



# Fungal Planet description sheets: 1781–1866

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## Key words:

ITS nrDNA barcodes  
LSU  
new taxa  
systematics

**Abstract:** Novel species of fungi described in this study include those from various countries as follows:

**Argentina**, *Septoria reinamora* on leaf spots of *Mutisia spinosa*. **Australia**, *Cortinarius albofolliculus* on mossy soil, *Cortinarius descensoriformis* among leaf litter, *Cortinarius kaki* among leaf litter, *Cortinarius lissosporus* in leaf litter, *Cortinarius malogranatus* in leaf litter, *Cortinarius meletlac* on soil in mixed forest, *Cortinarius sebosioides* in long decayed wood litter, *Helicogermisli australiensis* as an endophyte from healthy leaves of *Archontophoenix cunninghamiana*, *Puccinia clemensiorum* on culms of *Eleocharis ochrostachys*, *Puccinia geethae* on leaves of *Cyperus brevifolius*, *Puccinia marjaniae* on leaves of *Nymphoides indica*, *Puccinia scleriae-rugosae* on leaves of *Scleria rugosa*. **Brazil**, *Dactylaria calliandrae* on living leaf of *Calliandra tweediei*, *Mucor cerradoensis* from soil, *Musicillium palmae* on living leaves of unidentified palm species, *Neodendryphiella agapanthi* from stalks of *Agapanthus praecox*, *Parafusicladium riodejaneiroanum* on living leaves of native bamboo, *Parapendiella melastomatis* on living leaves of unidentified *Melastomataceae*, *Pararamichloridium ouopretoense* on living leaves of unidentified *Poaceae*, *Pentagonomyces endophyticus* (incl. *Pentagonomyces gen. nov.*) as endophytic from roots of *Musa acuminata*, *Polyschema endophytica* from healthy roots of coffee plant, *Purimycetes endophyticus* as root endophyte of *Cattleya locatellii*, *Ramularia rhododendri* on living leaves of *Rhododendron* sp., *Staphylotrichum soli* from soil, *Trichoderma sexdentis* from leaves inside a nest of the leaf-cutting ant *Atta sexdens rubropilosa*, *Wiesneriomyces soli* from soil. **France**, *Cosmospora nemaniae* on dead or effete stromata of *Nemania cf. colliculosa*, *Inocybe alnobetulae* in subalpine green alder stands, *Stylonectria hygrophila* on dead twigs of *Betula pubescens*. **Germany**, *Coniochaeta corticalis* from bark humus, *Coniochaeta fermentaria* from fermentation residues from biogas plants, *Coniochaeta fibricola* from softwood fibres, *Coniochaeta weberae* from bark humus, *Inocybe canicularis* on calcareous to more acidic soil with conifers. **Iceland**, *Inocybe islandica*

**Citation:** Crous PW, Catcheside DEA, Catcheside PS, Alfenas AC, Alfenas RF, Barreto RW, Lebel T, Balashov S, Broadbridge J, Jurjević Ž, De la Peña-Lastra S, Hoffmann R, Mateos A, Riebesehl J, Shivas RG, Soliz Santander FF, Tan YP, Altés A, Bandini D, Carriconde F, Cazabonne J, Czachura P, Gryta H, Eyssartier G, Larsson E, Pereira OL, Rigueiro-Rodríguez A, Wingfield MJ, Ahmad W, Bibi S, Denman S, Esteve-Raventós F, Hussain S, Illescas T, Luangsa-ard JJ, Möller L, Mombert A, Noisripoom W, Olariaga I, Pancorbo F, Paz A, Piątek M, Polman-Short C, Suárez E, Afshan NS, Ali H, Arzanlou M, Ayer F, Barratt J, Bellanger J-M, Bidaud A, Bishop-Hurley SL, Bohm M, Bose T, Campo E, Chau NB, Çolak ÖF, Cordeiro TRL, Cruz MO, Custódio FA, Couceiro A, Darmostuk V, Dearnaley JDW, de Azevedo Santiago ALCM, de Freitas LWS, de J Yáñez-Morales M, Domnauer C, Dentinger B, Dhileepan K, De Souza JT, Dovana F, Eberhardt U, Eisevand P, Erhard A, Fachada V, García-Martín A, Groenewald M, Hammerbacher A, Harms K, Haroon S, Haqnawaz M, Henriques S, Hernández AJ, Jacobus LM, Jaen-Contreras D, Jangsantear P, Kaygusuz O, Knoppersen R, Kumar TKA, Lynch MJ, Mahiques R, Maraia GL, Marbach PAS, Mehrabi-Koushki M, Miller PR, Mongkolsamrit S, Moreau P-A, Oberlies NH, Oliveira JA, Orlovich D, Pérez-Méndez AS, Pinto A, Raja HA, Ramírez GH, Raphael B, Rodrigues A, Rodrigues H, Ramos DO, Safi A, Sarwar S, Saar I, Sánchez RM, Santana JS, Scrace J, Sales LS, Silva LNP, Stryjak-Bogacka M, Tacconi A, Thanh VN, Thomas A, Thuy NT, Toome S, Valdez-Carrazco JM, van Vuuren NI, Vasey J, Vauras J, Vila-Viçosa C, Villarreal M, Visagie CM, Vizzini A, Whiteside EJ, Groenewald JZ. (2025). Fungal Planet description sheets: 1781–1866. *Persoonia* 54: 327–587. doi: 10.3114/persoonia.2025.54.10

**Received:** 15 May 2025; **Accepted:** 26 May 2025; **Effectively published online:** 8 July 2025

**Corresponding editor:** R. Zare

**Abstract:**

associated with *Dryas octopetala*. **India**, *Vishniacozyma indica* on dead twigs. **Iran**, *Botryotrichum lycii* on rotten leaf of *Lycium depressum*. **Italy**, *Cuphophyllus dolomiticus* among *Salix retusa*, *Salix reticulata* and *Dryas octopetala*, *Inocybe subentolomospora* on moss with the presence of *Alnus incana*, *Populus nigra* and *Salix* spp. **Malaysia**, *Catenulostroma pellitae* on leaf spots of *Eucalyptus pellita*. **Mexico**, *Colletotrichum mexicanus* from fruit of *Persea americana* cv. Hass. **New Caledonia (France)**, *Cortinarius caeloculus*, *Cortinarius luteigemellus* and *Cortinarius perpensus* on soil under *Nothofagus aequilateralis*. **New Zealand**, *Cytospora braithwaitei* on branch of *Malus domestica*. **Pakistan**, *Callistosporium khalidii* on humus soil, *Entoloma lilacinum* on litter in conifer forest, *Laccaria decolorans* on litter in broad-leaved subtropical forest. **Poland**, *Pseudoneoconiothyrium modrzyanum* from resin of *Larix decidua* ssp. *polonica*, *Tuberculiforma enigmatica* isolated from sooty mould community on *Quercus robur* leaves. **Portugal**, *Clavulus hemisphaericus* (incl. *Clavulus* gen. nov.) on mossy slopes and under *Laurus* leaf litter, *Entoloma daegae* on sandy, granitic soil, *Hygrocybe aurantiocitrina* under laurel forest, *Hygrocybe sanguineolutea* gregarious in laurel forest, *Hygrocybe vulcanica* on mossy areas of laurel forest areas, *Pachyphlodes algarvensis* on sandy soil under *Cistus salvifolius*, *Quercus suber* and *Pinus pinea*. **South Africa**, *Amycosphaerella podalyriae* on leaf of *Podalyria calyptata*, *Erythrobasidium eucalypti* from the gut of *Gonipterus* sp., *Letendreaa goniomae* on leaves of *Gonioma kamassi*, *Pezicula brabeji* and *Sphaerulina brabeji* on twigs of *Brabejum stellatifolium*, *Stachybotrys conicosiae* on dead flower head of *Conicosia elongata*, *Talaromyces ignescens* from soil. **Spain**, *Cortinarius phaeobrunneus* on soil under *Quercus ilex* and *Q. faginea*, *Inocybe pini-halepensis* among grass and fallen leaves of *Pinus halepensis*, *Inocybe subporcorum* in sandy soils under *Quercus ilex* subsp. *ballota* and *Pinus pinaster*, *Mycena morenoi* on dead leaves of *Betula pubescens* and *Salix atrocinerea*, *Pachyphlodes iberica* on clayey and loamy soil under *Quercus ilex* and *Quercus rotundifolia*, *Ramariopsis coronata* in laurel forest. **Switzerland**, *Inocybe minata* in a bog on very wet acidic soil with *Salix* spp. and *Betula* spp. **Thailand**, *Hypocrella khonsanitii* on scale insects (*Coccidae*), *Petchiella hymenopterorum* on hymenopteran pupae in the nest (*Hymenoptera*). **Trinidad and Tobago**, *Neodevriesia maravalensis* from office swab. **Türkiye**, *Russula anatolica* under *Quercus vulcanica*. **UK**, *Paracylindrosporium dactylorhizae* (incl. *Paracylindrosporium* gen. nov.) on leaf spots of *Dactylorhiza* sp., *Niesslia hepworthiae* and *Niesslia libertiae* on living leaves of *Libertia grandiflora*. **Ukraine**, *Lichenohendersonia cetrariae* on thallus of terricolous *Cetraria aculeata*. **USA**, *Atromagnispora indianensis* (incl. *Atromagnispora* gen. nov.) on submerged wood in a freshwater stream, *Cytospora michiganensis* from utility room (settle plate), *Exophiala aeris* from air (settle plate), *Hongoboletus americanus* from mixed pine-hardwood forest, *Lorrainsmithia pennsylvanica* from bedroom, air, *Superstratomyces massachusettsanus* from lyse buffer. **Vietnam**, *Aspergillus halopiscium* on dry marine anchovy *Stolephorus commersonii*. Morphological and culture characteristics are supported by DNA barcodes.

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## ACKNOWLEDGEMENTS

The work of P.W. Crous and colleagues benefitted from funding by the European Union's Horizon 2020 research and innovation program (RISE) under the Marie Skłodowska-Curie grant agreement No. 101008129, project acronym "Mycobiomics", and the Dutch NWO Roadmap grant agreement No. 2020/ENW/00901156, project "Netherlands Infrastructure for Ecosystem and Biodiversity Analysis – Authoritative and Rapid Identification System for Essential biodiversity information" (acronym NIEBA-ARISE). V.N. Thanh and colleagues acknowledge funding from the Vietnam Ministry of Industry and Trade (2025.QuyGen.BO). H.A. Raja is grateful to the Indianapolis Zoo for a species conservation grant for the study of freshwater ascomycetes; N.H. Oberlies is grateful to the National Institute of Health via the National Cancer Institute (P01 CA125066). The study of A. Safi and colleagues was financially supported by a grant (SCU.AP1403.294) from the Research Council of Shahid Chamran University of Ahvaz. A.S. Pérez-Méndez is grateful to Secihti (CONAHCYT) and Colegio de Postgraduados Funders in México for providing the funds for this research. M. Vázquez-Sánchez at the Botanic Department at the Colegio de Postgraduados, is also thanked for her advice. F.F. Soliz Santander and colleagues are grateful to the German Federal Ministry of Food and Agriculture (BMEL) and the Fachagentur Nachwachsende Rohstoffe e. V. (FNR) by funding the project "Entwicklung und Bewertung von torfgeduzierten Produktionssystemen im Gartenbau (ToPGa)" (funding number 2220MT006A) and to A. Zaiser, K. Löhr and H. Gottfried for laboratory assistance. Floragard Vertriebs-GmbH (Oldenburg, Germany) and Klasmann-Deilmann Service GmbH (Geeste, Germany) are gratefully acknowledged for providing substrates for this study. J. Cazabonne and colleagues would like to thank M. Gardes for her involvement and invaluable help throughout the project, P. Jargeat for sequencing samples and carrying out the initial phylogenetic analyses, K. Dinh for her assistance in extracting and sequencing samples, and P. Vincenot for the line drawings of their new species. The authors would also like to thank P. Pirot for coining the name *Cortinarius caeloculus*. R. Mahiques and colleagues thank G. Corriol for providing information about an additional collection of *C. phaeobrunneus*. T. Lebel and co-authors acknowledge and respect the traditional custodians of Karta Pintingga (Kangaroo Island) and the Peramangk and Kaurna nations (Adelaide Hills), the land on which these specimens were collected, and recognize their deep spiritual connection and relationship to Country. They are grateful to the Australian Biological Resources Study for funding support (NTRGI000057), the Botanic Gardens & State Herbarium of South Australia for support of undergraduate interns (C. Polman-Short; J. Broadbridge 2024), fieldwork and access to laboratories for microscopy, and Flinders University for support of molecular data generation. Thank you to curation staff at MEL, AD, PERTH and OTA for their assistance. E. Larsson acknowledges the Swedish Taxonomy Initiative, SLU Artdatabanken, Uppsala, Sweden. S. Hussain and co-authors would like to express their sincere gratitude to colleagues at the Centre for Plant Sciences and Biodiversity, and staff of the Laboratory of Mycology and Plant Pathology, University of Swat. They also extend our thanks to Higher

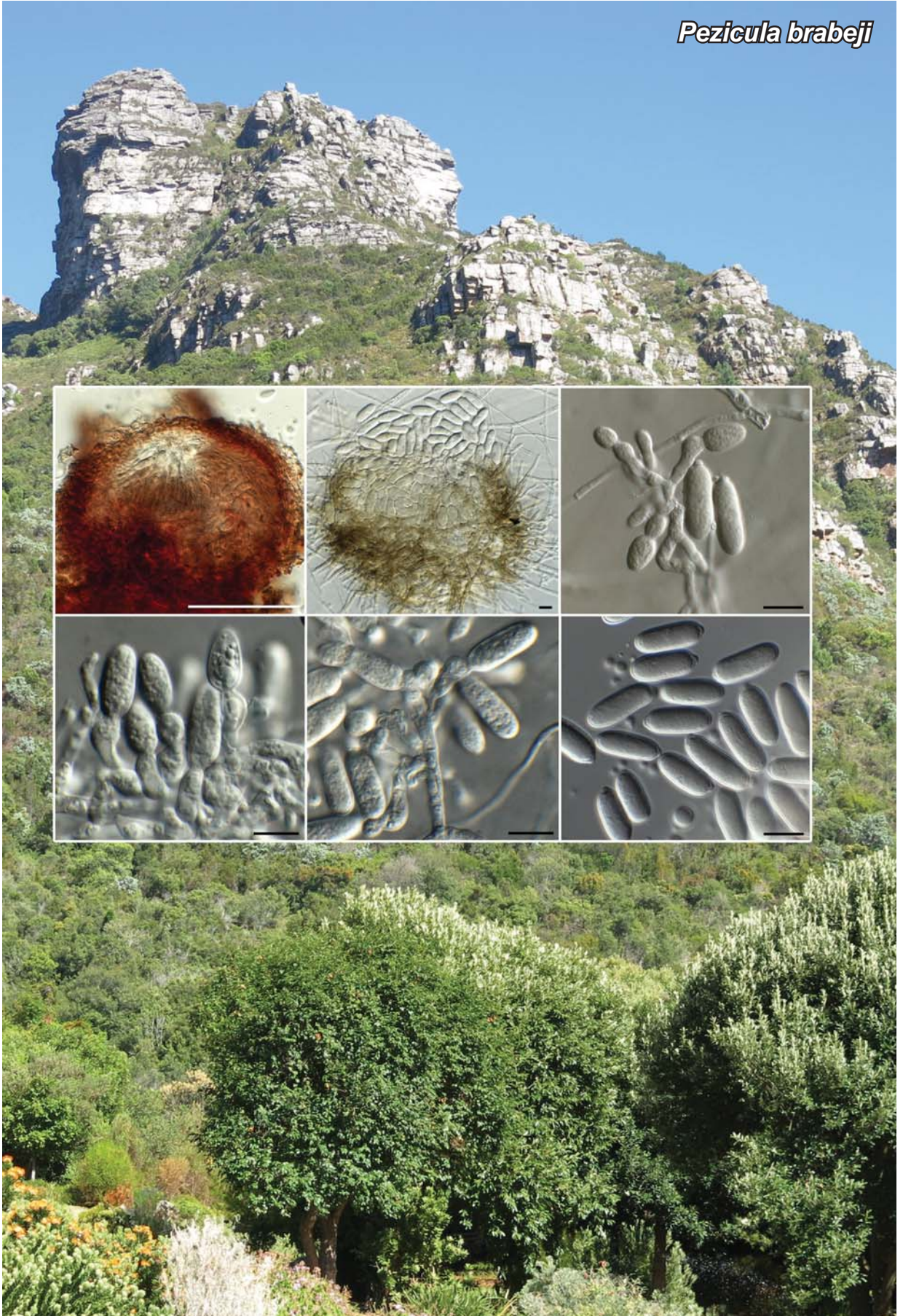
Education Commission, Islamabad, Govt. Pakistan for promoting and supporting research in the country. V. Fachada and colleagues are grateful to R. Ilanen for the precious help with the photographic plate layout. R. Knoppersen and colleagues thank Forestry South Africa for funding this study, with additional funding from the Forestry and Agricultural Biotechnology Institute and the University of Pretoria. S. De la Peña-Lastra and colleagues thank the Instituto das Florestas e Conservação da Natureza authorities and guards (Licence 01/IFCN/2021 – BIO MAD). The authors also thank E.B. Tejera and L. Quijada for the locations of some of the sampling areas. T. Illescas would like to thank to C. Morente for her help in researching documentation on the genus and compiling data. The Atlantic Islands National Maritime-Terrestrial Park authorities and guards are also acknowledged. A. Mateos and colleagues thank the Instituto das Florestas e Conservação da Natureza authorities and guards (Licence 01/IFCN/2021 – BIO MAD). The authors would like to thank E.B. Tejera and L. Quijada for the locations of some of the sampling areas. T. Illescas would like to thank C. Morente for her help in researching documentation on the genus and compiling data. They also thank the Secretaria Regional do Ambiente e Alterações Climáticas Açores for the permission granted for the sampling (Licença No. 16/2021/DRAAC). To the ECOTOX group for co-funding the trip. T. Illescas would like to thank to C. Morente for her help in researching documentation on the genus and compiling data. The study of W. Noisripoom and J.J. Luangsa-ard was financially supported by the National Science and Technology Development Agency (NSTDA), and the National Science, Research and Innovation Fund, Thailand Science Research and Innovation (TSRI) (Grant no. P2351531). M. Durand and various participants of the Journées Mycologiques de Beaufort contributed to the discovery of *Inocybe alnobetulae* on several spots of the French locality. G. Moreno and E. Horak contributed to the sample collection of *I. alnobetulae* in the green alder stands in Switzerland. D. Bandini and U. Eberhardt are grateful to A. Bond and L. Davis for the loan of type material of *Inocybe margaritispora* and to the Staatliches Museum f. Naturkunde Stuttgart and H. Thüs for their support. D. Bandini thanks F.-X. Boutard for the gift of a collection of *I. canicularis*. I. Saar was supported by the Estonian Research Council (grant PRG1170) and the Estonian Ministry of Education and Research (Centre of Excellence AgroCropFuture "Agroecology and new crops in future climates", TK200). F. Esteve-Raventós and colleagues acknowledge J.L. Siquier, J.C. Salom and J. Llistosella for their help in the collection of many samples in the Balearic Islands, and L. Parra for his nomenclatural advice. Furthermore, V. González, A. Caballero and G. Muñoz are thanked for handling collections and photographic material, while M. Cervini and E. Larsson are thanked for sharing some of their molecular data. J. Vauras acknowledges the FinBOL project of Finland and the association Kuopion Luonnon Ystävien Yhdistys. F. Dovana and colleagues thank L. Setti for the microscopy pictures and L. Poli for the collections and macro photos of *Inocybe subentolomospora*. The study of V. Darmostuk was supported by The National Scholarship Programme of the Slovak Republic and statutory funds from the W. Szafer Institute of Botany, Polish Academy of Sciences. L.W.S. de Freitas and co-authors express their gratitude to Conselho Nacional de Desenvolvimento Científico e

Tecnológico (CNPq) for the scholarship provided to L.W.S. de Freitas and for the research grant (CNPq 313401/2023-3) provided to A.L.C.M. de Azevedo Santiago. This manuscript was financed by the project “Morphological and molecular approaches to the knowledge of zygosporic fungal communities in the Atlantic Forest of Pernambuco and Paraíba, Brazil” (FACEPE APQ-1346-2.12/22). M.O. Cruz thanks Fundação de Amparo à Pesquisa do Estado de São Paulo (FAPESP) for a scholarship (# 2022/16087-7). DNA sequencing was funded by Fundação de Amparo à Pesquisa do Estado de São Paulo (FAPESP grant # 2019/03746-0). The authors are grateful to T.B. Gibertoni for providing soil samples. M. Villarreal and A. Couceiro thank H. Naviera, J.M. Traba and A. Vila-Sanjurjo from Vicerrectorado de Política Científica, Investigación y Transferencia, Universidade da Coruña (UDC) for extracting and sequencing the *M. morenoi* samples. J.S. Santana and colleagues were supported by the Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq), Coordenação de Aperfeiçoamento de Pessoal de Nível Superior - Brazil (CAPES) - Finance Code 001. They are also grateful to the Universidade Federal de Viçosa (UFV) for providing additional resources for this study and Sítio Barreiras Fruticultura LTDA for support in field works, transit and use of facilities. K. Bensch is acknowledged for help with the Latin name of the new taxa. S. Mongkolsamrit and colleagues were financially supported by the National Science and Technology Development Agency (NSTDA) the National Science, Research and Innovation Fund, Thailand Science Research and Innovation (TSRI) Grant no. P-2351531. They also thank A. Khonsanit for the photo illustration and N. Sawangkaew for identifying the insect hosts. J.A. Oliveira and colleagues were financially supported by the Brazilian Coffee Research and Development

Consortium (Consórcio Pesquisa Café, CBP&D/Café), Coordenação de Aperfeiçoamento de Pessoal de Nível Superior–Brasil (CAPES)–Finance Code 001, Fundação de Amparo à Pesquisa do Estado de Minas Gerais (FAPEMIG), and Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq). The study of P. Czachura was funded by the National Science Centre, Poland, under the project 2019/35/N/NZ9/04173. D.O. Ramos & O.L. Pereira are thankful to the Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq), Coordenação de Aperfeiçoamento de Pessoal de Nível Superior - Brasil (CAPES) - Finance Code 001, Fundação de Amparo à Pesquisa do Estado de Minas Gerais (FAPEMIG) for their financial support and the Núcleo de Pesquisa e Conservação de Orquídeas da UFV (NPCO) for the use of facilities. O. Kaygusuz thanks the Scientific and Technical Research Council of Türkiye (TUBITAK) in the 2219 International Postdoctoral Research Fellowship Programme (Grant No. 1059B192202880). G.H. Ramirez and R.M. Sánchez are grateful to the GENEtyC laboratory team (CERZOS–CONICET, Bahía Blanca) for their collaboration with molecular analyses of *Septoria reinamora*. The study of M. Piątek and co-authors was funded by the National Science Centre, Poland, under the project 2017/27/B/NZ9/02902. A. Thomas acknowledges financial support from Kerala State Council for Science Technology and Environment (KSCSTE) in the form of a research fellowship. A. Thomas & T.K.A. Kumar also thank the Chief Conservator of Forests & Chief Wildlife Warden, Kerala, for giving permission to conduct field work in the forest areas of Kerala State. A. Mombert thank J. Fournier for advice and a review of the descriptions, C. Vernillet for introducing him to the bois d’Apremont, and A. Greset for the background photo of *Stylonectria hygrophila*.



*Pezizula brabeji*



## *Pezicula brabeji* Crous, *sp. nov.*

*Etymology*: Name refers to the host genus it was isolated from, *Brabejum*.

*Classification*: *Dermateaceae*, *Helotiales*, *Leotiomycetidae*, *Leotiomyces*.

*Conidiomata* solitary, pycnidial to acervular, brown, subglobose, up to 200 µm diam.; wall of 3–6 layers of brown *textura angularis*; on SNA pycnidia at times with brown hyphae on outer layer. *Conidiophores* hyaline, smooth, branched or reduced to conidiogenous cells, up to 30 µm tall, doliform to subcylindrical, 5–12 × 4–6 µm; phialidic, at times proliferating percurrently at apex. *Conidia* hyaline, smooth, aseptate, guttulate, thick-walled, subcylindrical, straight to slightly curved, apex obtuse, tapering to truncate hilum, slightly protruding, 2 µm diam., (19–)22–25(–27) × (7–)8 µm.

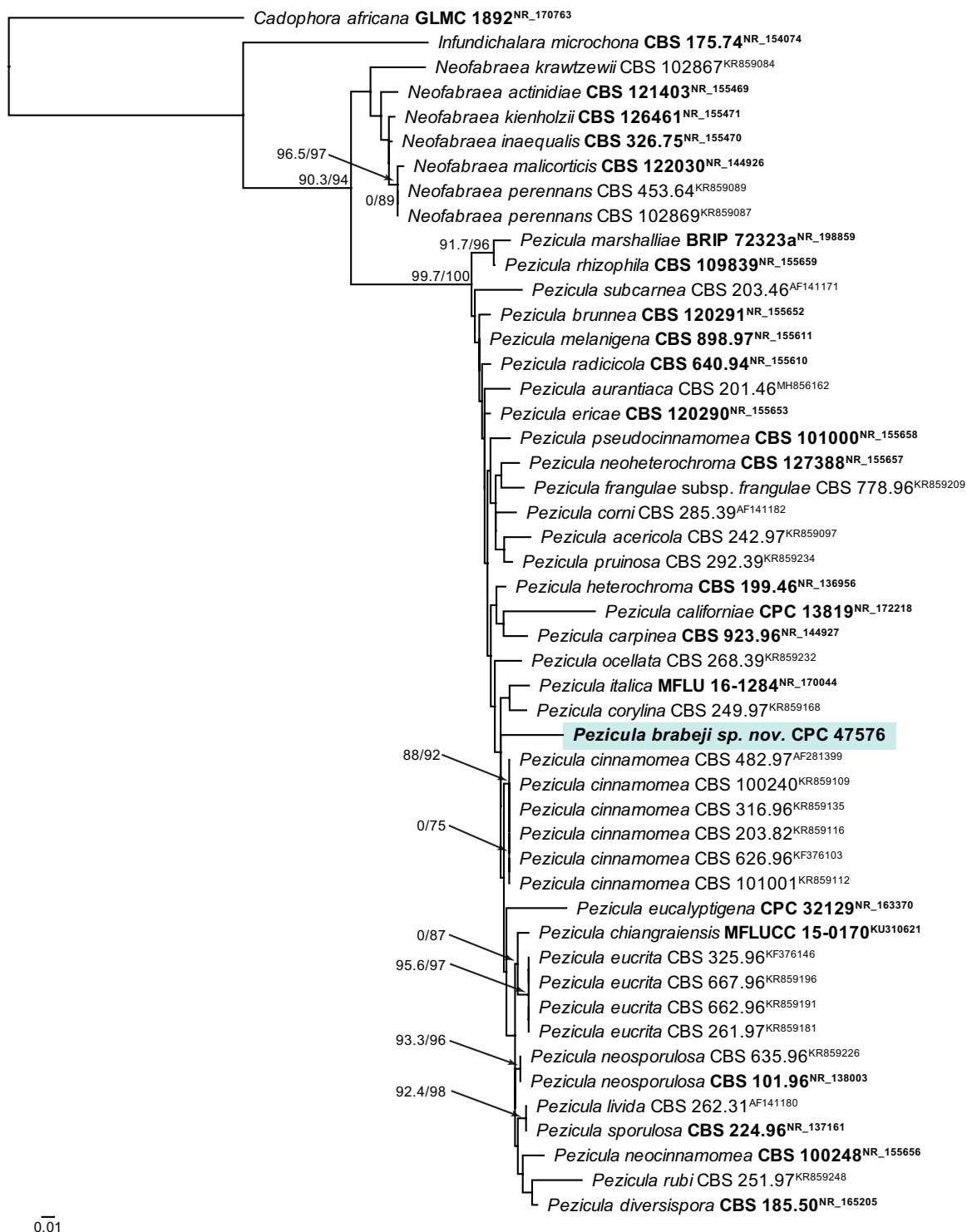
*Culture characteristics*: Colonies erumpent, spreading, with moderate aerial mycelium, and feathery, lobate margin, reaching 20 mm diam. after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse sienna, with diffuse sienna pigment in agar.

*Typus*: **South Africa**, Western Cape Province, Cape Town, Kirstenbosch, on twigs of *Brabejum stellatifolium* (*Proteaceae*), 22 Nov. 2023, P.W. Crous, HPC 4334 (**holotype** CBS H-25502; culture ex-type CPC 47576 = CBS 152301; ITS, LSU, *rpb2* and *tub2* sequences GenBank PV664921.1, PV664948.1, PV664013.1 and PV664048.1).

*Notes*: Species of *Pezicula* are common in regions with moderate climates, where they occur as saprobes on dead branches and twigs, or as endophytes (Chen *et al.* 2016). *Pezicula brabeji* is phylogenetically related to the homothallic *P. cinnamomea* [macroconidia (15.5–)26.3–29.6(–36.0) × (5.5–)9.3–9.8(–12.0) µm], but is distinct in having smaller conidia.

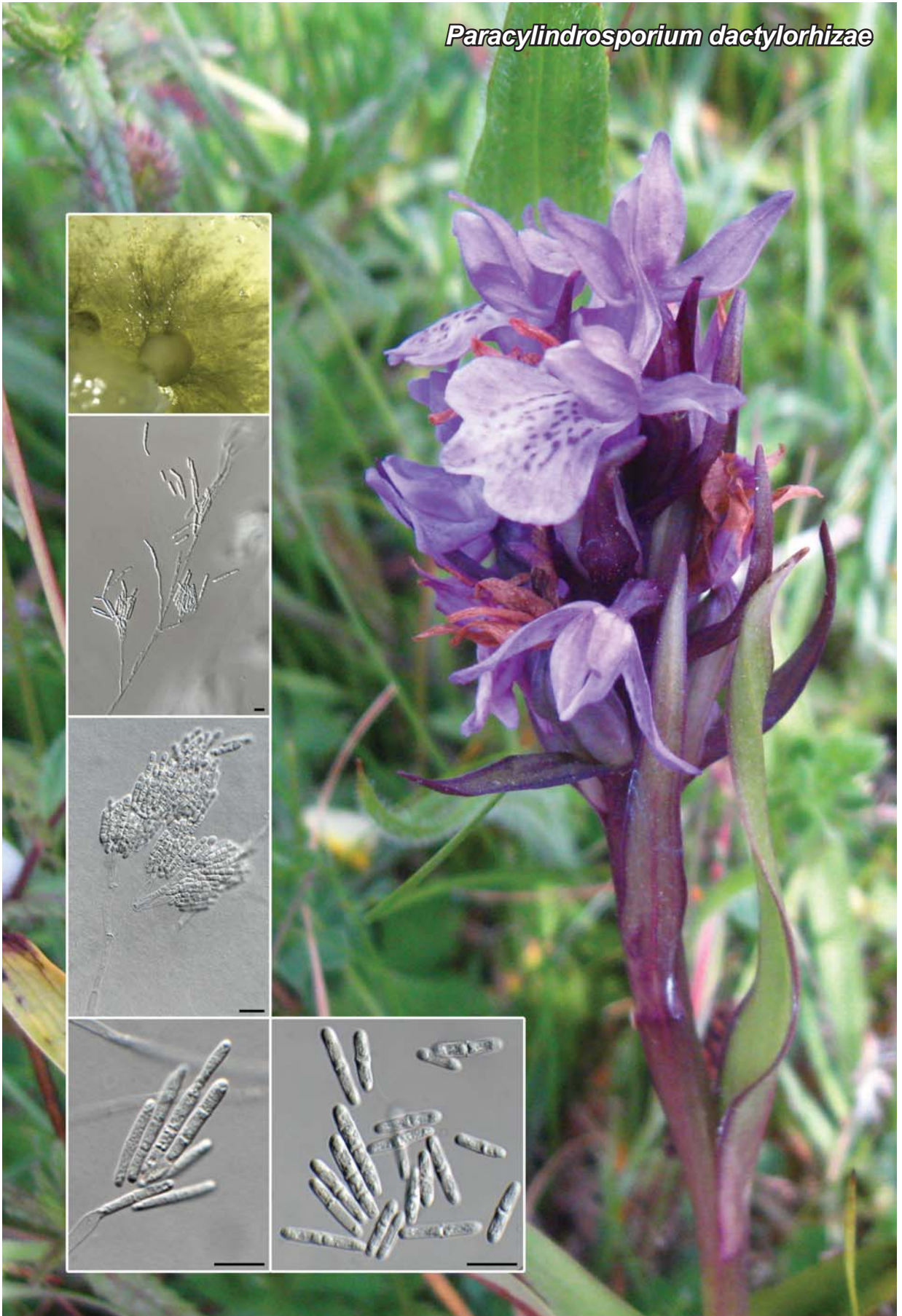
Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Pezicula cinnamomea* [strain CBS 226.96, GenBank KR859118.1; Identities = 515/538 (96 %), one gap (0 %)], *Pezicula sporulosa* [strain CBS 634.96, GenBank MH862602.1; Identities = 518/543 (95 %), four gaps (0 %)], and *Pezicula neosporulosa* [strain CBS 635.96, GenBank KR859226.1; Identities = 518/543 (95 %), four gaps (0 %)]. Closest hits using the **LSU** sequence are *Pezicula ocellata* [strain CBS 949.97, GenBank KR859025.1; Identities = 831/840 (99 %), no gaps], *Pezicula pruinosa* [strain CBS 292.39, GenBank KR859026.1; Identities = 828/837 (99 %), no gaps], and *Pezicula acericola* [strain CBS 240.97, GenBank KR858886.1; Identities = 830/840 (99 %), no gaps]. Closest hits using the **rpb2** (first part) sequence had highest similarity to *Pezicula neoheterochroma* [strain CBS 127388, GenBank KR859338.1; Identities = 849/877 (97 %), no gaps], *Pezicula eucrita* [strain CBS 259.97, GenBank KF376205.1; Identities = 850/880 (97 %), no gaps], and *Pezicula sporulosa* [strain CBS 225.96, GenBank KF376202.1; Identities = 847/880 (96 %), no gaps].

*Colour illustrations*: Kirstenbosch, Cape Town, South Africa. Conidiomata on synthetic nutrient-poor agar; conidiophores and conidiogenous cells giving rise to conidia; conidia. Scale bars: conidioma (left) = 100 µm; all others = 10 µm.



Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.4.0 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020, Mo *et al.* 2023) of the *Pezicula* ITS nucleotide alignment. Bootstrap support values from 1000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown), preceded by the SH-aLRT test value (only shown if the node has > 74 % bootstrap support). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Cadophora africana* (GLMC 1892; GenBank NR\_170763) and the novelty described here is highlighted with a coloured block and **bold** font. Alignment statistics: 49 strains including the outgroup; 538 characters including alignment gaps analysed; 214 distinct patterns, 111 parsimony-informative, 67 singleton sites, 360 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: SYM+I+R2. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.29050751).

*Paracylindrosporium dactylorhizae*





## *Paracylindrosporium* Scrace & Crous, *gen. nov.*

*Etymology:* Name refers to its similarity to *Cylindrosporium*.

*Classification:* *Ploettnerulaceae*, *Helotiales*, *Leotiomycetes*.

*Mycelium* consisting of hyaline, smooth, branched, septate hyphae. *Conidiophores* arising from superficial to immersed hyphae, erect, penicillate, terminal and intercalary on hyphae, subcylindrical with terminal penicillate conidiogenous

apparatus; primary branches subcylindrical, hyaline, smooth, 0–1-septate, giving rise to 1–4 *phialides*, hyaline, smooth, subcylindrical, with prominent flared collarettes. *Conidia* subcylindrical, mostly straight, hyaline, smooth, guttulate, apex obtuse, tapering to truncate hilum; conidia undergoing microcyclic conidiation, aggregating in mucoid mass.

*Type species:* *Paracylindrosporium dactylorhizae* Scrace & Crous

MB 859230

## *Paracylindrosporium dactylorhizae* Scrace & Crous, *sp. nov.*

*Etymology:* Name refers to the host it was isolated from, *Dactylorhiza*.

*Mycelium* consisting of hyaline, smooth, branched, septate, 3–4 µm diam. hyphae. *Conidiophores* arising from superficial to immersed hyphae, erect, penicillate, terminal and intercalary on hyphae, subcylindrical with terminal penicillate conidiogenous apparatus up to 160 µm tall; primary branches subcylindrical, hyaline, smooth, 0–1-septate, 15–45 × 3–4 µm, giving rise to 1–4 *phialides*, hyaline, smooth, subcylindrical, 7–15 × 2.5–3.5 µm, with prominent flared collarettes, 1–3 × 3–4 µm. *Conidia* subcylindrical, mostly straight, hyaline, smooth, guttulate, apex obtuse, tapering to truncate hilum, 2 µm diam., (0–)1–3(–4)-septate, (11–)15–20(–33) × (2.5–)3 µm; conidia undergoing microcyclic conidiation, aggregating in mucoid mass.

*Culture characteristics:* Colonies flat, spreading, with moderate aerial mycelium, and smooth, lobate margin, reaching 40 mm diam. after 2 wk at 25 °C. On MEA surface amber, and reverse umber to sienna.

*Typus:* **UK**, Lincolnshire, Skegness, Gibraltar Point National Nature Reserve, on leaf spots of *Dactylorhiza* sp. (*Orchidaceae*), 2023, *J. Scrace* [**holotype** CBS H-25507; culture ex-type CPC 46348 = CBS 152298; ITS, LSU, *actA*, *rpb1*, *rpb2* and *tef1* (first part) sequences GenBank PV664922.1, PV664949.1, PV663998.1, PV664010.1, PV664014.1 and PV664026.1].

*Additional material examined:* **UK**, Lincolnshire, Skegness, Gibraltar Point National Nature Reserve, on leaf spots of *Dactylorhiza* sp., 2023, *J. Scrace*, culture CPC 46267; ITS, LSU, *actA*, *rpb1*, *rpb2* and *tef1* (first part) sequences GenBank PV664923.1, PV664950.1, PV663999.1, PV664011.1, PV664015.1 and PV664027.1.

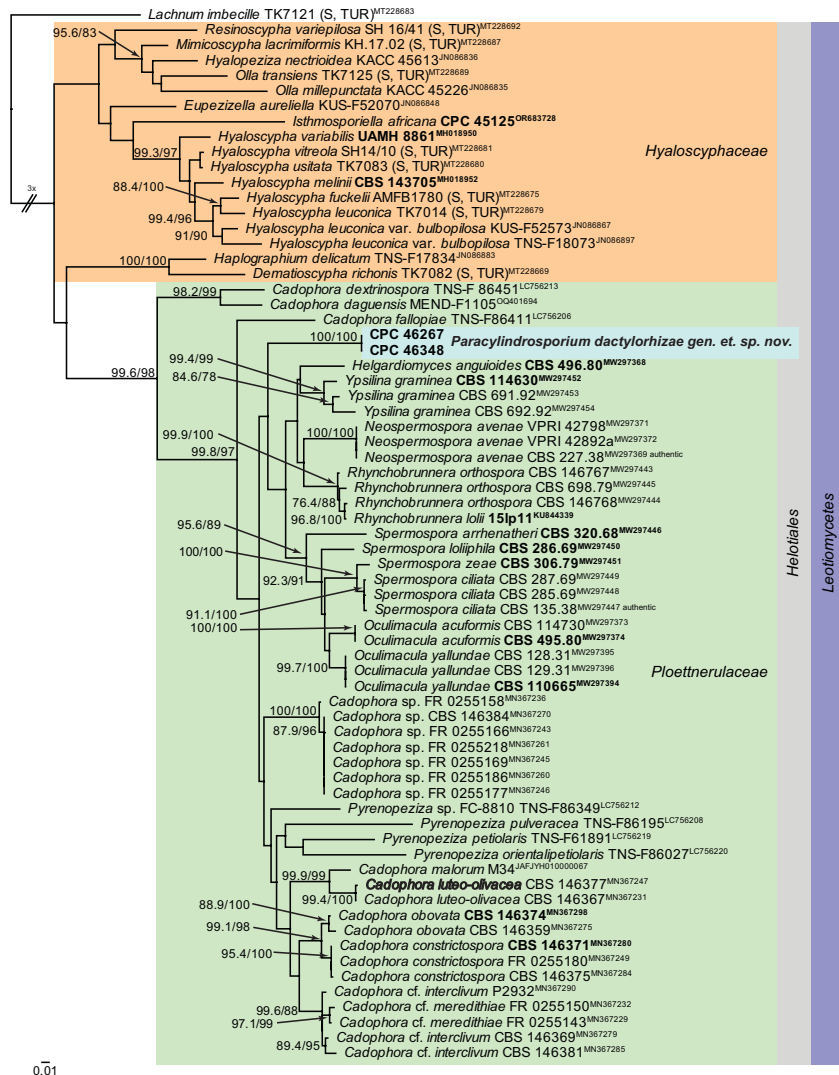
*Notes:* *Paracylindrosporium* is reminiscent of *Cylindrosporium* (type species *C. concentricum*) asexual morphs, which are treated as synonyms of *Pyrenopeziza*. No *Cylindrosporium* or *Pyrenopeziza* species are presently known from *Dactylorhiza* sp. *Paracylindrosporium dactylorhizae* is morphologically distinct in that it has relatively short conidia (up to 33 µm long) that are up to 4-septate (Hüseyn *et al.* 2007). *Paracylindrosporium dactylorhizae* causes *Dactylorhiza* “black death” of *Dactylorhiza* species in the UK. Koch’s postulates have been completed, with *P. dactylorhizae* confirmed as a very aggressive pathogen of this host (Scrace 2022). *Paracylindrosporium dactylorhizae* produces large numbers of conidia on leaves and flowers, suggesting that these propagules are most likely dispersed by rain splash.

Based on a megablast search of NCBI’s GenBank nucleotide database, the closest hits using the ITS sequence of CPC 46348 had highest similarity to *Pyrenopeziza subplicata* [strain CBS 338.58, GenBank MH857806.1; Identities = 571/600 (95 %), no gaps], *Pyrenopeziza eryngii* [strain CBS 329.58, GenBank MH857803.1; Identities = 567/601 (94 %), three gaps (0 %)], and *Spermospora zaeae* [strain CBS 306.79, GenBank MW298368.1; Identities = 547/583 (94 %), five gaps (0 %)]. The ITS sequences of CPC 46348 and 46267 are identical (600/600 nt). Closest hits using the LSU sequence of CPC 46267 are *Phialophora asteris* f. sp. *helianthi* [strain CBS 469.71, GenBank MH871990.1; Identities = 820/825 (99 %), no gaps], *Cadophora* cf. *meredithiae* [strain P2739, GenBank MN339408.1; Identities = 820/825 (99 %), no gaps], and *Cadophora malorum* [strain CBS 117865, GenBank MH874580.1; Identities = 819/825 (99 %), no gaps]. The LSU sequences of CPC 46348 and 46267 are identical (787/787 nt). Closest hits using the *actA* sequence of CPC 46348 had highest similarity to *Collembolispora aristata* [strain CPC 21145, GenBank KC005766.1; Identities = 591/663 (89 %), nine gaps (1 %)], *Spermospora loliiphila* [strain CBS 286.69, GenBank MW297295.1; Identities = 574/642 (89 %), four gaps (0 %)], and *Oculimacula acuformis* [strain CPC 34943, GenBank MW297205.1; Identities = 573/643 (89 %), six gaps (0 %)]. The *actA* sequences of CPC 46267 and 46348 are identical (648/648 nt). Closest hits using the *rpb1* sequence of CPC 46267 had highest similarity to *Cadophora interclivum* [strain BAG4, GenBank MF677905.1; Identities = 552/601 (92 %),

*Colour illustrations:* *Dactylorhiza* sp., Gibraltar Point National Nature Reserve, UK. Colony on synthetic nutrient-poor agar; conidiophores and conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.

no gaps], *Leptodophora orchidicola* [strain UAMH 8152, GenBank MF677909.1; Identities = 552/601 (92 %), no gaps], and *Cadophora meredithiae* [strain BAP6, GenBank MF677903.1; Identities = 548/600 (91 %), no gaps]. The *rpb1* sequences of CPC 46267 and 46348 are identical (740/740 nt). Closest hits using the *rpb2* (first part) sequence of CPC 46348 had highest similarity to *Cadophora cf. interclivum* [strain P2932, GenBank MN367290.1; Identities = 662/743 (89 %), no gaps], *Ypsilina graminea* [strain CBS 691.92, GenBank MW297453.1; Identities = 713/801 (89 %), no gaps], and *Neosporospora avenae* [strain CBS 388.64,

GenBank MW297370.1; Identities = 710/801 (89 %), no gaps]. The *rpb2* sequences of CPC 46267 and 46348 are identical (802/802 nt). Closest hits using the *tef1* (first part) sequence of CPC 46267 had highest similarity to *Rhexocercosporidium panacis* [strain C22-K9, GenBank MZ325592.1; Identities = 380/497 (76 %), 67 gaps (13 %)], *Cadophora infata* [strain MY759, GenBank MT921181.1; Identities = 379/501 (76 %), 75 gaps (14 %)], and *Oculimacula aculiformis* [strain CPC 34970, GenBank MW297472.1; Identities = 379/499 (76 %), 67 gaps (13 %)]. The *tef1* sequences of CPC 46267 and 46348 are identical (523/523 nt).



Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.4.0 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020, Mo *et al.* 2023) of the Ploettnerulaceae *rpb2* nucleotide alignment. Bootstrap support values from 1000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown), preceded by the SH-aLRT test value (only shown if the node has > 74 % bootstrap support). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Lachnum imbecille* [TK7121 (S, TUR); GenBank MT228683] and the novelty described here is highlighted with a coloured block and **bold** font. Families, orders and the class are shown to the right of the tree in coloured blocks. The root branch was shortened to facilitate layout. Alignment statistics: 69 strains including the outgroup; 824 characters including alignment gaps analysed: 447 distinct patterns, 323 parsimony-informative, 45 singleton sites, 456 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: SYM+I+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.29050751).



*Amycosphaerella podalyriae*



## *Amycosphaerella podalyriae* Crous, *sp. nov.*

**Etymology:** Name refers to the host genus from which it was isolated, *Podalyria*.

**Classification:** *Mycosphaerellaceae*, *Mycosphaerellales*, *Dothideomycetidae*, *Dothideomycetes*.

**Leaf spots** amphigenous, subcircular, brown with raised dark brown border, 2–5 mm diam. **Conidiomata** hypophyllous. **Stromata** well-developed, erumpent, up to 150 µm diam., of brown pseudoparenchymatal cells, giving rise to conidiophores. **Conidiophores** aggregated, subcylindrical, straight to geniculous-sinuous, brown, finely roughened, 1–2-septate, unbranched, 20–50 × 4–7 µm. **Conidiogenous cells** integrated, terminal, subcylindrical, brown, finely verruculose, proliferating percurrently at apex, 15–30 × 4–6 µm. **Conidia** solitary, brown, guttulate, smooth, narrowly obclavate, flexuous, apex subobtuse, base obconically truncate, 3(–3.5) µm, with minute marginal frill, 3–16-septate, (32–)75–100(–120) × (4–)5(–6) µm.

**Culture characteristics:** Colonies erumpent, spreading, with moderate aerial mycelium, surface folded, and smooth, lobate margin, reaching 10 mm diam. after 2 wk at 25 °C. On MEA, PDA and OA surface pale olivaceous grey to olivaceous grey, and reverse olivaceous grey.

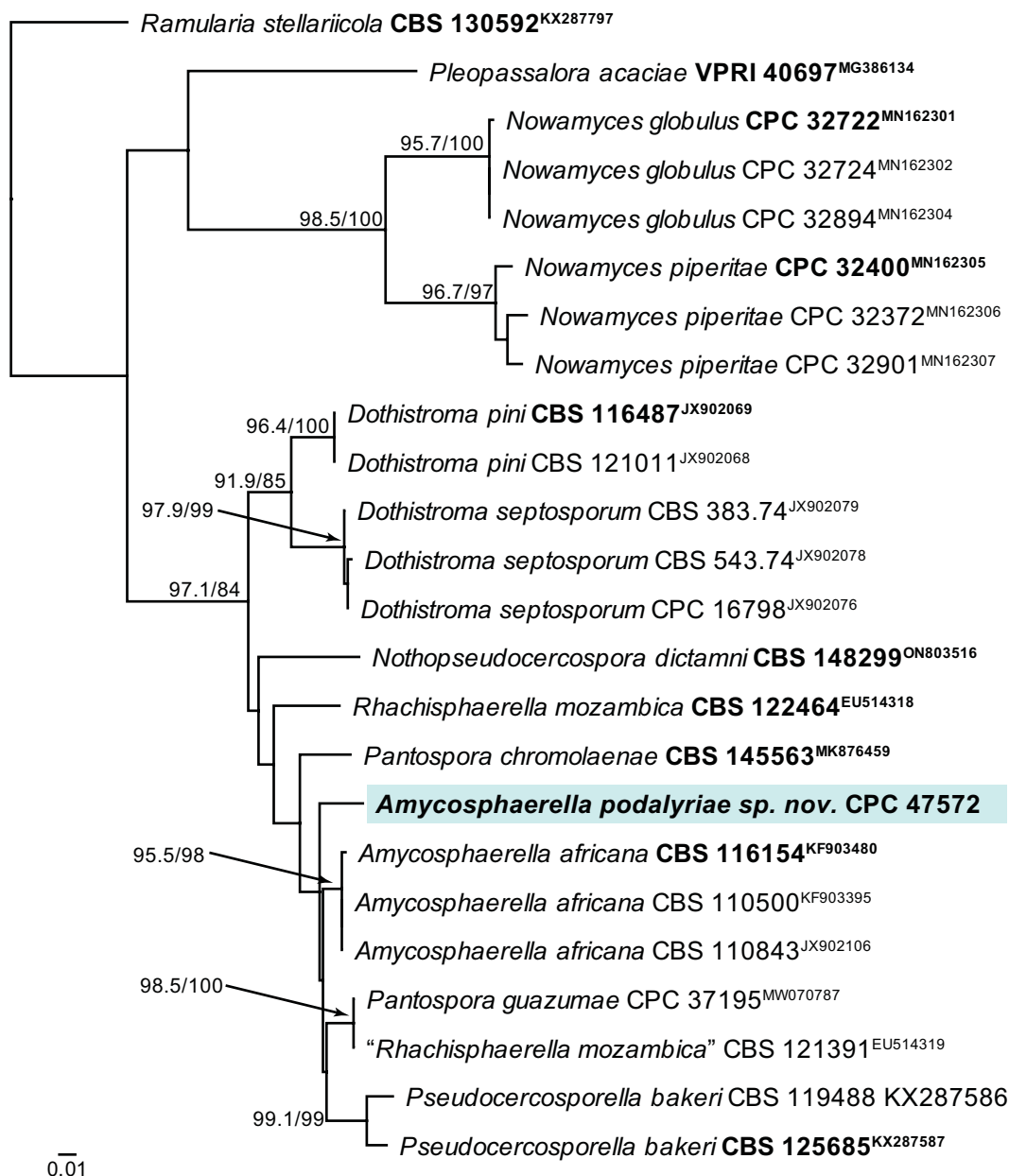
**Typus:** **South Africa**, Western Cape Province, Silvermine, on leaf of *Podalyria calyptrata* (*Fabaceae*), 1 Dec. 2023, *P.W. Crous*, HPC 4331 [**holotype** CBS H-25511; culture ex-type CPC 47572 = CBS 152224; ITS, LSU, *actA* and *tef1* (first part) sequences GenBank PV664924.1, PV664951.1, PV664000.1 and PV664028.1].

**Notes:** *Amycosphaerella* is a genus of foliar pathogens, presently known from two sexual species, *A. africana* (on *Buckinghamia* and *Eucalyptus*), and *A. keniensis* (on *Eucalyptus* and *Musa*) (Videira *et al.* 2017). Because *A. podalyriae* is only known from its asexual morph, it is not possible to compare these taxa morphologically, although the

host, *Podalyria*, is quite distinct from the other known hosts of *Amycosphaerella*. Phylogenetically, *A. podalyriae* is distinct from other known species in the genus.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Pantospora guazumae* [strain CIRAD-AUS 130, GenBank MW063438.1; Identities = 503/505 (99 %), one gap (0 %)], *Amycosphaerella africana* [as *Mycosphaerella aurantia*; strain UY483, GenBank EU853468.1; Identities = 503/505 (99 %), one gap (0 %)], *Pseudocercospora bidentis* [strain COAD 1019, GenBank KF421114.1; Identities = 494/497 (99 %), two gaps (0 %)], and *Rhachisphaerella mozambica* [as *Mycosphaerella mozambica*; strain CBS 121391, GenBank EU514258.1; Identities = 492/495 (99 %), one gap (0 %)]. Closest hits using the LSU sequence are *Mycosphaerella buckinghamiae* [strain CBS 112175, GenBank EU707856.2; Identities = 806/809 (99 %), no gaps], *Amycosphaerella africana* [strain CBS 110843, GenBank GQ852602.1; Identities = 806/809 (99 %), no gaps], and *Pseudocercospora tibouchinigena* [strain CBS 116462, GenBank GU253839.1; Identities = 806/809 (99 %), no gaps]. Closest hits using the *actA* sequence had highest similarity to *Pantospora guazumae* [strain CIRAD-AUS 130, GenBank MW070787.1; Identities = 552/571 (97 %), no gaps], *Amycosphaerella africana* [as *Mycosphaerella ellipsoidea*; strain CBS 110843, GenBank JX902106.1; Identities = 514/532 (97 %), one gap (0 %)], and *Rhachisphaerella mozambica* [as *Mycosphaerella mozambica*; strain CBS 121391, GenBank EU514319.1; Identities = 505/524 (96 %), no gaps]. Closest hits using the *tef1* (first part) sequence had highest similarity to *Amycosphaerella africana* [strain CBS 144635, GenBank MK442688.1; Identities = 441/482 (91 %), five gaps (1 %)], *Pantospora guazumae* [strain CIRAD-AUS 130, GenBank MW071106.1; Identities = 441/485 (91 %), five gaps (1 %)], and *Pseudocercospora bakeri* [strain CBS 119488, GenBank KX287862.1; Identities = 416/472 (88 %), 13 gaps (2 %)].

**Colour illustrations:** *Podalyria calyptrata*, Silvermine, Western Cape Province, South Africa. Conidiophores and conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.



Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.4.0 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020, Mo *et al.* 2023) of the *Amycosphaerella actA* nucleotide alignment. Bootstrap support values from 1000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown), preceded by the SH-aLRT test value (only shown if the node has > 74 % bootstrap support). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Ramularia stellariicola* (CBS 130592; GenBank KX287797) and the novelty described here is highlighted with a coloured block and **bold** font. Alignment statistics: 24 strains including the outgroup; 526 characters including alignment gaps analysed: 168 distinct patterns, 124 parsimony-informative, 34 singleton sites, 368 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TPM2u+F+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.29050751).





## *Ramularia rhododendri* Crous, *sp. nov.*

*Etymology:* Name refers to the host genus it was isolated from, *Rhododendron*.

*Classification:* *Mycosphaerellaceae*, *Mycosphaerellales*, *Dothideomycetidae*, *Dothideomycetes*.

*Mycelium* consisting of hyaline, smooth, branched, septate, 2–2.5 µm diam. hyphae. *Conidiophores* solitary, erect, subcylindrical, reduced to conidiogenous cells on hyphae, or 1–3-septate, 3–50 × 2–2.5 µm. *Conidiogenous cells* integrated, terminal and intercalary, 3–25 × 2–2.5 µm; scars thickened, darkened, refractive, 0.5–1 µm diam. *Conidia* in branched chains, hyaline, smooth, guttulate, fusoid to fusoid-ellipsoid, aseptate; ramoconidia 13–20 × 2.5–3 µm; conidia (7–)8–10(–12) × 2.5–3 µm; loci thickened, darkened, refractive, 0.5–1 µm diam.

*Culture characteristics:* Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 8 mm diam. after 2 wk at 25 °C. On MEA, PDA and OA surface olivaceous buff, reverse olivaceous.

*Typus:* **Brazil**, Minas Gerais, Caraça, on living leaves of *Rhododendron* sp. (*Ericaceae*), Feb. 2024, P.W. Crous, HPC 4383 [holotype CBS H-25709; culture ex-type COAD 3985 = CPC 47892; ITS, LSU, *actA*, *rpb2* and *tef1* (first part) sequences GenBank PV664925.1, PV664952.1, PV664001.1, PV664016.1 and PV664029.1].

*Notes:* *Ramularia* is a genus of foliar pathogens with a wide distribution, causing leaf spots, necrosis or chlorosis of numerous host plants. Presently no species are known from *Rhododendron* (Braun 1995, 1998). Phylogenetically, *R. rhododendri* is distinct from other species presently known from their DNA, or that have been recorded on *Rhododendron* spp.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Ramularia nyssicola* [strain CBS 127664, GenBank MH864616.1; Identities = 495/509 (97 %), seven gaps (1 %)], *Ramularia punctiformis* [strain CBS 113265, GenBank EU167569.1; Identities = 489/503 (97 %), one gap (0 %)], and *Ramularia weberiana* [strain CBS 136.23, GenBank NR\_175082.1; Identities = 482/496 (97 %), two gaps (0 %)]. Closest hits using the **LSU** sequence are *Ramularia deusta* var. *deusta* [strain CBS 473.50, GenBank KX287101.1; Identities = 838/841 (99 %), no gaps], *Ramularia nyssicola* [strain CBS 127665, GenBank NG\_070531.1; Identities = 853/857 (99 %), no gaps], and *Ramularia osterici* [strain CPC 10750, GenBank KX287185.1; Identities = 852/856 (99 %), no gaps]. Closest hits using the **actA** sequence had highest similarity to *Ramularia armoraciae* [strain CBS 241.90, GenBank KX287613.1; Identities = 463/497 (93 %), three gaps (0 %)], *Ramularia tricherae* [strain CBS 108974, GenBank KX287799.1; Identities = 462/497 (93 %), three gaps (0 %)], and *Ramularia nyssicola* [strain CBS 127664, GenBank KP894339.1; Identities = 527/573 (92 %), eight gaps (1 %)]. Closest hits using the **rpb2** (first part) sequence had highest similarity to *Ramularia nyssicola* [strain CBS 127664, GenBank KP894670.1; Identities = 770/852 (90 %), no gaps], *Ramularia unterseheri* [strain CPC 25740, GenBank KP894713.1; Identities = 718/856 (84 %), four gaps (0 %)], and *Ramularia vizellae* [strain CPC 25729, GenBank KP894753.1; Identities = 717/855 (84 %), two gaps (0 %)]. Closest hits using the **tef1** (first part) sequence had highest similarity to *Ramularia nyssicola* [strain CBS 127665, GenBank KJ504680.1; Identities = 321/356 (90 %), eight gaps (2 %)], *Ramularia hydrangeae-macrophyllae* [strain CBS 122273, GenBank KX287994.1; Identities = 326/369 (88 %), 15 gaps (4 %)], and *Ramularia asteris* [strain CBS 131.21, GenBank KX287893.1; Identities = 320/365 (88 %), 10 gaps (2 %)].

*Colour illustrations:* Leaves of *Rhododendron* sp., Caraça, Minas Gerais, Brazil. (Left column, *Ramularia rhododendri*). Conidiophores and conidiogenous cells giving rise to conidia; conidia. (Right column, *Staphylotrichum soli*). Conidiophores and conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.

## *Staphylotrichum soli* Crous, *sp. nov.*

*Etymology*: Name refers to the fact that it was isolated from soil.

*Classification*: Chaetomiaceae, Sordariales, Sordariomycetidae, Sordariomycetes.

*Mycelium* consisting of hyaline, septate, branched, 2.5–3.5 µm diam. hyphae. *Conidiogenous cells* integrated on hyphae as lateral hyphal pegs, hyaline, smooth, cylindrical, 3–20 × 2.5–3 µm. *Conidia* solitary, globose to subglobose to obovoid, hyaline to pale brown, thick-walled, smooth, (9–)10–12(–13) µm diam.

