diam. Trametal hyphae distinct, hyaline, thin or thick-walled, moderately branched, smooth, subparallel, 2–3.5 µm in diam. Cystidia absent. Crystals usually present, bipyradic, aggregated. Basidia cylindrical with a slight median constriction, hyaline,



**Fig. 193** Phylogram generated from maximum likelihood analysis based on nITS and nLSU sequences. The dataset contained 92 representative accessions with 1583 characters including gaps. *Crypto-*

*coccus depauperatus* were used as outgroup (Malysheva et al. 2015). Type strains are in bold and newly generated sequence is in blue



thin-walled, with 4 sterigmata and a basal clamp connection,  $15\text{--}20 \times 5\text{--}6\text{ }\mu\text{m}$ ; *basidioles* in shape similar to basidia, but slightly smaller. *Basidiospores* abundant, ellipsoid, hyaline, thin to slightly thick-walled, aculeate, with numerous tubercles on spines, IKI–, CB–,  $(3\text{--})3.3\text{--}4(-4.3) \times 2.7\text{--}3.2\text{ }\mu\text{m}$ ,  $L = 3.7\text{ }\mu\text{m}$ ,  $W = 3\text{ }\mu\text{m}$ ,  $Q = 1.2$  ( $n = 30/1$ ).

**Material examined:** Brazil, Pernambuco State, Recife, Recife Botanical Garden, on fallen angiosperm trunk, 16 May 2017, Yu-Cheng Dai, Dai 17433 (BJFC024964, **holotype**; isotype in HMAS).

**GenBank numbers:** ITS = OM523507, LSU = OM339314.

**Notes:** *Trechispora tuberculata* resembles *T. constricta* by hydroid hymenophore; however, *T. constricta* differs in the presence of thick-walled generative hyphae and aculeate basidiospores with a slight constriction in the middle-upper part of spines (Liu et al. 2022b).

### **Tremellomycetes** Doweld.

**Notes:** For the latest updated account of *Tremellomycetes* see Liu et al. (2020).

### **Tremellales** Fr.

**Notes:** For the latest updated account of *Tremellales* see Liu et al. (2020).

### **Tremellaceae** Fr.

**Notes:** For the latest updated account of *Tremellaceae* see Fan et al. (2021).

### **Tremella** Pers.

**Notes:** For the latest updated account of *Tremella* see Liu et al. (2015b), Fan et al. (2021).

### ***Tremella sairandhriana*** A. Thomas & T.K.A. Kumar, *sp. nov.*

**Mycobank number:** MB 844398; **Facesoffungi number:** FoF11779; Fig. 192

**Etymology:** refers to the collection locality.

**Holotype:** ZGCAT89.

**Diagnosis:** The species is characterised by whitish, resupinate, cerebriform basidiomes, and clamped hyphidia, and conidial formation from sterigmata. This species differs from the closely related *T. resupinata* by their larger basidiomes, presence of hyphidia and conidia borne on sterigmata.

**Basidiomes** medium sized,  $10\text{--}45 \times 1.5\text{--}3.5\text{ mm}$ , soft gelatinous, resupinate, cerebriform, sessile, broadly attached, easy to separate from the substratum. **Margin** sometimes wavy, white to pale yellowish white when fresh and pale yellowish brown when dry. **Spore print** whitish.

**Hymenium** pale brown in water. **Hyphidia**  $3\text{--}7\text{ }\mu\text{m}$ , branched, septate, thick-walled, with clamp connections. **Basidia**  $27\text{--}35 \times 26\text{--}27.5\text{ }\mu\text{m}$ , globose to subglobose,

two to four celled, longitudinally, transversely (rare), or obliquely septate, thin-walled, guttulate, hyaline, with basal clamp connection. *Basidioles* clavate to obovoid. *Sterigma*  $59\text{--}96 \times 6.5\text{--}9\text{ }\mu\text{m}$ , sometimes with swollen tip (up to  $11\text{ }\mu\text{m}$ ), septate, branched, occasionally producing conidia. *Conidia* from sterigma  $3\text{--}7 \times 3\text{--}7\text{ }\mu\text{m}$ , globose, hyaline, smooth, thin-walled. *Basidiospores*  $16\text{--}19 \times 17\text{--}20\text{ }\mu\text{m}$  ( $Q = 0.84\text{--}1\text{ }\mu\text{m}$ ,  $Q_m = 0.96\text{ }\mu\text{m}$ ), globose to subglobose, hyaline, thin-walled, smooth, guttulate, apiculate. *Secondary spore* production, and yeast cell formation from basidiospores observed. *Yeast cells*  $3\text{--}7 \times 3\text{--}7\text{ }\mu\text{m}$ , globose, subglobose, broadly ellipsoid. *Vesicles*  $10.4\text{--}12.7 \times 5.9\text{--}7.8\text{ }\mu\text{m}$ , ellipsoid, oval, thick-walled. *Swollen cells* absent. *Tramal hyphae*  $2\text{--}5.5\text{ }\mu\text{m}$  wide, slightly thick- to thick-walled, branched, smooth, hyaline, frequently anastomosing, with clamp connections. *Haustoria* abundant on hyphidia and subhymenium, rarely branching, with basal clamp connection, sometimes with forked tip.

**Habitat and distribution:** On unidentified fungal host growing on dead and decaying wood log.

**Material examined:** India, Kerala State, Palakkad District, Silent Valley National Park, 4 July 2019, A. Thomas, ZGCAT89 (**holotype**).

**GenBank numbers:** ITS = ON668075, LSU = ON668076.

**Notes:** *Tremella sairandhriana* is characterised by whitish, resupinate basidiomes, presence of hyphidia, globose to subglobose basidia, formation of conidia from sterigmata, and rarely branching haustoria. Among the whitish *Tremella* members, *T. sairandhriana* show close similarity to *T. resupinata* in the resupinate nature of basidiomes and larger size of basidia and basidiospores. However, *T. sairandhriana* differs from *T. resupinata* in the following characters: relatively large basidiomes, branched, septate, thick-walled, clamped hyphidia, and conidial formation from sterigmata.

*Tremella cheejenii* has similarity with *T. sairandhriana* in its whitish cerebriform basidiomes, and in the formation of conidia from sterigmata. However, *T. cheejenii* has smaller basidiospores ( $5\text{--}10\text{ }\mu\text{m}$ ) when compared to *T. sairandhriana*. *Tremella latispora* also have whitish basidiomes and are similar in morphology with *T. sairandhriana*, but *T. latispora* differs by their smaller basidia ( $17.2\text{--}24.0\text{ }\mu\text{m}$ ) and basidiospores ( $10.1\text{--}11.8\text{ }\mu\text{m}$ , Fan et al. 2021).

In the molecular phylogenetic analysis, *T. sairandhriana* clusters with *T. resupinata* (Fig. 193), and is a sister clade to the *T. fibulifera* complex of Fan et al. (2021). Members of *T. fibulifera* complex are morphologically characterised by cerebriform whitish basidiome and abundant clamp connections (Fan et al. 2021). The resupinate nature of basidiome, and the larger sized basidia and basidiospores of *T. sairandhriana* and *T. resupinata* segregate them from the *T. fibulifera* complex.

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## Declarations

**Conflict of interest** The authors declare that they have no conflict of interest.

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