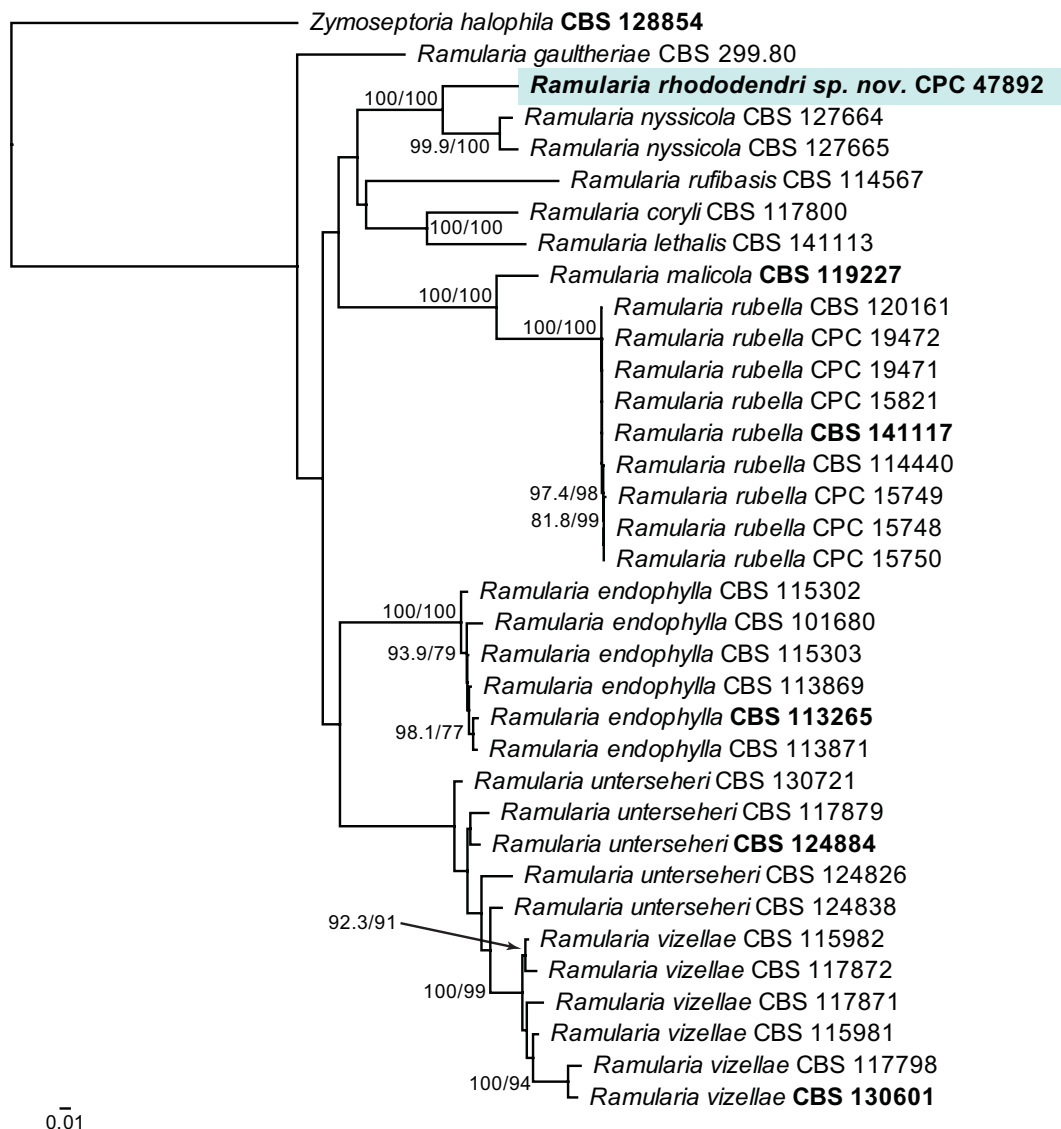
*Culture characteristics*: Colonies flat, spreading, with sparse aerial mycelium and smooth, even margin, reaching 15 mm diam. after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse sienna.

*Typus*: **Brazil**, Minas Gerais, Caraça, from soil, Feb. 2024, *P.W. Crous* [**holotype** CBS H-25713; culture ex-type COAD 3988 = CPC 47994; ITS, LSU, *rpb2*, *tef1* (second part) and *tub2* sequences GenBank PV664926.1, PV664953.1, PV664017.1, PV664041.1 and PV664049.1].

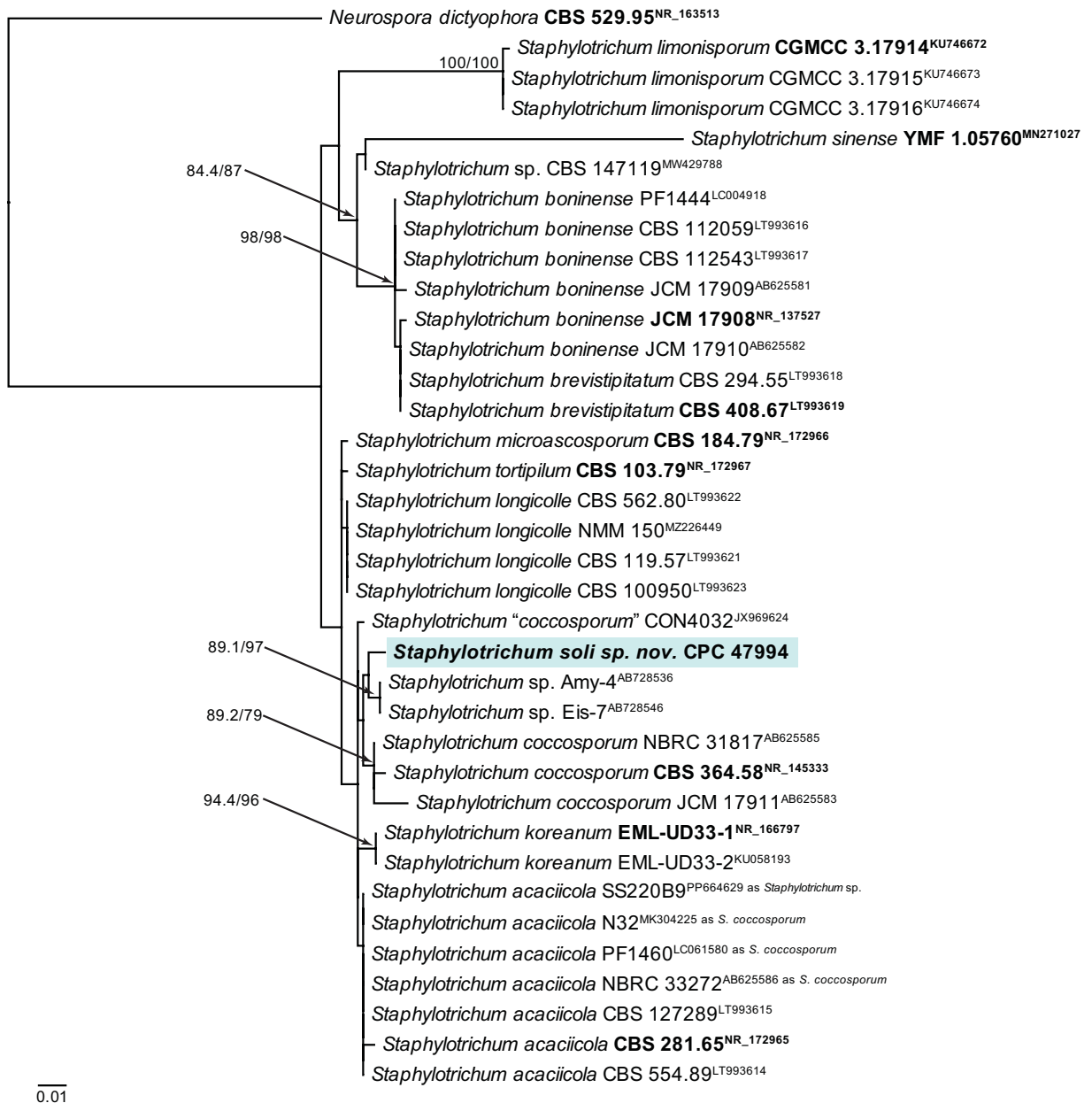
*Notes*: *Staphylotrichum* is characterized by having apically branched macronematous conidiophores with terminal denticle-like conidiogenous cells. Denticles are cylindrical or pimple-like, and globose conidia are aseptate, hyaline to pale brown, smooth or slightly verrucose (Wang *et al.* 2019). *Staphylotrichum soli* is related to but distinct from *S. coccosporum* [conidia globose, subglobose, occasionally obovoid or pyriform, (7.5–)8.5–11.5(–13.5) × (7.5–)8–10(–11) µm].

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Staphylotrichum* sp. [strain

SS220B9, GenBank PP664629.1; Identities = 466/470 (99 %), no gaps], *Staphylotrichum coccosporum* [strain PF1460, GenBank LC061580.1; Identities = 544/551 (99 %), one gap (0 %)], and *Staphylotrichum longicolle* [strain CBS 562.80, GenBank LT993622.1; Identities = 517/524 (99 %), one gap (0 %)]. Closest hits using the **LSU** sequence are *Staphylotrichum coccosporum* [strain CBS 281.65, GenBank MH870205.1; Identities = 804/805 (99 %), no gaps], *Plectosphaerella tabeijunkoae* [strain BRIP 74902a, GenBank OR510673.1; Identities = 801/805 (99 %), no gaps], and *Staphylotrichum tortipilum* [strain CBS 103.79, GenBank NG\_243693.1; Identities = 799/805 (99 %), no gaps]. Closest hits using the **rpb2** (first part) sequence had highest similarity to *Staphylotrichum coccosporum* [strain CBS 364.58, GenBank LT993539.1; Identities = 821/848 (97 %), no gaps], *Staphylotrichum acaciicola* [strain CBS 127289, GenBank LT993534.1; Identities = 819/848 (97 %), no gaps], and *Staphylotrichum microascosporum* [strain CBS 184.79, GenBank LT993543.1; Identities = 807/848 (95 %), no gaps]. Closest hits using the **tef1** (second part) sequence had highest similarity to *Staphylotrichum limonisporum* [strain LC5707, GenBank KX855219.1; Identities = 867/908 (95 %), five gaps (0 %)], *Podospora pseudocomata* [strain CBS 415.72M, GenBank XM\_062886409.1; Identities = 876/933 (94 %), two gaps (0 %)], and *Collariella carteri* [strain E37, GenBank MG890173.1; Identities = 855/902 (95 %), two gaps (0 %)]. Closest hits using the **tub2** sequence had distant similarity to *Staphylotrichum coccosporum* [strain CBS 364.58, GenBank LT993701.1; Identities = 662/762 (87 %), 44 gaps (5 %)], *Staphylotrichum acaciicola* [strain CBS 281.65, GenBank LT993694.1; Identities = 659/771 (85 %), 45 gaps (5 %)], and *Staphylotrichum sinense* [strain CGMCC 3.19631, GenBank MN340040.2; Identities = 636/793 (80 %), 81 gaps (10 %)].



Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.4.0 (Kalyanamoorthy *et al.* 2017, Minh *et al.* 2020, Mo *et al.* 2023) of the *Ramularia rpb2*/ITS/*actA*/*gapdh*/*tef1* nucleotide alignment. Bootstrap support values from 1000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown), preceded by the SH-aLRT test value (only shown if the node has > 74 % bootstrap support). Culture collection or specimen voucher numbers. For GenBank accession numbers of included sequences, see Videira *et al.* (2016). Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Zymoseptoria halophila* (CBS 128854) and the novelty described here is highlighted with a coloured block and **bold** font. Alignment statistics: 35 strains including the outgroup; 2509 characters including alignment gaps analysed: 910 distinct patterns, 708 parsimony-informative, 232 singleton sites, 1569 constant sites. The best-fit models identified for the different partitions in IQ-TREE using the TESTNEW option was: *rpb2*: TN+F+G4; ITS: TNe+I+R2; *actA*: TIM2e+G4; *gapdh*: HKY+F+I+G4; *tef1*: TIM3+F+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.29050751).



Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.4.0 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020, Mo *et al.* 2023) of the *Staphylotrichum* ITS nucleotide alignment. Bootstrap support values from 1000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown), preceded by the SH-aLRT test value (only shown if the node has > 74 % bootstrap support). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Neurospora dictyophora* (CBS 529.95; GenBank NR\_163513) and the novelty described here is highlighted with a coloured block and **bold** font. Alignment statistics: 36 strains including the outgroup; 571 characters including alignment gaps analysed: 164 distinct patterns, 53 parsimony-informative, 103 singleton sites, 415 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TNe+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.29050751).

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*Stachybotrys conicosiae*



## *Stachybotrys conicosiae* Crous, *sp. nov.*

*Etymology*: Name refers to the host genus it was isolated from, *Conicosia*.

*Classification*: *Stachybotryaceae*, *Hypocreales*, *Hypocreomycetidae*, *Sordariomycetes*.

*Mycelium* consisting of hyaline, smooth, branched, septate, 1.5–2 µm diam. hyphae. *Conidiophores* solitary, erect, thin-walled, hyaline to subhyaline, smooth, 1-septate, 65–120 × 5–7 µm, bearing 6–8 terminal conidiogenous cells. *Conidiogenous cells* phialidic, clavate to subclavate, subhyaline, smooth, 8–12 × (5–)6–7 µm, with apical collarettes. *Conidia* aseptate, ellipsoid-fusoid, thick-walled, dark brown, verruculose, apex obtuse, base truncate, (7–)8–9(–10) × 3.5–4 µm.

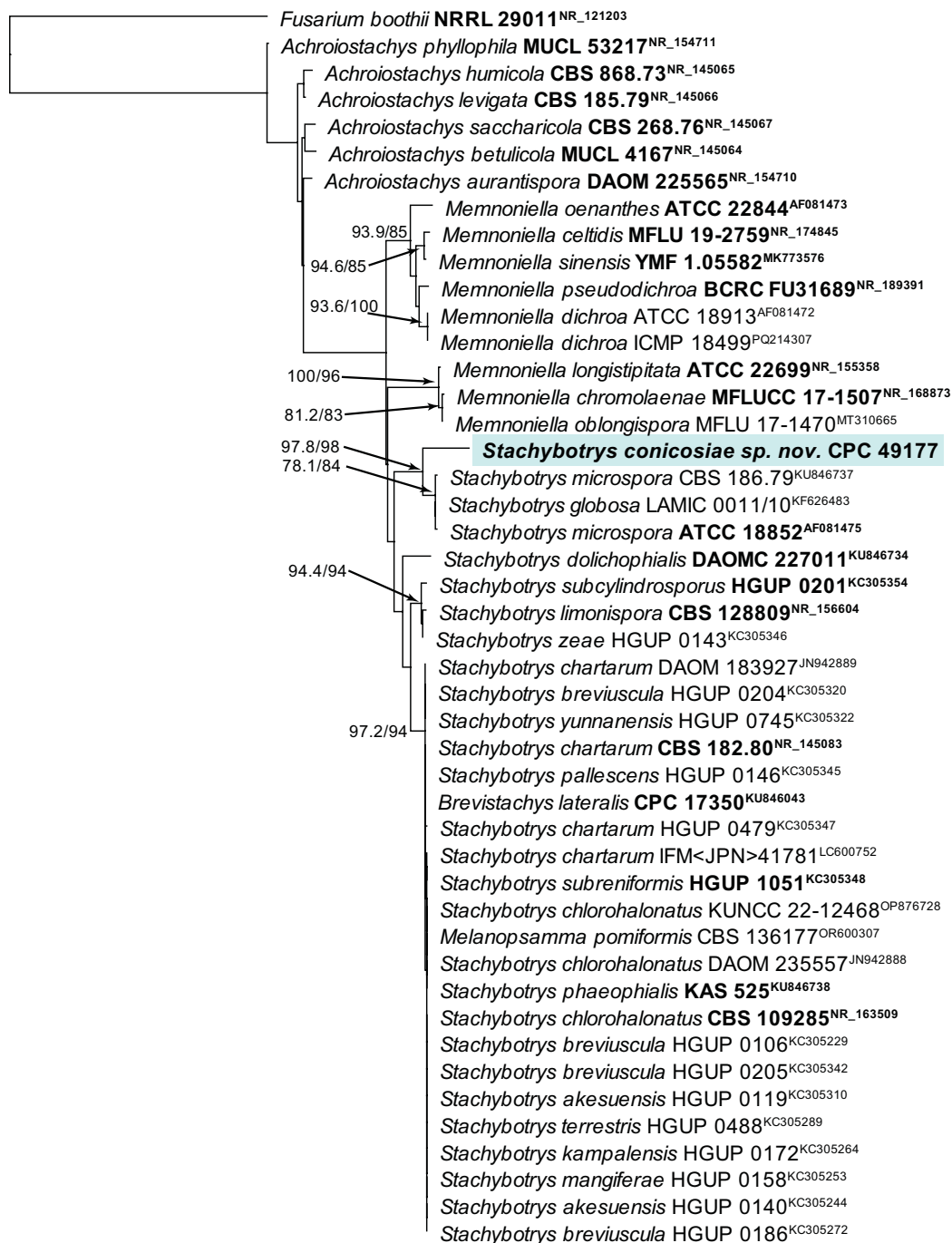
*Culture characteristics*: Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 15 mm diam. after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse luteous.

*Typus*: **South Africa**, Western Cape Province, Clanwilliam, on dead flower head of *Conicosia elongata* (*Aizoaceae*), Aug. 2024, *M.J. Wingfield*, HPC 4555 [holotype CBS H-25747; culture ex-type CPC 49177 = CBS 153455; ITS, LSU, *cmdA*, *rpb2* and *tef1* (first part) sequences GenBank PV664927.1, PV664954.1, PV664007.1, PV664018.1 and PV664030.1].

*Notes*: Lombard *et al.* (2016) redefined *Stachybotrys* and restricted it to species having conidiophores branching at the basal septum and the forming thick-walled conidia. *Stachybotrys conicosiae* is phylogenetically closely related to *S. subsylvatica* [conidiophores 30–65 × 3–5 µm, conidia (5–)5.5–6.5(–7) × 3–4 µm (av. 6 × 4 µm); Lombard *et al.* 2016], but is morphologically distinct, having longer conidiophores and conidia.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Stachybotrys subsylvatica* [strain CBS 126205, GenBank NR\_145084.1; Identities = 532/549 (97 %), seven gaps (1 %)], *Stachybotrys musae* [strain MFLUCC 20-0188, GenBank NR\_173231.1; Identities = 481/501 (96 %), no gaps], and *Stachybotrys microspora* [strain CBS 186.79, GenBank KU846737.1; Identities = 512/545 (94 %), two gaps (0 %)]. Closest hits using the **LSU** sequence are *Stachybotrys subsylvatica* [strain CBS 126205, GenBank NG\_058225.1; Identities = 812/819 (99 %), no gaps], *Stachybotrys microspora* [strain LAMIC0006/06, GenBank KP893309.1; Identities = 834/842 (99 %), one gap (0 %)], and *Stachybotrys globosa* [strain LAMIC0011/10, GenBank KP893316.1; Identities = 830/838 (99 %), one gap (0 %)]. Closest hits using the **cmdA** sequence had highest similarity to *Stachybotrys subsylvatica* [strain CBS 126205, GenBank KU846634.1; Identities = 579/654 (89 %), one gap (0 %)], *Stachybotrys musae* [strain MFLUCC 20-0152, GenBank MW480231.1; Identities = 477/556 (86 %), 20 gaps (3 %)], and *Stachybotrys microspora* [strain CBS 186.79, GenBank KU846631.1; Identities = 519/621 (84 %), eight gaps (1 %)]. Closest hits using the **rpb2** (first part) sequence had highest similarity to *Stachybotrys musae* [strain MFLUCC 20-0152, GenBank MW480229.1; Identities = 731/785 (93 %), two gaps (0 %)], *Stachybotrys subsylvatica* [strain CBS 126205, GenBank KU846964.1; Identities = 667/721 (93 %), no gaps], and *Stachybotrys microspora* [strain CBS 186.79, GenBank DQ676580.1; Identities = 590/640 (92 %), no gaps]. Closest hits using the **tef1** (first part) sequence had highest similarity to *Stachybotrys subsylvatica* [strain CBS 126205, GenBank KU847064.1; Identities = 377/458 (82 %), 17 gaps (3 %)], *Stachybotrys microspora* [strain CBS 186.79, GenBank KU847060.1; Identities = 366/462 (79 %), 31 gaps (6 %)], and *Stachybotrys reniformis* [strain CBS 976.95, GenBank KU847062.1; Identities = 341/430 (79 %), 24 gaps (5 %)].

*Colour illustrations*: *Conicosia elongata* flower, Clanwilliam, Western Cape Province, South Africa. Colony sporulating on synthetic nutrient-poor agar; conidiophores and conidiogenous cells giving rise to conidia; conidia. Scale bars = 10 µm.



0.01

Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.4.0 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020, Mo *et al.* 2023) of the *Stachybotrys* ITS nucleotide alignment. Bootstrap support values from 1000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown), preceded by the SH-aLRT test value (only shown if the node has > 74 % bootstrap support). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Fusarium boothii* (NRRL 29011; GenBank NR\_121203) and the novelty described here is highlighted with a coloured block and **bold** font. Alignment statistics: 46 strains including the outgroup; 584 characters including alignment gaps analysed; 224 distinct patterns, 105 parsimony-informative, 75 singleton sites, 404 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TNe+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.29050751).

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*Wiesneriomyces soli*





## *Wiesneriomyces soli* Crous, *sp. nov.*

*Etymology:* Name refers to the substrate it was isolated from, soil.

*Classification:* *Wiesneriomycetaceae*,  
*Wiesneriomycetales*, *Dothideomycetes*.

*Conidiomata* sporodochial, septate on dark pseudoparenchymatous stalk. *Setae* subulate, apex acute, 5–7-septate, thick-walled, brown, up to 250 µm tall, 10–13 µm wide at base. *Conidiophores* erect, branched, pale brown, smooth, up to 50 µm tall, 3–4 µm diam. *Conidiogenous cells* terminal, clavate, hyaline, 8–12 × 3–4 µm. *Conidia* hyaline, smooth, guttulate, slightly curved, cylindrical, (60–)65–75(–80) × (2.5–)3 µm, with 5–8 cells, separated by short isthmi, ends cells acutely rounded; individual cells 8–10 µm long, except apical cell shorter, 3–8 µm long.

*Culture characteristics:* Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 10 mm diam. after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse olivaceous grey.

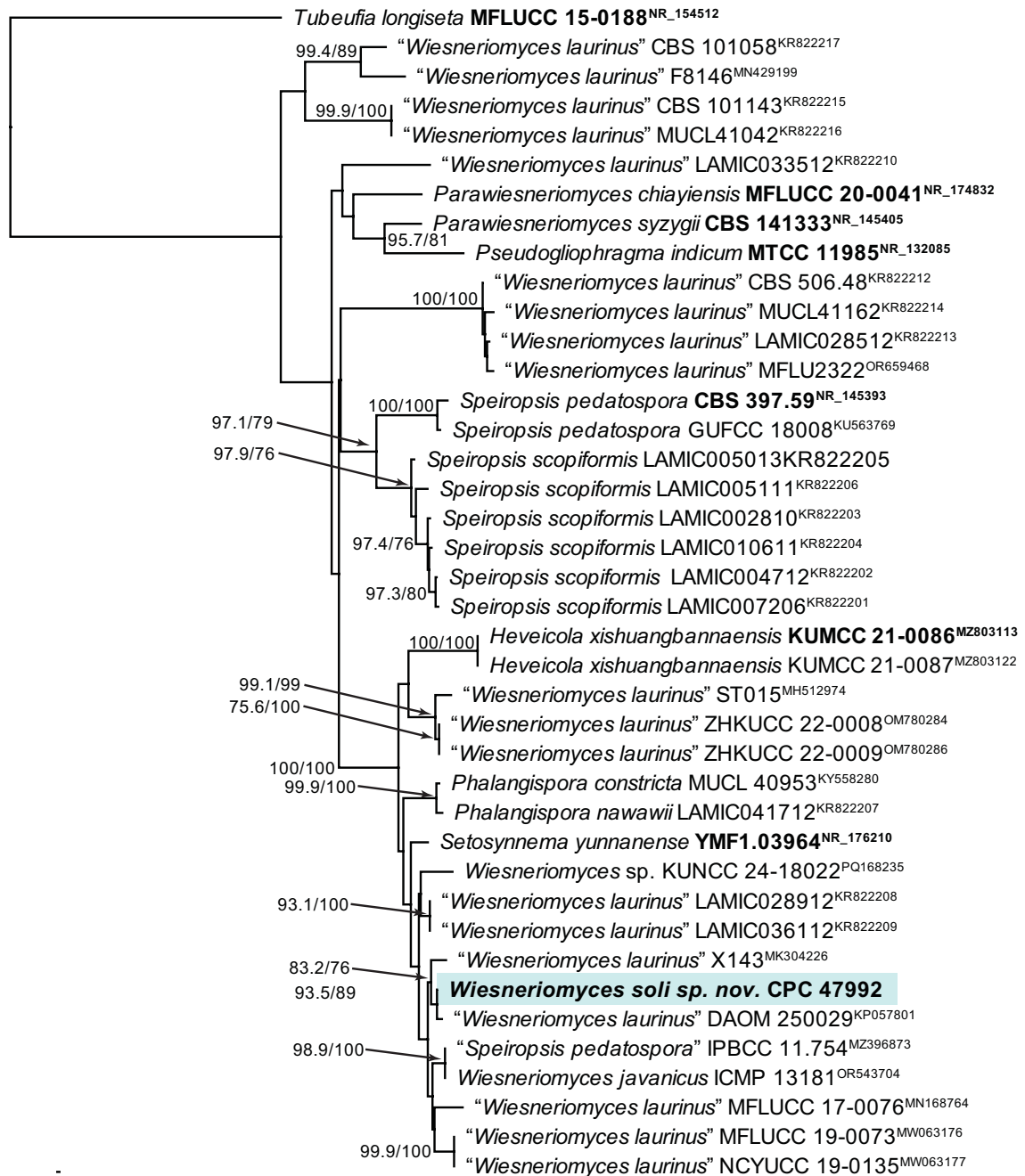
*Typus:* **Brazil**, Minas Gerais, Caraça, from soil, Feb. 2024, *P.W. Crous* [holotype CBS H-25712; culture ex-type COAD 3995 = CPC 47992; ITS, LSU, *rpb2* and *tef1* (second part) sequences GenBank PV664928.1, PV664955.1, PV664019.1 and PV664042.1].

*Notes:* Species of *Wiesneriomyces* occur in tropical areas, are saprobic, and are mostly found on leaf litter. *Wiesneriomyces soli* is phylogenetically close to *W. laurinus* (conidiomata with incurved setae arising from a sporodochial stalk; conidial cells 10–12 µm long, 3–4.5 µm wide), but distinct in lacking

incurved setae, and having shorter individual conidial propagules (Suetrong *et al.* 2014).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Wiesneriomyces laurinus* [strain DAOM 250029, GenBank KP057801.1; Identities = 551/560 (98 %), five gaps (0 %)], *Wiesneriomyces javanicus* [strain ICMP 13181, GenBank OR543704.1; Identities = 561/585 (96 %), seven gaps (1 %)], and *Speiropsis pedatospora* [strain JbD11, GenBank MZ396873.1; Identities = 560/586 (96 %), eight gaps (1 %)]. Closest hits using the LSU sequence are *Wiesneriomyces javanicus* [strain YMF1.04036, GenBank MH985636.1; Identities = 840/842 (99 %), no gaps], *Wiesneriomyces laurinus* [strain BCC9453, GenBank KJ425458.1; Identities = 832/834 (99 %), no gaps], and *Phalangispora constricta* [strain YMF1.02197, GenBank MH031751.1; Identities = 838/852 (98 %), no gaps]. Closest hits using the *rpb2* (first part) sequence had highest similarity to *Wiesneriomyces javanicus* [strain YMF1.04044, GenBank MK267286.1; Identities = 872/904 (96 %), no gaps], *Setosynnema yunnanense* [strain YMF1.02680, GenBank MK267284.1; Identities = 803/903 (89 %), no gaps], and *Phalangispora constricta* [strain YMF1.02197, GenBank MK049171.1; Identities = 619/725 (85 %), no gaps]. Closest hits using the *tef1* (second part) sequence had highest similarity to *Wiesneriomyces javanicus* [GenBank MK267293.1; Identities = 828/850 (97 %), one gap (0 %)], *Wiesneriomyces laurinus* [strain MFLUCC 17-0076, GenBank MT050455.1; Identities = 812/850 (96 %), no gaps], and *Setosynnema yunnanense* [GenBank MK267290.1; Identities = 807/863 (94 %), two gaps (0 %)].

*Colour illustrations:* Hiking trail in Caraça, Minas Gerais, Brazil. Colony sporulating on oatmeal agar; conidiomata with setae; conidia. Scale bars = 10 µm.



0.01

Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.4.0 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020, Mo *et al.* 2023) of the *Wiesneriomyces* ITS nucleotide alignment. Bootstrap support values from 1000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown), preceded by the SH-aLRT test value (only shown if the node has > 74 % bootstrap support). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in bold font. The tree was rooted to *Tubeufia longiseta* (MFLUCC 15-0188; GenBank NR\_154512) and the novelty described here is highlighted with a coloured block and bold font. Alignment statistics: 40 strains including the outgroup; 670 characters including alignment gaps analysed: 392 distinct patterns, 267 parsimony-informative, 79 singleton sites, 324 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TIM2e+I+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.29050751).

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*Exophiala aeris*



## *Exophiala aeris* Crous & Jurjević, *sp. nov.*

*Etymology:* Name refers to the fact that it was isolated from air via a settle plate method.

*Classification:* *Herpotrichiellaceae*, *Chaetothyriales*, *Chaetothyriomycetidae*, *Eurotiomycetes*.

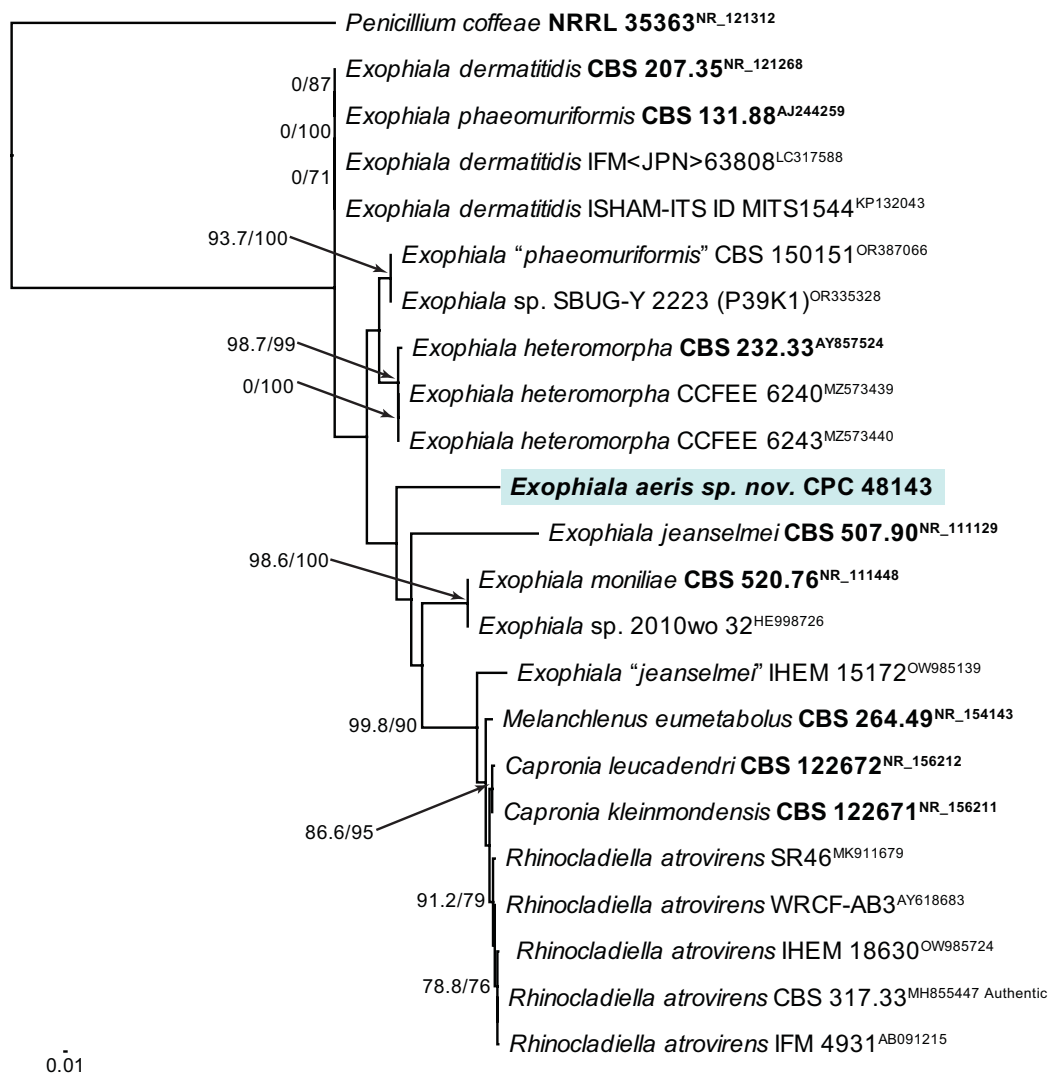
*Mycelium* consisting of pale brown, smooth, septate, branched, 1.5–2 µm diam. hyphae. *Conidiophores* reduced to lateral phialidic pegs on hyphae, or erect subcylindrical, unbranched, 1–5-septate, straight to flexuous, up to 50 µm tall, 2.5–3 µm wide, normally constricted at septa. *Conidiogenous cells* ellipsoid to fusoid-ellipsoid, pale brown, smooth, 3–6 × 2.5–3 µm, with cylindrical phialidic peg, 1–2 × 1 µm. *Conidia* solitary, aggregating in mucoid mass, pale brown, smooth, guttulate, ellipsoid, (3–)4(–5) × (1.5–)2.5(–3) µm.

*Culture characteristics:* Colonies erumpent, spreading, with sparse aerial mycelium and smooth, lobate margin, reaching 5 mm diam. after 2 wk at 25 °C. On MEA, CYA, PDA and OA surface and reverse dark mouse grey. No growth at 37 °C on CYA.

*Typus:* **USA**, Massachusetts, Springfield, living room, air (settle plate), Feb. 2024, Z. Jurjević, 5920 [**holotype** CBS H-25730; culture ex-type CPC 48143 = CBS 151647; ITS and *tef1* (first part) sequences GenBank PV664929.1 and PV664031.1].

*Notes:* *Exophiala* is a genus of *Herpotrichiellaceae* with members that are usually referred to as black yeasts. Species are known to have wide host ranges, and characterized by annelidic phialides that give rise to mucoid heads of pigmented conidia. *Exophiala aeris* is phylogenetically distinct from other members in this complex. The genus *Exophiala* is polyphyletic and in need of revision.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Exophiala moniliae* [strain CBS 520.76, GenBank NR\_111448.1; Identities = 459/532 (86 %), 32 gaps (6 %)], *Capronia kleinmondensis* [strain CBS 122671, GenBank NR\_156211.1; Identities = 471/548 (86 %), 29 gaps (5 %)], and *Capronia leucadendri* [strain CBS 122672, GenBank NR\_156212.1; Identities = 470/548 (86 %), 29 gaps (5 %)]. Closest hits using the **tef1** (first part) sequence had highest similarity to *Exophiala nishimurae* [strain IFM 41855, GenBank LC149408.1; Identities = 209/251 (83 %), 11 gaps (4 %)], *Exophiala bergeri* [strain RBG7236, GenBank OP066900.1; Identities = 231/287 (80 %), 14 gaps (4 %)], and *Dermatocarpon minutum* [strain AFTOL-ID 91, GenBank DQ782893.1; Identities = 161/177 (91 %), two gaps (1 %)].



Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.4.0 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020, Mo *et al.* 2023) of the *Exophiala* ITS nucleotide alignment. Bootstrap support values from 1000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown), preceded by the SH-aLRT test value (only shown if the node has > 74 % bootstrap support). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Penicillium coffeae* (NRRL 35363; GenBank NR\_121312) and the novelty described here is highlighted with a coloured block and **bold** font. Alignment statistics: 23 strains including the outgroup; 634 characters including alignment gaps analysed: 273 distinct patterns, 164 parsimony-informative, 123 singleton sites, 347 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TIM2+F+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.29050751).

*Sphaerulina brabeji*





## *Sphaerulina brabeji* Crous, *sp. nov.*

*Etymology:* Name refers to the host genus it was isolated from, *Brabejum*.

*Classification:* *Mycosphaerellaceae*, *Mycosphaerellales*, *Dothideomycetidae*, *Dothideomycetes*.

*Conidiomata* erumpent, pycnidial solitary, 250–300 µm diam.; wall of 3–6 layers of dark brown textura angularis. *Conidiophores* hyaline, smooth, subcylindrical, straight to geniculate-sinuous, branched at base or not, or reduced to conidiogenous cells, 0–2-septate, 20–30 × 5–7 µm. *Conidiogenous cells* terminal or intercalary, hyaline, smooth, proliferating percurrently or sympodially, 10–20 × 3–5 µm. *Conidia* solitary, hyaline, smooth, guttulate, subcylindrical, straight to flexuous, with apical taper, apex subobtuse, base truncate, 2–2.5 µm, 1–8-septate, (38–)60–70(–75) × 2.5–3 µm; undergoing microcyclic conidiation in culture.

*Culture characteristics:* Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 5 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse olivaceous grey.

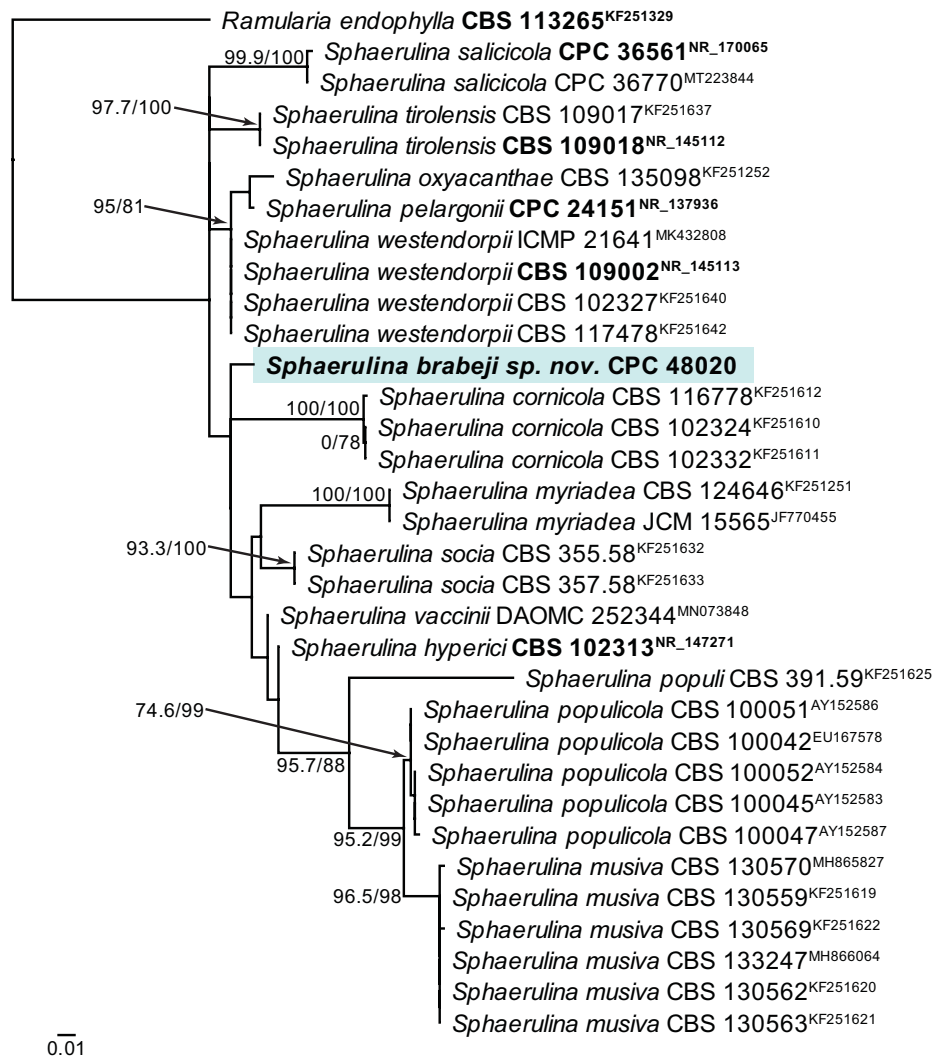
*Typus:* **South Africa**, Western Cape Province, Cape Town, Kirstenbosch, on twigs of *Brabejum stellatifolium* (*Proteaceae*), 22 Nov. 2023, P.W. Crous, HPC 4334 [**holotype** CBS H-25719; culture ex-type CPC 48020 = CBS 153463; ITS, LSU, *actA*, *cmdA*, *rpb2*, *tef1* (first part) and *tub2* sequences GenBank PV664930.1, PV664956.1, PV664002.1, PV664008.1, PV664020.1, PV664032.1 and PV664050.1].

*Notes:* *Sphaerulina* contains numerous leaf spot pathogens that can easily be confused with species of *Septoria*, also having mycosphaerella-like sexual morphs. *Sphaerulina brabeji* is phylogenetically related to *Sphaerulina hyperici* [on *Hypericum* spp.; conidia 24–55(–63) × 2.5–3.5 µm, 1–3(–5)-septate; Verkley *et al.* 2013], but distinct in having longer conidia with more septa. This is the first *Sphaerulina* sp. reported from *Brabejum*.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Sphaerulina hyperici* [strain CBS 102313, GenBank NR\_147271.1; Identities = 482/493 (98 %), five gaps (1 %)], *Sphaerulina berberidis* [strain FC-4020, GenBank LC206674.1; Identities = 494/506 (98 %), three

gaps (0 %)], and *Sphaerulina cercidis* [strain CBS 128634, GenBank MH865061.1; Identities = 493/505 (98 %), two gaps (0 %)]. Closest hits using the **LSU** sequence are *Sphaerulina azaleae* [strain KACC44227, GenBank MK578201.1; Identities = 839/840 (99 %), no gaps], *Sphaerulina patriniae* [strain CBS 128653, GenBank MH876542.1; Identities = 839/840 (99 %), no gaps], and *Sphaerulina chaenomelis* [as *Pseudocercospora chaenomelis*; strain CBS 131897, GenBank GU253834.1; Identities = 839/840 (99 %), no gaps]. Closest hits using the **actA** sequence had highest similarity to *Sphaerulina azaleae* [strain KACC 44227, GenBank MK584565.1; Identities = 518/550 (94 %), one gap (0 %)], *Sphaerulina cercidis* [strain CBS 118910, GenBank KF903507.1; Identities = 471/508 (93 %), one gap (0 %)], and *Septoria salicicola* [strain CPC 36569, GenBank MT223757.1; Identities = 501/553 (91 %), three gaps (0 %)]. Closest hits using the **cmdA** sequence had highest similarity to *Sphaerulina socia* [strain CBS 355.58, GenBank KF254284.1; Identities = 374/400 (94 %), two gaps (0 %)], *Sphaerulina berberidis* [strain CBS 324.52, GenBank KF254253.1; Identities = 393/433 (91 %), nine gaps (2 %)], and *Sphaerulina chaenomelis* [strain MUCC<JPN>:1510, GenBank OR507810.1; Identities = 392/433 (91 %), nine gaps (2 %)]. Closest hits using the **rpb2** (first part) sequence had highest similarity to *Mycosphaerella harthensis* [strain CBS 325.52, GenBank MF951675.1; Identities = 643/725 (89 %), two gaps (0 %)], *Sphaerulina koreana* [strain CBS 135462, GenBank KX288707.1; Identities = 686/786 (87 %), no gaps], and *Sphaerulina berberidis* [strain En26-1, GenBank OK431475.1; Identities = 742/852 (87 %), four gaps (0 %)]. Closest hits using the **tef1** (first part) sequence had highest similarity to *Sphaerulina socia* [strain CBS 355.58, GenBank KF253579.1; Identities = 320/352 (91 %), two gaps (0 %)], *Sphaerulina chaenomelis* [voucher GUCC 2595.1, GenBank MW113690.1; Identities = 317/348 (91 %), five gaps (1 %)], and *Sphaerulina gei* [strain CBS 128616, GenBank KF253561.1; Identities = 310/340 (91 %), two gaps (0 %)]. Closest hits using the **tub2** sequence had highest similarity to *Sphaerulina socia* [strain CBS 355.58, GenBank KF253094.1; Identities = 293/316 (93 %), two gaps (0 %)], *Sphaerulina berberidis* [strain CBS 324.52, GenBank KF253067.1; Identities = 221/239 (92 %), two gaps (0 %)], and *Sphaerulina juglandis* [strain MUCC<JPN>:1475, GenBank OR637381.1; Identities = 240/269 (89 %), eight gaps (2 %)].

*Colour illustrations:* Leaves of *Brabejum stellatifolium*, Kirstenbosch, Cape Town, South Africa. Conidiomata sporulating on synthetic nutrient-poor agar; conidiophores and conidiogenous cells giving rise to conidia on SNA; conidia. Scale bars = 10 µm.



Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.4.0 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020, Mo *et al.* 2023) of the *Sphaerulina* ITS nucleotide alignment. Bootstrap support values from 1000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown), preceded by the SH-aLRT test value (only shown if the node has > 74 % bootstrap support). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Ramularia endophylla* (CBS 113265; GenBank KF251329) and the novelty described here is highlighted with a coloured block and **bold** font. Alignment statistics: 33 strains including the outgroup; 584 characters including alignment gaps analysed: 153 distinct patterns, 90 parsimony-informative, 44 singleton sites, 450 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TN+I+R2. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.29050751).



*Neodendryphiella agapanthi*



## *Neodendryphiella agapanthi* Crous, *sp. nov.*

*Etymology*: Name refers to the host genus it was isolated from, *Agapanthus*.

*Classification*: Dictyosporiaceae, Pleosporales, Pleosporomycetidae, Dothideomycetes.

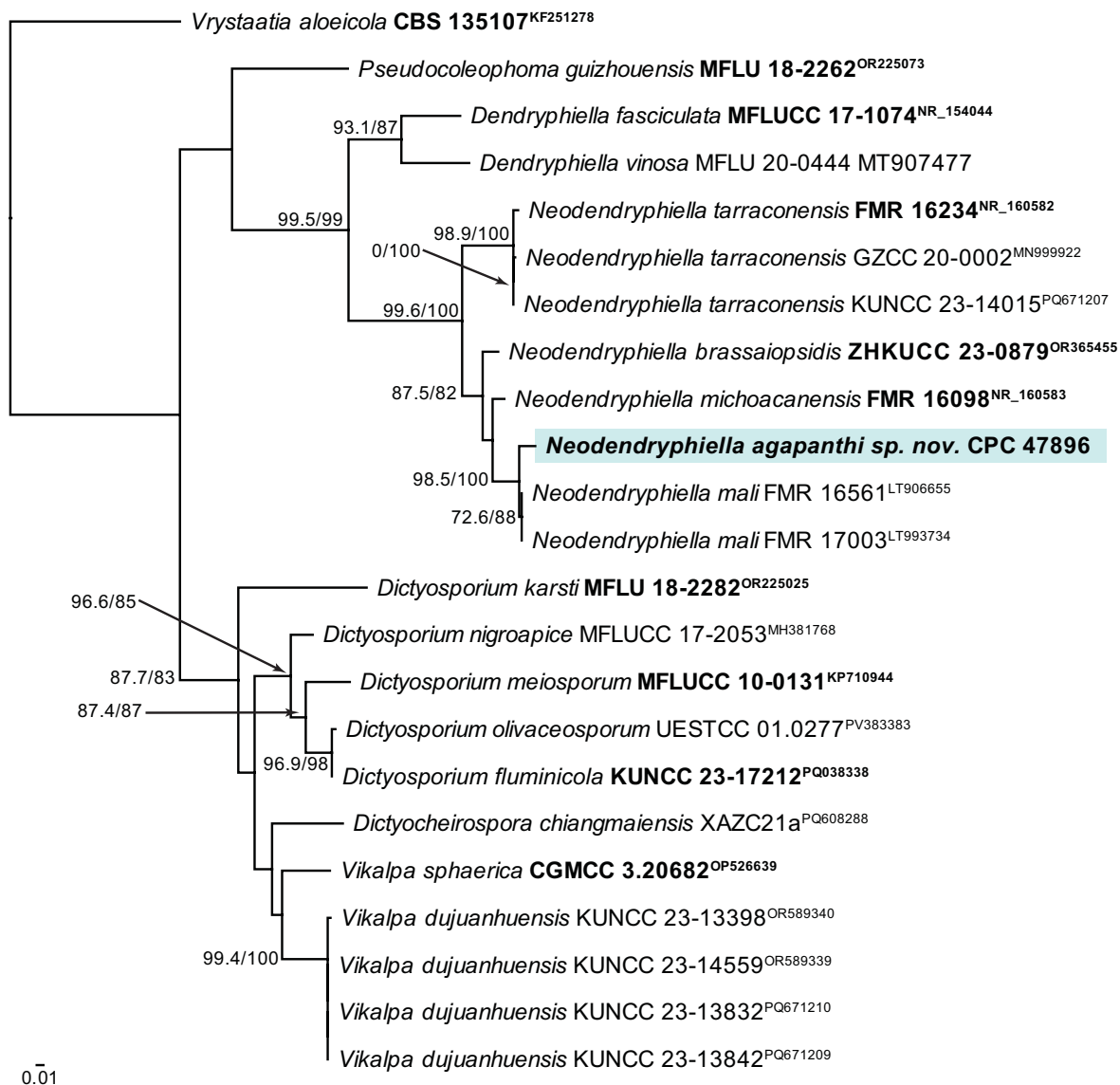
*Mycelium* of smooth, hyaline, branched, septate, 2.5–3 µm diam. hyphae. *Conidiophores* solitary, flexuous, subcylindrical, arising from superficial hyphae, brown, thick-walled, verruculose, guttulate, up to 300 µm tall, 4–6 µm wide, multiseptate, unbranched or branched at apex. *Conidiogenous cells* subcylindrical to subclavate, brown, verruculose, terminal and intercalary, polytretic (1–4), pores darkened, thickened, 1–1.5 µm diam. *Conidia* in branched chains, brown, verruculose, guttulate, straight with obtuse ends, pores thickened, darkened, 1–1.5 µm diam.; ramoconidia 1–3-septate, 15–17 × (5–)6 µm; conidia 1–2-septate, (9–)11–13(–15) × 5(–6) µm.

*Culture characteristics*: Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 10 mm diam. after 2 wk at 25 °C. On MEA surface honey, reverse isabelline; on PDA and OA surface and reverse umber.

*Typus*: **Brazil**, Minas Gerais, University of Viçosa campus, from stalks of *Agapanthus praecox* (*Amaryllidaceae*), Feb. 2024, P.W. Crous, HPC 4392 (**holotype** CBS H-25710; culture ex-type COAD 3989 = CPC 47896; ITS and LSU sequences GenBank PV664931.1 and PV664957.1).

*Notes*: *Neodendryphiella* was introduced as a new genus for a phylogenetically distinct lineage resembling *Dendryphiella* in general morphology. *Neodendryphiella agapanthi* is phylogenetically close to *N. mali*, although the latter has larger ramoconidia, (11–)15–17(–21) × 3–4 µm, and smaller, (0–)1-septate conidia, 4–15 × 3–5 µm (Iturrieta-González *et al.* 2018).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Neodendryphiella mali* [strain FMR 17003, GenBank LT993734.1; Identities = 488/499 (98 %), one gap (0 %)], and more distant hits to *Atrocalyx nordicus* [strain MAL27, GenBank MW759243.1; Identities = 343/385 (89 %), 11 gaps (2 %)], and *Lophiostoma cynaroidis* [strain CBS 123025, GenBank EU552138.1; Identities = 343/387 (89 %), 11 gaps (2 %)]. Closest hits using the **LSU** sequence are *Neodendryphiella mali* [strain FMR 17003, GenBank LT993735.1; Identities = 829/830 (99 %), no gaps], *Diplococcium asperum* [strain CBS 139.95, GenBank EF204493.1; Identities = 772/774 (99 %), no gaps], and *Neodendryphiella brassaiopsidis* [strain ZHKUCC 23-0879, GenBank NG\_243861.1; Identities = 823/828 (99 %), no gaps].



Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.4.0 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020, Mo *et al.* 2023) of the *Neodendryphiella* ITS nucleotide alignment. Bootstrap support values from 1000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown), preceded by the SH-aLRT test value (only shown if the node has > 74 % bootstrap support). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Vrystaatia aloicola* (CBS 135107; GenBank KF251278) and the novelty described here is highlighted with a coloured block and **bold** font. Alignment statistics: 23 strains including the outgroup; 579 characters including alignment gaps analysed: 330 distinct patterns, 187 parsimony-informative, 80 singleton sites, 312 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TIM2e+R2. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.29050751).

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*Parapenidiella melastomatis*





## *Parapenidiella melastomatis* Crous, *sp. nov.*

*Etymology:* Name refers to the host family it was isolated from, *Melastomataceae*.

*Classification:* *Teratosphaeriaceae*, *Mycosphaerellales*, *Dothideomycetidae*, *Dothideomycetes*.

*Mycelium* consisting of olivaceous, smooth, branched, septate, 1.5–2 µm diam. hyphae. *Conidiophores* reduced to conidiogenous cells on hyphae, solitary, integrated, subcylindrical, pale brown, smooth, 10–30 × 1.5–2 µm, with terminal or lateral scar, thickened, darkened, 1 µm diam. *Conidia* in branched chains, pale brown, smooth, guttulate, fusoid-ellipsoid; hila thickened, darkened, 0.5 µm diam.; ramoconidia 10–20 × 2–3 µm; conidia aseptate, (8–)9–12 × 2–3 µm.

*Culture characteristics:* Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 5 mm diam. after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse isabelline.

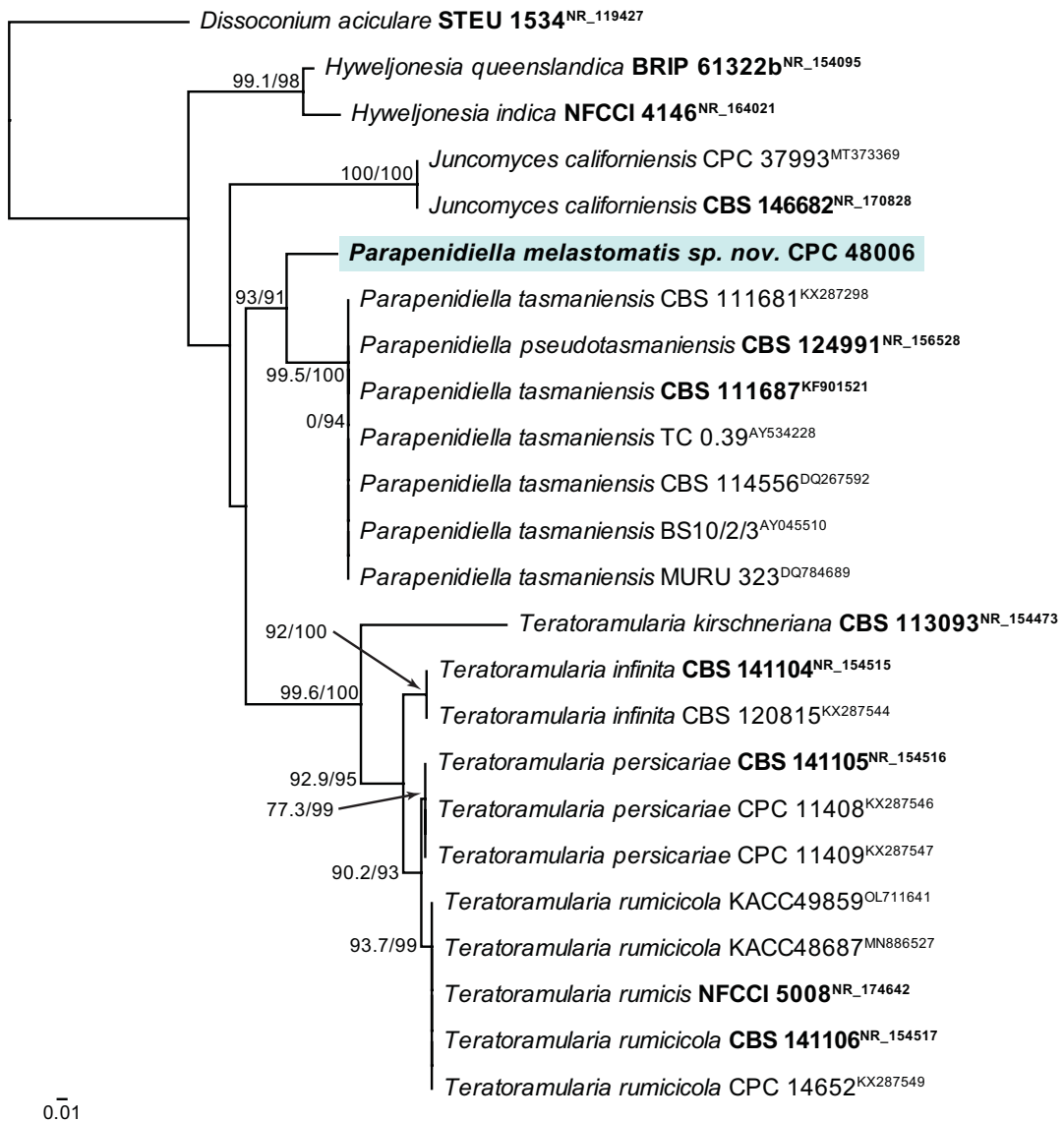
*Typus:* **Brazil**, Minas Gerais, Caraça, on living leaves of unidentified *Melastomataceae*, Feb. 2024, *P.W. Crous*, HPC 4402 [**holotype** CBS H-25716; culture ex-type COAD 3990 = CPC 48006; ITS, LSU, *actA* and *tef1* (first part) sequences GenBank PV664932.1, PV664958.1, PV664003.1 and PV664033.1].

*Notes:* *Parapenidiella* is distinguished by having pale brown, unbranched, penicillate conidiophores, with olivaceous to pale brown, branched conidial chains. *Parapenidiella melastomatis* is phylogenetically close to *P. tasmaniensis*, although the latter has larger, 0(–)1-septate, (4–)8–12(–20) × 2–2.5 µm conidia (Crous *et al.* 2012).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Parapenidiella tasmaniensis* [strain

BS10/2/3, GenBank AY045510.1; Identities = 458/520 (88 %), 30 gaps (5 %)], *Parapenidiella pseudotasmaniensis* [strain CBS 124991, GenBank NR\_156528.1; Identities = 448/511 (88 %), 31 gaps (6 %)], and *Teratoramularia rumicis* [strain NFCCI 5008, GenBank NR\_174642.1; Identities = 358/415 (86 %), 20 gaps (4 %)]. Closest hits using the **LSU** sequence are *Parapenidiella tasmaniensis* [strain CBS 111687, GenBank DQ246233.1; Identities = 865/870 (99 %), one gap (0 %)], *Parapenidiella pseudotasmaniensis* [strain CBS 124991, GenBank NG\_066269.1; Identities = 865/870 (99 %), one gap (0 %)], and *Teratoramularia kurodachikae* [strain BRIP 75800a, GenBank NG\_243398.1; Identities = 848/869 (98 %), one gap (0 %)]. Closest hits using the **actA** sequence had highest similarity to *Teratoramularia infinita* [strain CPC 19488, GenBank KX287828.1; Identities = 448/496 (90 %), three gaps (0 %)], *Ramularia hydrangeae-macrophyllae* [strain CPC 25903, GenBank KX287738.1; Identities = 450/498 (90 %), seven gaps (1 %)], and *Ramularia acroptili* [strain CPC 18723, GenBank KX287593.1; Identities = 449/498 (90 %), seven gaps (1 %)]. A blast2 comparison against the available sequences of *Parapenidiella tasmaniensis* (GenBank DQ147676.1, DQ147677.1, KF903451.1, KF903469.1, and KF903562.1) revealed a similarity of 81.5 to 88.5 %. Closest hits using the **tef1** (first part) sequence had distant partial similarity to *Pseudocercospora victoriae* [strain CBS 149428, GenBank PP405007.1; Identities = 176/191 (92 %), three gaps (1 %)], *Pseudophaeophleospora phormii* [strain CBS 144606, GenBank MK442711.1; Identities = 171/184 (93 %), one gap (0 %)], and *Zasmidium fructigenum* [GenBank OM165025.1; Identities = 170/184 (92 %), one gap (0 %)]. A blast2 comparison against the available sequences of *Parapenidiella tasmaniensis* (GenBank DQ235121.1, DQ235122.1, KF903150.1, KF903151.1, and KF903152.1) revealed a similarity of 69 % (GenBank DQ235121.1, DQ235122.1) to 91 % (GenBank KF903152.1).

*Colour illustrations:* Leaves of *Melastoma* sp., Caraça, Minas Gerais, Brazil. Conidiophores and conidiogenous cells giving rise to conidia on SNA; conidia. Scale bars = 10 µm.



Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.4.0 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020, Mo *et al.* 2023) of the *Parapendiella* ITS nucleotide alignment. Bootstrap support values from 1000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown), preceded by the SH-aLRT test value (only shown if the node has > 74 % bootstrap support). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Dissoconium aciculare* (STEU 1534; GenBank NR\_119427) and the novelty described here is highlighted with a coloured block and **bold** font. Alignment statistics: 24 strains including the outgroup; 547 characters including alignment gaps analysed: 241 distinct patterns, 147 parsimony-informative, 58 singleton sites, 342 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TIM2+F+I. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.29050751).

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*Pararamichloridium ouopretoense*



## *Pararamichloridium ouopretoense* Crous, *sp. nov.*

*Etymology:* Name refers to Ouro Preto, Brazil, the historic town where this fungus was collected.

*Classification:* *Pararamichloridiaceae*,  
*Pararamichloridiales*, *Sordariomycetes*.

*Mycelium* consisting of hyaline, smooth, branched, septate, 1.5–2 µm diam. hyphae. *Conidiophores* arising from superficial hyphae, solitary, erect, flexuous, subcylindrical, unbranched, brown, thick-walled, smooth, 1–4-septate, 50–150 × 4–5 µm. *Conidiogenous cells* 35–50 × 2–3 µm, integrated, terminal, pale brown, smooth, subcylindrical, forming a rachis with pimple-like denticles, 0.5–1 × 0.5 µm. *Conidia* solitary, aseptate, ellipsoid, guttulate, medium brown, covered in mucoid sheath giving conidia warty appearance, (6–)7(–8) × (3–)3.5(–4) µm.

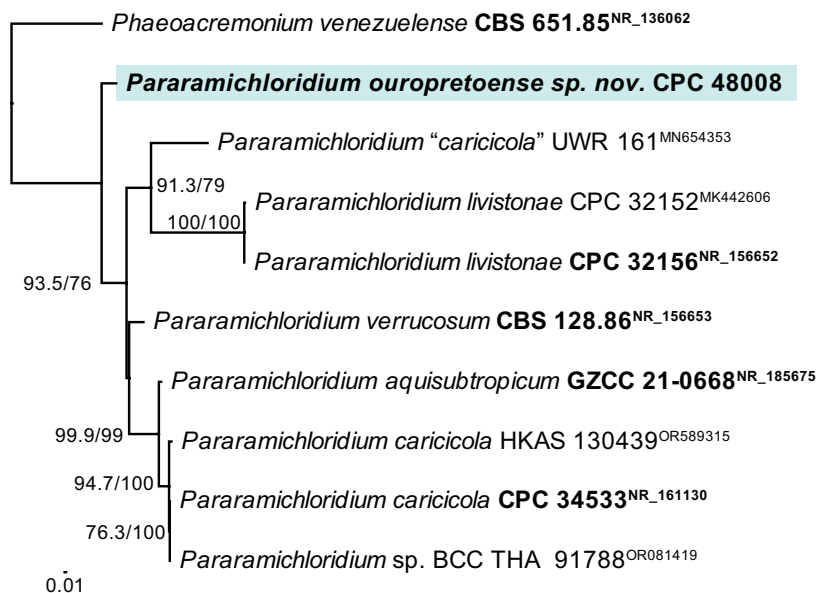
*Culture characteristics:* Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 15 mm diam. after 2 wk at 25 °C. On MEA surface ochreous, reverse umber; on PDA surface and reverse pale luteous; on OA surface buff.

*Typus:* **Brazil**, Minas Gerais, Ouro Preto, on living leaves of unidentified *Poaceae*, Feb. 2024, *P.W. Crous*, HPC 4405 (**holotype** CBS H-25717; culture ex-type COAD 3991 = CPC 48008; ITS and LSU sequences GenBank PV664933.1 and PV664959.1).

*Notes:* *Pararamichloridium* is a ramichloridium-like genus that presently includes four species. *Pararamichloridium ouopretoense* is phylogenetically close to *P. caricicola*, but distinct in that the latter has slightly smaller conidia, (4–)6–7(–8) × 3(–3.5) µm, and shorter conidiophores, 35–100 × 2.5–3 µm (Crous *et al.* 2018a).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Pararamichloridium caricicola* [strain CBS 145069, GenBank NR\_161130.1; Identities = 518/591 (88 %), 23 gaps (3 %)], *Pararamichloridium aquisubtropicum* [strain GZAAS 21-0382, GenBank NR\_185675.1; Identities = 506/579 (87 %), 29 gaps (5 %)], and *Pararamichloridium verrucosum* [strain CBS 128.86, GenBank NR\_156653.1; Identities = 496/574 (86 %), 44 gaps (7 %)]. Closest hits using the **LSU** sequence are *Pararamichloridium verrucosum* [strain CBS 128.86, GenBank NG\_057768.1; Identities = 820/839 (98 %), no gaps], *Pararamichloridium caricicola* [strain CBS 145069, GenBank NG\_066287.1; Identities = 842/862 (98 %), no gaps], and *Pararamichloridium aquisubtropicum* [strain GZAAS 21-0382, GenBank NG\_228929.1; Identities = 841/862 (98 %), no gaps].

*Colour illustrations:* Living leaves of unidentified *Poaceae*, Ouro Preto, Minas Gerais, Brazil. Conidiophores and conidiogenous cells giving rise to conidia on SNA; conidia. Scale bars = 10 µm.



Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.4.0 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020, Mo *et al.* 2023) of the *Pararamichloridium* ITS nucleotide alignment. Bootstrap support values from 1000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown), preceded by the SH-aLRT test value (only shown if the node has > 74 % bootstrap support). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Phaeoacremonium venezuelense* (CBS 651.85; GenBank NR\_136062) and the novelty described here is highlighted with a coloured block and **bold** font. Alignment statistics: 10 strains including the outgroup; 632 characters including alignment gaps analysed: 244 distinct patterns, 134 parsimony-informative, 87 singleton sites, 411 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TIM2+F+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.29050751).

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*Parafusicladium riodejaneiroanum*





## *Parafusicladium riodejaneiroanum* Crous, *sp. nov.*

*Etymology:* Name refers to the city where it was collected, Rio de Janeiro, Brazil.

*Classification:* *Symptoventuriaceae*, *Venturiales*, *Pleosporomycetidae*, *Dothideomycetes*.

*Mycelium* consisting of brown, smooth, branched, septate, 2–2.5 µm diam. hyphae. *Conidiophores* solitary, erect, subcylindrical, unbranched, straight to flexuous, brown, smooth, reduced to conidiogenous cells on hyphae without basal septum, or 1-septate, with septum in bottom third of conidiophore, 7–45 × 3–5 µm. *Conidiogenous cells* 7–40 × 3–5 µm, integrated, terminal, brown, smooth, with prominent sympodial denticles; scars cicatrized, slightly darkened or not, 0.5–1 µm diam. *Conidia* solitary, brown, guttulate, straight, medianly 1-septate, subcylindrical, apex obtuse, tapering at base to truncate hilum, 1 µm diam., slightly darkened, mostly solitary, rarely in chains of two conidia, (12–)13–15(–16) × (2.5–)3(–3.5) µm.

*Culture characteristics:* Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 5 mm diam. after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse umber.

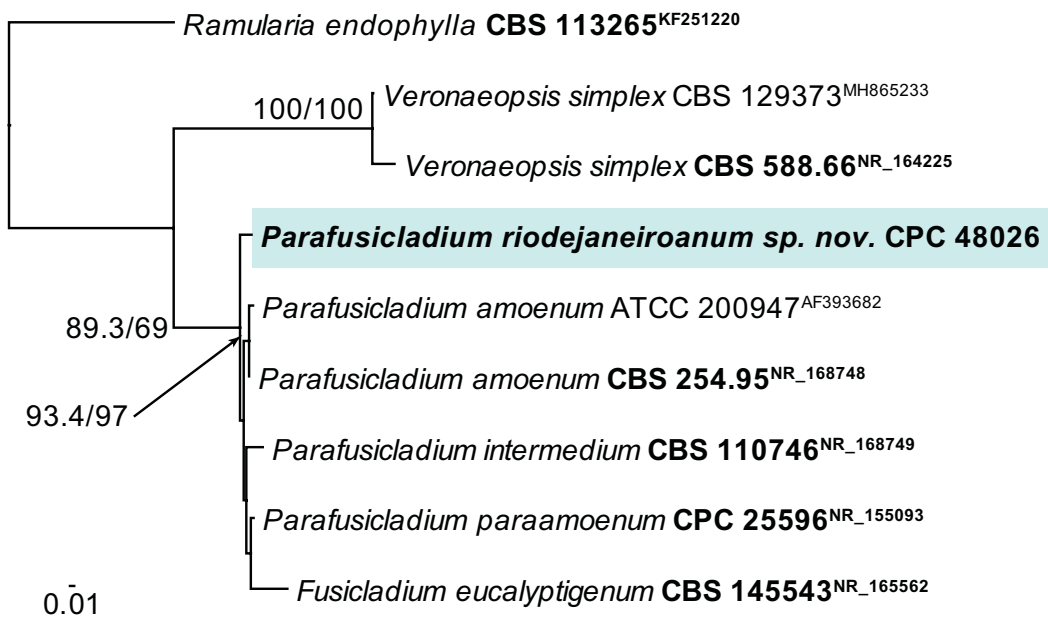
*Typus:* **Brazil**, Rio de Janeiro, on living leaves of native bamboo (*Poaceae*), Feb. 2024, *P.W. Crous*, HPC 4404 [**holotype** CBS H-25720; culture ex-type COAD 3992 = CPC 48026; ITS, LSU, *tef1* (first part) and *tub2* sequences GenBank PV664934.1, PV664960.1, PV664034.1 and PV664051.1].

*Notes:* *Parafusicladium* has erect, solitary, subcylindrical, brown to dark brown conidiophores, with smooth, brown, denticulate conidiogenous cells, and cylindrical to subcylindrical, subhyaline to pale brown conidia (Shen *et al.* 2020). *Parafusicladium riodejaneiro* is phylogenetically close

to *P. amoenum* (conidia fusoid, 0–1-septate, in simple chains, (6.0–)10.5–12.8(–17.3) × (1.5–)2.4–3.0(–3.8) µm; Ho *et al.* 1999), but differs in conidial morphology.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Parafusicladium amoenum* [strain CBS 254.95, GenBank NR\_168748.1; Identities = 512/530 (97 %), three gaps (0 %)], *Parafusicladium paraamoenum* [strain CBS 141322, GenBank NR\_155093.1; Identities = 512/533 (96 %), six gaps (1 %)], and *Parafusicladium intermedium* [strain CBS 110746, GenBank NR\_168749.1; Identities = 489/517 (95 %), five gaps (0 %)]. Closest hits using the LSU sequence are *Parafusicladium amoenum* [strain CBS 254.95, GenBank NG\_058242.1; Identities = 852/855 (99 %), no gaps], *Fusicladium eucalyptigenum* [strain CBS 145543, GenBank MK876431.1; Identities = 720/728 (99 %), no gaps], and *Fusicladium intermedium* [strain CBS 110746, GenBank EU035432.1; Identities = 848/858 (99 %), one gap (0 %)]. Closest hits using the *tef1* (first part) sequence had distant highest similarity to *Curvularia hawaiiensis* [strain DUCC15700, GenBank OR841149.1; Identities = 148/167 (89 %), no gaps], *Curvularia lunata* [voucher CRB-JD A112, GenBank MT793765.1; Identities = 143/159 (90 %), no gaps], and *Helminthosporium juglandinum* [strain L97, GenBank KY984445.1; Identities = 276/365 (76 %), 31 gaps (8 %)]. A blast2 comparison between our sequence and three unverified *Parafusicladium tef1* sequences (GenBank MK888730.1–MK888732.1) on GenBank revealed an average sequence similarity of 91 %. Closest hits using the *tub2* sequence had highest similarity to *Paraconiothyrium bonneyae* [voucher GZAAS 23-0804, GenBank OR902367.1; Identities = 400/508 (79 %), 27 gaps (5 %)], *Paraconiothyrium salinum* [strain CMG 49, GenBank MN380479.1; Identities = 396/503 (79 %), 16 gaps (3 %)], and *Curreya pityophila* [strain UTHSC DI16-357, GenBank LT796981.1; Identities = 380/479 (79 %), 16 gaps (3 %)].

*Colour illustrations:* View from Sugarloaf Mountain, Rio de Janeiro, Brazil. Conidiophores and conidiogenous cells giving rise to conidia on SNA; conidia. Scale bars = 10 µm.



Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.4.0 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020, Mo *et al.* 2023) of the *Parafusicladium* ITS nucleotide alignment. Bootstrap support values from 1000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown), preceded by the SH-aLRT test value (only shown if the node has > 74 % bootstrap support). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Ramularia endophylla* (CBS 113265; GenBank KF251220) and the novelty described here is highlighted with a coloured block and **bold** font. Alignment statistics: nine strains including the outgroup; 532 characters including alignment gaps analysed: 154 distinct patterns, 107 parsimony-informative, 100 singleton sites, 325 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TNe+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.29050751).

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*Stylonectria hygrophila*



***Stylonectria hygrophila* Mombert & Crous, *sp. nov.***

*Etymology:* The name refers to the occurrence of this species in a marshy locality.

*Classification:* *Nectriaceae*, *Hypocreales*, *Sordariomycetes*.

*Ascomata* perithecial, gregarious, in groups of 2–16, or solitary, erumpent to superficial with base remaining immersed in a hypostroma of fusarium-like sporodochia, arising from dead pyrenomycetes, broadly pyriform, 240–308 µm high, 234–288 µm diam. (av. 274–261 µm, n = 10), with a discoid papilla, red to dark red, turning dark purple in 5 % KOH, yellow in lactic acid, not collapsing when dry. *Ascomatal wall* smooth, 32–40 µm thick, composed of two regions: outer region 22–29 µm thick, of irregularly shaped thick-walled cells of *textura intricata* to *textura epidermoidea*; inner region 12–16 µm thick of thin-walled, flattened cells of *textura prismatica* to *textura angularis*. *Asci* unitunicate, subcylindrical, 64–79 × 5.6–6.9 µm, 8-spored, apices rounded and simple, uniseriate; evanescent, narrowly moniliform paraphyses, interspersed between asci. *Ascospores* ellipsoidal, 1-septate, often constricted at septum, (9.4–)9.6–11.3(–12.3) × (4.3–)4.6–5.4(–5.9) µm, (av. = 10.4 × 5 µm, n = 76), (Q = 1.7–2.1–2.5), smooth, thick-walled, hyaline at first, becoming pale golden brown at maturity (measurements from discharged mature ascospores). *Mycelium* consisting of hyaline, smooth, branched, septate, 2–2.5 µm diam. hyphae. Crystalline sporodochia superficial on CLA. *Conidiophores* solitary or aggregated in clusters to form sporodochia reduced to conidiogenous cells or 1–2-septate, branched, subcylindrical, hyaline, smooth, 10–40 × 2–3 µm. *Conidiogenous cells* hyaline, smooth, monophialidic, straight to curved, subcylindrical with apical taper, 10–20 × 2–3 µm, with inconspicuous collarette. *Conidia* solitary, aggregating in mucoid mass, hyaline, smooth, fusoid, apex subobtuse, curved, base tapered to truncate hilum, (0–)1-septate, (10–)22–27(–30) × (2–)2.5(–3) µm; larger conidia develop a slight constriction in the basal cell, appearing as a poorly developed foot cell, but mostly absent, along with *chlamydospores* and *microconidia*.

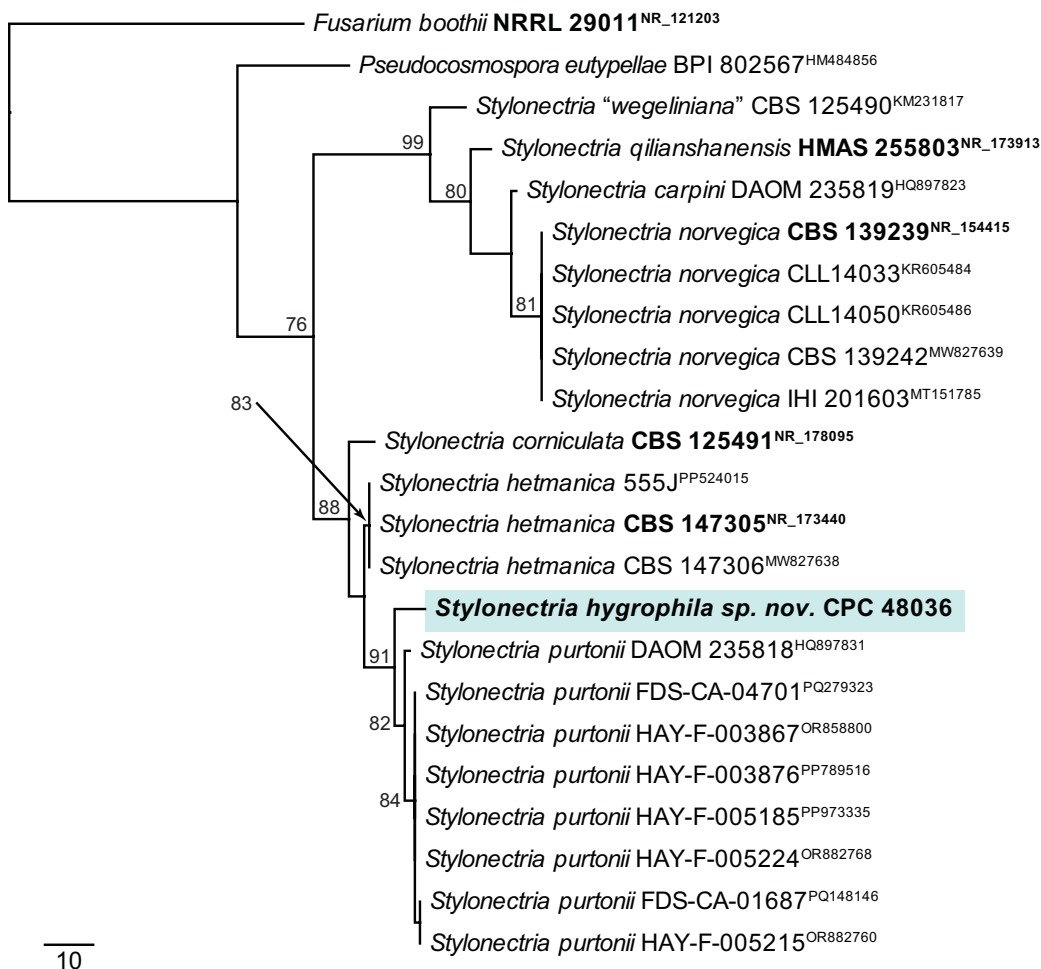
*Culture characteristics:* Colonies flat, spreading, with sparse aerial mycelium and smooth, lobate margin, reaching 17 mm diam. after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse saffron.

*Typus:* **France**, Haute-Saône (70), Saint-Germain, Réserve Naturelle de la Grande Pile, on unidentified *Diaporthales*, on dead twigs of *Betula pubescens* (*Betulaceae*), 47.73370° N 6.50264° E, 326 m a.s.l., 12 Mar. 2024, A. Mombert, CBNM0079 (**holotype** CBS H-25722; ex-type culture CPC 48036 = CBS 153465; ITS and LSU sequences GenBank PV664935.1 and PV664961.1).

*Notes:* *Stylonectria*, a fungicolous member of the *Nectriaceae*, occurs on old stromata of pyrenomycetes (Gräfenhan *et al.* 2011). The genus is characterized by having red cosmospore-like perithecia with a conspicuous flattened apical disc, giving rise to fusarioid asexual morphs in culture. *Stylonectria hygrophila* is phylogenetically distinct from species presently recognized in the genus. The phylogenetically closest species is *S. purtonii*, which is mainly distinguished by narrower ascospores 8–11 × 3.5–4.5 µm and shorter conidia 20–24 × 1.5–2 µm, (Lechat *et al.* 2021).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Stylonectria* sp. [strain MYB204, GenBank PQ699599.1; Identities = 507/509 (99 %), no gaps], *Stylonectria purtonii* [voucher HAY-F-003867, GenBank OR858800.1; Identities = 508/518 (98 %), no gaps], and *Stylonectria hetmanica* [strain CBS 147305, GenBank NR\_173440.1; Identities = 494/507 (97 %), three gaps (0 %)]. Closest hits using the **LSU** sequence are *Stylonectria appanata* [strain CBS 125489, GenBank KM231689.1; Identities = 822/829 (99 %), no gaps], *Stylonectria wegeliniana* [strain CBS 125490, GenBank KM231690.1; Identities = 819/829 (99 %), no gaps], and *Stylonectria corniculata* [strain CBS 125491, GenBank NG\_088024.1; Identities = 814/829 (98 %), no gaps].

*Colour illustrations:* Forest in Réserve Naturelle de la Grande Pile, France. Asci and ascospores; perithecia; conidiophores and conidiogenous cells giving rise to conidia on SNA. Scale bars: perithecia = 300 µm, all others = 10 µm.



The single most parsimonious tree obtained from a maximum parsimony phylogenetic analysis (PAUP\* v. 4.0a; Swofford 2003) of the *Stylonectria* ITS nucleotide alignment. The tree was rooted to *Fusarium boothii* (NRRL 29011; GenBank NR\_121203) and the scale bar indicates the number of changes. Parsimony bootstrap support values from 1000 replicates and > 74 % are shown at the nodes and the novelty described here is highlighted with a coloured block and **bold** font. Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. Alignment statistics: 23 strains including the outgroup; 529 characters including alignment gaps analysed: 379 constant, 94 variable and parsimony-uninformative and 56 parsimony-informative. Tree statistics: Tree Length = 231, Consistency Index = 0.870, Retention Index = 0.904, Rescaled Consistency Index = 0.786. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.29050751).

*Muscillium palmae*





## *Musicillium palmae* Crous, *sp. nov.*

*Etymology:* Name refers to its host, a species of palm.

*Classification:* *Trichosphaeriaceae*, *Trichosphaeriales*, *Hypocreomycetidae*, *Sordariomycetes*.

*Mycelium* consisting of hyaline, smooth, branched, septate, 2–3 µm diam. hyphae. *Conidiophores* dimorphic. Acremonium-like conidiophores reduced to solitary, hyaline, smooth, subulate phialides arising from superficial hyphae, 20–35 × 2–3 µm. *Macroconidiophores* subverticillate, erect, flexuous, unbranched, up to 400 µm tall, 3–3.5 µm wide at base, which lacks rhizoids; stipe brown, verruculose, multiseptate, becoming subhyaline towards apex, with verticillate arrangement of phialides, subulate, smooth, hyaline, 30–65 × 2.5–3 µm. *Conidia* solitary, aggregating in mucoid mass, hyaline, smooth, guttulate, aseptate, ellipsoid to subcylindrical, ends obtuse, (4–)5–6(–7) × (2–)2.5 µm.

*Culture characteristics:* Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 30 mm diam. after 2 wk at 25 °C. On MEA, PDA and OA surface umber with patches of dirty white, reverse umber.

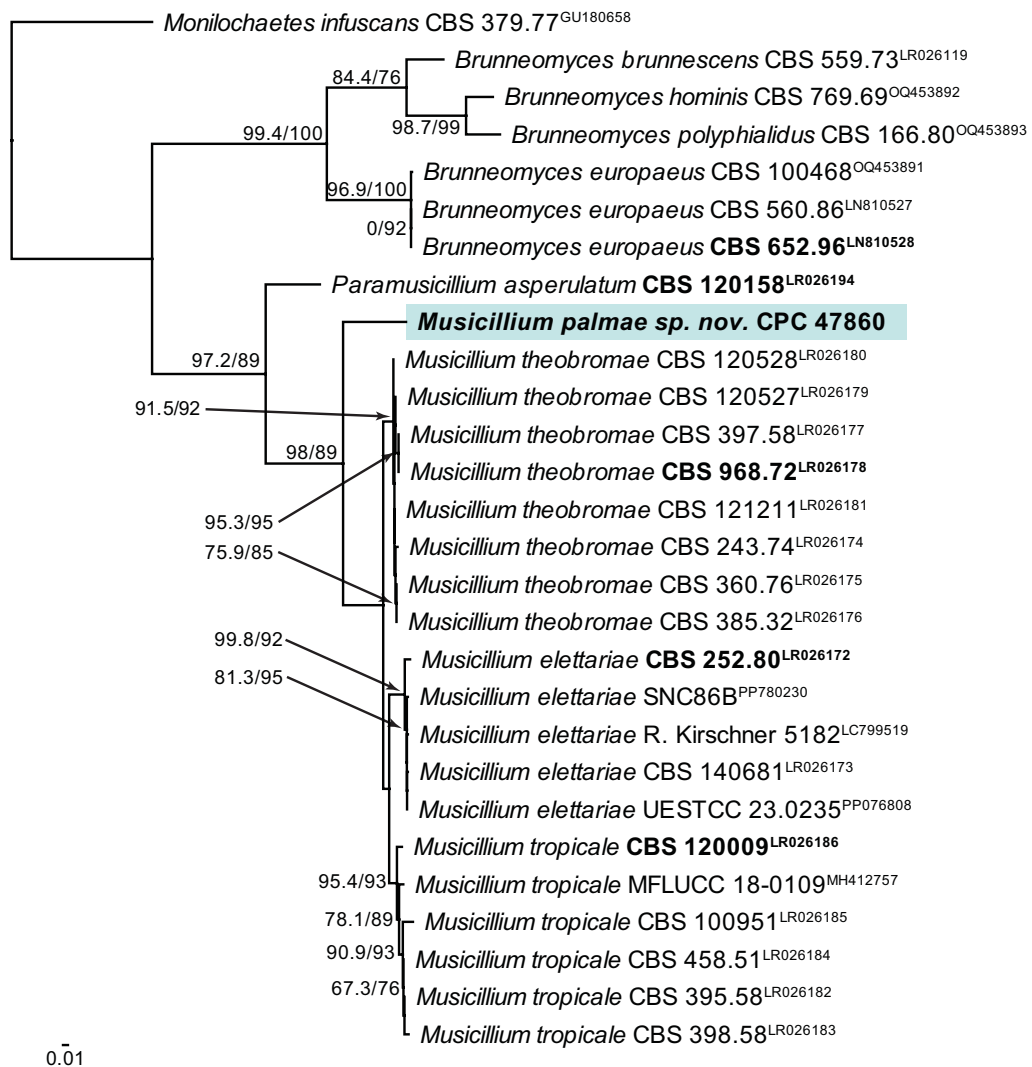
*Typus:* **Brazil**, Rio de Janeiro, on living leaves of unidentified palm species, Feb. 2024, *P.W. Crous*, HPC 4401 [**holotype** CBS H-25706; culture ex-type COAD 3993 = CPC 47860; ITS, LSU, *rpb2* and *tef1* (second part) sequences GenBank PV664936.1, PV664962.1, PV664021.1 and PV664043.1].

*Notes:* *Musicillium* is characterised by solitary pale brown conidiophores that are verticillate towards the apex, and have whorls of phialidic conidiogenous cells producing aseptate, hyaline conidia. *Musicillium palmae* is close to *Musicillium*

*theobromae* (conidiophores up to 220 µm long, phialides 15.8–35.4 µm long, conidia 3.4–5.3 × 1.7–2.6 µm; Giraldo & Crous 2019), but is morphologically distinct.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Musicillium theobromae* [strain NZ62, GenBank MK579179.1; Identities = 518/536 (97 %), four gaps (0 %)], *Musicillium elettariae* [strain SNC86B, GenBank PP592418.1; Identities = 516/536 (96 %), two gaps (0 %)], and *Musicillium tropicale* [strain MFLUCC 23-0232, GenBank PP809115.1; Identities = 487/507 (96 %), two gaps (0 %)]. Closest hits using the **LSU** sequence are *Musicillium elettariae* [strain SNC86B, GenBank PP621045.1; Identities = 852/854 (99 %), no gaps], *Musicillium elettariae* [as *Musicillium theobromae*; strain CBS 252.80, GenBank LR025899.1; Identities = 825/827 (99 %), no gaps], and *Paramusicillium asperulatum* [strain CBS 120158, GenBank NG\_242061.1; Identities = 813/827 (98 %), no gaps]. Closest hits using the **rpb2** (first part) sequence had highest similarity to *Paramusicillium asperulatum* [as *Musicillium theobromae*; strain CBS 120528, GenBank LR026180.1; Identities = 669/743 (90 %), no gaps], *Musicillium elettariae* [strain UESTCC 23.0235, GenBank PP076808.1; Identities = 701/787 (89 %), no gaps], and *Musicillium tropicale* [strain MFLUCC 23-0232, GenBank PP840928.1; Identities = 706/794 (89 %), no gaps]. Closest hits using the **tef1** (second part) sequence had highest similarity to *Musicillium elettariae* [strain SNC86B, GenBank PP740455.1; Identities = 869/891 (98 %), four gaps (0 %)], *Acrostalagmus luteoalbus* [strain CBS 149685, GenBank OQ989238.1; Identities = 850/905 (94 %), four gaps (0 %)], and *Musicillium tropicale* [strain MFLUCC 23-0232, GenBank PP866300.1; Identities = 784/811 (97 %), two gaps (0 %)].

*Colour illustrations:* Statue of Christ the Redeemer, Rio de Janeiro, Brazil. Conidiophores and conidiogenous cells giving rise to conidia on SNA; conidia. Scale bars = 10 µm.



Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.4.0 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020, Mo *et al.* 2023) of the *Musicillium rpb2* nucleotide alignment. Bootstrap support values from 1000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown), preceded by the SH-aLRT test value (only shown if the node has > 74 % bootstrap support). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Monilochaetes infuscans* (CBS 379.77; GenBank GU180658) and the novelty described here is highlighted with a coloured block and **bold** font. Alignment statistics: 28 strains including the outgroup; 743 characters including alignment gaps analysed: 275 distinct patterns, 242 parsimony-informative, 47 singleton sites, 454 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TN+I+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.29050751).

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*Dactylaria calliandrae*



***Dactylaria calliandrae* Crous, *sp. nov.***

*Etymology:* Name refers to the host genus it was isolated from, *Calliandra*.

*Classification:* *incertae sedis*, *Amphisphaeriales*, *Xylariomycetidae*, *Sordariomycetes*.

*Mycelium* consisting of hyaline, smooth, branched, septate, 2–3 µm diam. hyphae, eventually forming numerous hyphal coils. *Conidiophores* solitary, erect, subcylindrical, hyaline, smooth (appearing subhyaline with age), mostly reduced to conidiogenous cells (rarely with a supporting cell), tapering towards base, attached to aerial hyphae, 10–25 × 3–4 µm, forming a cluster of prominent cylindrical denticles, 1–3 × 1.5 µm, not thickened nor darkened. *Conidia* solitary, hyaline, smooth, guttulate, straight to slightly curved, spindle-shaped, apex subobtusate, base truncate, (2 µm diam.), widest in middle, (3–)5–6(–8)-septate, (37–)40–45(–47) × (2.5–)3 µm.

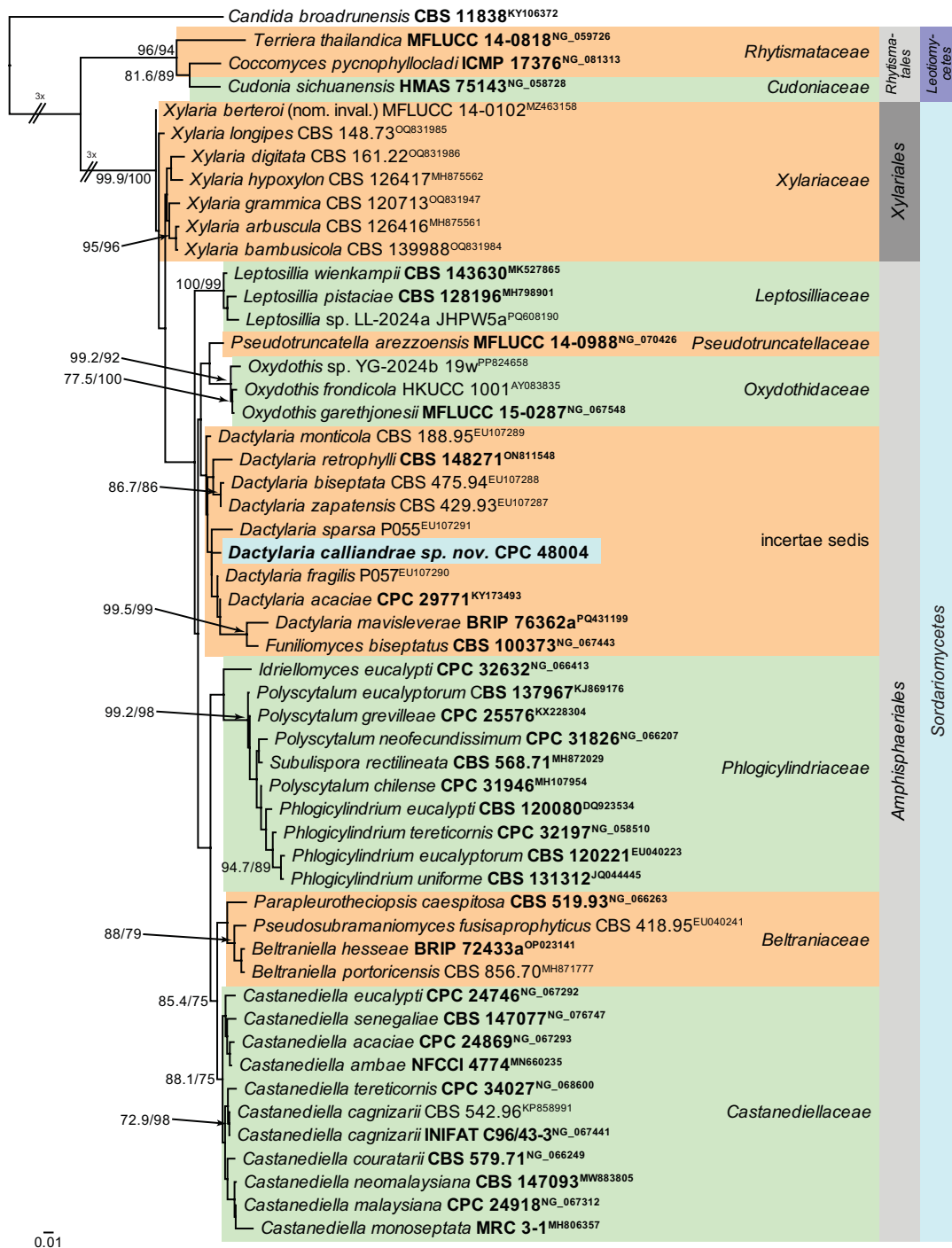
*Culture characteristics:* Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 10 mm diam. after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse buff.

*Typus:* **Brazil**, Minas Gerais, Viçosa, Clonar nursery, on living leaf of *Calliandra tweediei* (*Fabaceae*), 25 Feb. 2024, P.W. Crous, HPC 4399 [**holotype** CBS H-25715; culture ex-type COAD 3994 = CPC 48004; ITS, LSU, *rpb2* and *tef1* (second part) sequences GenBank PV664937.1, PV664963.1, PV664022.1 and PV664044.1].

*Notes:* The genus *Dactylaria* (type species *D. purpurella*) is heterogeneous and polyphyletic, with species frequently appearing to be mycoparasitic. *Dactylaria calliandrae* is

phylogenetically close to *D. acerosa* (conidia 3-septate), though distinct in having multi-septate conidia (de Hoog 1985). *Dactylaria* is in need of revision, pending recollection of its type species.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Dactylaria acerosa* [strain ICMP 13178, GenBank OR543730.1; Identities = 516/535 (96 %), no gaps], *Fusidium griseum* [strain Trtsf08, GenBank GU479905.1; Identities = 508/535 (95 %), three gaps (0 %)], and *Dactylaria retrophylli* [strain CBS 148271, GenBank NR\_184363.1; Identities = 491/547 (90 %), 20 gaps (3 %)]. Closest hits using the **LSU** sequence are *Dactylaria fragilis* [strain P057, GenBank EU107290.1; Identities = 836/847 (99 %), no gaps], *Dactylaria acaciae* [strain CPC 29771, GenBank KY173493.1; Identities = 806/818 (99 %), no gaps], and *Dactylaria zapatensis* [strain P056, GenBank EU107287.1; Identities = 837/850 (98 %), no gaps]. Closest hits using the **rpb2** (first part) sequence had distant similarity to *Melogramma campylosporium* [voucher MFLU 17-0348, GenBank MW658632.1; Identities = 706/888 (80 %), eight gaps (0 %)], *Brachiampulla verticillata* [strain ICMP 15065, GenBank MW147336.1; Identities = 693/886 (78 %), eight gaps (0 %)], and *Brachiampulla verticillata* [strain ICMP 15993, GenBank MW147337.1; Identities = 692/886 (78 %), eight gaps (0 %)]. Closest hits using the **tef1** (second part) sequence had distant similarity to *Beauveria bassiana* [strain 2641, GenBank AY531917.1; Identities = 766/839 (91 %), three gaps (0 %)], *Beauveria bassiana* [strain 1969, GenBank AY531907.1; Identities = 765/839 (91 %), three gaps (0 %)], and *Beauveria asiatica* [strain F1294, GenBank LC163544.1; Identities = 763/839 (91 %), three gaps (0 %)].



Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.4.0 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020, Mo *et al.* 2023) of the *Amphisphaeriales* LSU nucleotide alignment. Bootstrap support values from 1000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown), preceded by the SH-aLRT test value (only shown if the node has > 74 % bootstrap support). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Candida broadrunensis* (CBS 11838; GenBank KY106372) and the novelty described here is highlighted with a coloured block and **bold** font. Families, orders and the classes are shown to the right of the tree in coloured blocks. The root branch was shortened to facilitate layout. Alignment statistics: 53 strains including the outgroup; 835 characters including alignment gaps analysed; 243 distinct patterns, 193 parsimony-informative, 102 singleton sites, 540 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: GTR+F+R3. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.29050751).

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*Cosmospora nemaniae*





## *Cosmospora nemaniae* Mombert & Crous, *sp. nov.*

**Etymology:** Named for *Nemania*, the host genus it was isolated from.

**Classification:** Nectriaceae, Hypocreales, Hypocreomycetidae, Sordariomycetes.

**Ascomata** crowded on dead or effete stromata of *Nemania* cf. *colliculosa*, gregarious, subglobose, 200–276 µm high, 174–254 µm diam. (av. = 238 × 214 µm, n = 10), with a slightly acute papilla, smooth, red, becoming purple in 5 % KOH, yellow in lactic acid, laterally pinched when dry. **Ascomatal wall** smooth, 30–33 µm thick, composed of two regions: outer region 19–24 µm thick, composed of subglobose to ellipsoidal cells; inner region 7–12 µm thick, of thin-walled, ellipsoidal, elongate cells. **Asci** unitunicate, cylindrical, short-stipitate, 62–75 × 3.7–4.9 µm, containing 8 uniseriate ascospores, becoming narrowly clavate, 6–8 µm wide, with irregularly biseriate ascospores. **Paraphyses** evanescent, narrowly moniliform, 2–3 µm diam., interspersed between asci. **Ascospores** (7.5–)8.1–9.9(–10.8) × (3.9–)4.2–4.9(–5.3) µm (av. = 9 × 4.5 µm, n = 83), Q = 1.6–2–2.6, ellipsoidal, equally 1-septate, constricted at septum, strongly verrucose, hyaline at first, becoming pale yellowish brown when mature (measurements from discharged, mature ascospores). **Mycelium** consisting of hyaline, smooth, branched, septate, 2.5–3 µm diam. hyphae. **Conidiophores** solitary, erect, hyaline, smooth, flexuous, subcylindrical, reduced to conidiogenous cells on hyphae, or verticillate with terminal and intercalary whorls of phialides, up to 300 µm tall, 3–4 µm wide, multiseptate. **Conidiogenous cells** monophialidic, hyaline, smooth, subcylindrical, with apical taper, flexuous, 30–60 × 3–4 µm, with slightly flared collarette at apex. **Conidia** of two types. Predominant conidia aseptate, hyaline, smooth, guttulate, fusoid-ellipsoid, straight to slightly curved, apex subobtuse, tapering to truncate hilum, (6–)7–8(–10) × 2.5–3 µm. Abnormal conidia subcylindrical, aseptate, hyaline, smooth, (10–)11–13(–15) × 3–3.5 µm.

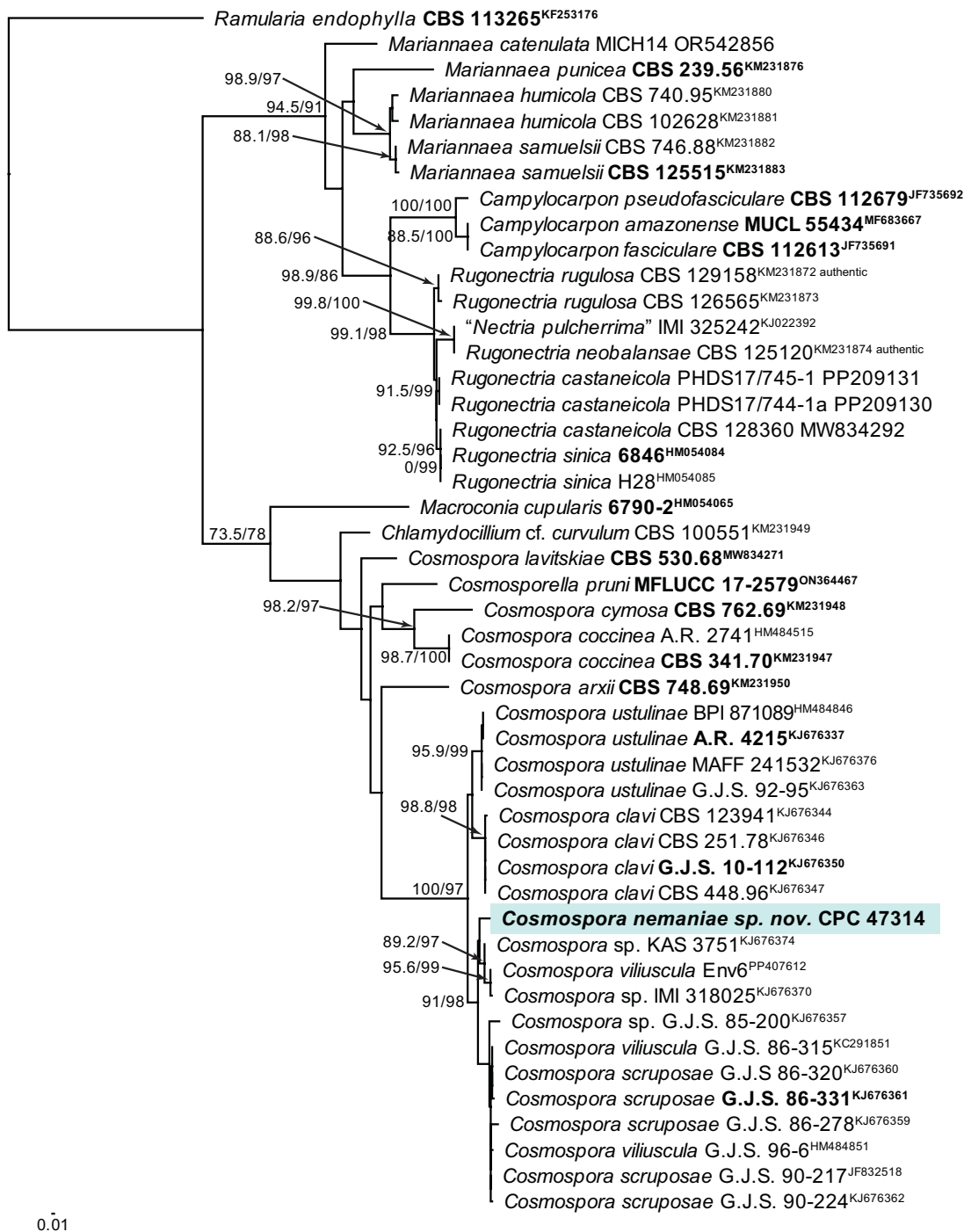
**Culture characteristics:** Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 10–15 mm diam. after 2 wk at 25 °C. On MEA, PDA and OA surface amber, with diffuse amber pigment, reverse honey.

**Typus:** France, Haute-Saône (70), Mantoche, bois d'Aprémont, on dead or effete stromata of *Nemania* cf. *colliculosa*, 198 m a.s.l., 47.418709°N, 5.494462°E, 31 Oct. 2023, A. Mombert & C. Vernillet, AM2310311 [holotype CBS H-25702; culture ex-type CPC 47314 = CBS 153517; ITS, LSU, *tef1* (first part) and *tef1* (second part) sequences GenBank PV664938.1, PV664964.1, PV664035.1 and PV664045.1].

**Notes:** Most cosmospora-like fungi have been shown to be mycoparasites of fungi in *Xylariaceae* and *Diatrypaceae* (Gräfenhan *et al.* 2011). Species of *Cosmospora* tend to be strongly host specific. Presently there are no species known from *Nemania* spp. *Cosmospora nemaniae* is characterized by subglobose ascomata with slightly acute papilla and strongly verrucose ascospores. The closest species is *C. ustulinae* and *C. xylariae*, which are distinguished in having narrowly obpyriform ascomata, and smaller ascospores (*C. ustulinae*, 6.0–8.5 × 2.5–5.0 µm, and *C. xylariae*, 8.5–9.5(–10) × 3.8–4.2 µm; Lechat & Fournier 2021). However, *C. nemaniae* is distinct from both of these species with an ITS similarity of 92.26 % and 91.77 % for *C. ustulinae* [as *Cosmospora* sp. '*ustulinae*'; ex-epitype strain AR4215, GenBank JN995619.1; Identities = 489/530 (92 %), 22 gaps (4 %)] and *C. xylariae* [holotype voucher JF19001, GenBank MZ955629.1; Identities = 457/498 (92 %), 22 gaps (4 %)], respectively. No *tef1* sequence of the latter species was available for inclusion in the phylogenetic tree.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Cosmospora coheniae* [strain BRIP 75895a, GenBank PQ806952.1; Identities = 638/650 (98 %), no gaps], *Cosmospora ustulinae* [as *Cosmospora* sp. '*ustulinae*'; strain AR4215, GenBank JN995619.1; Identities = 560/571 (98 %), no gaps], and *Cosmospora vilioscula* [strain G.J.S. 86-315, GenBank KC291748.1; Identities = 558/570 (98 %), no gaps]. Closest hits using the LSU sequence are *Cosmospora vilioscula* [strain CBS 455.96, GenBank GQ506003.1; Identities = 849/854 (99 %), no gaps], *Pseudocosmospora vilior* [strain CBS 126109, GenBank MH875480.1; Identities = 849/854 (99 %), no gaps], and *Cosmospora khandalensis* [strain CBS 356.65, GenBank NG\_069711.1; Identities = 848/854 (99 %), no gaps]. Closest hits using the *tef1* (first part) sequence had highest similarity to *Cosmospora vilioscula* [strain Env6, GenBank PP407612.1; Identities = 413/437 (95 %), five gaps (1 %)], *Cosmospora vilior* [strain G.J.S. 90-217, GenBank JF832518.1; Identities = 370/404 (92 %), 14 gaps (3 %)], and *Cosmospora scruposae* [strain G.J.S. 86-278, GenBank KJ676359.1; Identities = 240/264 (91 %), five gaps (1 %)]. Closest hits using the *tef1* (second part) sequence had highest similarity to *Cosmospora aquatica* [voucher S-350, GenBank MN200275.1; Identities = 829/865 (96 %), no gaps], *Neocosmospora solani* [as *Fusarium solani*; strain MB10A, GenBank LT615305.1; Identities = 880/936 (94 %), no gaps], and *Nectria haematococca* [strain GJS89-70, GenBank AY489624.1; Identities = 899/959 (94 %), two gaps (0 %)].

**Colour illustrations:** Forest at Mantoche, bois d'Aprémont, France. Section through perithecial wall; perithecia; asci with ascospores; colony sporulating on SNA; conidiophores and conidiogenous cells giving rise to conidia; conidia. Scale bars: perithecia = 200 µm; all others = 10 µm.



0.01

Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.4.0 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020, Mo *et al.* 2023) of the *Cosmospora tef1* (first part) nucleotide alignment. Bootstrap support values from 1000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown), preceded by the SH-aLRT test value (only shown if the node has > 74 % bootstrap support). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Ramularia endophylla* (CBS 113265; GenBank KF253176) and the novelty described here is highlighted with a coloured block and **bold** font. Alignment statistics: 47 strains including the outgroup; 381 characters including alignment gaps analysed: 345 distinct patterns, 234 parsimony-informative, 59 singleton sites, 88 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TPM2u+F+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.29050751).

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*Neodevriesia maravalensis*



## *Neodevriesia maravalensis* Crous & Jurjević, *sp. nov.*

*Etymology:* Name refers to Maraval, one of the northern suburbs of Trinidad's capital, Port of Spain, in Trinidad and Tobago.

*Classification:* *Neodevriesiaceae*, *Mycosphaerellales*, *Dothideomycetidae*, *Dothideomycetes*.

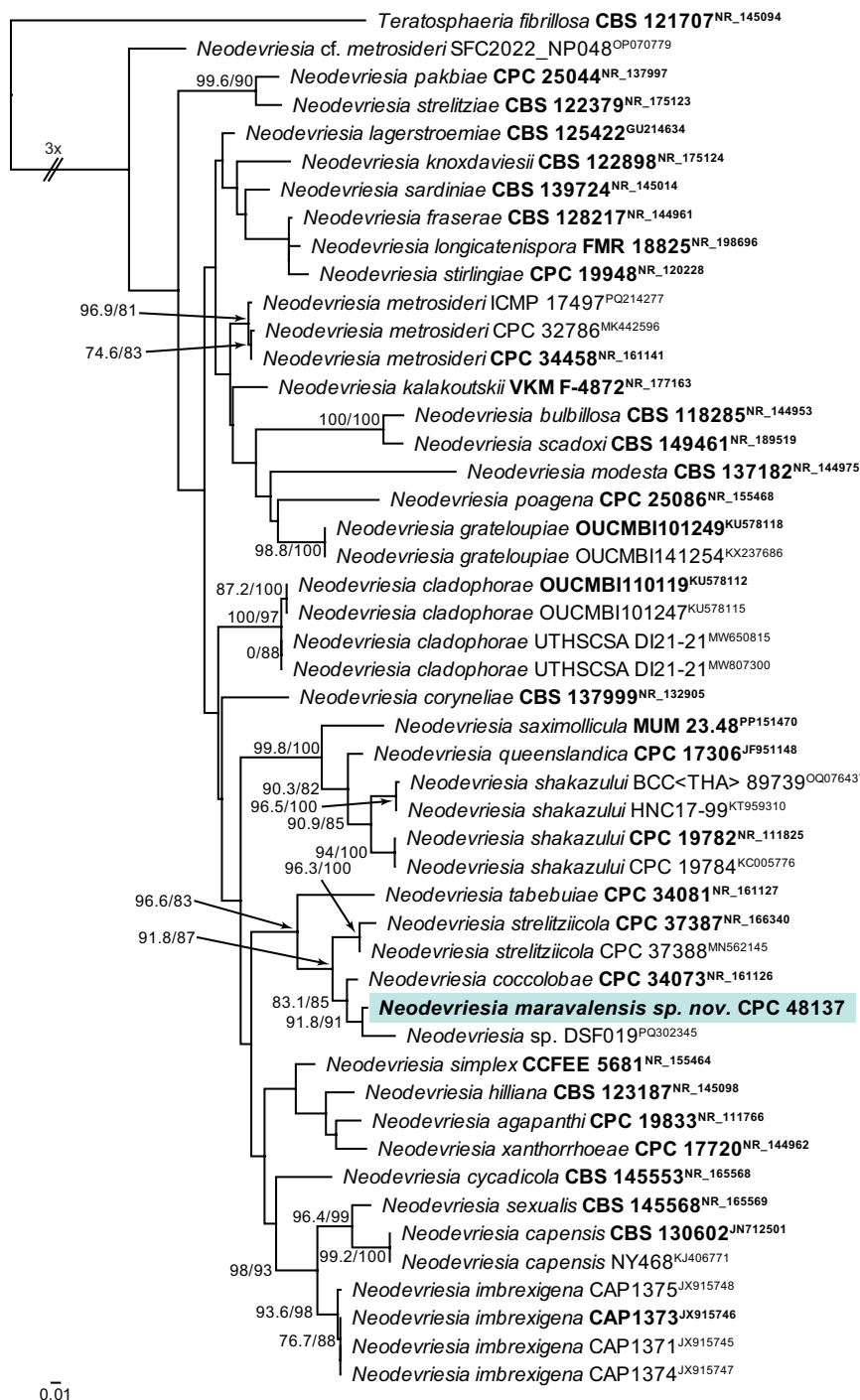
*Mycelium* of brown, smooth, branched, septate, 2.5–3 µm diam. hyphae. *Conidiophores* solitary, erect, subcylindrical, brown, smooth, unbranched, 1–3-septate, 15–80 × 2.5–3 µm. *Conidiogenous cells* integrated, terminal, subcylindrical, brown, smooth, 10–20 × 2.5–3 µm; loci thickened, darkened, sympodial at apex, 1.5–2 µm diam. *Conidiogenous apparatus* penicillate, *conidia* brown, aseptate, subcylindrical to fusoid-ellipsoid; ramoconidia 10–15 × 2.5–3 µm, conidia (8–)10–11(–12) × 2(–2.5) µm; hila thickened, darkened, 0.5–1 µm diam.

*Culture characteristics:* Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 5 mm diam. after 2 wk at 25 °C. On MEA, CYA, PDA and OA surface olivaceous grey, reverse iron grey. No growth at 37 °C on CYA.

*Typus:* **Trinidad and Tobago**, Maraval, wires in plenum (office), swab, Jan. 2005, Z. Jurjević, 5907 (**holotype** CBS H-25729; culture ex-type CPC 48137 = CBS 151634; ITS and LSU sequences GenBank PV664939.1 and PV664965.1).

*Notes:* *Neodevriesia* is a hyphomycetous genus, characterized by having medium brown, unbranched conidiophores, thick-walled, medium brown, rarely septate conidia, occurring in short and mostly unbranched conidial chains, and lacking chlamydospores. *Neodevriesia maravalensis* is related to *N. coccolobae* [conidia 0(–1)-septate, pale brown, smooth, subcylindrical to narrowly fusoid, (6–)7–8(–10) × (2–)2.5(–3) µm; Crous *et al.* 2018a], but distinct in having longer conidia.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Neodevriesia* sp. [strain DSF019, GenBank PQ302345.1; Identities = 495/498 (99 %), no gaps], *Neodevriesia coccolobae* [strain CBS 145064, GenBank NR\_161126.1; Identities = 510/522 (98 %), one gap (0 %)], and *Neodevriesia strelitzicola* [strain NTOU 4478, GenBank MZ422997.1; Identities = 517/536 (96 %), four gaps (0 %)]. Closest hits using the **LSU** sequence are *Neodevriesia coccolobae* [strain CBS 145064, GenBank NG\_066285.1; Identities = 828/829 (99 %), no gaps], *Neodevriesia strelitzicola* [strain CPC 37387, GenBank MN567651.1; Identities = 790/792 (99 %), no gaps], and *Neodevriesia cladophorae* [voucher OUCMB110119, GenBank KU578114.1; Identities = 798/805 (99 %), no gaps].



Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.4.0 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020, Mo *et al.* 2023) of the *Neodevriesia* ITS nucleotide alignment. Bootstrap support values from 1000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown), preceded by the SH-aLRT test value (only shown if the node has > 74 % bootstrap support). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in bold font. The tree was rooted to *Teratosphaeria fibrillosa* (CBS 121707; GenBank NR\_145094) and the novel species described here is highlighted with a coloured block and bold font. The root branch was shortened to facilitate layout. Alignment statistics: 49 strains including the outgroup; 570 characters including alignment gaps analysed: 291 distinct patterns, 155 parsimony-informative, 90 singleton sites, 325 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TNe+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.29050751).

*Niesslia hepworthiae*





## *Niesslia hepworthiae* Crous, *sp. nov.*

**Etymology:** Named in honour of the English artist and sculptor, Dame Jocelyn Barbara Hepworth (10 January 1903 – 20 May 1975). The fungus was collected in the garden next to her studio, in St Ives, Cornwall, England.

**Classification:** *Niessliaceae*, *Hypocreales*, *Hypocreomycetidae*, *Sordariomycetes*.

**Mycelium** of hyaline, smooth, branched, septate, 1.5–2 µm diam. hyphae. **Conidiophores** solitary, reduced to conidiogenous cells, or aggregated in sporodochia, 200–250 µm diam., with pinkish mucoid conidial mass; conidiophores subcylindrical, 0–1-septate, up to 25 µm tall, giving rise to 1–4 conidiogenous cells in rosette, 10–15 × 1.5–2 µm, with cylindrical phialidic collarette. Solitary conidiogenous cells up to 35 µm tall, with lateral walls slightly thickened, typical of *Monocillium*. **Conidia** solitary, aseptate, hyaline, smooth, guttulate, fusoid-ellipsoid, apex subobtuse, base with truncate hilum, 1–1.5 µm diam., (5–)6 × 2(–2.5) µm.

**Culture characteristics:** Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 20 mm diam. after 2 wk at 25 °C. On MEA, PDA and OA surface salmon, reverse salmon to ochreous.

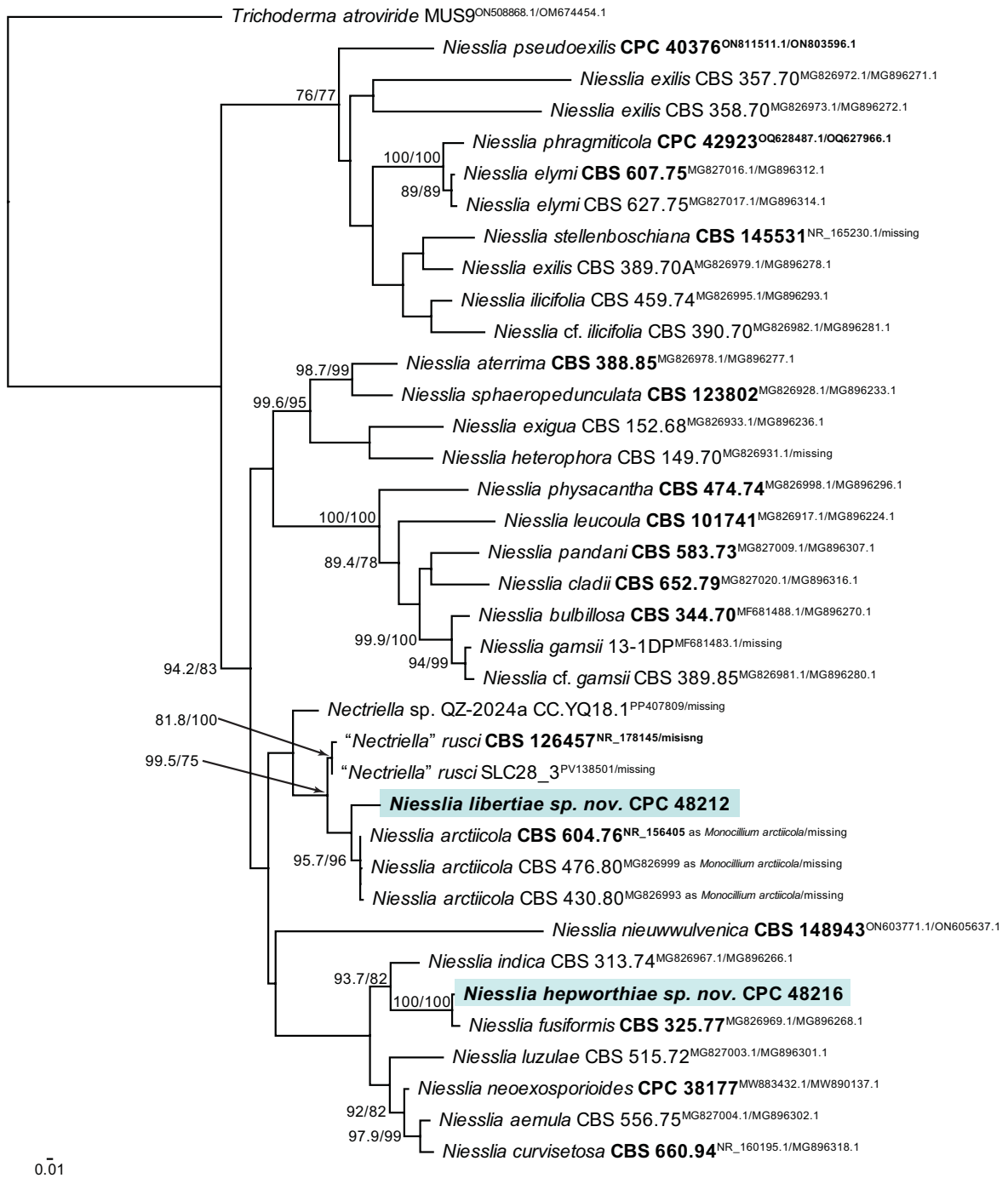
**Typus:** UK, England, Cornwall, St. Ives, Barbara Hepworth Museum and Sculpture Garden, on living leaf of *Libertia grandiflora* (*Iridaceae*), 8 May 2024, P.W. Crous & K.L. Crous, HPC 4473 [**holotype** CBS H-25736; culture ex-type CPC 48216 = CBS 153518; ITS, LSU, *actA*, *tef1* (first part) and *tub2* sequences GenBank PV664940.1, PV664966.1, PV664004.1, PV664036.1 and PV664052.1].

**Notes:** *Niesslia hepworthiae* is closely related to *Niesslia neoexosporioides* [stipes terminating in clavate vesicles, and conidia (7–)8–10(–14) × 2(–2.5) µm; Crous *et al.* 2021]. The most obvious difference, however, is that *N. hepworthiae* forms pinkish sporodochia in culture, which has not been

observed in other species of *Niesslia*. Another species described in this set from the same country and host, *N. libertiae*, is distinct based on its molecular phylogeny.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Niesslia* sp. [strain CBS 325.77, GenBank MG826969.1; Identities = 571/581 (98 %), six gaps (1 %)], *Monocillium indicum* [strain CBS 182.65, GenBank MH858535.1; Identities = 485/500 (97 %), two gaps (0 %)], and *Niesslia exosporioides* [strain CBS 515.72, GenBank MG827003.1; Identities = 554/589 (94 %), 17 gaps (2 %)]. Closest hits using the **LSU** sequence are *Niesslia neoexosporioides* [strain CBS 146810, GenBank NG\_076714.1; Identities = 880/883 (99 %), no gaps], *Niesslia exosporioides* [strain CBS 515.72, GenBank MH872254.1; Identities = 804/807 (99 %), no gaps], and *Monocillium curvisetosum* [strain CBS 660.94, GenBank MH874141.1; Identities = 878/884 (99 %), one gap (0 %)]. Closest hits using the **actA** sequence had highest similarity to *Niesslia neoexosporioides* [strain CPC 38177, GenBank MW890027.1; Identities = 598/690 (87 %), 28 gaps (4 %)], and *Niesslia nieuwwulvenica* [strain CPC 41374, GenBank ON605620.1; Identities = 479/546 (88 %), 17 gaps (3 %)]. Closest hits using the **tef1** (first part) sequence had highest similarity to *Niesslia neoexosporioides* [strain CPC 38177, GenBank MW890097.1; Identities = 289/351 (82 %), 24 gaps (6 %)], *Xenomyrothecium tongaense* [strain CBS 598.80, GenBank KU847314.1; Identities = 205/229 (90 %), 11 gaps (4 %)], and *Calonectria variabilis* [strain CBS 112691, GenBank GQ267335.1; Identities = 202/229 (88 %), 10 gaps (4 %)]. Closest hits using the **tub2** sequence had highest similarity to *Niesslia neoexosporioides* [strain CPC 38177, GenBank MW890137.1; Identities = 507/656 (77 %), 43 gaps (6 %)], *Thelonectria yunnanica* [strain HMAS 183564, GenBank JQ836660.1; Identities = 323/415 (78 %), 31 gaps (7 %)], and *Neonectria ditissimopsis* [strain 5743, GenBank JF268728.1; Identities = 321/419 (77 %), 46 gaps (10 %)].

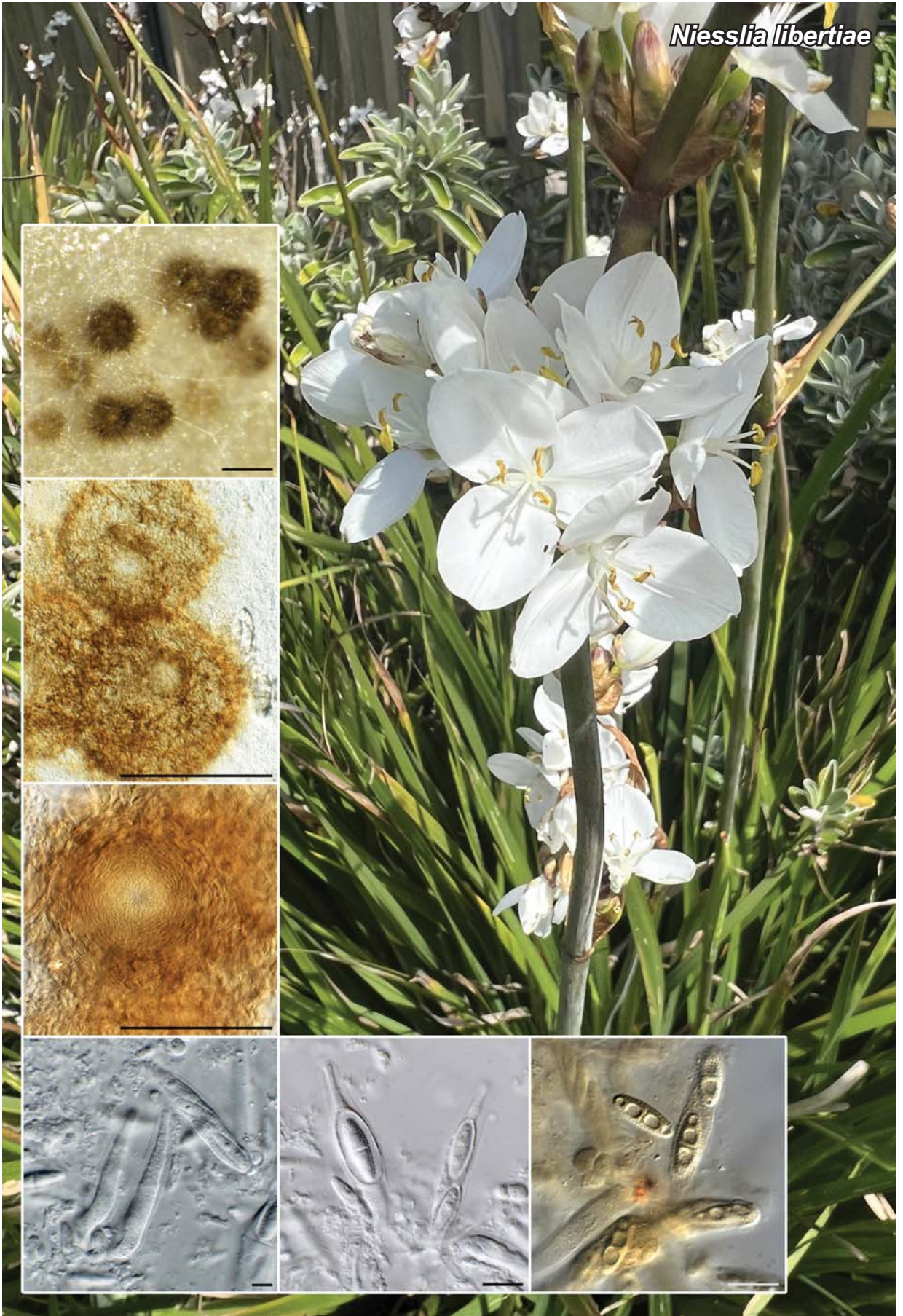
**Colour illustrations:** *Libertia grandiflora* in garden of Barbara Hepworth's Museum and Sculpture Garden, St. Ives, Cornwall, UK. Sporodochia on SNA; conidiophores and conidiogenous cells giving rise to conidia on SNA; conidia. Scale bars = 10 µm.



Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.4.0 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020, Mo *et al.* 2023) of the *Niesslia* ITS/*tub2* nucleotide alignment. Bootstrap support values from 1000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown), preceded by the SH-aLRT test value (only shown if the node has > 74 % bootstrap support). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Trichoderma atroviride* (MUS91; GenBank ON508868.1/OM674454.) and the novelties described in this set are highlighted with coloured blocks and **bold** font. Alignment statistics: 37 strains including the outgroup; 1127 characters including alignment gaps analysed: 683 distinct patterns, 423 parsimony-informative, 140 singleton sites, 564 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: ITS: TIM2+F+I+G4; *tub2*: TN+F+I+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.29050751).



*Niesslia libertiae*



***Niesslia libertiae* Crous, *sp. nov.***

*Etymology*: Name refers to the host genus it was collected from, *Libertia*.

*Classification*: *Niessliaceae*, *Hypocreales*, *Hypocreomycetidae*, *Sordariomycetes*.

*Ascomata* solitary, erumpent to superficial, globose, 70–150 µm diam., pale brown, surrounded by brown, thick-walled setae, unbranched, apices obtuse, 25–70 × 2.5–3.5 µm. *Ostiole* central, filled with hyaline, septate periphyses, up to 25 µm tall, 2–3 µm wide; perithecial wall of 6–8 layers of pale brown textura angularis. *Asci* 8-spored, hyaline, smooth, subcylindrical, apex obtuse, base bluntly rounded, straight to slightly curved, 45–55 × 9–11 µm, apex not staining in Melzer's reagent. *Ascospores* bi- to triseriate, fusoid-ellipsoid, ends subobtusely, widest at median septum, guttulate, initially hyaline, becoming pale brown and verruculose, surrounded by a prominent mucoid sheath (up to 3 µm diam.), (16–)17–18(–19) × (5.5–)6(–7) µm. *Asexual morph* not observed in culture or in vivo.

*Culture characteristics*: Colonies flat, spreading, with moderate aerial mycelium and smooth, lobate margin (feathery on PDA), reaching 15 mm diam. after 2 wk at 25 °C. On MEA, PDA and OA surface dirty white, reverse buff.

*Typus*: **UK**, England, Cornwall, Mousehole, on living leaf of *Libertia grandiflora* (*Iridaceae*), 8 May 2024, *P. W. Crous*, HPC 4472 [**holotype** CBS H-25735; culture ex-type CPC 48212 = CBS 153519; ITS, LSU, *actA*, *tef1* (first part) and *tub2* sequences GenBank PV664941.1, PV664967.1, PV664005.1, PV664037.1 and PV664053.1].

*Notes*: *Niesslia*, as circumscribed by Gams *et al.* (2019) is polyphyletic. *Niesslia libertiae* is introduced as novel, phylogenetically distinct species, which is only known from its sexual morph. Based on the key provided by Gams *et al.* (2019), it keys out to *N. striatipora*, but ascospores are not striate, and an asexual morph did not develop in culture. Sequences deposited for *Nectriella rusci* appear to be incorrect. Another species described in this set from the same country and host, *N. hepworthiae*, is distinct based on its molecular phylogeny (see phylogenetic tree included with that species).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Monocillium arctiicola* [strain CBS 604.76, GenBank NR\_156405.1; Identities = 577/594 (97 %), four gaps (0 %)], *Nectriella rusci* [strain CBS 126457, GenBank NR\_178145.1; Identities = 574/593 (97 %), six gaps (1 %)], and *Monocillium indicum* [strain SDT34-22, GenBank JX077045.1; Identities = 310/331 (94 %), nine gaps (2 %)]. Closest hits using the **LSU** sequence are *Nectriella rusci* [strain CBS 126457, GenBank NG\_088080.1; Identities = 862/870 (99 %), no gaps], *Monocillium arctiicola* [strain CBS 604.76, GenBank NG\_058531.1; Identities = 847/858 (99 %), two gaps (0 %)], and *Niesslia exosporioides* [strain CBS 515.72, GenBank MH872254.1; Identities = 796/807 (99 %), one gap (0 %)]. Closest hits using the *actA* sequence had highest similarity to *Niesslia neoexosporioides* [strain CPC 38177, GenBank MW890027.1; Identities = 391/408 (96 %), no gaps], *Corallomycetella elegans* [strain CBS 275.60, GenBank KM231237.1; Identities = 476/528 (90 %), 18 gaps (3 %)], and *Gliocephalotrichum longibrachium* [strain CBS 126571, GenBank KM231117.1; Identities = 459/508 (90 %), six gaps (1 %)]. Closest hits using the *tef1* (first part) sequence had highest similarity to *Niesslia neoexosporioides* [strain CPC 38177, GenBank MW890097.1; Identities = 280/342 (82 %), 20 gaps (5 %)], and *Niesslia nieuwwulvenica* [strain CPC 41374, GenBank ON605629.1; Identities = 266/329 (81 %), 19 gaps (5 %)]. Closest hits using the *tub2* sequence had distant partial similarity to *Niesslia neoexosporioides* [strain CBS 148284, GenBank ON803595.1; Identities = 298/379 (79 %), 29 gaps (7 %)], *Striaticonidium panamaense* [strain CPC 46539, GenBank PQ504942.1; Identities = 213/264 (81 %), 14 gaps (5 %)], and *Fusicolla aquaeductum* [strain KUMCC 17-0320, GenBank MH087222.1; Identities = 272/346 (79 %), 23 gaps (6 %)].

For phylogenetic tree, see *Niesslia hepworthiae* (FP 1799).

*Colour illustrations*: *Libertia grandiflora* flowers in Mousehole, Cornwall, England. *Ascomata* on oatmeal agar; close-up of ostiole; asci with ascospores; ascospores in Melzer's reagent. Scale bars: *ascomata* = 150 µm; *ostiole* = 75 µm; all others = 10 µm.



*Letendraea goniomae*



## *Letendraea goniomae* Crous, *sp. nov.*

*Etymology*: Name refers to the host genus it was collected from, *Gonioma*.

*Classification*: *Tubeufiaceae*, *Tubeufiales*, *Dothideomycetes*.

*Ascomata* pseudothecial, 150–200 µm diam., separate, immersed, pale brown, with central ostiole, and wall of 3–6 layers of pale brown textura angularis. *Pseudoparaphyses* numerous, unbranched, anastomosing, cellular, 2–2.5 µm diam. *Asci* 8-spored, bitunicate, cylindrical-clavate, short pedicellate, with visible ocular chamber, 50–65 × 7–8 µm. *Ascospores* 3- to multiseriate, medianly 1-septate, constricted at septum, widest and swollen above median septum, fusoid, brown, verruculose, (13–)15–16(–17) × (3.5–)4 µm.

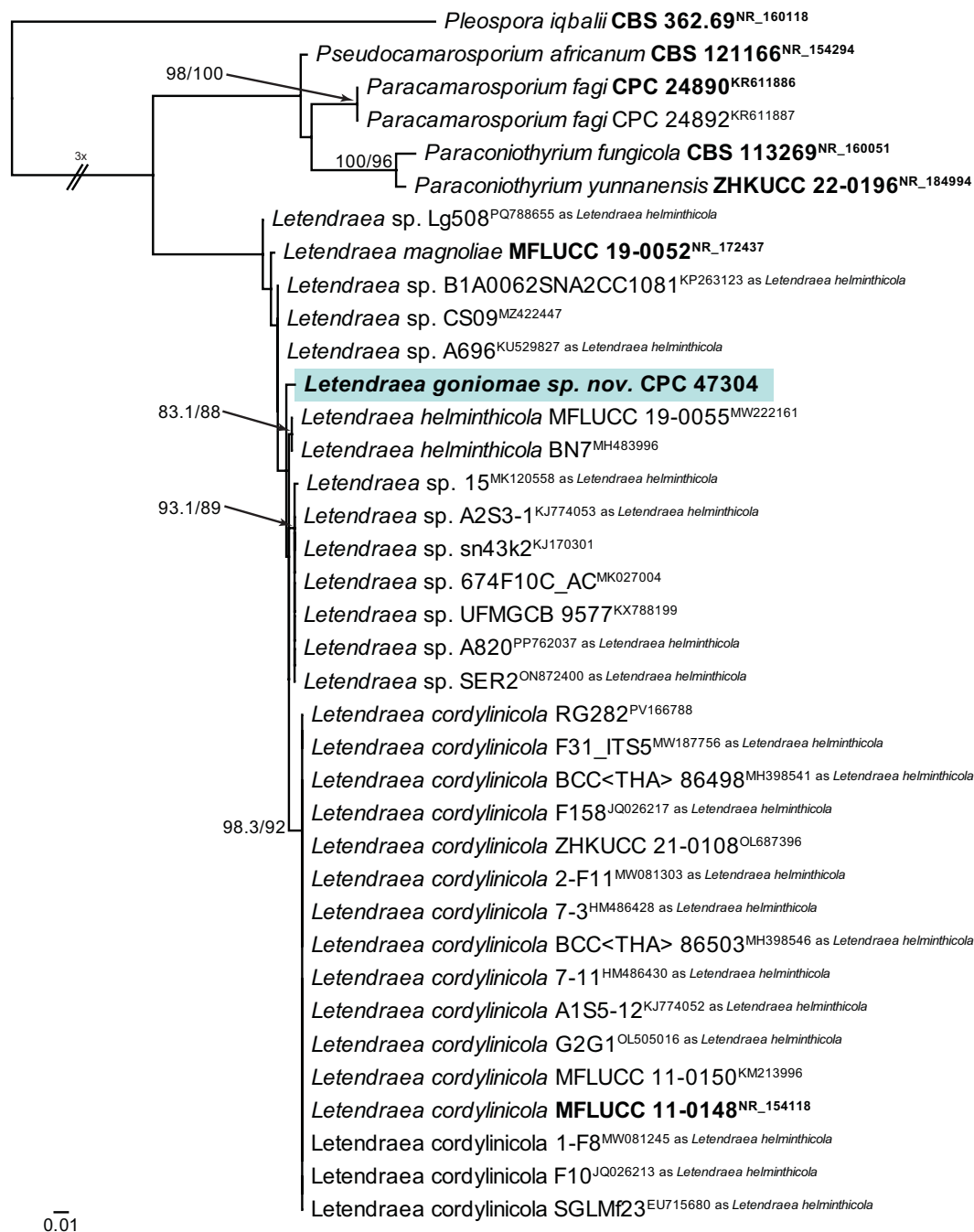
*Culture characteristics*: Colonies flat, spreading, with moderate aerial mycelium and smooth, even margin, covering dish after 2 wk at 25 °C. On MEA surface pale luteous, reverse sienna; on PDA and OA surface and reverse saffron.

*Typus*: **South Africa**, Western Cape Province, Knysna, Groenkop Forest, on leaves of *Gonioma kamassi* (*Apocynaceae*), Oct. 2023, M.J. Wingfield, HPC 4305 [**holotype** CBS H-25701, culture ex-type CPC 47304 = CBS 153525; ITS, LSU and *tef1* (second part) sequences GenBank PV664942.1, PV664968.1 and PV664046.1].

*Notes*: *Letendraea goniomae* is closely related to isolates identified as *Letendraea helminthicola* (asci 60–70 × 10–14 µm, ascospores 12–15 × 4.5–6 µm; Petch 1938), and *Letendraea cordylinicola* [asci (51–)55–60(–68) × (8–)10–12 µm, ascospores 13–15 × 3–4 µm; Ariyawansa *et al.* 2014], but differs in the size of its ascospores.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Letendraea cordylinicola* [strain MFLUCC 11-0150, GenBank KM213996.1; Identities = 505/511 (99 %), one gap (0 %)], *Letendraea helminthicola* [strain BCC<THA> 86498, GenBank MH398541.1; Identities = 505/511 (99 %), one gap (0 %)], and *Nemania diffusa* [strain CBS 275.72, GenBank MH860472.1; Identities = 505/512 (99 %), two gaps (0 %)]. Closest hits using the **LSU** sequence are *Letendraea helminthicola* [strain MFLUCC 19-0055, GenBank MW209732.1; Identities = 848/848 (100 %), no gaps], *Letendraea eurotioides* [strain CBS 212.31, GenBank AY787935.1; Identities = 845/846 (99 %), no gaps], and *Letendraea cordylinicola* [strain ZHKUCC 21-0108, GenBank OL687397.1; Identities = 870/873 (99 %), one gap (0 %)]. Closest hits using the **tef1** (second part) sequence had highest similarity to *Letendraea helminthicola* [strain CBS 884.85, GenBank MK404174.1; Identities = 863/882 (98 %), no gaps], *Paraconiothyrium brasiliense* [strain UTHSC DI16-311, GenBank LT797116.1; Identities = 874/907 (96 %), two gaps (0 %)], and *Didymosphaeria rubiulmifolii* [strain MFLUCC 16-1000, GenBank MT394734.1; Identities = 868/901 (96 %), two gaps (0 %)].

*Colour illustrations*: Groenkop Forest, Knysna, South Africa. Ascomata on pine needle agar; asci with ascospores; ascospores. Scale bars: ascomata = 200 µm; all others = 10 µm.

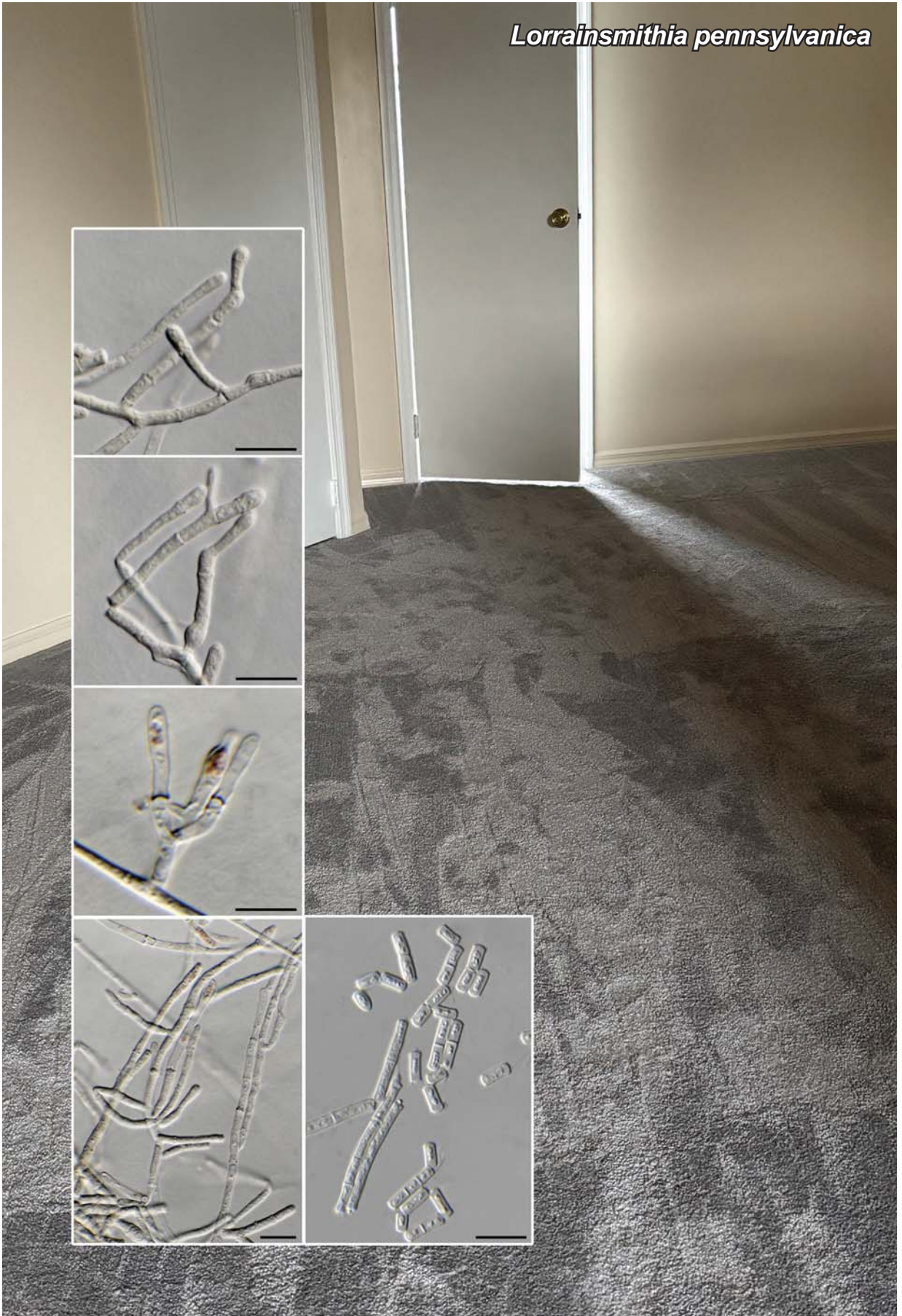


Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.4.0 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020, Mo *et al.* 2023) of the *Letendraea* ITS nucleotide alignment. Bootstrap support values from 1000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown), preceded by the SH-aLRT test value (only shown if the node has > 74 % bootstrap support). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Pleospora iqbalii* (CBS 362.69; GenBank NR\_160118) and the novelty described here is highlighted with a coloured block and **bold** font. The root branch was shortened to facilitate layout. Alignment statistics: 37 strains including the outgroup; 674 characters including alignment gaps analysed; 188 distinct patterns, 87 parsimony-informative, 89 singleton sites, 498 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TNe+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.29050751).

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*Lorrainsmithia pennsylvanica*





## *Lorrainsmithia pennsylvanica* Crous & Jurjević, *sp. nov.*

*Etymology:* Name refers to the state of Pennsylvania, USA, where it was collected.

*Classification:* *incertae sedis*, *Pleosporales*, *Dothideomycetes*.

*Mycelium* consisting of hyaline, smooth, branched, septate, 1.5–3 µm diam. hyphae. Hyphae separating into *phragmoconidia*, cylindrical with truncate ends, smooth, hyaline, guttulate, 0–2-septate, aseptate conidia (3.5–)4–5(–7) × (2.5–)3 µm.

*Culture characteristics:* Colonies erumpent, spreading, with moderate aerial mycelium and smooth, lobate margin, reaching 20 mm diam. after 2 wk at 25 °C. On MEA surface and reverse umber with diffuse umber pigment; on PDA surface and reverse umber with diffuse red pigment; on OA surface red. No growth at 37 °C on CYA.

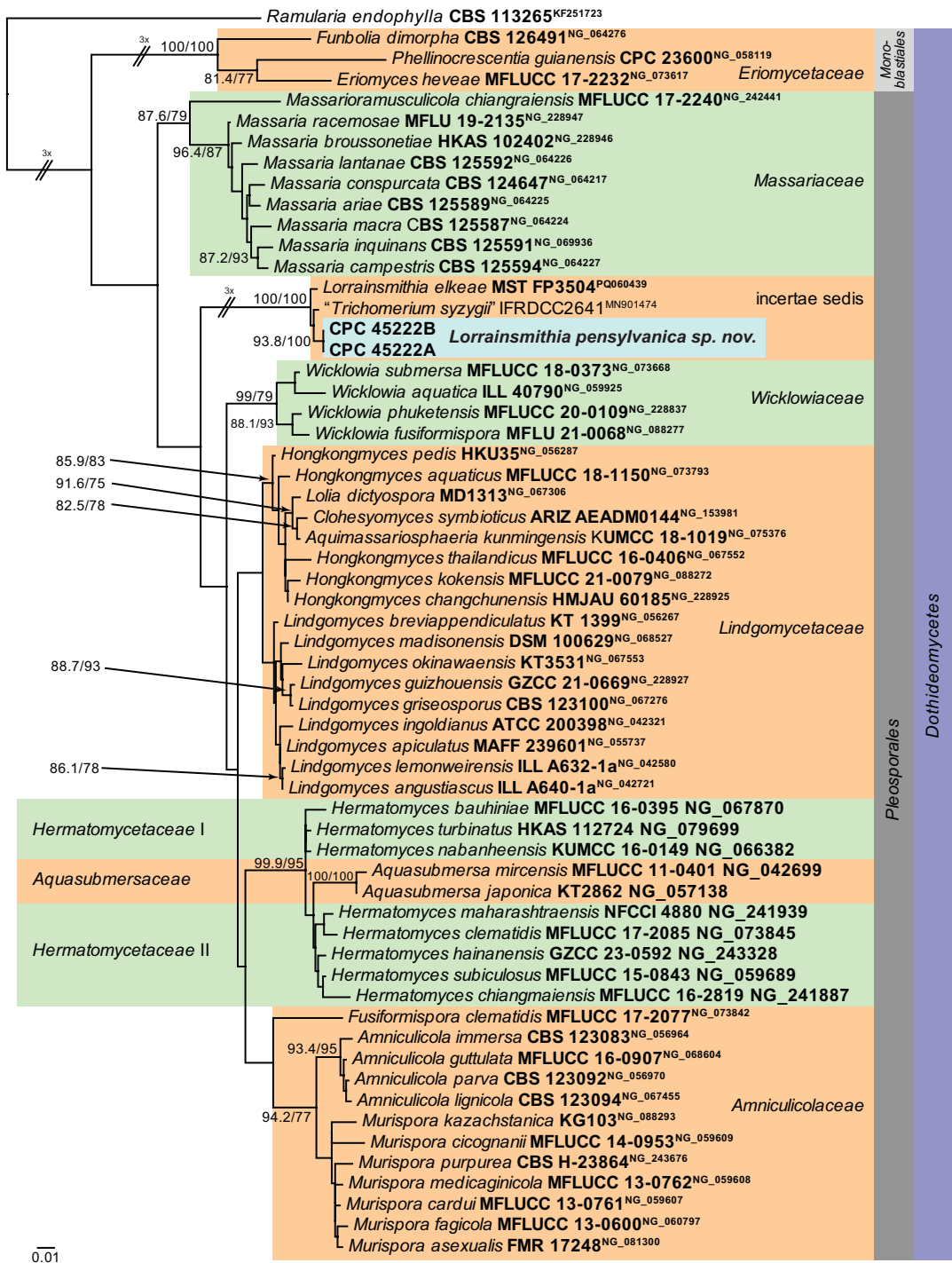
*Typus:* USA, Pennsylvania, Bath, from bedroom, air, 14 Sep. 2022, Z. Jurjević, 5748 (**holotype** CBS H-25698; culture ex-type CPC 45222A = CBS 153526; ITS, LSU and *tub2* sequences GenBank PV664943.1, PV664969.1 and PV664054.1); *ibid.*, culture CPC 45222B; ITS, LSU, *rpb1* and *tub2* sequences GenBank PV664944.1, PV664970.1, PV664012.1 and PV664055.1.

*Notes:* *Lorrainsmithia pennsylvanica* is phylogenetically related to *Lorrainsmithia elkeae*, described from an unidentified dead spider in New South Wales, Australia. Unfortunately the description lacks any morphological details, so these two species can only be compared based on their DNA phylogeny, which places them as two taxa within *Lorrainsmithia* (Tan *et al.* 2024).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence of CPC 45222A had highest similarity to *Dothideomycetes* sp.

NF-3 [strain 2015-F-276, GenBank KU892279.1; Identities = 497/501 (99 %), no gaps], "*Trichomerium syzygii*" [strain IFRDCC2641, GenBank MN901487.1; Identities = 495/514 (96 %), one gap (0 %)], *Lorrainsmithia elkeae* [strain MST-FP3504, GenBank PQ066529.1; Identities = 488/514 (95 %), two gaps (0 %)], and *Pseudocercospora sphaerellae-eugeniae* [strain P111, GenBank KC731558.1; Identities = 415/445 (93 %), five gaps (1 %)]. The sequence in the blast result listed as *Trichomerium syzygii* is not conspecific with the ex-type sequence of that species (GenBank NR\_170066.1, < 90 % overall sequence homology). The ITS sequences of CPC 45222A and CPC 45222B are 100 % (500/500 nt) identical. Closest hits using the LSU sequence of CPC 45222A are "*Trichomerium syzygii*" [strain IFRDCC2641, GenBank MN901474.1; Identities = 798/804 (99 %), no gaps], *Lorrainsmithia elkeae* [strain MST-FP3504, GenBank PQ060439.1; Identities = 806/814 (99 %), no gaps], and *Hermatomyces sphaericus* [voucher C415, GenBank MK348002.1; Identities = 774/853 (91 %), five gaps (0 %)]. The sequence in the blast result listed as *Trichomerium syzygii* is not conspecific with the ex-type sequence of that species (GenBank NG\_074428.1, < 83 % overall sequence homology). The LSU sequences of CPC 45222A and CPC 45222B are 100 % (841/841 nt) identical. No significant hits were obtained when the *rpb1* sequence of CPC 45222B was used in blastn and megablast searches. Closest hits using the *tub2* sequence of CPC 45222A had distant similarity to *Crassiclypeus aquaticus* [strain KH 104, GenBank LC312615.1; Identities = 396/506 (78 %), 36 gaps (7 %)], *Preussia intermedia* [strain 18THES003, GenBank MT881987.1; Identities = 265/322 (82 %), 11 gaps (3 %)], and *Corynespora smithii* [strain NBRC8162, GenBank AB539436.1; Identities = 334/423 (79 %), 30 gaps (7 %)]. The *tub2* sequences of CPC 45222A and 45222B are identical (611/611 nt).

*Colour illustrations:* Bedroom floor in Bath, PA, USA. Conidiophores and conidiogenous cells giving rise to conidia on SNA; conidia. Scale bars = 10 µm.



Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.4.0 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020, Mo *et al.* 2023) of the *Pleosporales* LSU nucleotide alignment. Bootstrap support values from 1000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown), preceded by the SH-aLRT test value (only shown if the node has > 74 % bootstrap support). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Ramularia endophylla* (CBS 113265; GenBank KF251723) and the novelty described here is highlighted with a coloured block and **bold** font. Families, orders and the class are shown to the left and right of the tree in coloured blocks. Some branches were shortened to facilitate layout. Alignment statistics: 60 strains including the outgroup; 812 characters including alignment gaps analysed: 279 distinct patterns, 209 parsimony-informative, 63 singleton sites, 540 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TN+F+I+R3. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.29050751).



*Catenulostroma pellitae*



## *Catenulostroma pellitae* Crous, *sp. nov.*

**Etymology:** Name refers to the *Eucalyptus* species it was isolated from, *E. pellita*.

**Classification:** *Teratosphaeriaceae*, *Mycosphaerellales*, *Dothideomycetidae*, *Dothideomycetes*.

**Ascomata** amphigenous on leaf litter, black, erumpent, aggregated in clusters, up to 100 µm diam; wall consisting of 2–3 layers of medium brown textura angularis. **Asci** paraphysate, fasciculate, bitunicate, sessile, obovoid to broadly ellipsoid, straight to slightly curved, 8-spored, 20–30 × 7–9 µm. **Ascospores** tri- to multiseriate, overlapping, hyaline, guttulate, thin-walled, straight, fusoid-ellipsoidal with obtuse ends, widest in middle of apical cell, constricted at the septum, tapering towards both ends, but more prominently towards the lower end, (8–)10–11(–13) × 2.5(–3) µm; germinating ascospores on MEA germinate from both polar ends, with germ tubes parallel to the long axis of the spore, constricted at septum, distorting, with mucoid sheath visible, also starting lateral germ tubes from original spore, 3.5–4.5 µm wide.

**Culture characteristics:** Colonies erumpent, spreading, surface folded with moderate aerial mycelium and smooth, lobate margin, reaching 5 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface and reverse iron grey.

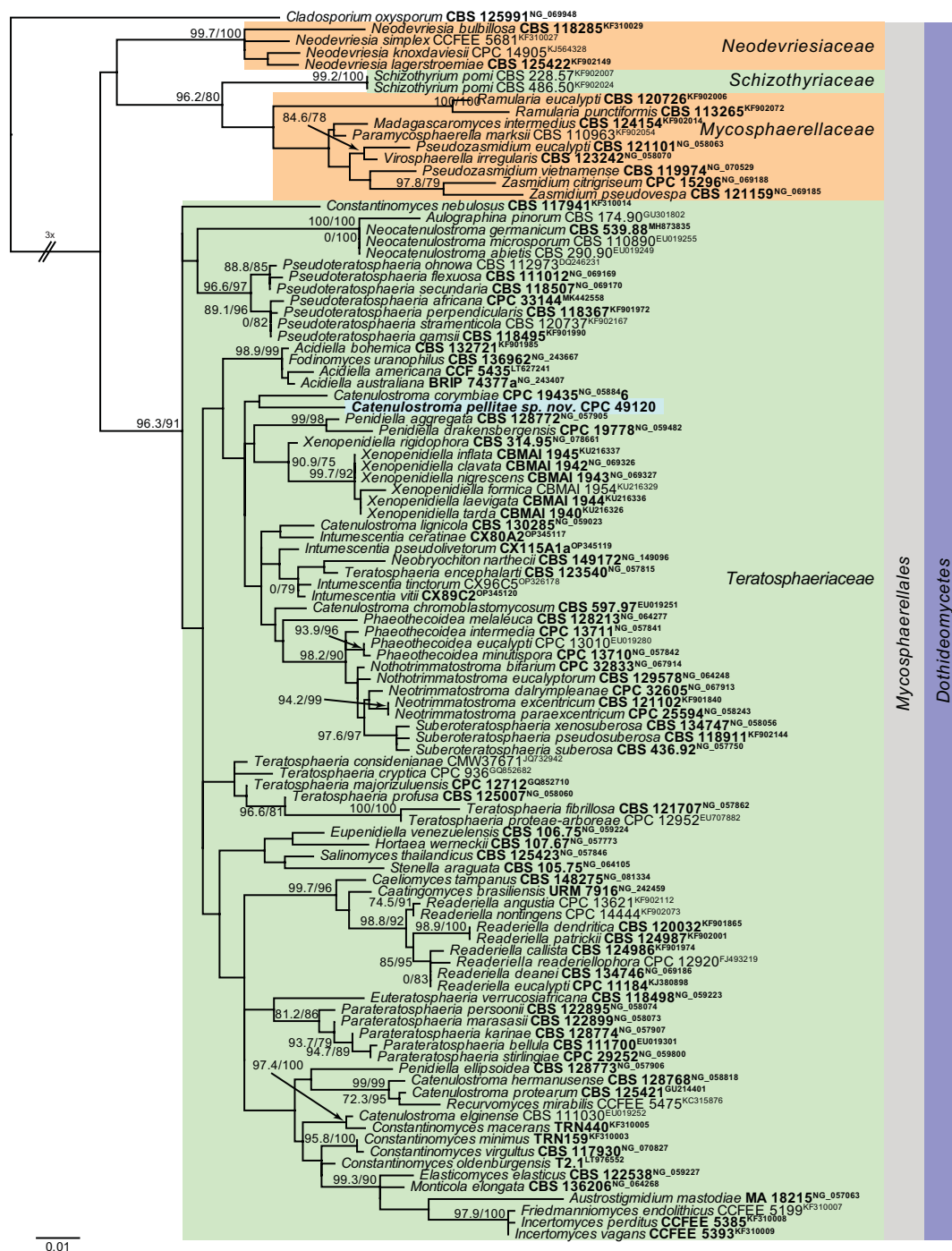
**Typus:** **Malaysia**, on leaf spots of *Eucalyptus pellita* (*Myrtaceae*), Jul. 2015, *M.J. Wingfield*, HPC 4516 [**holotype** CBS H-25743; culture ex-type CPC 49120 = CBS 153528; ITS, LSU, *cmdA*, *rpb2*, *tef1* (first part) and *tub2* sequences GenBank PV664945.1, PV664971.1, PV664009.1, PV664023.1, PV664038.1 and PV664056.1].

**Notes:** *Catenulostroma pellitae* is related to *C. corymbia*, a sexual species described from *Corymbia* leaves collected in Australia. It is distinguished in having smaller ascospores, 7–8(–10) × (2–)3(–3.5) µm, and also produces an asexual morph in culture (Crous *et al.* 2012), which is not observed in *C. pellitae*.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence

had highest similarity to *Catenulostroma elginense* [strain STE-U 1958, GenBank NR\_145089.1; Identities = 337/384 (88 %), 24 gaps (6 %)], *Euteratosphaeria verrucosiafricana* [strain CPC 11167, GenBank NR\_164213.1; Identities = 358/416 (86 %), 22 gaps (5 %)], and *Constantinomyces macerans* [strain TRN 440, GenBank NR\_164011.1; Identities = 371/432 (86 %), 29 gaps (6 %)]. Closest hits using the **LSU** sequence are *Catenulostroma chromoblastomycosum* [strain CBS 597.97, GenBank EU019251.2; Identities = 869/885 (98 %), no gaps], *Teratosphaeria encephalarti* [strain CBS 123541, GenBank FJ372414.1; Identities = 833/853 (98 %), no gaps], and *Catenulostroma corymbiae* [strain CPC 19435, GenBank KC005804.1; Identities = 864/885 (98 %), no gaps]. Closest hits using the **cmdA** sequence had highest similarity to *Austroafricana parva* [strain CPC 12249, GenBank KF902533.1; Identities = 378/448 (84 %), nine gaps (2 %)], *Teratosphaericola pseudoafricana* [strain CBS 111168, GenBank KF902782.1; Identities = 383/456 (84 %), 26 gaps (5 %)], and *Teratosphaeria majorizuluensis* [strain CBS 120040, GenBank KF902733.1; Identities = 328/374 (88 %), three gaps (0 %)]. Closest hits using the **rpb2** (first part) sequence had highest similarity to *Intumescencia ceratinae* [strain CX80A2, GenBank OP354474.1; Identities = 696/861 (81 %), one gap (0 %)], *Neobryochiton narthecii* [strain CBS 149172, GenBank ON803547.1; Identities = 658/824 (80 %), no gaps], and *Aulographina pinorum* [strain CBS 174.90, GenBank GU371737.1; Identities = 690/890 (78 %), seven gaps (0 %)]. Closest hits using the **tef1** (first part) sequence had highest similarity to *Xenopenidiella tarda* [strain DOC343, GenBank KU216353.1; Identities = 164/171 (96 %), no gaps], *Xenopenidiella inflata* [strain 87N, GenBank KU216359.1; Identities = 163/171 (95 %), no gaps], and *Pseudoteratosphaeria africana* [strain CBS 144597, GenBank MK442712.1; Identities = 179/187 (96 %), no gaps]. Closest hits using the **tub2** sequence had highest similarity to *Devriesia shelburniensis* [strain CBS 115876, GenBank KF442467.1; Identities = 292/351 (83 %), 22 gaps (6 %)], *Meristemomyces frigidus* [strain CCFEE 5508, GenBank KF546750.1; Identities = 282/349 (81 %), 15 gaps (4 %)], and *Petrophila incerta* [strain TRN139b, GenBank KF546769.1; Identities = 279/347 (80 %), six gaps (1 %)].

**Colour illustrations:** *Eucalyptus* forest in Malaysia. Section through pseudothecium; erumpent pseudothecia on leaf tissue; asci with ascospores; germinating ascospore. Scale bars: pseudothecium = 50 µm; all others = 10 µm.

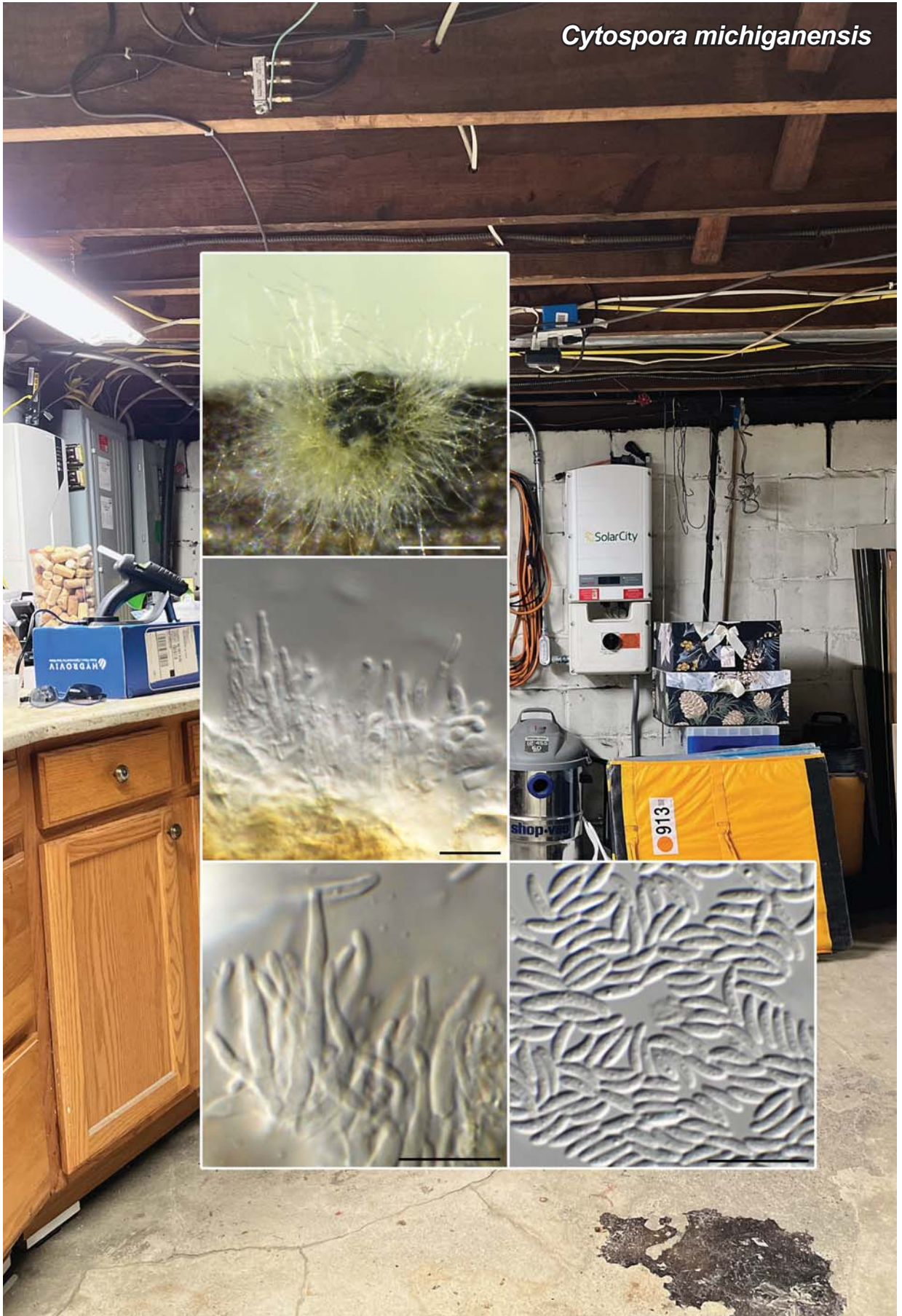


Most likely phylogenetic tree obtained from the maximum likelihood analysis with IQ-TREE v. 2.4.0 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020, Mo *et al.* 2023) of the *Mycosphaerellales* LSU nucleotide alignment. Bootstrap support values from 1000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown), preceded by the SH-aLRT test value (only shown if the node has > 74 % bootstrap support). Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Cladosporium oxysporum* (CBS 125991; GenBank NG\_069948) and the novelty described here is highlighted with a coloured block and **bold** font. Families, the order and the class are shown to the right of the tree in coloured blocks. The root branch was shortened to facilitate layout. Alignment statistics: 104 strains including the outgroup; 756 characters including alignment gaps analysed: 266 distinct patterns, 172 parsimony-informative, 58 singleton sites, 526 constant sites. The best-fit model identified for the entire alignment in IQ-TREE using the TESTNEW option was: TIM2e+I+R3. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.29050751).

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*Cytospora michiganensis*





## *Cytospora michiganensis* Crous & Jurjević, *sp. nov.*

**Etymology:** Name refers to Michigan, USA, where this fungus was collected.

**Classification:** *Cytosporaceae*, *Diaporthales*, *Sordariomycetidae*, *Sordariomycetes*.

**Conidiomata** on pine needle agar solitary, immersed, becoming erumpent, pycnidial, multilocular, brown, globose, 150–200 µm diam.; wall of 3–4 layers of pale brown *textura angularis*. **Conidiophores** lining inner cavity, hyaline, smooth, subcylindrical, branched, 1–2-septate, 10–20 × 2.5–3 µm. **Conidiogenous cells** hyaline, subcylindrical, tapering towards phialidic apex, terminal and intercalary, 7–10 × 2–2.5 µm. **Conidia** solitary, hyaline, smooth, aseptate, subcylindrical, curved, apex subobtuse, base truncate, 5–6(–7) × 1.5 µm.

**Culture characteristics:** Colonies flat, spreading, with moderate aerial mycelium, covering dish after 2 wk at 25 °C. On MEA, CYA, PDA and OA surface and reverse scarlet. Grows 4 mm / 7 d at 37 °C on CYA.

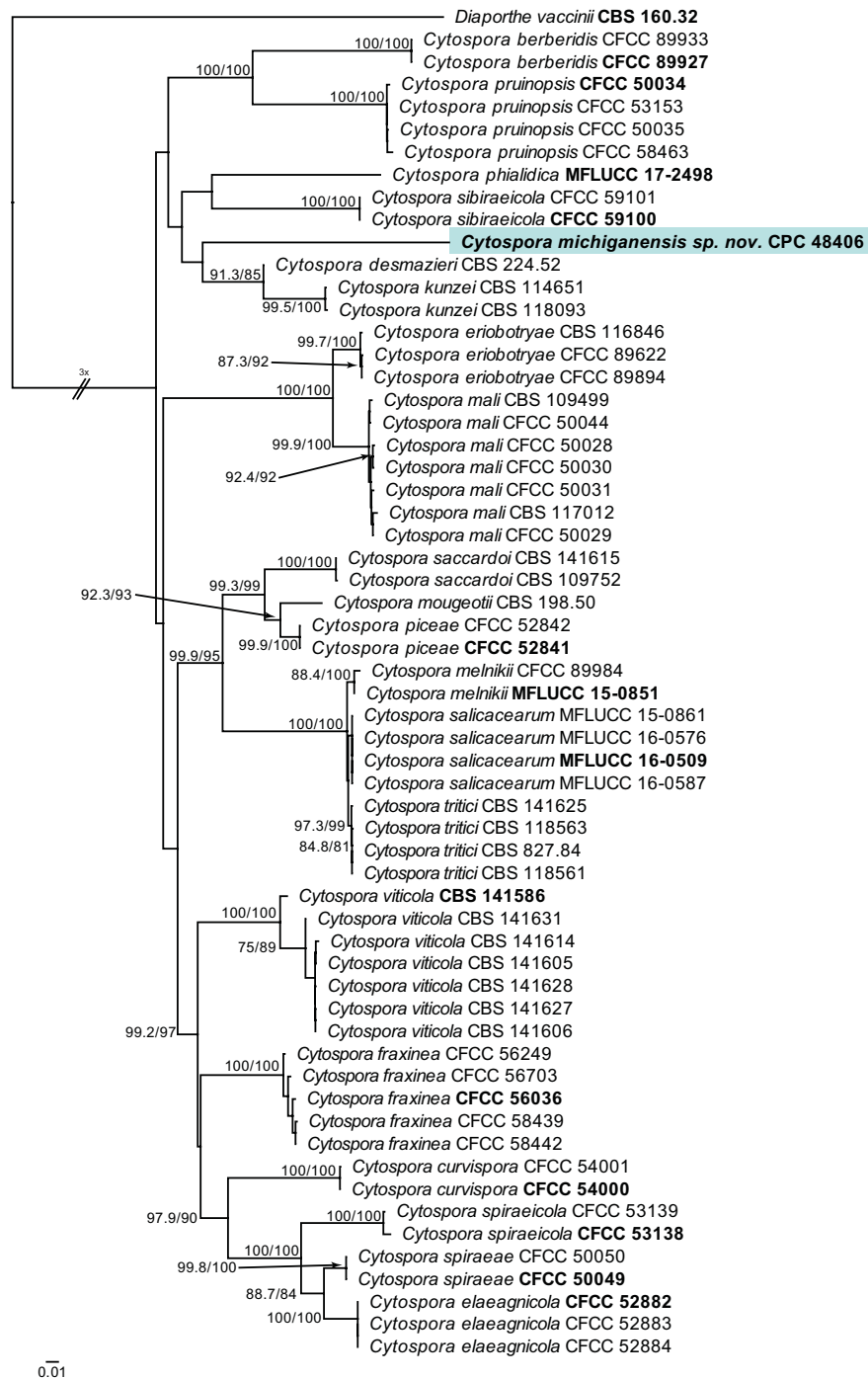
**Typus:** **USA**, Michigan, Farmington Hills, from utility room (settle plate), Apr. 2024, Z. Jurjević, 5934 [**holotype** CBS H-25739; culture ex-type CPC 48406 = CBS 153530; ITS, LSU, *actA*, *rpb2*, *tef1* (first part) and *tub2* sequences GenBank PV664946.1, PV664972.1, PV664006.1, PV664024.1, PV664039.1 and PV664057.1].

**Notes:** *Cytospora* contains numerous important canker pathogens of woody host plants (Lin *et al.* 2024). *Cytospora michiganensis* is phylogenetically related but distinct from various species of *Cytospora*, and is thus introduced as new. Because it was trapped from air via a settle plate, its host plant remains unknown.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Cytospora desmazieri* [strain CBS 197.42, GenBank KY051908.1; Identities = 529/559 (95 %), 17 gaps (3 %)], *Cytospora pruinosa* [strain FeC38, GenBank

MW447045.1; Identities = 564/597 (94 %), 16 gaps (2 %)], and *Cytospora leucostoma* [strain Z5-4-1, GenBank MN907640.1; Identities = 557/591 (94 %), 19 gaps (3 %)]. Closest hits using the **LSU** sequence are *Cytospora pruinosa* [as *Valsa pruinosa*; strain CBS 133.25, GenBank MH866316.1; Identities = 880/885 (99 %), no gaps], *Cytospora desmazieri* [as *Valsa pini*; strain CBS 197.42, GenBank MH867615.1; Identities = 880/885 (99 %), one gap (0 %)], and *Cytospora mali* [strain ARI-15-US, GenBank PP976972.1; Identities = 851/856 (99 %), no gaps]. Closest hits using the **actA** sequence had highest similarity to *Cytospora leucostoma* [strain CFCC 54682, GenBank MW815943.1; Identities = 144/167 (86 %), 12 gaps (7 %)], *Cytospora carpobroticola* [strain CPC 47120, GenBank PQ497710.1; Identities = 144/170 (85 %), 17 gaps (10 %)], and *Cytospora pavettae* [strain CBS 145562, GenBank MK876457.1; Identities = 137/166 (83 %), 10 gaps (6 %)]. Closest hits using the **rpb2** (first part) sequence had highest similarity to *Cytospora pruinopsis* [strain 20210416-YuS, GenBank OM274066.1; Identities = 834/922 (90 %), no gaps], *Cytospora viticola* [strain CBS 143162, GenBank MH108002.1; Identities = 768/854 (90 %), no gaps], and *Cytospora salicacearum* [strain shd162, GenBank MW824357.1; Identities = 828/922 (90 %), no gaps]. Closest hits using the **tef1** (first part) sequence had highest similarity to *Cytospora viticola* [strain CBS 143162, GenBank MH108014.1; Identities = 290/329 (88 %), 17 gaps (5 %)], *Cytospora piceae* [strain CFCC 52841, GenBank MH820402.1; Identities = 283/324 (87 %), 17 gaps (5 %)], and *Cytospora elaeagnicola* [strain 1322-2, GenBank MG230584.1; Identities = 282/323 (87 %), 17 gaps (5 %)]. Closest hits using the **tub2** sequence had highest similarity to *Cytospora bungeanae* [strain CFCC 50495, GenBank MH933563.1; Identities = 457/585 (78 %), 52 gaps (8 %)], *Cytospora pruinopsis* [strain CFCC 50034, GenBank KP310819.1; Identities = 583/781 (75 %), 107 gaps (13 %)], and *Cytospora mali* [strain CFCC 50030, GenBank MH933579.1; Identities = 540/696 (78 %), 83 gaps (11 %)].

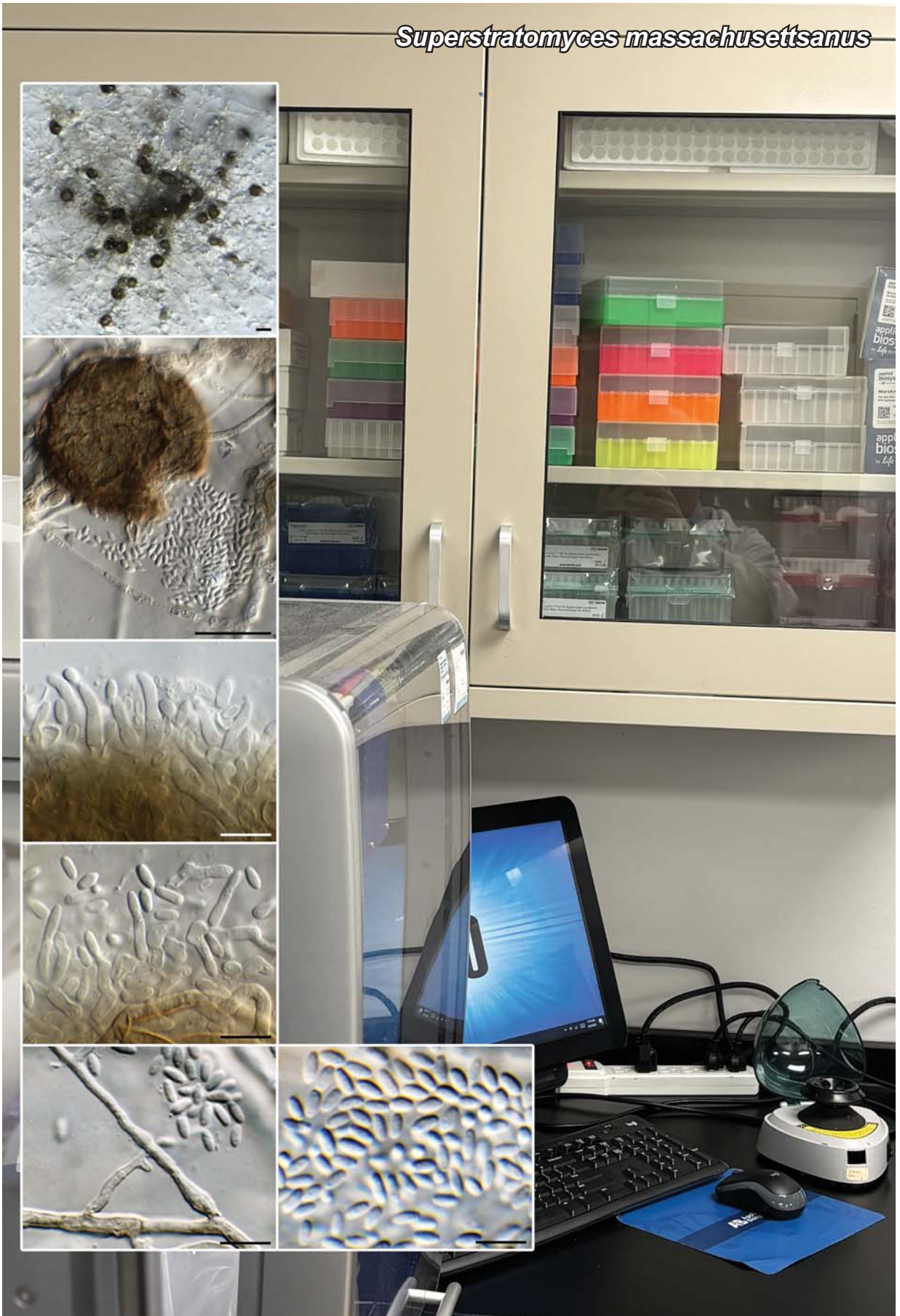
**Colour illustrations:** Utility room, Farmington Hills, MI, USA. Conidioma on pine needle agar; Conidiophores and conidiogenous cells giving rise to conidia on SNA; conidia. Scale bars: conidioma = 200 µm; all others = 10 µm.



Most likely phylogram obtained from the maximum likelihood analysis with IQ-TREE v. 2.4.0 (Kalyaanamoorthy *et al.* 2017, Minh *et al.* 2020, Mo *et al.* 2023) of the *Cytospora* ITS/*actA*/*rpb2*/*tef1*/*tub2* nucleotide alignment. Bootstrap support values from 1000 non-parametric bootstrap replicates are shown at the nodes (> 74 % are shown), preceded by the SH-aLRT test value (only shown if the node has > 74 % bootstrap support). Culture collection or specimen voucher numbers are indicated for all species. For GenBank accession numbers of included sequences, see Lin *et al.* (2024). Sequences from material with a type status are indicated in **bold** font. The tree was rooted to *Diaporthe vaccinii* (CBS 160.32) and the novelty described here is highlighted with a coloured block and **bold** font. The root branch was shortened to facilitate layout. Alignment statistics: 60 strains including the outgroup; 2756 characters including alignment gaps analysed; 1319 distinct patterns, 933 parsimony-informative, 196 singleton sites, 1627 constant sites. The best-fit model identified for each partition in IQ-TREE using the TESTNEW option was: ITS: TIM2e+I+G4; *actA*: TIM2e+G4; *rpb2*: TNe+G4; *tef1*: TPM2u+F+I+G4; *tub2*: HKY+F+I+G4. The scale bar shows the expected number of nucleotide substitutions per site. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.29050751).



# *Superstratomyces massachusettsanus*



## *Superstratomyces massachusettsanus* Crous & Jurjević, *sp. nov.*

*Etymology*: Name refers to Massachusetts, USA, where this fungus was collected.

*Classification*: *Superstratomycetaceae*,  
*Superstratomycetales*, *Dothideomycetes*.

*Conidiomata* pycnidial, solitary or aggregated, globose, brown, 50–80 µm diam., with central ostiole; wall of 3–4 layers of brown textura angularis. *Conidiophores* lining inner cavity, subcylindrical, hyaline, smooth, branched, 1–2-septate, 10–18 × 2.5–3 µm. *Conidiogenous cells* integrated, terminal and intercalary, phialidic, 3–10 × 2.5–3 µm. *Conidia* solitary, hyaline, smooth, aseptate, guttulate, ellipsoid with obtuse ends, 3–5 × 2(–2.5) µm.

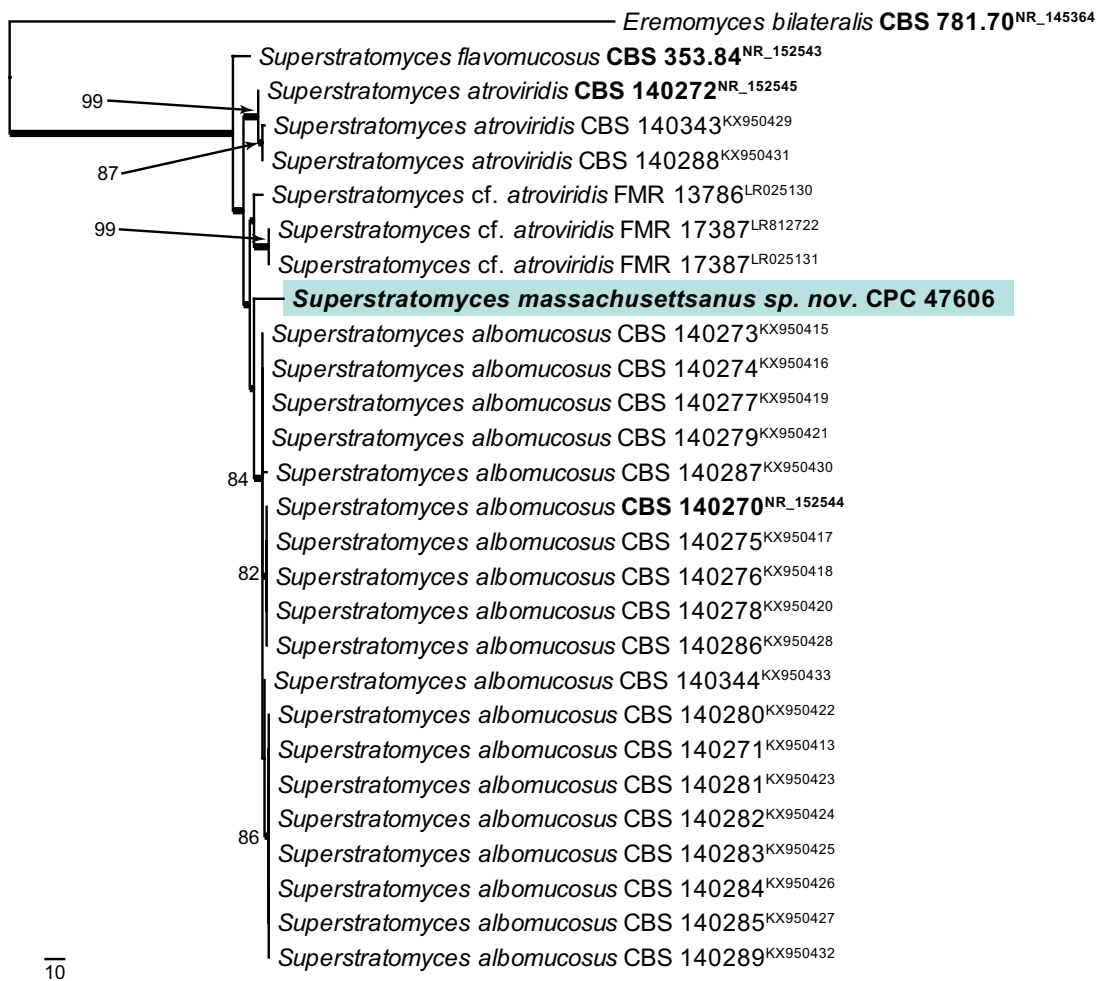
*Culture characteristics*: Colonies erumpent, spreading, surface folded with moderate aerial mycelium and smooth, lobate margin, reaching 10 mm diam. after 2 wk at 25 °C. On MEA, PDA and OA surface olivaceous grey, reverse iron grey. No growth at 37 °C on CYA.

*Typus*: **USA**, Massachusetts, Charlestown, from lyse buffer, Aug. 2024, Z. Jurjević, 5860 [**holotype** CBS H-25703; culture ex-type CPC 47606 = CBS 153531; ITS, LSU, *rpb2*, *tef1* (first part), *tef1* (second part) and *tub2* sequences GenBank PV664947.1, PV664973.1, PV664025.1, PV664040.1, PV664047.1 and PV664058.1].

*Notes*: *Superstratomyces* is characterised by brown pycnidial conidiomata, phialidic conidiogenous cells and hyaline, aseptate conidia (van Nieuwenhuijzen *et al.* 2016). *Superstratomyces massachusettsanus* is morphologically similar to *S. albomucosus*, except for its smaller conidiomata (conidia 2.8–6.0 × 1.5–3.0 µm, conidiomata 80–300 µm diam.; van Nieuwenhuijzen *et al.* 2016), but phylogenetically distinct.

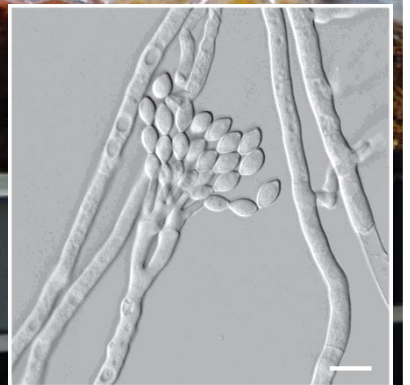
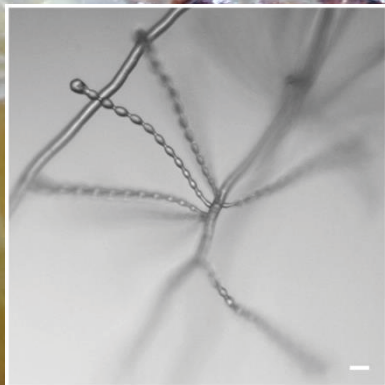
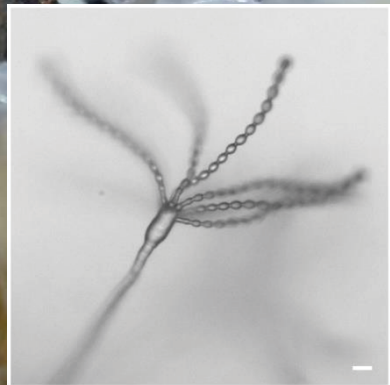
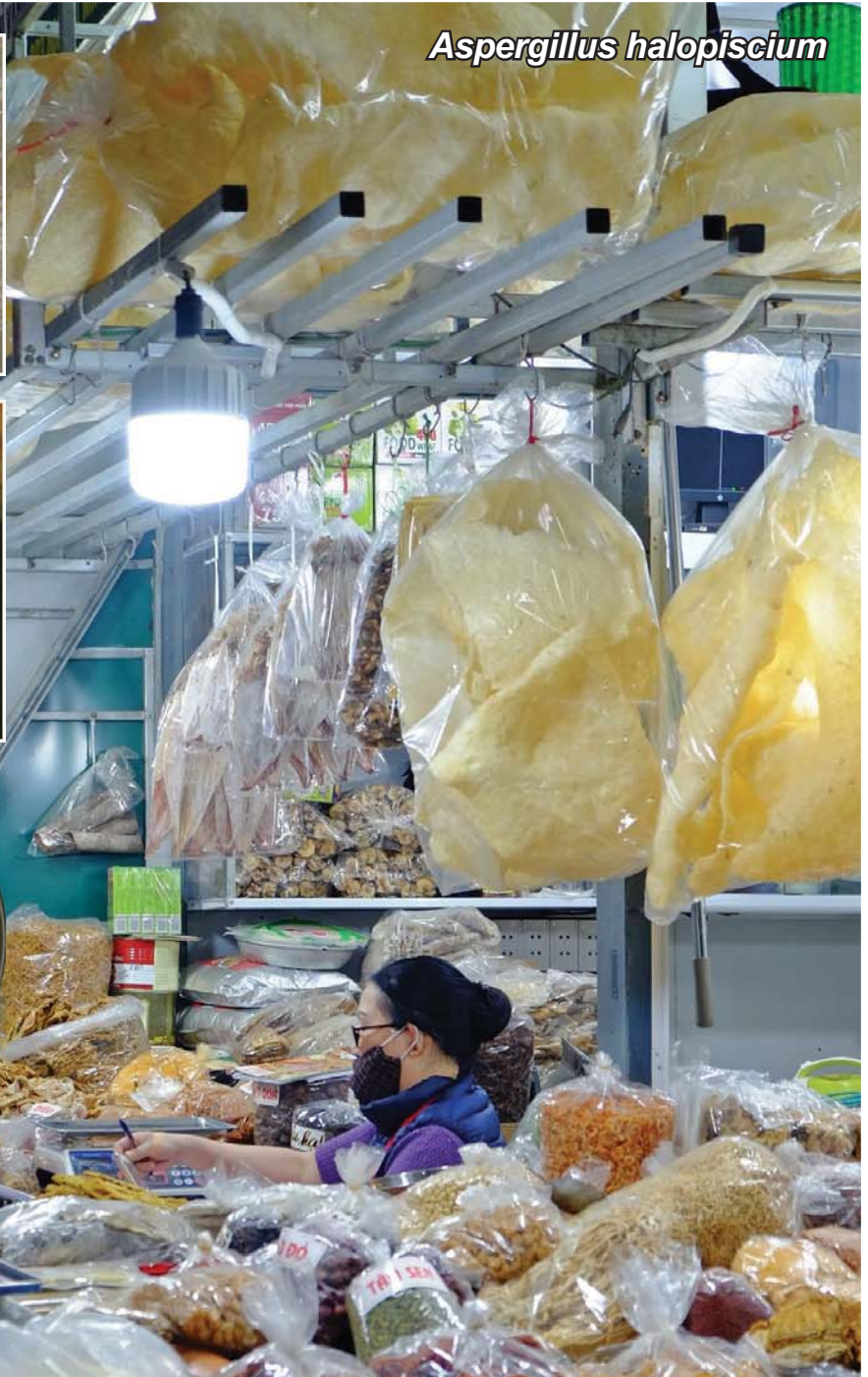
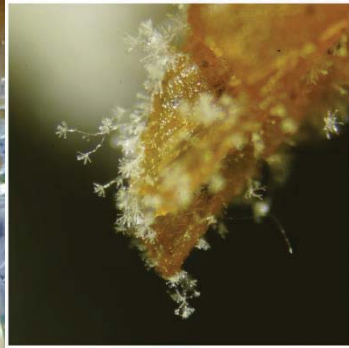
Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Superstratomyces albomucosus* [strain DTO 305-E3, GenBank KX950433.1; Identities = 900/926 (97 %), five gaps (0 %)], *Superstratomyces albomucosus* [strain CBS 140270, GenBank NR\_152544.1; Identities = 802/818 (98 %), two gaps (0 %)], *Superstratomyces flavomucosus* [strain CBS 353.84, GenBank NR\_152543.1; Identities = 890/926 (96 %), six gaps (0 %)], and *Superstratomyces atroviridis* [strain CBS 140272, GenBank NR\_152545.1; Identities = 797/818 (97 %), one gap (0 %)]. Closest hits using the **LSU** sequence are *Superstratomyces albomucosus* [strain DTO 277-D2, GenBank KX950439.1; Identities = 814/816 (99 %), no gaps], *Superstratomyces flavomucosus* [strain DTO 305-C3, GenBank KX950438.1; Identities = 814/816 (99 %), no gaps], and *Superstratomyces atroviridis* [strain CBS 140272, GenBank NG\_058271.1; Identities = 814/816 (99 %), no gaps]. Closest hits using the **rpb2** (first part) sequence had highest similarity to *Superstratomyces atroviridis* [strain FMR 17387, GenBank LR812723.1; Identities = 816/904 (90 %), one gap (0 %)], *Farlowiella carmichaeliana* [strain AFTOL-ID 1787, GenBank DQ677989.1; Identities = 383/488 (78 %), four gaps (0 %)], and *Herpotrichia juniperi* [strain HFRN18-240, GenBank LC618860.1; Identities = 685/932 (73 %), 55 gaps (5 %)]. No significant hits were obtained when the **tef1** (first part) and **tub2** sequences were used in blastn and megablast searches. Closest hits using the **tef1** (second part) sequence had highest similarity to *Superstratomyces atroviridis* [strain FMR 17387, GenBank LR812724.1; Identities = 416/421 (99 %), no gaps], *Superstratomyces albomucosus* [strain DTO 277-D2, GenBank KX950471.1; Identities = 434/441 (98 %), no gaps], and *Superstratomyces flavomucosus* [strain DTO 305-C3, GenBank KX950470.1; Identities = 435/443 (98 %), no gaps].

*Colour illustrations*: Laboratory in Charlestown, MA, USA. Conidiomata on SNA; pycnidial conidioma; Conidiophores and conidiogenous cells giving rise to conidia on SNA; conidia. Scale bars: conidiomata = 80 µm; conidioma = 40 µm; all others = 10 µm.



The first of two equally most parsimonious trees obtained from a maximum parsimony phylogenetic analysis (PAUP\* v. 4.0a; Swofford 2003) of the *Superstratomyces* ITS nucleotide alignment. The tree was rooted to *Eremomyces bilateralis* (CBS 781.70; GenBank NR\_145364) and the scale bar indicates the number of changes. Parsimony bootstrap support values from 1000 replicates and > 74 % are shown at the nodes and the novelty described here is highlighted with a coloured block and **bold** font. Culture collection or specimen voucher numbers and GenBank accession numbers (superscript) are indicated for all species. Sequences from material with a type status are indicated in **bold** font. Branches present in the strict consensus tree are thickened. Alignment statistics: 28 strains including the outgroup; 715 characters including alignment gaps analysed: 303 constant, 379 variable and parsimony-uninformative and 33 parsimony-informative. Tree statistics: Tree Length = 459, Consistency Index = 0.965, Retention Index = 0.863, Rescaled Consistency Index = 0.833. The alignment and tree were deposited at figshare.com (doi: 10.6084/m9.figshare.29050751).

*Aspergillus halopiscium*





# *Aspergillus halopiscium* V.N. Thanh, N.T. Thuy & N.B. Chau, *sp. nov.*

**Etymology:** Name refers to the habitat where the fungus was found (salted fish).

**Classification:** *Aspergillaceae*, *Eurotiales*,  
*Eurotiomycetidae*, *Eurotiomycetes*.

**Sexual structures** not observed. *Hyphae* hyaline, smooth, 3.5–6.0 µm diam., branched, septate. *Conidiophores* develop from submerged or aerial mycelia, may be branched or unbranched, subcylindrical to ampulliform, hyaline, smooth, and either poly- or monophialidic. *Phialides* arise directly from the conidiophore without a septum at the base and may be verticillate or irregularly branched, measuring 1.5–2.5 × 6–8 µm. *Conidia* occur in short chains (up to 15), are fusoid to ellipsoid, with both ends symmetrically tapered and truncated, thin-walled, aseptate, hyaline, smooth, (3.5–)4–5(–6) × (6–)7–8(–9) µm.

**Culture characteristics:** The fungus is halophilic, tolerant of up to 15 % NaCl, with optimal growth at 5 % NaCl. Without NaCl addition, growth is restricted and slow, with raised colonies. On malt extract agar (MEA) containing 5 % NaCl, colonies are white, flat, spreading, velvety, entire, and wrinkled at the center, with no diffused pigmentation, reaching 25–30 mm diam. after 2 wk at 30 °C. Optimal growth occurs on diluted fish sauce agar, forming white, flat, spreading, chalky colonies with an entire margin and radiating wrinkles, reaching 35–40 mm diam. after 2 wk at 30 °C.

**Habit, habitat and distribution:** *Aspergillus halopiscium* is a halophilic fungus obtained from dried marine anchovies and fish sauce production facilities in Vietnam.

**Typus:** Vietnam, Hanoi, 10°38'N, 106°58'E, 10 m a.s.l., dry marine anchovy *Stolephorus commersonnii*, May 2019, V.N. Thanh (**holotype** and culture ex-type permanently preserved in a metabolically inactive state OHFS 14.1; ITS-LSU, *cmdA*, *rpb2*, and *tub2* sequences GenBank MW473703, PV568286, PV568287, and PV568286).

**Additional material examined:** Vietnam, Hanoi, 10°38'N, 106°58'E, 10 m a.s.l., dry marine anchovies *Stolephorus commersonnii*, May 2019, V.N. Thanh, culture OHFS 31.1; ITS-LSU, *tub2*, and *cmdA* sequences GenBank MW473706, MW473708, and MW551940; Phu Quoc Island, 10°10'N

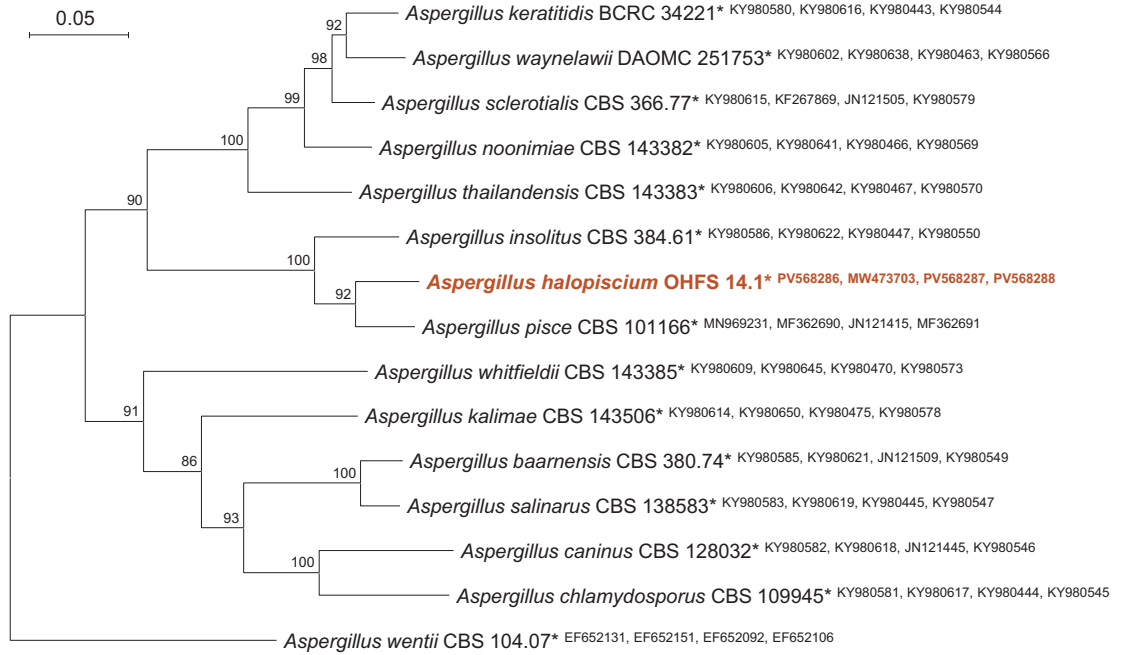
104°02'E, 17 m a.s.l., leakage from a wooden fish sauce tank (*Stolephorus commersonnii*), Aug. 2019, V.N. Thanh, culture VCIM 5445; ITS-LSU and *rpb2* sequences GenBank MW473702 and MW473707.

**Notes:** In a study on the diversity of halotolerant fungi associated with salted fish products (dried marine fish) and fish sauce production facilities in Vietnam, three strains of *Aspergillus* subgenus *Polypaecilum* were obtained by placing the samples on diluted fish sauce agar (1 % amino acids, 7 % NaCl, 2 % agar). The strains were morphologically similar, and nearly identical in the ITS-LSU sequences (1–2 differences in 1178 nuc.). Although the fungus produced both poly- and monophialidic conidiophores, the former was more frequent and well-developed. The strains were halophilic. On MEA, they formed compact and raised colonies, suggesting stressed conditions. Growth was enhanced with the addition of NaCl at concentrations of 5–10 %. Growth was poor at 15 % NaCl, and no growth was observed at 20 % NaCl. Fungal growth on both MEA and fish sauce agar produced a strong ammonia odour, indicating a high level of deamination activity.

Based on a megablast search of NCBI's GenBank nucleotide database, the **ITS** sequence had highest similarity to *Aspergillus pisce* [strain CBS 101166<sup>T</sup>, GenBank NR\_172275.1; Identities = 475/513 (93 %), 25 gaps (4 %)], and *Aspergillus insolitus* [strain CBS 384.61<sup>T</sup>, GenBank NR\_154978.1; Identities = 448/488 (92 %), 24 gaps (4 %)]. Closest hits using the **LSU** sequence are *Aspergillus insolitus* [strain CBS 384.61<sup>T</sup>, GenBank MH869664.1; Identities = 652/656 (99 %) one gap (0 %)], and *Aspergillus caninus* [strain CBS 128032<sup>T</sup>, GenBank NG\_064243.1; Identities = 601/621 (97 %), four gaps (0 %)]. The closest hit using the **rpb2** sequence is *Aspergillus pisce* [strain CBS 101166<sup>T</sup>, GenBank JN121415.1; Identities = 897/951 (94 %), no gaps]. The closest hit using the **tub2** sequence is *Aspergillus pisce* [strain CBS 101166<sup>T</sup>, GenBank MF362691.1; Identities = 402/439 (92 %), 10 gaps (2 %)]. The closest hit using the **cmdA** sequence is *Aspergillus pisce* [strain CBS 101166<sup>T</sup>, GenBank MN969231.1; Identities = 474/502 (94 %), two gaps (0 %)].

**Supplementary material:** doi: 10.6084/m9.figshare.28602518 (alignments and phylogenetic trees).

**Colour illustrations:** Vietnam, Hanoi, a shop selling dried food products, including dried marine anchovies *Stolephorus commersonnii* (photo credit V.N. Thanh). *Aspergillus halopiscium* on an anchovy, and closeup photo (top); *Aspergillus halopiscium* on fish sauce agar after 10 d at 30 °C; conidiophores and conidia (bottom row). Scale bars = 10 µm.



Maximum likelihood tree based on *cmdA*, ITS, *rpb2*, and *tub2* sequences of *Aspergillus halopiscium* and related *Aspergillus* species. The maximum likelihood analysis was performed using the Tamura-Nei model (Tamura & Nei 1993) in MEGA v. 12 (Kumar *et al.* 2024). Bootstrap support values greater than 50 % are given at the nodes. GenBank accession numbers are indicated (superscript). Novel taxa are indicated in **bold**. Ex-type strains are indicated with asterisks (\*).



*Atromagnispora indianensis*



Fungal Planet 1807

MB 857536

## *Atromagnispora* Raja, L.M. Jacobus, Henriques & Oberlies, *gen. nov.*

*Etymology*: “*atrum*” in Latin meaning dark and “*magnus*” in Latin meaning large referring to the dark and large ascospores of the fungus.

*Classification*: Pleosporales, Lindgomycetaceae, Dothideomycetes.

*Ascomata* on wood, black, carbonaceous, solitary or grouped, globose to subglobose, superficial to partially immersed. *Ostiolate* with a short neck. *Peridium* thick-walled, areolate in surface view. *Hamathecium* comprising numerous cellular pseudoparaphyses, septate, embedded in a gelatinous matrix. *Asci* eight-spored, bitunicate, fissitunicate, globose

to subglobose with a short stalk or not, thick-walled, mostly deliquescent at maturity, without an apical ring. *Ascospores* broadly fusoid to ellipsoidal, bi- to triseriate, 1-septate bi-apiculate, with hyaline, bipolar papillae. Young ascospores hyaline, filled with lipid droplets, surrounded by large, thick-walled, striated sheath as well as an outer thin mucilaginous sheath which expands in the water; mature ascospores become dark brown to black and rough walled to reticulate or warted in surface view.

*Type species*: *Atromagnispora indianensis* Raja, L.M. Jacobus, Henriques & Oberlies

MB 857537

## *Atromagnispora indianensis* Raja, L.M. Jacobus, Henriques & Oberlies, *sp. nov.*

*Etymology*: “*indianensis*” name refers to the state of Indiana where the fungus is presently known.

*Ascomata* on wood 265–335 × 270–346 µm, black, carbonaceous, solitary or grouped, globose to subglobose, superficial to partially immersed with a plume of large, black ascospores oozing out of the ostiole. *Ostiolate* with a short neck. Ostiole rounded, 40–50 µm wide. *Peridium* thick-walled and areolate in surface view. *Hamathecium* comprising numerous cellular pseudoparaphyses, septate, 2–3 µm wide, embedded in a gelatinous matrix. *Asci* eight-spored, bitunicate, fissitunicate, globose to subglobose with a short stalk, thick-walled, most deliquescent at maturity, without an apical ring, 102–192 × 57–140 µm (av. and SD = 150 ± 32 × 104 ± 26 µm, n = 20). *Ascospores* bi- to triseriate, broadly fusiform to ellipsoidal, hyaline when young, 61–81 × 26–34 µm (av. and SD = 75 ± 5 × 30 ± 2 µm, n = 20), 1-septate, bi-apiculate, filled with lipid droplets, with hyaline bipolar papilla, 5–7 × 6–7 µm, surrounded by large, thick, striated sheath, 10–14 µm wide at the apex and 6–10 µm wide at the sides; as well as an outer thin-walled mucilaginous sheath which expands in the water, 10–20 µm wide. Older ascospores 89–120 × 47–62 µm (av. and SD = 106 ± 7 × 53 ± 4 µm,

n = 30) at first lightly pigmented and pale brown with two large guttules; as the ascospores age further, the sheath and the bipolar papillae begin to get appressed to the older ascospores; mature ascospores become dark brown, septum darkens towards the periphery, rough walled to reticulate or warted in surface view; ultimately becoming dark black. Older ascospores germinating at the apices. *Asexual morph* unknown.

*Culture characteristics*: On peptone yeast glucose (PYG), colonies grow slowly, attaining 25–30 mm diam. after 30 d at 25 °C on a 12-h light/dark cycle. The aerial mycelium appears whitish gray to pale brown, circular in shape, raised and flocculose in the center that has a marginal zone of pale brown mycelium. The hyphae are both aerial and submerged, septate, and measure 2–3 µm in width. Reverse side of the colony is opaque, ranging from dark to pale brown, and a light brown pigment is exuded into the surrounding agar.

*Habit, habitat and distribution*: Submerged wood, freshwater stream in Indiana, USA.

*Typus*: USA, Indiana, Martin County, East Fork White River at Hindostan Falls, lower boat ramp, 38°37'20.3"N, 86°50'51.7"W, 20 Jul. 2024, water temperature 26 °C, pH 8.5, L.M. Jacobus & S. Henriques, G1216 (**holotype** ILLS00123000); ex-type living culture CBS 153515, single ascospore isolate from holotype; GenBank ITS LSU and *tef1-α* sequences PV068212, PV068213, PV061841, PV061842, PV061008, PV061009.

*Notes*: The ascomycete fungal genus that comes to mind when the morphological characters of the new genus are examined under the microscope, is *Caryospora*, *Astrosphaeriellaceae*, *Pleosporales*, *Ascomycota*. Mainly resembling *C. aquatica*, *C. minima*, and *C. quercus* (Dong *et al.* 2020b). However, the combination of characters, in *At. indianensis* such as

*Colour illustrations*: East Fork White River, Indiana, USA (photo credit: L.M. Jacobus). *Atromagnispora indianensis* from holotype; ascomata on wood, note arrow indicating ascospores oozing out of the ostiole; squash mount of peridial wall in surface view; pseudoparaphyses; thick-walled ascus with ascospores; ascus showing dark brown one-septate ascospores; note arrow showing ascus stalk; young ascospore with large, thick, striated sheath and note arrow indicating outer thin-walled mucilaginous sheath which expands in the water; ascospore morphology from young, hyaline to dark brown to black; note arrows showing the bipolar papillae. Scale bars: ascomata = 200 µm; peridial wall = 20 µm; ascus and ascospores = 20 µm and 50 µm; pseudoparaphyses = 10 µm.



large, thick-walled globose to subglobose asci, cellular pseudoparaphyses, large ascospores (89–120 × 47–62 µm), with a striated and mucilaginous sheath with hyaline bipolar papillae, differentiate *Atromagnispora* from *Caryospora*. Although, a two-layered sheath is also seen in *C. quercus*, (Dong *et al.* 2020b) and a large sheath, which spreads in water is present in *C. minima* (Hyde *et al.* 1998), when observed more closely, these fungi have vastly different sheaths surrounding their ascospores. *Atromagnispora indianensis* also morphologically resembles *C. callicarpa* in the size of the dark brown ascospores and presence of bipolar apical cells. However, *At. indianensis* differs from *C. callicarpa* in not having a dark band of septa and has a different pattern of striations compared to *C. callicarpa* (Hawksworth *et al.* 2010). In addition, *Caryospora* shows phylogenetic affiliation with the family *Astrosphaeriellaceae*, (Dong *et al.* 2020b) whereas *Atromagnispora* shows phylogenetic affinity to the *Lindgomycetaceae*, *Pleosporales* (Hirayama *et al.* 2010, Raja *et al.* 2017; present study).

Another freshwater genus which bears superficial similarities to *Atromagnispora* is *Angustospora nilensis* (Li *et al.* 2016). However, *At. indianensis* differs from *An. nilensis* in both morphological characters and phylogenetic position. *Atromagnispora* is phylogenetically related to *Lindgomycetaceae*, whereas *An. nilensis* shows relatedness to the *Testudinaceae* (Li *et al.* 2016). Morphologically, *At. indianensis* differs from *An. nilensis* in ascus, and ascospore morphology; the asci in *At. indianensis* are thick-walled, globose to subglobose, while *An. nilensis* has clavate asci. The ascospores of *At. indianensis* are larger, fusiform when hyaline have a striated and large mucilaginous sheath, with reticulate pattern on the mature ascospore surface; characters largely absent in ascospores of *An. nilensis*.

Interestingly, the morphology of ascospores of *Atromagnispora* also resembles that *Ascomauritiana* (Ranghoo & Hyde 1999), when they are seen on the surface of wood substrate after oozing out of the ascomata ostiole, albeit only superficially.

In addition, Raja *et al.* (2010) conducted a comparison of seven morphologically similar members (*Alascospora evergladensis*, *Caryospora putaminum*, *Zopfia rhizophila*, *Pontoporeia biturbinata*, *Zopfiofoveola punctata*, *Testudina terrestris*, *Verruculina enalia*) of the *Pleosporales*, which were collected from various habitats, including terrestrial,

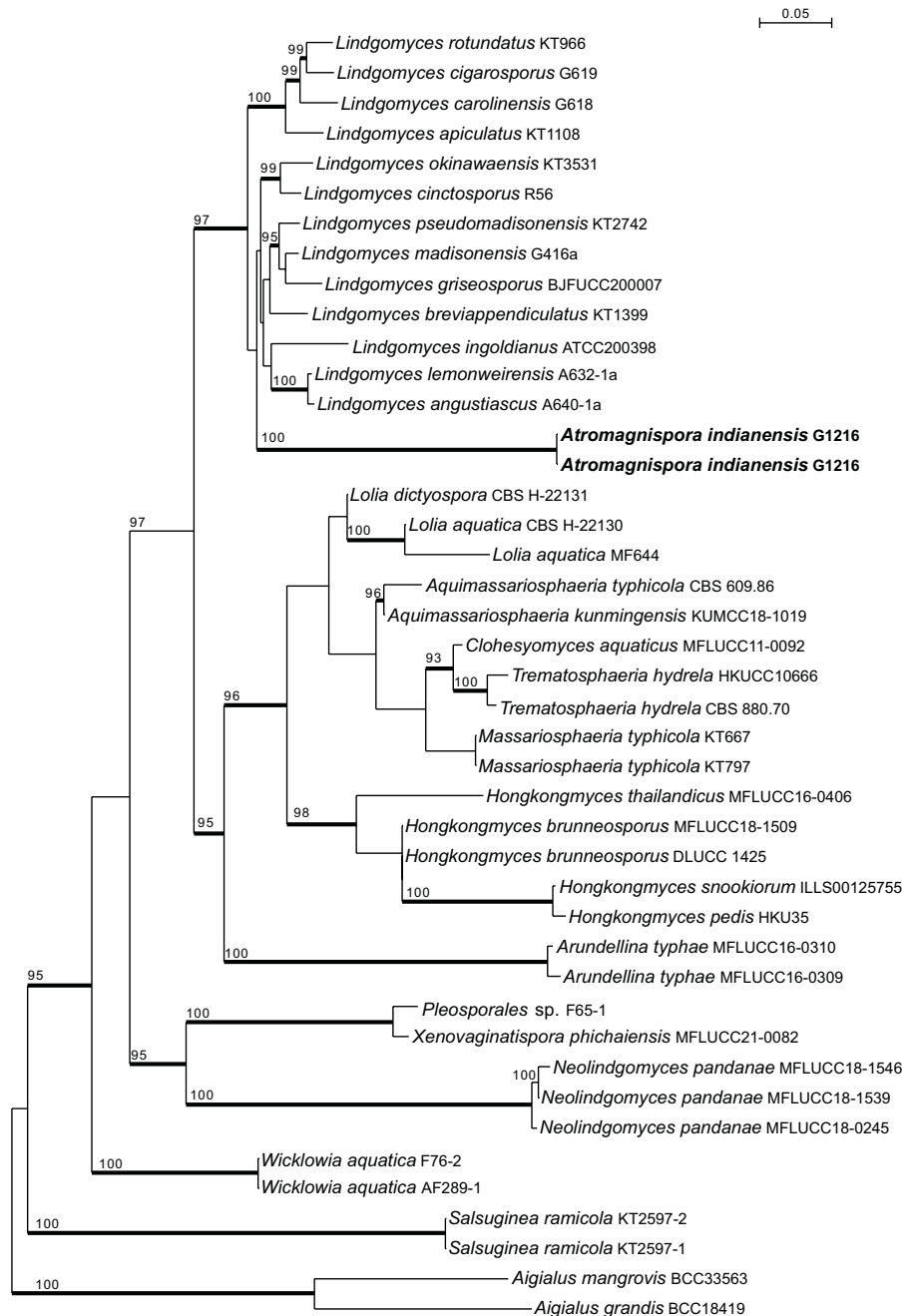
freshwater, mangrove, and marine environments. All these fungi feature thick-walled, globose to subglobose and clavate to cylindrical asci and produce ellipsoidal, mature dark brown to black, 1-septate ascospores. These ascospores may have a rough-walled surface and may or may not possess bipolar papillae. The newly identified genus, *At. indianensis* is distinct from these seven genera as it occurs on submerged wood in freshwater and is distinguished by its large broadly fusiform to ellipsoidal ascospores, as well as a combination of a striated and expanding gelatinous sheaths, which is evident in young ascospores. In addition, the ascospores of *At. indianensis* are equipped with hyaline, bipolar papillae, and reticulate ornamentation on the surface; characters that are largely absent in the aforementioned taxa.

Molecular phylogenetic analysis based on combined partial 28S nrRNA and *tef1-α* also confirm that *A. indianensis* is distinct from *Caryospora*, *Angustospora* and *Zopfia* (Supplementary material).

*Atromagnispora indianensis* is also morphologically similar to *Zopfia* (Hawksworth 1979, Hawksworth & Booth 1974) in having globose, thick-walled asci, and dark brown to black, ornamented ellipsoidal ascospores with bipolar papillae. However, *A. indianensis* differs from *Zopfia* in having ostiolate ascomata and larger ascospores with two different types of sheaths in younger ascospores. The peridial wall of *A. indianensis* appears to be areolate in surface view, while *Zopfia* spp. show a cephalothecoid wall (Hawksworth & Booth 1974). Lundqvist (1972) referred to the cephalothecoid peridium wall as “areolate” which is similar to what we observe in *A. indianensis*; but the term “cephalothecoid” was retained for fungi in the genus *Zopfia* (Hawksworth and Booth 1974). Moreover, molecular phylogenetic analysis based on combined 28S nrRNA and *tef1-α* sequence data confirm that *A. indianensis* is distinct from *Zopfia rhizophila* (Supplementary material).

*Atromagnispora indianensis* is an unusual morphological clade in the *Lindgomycetaceae* (Pers. comm., K. Tanaka, 2025).

*Supplementary material:* <https://figshare.com/s/ffd85112937197b99a99> (alignments, table with accession numbers, and additional phylogenetic trees).

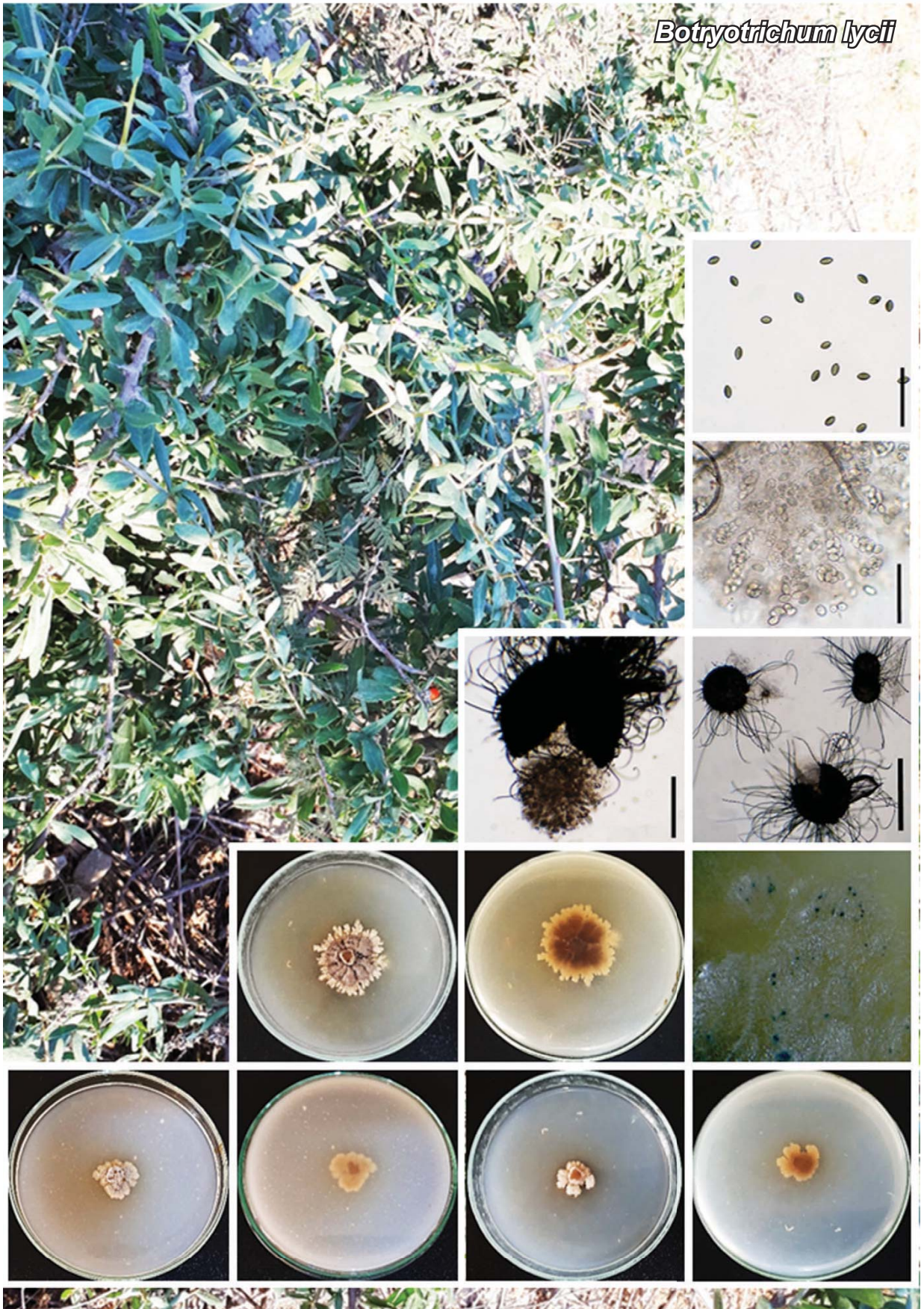


Phylogram of the most likely tree ( $-lnL = 20235.978$ ) from an IQ-TREE v. 2.2.0 analysis (Nguyen *et al.* 2015) of 43 taxa based on ITS, partial 28S nrRNA, and *tef1- $\alpha$*  (alignment length 4337 bp) under the Edge-linked partition model for 5000 ultrafast bootstrap replicates (Minh *et al.* 2013) using PhyloSuite v. 1.2.3 (Xiang *et al.* 2023). Numbers refer to UFBoot support values  $\geq 90$  %. Nodes  $\geq 95$  % are considered strongly supported. Thickened branches indicate significant Bayesian posterior probabilities  $\geq 95$  %. Bayesian analyses were run for 10 M generations using MrBayes v. 3.2 (Ronquist *et al.* 2012) under the GTR+G model for the ITS region, the TIEMF+I+G model for the partial 28S nrRNA gene region, and TRN+G model for *tef1- $\alpha$*  using PartitionFinder2 (Lanfear *et al.* 2017). ClipKit (<https://dev-clipkit.genomelybio.com/#/>) (Steenwyk *et al.* 2020) was used to remove ambiguous characters from the alignments of each region prior to concatenation using SequenceMatrix v.1.0 (Vaidya *et al.* 2011). The new genus is highlighted in **bold**. Scale bar indicates the expected number of nucleotide substitutions per site. Taxon sampling was performed as per Dan-Feng *et al.* (2021) and Boonmee *et al.* (2021).

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*Botryotrichum lycii*



***Botryotrichum lycii* Safi & M. Mehrabi-Koushki, *sp. nov.***

*Etymology*: Named after the host genus from which it was isolated, *Lycium*.

*Classification*: Chaetomiaceae, Sordariales, Sordariomycetes.

Morphology on potato dextrose agar (PDA): *Ascomata* semi-immersed to immersed in the agar, solitary, ostiolate, dark brown to black, globose to subglobose, (76.5–)121.5–302(–385) × (98–)115.5–302 µm, 95 % confidence limits = 195.5–227.5 × 185–216 µm ( ± SD = 211.6 ± 56.8 × 200.5 ± 55 µm, n = 50). *Ascomatal wall* dark brown, *textura intricata* or *epidermoidea* in surface. *Ascomatal hairs* covering the whole *ascomata*, hyphal-like, smooth, flexuous or slightly undulate, dark brown to black, paler towards the tips, 2.4–6 µm diam near the base, varying in length. *Asci* clavate, spore-bearing part (17–)21.5–45.5 × 10–24 µm, n = 50, with stalks (18–)20.5–38(–47) × 4.3–8.8 µm long, n = 40, containing eight irregularly arranged or biseriolate *ascospores*. *Ascospores* aseptate, smooth, olive brown, amygdaliform to fusiform, with an apical germ pore, 10–17 × 7–10 µm, 95 % confidence limits = 14–14.5 × 8.5–9 µm ( ± SD = 14.3 ± 1.1 × 8.6 ± 0.6 µm, n = 50). *Asexual morph* not observed.

*Culture characteristics*: Colonies on PDA reaching 16 mm diam. after 12 d of incubation at 25 ± 0.5 °C, and 20 mm diam. at 30 ± 0.5 °C, creamy to pale brown, irregular with undulate margin; reverse creamy brown with irregular margin. Colonies on oatmeal agar (OA) reaching 15 mm diam. after 8 d of incubation at 25 ± 0.5 °C, and 14 mm diam. at 30 ± 0.5 °C, grey in the centre with irregular light brown margin, *ascoma* scattered on colony as black dots; reverse pale brown with irregular margin.

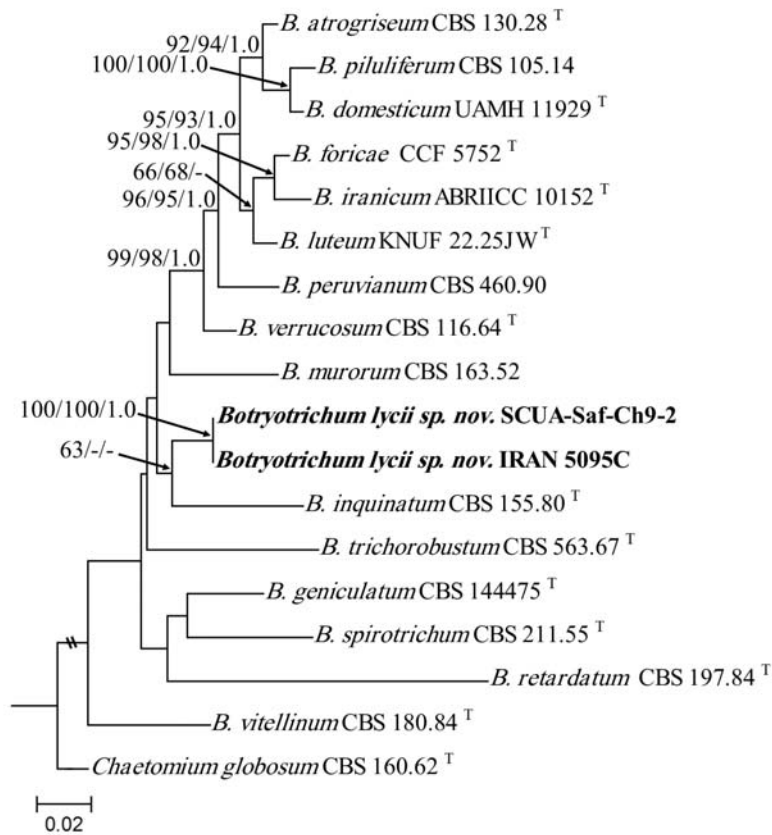
*Typus*: Iran, Khuzestan Province, Shadegan, isolated from rotten leaf of *Lycium depressum* (*Solanaceae*), Dec. 2022, A. Safi (**holotype** IRAN 18535F, culture ex-type IRAN 5095C = SCUA-Saf-Ch9; ITS, *tub2* and *rpb2* sequences GenBank PV166307, PV173108 and PV173110).

*Additional material examined*: Iran, Khuzestan Province, Shadegan, isolated from rotten leaf of *L. depressum*, Dec. 2022, A. Safi, culture SCUA-Saf-Ch9-2; ITS, *tub2* and *rpb2* sequences GenBank PV166308, PV173109 and PV173111.

*Notes*: The closest match in the BLASTn search for ITS and *tub2* sequences of *Botryotrichum lycii* IRAN 5095C was *B. verrucosum* strain CBS 116.64 (ITS: GenBank NR168165, identities = 99.2 %; *tub2*: GenBank LT993648, identities = 94.4 %), and for *rpb2* sequences was *B. inquinatum* strain CBS 155.80 (*rpb2*: GenBank MK919345, identities = 94.8 %). *Botryotrichum lycii* is phylogenetically related to *B. inquinatum* (MLBS 65 %). This new species and the ex-type strain of *B. inquinatum* (CBS 155.80) showed 5 bp difference (1.3 %) across 363 nucleotides of the ITS region, 46 bp difference (9.3 %) across 497 nucleotides of the *tub2* region, and 28 bp difference (5.1 %) across 557 nucleotides of the *rpb2* region. Morphologically, *B. lycii* can be distinguished from *B. inquinatum* by smaller *ascomata* [(76.5–)121.5–302(–385) × (98–)115.5–302 µm vs (120–)175–330 µm diam.] and *ascospores* 10–17 × 7–10 µm vs (16–)17–19(–20.5) × (11.5–)12.5–14.5 µm; Wang *et al.* 2022]. *Botryotrichum inquinatum* was introduced with the description of strains obtained from desert soil in Egypt and sewage sludge in Japan (Wang *et al.* 2022), while the strains of *B. lycii* were isolated from rotten leaves of *Lycium depressum*.

*Supplementary material*: The composite alignment and supplementary table showing the accession numbers of the sequences used in the phylogenetic analysis were deposited at figshare.com (DOI: 10.6084/m9.figshare.28832372).

*Colour illustrations*: *Lycium depressum*, Shadegan, Khuzestan Province, Iran. From bottom to top and left to right: 12-d-old colony on OA and PDA in surface and reverse, respectively; a 30-d-old colony on PDA in surface and reverse, respectively; *ascomata*; *asci*; *ascospores*. Scale bars: *ascomata* = 70 µm; *asci* and *ascospores* = 20 µm.



RAxML phylogenetic tree constructed from a maximum likelihood analysis based on the combined ITS, *tub2* and *rpb2* sequences of *Botryotrichum* species. The tree was rooted to *Chaetomium globosum* strain CBS 160.62. Bootstrap support values (MLBS, MPBS, respectively) obtained in maximum likelihood (ML, TrN + G) and maximum parsimony (MP) analyses > 50 % and Bayesian posterior probability values (BPP) ≥ 0.5 are shown at the nodes, respectively (Software used: ML: raxmlGUI v. 2.0 beta, Edler *et al.* 2019; MP: MEGA v. 7, Tamura *et al.* 2013; BI: jModelTest 2 and MrBayes v. 3.2.6, Darriba *et al.* 2012, Ronquist *et al.* 2012). The new taxon is indicated in **bold**.

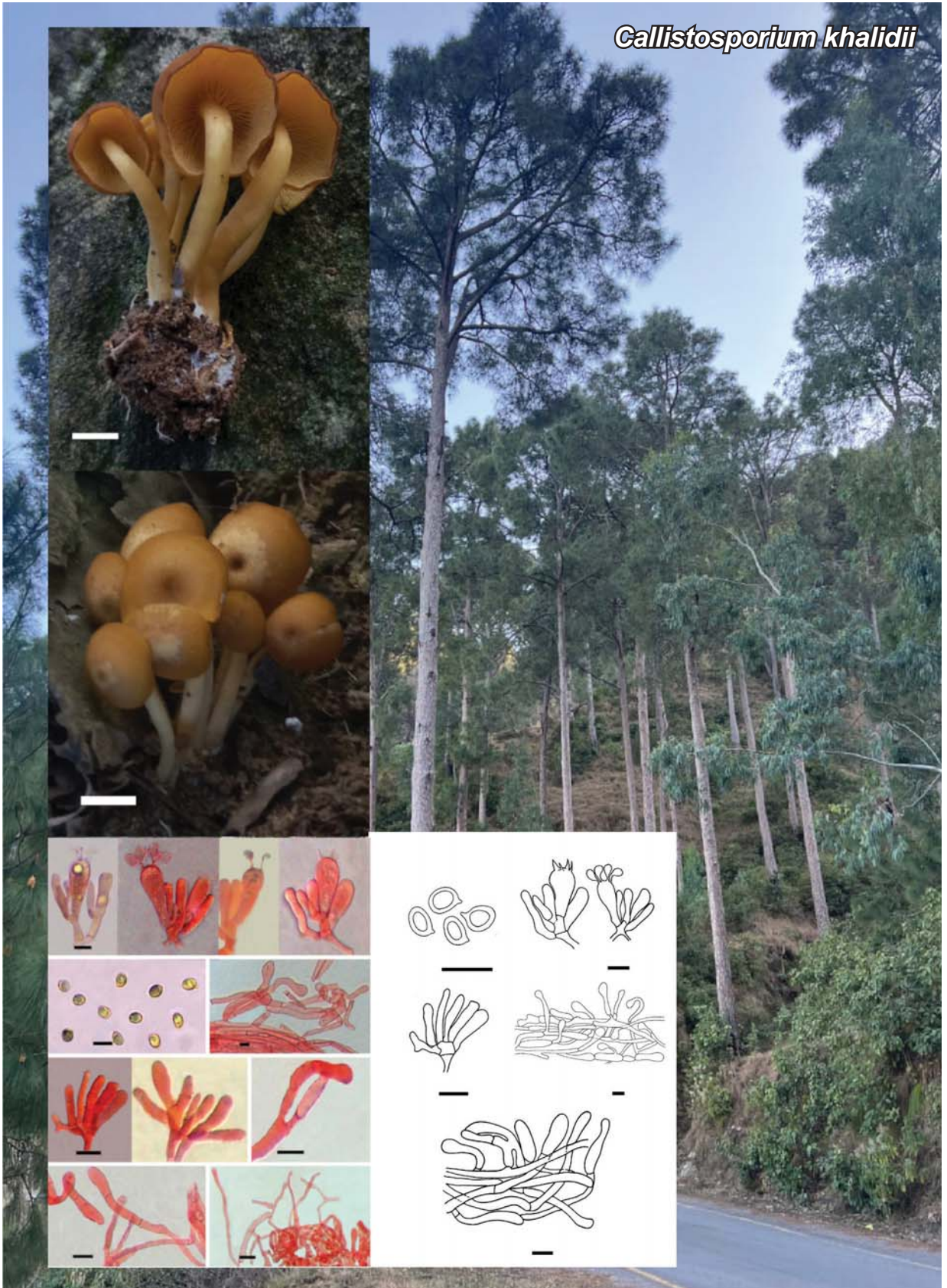
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*Callistosporium khalidii*





# *Callistosporium khalidii* S. Haroon, M. Haqnawaz, H. Ali, S. Sarwar & Afshan, *sp. nov.*

**Etymology:** The specific epithet “khalidii” (Latin) is named in honour of the distinguished mycologist, Prof. Dr Abdul Nair Khalid, in recognition of his significant contributions to fungal taxonomy in Pakistan.

**Classification:** *Callistosporiaceae*, *Agaricales*, *Agaricomycetes*.

**Basidiomata** small in size. *Pileus* 1.5–2.1 cm diam., pulvinate to parabolic, depressed, incurved margin, dull yellow orange at centre (10 YR 7/3; Munsell 1975), orange at margin (7.5 YR 6/6), smooth texture, entire, even or regulate margin of the cap. *Lamellae* short decurrent, narrow, tapering, sub distant, pale yellow (25 YR 8/4), even and entire margin of the gills, smooth, 1–2 tiers. *Stipe* 20–30 mm long and 2–4 mm wide, central, compressed to flexuous, pale yellow (7.5 Y 8/3), smooth; *volva* and *annulus* absent; *taste* and *odour* not distinctive. *Basidiospores* [30/1/7 (1.6–)1.8–2.7(–2.8) × (1.0–)1.1–1.8(–1.9) μm, avl × avw 1.4 × 2.2. Q 1.17–2.0, Qav 1.51, thin-walled, amygdaliform in side view, ellipsoid in front view, apiculate, guttulate, apiculate, smooth, hyaline with yellow to green guttule in 5 % KOH. *Basidia* (7.8–)8.3–24.1(–26.2) × (2.4–)2.5–5.9(–6.0) μm (avl × avw, 17.3 × 4.28), thin-walled, multi guttulate, 4 sterigmata, clavate to broadly clavate, cytoplasmic content hyaline while guttules appear greenish in 5 % KOH. *Cheilocystidia* (6.7–)7.4–13.0(–16.6) × (0.7–)0.9–1.8(–2.3) μm (avl × avw, 9.77 × 1.28), clavate, cylindrical, subcapitate and slightly flexuose with round apex, thin-walled, smooth, clamp connection present, hyaline in 5 % KOH. *Pleurocystidia* absent. *Hymenophoral trama* subregular to slightly divergent. *Pileipellis* 3.1–6.9 μm diam., interwoven, intricate trichoderm irregularly arranged, branched, thin-walled, septate, granulous pigments present, no clamp connection, capitate ends. *Pileocystediya* (9.0–)11.8–66.6(–67.8) × (1.4–)1.6–13.1(–14.6) μm (avl × avw, 25 × 4.99), pileus with scattered emergent terminal elements, cylindrical to slightly flexuose and narrowly clavate to long erect clavate, capitate to subcapitate apex, thin walled, hyaline in 5 % KOH. *Stipeipellis* 1.2–15.1 μm wide, thin-walled, irregularly arranged hyphae, septate, branched, intricate trichoderm capitate ends, dense granulous pigments present, no clamp connection, hyaline in 5 % KOH. *Caulocystidia* (7.8–)8.3–24.1(–26.2) × (2.4–)2.5–5.9(–6.0) μm (avl × avw, 43.5 × 10.6), cylindrical, capitate to subcapitate, ellipsoid, sphaeropedunculate, lecythiform, clavate, thin-walled, present on whole stipe, with rounded, capitate to subcapitate apex.

**Colour illustrations:** Pakistan, Azad Jammu and Kashmir, District Bhimber, Tehsil Samahni, 798 m a.s.l., humus soil, gregariously near the base of the trunk of fresh pine tree in coniferous forest. Basidiomata of *Callistosporium khalidii* in natural habitat; line drawings of basidia, basidiospores, cheilocystidia, pileus and stipe elements; basidiospores in 5 % KOH and Congo red. Scale bars: basidiomata = 10 μm; micromorphology = 5 μm.

**Habit, habitat and distribution:** Gregarious, in coniferous forest near rhizosphere area of conifer trees on soil rich in organic matter.

**Typus:** **Pakistan**, Azad Jammu and Kashmir, District Bhimber, Tehsil Samahni, 798 m a.s.l., humus soil, gregariously on rhizosphere area of pine trees in coniferous forest, Aug. 2024, S. Haroon SH56 (**holotype** LAH38566, ITS and LSU sequences GenBank PV093926 and PV105648).

**Additional material examined:** **Pakistan**, Azad Jammu and Kashmir, District Bhimber, Tehsil Samahni, 798 m a.s.l., humus soil, gregariously near rhizosphere of pine trees in coniferous forest, Sep. 2024, S. Haroon SH102, LAH38565, ITS and LSU sequences GenBank PV110979 and PV110980.

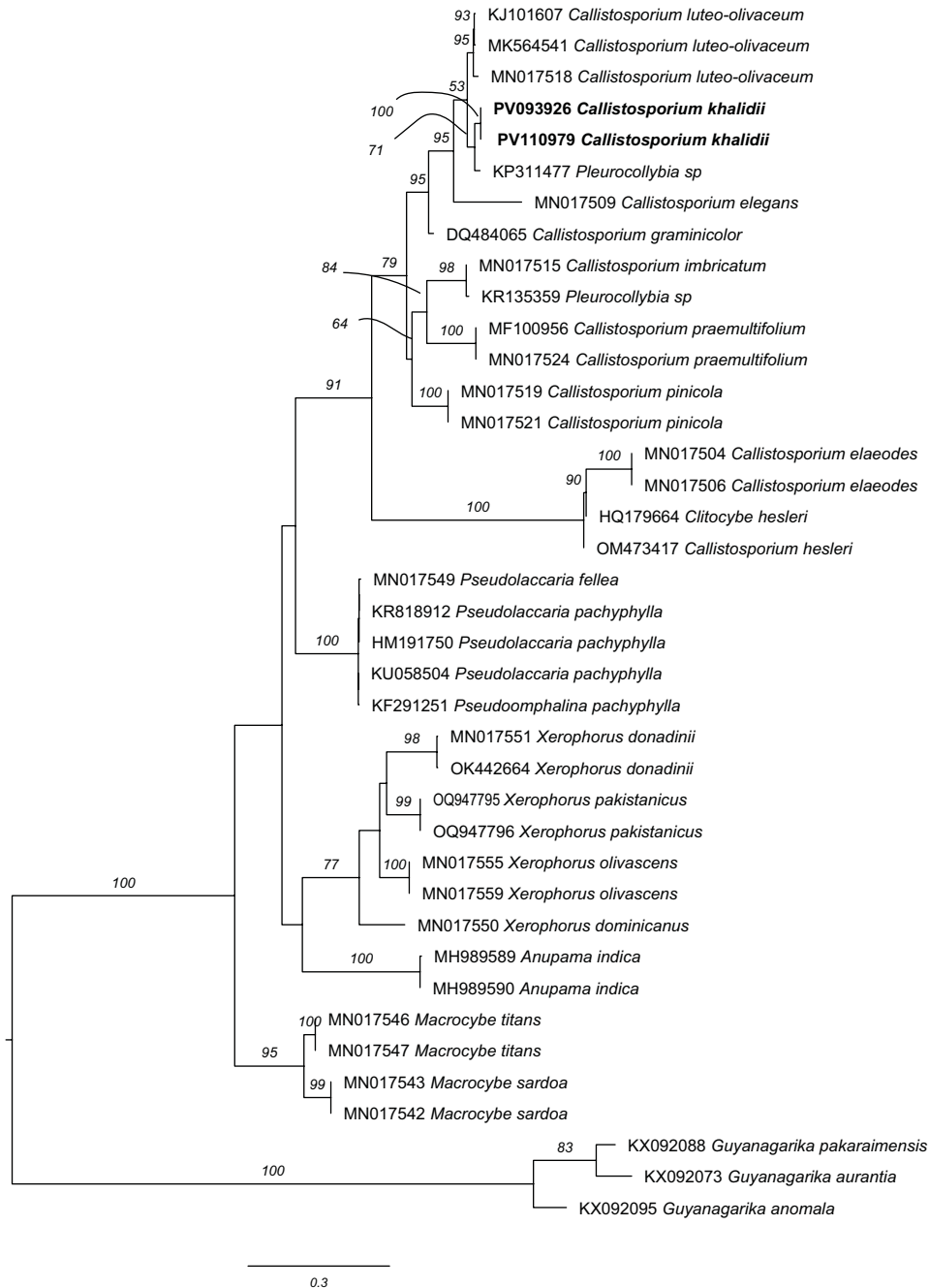
**Notes:** Morphological, anatomical, and phylogenetic analyses reveal that *C. khalidii* is closely related to *C. luteoolivaceum* (Italy), *C. graminicolor*, and *C. elegans* (Saba & Khalid 2014, Vizzini *et al.* 2020, Xu *et al.* 2021). *Callistosporium khalidii* forms a distinct clade with a high bootstrap support, distinguishing it from *C. luteo-olivaceum* found in Italy. Furthermore, it is characterized by a pulvinate to parabolic pileus with a depressed centre and incurved margins, smooth orange surface with a dull yellow orange centre, decurrent lamellae, central stipe, and amygdaliform spores in side view and ellipsoid in front view, av. 1.4–2.2 μm. Additionally, it possesses capitate to subcapitate, ellipsoid, sphaeropedunculate, lecythiform caulocystidia. In contrast, *C. luteo-olivaceum* reported from the USA exhibits a slightly hemispherical, convex to flat-convex pileus with straight, striate margins, velutinous, yellowish brown to olive brown surface, emarginated, ventricose lamellae, eccentric stipe, and ellipsoid spores adaxially flattened in side view, av. 3.7–5.5 μm, as well as lageniform, sometimes flexuose, bilobed caulocystidia (Moser 1986, Martin 2012, Vesterholt & Holec 2012, Saba & Khalid 2014, Jančovičová *et al.* 2016, Picciola & Zugna 2017). *Callistosporium graminicolor* differs from *C. khalidii* because of its larger spores (6.0–8.0 × 4.0–5.5 μm) (Vizzini *et al.* 2020, Kaygusuz & Demirak 2022). *Callistosporium elegans* is another closely related species reported from Belize, is distinguished from our taxon by its hemispheric to broadly convex pileus with inrolled margin, maroon or brick red, sulcate-striate cap of margin, glabrous but granulose at the centre, and hygrophanous pileus, adnate, sinuate or sub-arcuate-decurrent lamellae, ellipsoid to ovoid large spores, av. 3.3 × 4.9 μm and subcapitate to bilobed cheilocystidia (Desjardin & Perry 2017).

A BLAST analysis revealed that the ITS sequences exhibited 97.39 % similarity with *Pleurocollybia* sp. (GenBank KP311477, unpublished), while the LSU sequences displayed 99.11 % similarity with *Pleurocollybia* sp. (GenBank KP311402, unpublished). For the phylogenetic analysis, a dataset of 36 ITS sequences, including *Guyanagarika pakaraimensis* (GenBank KX092106), *Guyanagarika aurantia* (GenBank KX092073), and *Guyanagarika anomala*

(GenBank KX092095) as outgroups, was assembled. The LSU dataset comprised 29 sequences retrieved from GenBank, with *Guyanagarika pakaraimensis* (GenBank KX092106) serving as an outgroup. In the phylogenetic analysis, the ITS tree indicated that our sequences formed an independent clade with *Pleurocollybia* sp. (GenBank KP311477), with strong bootstrap support. Similarly, the LSU

tree demonstrated that our sequences formed an independent clade with *Pleurocollybia* sp. (GenBank KP311402), also with strong bootstrap support.

*Supplementary material:* <https://figshare.com/s/adb79f06bf207a50489a> (phylogenetic tree).



The concatenated ITS dataset was analysed using the RAxML-HPC2 v. 8.2.10 tool on the XSEDE platform within CIPRES Gateway v. 3.1 (Miller *et al.* 2010, Stamatakis 2014). This analysis incorporated 1000 bootstrap replicates and employed the GTR + Gamma substitution model. The resulting tree was visualized using FigTree v. 1.4.2 (Rambaut 2014). The novel species is shown in **bold** font.



*Clavulus hemisphaericus*



***Clavulus* A. Mateos, De la Peña-Lastra & Olariaga, *gen. nov.***

*Etymology:* The epithet refers to the small clove-like shape of the basidiomata.

*Classification:* *Clavariaceae*, *Agaricales*, *Agaricomycetes*.

*Basidiomata* clavarioid, reminiscent of craterelloid or physalacrioid forms. *Fertile part* solid, with hymenium covering the upper surface. *Stipe* central, smooth, and translucent when wet. *Surface* white, pubescent, drying pale yellow. *Context* thin, indistinct *taste* and *odour*. *Spores* globose to broadly ovoid, hyaline, with a prominent apiculus. *Basidia* cylindrical-clavate, clampless. *Hymenium* with irregular crystallized deposits. *Leptocystidia* pyriform to clavate, immersed; *gloeocystidia* obovoid, scattered. *Hyphal system* monomitic, dextrinoid in Melzer's reagent. *Ecology* gregarious, associated with decaying wood in forested areas.

*Type species:* *Clavulus hemisphaericus* A. Mateos, De la Peña-Lastra & Olariaga

*Notes:* The new genus *Clavulus* is nested within *Clavariaceae* in the combined analyses inferred from the nr5.8S, nrLSU (28S), nrSSU (18S), *RPB1*, *RPB2* and *TEF1* regions, holding a position basal to the genus *Clavulinopsis* (see Supplementary material). Additionally, megablast searches in NCBI's GenBank nucleotide database retrieve as closer hits sequences attributed to *Clavariaceae* and especially *Clavulinopsis*. *Clavulus* differs from *Clavulinopsis* in having reduced clavarioid basidiomata with a claviform fertile part, the absence of clamps – basidiomata are devoid of clamps in *Clavulinopsis*, always have 2-spored basidia and are derived from a parthenogenetic reproduction mode –, presence of cystidia and crystallized deposits among contextual hyphae.

MB 857873

***Clavulus hemisphaericus* A. Mateos, De la Peña-Lastra & Olariaga, *sp. nov.***

*Etymology:* The epithet refers to the form of the capitulum, which is regularly hemispherical.

*Basidiomata* gregarious, clavarioid, reminiscent of craterelloid or physalacrioid basidiomata, unbranched, small-sized, 0.8–2.6 mm high. *Fertile part* as a hemispherical head, 0.2–1.2 mm diam., solid, with the hymenium covering the upper convex surface, with an inrolled margin, regular at first and then somewhat wavy, the lower concave part sterile, formed by folds or low veins, irregular and distant. *Stipe* central, gradually broader towards the apex and fusing with the fertile part, with the smooth part until 3/5 of its height, 0.3–1.2 mm high, terete in section 0.04–0.08 mm broad. The stipe surface is smooth or slightly pruinose, generally white, but the stipe is translucent when wet, pubescent and slightly grey; upon drying pale yellow and reddish brown tones appear at the stipe apex. *Context* exiguous, concolourous to cutis, without distinct *taste* and *odour*. *Basidiospores* (4.9–)5.1–5.5–5.7(–6.7) × (4.7–)4.9–5.3–5.7(–6.5) µm; Q = 1–1.05–1.09(–1.1); N = 30; Ve = 80 µm<sup>3</sup>, globose to subglobose, broadly ovoid to fig-shaped, with a large yellowish greenish guttule, with a prominent apiculus of up to 1.7 × 1.2 µm, hyaline, without iodine reactions, congophilous. *Basidia* 18–39 × 5–6.5 µm, (2–)4-spored, cylindrical-clavate, with sterigmata of

up to 4 µm long, clampless. *Hymenium* and *subhymenium* with abundant, amorphous, irregular, crystallized deposits among hyphae, sometimes, bipyramidal or baculiform and concentrically striate. *Leptocystidia* (10.9–)21.5–27.0(–32.7) × (5.5–)5.54–7.5(–8.0) µm, pyriform to clavate, immersed; *gloeocystidia* scattered in the hymenium, obovoid to sphaeropedunculate, 16.3–21.9 × (8.2–)10.3–12.9(–13.8) µm. *Hyphal system* monomitic, formed by generative hyphae, subparallel-arranged, 3–5 µm broad in the stipe context, dextrinoid in Melzer's reagent, with oily guttules and abundant crystals, clampless.

*Distribution:* Currently known only from the type location in Madeira.

*Typus:* **Portugal**, Madeira, Ribeira da Janela, Fanal, N32°48'55.9", W17°08'54.2", 1100 m a.s.l., gregarious, on mossy slopes and under *Laurus* leaf litter in laurel forests, 11 Nov. 2021, A. Mateos & S. De la Peña-Lastra (**holotype** AMI-SPL891; ITS2 and LSU sequences GenBank PV211422 and PV211426).

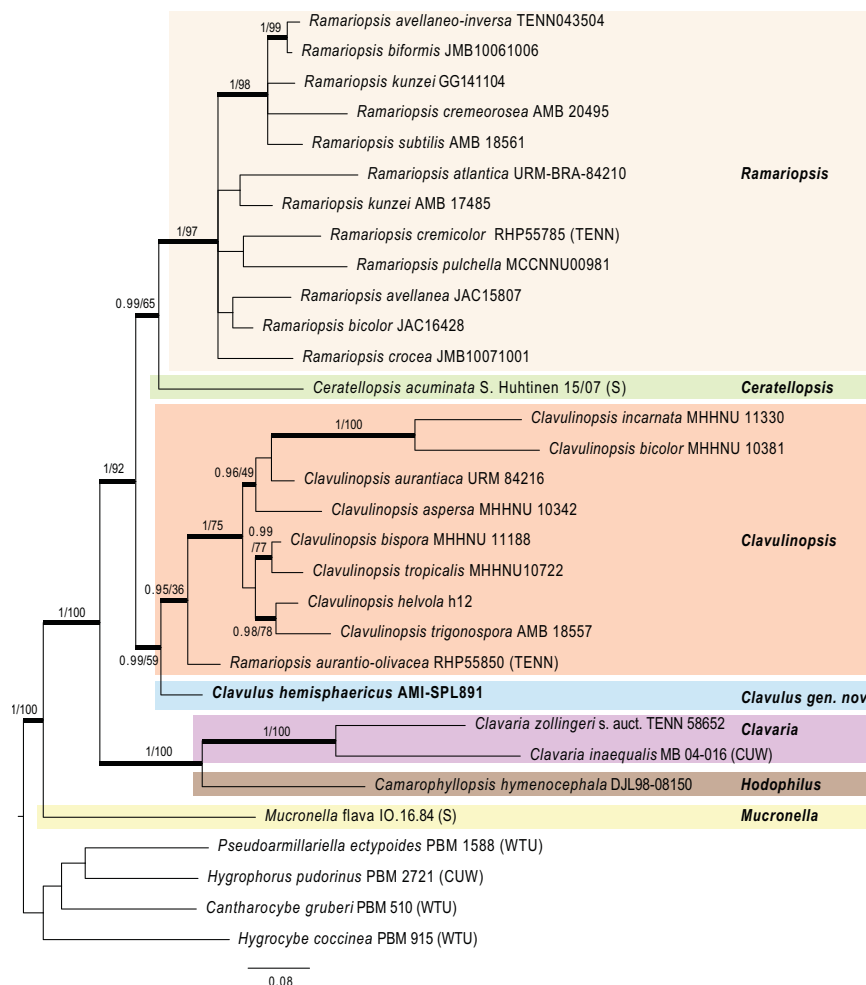
*Notes:* *Clavulus hemisphaericus* does not fit in any described genus within the *Clavariaceae*, within which it belongs according to our multigene analyses. Other genera with reduced clavarioid basidiomata are *Ceratellopsis* and *Hirticlavula*. The former, *Ceratellopsis*, differs in the spear-shaped basidiomata with a sterile apex, smaller non-globose spores, absence of cystidia and presence of clamps (Olariaga *et al.* 2020). Furthermore, sequences of *C. hemisphaericus* did not show affinity to the sequences of the type of *Ceratellopsis*, *C. acuminata*. The latter, *Hirticlavula*, with its only species *H. elegans* is characterized by a narrowly claviform fertile part, a stipe furnished with long septate hairs and its LSU sequence nests sister to *Clavaria* (Petersen *et*

*Colour illustrations:* Portugal, Azores, Terceira, Ribeira da Janela, Fanal, forest of *Laurus novocanariensis*, where the holotype of *Clavulus hemisphaericus* was collected. Left column: basidiomata of the holotype. Right column: upper photo shows basidiospores (H<sub>2</sub>O in right, IKI-2 in left); middle photo is a section of the fertile part (left, H<sub>2</sub>O), trama hyphal system (middle, IKI-2) and section of basidiomata rehydrated (right, H<sub>2</sub>O); and the bottom photo is basidia and hymenophore (upper, H<sub>2</sub>O), leptocystidia and gloeocystidia (bottom and right, IKI-2), crystals (bottom and right). Scale bars: basidiomata (rehydrated) = 500 µm; hymenial section (upper) = 100 µm; hymenial section (bottom) = 50 µm; all others = 10 µm.



al. 2014). The phylogenetically closest genus to *Clavulus* is *Clavulinopsis* (see Supplementary material), to which *Clavulus* is basal and together form a monophyletic clade (BPP 1). Including *Clavulus* in *Clavulinopsis* would require a profound emendation of *Clavulinopsis* – as circumscribed by Corner (1950), Petersen (1968) and subsequent authors – for it to include a species with reduced and claviform basidiomata, without clamps and with cystidia. Considering this, the decision of accommodating *Clavulus hemisphaericus* in a separate genus is rendered more appropriate and useful for the mycological community. *Clavaria*, another genus with clampless hyphae, differs like *Clavulinopsis* in comprising species with larger cylindrical to narrowly claviform basidiomata and devoid of cystidia. *Clavicornia*, allied to the *Clavaria* s. lat. clade, is reminiscent of *Clavulus* because of its apically truncated basidiomata, but its species have cystidia and bear scattered clamps at basidia. *Alloclavaria*, devoid of clamps and producing cystidia, differs

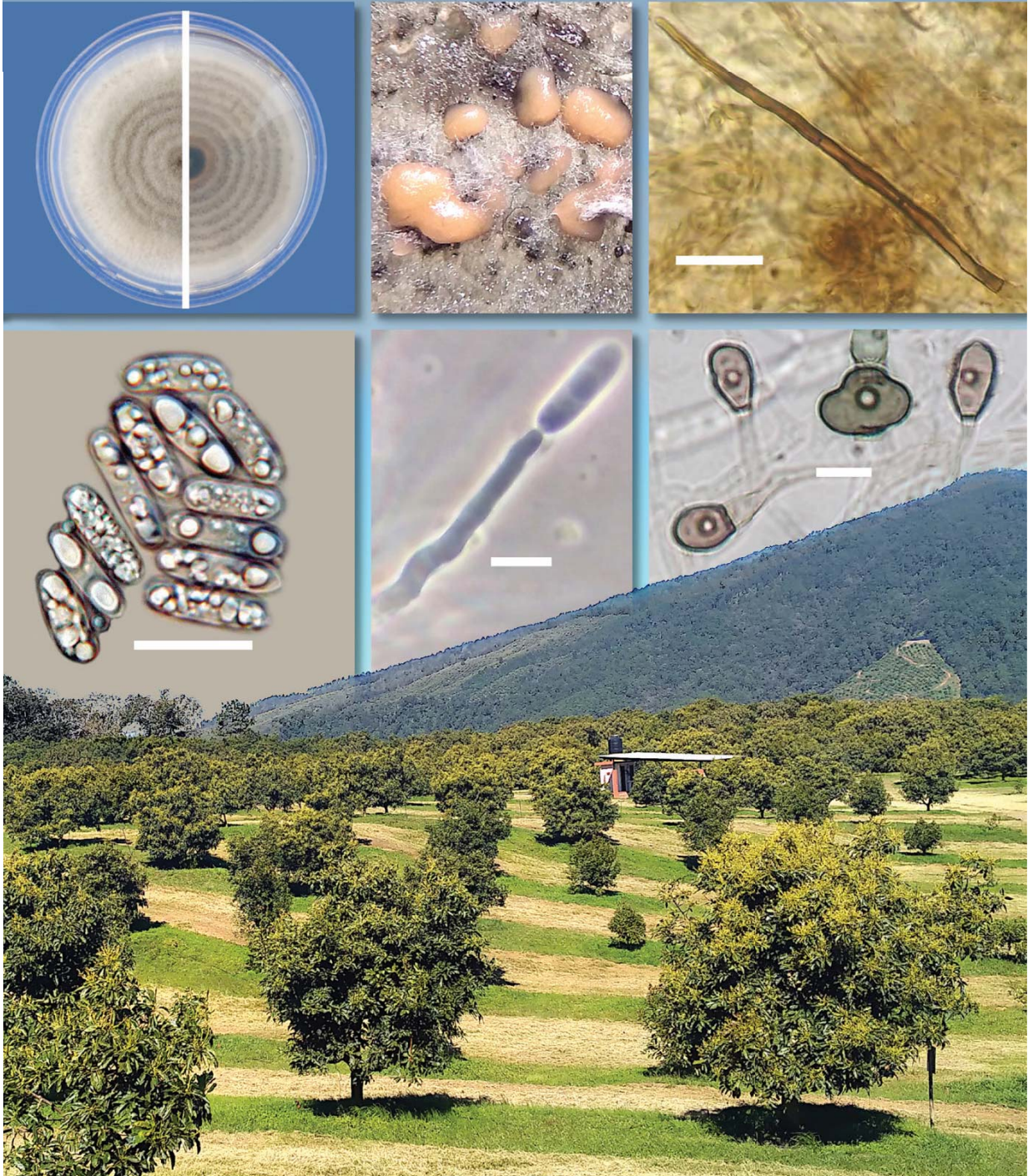
in its cylindrical basidiomata and belongs furthermore to the *Hymenochaetales* (Dentinger & McLaughlin 2006). Species of *Physalacria*, producing vaguely similar basidiomata with cystidia, have clamp connections and belong outside the *Clavariales*. Blast searches using ITS and LSU sequences retrieve as closest matches sequences from several species of *Clavulinopsis* and *Ramariopsis*. Closest matches with ITS sequences identified to species level are *Ramariopsis crocea* (87.32 %, GenBank MK607557) and *Clavulinopsis corallinorosacea* (86.58 %, GenBank KP257144), whereas closest matches with LSU sequences identified to species level are *Clavulinopsis bispora* (96.41 %, GenBank NG\_242117.1) and *Clavulinopsis corallinorosacea* (96.20 %, GenBank HQ877707). Nevertheless, all species placed in *Clavulinopsis* and *Ramariopsis* have larger clavarioid basidiomata, possess clamps and lack cystidia. Considering all this, we consider the description of a new genus and species to be justified. **Supplementary material:** doi: 10.6084/m9.figshare.28870169 (Alignment); 10.6084/m9.figshare.28870376 (table).



Best tree of the Maximum Likelihood analysis in IQ-TREE 1.16.12 (Nguyen *et al.* 2015) of selected sequences of *Clavariales* from a concatenated dataset of the 5.8S-28S-18S-*RPB1*-*RPB2*-*TEF1*-regions. Maximum Likelihood standard bootstrap support values (ML-Boot)/Bayesian posterior probabilities (PP) are shown on branches, ordered as ML-UFBoot/PP. Thickened branches received support in both analyses (ML-Boot ≥ 70 % and/or PP ≥ 0.95). Values are provided for nodes supported at least in one analysis. Genera are indicated by vertical bars.

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*Colletotrichum mexicanus*





# *Colletotrichum mexicanus* A.S. Pérez-Méndez, M.J. Yáñez-Morales & A.J. Hernández, *sp. nov.*

**Etymology:** The name refers to the location, México state, Mexico, from where this species was collected.

**Classification:** *Glomerellaceae*, *Glomerellales*, *Sordariomycetes*.

**Sexual morph** not observed. **Asexual morph** on 2 % potato dextrose agar (PDA). **Vegetative hyphae** 2–6 µm diam., hyaline to brownish, smooth-walled, septate, branched. **Conidiomata** acervular. **Setae** moderately observed, medium brown, some setae pale brown toward the tip and base, smooth-walled and thick-walled, 40–109 µm long, 1–3(–4)-septate, base rarely inflated, 4–7 µm diam., tip rounded and rarely producing a conidium. **Conidiogenous cells** hyaline, smooth-walled, cylindrical, 10–22(–29) × 2–4 µm, opening 1 µm diam. **Conidia** hyaline, smooth-walled, aseptate, straight, oblong to cylindrical, apex rounded and base slightly narrowing to truncate hilum, hilum sometimes slightly visible, cytoplasm guttulate, often with two large polar guttules, sometimes also one in the centre, or guttules dispersed along the cytoplasm, 15–20(–29) × 4–6(–7) µm (av. ± SD = 17 × 5 µm ± 1.5 × 0.7), L/W ratio = 3.5. **Appressoria** (on slide culture from conidia) single, pale brown and medium brown, subglobose, ellipsoid, clavate, with entire or slightly undulate margin, (7–)9–17 × 5–8 µm in 5 d (av. ± DS = 12 ± 3.1 × 6 ± 0.9).

**Culture characteristics** (fluorescent white light/near UV 12 h photoperiod, 20 °C after 10 and 20 d; colony diam range was determined in triplicate plates): Colonies on 2 % PDA: margin entire and whitish, aerial mycelium dense-cottony with tufts, pale mouse grey to slightly olivaceous, with dark zonations, centre whitish, conidia in mass under aerial mycelia pale salmon (colony-centre and at the margin), reverse blackish in the centre, olivaceous with dark zonations towards the margin; growth diam. 62–68 mm in 10 d. On oatmeal agar (OA): entire margin, aerial mycelium sparse, surface with whitish and slightly olivaceous sections, reverse whitish; growth diam. 72–73 mm in 10 d, conidia in mass pale salmon, rarely observed. On synthetic nutrient-poor agar (SNA) with filter paper: colonies with slightly raised hyphae and with undulate margin, moderate whitish aerial mycelium, and pale mouse grey zonations, reverse whitish; growth diam. 58–61 mm in 10 d, and few light salmon conidia mass in the centre of the SNA colony; on filter paper no conidia mass observed, only pale mouse grey moderate to abundant aerial mycelium and immersed blackish structures. On SNA with pine needles: flat with entire margin, sparse whitish aerial mycelium, reverse whitish; growth diam. 79 mm in 10 d; and on pine needles

abundant acervuli and large pale orange conidia masses. After 20 d, colony growth diam. 85 mm on the four cultures (OA, PDA, SNA with filter paper and SNA with pine needles).

**Typus:** **Mexico**, Santiago Cuautlalpan, state of México, 19.42N, -98.90W, 2253 m a.s.l., healthy pulp in fruit of *Persea americana* cv. Hass (*Lauraceae*), 19 Mar. 2021, A.S. Pérez-Méndez (**holotype** CMPH 235, culture ex-holotype CP CC040 = CP-766; ITS, *act*, *chs-1*, *gapdh*, and *tub2* sequences GenBank OQ969851, OR123421, PP271387, OR734201, and OR241008).

**Additional materials examined:** **Mexico**, Santiago Cuautlalpan, state of México, 19.42 N, -98.90W, 2253 m a.s.l., healthy pulp in fruit of *P. americana* cv. Hass (supermarket fruit), 29 Mar. 2021, A.S. Pérez-Méndez, cultures CP CC041 (= CP-767), CP CC042 (= CP-769) and CP CC043 (= CP-773); ITS, *act*, *chs-1*, *gapdh*, and *tub2* sequences GenBank OQ969852, OR241014, PP271388, OR734202, and OR241009; OQ969853, OR241015, PP271389, OR734203, and OR241010; OQ969854, OR241016, PP271390, OR734204, and OR241011, respectively; Uruapan, state of Michoacan, 19.42N, -101.78W, 1907 m a.s.l., symptomatic pulp in fruit of *P. americana* cv. Hass (plantation), 3 Jul. 2021, A.S. Pérez-Méndez, cultures CP CC044 (= CP-820) and CP CC045 (= CP-828), ITS, *act*, *chs-1*, *gapdh*, and *tub2* sequences GenBank OQ969855, OR123422, PP271391, OR734205, and OR241012; OQ969856, OR123423, PP271392, OR734206, and OR241013, respectively.

**Notes:** The phylogenetic analysis indicates that *C. mexicanus* is most closely related with isolates of an undescribed *Colletotrichum* sp. (CPO 27.941, CPO 27.1007, and CPO 27.1010) isolated from preharvest avocado fruit (*P. americana*) with anthracnose symptoms in México (Fuentes-Aragón *et al.* 2020). Another isolate (Q026), was less closely related to *C. mexicanus*. Furthermore, morphologically, *C. mexicanus* conidia were larger (av. = 17 × 5 µm) than those of the *Colletotrichum* sp. isolate Q026 from Andean blackberry in Colombia (Afanador-Kafuri *et al.* 2014). *Colletotrichum pyriformiae*, a species isolated from pear leaves and fruit in China (Fu *et al.* 2019) was the least strongly related to *C. mexicanus* and also differed morphologically. *Colletotrichum mexicanus* strains did not form sexual morphs in culture (PDA, OA, SNA) whereas *C. pyriformiae* did (same incubation conditions) (Fu *et al.* 2019). On PDA and OA, the conidia of *C. mexicanus* were smaller [(12–)13–18(–19) × 4–6(–7) µm and (13–)14–18(–21) × 3–5(–6) µm, respectively] than those of *C. pyriformiae* (14–23 × 5.5–7 µm and 15.5–21.5 ×

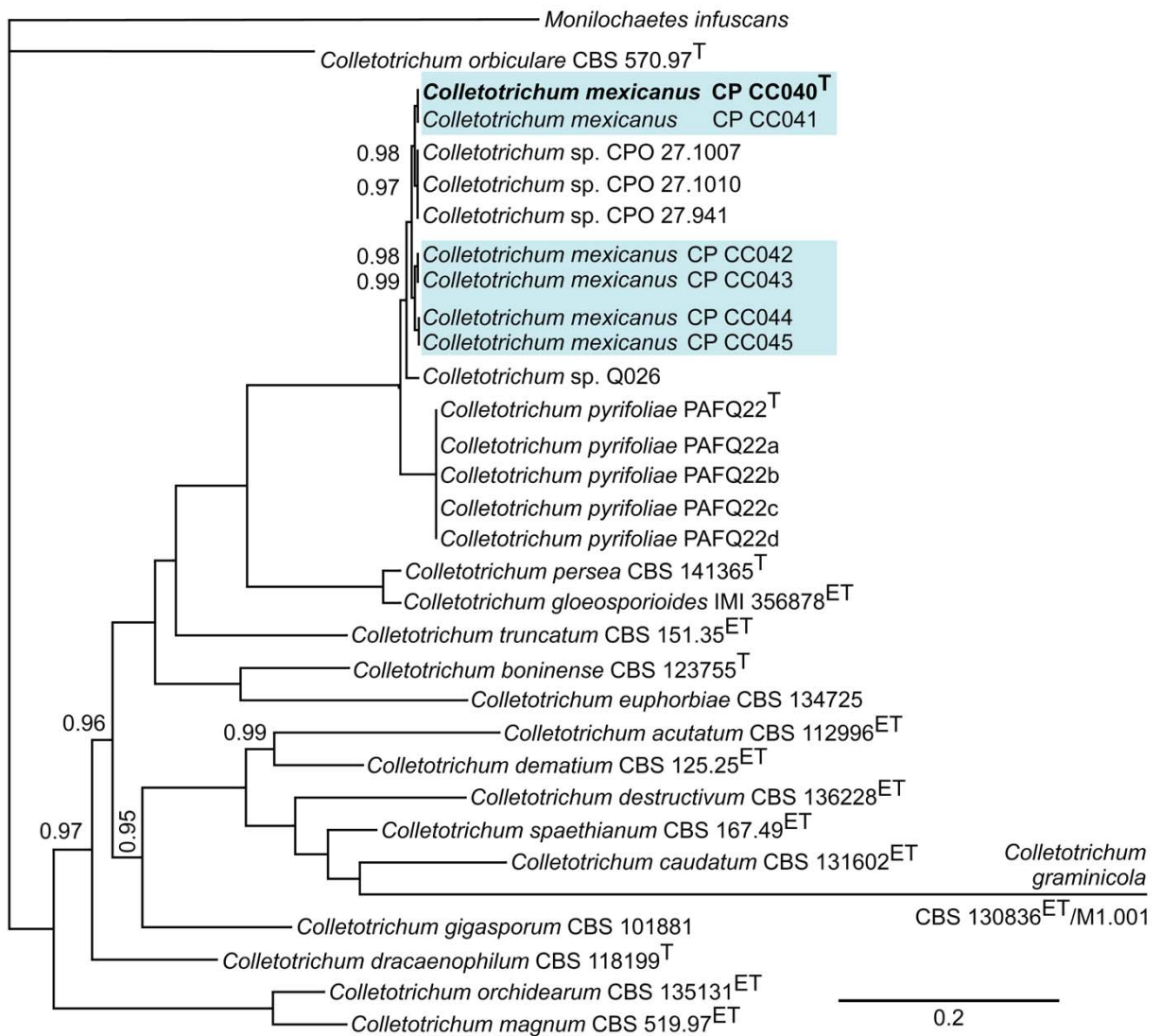
**Colour illustrations:** *Persea americana* cv. Hass flowering plantation in Uruapan, Michoacán, Mexico. Colony surface and reverse on 2 % PDA; conidiomata; setae; guttulate hyaline conidia; conidiogenous cell giving rise to conidia; appressoria. Scale bars: setae and conidia = 20 µm; conidiogenous cell = 5 µm; appressoria = 10 µm.

5–6.5 µm, respectively) (no conidial formation was observed on SNA with *C. mexicanus*, while *C. pyriformis* formed conidia on SNA) (Fu *et al.* 2019).

A megablast search of the NCBI GenBank nucleotide database with six sequences of *Colletotrichum mexicanus* (CP CC040 to CP CC045) generated the following BLASTn results. The closest hits using ITS sequences showed the highest similarity to four unnamed *Colletotrichum* strains CPO 27.941, CPO 27.1007, and CPO 27.1010, and Q026 (GenBank MN744300, MN744301, MN744302, and JN715839, respectively); Identity values (range) of the six *C. mexicanus* sequences were 554–575/555–577 (99–100 %), 550–563/551–565 (99–100 %), 547–568/548–570 (99–100 %), and 534–572/536–573 (99–100 %), with no gaps. The lower similarity to *Colletotrichum pyriformis* (ex-type strain PAFQ22, GenBank NR\_160840); Identity range, 518–526/523–530 (99 %), one gap (0 %). The closest hits using the *act* sequence were highest in similarity to unnamed *Colletotrichum* strain Q026, and strains CPO 27.1007, CPO 27.941, and CPO 27.1010 (GenBank KC859970, MN746535, MN746534, and MN746536, respectively); identity value ranges were 274–284/275–285 (99 %), 263–274/263–274 (100 %), 263–269/263–269 (100 %), and 262–263/262–263 (100 %), with no gaps. The lower similarity to *Colletotrichum pyriformis* (ex-type strain PAFQ22, GenBank MG747768); Identity = 243/251 (97 %), two gaps (0 %). The closest hits generated using the *chs-1* sequence were highest in similarity to unnamed *Colletotrichum* strains CPO 27.941, CPO 27.1007, and CPO 27.1010, and strain Q026 (GenBank MN746563, MN746564, MN746565, and KC859995, respectively); Identity values were 298/299

(99 %), 289/290 (99 %), 287/288 (99 %), and 287/291 (99 %) respectively; zero and one gap (0 %). The lower similarity to *Colletotrichum pyriformis* (ex-type strain PAFQ22, GenBank MG747914); Identity = 233/292 (98 %), with no gaps. The closest hits generated using the *gapdh* sequence were highest in similarity to unnamed *Colletotrichum* strains CPO 27.941, CPO 27.1007, and CPO 27.1010, and strain Q026 (GenBank MN737360, MN737361, MN737362, and KC860013, respectively); Identity value ranges were 251–255/257–261 (98 %), 248–252/254–258 (98 %), 247–251/253–257 (98 %), and 251–252/257–261 (96–98 %) respectively; zero and four gaps (0–1 %). The lower similarity to *Colletotrichum pyriformis* (ex-type strain PAFQ22, GenBank MG747996); Identity = 208–209/230–234 (89–91 %), three and seven gaps (1–2 %). The closest hits generated using the *tub2* sequence were highest in similarity to unnamed *Colletotrichum* strains CPO 27.941, CPO 27.1010, and CPO 27.1007, and strain Q026 (GenBank MN848375, MN848377, MN848376, and KC860039, respectively); Identity value ranges = 718–753/718–753 (100 %), 714–746/714–746 (100 %), 709–741/709–741 (100 %), and 431/437 (99 %), no gaps. The lower similarity to *Colletotrichum pyriformis* (strain PAFQ22d, GenBank MG874845); Identity = 475/488 (97 %), no gaps.

*Supplementary material:* doi: 10.6084/m9.figshare.28226306 (table, alignment and tree were deposited at figshare.com).



Bayesian phylogenetic analysis of the combined ITS, *act*, *chs-1*, *gapdh* and *tub2* sequences alignments of *Colletotrichum mexicanus*. Bayesian posterior probability (pp  $\geq$  0.90) values are indicated at the nodes. Culture collection numbers are indicated for all species and GenBank accession numbers in the supplementary table. *Monilochaetes infuscans* (CBS 869.96) was the outgroup and the novelty described highlighted with coloured block and the type specimen with **bold** font. Twenty-five strains of *Colletotrichum* spp. and the outgroup were included. The tree was constructed with MrBayes v. 3.2 software (Ronquist *et al.* 2012), and the Mesquite v. 3.7 software (Maddison & Maddison 2021) was used to view and edit the matrices. A Bayesian analysis using the General Time Reversible model was selected, with likelihood parameters settings number of substitution types (nst = 6), with a proportion of sites invariable and the rest drawn from the gamma distribution (rate = invgamma) with 2 M generations sampled every 100 generations. The first 250000 generations were discarded as the chains were converging (burn-in period). The scale bar shows the number of expected changes per site. T (ex-holotype) and ET (ex-epitype) (superscript) = type strains used in this analysis.

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*Coniochaeta corticalis*





## *Coniochaeta corticalis* R. Hoffmann & Riebesehl, *sp. nov.*

**Etymology:** Named after the substrate, bark humus for horticultural use.

**Classification:** *Coniochaetaceae*, *Coniochaetales*, *Sordariomycetes*.

*Conidiogenous cells* formed directly on hyphae, ampulliform, constricted base. *Conidia* solitary, aseptate, hyaline, smooth-walled, ellipsoidal, apex obtuse, 2.5–3.9 × 1.9–2.7 μm (av. 3.3 × 2.3 μm). *Hyphae* hyaline, septate, smooth-walled. *Chlamydospores* absent.

**Culture characteristics:** Colonies on potato dextrose agar flat, with aerial hyphae and folded surface, margins irregular, reaching 78 mm diam. after 57 d at room temperature (approx. 22 °C) with natural dark light cycle. Surface dark reddish brown to black with white aerial hyphae, surface dull, reverse dark reddish brown to black (colours after Rayner 1970).

**Typus:** **Germany**, Lower Saxony, Braunschweig, 52°16'37"N, 10°33'53"E, 80 m a.s.l., isolated from horticultural substrate consisting of bark humus (mainly from *Abies* sp., *Picea* sp. and *Pinus* sp. (*Pinaceae*), 14 Jun. 2023, F.F. Soliz Santander (**holotype** JKI-GP-23-050, culture ex-type DSM 119705, ITS, LSU, *TEF* and TUB2 sequences GenBank PV272673, PV259250, PV287720 and PV287716).

**Notes:** Based on the ITS alignment phylogenetic analysis, the closest phylogenetic neighbours are *Coniochaeta lignicola* (GenBank NR\_111520; difference = 0.42 %), *C. velutina* (GenBank GQ154544; difference = 1.06 %), *C. weberae* (GenBank PV272675; difference = 0.84 %), *C. luteoviridis* (GenBank NR\_154769; difference = 1.27 %) and *C. mutabilis* (GenBank NR\_111519; difference = 1.27 %).

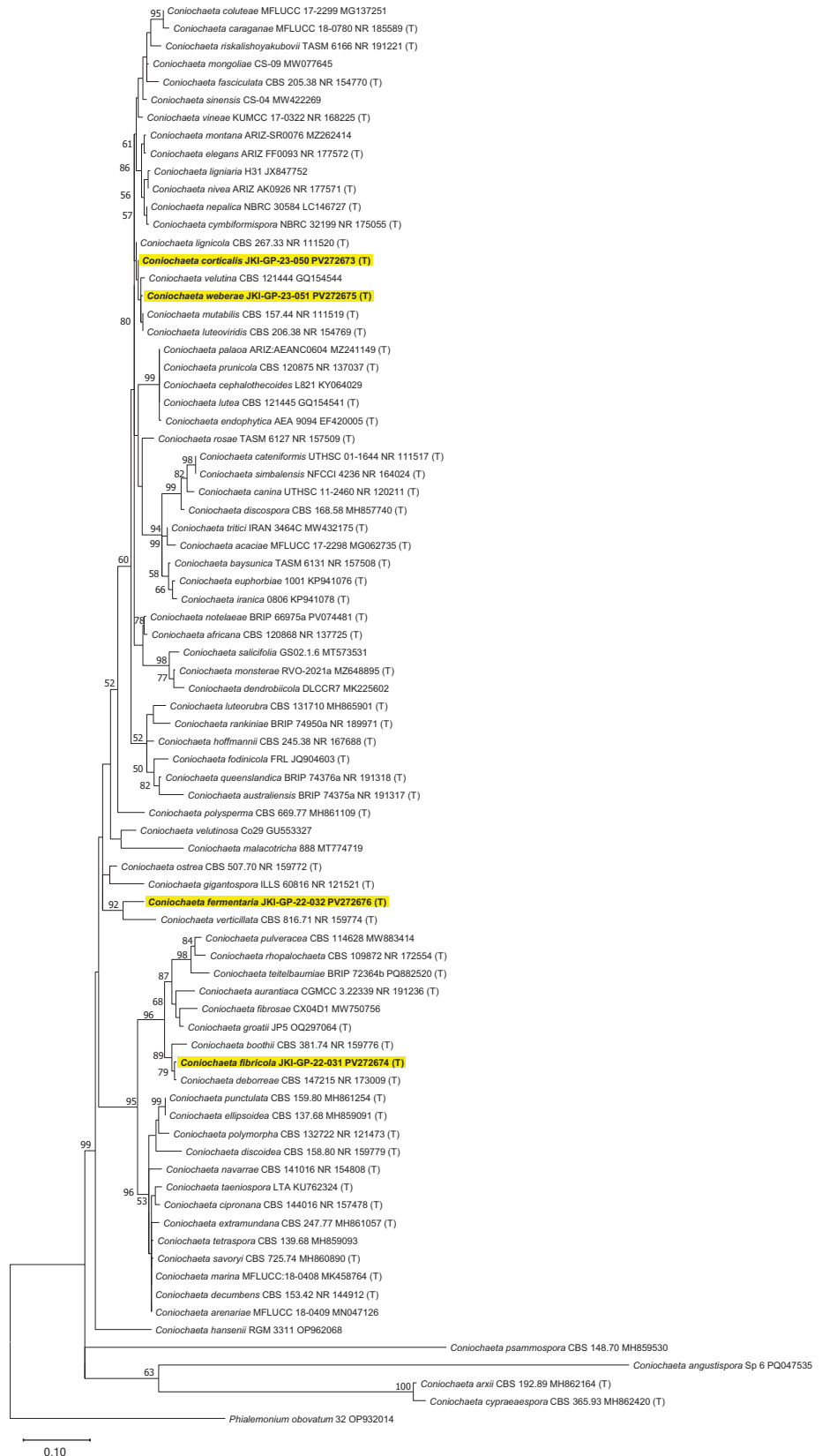
*Coniochaeta corticalis* is morphologically characterised by dark reddish brown to black colonies with white aerial hyphae and a folded surface on the agar plate. As these characteristics are also present in several other species in *Coniochaeta*; the morphological comparison of the closest species is based on conidial morphology. Although the shape of the conidia is similar in *C. corticalis* and the closest relatives, the sizes differ. The conidia from *C. lignicola* and *C. velutina* are longer and narrower (*C. lignicola* = 3–4.5 × 1.5–2 μm; *C. velutina* = 3.5–6 × 1.2–2 μm), and longer from *C. luteoviridis* and *C. mutabilis* (*C. luteoviridis* = 4.5–7 × 1.8–2.5 μm; *C. mutabilis* = 4–6 × 1.5–2 μm). In addition, chlamydospores are present in *C. mutabilis* and *C. luteoviridis* (Weber 2002) and absent in *C. corticalis*. A comparison of the morphological features of *C. corticalis* with all other *Coniochaeta* species without online available DNA sequences show also no matches.

**Supplementary material:** doi: 10.6084/m9.figshare.28590347 (alignment).

**Colour illustrations:** Greenhouse and the substrate from which the fungus was isolated. Colony on PDA agar; hyphae with conidiogenous cells; conidia. Scale bars = 10 μm.

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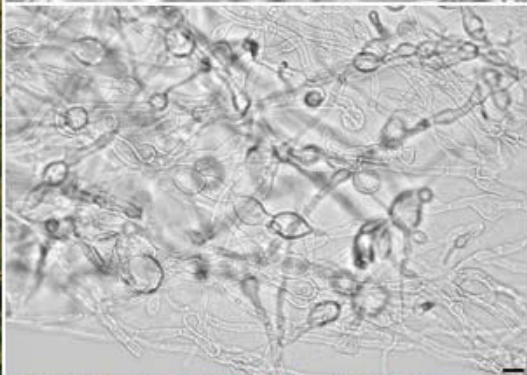
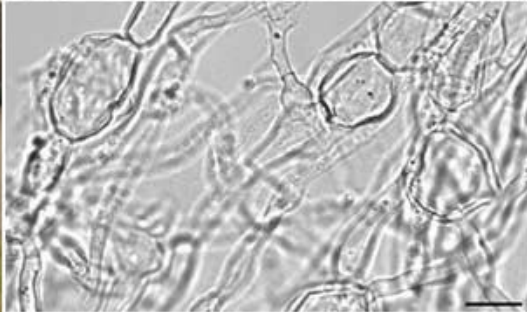
F.F. Soliz Santander & J. Riebesehl, Julius Kühn Institute, Institute for Plant Protection in Horticulture and Urban Green, Messeweg 11-12, 38104, Braunschweig, Germany; e-mail: fabianfabriciosoliz@gmail.com & janett.riebesehl@julius-kuehn.de



Maximum Likelihood tree obtained by analysis of ITS sequences from *C. corticalis*, *C. fermentaria*, *C. fibricola*, *C. weberae* (bold, yellow) and other *Coniochaeta* species, based on available sequences from GenBank. Phylogenetic analysis was conducted in MEGA v. 11 (Tamura *et al.* 2021) using the K2+G+I model suggested by the MEGA v. 11 model selection tool with 95 % site coverage cutoff, partial deletion for gap treatment and 1000 bootstrap replications. The underlying alignment was calculated by MAFFT v. 7 (Katoch *et al.* 2019) using the L-INS-i method. Sequences from type material are labelled with (T).



*Coniochaeta fermentaria*



## *Coniochaeta fermentaria* R. Hoffmann & Riebesehl, *sp. nov.*

*Etymology*: Named after substrate, fermentation residues from biogas plants.

*Classification*: *Coniochaetaceae*, *Coniochaetales*, *Sordariomycetes*.

*Conidiogenous cells* formed directly on hyphae. *Conidia* solitary, aseptate, hyaline, smooth-walled, ellipsoid, apex obtuse or pointed on one side, 3.6–5.1 × 1.5–2.2 µm (av. 4.4 × 1.7 µm). *Hyphae* hyaline, septate, smooth-walled. *Chlamydospores* solitary or in short chains, hyaline, thick-walled, ellipsoid or globose in shape, measuring 11.7–20.2 × 7.3–14.5 µm (av. 15.5 × 10.3 µm).

*Culture characteristics*: Colonies on potato dextrose agar flat, margin irregular, dense, reaching 68 mm diam. after 57 d at room temperature (approx. 22 °C) with natural dark light cycle. Surface dull, white to light yellow with folded surface in the middle, reverse same colour scheme (colours after Rayner 1970).

*Typus*: **Germany**, Lower Saxony, Braunschweig, 52°16'37"N, 10°33'53"E, 80 m a.s.l., isolated from fermentation residues from biogas plants [consisting of 70 % *Zea mays* (*Poaceae*) and 30 % manure] that were fermented for 4 mo under addition of sawdust, 21 Feb. 2022, *F.F. Soliz Santander* (**holotype** JKI-GP-22-032, culture ex-type DSM 119708, ITS, LSU, *TEF* and *TUB2* sequences GenBank PV272676, PV259253, PV287723 and PV287719).

*Notes*: Based on the ITS alignment phylogenetic analysis, the closest phylogenetic neighbour is *Coniochaeta verticillata* (GenBank NR\_159772; Identity = 8.86 %). However, the distance between *Coniochaeta verticillata* and *Coniochaeta fermentaria* suggests a novel species.

*Coniochaeta fermentaria* is morphologically characterised by white to light yellow colonies with a very solid leathery surface. These characteristics distinguish *Coniochaeta fermentaria* from many other known species within the genus. A comparison of the morphological features of *C. fermentaria* with all other *Coniochaeta* species without online available DNA sequences show also no matches.

For phylogenetic tree, see *Coniochaeta corticalis* (FP 1812).

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*Colour illustrations*: Greenhouse and the substrate from which the fungus was isolated. Colony on PDA agar; hyphae and chlamydospores. Scale bars = 10 µm.

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*Coniochaeta fibricola*



## *Coniochaeta fibricola* R. Hoffmann & Riebesehl, *sp. nov.*

*Etymology*: Named after the substrate, wood fibres for horticultural use.

*Classification*: *Coniochaetaceae*, *Coniochaetales*, *Sordariomycetes*.

*Conidiogenous cells* formed directly on hyphae, mostly reduced to protrusions. *Conidia* solitary, aseptate, hyaline, smooth-walled, ellipsoidal, partly arched, apex obtuse, 2.7–4.8 × 2.2–3.3 µm (av. 3.7 × 2.8 µm). *Hyphae* hyaline, septate, smooth-walled. *Chlamydospores* absent.

*Culture characteristics*: Colonies on potato dextrose agar flat, with aerial hyphae at the centre, folded surface at the centre, margin entire, dense, reaching 83 mm diam. after 57 d at room temperature (approx. 22 °C) with natural dark light cycle. Surface dull, moderate brown with white aerial hyphae at the centre, centre surrounded by pale yellow part, white at the periphery, reverse same colour scheme (colours after Rayner 1970).

*Typus*: **Germany**, Lower Saxony, Braunschweig, 52°16'37"N, 10°33'53"E, 80 m a.s.l., isolated from horticultural substrate consisting of softwood fibres [mainly from *Picea* sp. and *Pinus* sp. (*Pinaceae*)], 23 Aug. 2022, F.F. Soliz Santander (**holotype** JKI-GP-22-031, culture ex-type DSM 119706, ITS, LSU, TEF and TUB2 sequences GenBank PV272674, PV259251, PV287721 and PV287717).

*Notes*: Based on the ITS alignment phylogenetic analysis, the closest phylogenetic neighbours are *Coniochaeta deborreae* (GenBank NR\_173009; Identity = 0.42 %) and *C. boothii* (GenBank NR\_159776; Identity = 2.37 %).

*Coniochaeta fibricola* is morphologically characterised by moderate brown colonies with aerial hyphae at the centre. As the brownish surface and aerial hyphae are also present in several other species of *Coniochaeta*, the morphological comparison of the closest species is based on conidial morphology. Although the shape of the conidia is similar in *C. fibricola* and its phylogenetic closest species *C. deborreae*, the size differs. The conidia from *C. deborreae* have almost the same length but are thinner (*C. deborreae* = 2.5–4 × 1.5–2 µm) in comparison to those of *C. fibricola* (Crous *et al.* 2021). In addition, chlamydospores are present in *C. deborreae* and absent in the newly described species. A comparison of the morphological features of *C. fibricola* with all other *Coniochaeta* species without online available DNA sequences show also no matches.

For phylogenetic tree, see *Coniochaeta corticalis* (FP 1812).

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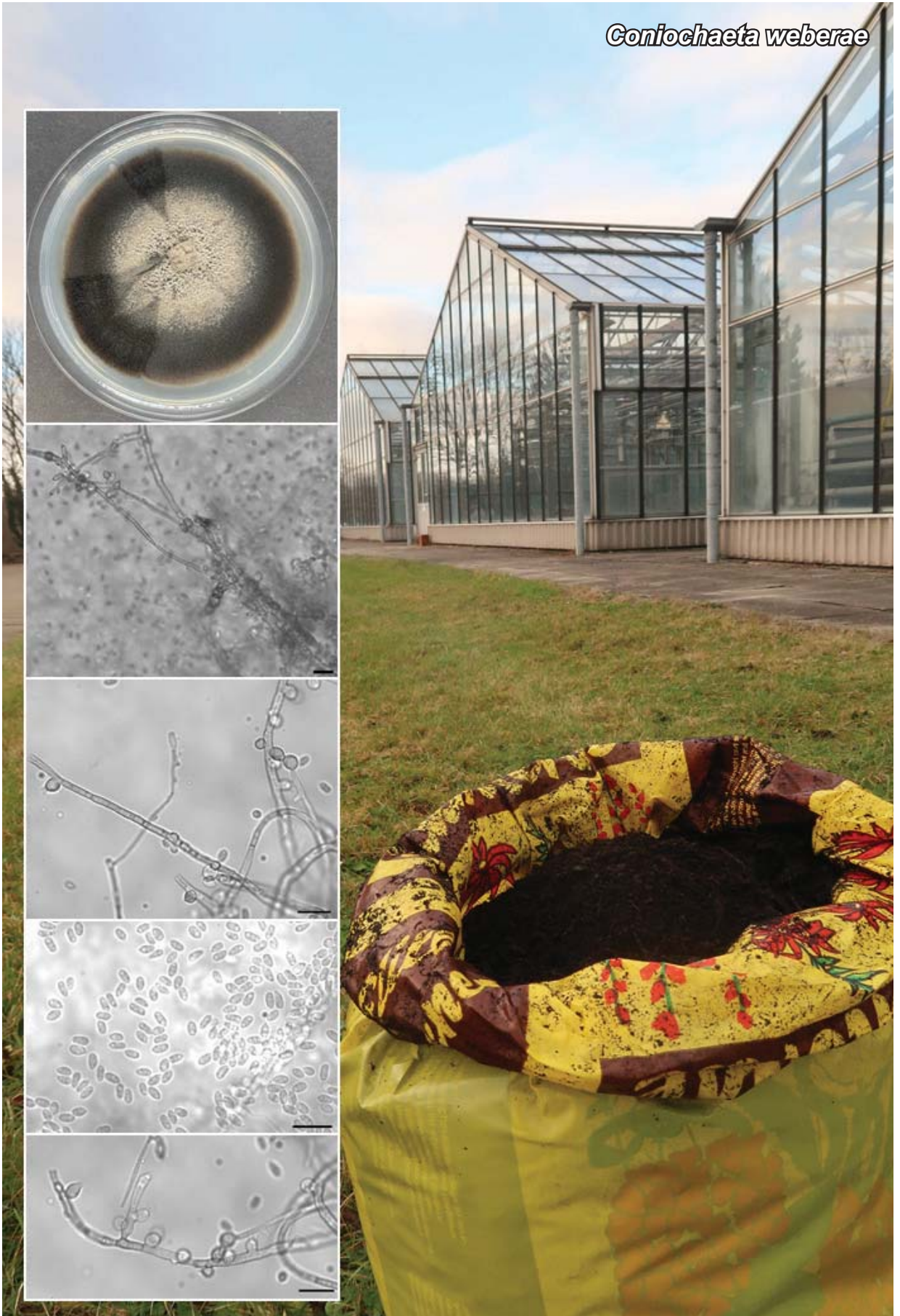
*Colour illustrations*: Greenhouse and the substrate from which the fungus was isolated. Colony on PDA agar; conidia; hyphae with conidiogenous cells. Scale bars = 10 µm.

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*Coniochaeta weberae*



## *Coniochaeta weberae* R. Hoffmann & Riebesehl, *sp. nov.*

*Etymology*: Named after Evi Weber, a mycologist who contributed an important morphological study to the genus *Coniochaeta*.

*Classification*: *Coniochaetaceae*, *Coniochaetales*, *Sordariomycetes*.

*Conidiogenous cells* formed directly on hyphae, mostly reduced to protrusions. *Conidia* solitary, aseptate, hyaline, smooth-walled, ellipsoid, apex obtuse or pointed on one side, 3.3–5.1 × 1.6–3.6 µm (av. 4.0 × 2.4 µm). *Hyphae* hyaline, septate, smooth-walled. *Chlamydospores* absent.

*Culture characteristics*: Colonies on potato dextrose agar flat, with aerial hyphae most densely in the middle, margin entire, dense, reaching 88 mm diam. after 50 d at room temperature (approx. 22 °C) with natural dark light cycle. Surface dull, dark greyish red with white aerial hyphae, reverse dark greyish red to black and pale dark greyish red at the edges (colours after Rayner 1970).

*Typus*: **Germany**, Lower Saxony, Braunschweig, 52°16'37"N, 10°33'53"E, 80 m a.s.l., isolated from horticultural substrate consisting of bark humus [mainly from *Abies* sp., *Picea* sp. and *Pinus* sp. (*Pinaceae*)], 14 Jun. 2023, F.F. Soliz Santander (**holotype** JKI-GP-23-051, culture ex-type DSM 119707, ITS, LSU, *TEF* and *TUB2* sequences GenBank PV272675, PV259252, PV287722 and PV287718).

*Notes*: Based on the ITS alignment phylogenetic analysis, the closest phylogenetic neighbours are *Coniochaeta corticalis* (GenBank PV272673; difference = 0.84 %), *C. velutina* (GenBank GQ154544; Identity = 1.28 %), *C. lignicola* (GenBank NR\_111520; Identity = 0.85 %), *C. luteoviridis* (GenBank NR\_154769; difference = 1.28 %) and *C. mutabilis* (GenBank NR\_111519; difference = 1.06 %).

*Coniochaeta weberae* is morphologically characterised by dark greyish red colonies with aerial hyphae. As the surface colour with aerial hyphae are also present in several other species within the *Coniochaeta* genus, the morphological comparison of the closest species is based on the conidia. Although the shape of the conidia is similar in comparison to *C. weberae* and those of *C. velutina* and *C. lignicola*, but the size differs, particularly in the width of the conidia. The conidia of *C. corticalis* (2.5–3.9 × 1.9–2.7 µm), *C. lignicola* (3–4.5 × 1.5–2 µm), *C. velutina* (3.5–6 × 1.2–2 µm), *C. luteoviridis* (4.5–7 × 1.8–2.5 µm) and *C. mutabilis* (4–6 × 1.5–2 µm) are narrower in comparison to those of *C. weberae*. The conidia length overlap partly more, but especially in *C. luteoviridis* the conidia are longer. In addition, chlamydospores are present in *C. mutabilis* and *C. luteoviridis* (Weber 2002) and absent in *C. weberae*. A comparison of the morphological features of *C. weberae* with all other *Coniochaeta* species without online available DNA sequences show also no matches.

For phylogenetic tree, see *Coniochaeta corticalis* (FP 1812).

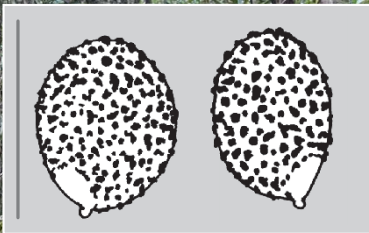
*Colour illustrations*: Greenhouse and the substrate from which the fungus was isolated. Colony on PDA agar; hyphae with conidiogenous cells; conidia; hyphae with conidiogenous cells. Scale bars = 10 µm.

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*Cortinarius caeloculus*



# *Cortinarius caeloculus* Cazabonne, Eyssart., Carriconde & Gryta, *sp. nov.*

*Etymology:* Named after the cap which seems to be composed of a sky-blue iris surrounding an ochre centre, from the Latin *caelum*, “sky”, and *oculus*, “eye”.

*Classification:* Cortinariaceae, Agaricales, Agaricomycetes.

*Cap* 5–20 mm diam., hemispherical to convex without umbo, dry and fibrillose to minutely felted, deep blue-lilac, grey-lilac blue, violaceous blue or grey blue at the margin then gradually fading to ochre or pale yellow brown towards the disc, maybe slightly hygrophanous; margin sometimes striate or even sulcate on very wet specimens; velar remnants absent. *Gills* emarginate, subdistant to distant, deep lilac turning rusty brown; edge concolorous. *Stipe* 15–30 × 1.5–2 mm, subcylindrical, concolorous; cortina and veil white, tenuous; mycelium (always?) lilac. *Flesh* thin, *taste* and *odour* not noted. *Spores* (on stipe) (6.6–)7.0–7.4–7.9(–8.7) × (4.9–)5.2–5.6–5.9(–6.3) µm, Q = (1.2–)1.24–1.3–1.4(–1.6), n = 147, ellipsoid, widely ellipsoid to subglobose, rather minutely and regularly verrucose, rusty brown, not dextrinoid. *Basidia* on average 25 × 8.5 µm, tetrasporic, clavate. *Cystidia* absent. *Pileipellis* composed of a very thin epicutis of repent non-gelatinized hyphae 4–8 µm wide, on a subcellular subcutis with up to 30 µm wide elements; pigment parietal, yellowish in KOH. *Clamp connections* present in all parts.

*Typus:* **France**, New Caledonia, pic du Grand Kaori, 22°16'49.80"S, 166°53'40.80"E, 260 m a.s.l., on soil under *Nothofagus aequilateralis* (*Nothofagaceae*), 28 May 2013, *F. Carriconde*, PGK 13-050 (**holotype** PC0142595; ITS sequence GenBank PQ340587).

*Additional material examined.* **France**, New Caledonia, col de Yaté, 22°10'7.20"S, 166°53'36.60"E, 320 m a.s.l., basidiocarps, under *N. aequilateralis*, 27 Jun. 2013, *F. Carriconde*, CY13-56 (ITS sequence GenBank PQ340585) and CY13-070 (ITS sequence GenBank KY774074); col de Yaté, in mixed forest, 22°10'7.08"S, 166°53'41.61"E, 340 m a.s.l., basidiocarps, 27 Jun. 2013, *F. Carriconde*, CY13-083 (ITS sequence GenBank PQ340586); pic du Grand Kaori, 22°16'49.80"S, 166°53'40.80"E, 260 m a.s.l., basidiocarp under *N. aequilateralis*, 22 Jul. 2013, *F. Carriconde*, PGK13-105 (ITS sequence GenBank PQ340588).

*Notes:* The genus *Cortinarius* s. lat. is probably the largest ectomycorrhizal genus of the order *Agaricales*, with a cosmopolitan distribution of over 3000 described species (Roskov *et al.* 2019). While the taxonomy and diversity of this genus are relatively well-known in western Central Europe (Liimatainen *et al.* 2020, Szabó *et al.* 2023), many of the world's zones remain totally under-studied, especially in the

tropics. Indeed, in the New Caledonian rainforests, among the 142 OTUs identified as *Cortinarius* by Carriconde *et al.* (2019), only one OTU was assigned at the species level, *C. picoides*. Similarly, in their checklist of New Caledonian Basidiomycota, Horak & Mouchacca (1998) reported only three identified species. The three new species described here (see following pages) belong to the sect. *Anomali*, which has expanded considerably in recent years (Eyssartier *et al.* 2014, Dima *et al.* 2016, 2021, Zhang *et al.* 2023). The phylogeny of *Cortinarius* sect. *Anomali* inferred from rDNA ITS sequences (phylogenetic tree below and Supplementary Fig. S1) revealed a core group including only specimens from the Northern Hemisphere and several paraphyletic basal lineages encompassing specimens mainly from Oceania and a few from South America. Similar phylogenetic topologies were previously reported for this section (Dima *et al.* 2016, 2021, Zhang *et al.* 2023) and could suggest a southern origin of the section *Anomali*. The three newly described species are well-defined as they appear clearly monophyletic and strongly supported. These three species are phylogenetically placed among basal lineages of *Cortinarius* sect. *Anomali* but with often poor support as to their exact position.

*Cortinarius caeloculus* is morphologically closely related to the recently described *C. cinnamomeoillicinus* and *C. tropicus* from China, but it differs from these species by several morphological, habitat, and molecular aspects. *Cortinarius cinnamomeoillicinus* has larger caps (15–52 mm) and longer stipes (30–70 mm long), adnate gills, longer and slightly narrower basidia (29–33 × 6–7 µm), and a lilac pileal surface with overall paler and more greyish colours (Zhang *et al.* 2023), lacking the cap's blueish shades characteristic of *C. caeloculus*. *Cortinarius cinnamomeoillicinus* is currently known only from tropical Guizhou and Yunnan (China) and is found under *Fagaceae* or *Pinaceae*, while *C. caeloculus* is known only from New Caledonian collections found under *Nothofagus*. *Cortinarius tropicus* has also larger caps (20–45 mm) and longer stipes (50–80 mm long), an umbonate pileus, a whitish basal mycelium, longer and slightly wider basidia (30–42 × 7–11 µm), and generally darker violet colours (especially on mature specimens), a cream to pale violet margin, and is found only in tropical Yunnan (China) under *Fagaceae* (Zhang *et al.* 2023). *Cortinarius nothoanomalus*, described from Argentina under *Nothofagus*, forms larger spores (10–11 × 4.8–6.3 µm; Moser & Horak 1975). *Cortinarius laquellus*, from *Nothofagetis* in New Zealand, is also very close, but its spores are narrower, more elliptic to subamygdaloid, and measure 6.5–8.5 × 4–5.2 µm (Sooop 2005).

Based on a blast search (MEGABLAST), the ITS sequence of *C. caeloculus* has only 92.2 % and 90.9 % of identities with ITS sequences of *C. tropicus* and *C. cinnamomeoillicinus* respectively. Moreover, the phylogeny inferred from ITS sequences reveals that while *C. cinnamomeoillicinus* and *C. tropicus* are phylogenetically placed in the core group of *Cortinarius* sect. *Anomali*, *C. caeloculus* is placed among basal lineages of this section,

*Colour illustrations:* New Caledonia, at the pic du Grand Kaori location, in a rainforest dominated at the canopy layer by *Nothofagus aequilateralis*. *Cortinarius caeloculus* (holotype); spores from the holotype. Scale bars: basidiomata = 1 cm; spores = 10 µm.

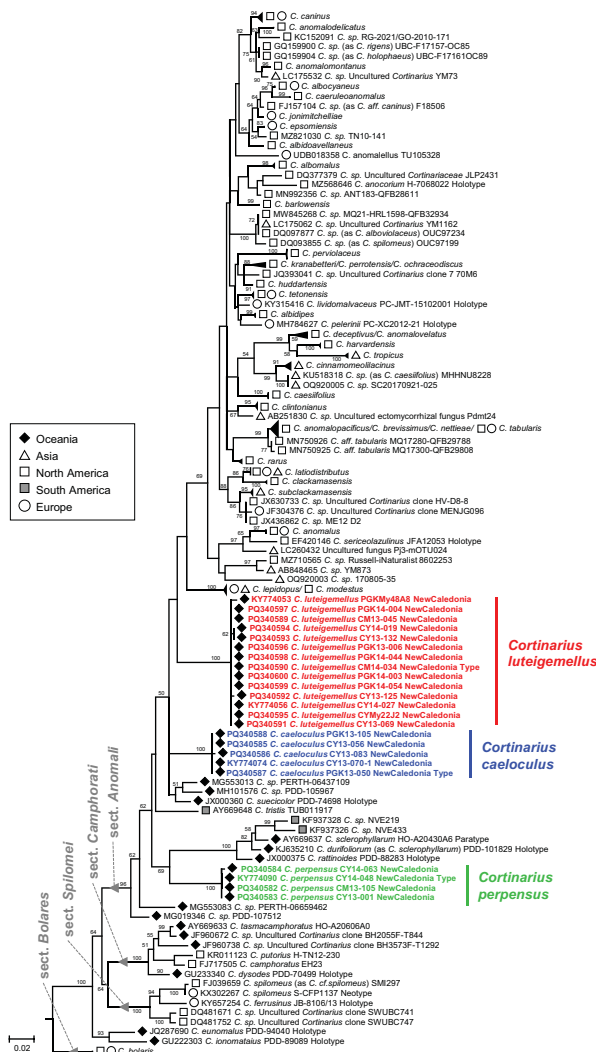


Key to the described species

1. Evident yellow veil forming girdles on the stipe and sometimes remnants at the margin of the cap... *Cortinarius luteigemellus*
1. Veil tenuous, less evident..... 2
2. Cystidia absent. Cap of a beautiful deep blue-lilac, grey-lilac blue, violaceous blue or grey blue, becoming ochraceous-yellow towards the centre ..... *Cortinarius caeloculus*
2. Cystidia abundant on the lamellar edge, clavate, subcylindrical or fusoid. Cap lilac brown, chestnut brown, ochraceous towards the disc..... *Cortinarius perpensus*

with as the closest lineage, a lineage containing *C. suecicolor* holotype and two indeterminate samples from Australia and New Zealand (specimens PERTH 06437109 and PDD 105967 New Zealand with GenBank accessions MG553013 and MH101576 respectively). At the intraspecies level, ITS sequence similarities between the five analysed samples of *C. caeloculus* range between 99.4 and 100 %.

*Supplementary material:* Alignment of ITS sequences, expanded phylogenetic tree and tables are available in the Figshare Data Repository doi: 10.6084/m9.figshare.28847843.



Synthetic maximum likelihood (ML) tree of *Cortinarius* sect. *Anomali* and closely related sections showing the phylogenetic positions of the three newly described species from New Caledonia. The tree is based on a nuclear ribosomal ITS sequences alignment. Sequences of well defined species are collapsed (see complete tree in supplementary material). Sequences of the New Caledonian species are in bold and colored in red, blue and green for *Cortinarius luteigemellus*, *Cortinarius caeloculus* and *Cortinarius perpensus* respectively. The tree is rooted with *Cortinarius bolaris*. The ML bootstrap support values above 50 % are presented. The scale bar gives the expected number of changes per site. Symbols refer to the geographic origin of accessions included in the complete tree (see legend).

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*Cortinarius luteigemellus*





# *Cortinarius luteigemellus* Cazabonne, Eyssart., Carriconde & Gryta, *sp. nov.*

*Etymology:* From the Latin *luteus*, “yellow”, and *gemellus*, “twin”, because of its similarities with *Cortinarius caeloculus*, but distinguished by its yellow veil.

*Classification:* Cortinariaceae, Agaricales, Agaricomycetes.

*Cap* 14–45 mm diam., conico-convex then plano-convex, grey blue, greyish cream, ochraceous yellow or ochraceous brown at centre, with yellow veil remnants at the margin. *Gills* emarginate, subdistant to distant, at first deep lilac then rusty brown; edge concolourous. *Stipe* 45–60 × (1–)3–5 mm subcylindrical or slightly clavate; veil yellow forming evident girdles. *Flesh* thin, *taste* and *odour* not noted. *Spores* (on stipe) (6.7–)7.2–7.7–8.1(–9.0) × (5.0–)6.1–6.5–6.9(–7.2) μm, Q = (1.1–)1.11–1.2–1.2(–1.3) μm, n = 309, subglobose to slightly subglobose, rather minutely and regularly verrucose, rusty brown, not dextrinoid. *Basidia* 32–38(–45) × (7.5–)9–11 μm, tetrasporic, rarely bisporic, clavate. *Marginal cells* absent. *Pileipellis* composed of a thin epicutis of repent non gelatinized hyphae 4–10(–15) μm wide, on a subcellular subcutis with up to 30 μm wide elements; pigment parietal, yellowish in KOH. *Clamp connections* present.

*Typus.* France, New Caledonia, col de Mourange, 22°12'7.38"S, 166°40'21.66"E, 340 m a.s.l., on soil under *Nothofagus aequilateralis* (*Nothofagaceae*), 17 Feb. 2014, F. Carriconde, CM14-034 (**holotype** PC0142593; ITS sequence NCBI GenBank PQ340590).

*Additional material examined:* France, New Caledonia, col de Mourange, 22°12'7.38"S, 166°40'21.66"E, 340 m a.s.l., basidiocarps under *N. aequilateralis*, 21 May 2013, F. Carriconde, CM13-045 (ITS sequence GenBank PQ340589); col de Yaté, 22°10'7.20"S 166°53'36.60"E, 320 m a.s.l., basidiocarps under *N. aequilateralis*, 27 Jun. 2013, F. Carriconde, CY13-069 (ITS sequence GenBank PQ340591); *ibid.*, 24 Jul. 2013, F. Carriconde, CY13-125 (ITS sequence GenBank PQ340592); col de Yaté, in mixed forest, 22°10'7.08"S 166°53'41.61"E, 340 m a.s.l., basidiocarp, 24 Jul. 2013, F. Carriconde, CY13-132 (ITS sequence GenBank PQ340593); *ibid.*, 29 Jan. 2014, F. Carriconde, CY14-019 (ITS sequence GenBank PQ340594); *ibid.*, 26 Feb. 2014, F. Carriconde, CY14-027 (ITS sequence GenBank KY774056); *ibid.*, ectomycorrhiza, 26 Apr. 2012, F. Carriconde, CYMy22J2 (ITS sequence GenBank PQ340595); pic du Grand Kaori, 22°16'49.80"S 166°53'40.80"E, 260 m a.s.l., basidiocarps under *Nothofagus aequilateralis*, 5 Apr. 2013, F. Carriconde, PGK13-006 (ITS sequence GenBank PQ340596); *ibid.*,

22 Jan. 2014, F. Carriconde, PGK14-003 (ITS sequence GenBank PQ340600) and PGK14-004 (ITS sequence GenBank PQ340597); *ibid.*, 24 Feb. 2014, F. Carriconde, PGK14-044 (ITS sequence GenBank PQ340598) and PGK14-054 (ITS sequence GenBank PQ340599); *ibid.*, ectomycorrhiza, 23 Apr. 2012, F. Carriconde, PGKMy48A8 (ITS sequence GenBank KY774053).

*Notes:* *Cortinarius luteigemellus* is morphologically similar to the newly described species *C. caeloculus* recorded in New Caledonia (see previous pages), but features an evident yellow veil forming girdles compared to the tenuous white veil of *C. caeloculus*. Moreover, *C. caeloculus* has smaller caps, shorter and narrower stipes, narrower spores, and shorter and narrower basidia (see previous pages). It is also clearly genetically different with only 92.2 % of identity between ITS sequences of the types of these two species. On a phylogenetic tree based on rDNA ITS sequences alignment, *C. luteigemellus* is a well-differentiated species (100 % bootstrap support value) with slight intraspecific variations in ITS sequences (between 0 and 0.7 % recorded among the fourteen samples analysed) and is rather placed among basal lineages of *Cortinarius* sect. *Anomali*. Phylogenetically, the closest lineages of *C. luteigemellus* are the newly described species *C. caeloculus*, a lineage containing the holotype of *C. suecicolor* and two indeterminate species from Australia and New Zealand, and a lineage including *C. lepidopus* and *C. modestus*. *Cortinarius suecicolor* has cap and stipe sizes like *C. luteigemellus* and a greyish blue cap with an ochraceous disc and is found under *Nothofagus* (Sooop 2002). However, it has saturated grey blue gills, slightly smaller spores, forms cystidia (unlike *C. caeloculus* as well), and was described from New Zealand. Morphologically, *C. lepidopus* has a garland-shaped yellow veil and similar spores in size as *C. luteigemellus* (see Eyssartier *et al.* 2014). Still, contrary to *C. luteigemellus* and *C. caeloculus*, it lacks lilac, violaceous, or grey blue tones, rather featuring brown and reddish colours on the cap. Similarly, *C. modestus* has clearly brownish caps, and is, at present, considered a North American taxon (see Dima *et al.* 2021).

A blast analysis (MEGABLAST) performed with the ITS sequence of *C. luteigemellus* type reveals 94.3 %, 94.2 %, 94.0 % and 93.7 % of identities with *C. rarus* holotype (GenBank accession MZ663800), *C. pelerinii* (GenBank accession MH784627), *C. modestus* holotype (GenBank accession MZ580446) and *C. suecicolor* holotype (GenBank accession JX000360).

For phylogenetic tree, see *Cortinarius caeloculus* (FP 1816).

*Colour illustrations:* New Caledonia, at the col de Mourange location, in a rainforest dominated at the canopy layer by *N. aequilateralis*. *Cortinarius luteigemellus* (holotype); spores from the holotype. Scale bars: basidiomata = 1 cm; spores = 10 μm.

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*Cortinarius perpensus*



# *Cortinarius perpensus* Cazabonne, Eyssart., Carriconde & Gryta, *sp. nov.*

**Etymology:** From the Latin *perpensus*, “examined, checked”, because this species must be studied carefully to be correctly identified.

**Classification:** *Cortinariaceae*, *Agaricales*, *Agaricomycetes*.

**Cap** 5–15 mm diam., lilac brown, chestnut brown, ochraceous towards the disc, striate at the margin in age. **Gills** emarginate, subdistant to distant, at first deep lilac then rusty brown; with fimbriate sterile edge. **Stipe** 20–45 × 1–3 mm, subcylindrical, lilac-blue; veil poorly developed, yellow. **Flesh** thin, **taste** and **odour** not noted. **Spores** (on lamellae) (7.1–)7.6–8.2–8.7(–9.3) × (6.0–)6.3–6.7–7.0(–7.8) μm, Q = 1.1–1.2–1.3, n = 259, subglobose to slightly subglobose, regularly verrucose, rusty brown, not dextrinoid. **Basidia** 35–40 × 8–10 μm, clavate, tetrasporic. **Cystidia** numerous on the lamellar edge, clavate, subcylindrical or fusoid, measuring (23.6–)27.1–42.3(–46.1) × (6–)6.9–27.7(–34.2) μm. **Pileipellis** composed of a thin cutis of well-differentiated hyphae, many numerous free extremities, (5–)10–15 μm wide, on a subcellular hypoderm. **Clamp connections** present in all parts.

**Typus.** France, New Caledonia, col de Yaté, 22°10'7.20"S, 166°53'36.60"E, 320 m a.s.l., on soil under *Nothofagus aequilateralis* (*Nothofagaceae*), 26 Mar. 2014, CY14-048 (**holotype** PC0142594; ITS sequence GenBank KY774090).

**Additional material examined.** France, New Caledonia, col de Mouirange, 22°12'4.38"S, 166°40'10.26"E, 320 m a.s.l., basidiocarp under *Arillastrum gummiferum*, 17 Jun. 2013, F. Carriconde, CM13-105 (ITS sequence GenBank PQ340582); col de Yaté, 22°10'7.20"S, 166°53'36.60"E, 320 m a.s.l., basidiocarps under *Nothofagus aequilateralis*, 8 Apr. 2013, F. Carriconde, CY13-001 (ITS sequence GenBank PQ340583) and in mixed forest, 22°10'7.08"S, 166°53'41.61"E, 340 m a.s.l., 26 Mar. 2014, F. Carriconde, CY14-063 (ITS sequence GenBank PQ340584).

**Colour illustrations:** New Caledonia, at the col de Mouirange location, in a rainforest dominated at the canopy layer by *Arillastrum gummiferum* (*Myrtaceae*). *Cortinarius perpensus* (holotype); spores from the holotype. Scale bars: basidiomata = 1 cm; spores = 10 μm.

**Notes:** The main morphological difference with the two other newly described New Caledonian species is the presence and abundance of cystidia on the lamellar edge. Moreover, although *C. caeloculus* and *C. perpensus* are similar in size, *C. perpensus* has a more conical cap, a brownish chestnut disc, and larger spores. *Cortinarius luteigemellus* is clearly a larger species, with a light ochre brown disc, a yellow veil, and overall, more greyish colour shades. On the phylogenetic analysis based on rDNA ITS sequences alignment, *C. perpensus* is a well-differentiated species (100 % bootstrap value) among basal lineages of *Cortinarius* sect. *Anomali*. *Cortinarius perpensus* is sister to a lineage including *C. rattinoides* holotype, *C. durifoliorum* holotype, *C. sclerophyllum* paratype and two indeterminate samples from Colombia (specimens NVE219 and NVE433 with GenBank accessions KF937326 and KF937328). Like *C. perpensus*, *C. rattinoides* is found under *Nothofagus* spp. and forms clavate marginal elements, but they are not as numerous and are significantly smaller (15–25 × 5–7 μm). Contrary to *C. perpensus*, *C. rattinoides* has also larger caps (15–40 mm diam.), longer and larger stipes (40–75 × 2–5 mm), but smaller basidia (20–25 × 7 μm) and slightly narrower spores. Moreover, *C. rattinoides* features dark violet gills and generally more reddish, brick and brown shade colours (Gasparini & Soop 2008). The New Zealand *C. durifoliorum* is also found in *Nothofagus* forests and forms clavate cystidia, but it has larger caps (15–50 mm diam.) and stipes (35–105 × 2–6 mm), smaller cystidia (17–25 × 7–9 μm) and shorter basidia (20–27 × 7–9 μm), as well as brown-red fibrils on the cap and dark reddish fringes bands and fibrils on the stipe (Soop *et al.* 2018). *Cortinarius sclerophyllum* is morphologically highly similar to *C. durifoliorum*, but the caps and gills tend to display more violet shades (Soop *et al.* 2018).

A blast analysis (MEGABLAST) performed with the ITS sequence of *C. perpensus* type shows 92.3 %, 91.9 % and 91.9 % of identities with ITS sequences of *C. rattinoides* holotype (GenBank accession JX000375), *C. durifoliorum* (GenBank accession KJ635210) and *C. sclerophyllum* paratype (GenBank accession AY669637), respectively. Within the *C. perpensus* species, ITS sequence similarities among the four samples varied between 99.9 and 99.7 %.

For phylogenetic tree, see *Cortinarius caeloculus* (FP 1816).

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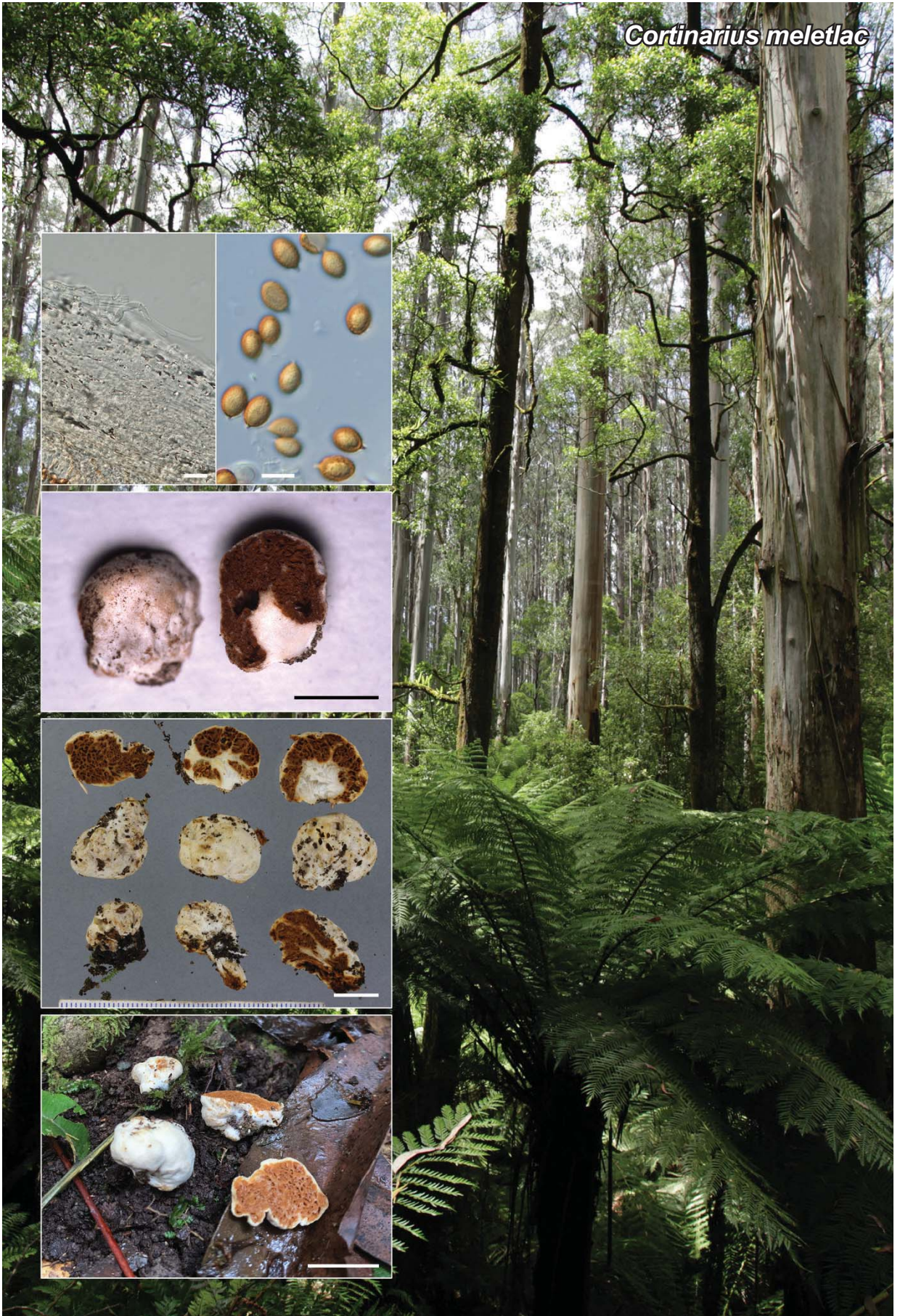
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*Cortinarius meletiac*



Fungal Planet 1819

MB 857740

## *Cortinarius meletlac* Polman-Short, J. Barratt, Orlovich & T. Lebel, *sp. nov.*

*Etymology:* For the Latin, mel = honey, lac = milk direct Latin translation "milk and honey", for the overall appearance of the basidiomes with silvery white pileus and cinnamon-honey coloured hymenophore.

*Classification:* Cortinariaceae, Agaricales, Agaricomycetes.

*Basidiomata* hypogaeal, sporulating in clusters beneath leaf litter. *Pileus* 7–17 × 7–13 mm, turbinate, smooth to finely felty or scurfy or pulverulent with some furrowing towards the base, silvery white to light grey, handling darker; context thin, white in cross section. *Hymenophore* loculate, chambers small, irregular and labyrinthine, tawny, chestnut or cinnamon – honey brown becoming dark brown in colour, trama inconspicuous appearing watery. *Stipe-collumella* central, percurrent or not, some branching, when percurrent 0.5–2 mm broad, when not percurrent 5 mm at base tapering to 2–3 mm wide at apex, inserted, white to cream, darkening to dull yellowish after being cut, may take up the bottom two thirds of the basidiomata; margin completely attached to partial veil. *Universal veil* appears to be absent or indistinguishable from pellis. *Cortina/Partial veil* white, thick, fibrous, persistent. *Basal mycelium* white. *Odour* and *taste* slightly phenol or naphthalene, when fresh, in dried material pleasant earthy. *Spores en masse* dark brown. *Chemical tests* 15 % KOH no reaction on surface or flesh. *Basidiospores* (6.5–)7–9.5 × (4–)4.5–6.5 µm, [av. 7.9 ± 1.5 × 5.2 ± 1.1 µm, Q= 1.3–1.7 (n = 46)], ellipsoid to subovoid, mostly axially symmetrical, thin-walled, golden to faint ochre-brown in KOH, ornamentation of verrucose warts < 0.5 µm high; hilar appendix prominent up to 1.5 µm long, tapering. *Basidia* (14–)17–28(–31) × 4–8(–9 µm, (av. 22.2 ± 8.1 × 6.1 ± 3, Q= 2.4–6.6, n = 29) typically clavate and sometimes bulging at apex, or sometimes irregular and asymmetrical, hyaline, typically 2-spored, but occasionally 4-spored; sterigmata tapering, up to 5 µm long. *Cystidia* absent. *Hymenophoral trama* 20–50 µm wide, composed of interwoven inflated septate hyphae, 2–7 µm broad, hyaline or patchily golden to orange pigmented towards subhymenium. *Subhymenium* 20–80 µm broad, composed of interwoven hyphae 3–5 µm diam. and irregularly shaped inflated hyphae, 5–8 µm broad, hyaline or faint golden-brown pigmented in some sections. *Pileipellis* a layer 30–70 µm broad, not forming a distinct cutis, composed of interwoven, disorganised hyaline hyphae 2–6 µm broad and inflated hyphae 5–15 µm broad, often splaying at surface, becoming somewhat parallel in context. *Context* 50–300 µm broad, composed of inflated cells 3–8 µm broad, hyaline or light golden-brown pigmented. *Clamp connections* observed in pileipellis.

*Colour illustrations:* Tall, wet *Eucalyptus regnans* forest, mixed *Acacia* and *Dicksonia* understorey, Nungatta State Forest, NSW, Australia. Basidiomata (OTA73242) in the field at Orokonui Ecosanctuary (NZ) under *Eucalyptus regnans* with mixed shrubby understorey; basidiomata in lab OTA73242; basidiomata in lab type MEL2314531; microscopic elements: golden basidiospores; pileipellis structure. Scale bars: basidiomata = 10 mm; spores = 10 µm; pileipellis = 20 µm.

*Habit, habitat and distribution:* Hypogaeal in tall, wet mixed eucalypt forest, *Eucalyptus obliqua* with *Acacia dealbata* understorey or *Eucalyptus regnans* with *Leptospermum* spp. and *Eucalyptus* rough bark in Eastern Australia. Also found in introduced *Eucalyptus regnans* plantations in New Zealand. May to July.

*Typus:* **Australia**, New South Wales, South Coast, off Nungatta Road, 3.35 km from Junction of Inlay and Nungatta Road, off small track to east, 6 Jun. 2002, T. Lebel TL1437 (**holotype** MEL 2314531; ITS and LSU sequences GenBank PV226111 and PV226114).

*Additional material examined:* **Australia**, Tasmania, Eaglehawk Neck, 18 May 1991, J.M. Trappe, H5330 (PERTH 07669666; ITS sequence GenBank DQ328119); Victoria, Warrandyte State Park, Black Flat. South eastern corner of reserve, ca 150 m up south facing slope from parking lot, 28 Jul. 1999, T. Lebel, TL99 (MEL 2061024; ITS and LSU sequences GenBank PV226110 and PV226115); 2.4 km N of Baw Baw National Park, 16 Jun. 1994, J.M. Trappe, H6784 (PERTH 07668759; ITS sequence GenBank DQ328200); Murrangowar Forest Management Block, Junction of Bourke Street and Morrison's Track, Site R12, in *Eucalyptus obliqua* forest, 18 Jul. 1996, T. Mitchell, AWC480 (MEL 2057558; ITS sequence GenBank DQ328103); Eildon State Forest, Mallet Creek, 16 Jun. 1994, J.M. Trappe, H6593 (PERTH 07647425). **New Zealand**, Otago, Orokonui, *Eucalyptus regnans* plantation, 1 Apr. 2004, D. Orlovich DAO OR017 (OTA60213; ITS sequence GenBank MN846509); Otago, Orokonui Ecosanctuary, *Eucalyptus regnans* plantation with mixed understorey, 27 May 2021, D. Orlovich DAO 2021/288 (OTA73242; ITS sequence GenBank OQ065062).

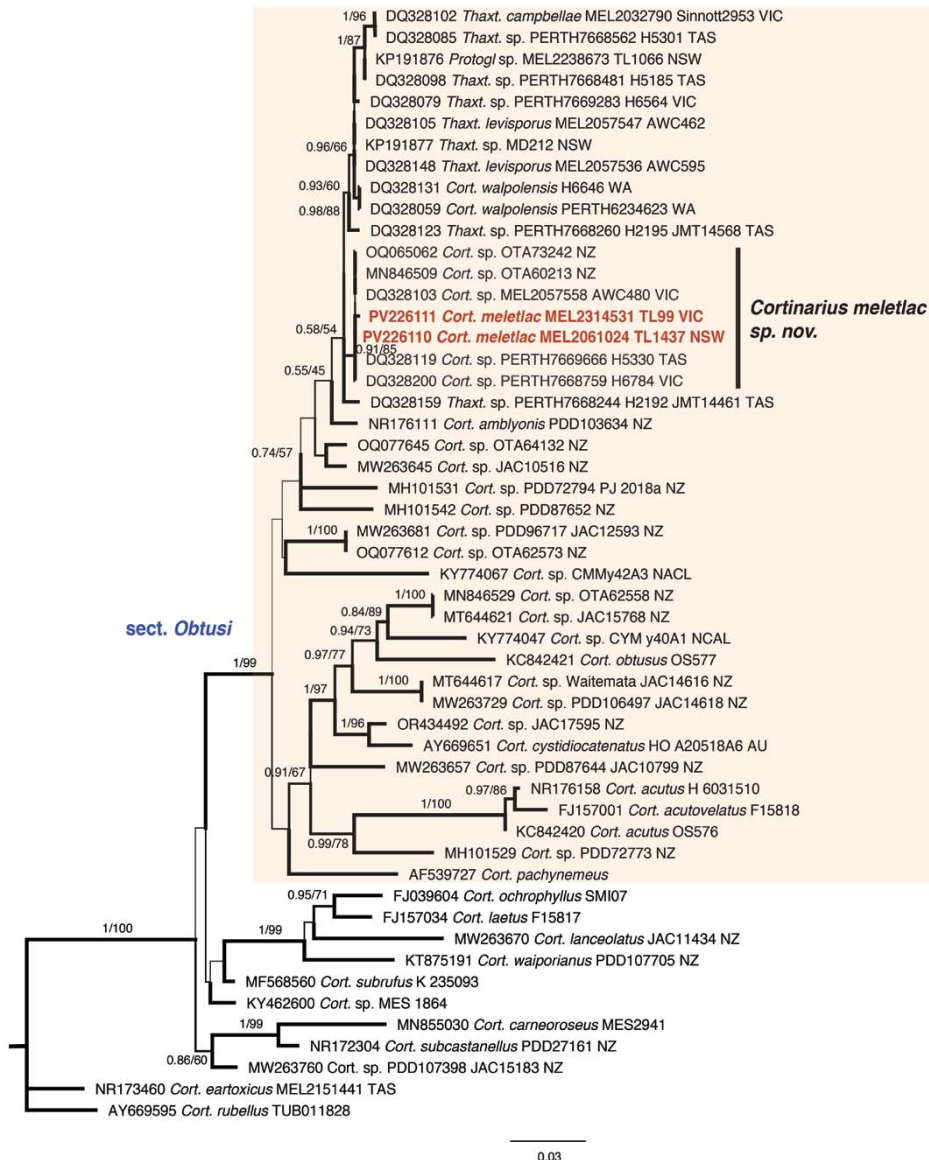
*Notes:* *Cortinarius meletlac* is distributed across south-eastern Australia and introduced with *Eucalyptus regnans* plantations in New Zealand. Analysis of molecular data (ITS-LSU) places *C. meletlac* (BS 0.91 / PP 85) in a weakly supported clade (BS 0.58 / PP 54) close to several other undescribed Australian sequestrate taxa and *C. walpolensis* (Francis & Bougher 2004). The epithets '*campbellae*' and '*levisporus*' have been applied broadly to sequestrate collections that, on sequencing, are in multiple distantly related clades within the *Cortinarioid* lineage; thus the sequences in this clade are considered as undescribed species until type material can be analysed. The sister group to *C. meletlac* includes *C. amblyonis* (Soop 2016) and two other undescribed mushroom-forming species found in New Zealand, and a sequence from New Caledonia (GenBank KY774067). Within *C. meletlac*, two sequences from New Zealand collections made under *Eucalyptus regnans* support the notion that this is a native Australian species that has been introduced into New Zealand with eucalypt plantations.

*Cortinarius meletlac* differs from *C. walpolensis* (Francis & Bougher 2004) in having a silvery white scurfy or pulverulent pileus, and in lacking the scattered cinnamon fibrils seen in *C. walpolensis*. Both pellis structure and spores of *C. meletlac*



and *C. walpolensis* are remarkably similar, with spores falling within the same size range, golden brown colour and ornamentation of small warty rods less than 0.5 µm high. One small distinguishing feature is that *C. meletlac* typically has basidia that are mostly 2-spored, differing from *C. walpolensis* which are 4-spored. Various combinations of macro- and micro- characters also distinguish *C. meletlac* from the un-named sequestrate taxa in this clade, particularly pellis structure (more layers, and/or pileipellis gelatinised), and size/shape of the hymenophoral chambers (i.e. more labyrinthine lamellate). Morphologically, none of the sequestrate taxa or un-named collections in this clade resemble *C. amblyonis*

(Soop 2016), which has rather delicate tan to reddish brown basidiomes. *Cortinarius amblyonis* is considered a typical member of section *Obtusi*, with the small dry red-brown pileus, whitish stipe, and faint iodoform odour, but lacks the differentiated cheilocystidia prominent in the lamellae of other taxa in the section (Soop 2016, Soop *et al.* 2019). None of the sequestrate taxa in this clade have prominent cheilocystidia. Although extensively sampled, no Australian mushroom-forming species of *Cortinarius* currently fall within this group. Further gene regions and investigation of more collections is required to resolve relationships in this complex.



RAxML v. 8 (Stamatakis 2014) phylogenetic tree obtained for ITS-nrDNA from a selection of species in *Cortinarius* section *Obtusi* and other taxa. **Bold lines** indicate posterior probabilities and bootstrap support values (MrBayes v. 3.2.6; Huelsenbeck & Ronquist 2001) from maximum likelihood ( $\geq 0.75$  PP /  $\geq 50$  % BS; values below these are not shown). **Bold text** indicates sequences generated for this study. Genus abbreviations (names as in GenBank): Cort. = *Cortinarius*, Thaxt. = *Thaxterogaster*, Protogl. = *Protoglossum*.

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*Cortinarius phaeobrunneus*





# *Cortinarius phaeobrunneus* †Bidaud, Mahiques, E. Suárez & Bellanger, *sp. nov.*

*Etymology:* Named after the brown to blackish discolouration of basidiomata, from the Greek *phaeo*, “dark”, and the Latin *brunneus*, “brown”.

*Classification:* Cortinariaceae, Agaricales, Agaricomycetes.

*Pileus* 15–70 mm diam, convex, lobate flexuous, sometimes broadly umbonate, fleshy at centre, with thin and incised silvery-white margin, hygrophanous, pale brown, reddish brown to chestnut brown, dehydrating as concentric zones with centre remaining darker, blackening as exsiccate, covered by a loose white fibrillose veil, denser at margin. *Gills* emarginate, broad, wide, spaced, ventricose, light brown to tawny brown, turning to dark brown; edge serrulate, whitish in early stages. *Stipe* 45–90 × 6–20 mm, clavate, filled but soft, covered on its lowest third by a sheeting white veil sometimes forming an annular zone, with silvery fibrils on the upper part, masking a brownish background; slight metallic blue hues sometimes visible at apex. *Flesh* woolly, whitish in the pileus, brown in the stipe, dark brown at base; *smell* null or weakly soapy or herbaceous. *Spores* 8–9.5–11.5 × 5–6.2–7.5 µm, Q = 1.4–1.5–1.8 (n > 30) ellipsoid to broadly subamygdaliform, punctate to finely warty, more prominent at apex. *Basidia* tetrasporic, clavate, 30–33 × 8–12 µm. Sterile marginal cells clavate, 5–13 µm wide. *Pileipellis* a cutis of radial hyphae (4–7 µm wide) with obtuse, appressed free ends, mixed with thinner velar hyphae (2–3 µm wide), dissociated on the surface; subcutis slightly differentiated, consisting in short septate articles (10–25 µm long), vesicular for the largest ones; yellow-brown parietal pigment, coating. *Clamp-connections* present.

*Typus:* Spain, Teruel, Formiche Alto, Barranco del Monte, 40°20'50"N, 0°52'54"E, 1190 m a.s.l., under *Quercus ilex* and *Q. faginea* (Fagaceae), with some *Pinus sylvestris* (Pinaceae), 20 Oct. 2022, E. Suárez, MES-4838 (holotype VAL-Myco 1765, isotype in herb. RM; ITS and LSU sequences GenBank PV263593 and PV390007).

*Additional materials examined:* France, Ain, Bellegarde-en-Valserine, Mussel, 500 m a.s.l., on a clay-limestone soil under *P. sylvestris*, 1 Oct. 1997, R. Fillion, RF 97.41 (ITS sequence GenBank PV263594); Ardèche, Lagorce, Bois d'Ajude, 150 m a.s.l., on calcareous soil under *Q. ilex*, 9 Nov. 2004, A. Bidaud, AB 04-11-524 (ITS sequence GenBank PV263595); *ibid.*, Rocle, 200 m a.s.l., on calcareous soil under *Q. ilex*, 22 Oct. 2018, A. Bidaud & G. Raffini, AB 18-11-190 (ITS

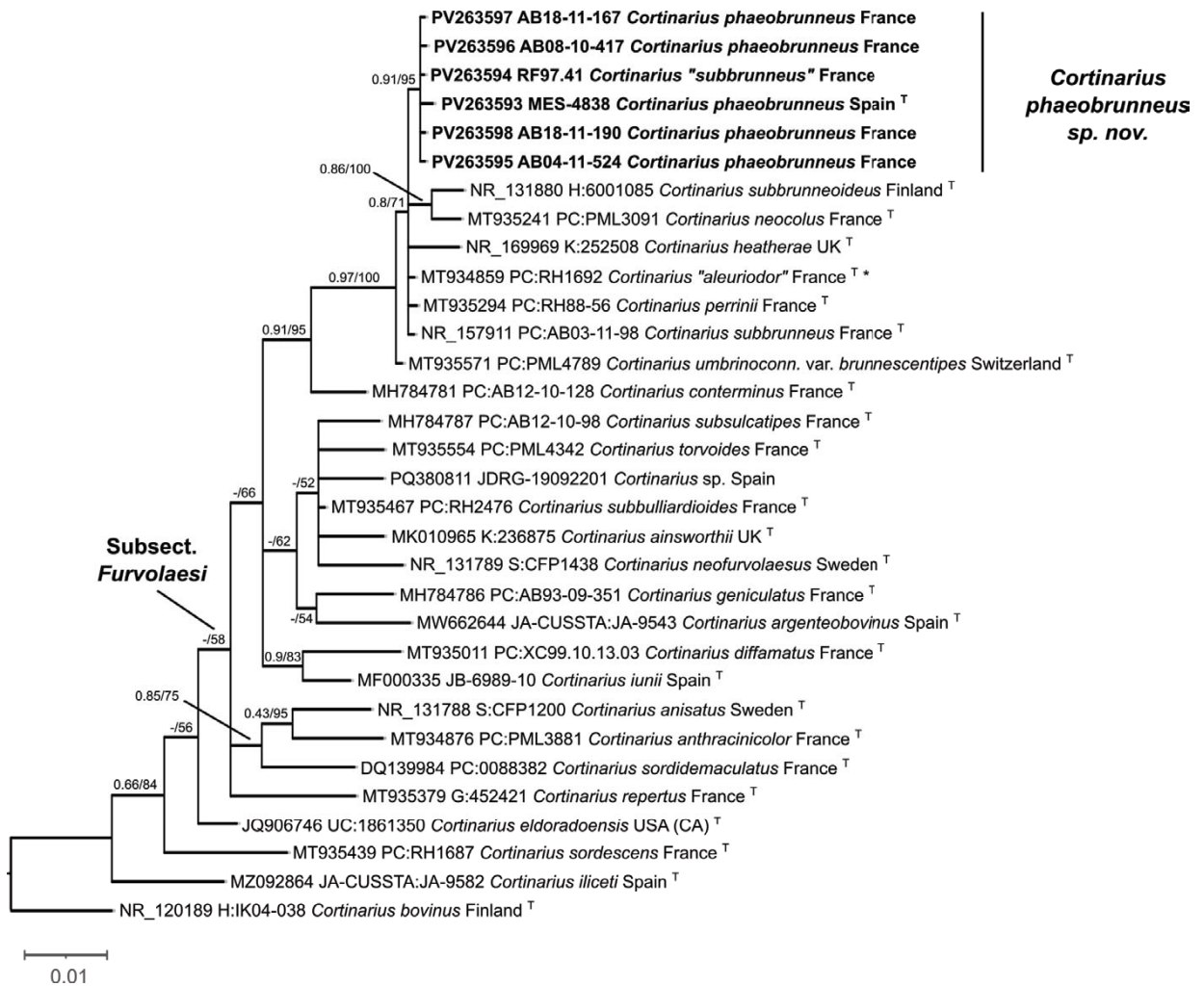
sequence GenBank PV263598); *ibid.*, 15 Nov. 2018, A. Bidaud & G. Raffini, AB 18-11-167 (ITS sequence GenBank PV263597); Gard, Saint-Jean-du-Pin, Tresmont, 300 m a.s.l., on calcareous soil under *Q. ilex*, 31 Oct. 2008, A. Bidaud, AB 08-10-417 (ITS sequence GenBank PV263596).

*Notes:* *Cortinarius phaeobrunneus* currently constitutes a strongly supported lineage of the recently revised section *Bovini*, and nests within the poorly supported subsection *Furvolaei* (Liimatainen *et al.* 2020, Schmidt-Stohn *et al.* 2025). Phylogenetically, the species is closest to *C. perrinii* (syn. *C. subbrunneus*), from which it differs by four evolutionary events (two substitutions and two indels) at the ITS locus. Because of this short phylogenetic distance and limited taxon sampling of the species, the authors of the *Atlas des cortinaires* have previously described one collection of *C. phaeobrunneus* (RF 97.41, under *C. subbrunneus*) as *C. perrinii*, in spite of morphological (abundant veil at stipe base and blue hues in the upper part of the stipe) and ecological (loamy soil under *Pinus sylvestris* vs acidic soil under *Picea abies*) differences (Bidaud *et al.* 2015, f. 1420, pl. 960). Additional sequenced collections of both species in the past decade indicates that 1) despite being not numerous, the substitutions and indels distinguishing the two clades are fixed, with no evidence of gene flow between corresponding populations, and 2) neighbouring species in this group such as *C. neocolus*, *C. heatherae*, and *C. subbrunneoideus* are also distant to each other and to *C. phaeobrunneus* and *C. perrinii*, by similarly short phylogenetic distances (e.g. *C. heatherae*/*C. perrinii* = *C. neocolus*/*C. perrinii* = *C. subbrunneoideus*/*C. perrinii* = 8 evolutionary events). Considering the morphological and ecological differences distinguishing these five species, these observations support the reproductive isolation of *C. phaeobrunneus* within a group of bovinoid taxa that may have radiated relatively recently from their latest common ancestor.

Morphologically, *C. phaeobrunneus* can be distinguished from its closest lookalikes by the usually abundant white veil covering at least the lower part of the stipe. The species seems also thermophilic, calciphilous and associated to Mediterranean *Quercus*- or *Pinus*-dominated woodlands, although a late collection from the central French Pyrénées, under *Fagus sylvatica*, suggests *C. phaeobrunneus* may be more broadly distributed (G. Corriol, pers. comm., not included here). In the same Mediterranean biomes and from the same subsection, *C. subbulliardoides* (syn. *C. tacitus*) is not rare and could be confused with *C. phaeobrunneus*. However, this species displays less developed veil and more reddish hues on the pileus.

*Supplementary material:* Alignment of *Cortinarius* subsection *Furvolaei*. <https://doi.org/10.6084/m9.figshare.28590782.v1>.

*Colour illustrations:* Holotype collection area at Barranco del Monte, Formiche Alto, Teruel, Spain. Basidiomata *in situ*, coll. AB 08-10-417 (top left); coll. AB 18-11-190 (middle left); AB 18-11-167 (bottom left); MES-4838 (bottom right, holotype). Scale bars = 1 cm.



Bayesian inference phylogenetic analysis of 32 ITS sequences representing subsect. *Furvolaesi* as introduced by Liimatainen *et al.* (2020). Numbers on branches indicate SH-aLRT and BPP support values, significant when  $\geq 0.82$  and  $\geq 95\%$ , respectively. Sequences newly generated for the present study are highlighted in **bold** and those from type material are marked by a suffix superscript T. The asterisk indicates a likely wrong sequence according to Schmidt-Stohn *et al.* (2025). All analyses were performed online at NGPhylogeny.fr (Lemoine *et al.* 2019).

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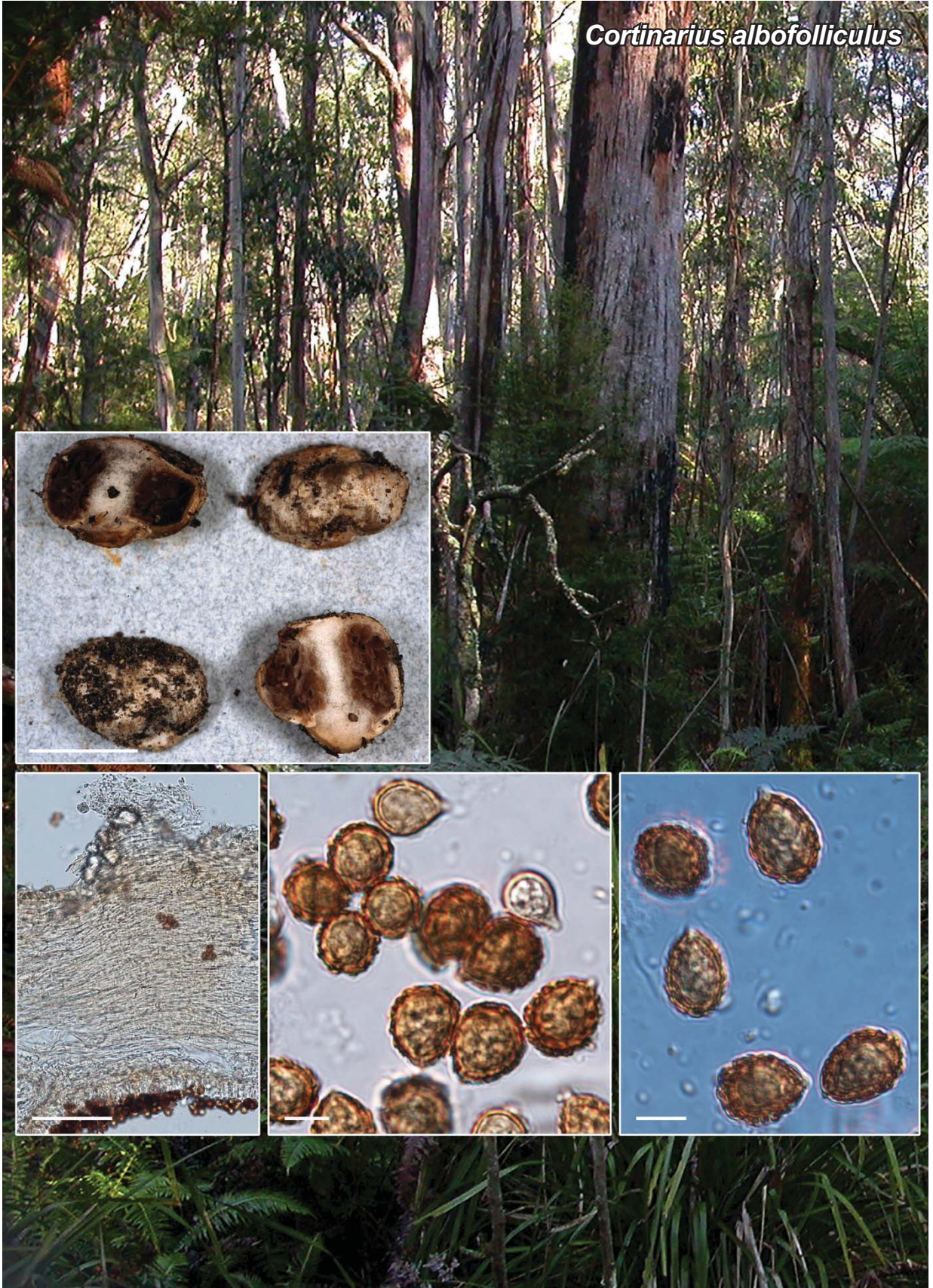
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*Cortinarius albofolliculus*



***Cortinarius albofolliculus* Polman-Short & T. Lebel, *sp. nov.***

*Etymology:* In reference to the silvery white colour and overall appearance of the basidiomes, *albofolliculus* (L. for *albo* = white, *folliculus* = small bag).

*Classification:* Cortinariaceae, Agaricales, Agaricomycetes.

*Basidiomata* 5–16 mm diam. × 5–12 mm high, globose to subglobose with slightly bulbous base; surface completely covered with silvery grey, silky, thin white to pale cream in patches universal veil, easily rubbing off, pileus handling tawny to dull brown; flesh white to translucent grey in cross-section. *Hymenophore* labyrinthine loculate, rich chestnut brown to cocoa brown. *Stipe-columella* 1–3 mm diam. × 5–8(–12) mm high, percurrent, central, solid, white, silky, extending into a basal bulb 3–5 mm diam. × 1–3 mm high, handling brownish; *context* fibrous, white, occasionally appearing silver to translucent. *Universal veil* silky white, dry, delicate and easily rubbing off, persistent, remaining attached to pileus rim and stipe base. *Partial veil/Cortina* cobwebby, silky white, persistent. *Odour* not recorded. *Basal rhizomorphs* white. *Basidiospores* (12.9–)13.5–15.25(–16.25) × (9.5–)10.0–12.0(–13.0) µm, (14.03 ± 1.15 × 11.16 ± 0.97, Q= 1.1–1.5, n = 56), subglobose to obovate, thick-walled, ornamentation roughly warty-nodulose 0.5–1.5 µm high, deep orange brown in water or 3 % KOH. *Basidia* 33–51 × 11–13.5 µm, narrowly clavate, unpigmented; mostly 4-spored, occasionally 2- or 3-spored, sterigmata 3–5 µm long. *Cystidia* 20–38 × 6–9 µm, cylindrical to narrow clavate, unpigmented, scattered in hymenium. *Hymenophoral trama* 30–90 µm wide, of loosely interwoven hyaline inflated hyphae 8–15.5 µm diam. *Subhymenium* 15–35 µm wide, of inflated hyaline hyphae 7.5–15.0 µm diam., appearing pseudoparenchymatous. *Pileipellis* 25–135 µm wide, forming a thin, patchy, ixocutis of mostly horizontal hyphae 2–5.5 µm diam., embedded in a gelatinised matrix, with occasional upright tips protruding beyond, and scattered patches of hyaline or faintly golden crystals. *Pileus context* 130–350 µm wide, of slightly inflated, short-septate interwoven hyphae 8–15 µm diam., sometimes appearing brick-like, patchily golden pigmented or slightly pigmented throughout. *Clamp connections* observed in hymenophoral trama and pileipellis.

*Habit, habitat and distribution:* Embedded in long decayed wood, deep leaf litter and/or mossy soil, in *Eucalyptus* forest, fruiting in small clusters. Australia (New South Wales) distribution.

*Typus:* **Australia**, New South Wales, South Coast, Off Imlay road to south, 1.6 km west of junction with Wog Way (TL site MGS 7.2), 30 May 2001, T. Lebel, H. Bender & J. Zdraveski TL471 (**holotype** MEL 2314445; ITS and LSU sequences GenBank PQ472589 and PQ472610).

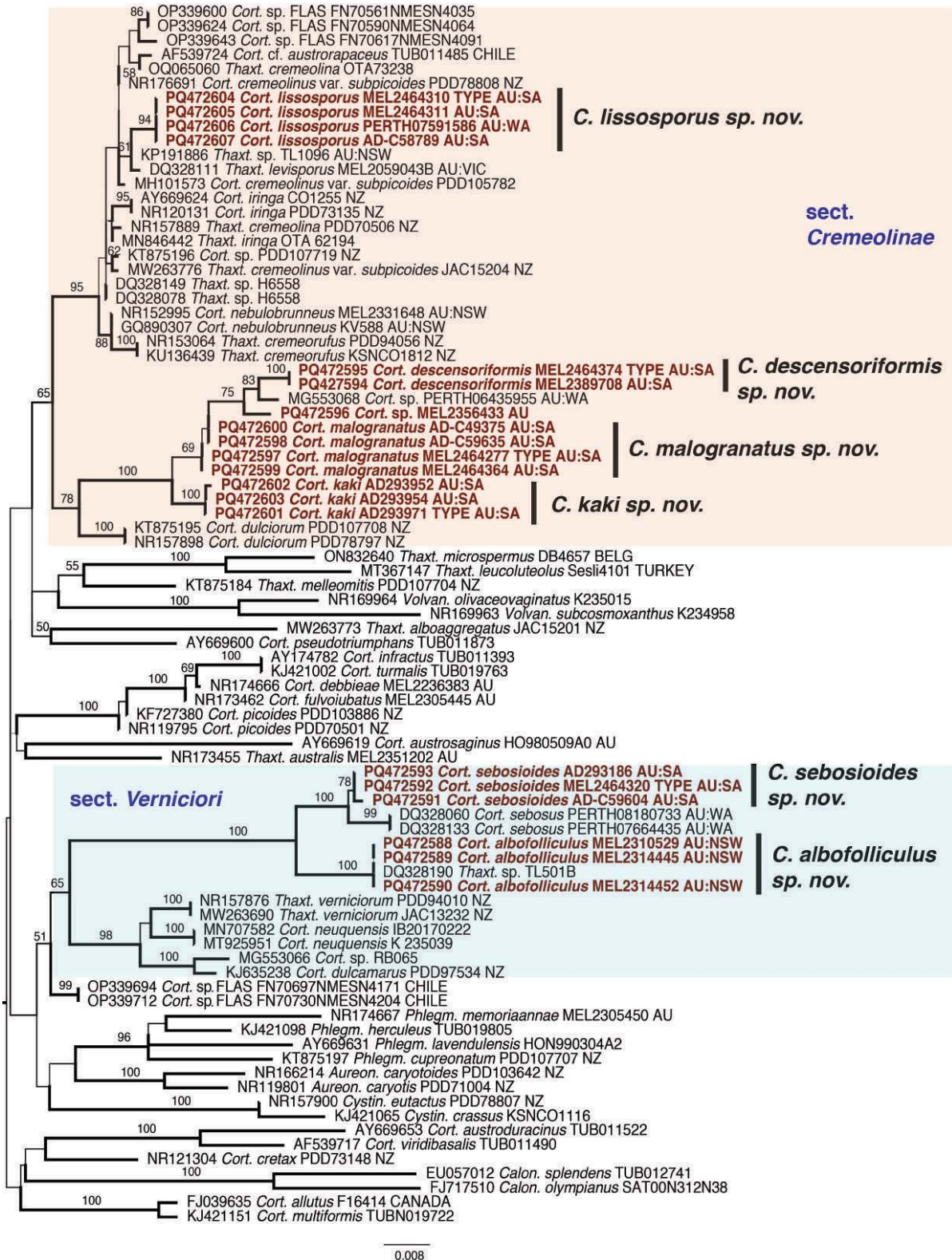
*Colour illustrations:* Long unburnt *Eucalyptus* woodland dominated by *E. cypellocarpa* with *Xanthorrhoea* spp. and *Cyathus australis* (tree fern) understory, Nungatta State Forest, New South Wales, Australia, holotype site. Basidiomata in lab and field; microscopic elements: cross-section of pileipellis and hymenium in KOH; orange-brown, thick-walled ornamented basidiospores in water. Scale bars: basidiomata = 10 mm; pileipellis = 100 µm; spores = 10 µm.

*Additional material examined:* **Australia**, New South Wales, South Coast, Off Nungatta Road, 3.35 km from junction with Imlay Road, to the west of Nungatta Road (TL site MGS 3.1), 31 May 2001, S.H. Lewis, TL496 (MEL 2310529; ITS and LSU sequences GenBank PQ472588 and PQ472609); South Coast, Off Nungatta Road, 3.35 km from junction with Imlay Road, to the west of Nungatta Road (TL site MGS 3.1), 31 May 2001, H. Bender, TL493 (environmental sample, single basidiome); South Coast, Odd Reef road east, 2.8 km south of junction with Laings road, west side of road, (TL site SAM 1.1), 4 Jun. 2002, J.M. Trappe, TL1264 (MEL 2314452; ITS and LSU sequences GenBank PQ472590 and PQ472611); South Coast, Off Nungatta Road, 3.35 km from junction with Imlay Road, to the west of Nungatta Road (TL site MGS 3.1), 31 May 2001, S.H. Lewis, H. Bender, J. Zdravevski, J. Tonkin & T. Lebel, TL501B (MEL 2310526B; ITS sequence GenBank DQ328190).

*Notes:* Basidiomes of *C. albofolliculus* resemble those of *C. walpolensis* (Francis & Bougher 2004) and several undescribed taxa, in the loculate brown hymenophore, the truncate or percurrent stipe-columella. However, *C. albofolliculus* lacks the cinnamon fibrils that *C. walpolensis* basidiomes have, though these are fragile and easily rubbed off during collection. Microscopically *C. albofolliculus* has considerably larger spores (av. 14.03 × 11.16 µm) with more robust warts up to 1.5 µm high, than *C. walpolensis* (av. 8.0 × 5.0 µm) with small warts up to 0.5 µm high. The larger spores and more robust spore ornamentation are consistent with those of *C. sebosus* and *C. sebosoides*. In terms of distribution, there is no overlap, as *C. albofolliculus* is currently known only from southern New South Wales, *C. walpolensis* and *C. sebosus* from southern Western Australia, and *C. sebosoides* from southern South Australia.

*Cortinarius albofolliculus* is a strongly supported taxon (BS 100/ PP 1.0) placed in strongly supported clade (BS 100/ PP 1.0) with the sequestrate taxa *C. sebosus* and *C. sebosoides* *sp. nov.* In this analysis, these sequestrate taxa are placed in a poorly supported (BS 30/ PP 0.69) sect. *Verniciori* (Liimatainen *et al.* 2022) clade that includes *C. neuquensis* (Salgado Salomon *et al.* 2021) from Argentina (light ochre brown to reddish glutinous pileus with pale cinnamon universal veil), *C. verniciorum* (Soop 2013) and *C. dulcamarus* (Soop 2016) from New Zealand (orange brown basidiomes with strongly viscid pilei), and *Cortinarius* sp. (MG553066, RB065) from Western Australia. The basidiomata of the sequestrate taxa do not resemble the mushroom counterparts in this poorly supported clade, lacking any viscosity, and generally lacking any hints of orange or reddish colouration. In a much broader sampling of species, (ITS only; unpubl.), all three sequestrate taxa *C. sebosoides* *sp. nov.*, *C. albofolliculus* *sp. nov.* and *C. sebosus* remain in a strongly supported (PP 0.9) clade with *C. verniciorum*, *C. neuquensis* and an undescribed species from Chile (OP339712).

*Supplementary material:* Please contact the author (T. Lebel) for any queries regarding alignments or other data.



RxML v. 8 (Stamatakis 2014) phylogenetic tree obtained from the ITS-LSU-nrDNA for a selection of cortinarioid species. Bold lines indicate bootstrap support values for maximum likelihood ( $\geq 50$  % BS, values below this threshold not shown). **Bold** red text indicates sequences generated for this study: *C. malogranatus* sp. nov., *C. lissosporus* sp. nov., *C. kaki* sp. nov., *C. descensoriformis* sp. nov., *C. sebosoides* sp. nov., and *C. albofolliculus* sp. nov. Genus abbreviations (names as in GenBank): *Cort.* = *Cortinarius*, *Thaxt.* = *Thaxterogaster*, *Volvan.* = *Volvanarius*, *Phlegm.* = *Phlegmacium*, *Aureon.* = *Aureonarius*, *Cystin.* = *Cystinariius*, *Calon.* = *Calonarius*.

*Cortinarius descensoriformis*





## *Cortinarius descensoriformis* Broadbridge & T. Lebel, *sp. nov.*

**Etymology:** In reference to the overall shape of the basidiomes with persistent veil, short stipe-columella and basal bulb giving the appearance of a parachute, *descensoria* (L. for descent or descending), and *formis* (L. to appear similar to).

**Classification:** *Cortinariaceae*, *Agaricales*, *Agaricomycetes*.

**Basidiomata** emergent to hypogaeal under leaf litter, embedded in dense mycelial mat with integrated leaf litter. *Xanthorrhoea* an associated species in *Eucalyptus cladocalyx* open woodland. *Pileus* 5–25 mm diam. × 3–14 mm high, globose to subglobose to flattened turbinate apex, occasionally plane to slightly indented, finely fibrillose, dry, margin in-rolled but not attached to stipe, fine white universal veil completely encasing fruit body, persistent and easily rubbed off, overlying chestnut to honey coloured pellis. *Hymenophore* lamellate to sublamellate-labyrinthine, deep rusty yellow brown to rich brown, exposed at base where cortina has torn. *Stipe-columella* 3–8 mm diam., percurrent, solid, central, broad at apex tapering to central columella then extending into a prominent marginate basal bulb 4–9 mm diam. × 2–4 mm high; *context* white to translucent, staining rusty orange at edges of pellis and occasionally base when cut. *Universal veil* silky white, dry, thin and easily rubbing off, persistent in patches on apex of basidiomata. *Cortina* white, thick, persistent, not breaking readily, solid to occasionally arachnoid as pileus expands. *Spore drop* rusty brown on inside of cortina. *Odour* not recorded fresh, dried specimens produce ‘wet dog’ odour. *Basal rhizomorphs* white.

**Basidiospores** (7.0–)8.0–10.0(–11.0) × 5.5–7.0 μm (9 ± 0.7 × 5.7 ± 0.5, Q = 1.2–1.8, n = 75), thin-walled, asymmetric, ellipsoid to occasionally ovate, light olive brown to orange brown in water and 3 % KOH, very finely ornamented with isolated warts 0.5–1.0 μm high, immature spores can appear smooth; tapering slightly at point of attachment. *Basidia* (12.8–)21.0–24.5(–34.0) × 5.3–8.0 μm (22.3 ± 6.7 × 0.9 ± 1, Q = 1.8–4.6, n = 17), clavate to cylindrical, hyaline, length highly variable; 2- or 4-spored, sterigmata conical, 2–3 μm long, *Cheilocystidia* absent. *Pleurocystidia* absent. *Hymenophoral trama* 50–100 μm wide, of short parallel, hyaline interwoven septate hyaline hyphae 8–14 μm diam. *Subhymenium* 20–30 μm wide, of hyaline slightly inflated hyphae 8–15 μm diam. *Pileipellis* 2-layered, an epicutis 30–110 μm wide, consisting of very fine hyaline hyphae 2.0–4.5 μm diam. that widen closer to context to 6.0 μm diam., with septate terminal cylindrical elements forming a patchy upright thin turf, overlying a

subcutis 50–200 μm wide, of golden brown to deep brown pigmented inflated hyphae 25–35 × 14–25 μm. *Pileus context* 450–1000 μm wide, of interwoven hyaline hyphae 3–5 μm diam. intermixed with abundant inflated elements 10–18 × 6–15 μm. *Clamp connections* observed in pileipellis.

**Habit, habitat and distribution:** Basidiomata emergent to hypogaeal under leaf litter, embedded in dense mycelial mat with integrated leaf litter. *Xanthorrhoea* sp. and associated small shrubs in *Eucalyptus cladocalyx* open woodland. Currently known only from Kangaroo Island, South Australia.

**Typus:** **Australia**, South Australia, Kangaroo Island, De Mole Site off Jumpoff Road, within 200 m of gate on track, 24 Jun. 2017, T. Lebel & D.E.A. Catcheside, TL2885 (**holotype** MEL 2464374; ITS and LSU sequences GenBank PQ472595 and PQ472615).

**Additional materials examined:** **Australia**, South Australia, Kangaroo Island, De Mole Site off Jumpoff Road, 22 Jun. 2015, T. Lebel & H.P. Vonow, PSC4200-TL2707 (AD-C 59625, MEL 2389708; ITS and LSU sequences GenBank PQ472594 and PQ472614); Kangaroo Island, De Mole Site off Jumpoff Road, near gate on upper ridge, 29 Jun. 2016, T. Lebel, D.E.A. Catcheside & H.P. Vonow, TL2842 (MEL 2464351); Kangaroo Island, De Mole Site off Jumpoff Road, near gate on upper ridge, 23 Jun. 2018, P.S. Catcheside, D.E.A. Catcheside & H.P. Vonow, PSC4592 (AD-C 61232).

**Notes:** Basidiomes of *C. descensoriformis* resemble those of *C. debbieae* (Trappe & Claridge 2003) except the stipe-columella is less robust and much shorter, with an obvious bulbous marginate base and the lamellae are pale tan initially but become a very rich orange brown rather than dull brown as in *C. debbiae*. *Cortinarius descensoriformis* basidiomes also strongly resemble those of *C. globuliformis* but lack the bright yellow colouring of the basidiome or the mycelium (Bougher & Malajczuk 1986).

*Cortinarius descensoriformis* sits within a small strongly supported clade with several other sequestrate taxa including *C. malogranatus* *sp. nov.*, *Cortinarius* *sp.* (MEL2356433) and *C. kaki* *sp. nov.*, and an undescribed taxon with mushroom basidiome form *Cortinarius* *sp.* (RB607, PERTH06435955). Almost all the species in this clade have basidiomes with a persistent white to silvery universal veil overlying a creamy tan to brown dry or slimy pileus, and a somewhat bulbous stipe base. The exception is the collection *Cortinarius* *sp.* (RB607, PERTH06435955), which according to the accompanying notes has a glutinous orange tan to yellowish pileus. Several other species with mushroom basidiome forms, *C. dulciorum*, *C. iringa*, *C. cremeorufus*, *C. cremeolinus*, and *C. cremeolinus* var. *subpicoides* from New Zealand, and *C. “rapaceus* var. *luridus”* (GenBank AF539724 = *C. cf. austrorapaceus*; Soop *et al.* 2023) and *Cortinarius* *sp.* (GenBank OP339643, etc.) from Chile, are in a poorly supported broader sect. *Cremeolinæ* clade (BS 55/ PP 0.59; Soop *et al.* 2019, 2023), with three sequestrate taxa from Australia, *C. nebulobrunneus* (Danks *et al.* 2010), *C. lissosporus* *sp. nov.* and *Cortinarius* *sp.* (H6558).

**Colour illustrations:** Long unburnt *Eucalyptus* woodland dominated by *E. cladocalyx* with *Xanthorrhoea* *sp.* understorey, Flinders Chase National Park, Kangaroo Island, Australia, holotype site. Basidiomata in field; microscopic elements: ornamented basidiospores in water; SEM of basidiospores showing spore walls. Scale bars: basidiomata = 10 mm; spores and SEM spores = 10 μm.

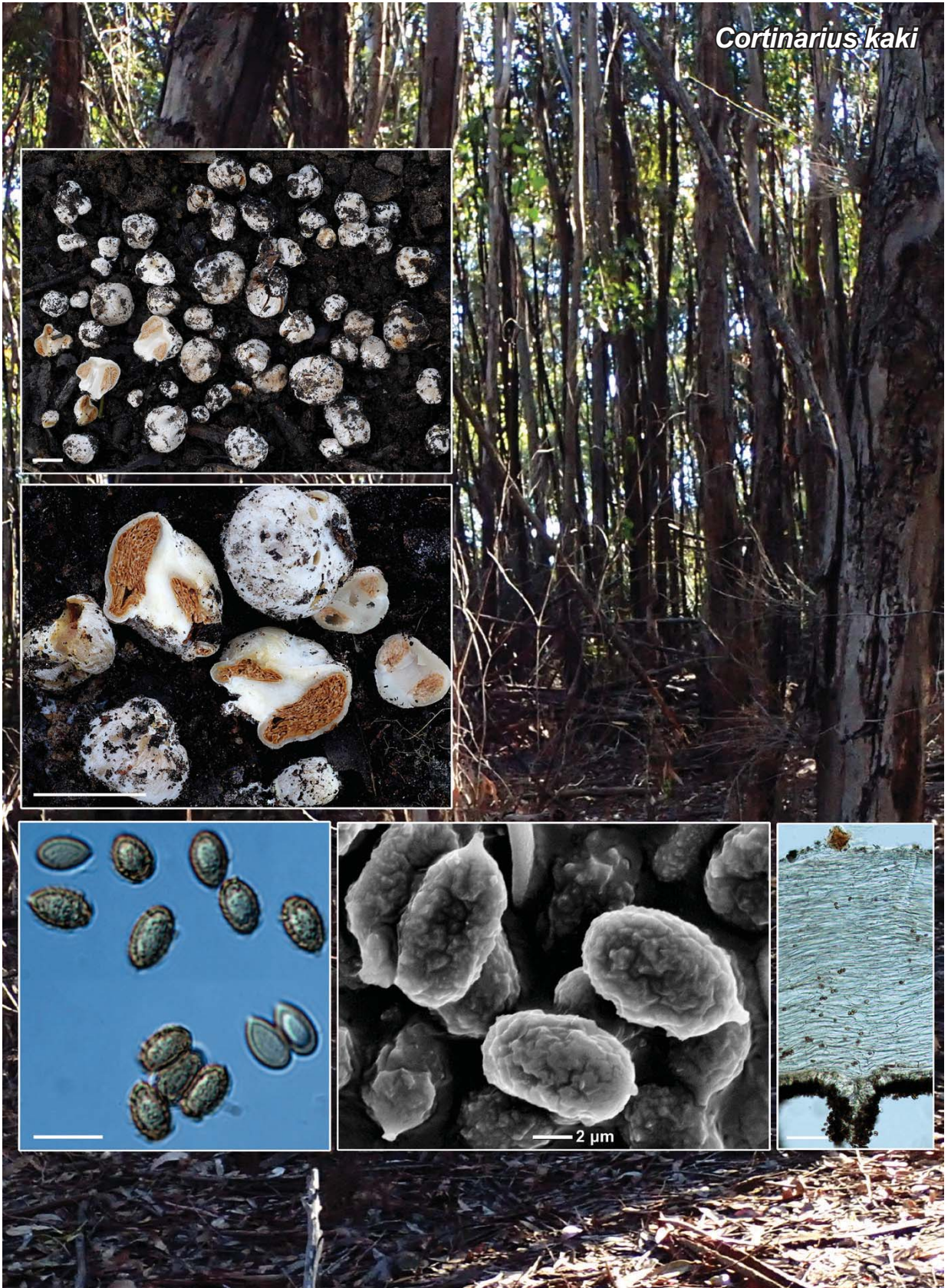
Discussion continues over whether the splitting of the old genus *Cortinarius* into 10 genera, with seven described as new (Liimatainen *et al.* 2022), was a little hasty (Gallone *et*

*al.* 2024). We have therefore maintained the use of the genus name *Cortinarius*, rather than utilizing *Thaxterogaster*, for this new species.

For phylogenetic tree, see *Cortinarius albofolliculus* (FP 1821).



*Cortinarius kaki*



***Cortinarius kaki* Broadbridge & T. Lebel, *sp. nov.***

*Etymology:* From the Japanese term for persimmon (*Diosporus kaki*) and the dye obtained from persimmon which is “kaki”, in reference to the colour of the spore mass. The fabric that results from dyeing with this pigment is called kakishibu.

*Classification:* Cortinariaceae, Agaricales, Agaricomycetes.

*Basidiomata* hypogaeal, sporulating in large numbers in clusters or singly in deep leaf litter. *Pileus* 5–21 mm diam. × 4–17 mm high, occasionally turbinate, often subglobose, irregularly folded and appressed where 2–3 sporocarps are close together, apex initially convex becoming planoconvex, dry, silky white with a thin universal veil easily rubbed off, overlying dull tan to grey translucent pileus. *Hymenophore* sublamellate to labyrinthine-loculate, initially pale dull tan becoming buff with maturity, turning light rusty brown to honey brown or bright ochre in older specimens. *Stipe-columella* 2–5(–6) mm diam., percurrent, central, solid, waxy white translucent, context remaining white or staining yellowish orange in some specimens, extending into a white basal bulb at base of stipe, ± 3–9 mm diam., with white ‘rim’ from cottony, persistent veil. *Cortina* white, persistent, staining yellow to tan brown on handling. *Odour* chlorine to floral, occasionally odourless. *Basal mycelium* white. *Basidiospores* (8.0–)9.0–10.5(–11.0) × 5.0–6.5 µm (mean 9.66 ± 0.77 × 5.98 ± 0.4, Q= 1.37–2.1, n = 32), ellipsoid to oblong, thick-walled, finely to roughly warty, ornamentation up to 1 µm high, note immature spores appearing smooth and hyaline or pale yellow, mature spores golden to rust coloured in KOH. *Basidia* 20.0–24.4(–30.4) × (7.0–)8.0–9.8 µm (av. 23.4 ± 4.9 × 8.7 ± 7, Q= 2.1–3.4, n = 6), 4-spored, clavate, smooth. *Cheilocystidia* and *pleurocystidia* not observed. *Hymenophoral trama* 180–500 µm wide, composed of parallel, interwoven hyaline hyphae 4.7–9.0 µm diam., that are occasionally inflated up to 15 µm. *Subhymenium* hyphae appearing similar to those present in hymenophoral trama. *Pileipellis* a cutis, 20–70 µm wide, composed of thin hyaline hyphae 2–4.5 µm diam, overlying a broad context, 180–600 µm wide, of interwoven, parallel, “brick-like”, septate hyphae 4.5–11 µm diam.; areas of golden pigment sparse but throughout pileipellis. *Clamp connections* not observed.

*Habit, habitat and distribution:* Sporulating in large numbers in clusters or singly in deep leaf litter under *Eucalyptus* spp in open woodland with low herbaceous layer. Currently known only from Kangaroo Island, South Australia.

*Colour illustrations:* *Eucalyptus* open woodland with mixed low shrub and *Xanthorrhoea* sp understorey, Flinders Chase National Park, Kangaroo Island, Australia, holotype site. Basidiomata in field and lab; microscopic elements: ornamented basidiospores in water; SEM of basidiospores showing irregular ornamentation. Scale bars: basidiomata = 10 mm; spores and SEM spores = 10 µm.

*Typus:* **Australia**, South Australia, Kangaroo Island, Flinders Chase National Park, along track from Mays Cottage to Platypus waterholes, woodland on first ridge, 27 Jun. 2016, T. Lebel, H.P. Vonow & D.E.A. Catcheside, TL2824 (**holotype** AD 293971, **isotype** MEL 2464333; ITS and LSU sequences GenBank PQ472601 and PQ472620).

*Additional materials examined:* **Australia**, South Australia, Kangaroo Island, Flinders Chase National Park, along main Visitors Centre track from Mays Cottage to Platypus waterholes, 23 Jun. 2019, T. Lebel, TL3127 (AD 293952; ITS and LSU sequences GenBank PQ472602 and PQ472621); Kangaroo Island, Flinders Chase National Park, along track from Mays Cottage to Platypus waterholes, lunch stop ridge, 23 Jun. 2019, T. Lebel, TL3129 (AD 293954; ITS sequence GenBank PQ472603).

*Notes:* *Cortinarius kaki* differs from *C. walpolensis* (Francis & Bougher 2004) in the lack of cinnamon fibrils on the pale pileus surface that inconsistently stain brown, more robust basal bulb to stipe and robust percurrent stipe, and lack of yellow pigmentation in pileipellis or context in *C. kaki*. *Cortinarius kaki* sits within a small strongly supported clade (BS 100/ PP 1.0) with several other sequestrate taxa *C. descensoriformis* *sp. nov.*, *Cortinarius* *sp.* (MEL2356433) and *C. malogranatus* *sp. nov.*, and an undescribed taxon with mushroom basidiome form *Cortinarius* *sp.* (RB607, PERTH06435955). Almost all the species in this clade have basidiomes with a persistent white to silvery universal veil overlying a creamy tan to brown dry or slimy pileus, and a somewhat bulbous stipe base. The exception is the collection *Cortinarius* *sp.* (RB607, PERTH06435955), which according to the accompanying notes has a glutinous orange tan to yellowish pileus. Several other species with mushroom basidiome forms, *C. dulciorum*, *C. iringa*, *C. cremeorufus*, *C. cremeolinus*, and *C. cremeolinus* var. *subpicoides* from New Zealand, and *C. “rapaceus* var. *luridus”* (GenBank AF539724 = *C. cf. austrorapaceus*; Soop *et al.* 2023) and *Cortinarius* *sp.* (GenBank OP339643, etc.) from Chile, are in a poorly supported broader sect. *Cremeoliniae* clade (BS 55/ PP 0.59; Soop *et al.* 2019, 2023), with three sequestrate taxa from Australia, *C. nebulobrunneus* (Danks *et al.* 2010), *C. lissosporus* *sp. nov.* and *Cortinarius* *sp.* (H6558).

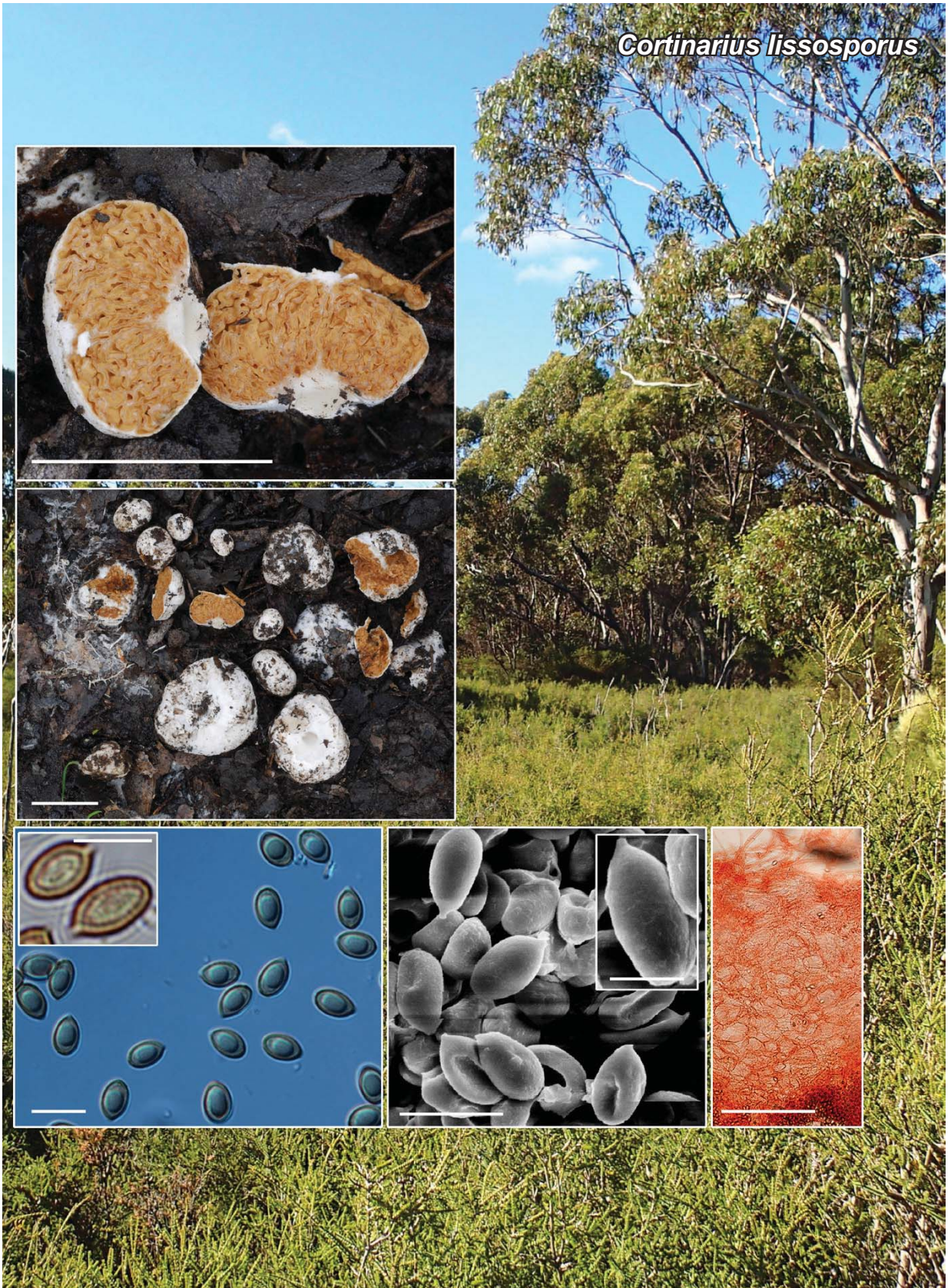
Discussion continues over whether the splitting of the old genus *Cortinarius* into 10 genera, with seven described as new (Liimatainen *et al.* 2022), was a little hasty (Gallone *et al.* 2024). We have therefore maintained the use of the genus name *Cortinarius*, rather than utilizing *Thaxterogaster*, for this new species.

For phylogenetic tree, see *Cortinarius albofolliculus* (FP 1821).

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*Cortinarius lissosporus*



***Cortinarius lissosporus* Broadbridge & T. Lebel, *sp. nov.***

*Etymology*: Alluding to the smooth appearance of the spores, *lisso* (GK. for smooth), which is not very common in the genus.

*Classification*: *Cortinariaceae*, *Agaricales*, *Agaricomycetes*.

*Basidiomata* hypogaeal in clusters, well embedded in leaf litter and organic layer. *Pileus* 6–40 mm diam. × 5–35 mm high, globose to subglobose, occasionally flattened, with planoconvex to convex apex and some furrowing or ridging in older specimens, smooth to faintly fibrillose silky, easily rubbed off, dry, white to ivory coloured; flesh up to 0.8 mm thick, white to cream coloured. *Hymenophore* loculate, chambers fine, labyrinthine, initially bright yellowish brown, burnt amber or sienna, becoming bright orangish rusty brown to cinnamon in age. *Stipe* 1–5 mm high × 3–8 mm diam., present as an inserted bulbous basal pad, barely exerted beyond pileus, white, dry, cottony; context white to translucent; *columella* absent or present as narrow white percurrent strand 0.5 mm diam. *Universal veil* white, silky thin layer completely encasing pileus, becoming cottony, with robust attachment between basal pad margin and pileus, persistent. *Cortina* (*partial veil*) present, white, fragile. *Basal mycelium* white. *Odour* faint chlorine. *Basidiospores* (7.0–)8.0–9.0(–9.5) × (4.5–)5.0–6.0 μm, (av. 8.21 ± 0.62 × 5.22 ± 0.40, Q = 1.37–1.94, n = 51), broadly ellipsoid to lemon shaped with somewhat tapering point of attachment, symmetrical, thick walled, pigmented golden, appearing smooth or unornamented in KOH or water but very fine lines and flat warts barely visible under SEM. *Basidia* (13.5–)17.0–25.0(–29.9) × 5.5–8.0 μm, (av. 22.35 ± 4.9 × 6.62 ± 0.87, n = 23), slightly clavate, unpigmented, appear long due to length/width ratio, 4-spored. *Cystidia* absent. *Hymenophoral trama* 30–50 μm wide, of highly inflated septate hyaline hyphae, 14–23 μm diam., interwoven and appearing parenchymatous. *Subhymenium* of hyaline hyphae, 6–13 × 4–11 μm diam., interwoven and narrower than hymenial trama hyphae. *Pileipellis* 15–65 μm wide, a narrow cutis composed of thin, loosely interwoven septate hyphae 3–8 μm diam., that extend past pileus surface in a patchy tomentum, smooth walled though occasionally with very fine crystalline ornamentation, golden brown pigmentation in parts; overlying a broad context 110–450 μm wide, of loosely interwoven highly inflated hyaline hyphae 15–24 μm diam., appearing parenchymatous in patches. *Clamp connections* observed within hymenophoral trama and pileipellis.

*Habitat, habitat and distribution*: Hypogaeal in clusters, well embedded in leaf litter and organic layer under old *Melaleuca* sp. and *Callitris* sp. in swampy areas of heathland with lots of downed wood of varying diameter, in mixed *Eucalyptus* woodland. Currently known from Kangaroo Island, South Australia and southwest Western Australia.

*Typus*: **Australia**, South Australia, Kangaroo Island, Flinders Chase National Park, Platypus Waterholes Track, *Melaleuca* sp. and *Callitris* sp. old stand of dead trees, 25 Jun. 2016, T. Lebel, P.S. Catcheside, D.E.A. Catcheside & H.P. Vonow, TL2801 (**holotype** AD 293977, **isotype** MEL 2464310; ITS sequence GenBank PQ472604).

*Additional materials examined*: **Australia**, South Australia, Kangaroo Island, Flinders Chase National Park, Platypus Waterholes Track, under old *Melaleuca* sp. and *Callitris* sp., southern side of path, 25 Jun. 2016, T. Lebel, P.S. Catcheside, D.E.A. Catcheside & H.P. Vonow, TL2802 (AD 293970, MEL 2464311; ITS sequence GenBank PQ472605); Deep Creek National Park, Stringybark Walking track, eucalypt woodland, 15 Jul. 2005, P.S. Catcheside & D.E.A. Catcheside, PSC2244 (AD-C 52872); Deep Creek National Park, Wildflower Walk track, in open mossy compacted soil, 6 Jul. 2013, T.M. Bridle, TMB1613 (AD-C 58789; ITS and LSU sequences GenBank PQ472607 and PQ472622); Western Australia, Boyicup, *Eucalyptus* woodland, 1 Jul. 1975, P. Christensen, JMT5456 (PERTH 07591586; ITS sequence GenBank PQ472606).

*Notes*: *Cortinarius lissosporus* might be easily confused with sequestrate species of *Austropaxillus* (= *Gymnopaxillus*) or *Descolea* (= *Hysterogaster*) in the white to pale creamy basidiomes with pale tan to burnt sienna loculate hymenophore, reduced stipe-columella and smooth appearance of the spores. However, the spores of both *Austropaxillus* and *Descolea* are considerably larger, typically 13–22 μm long, and are dextrinoid in Melzer's reagent. *Cortinarius lissosporus* basidiomes also resemble those of *C. walpolensis* (Francis & Bougher 2004), but the spores appear smooth, unlike *C. walpolensis* spores which are ornamented with obvious irregular fine low warts and rods (up to 0.5 μm high). Analysis of molecular data (ITS–LSU) places *Cortinarius lissosporus* in a moderately supported clade (BS 60/ PP 0.86) with two sequences from undescribed Australian sequestrate species *Cortinarius* sp. (GenBank KP191886) and *Cortinarius* aff. *levisporus* (GenBank DQ328111). From the field notes these two collections have similar macromorphology to the new species but differ microscopically.

*Colour illustrations*: Mixed *Eucalyptus* woodland dominated by *Melaleuca* sp. and *Callitris* sp. with mixed heathland understorey, 4 yrs after fire, Flinders Chase National Park, Kangaroo Island, Australia, holotype site. Basidiomata in the field; microscopic elements: smooth spores in water; SEM of basidiospores showing very low ornamentation on some spores. Scale bars: basidiomata = 10 mm; spores 10 and SEM spores = 10 μm.



These taxa are all part of a strongly supported clade (BS 92/ PP 1.0) in a poorly supported sect. *Cremeolinae* (Soop *et al.* 2019, 2023) of several taxa with mushroom basidiomata form including *C. iringa*, *C. cremeorufus*, *C. cremeolinus*, and *C. cremeolinus* var. *subpicoides* from New Zealand, and *C. "rapaceus* var. *luridus*" (GenBank AF539724 = *C. cf. austrorapaceus* Soop *et al.* 2023) and *Cortinarius* sp. (GenBank OP339624, etc.) from Chile. The sequestrate *Cortinarius nebulobrunneus* has robust, almost agaricoid basidiomes, with a fine white bloom of universal veil over a pale tan pileus, darker hymenophore, and ellipsoid, finely warty spores (Danks *et al.* 2010). All taxa in this clade have spores that appear smooth or with low (< 0.8 µm high) fine ornamentation.

Discussion continues over whether the splitting of the old genus *Cortinarius* into 10 genera, with seven described as new (Liimatainen *et al.* 2022), was a little hasty (Gallone *et al.* 2024). We have therefore maintained the use of the genus name *Cortinarius*, rather than utilizing *Thaxterogaster*, for this new species.

For phylogenetic tree, see *Cortinarius albofolliculus* (FP 1821).

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*Cortinarius malogranatus*





## *Cortinarius malogranatus* Broadbridge & T. Lebel, *sp. nov.*

**Etymology:** In reference to the overall appearance of the deep purple brown, thick-walled spores in the hymenophore which are reminiscent of the interior of a pomegranate, *malogranata* (L. for pomegranate, “apple with many seeds”).

**Classification:** *Cortinariaceae*, *Agaricales*, *Agaricomycetes*.

**Basidiomata** hypogaeal, fruiting singly or in small clusters, embedded in a dense mat of slightly gummy mycelium and fine leaf litter. **Pileus** 8–22(–25) mm diam. × 8–16 mm high, turbinate to parachute shaped becoming planoconvex with occasionally shallowly depressed apex at maturity, surface dry; silvery white to smokey grey translucent sheen from overlying very fine white universal veil completely encasing younger basidiomes, overlying pale cream to translucent tissue underneath, occasionally with metallic blue-green sheen in mature basidiomes or where veil is eroded with handling; **pellis** context ± 1–3 mm thick at apex, narrowing to 0.5–1.0 mm at margin, moist, waxy-cartilaginous, translucent pale cream to pale tan, margin remaining incurved at maturity. **Hymenophore** labyrinthine sublamellate, irregular in shape, initially dull pale brown becoming rich dark brown. **Stipe-columella** 3–8 mm diam., white, dry, percurrent, robust, central, cylindrical, expanding into a bulbous base which barely protrudes beyond pileus margin, apparent as thin white disc at base of stipe-columella when viewed on upturned basidiomes; context translucent to cartilaginous, staining yellowish to orange at outer edges of pileus and base when cut in some basidiomes. **Universal veil** white, dry, fibrillose fine bloom over whole basidiome, thin, easily removed by rubbing, remaining attached from pellis to the basal bulb, persistent. **Cortina (partial veil)** present as a barely visible, fine, white, short layer between basal bulb margin and pileus margin. **Spore colour** dark brown en masse. **Odour** none or sometimes chlorine to faintly floral. **Basal mycelium** white. **Basidiospores** (13.2–)16.0–20.0(–23.4) × 13.0–17.0(–21.5) μm, (av. 17.9 ± 2.1 × 16.3 ± 2.1, Q= 0.9–1.5, n = 74), mostly globose, occasionally subglobose and slightly asymmetrical, thick walled, finely ornamented with flat topped broad pegs and ridges 0.8–2.0 μm high, barely visible beneath utricle, heavily pigmented deep purple-brown; point of attachment quite defined. **Basidia** (16.6–)25–44(–66) × (6.9–)10.0–16.0(–18.7) μm, (av. 39.7 ± 12.1 × 13.1 ± 3.3, Q = 1.7–7, n = 43), cylindrical to narrowly clavate, mostly 4-spored though occasionally 2- or 3-spored; sterigmata 3.5–5.4 μm long, robust. **Cheilocystidia** not observed. **Pleurocystidia** not observed. **Hymenophoral trama** 35–80 μm wide, of hyphae

arranged linearly “brick-like”, slightly inflated in areas, 5–15(–26) μm, unpigmented or with subtle golden pigment towards subhymenium. **Subhymenium** 14–30 μm wide, composed of both thin hyaline hyphae and inflated hyphae, 3–5 μm diam. **Pileipellis** 10–45 μm wide, a cutis composed of thin, loosely interwoven hyphae 2.4–5.7(–7.5) μm, with very fine golden ornamentation scattered on walls, overlying a broad context, 165–560 μm wide, composed of hyphae 4.8–15.7 μm diam., with faintly golden content in patches. **Clamp connections** observed in pellis hyphae.

**Habit, habitat and distribution:** Fruiting singly or in small clusters, embedded in a dense mat of slightly gummy mycelium and fine leaf litter in *Eucalyptus cladocalyx* open woodland in deep leaf litter. Associated plants *Xanthorrhoea* and small shrubs. Known from southern South Australia.

**Typus:** **Australia**, South Australia, Kangaroo Island, De Mole site at end of Jumpoff Road off the Playford Highway, to east of track to bridge into nearby creekline, *Eucalyptus* open woodland in deep leaf litter, 22 Jun. 2016, T. Lebel, P.S. Catcheside & D.E.A. Catcheside, TL2768 (**holotype** AD 293974, **isotype** MEL 2464277; ITS sequence GenBank PQ472597).

**Additional materials examined:** **Australia**, South Australia, Kangaroo Island, Rocky River track near bridge, 27 Jun. 2004, P.S. Catcheside & D.E.A. Catcheside, PSC1981 (AD-C 49375; ITS and LSU GenBank PQ472600 and PQ472618); Kangaroo Island, De Mole Site at end of Jumpoff Road off the Playford Highway, Site 2, 23 Jun. 2015, T. Lebel & P.S. Catcheside, TL2708/PSC4249 (AD-C 59635, MEL 2389706; ITS and LSU sequences GenBank PQ472598 and PQ472617); Kangaroo Island, Rocky River Bridge track, 23 Jun. 2017, H.P. Vonow, G. Scott & S. Giacopini, TL2875 (AD 293975, MEL 2464364; ITS and LSU sequences GenBank PQ472599 and PQ472619); Kangaroo Island, Flinders Chase National Park, Rocky River track near bridge, 19 Jul. 2005, P.S. Catcheside, PSC2276 (AD-C 52859); Kangaroo Island, Flinders Chase National Park, Rocky River track, 19 Jul. 2006, P.S. Catcheside, PSC2587 (AD-C 54661).

**Notes:** *Cortinarius malogranatus* resembles another sequestrate species, *C. sebosus* from Western Australia (Francis & Bougher 2004), in the sublamellate brown hymenophore and reasonably robust stipe-columella. However, the pileus of *C. malogranatus* is dry not slightly viscid, and silvery white to smokey grey (due to the persistent universal veil) or sometimes metallic blue grey in older basidiomes, versus the creamy yellow, greenish grey or slightly purple pileus of *C. sebosus*. In microscopic characters, *C. sebosus* consistently has 2- rather than 4-spored basidia. Furthermore, analysis of molecular data (ITS) places *C. malogranatus* sp (BS 42 / PP 0.84) in a completely different lineage within *Cortinarius*, sect. *Cremeolinae*, to *C. sebosus* (placement in sect. *Verniciori*, Liimatainen *et al.* 2022, with low support BS 30/ PP 0.69). *Cortinarius malogranatus* sits within a small strongly supported clade (BS 100/ PP 1.0) with several other sequestrate taxa *C. descensiformis* sp. nov.,

**Colour illustrations:** Long unburnt *Eucalyptus* woodland dominated by *E. cladocalyx* with *Xanthorrhoea* sp. understory, Flinders Chase National Park, Kangaroo Island, Australia, holotype site. Basidiomata in lab and field; microscopic elements: deep purple-brown, thick-walled ornamented basidiospores in water; SEM of basidiospores showing spore walls. Scale bars: basidiomata = 10 mm; spores and SEM spores = 10 μm.

*Cortinarius* sp. (MEL2356433) and *C. kaki* sp. nov., and an undescribed taxon with mushroom basidiome form *Cortinarius* sp. (RB607, PERTH06435955). Almost all the species in this clade have basidiomes with a persistent white to silvery universal veil overlying a creamy tan to brown dry or slimy pileus, and a somewhat bulbous stipe base. The exception is the collection *Cortinarius* sp. (RB607, PERTH06435955), which according to the accompanying notes has a glutinous orange tan to yellowish pileus. Several other species with mushroom basidiome forms, *C. dulciorum*, *C. iringa*, *C. cremeorufus*, *C. cremeolinus*, and *C. cremeolinus* var. *subpicoides* from New Zealand, and *C. "rapaceus* var. *luridus*" (GenBank AF539724 = *C. cf. austrorapaceus*; Soop *et al.* 2023) and *Cortinarius* sp. (GenBank OP339643, etc.) from

Chile, are in a poorly supported broader sect. *Cremeolinae* clade (BS 55/ PP 0.59; Soop *et al.* 2019, 2023), with three sequesterate taxa from Australia, *C. nebulobrunneus* (Danks *et al.* 2010), *C. lissosporus* sp. nov. and *Cortinarius* sp. (H6558). Variation in the barcode genes ITS and LSU is low in sect. *Cremeolinae*, and further genes are required to disentangle close relationships within this clade of Southern Hemisphere taxa.

Discussion continues over whether the splitting of the old genus *Cortinarius* into 10 genera, with seven described as new (Liimatainen *et al.* 2022), was a little hasty (Gallone *et al.* 2024). We have therefore maintained the use of the genus name *Cortinarius*, rather than utilizing *Thaxterogaster*, for this new species.

For phylogenetic tree, see *Cortinarius albofolliculus* (FP 1821).



*Cortinarius sebosoides*



***Cortinarius sebosoides* Broadbridge & T. Lebel, *sp. nov.***

*Etymology:* In reference to the close relationship, and resemblance to, *Cortinarius sebosus*.

*Classification:* *Cortinariaceae*, *Agaricales*, *Agaricomycetes*.

*Basidiomata* embedded in long decayed wood litter and/or mossy soil, not solitary. *Pileus* 5–13 mm diam. × 5–15 mm high, turbinate or elongate to flattened with distinctly bulbous base; surface completely covered with silvery silky thin white to pale cream in patches universal veil, easily rubbing off, overlying dark grey to warm tan translucent flesh. *Hymenophore* sublammellate to lamellate, few cross connections, colour initially buff brown to rich chestnut brown to cocoa brown. *Stipe-columella* 2.5 × 3.5(–4) mm diam. × 8–12(–14) mm high, percurrent, central, solid, white, silky, dry, extending into a broad basal bulb 3–8(–11) mm diam. × 2–4 mm high, with patches of orange tinges on some specimens or presenting as an orange-tinged rim (fragile, easily rubbed off); *context* fibrous, white, occasionally appearing silver to translucent, staining orangish around outer edge when freshly cut. *Universal veil* silky white, dry, relatively thick but easily rubbing off, persistent remaining attached to pileus rim and stipe base. *Partial veil/Cortina* cobwebby, fragile, thin, silky white, remaining attached. *Odour* not recorded. *Basal rhizomorphs* white. *Basidiospores* (10.0–)13.0–17.6(–18.7) × 9.0–11.8(–13.0) μm, (14.8 ± 1.72 × 10.97 ± 1.01, Q = 1.1–1.7, n = 60), subglobose to obovate, thick-walled, ornamentation warty-nodulose 0.5–2 μm high, more prominent at spore apex, golden to rusty brown in water or 3 % KOH. *Basidia* 15–40 × 3–11 μm, (av. 30.7 ± 8.1 × 8.1 ± 3.1, Q = 2.6–7.9, n = 22), narrowly clavate, occasionally with faint golden pigment; mostly 2- or 4- spored, sometimes 1- or 3-spored, sterigmata 4–7 μm long. *Cystidia* 26–30 × 6–8 μm, smooth, clavate. *Hymenophoral trama* 40–250 μm wide, of loosely interwoven hyaline inflated hyphae 4.1–18.5 μm diam. *Subhymenium* 15–35 μm wide, of inflated hyphae 7.5–15.2 μm diam., hyphae golden fading to near translucent halfway across width. *Pileipellis* 47–99 μm wide, an ixocutis of mostly horizontal golden pigmented hyphae 1.8–4.0 μm diam. embedded in a gelatinised matrix, though on some specimens hyphal tips protruding from surface, hyphae smooth with occasional ornamentation appearing as small bumps throughout. *Pileus context* 180–340 μm wide, of highly inflated hyphae 11–20 μm diam., appearing parenchymatous, with patchy golden pigmentation. *Clamp connections* observed in hymenophoral trama and pileal context. *Pigment deposits* golden throughout the hymenophore.

*Habit, habitat and distribution:* Embedded in long decayed wood litter and/or mossy soil, fruiting in clusters in eucalypt woodland. Currently known from Kangaroo Island, southern South Australia.

*Typus:* **Australia**, South Australia, Kangaroo Island, Flinders Chase National Park, Ravine des Casoars near bridge, 26 Jun. 2016, *T. Lebel, P.S. Catcheside, D.E.A. Catcheside & H.P. Vonow*, TL2811 (**holotype** AD 293973, **isotype** MEL 2464320; ITS and LSU sequences GenBank PQ472592 and PQ472612).

*Additional materials examined:* **Australia**, South Australia, Kangaroo Island, Flinders Chase National Park, Ravine des Casoars, site 1 near bridge, 22 Jun. 2015, *H.P. Vonow*, PSC4192 (AD-C 59604; ITS sequence GenBank PQ472591); Adelaide Hills, Mylor Conservation Reserve off Whitehead Road, along edge of track, 4 Jun. 2023, *T. Lebel*, TL3575 (AD 293186; ITS and LSU sequences GenBank PQ472593 and PQ472613).

*Notes:* Basidiomes of *C. sebosoides* resemble those of *C. sebosus* (Francis & Bougher 2004) and *C. malogranatus sp. nov.* in the sublammellate brown hymenophore and reasonably robust stipe-columella. However, *C. sebosoides* lacks the yellow-, greenish grey or dull purple tinges present in *C. sebosus*, and has a basal bulb with patches of orange tinges or an orange-tinged rim and a stipe context that stains orangish around the outer edge when freshly cut. Unfortunately, the orange fibrils on the basal bulb are fragile and easily rubbed off during collection, thus are often missing from basidiomes. Microscopically *C. sebosoides* has mostly 4- rather than 2- spored basidia, slightly smaller and narrower spores (av. 14.8 × 11 μm) than *C. sebosus* (av. 17.5 × 12 μm), and a narrower ixocutis of golden pigmented rather than hyaline hyphae overlying a broad context of patchily pigmented hyphae. *Cortinarius sebosoides* (BS 61/ PP 0.9) is placed in a strongly supported clade (BS 100/ PP 1.0) with the sequestrate *C. sebosus* from Western Australia; there are consistent 4–6 bp difference between the two taxa in the ITS region. This, together with morphological differences, and lack of overlap in current distributions, encouraged us to describe *C. sebosoides* at the species rather than varietal level. A third sequestrate species, *C. albofolliculus sp. nov.*, is sister to these taxa. In this analysis, these sequestrate taxa are placed in a poorly supported (BS 30/ PP 0.69) sect. *Verniciori* (Liimatainen *et al.* 2022) clade that includes *C. neuquensis* from Argentina (light ochre brown to reddish glutinous pileus with pale cinnamon universal veil; Salgado Salomon *et al.*

*Colour illustrations:* *Eucalyptus* woodland with a mixture of mallee form *Eucalyptus* spp. with mixed heath shrub understory, Flinders Chase National Park, Kangaroo Island, Australia, holotype site. Basidiomata in field and lab; microscopic elements: section of pileipellis; SEM of basidiospores showing robust ornamentation. Scale bars: basidiomata = 10 mm; spores and SEM spores = 10 μm.

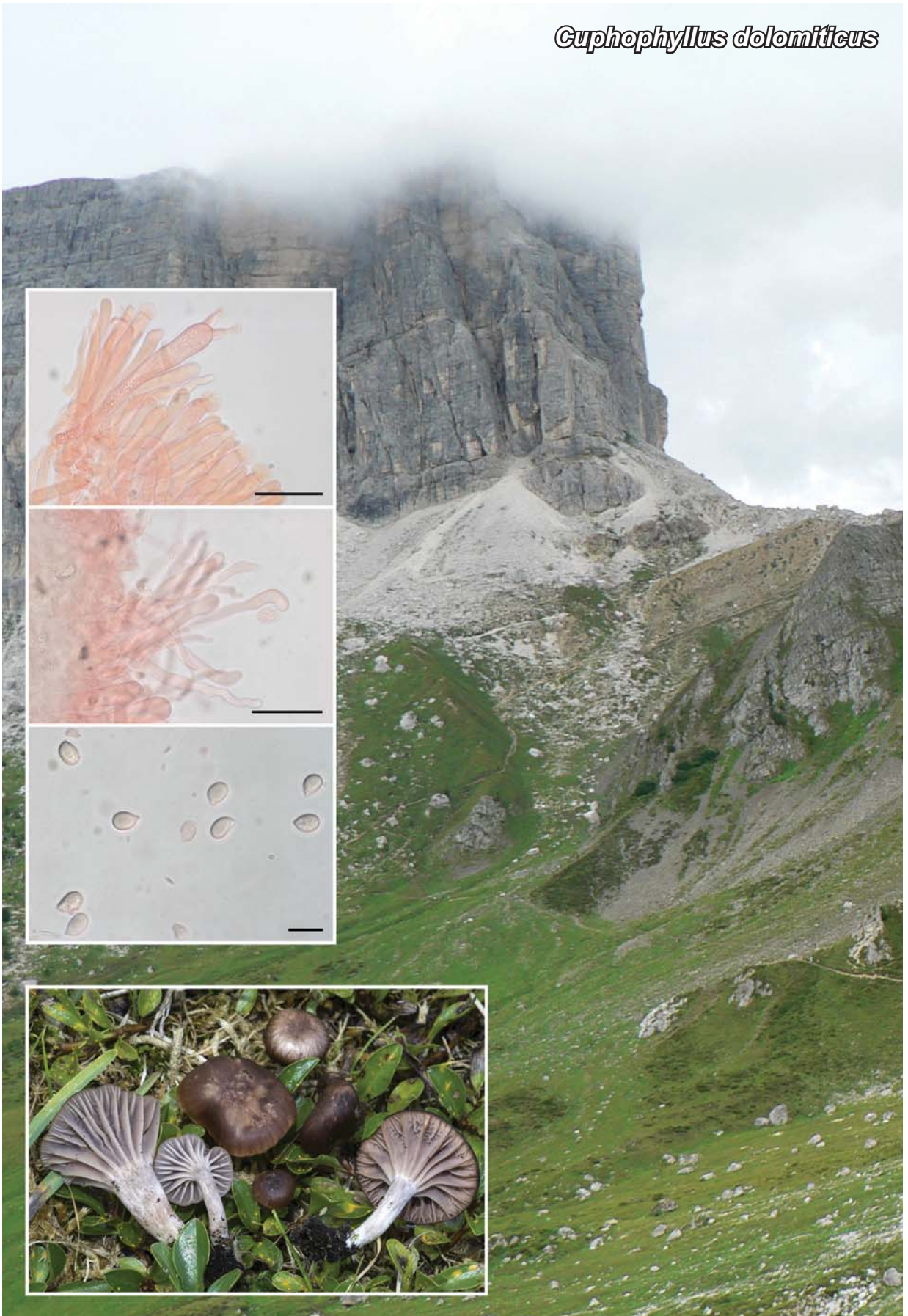


2021), *C. verniciorum* (Soop 2013) and *C. dulcamarus* from New Zealand (orange brown basidiomes with strongly viscid pilei; Soop 2016), and *Cortinarius* sp. (GenBank MG553066, RB065) from Western Australia. The basidiomata of the sequestrate taxa do not resemble the mushroom counterparts in this poorly supported clade, lacking any viscosity, and

generally lacking any hints of orange or reddish colouration. In a much broader sampling of species, (ITS only; unpub.), all three sequestrate taxa *C. sebosoides*, *C. albofolliculus* sp. nov. and *C. sebosus* remain in a strongly supported (PP 0.9) clade with *C. verniciorum*, *C. neuquensis* and an undescribed species from Chile (GenBank OP339712).

For phylogenetic tree, see *Cortinarius albofolliculus* (FP 1821).

*Cuphophyllus dolomiticus*





## *Cuphophyllus dolomiticus* E. Campo & E. Larss., *sp. nov.*

**Etymology:** Refers to the area, the Dolomites, where the species first was found.

**Classification:** *Hygrophoraceae*, *Agaricales*, *Agaricomycetes*.

*Basidiomata* clitocybioid. *Pileus* 5–25 mm diam., as young hemispheric to plano-convex with incurved margin, without or just low broad and blunt umbo, with age becoming plane, sometimes depressed with wavy and lobed margin, dry to subviscid, slightly wrinkled under the lens, sometimes translucently striate at margin up to 1/3 towards the centre, hygrophanous, first rather uniformly dark brown chocolate coloured with a weak purple violet tone, with age paler at margin, somewhat striate and fading. *Lamellae* short to rather deeply decurrent, arcuate, distant to subdistant, lamellae that reach the stipe = 16–25(–30), interspaced with lamellulae, a few furcate, intervening, first pale greyish, later greyish-brown with purple-violet tone usually with pale edge. *Stipe* 15–30 × 4–8 mm, cylindrical, usually thickest at the apex or upper half, sometimes tapering and often bending towards the base, dry, matt, fibrillose lengthwise, pale, whitish to greyish, with age getting a weak brown-violet tone. *Context* concolourous. *Smell* immediately pleasant almost sweetish then rubber, *taste* indistinct. Micro-morphology measured from fresh and dried material dehydrated in 3 % KOH and ammoniacal Congo red solution. *Basidiospores* (6.0–)8.1–8.6–9.1(–10.3) × (5.0–)5.4–5.7–6.1(–6.7) μm, n = 170, Q = 1.39–1.66, Q av. = 1.53, ovoid to broadly ellipsoid, a few lacrymoid, with a distinct and often oblique apiculus, often with a large drop, hyaline, white in deposit, non-amyloid. *Basidia* 47–53–58 × 7–8–9 μm, n = 25, Q av. = 6.6, narrowly clavate, 4-spored, 2-spored, a few 1-spored, hyaline, sterigmata 5.4–7.4 μm long. *Cheolocystidioid hairs* 28–46 × 3–4 μm, abundant on the lamellar edge, cylindrical, sinuous, normally with obtuse apex but also bifid, nodulose or capitate. *Lamellae trama* interwoven, made up of cylindrical hyphae 5–18 μm wide, some branched and inflated, weakly encrusted by ochraceous pigments. *Pileipellis* a cutis up to 30–80 μm thick with non-gelatinized radially interwoven hyphae 3–6 μm, incrustated with finely ochraceous granular pigments, hyphae in subpellis interwoven, hyaline 5–10 μm with inflated end cells up to 18 μm wide. *Stipitipellis* a cutis of thin parallel hyphae 2.5–5 μm wide, superficial hyphae are more or less covered with excrescences up to 13 μm long. At stipe apex scattered clusters of polymorphous caulocystidial hair-like structures 4–5 × 35–75 μm, with granular oily light refracting content, often inflated end cells up to 10 μm wide. *Clamp connections* frequent in all tissues.

**Colour illustrations:** *Cuphophyllus dolomiticus* habitat in the alpine zone in Val Cenera below Forcella Giau (photo E. Bizio). *In situ* basidiomata, photos of hymenium, basidiospores and caulocystidioid hairs of the holotype (GB-0207704). Scale bars: basidia and cheilocystidial hairs = 20 μm; spores = 10 μm.

**Ecology and distribution:** The species has been found in Italy and Sweden in the alpine zone, growing in nutrient rich habitats on calcareous ground among herbs and mosses, *Salix reticulata*, *S. retusa*, *S. polaris* and *Dryas octopetala*. Also, in the mid-boreal zone of Norway on grazed calcareous shallow soil by the sea. Our specimens were collected from mid-August to the first part of September. Blast search of NCBI's GenBank and the UNITE database recovered no additional data, suggesting the species to be rare or overlooked.

**Typus:** **Italy**, Veneto, Belluno, Forcella Giau, Colle S. Lucia, N46°28'32", E12°04'11", 2300 m a.s.l., in the alpine zone, dolomitic area, among *Salix retusa*, *Salix reticulata* and *Dryas octopetala*, 21 Aug. 2017, E. Campo & M.C. Magnozzi (**holotype** GB-0207704, **isotype** AMB 21057; ITS-LSU sequence GenBank PV069116).

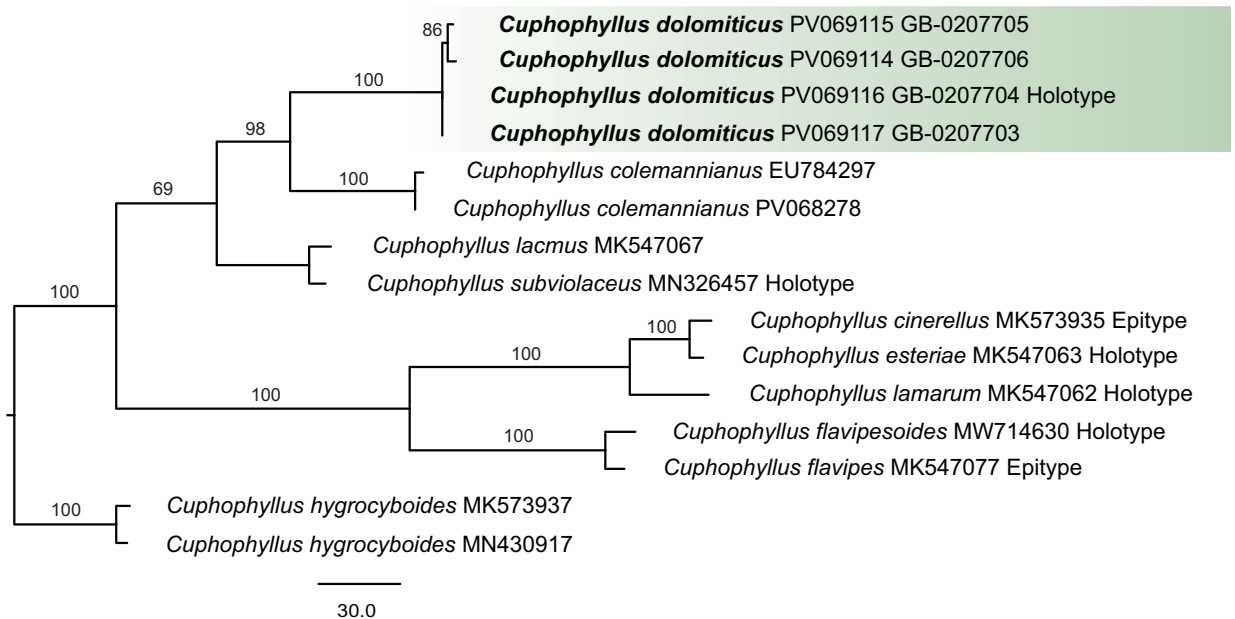
**Additional materials examined:** **Italy**, Veneto, Belluno, Colle S. Lucia, Forcella Giau, 2300 m a.s.l., dolomitic area among *Dryas octopetala* and *Salix retusa*, 22 Aug. 2015, E. Campo & M.C. Magnozzi (GB-0207705, ITS-LSU sequence GenBank PV069115); *ibid.*, Forcella Giau, alpine area on calcareous soil among *Salix retusa*, *Salix reticulata* and *Dryas octopetala*, 21 Aug. 2017, E. Campo & M.C. Magnozzi (GB-0207703, ITS-LSU sequence GenBank PV069117). **Norway**, Nordland, Fauske, on grazed calcareous shallow soil, on shore rock by the sea, in mid-boreal zone, 7 Sep. 2022, J.B. Jordal & K. Svingen, JBJ22-033 (OF-77092, ITS sequence GenBank PV299233). **Sweden**, Lule lappmark, Jokkmokk, Padjelanta NP, Sorjosjaure, in alpine meadow on calcareous ground with *Salix reticulata*, 17 Aug. 2016, E. Larsson, EL202-16 (GB-0207706; ITS-LSU sequence GenBank PV069114). **Collections studied for comparison:** *Cuphophyllus colemannianus*. **Italy**, Friuli Venezia Giulia, Pordenone, Arba, 210 m a.s.l., in a stable lawn among grass, 5 Dec. 2009, G. Zecchin (MCVE 25365); Vajont, Maniago in meadow among grass, 9 Nov. 2013, E. Campo (TUR-A199695). **Sweden**, Gotland, Gothem, Svalings, grazed forest meadow, 9 Oct. 2021, E. Larsson, 201-21 (ITS-LSU sequence GenBank PV068278). *Cuphophyllus cinerellus*. **Norway**, Troms, Storfjord, arctic tundra on siliceous soil among *Salix herbacea*, *Empetrum nigrum*, *Arctostaphylos alpinus* and *Betula nana*, 21 Aug. 2014, E. Campo (AMB 21059). **Sweden**, Lule lappmark, Jokkmokk, Padjelanta NP, Arranoajvve, alpine tundra among lichens, *Empetrum nigrum* and *Betula nana*, 11 Aug. 2016, E. Larsson (**epitype** GB-0156961; ITS-LSU sequence GenBank MK573935).

**Notes:** *Cuphophyllus dolomiticus* belongs in a complex of closely related and morphologically similar species that in Europe mainly are restricted to seminatural grasslands, meadows and wooded meadows (Arnolds 1990, Boertmann 2010). *Cuphophyllus dolomiticus* is similar and genetically most closely related to *C. colemannianus* but differs and can be discriminated by the small basidiomata, a pileus without umbo and dark brown chocolate colours, and lamellae that are greyish brown with a purple tone. The spores are on average somewhat smaller (in *C. colemannianus* 8–10 ×

5.5–6.8  $\mu\text{m}$ ), the cheilocystidioid hairs are abundant and longer up to 46  $\mu\text{m}$  (25  $\mu\text{m}$  in *C. colemannianus*) and the lamellae trama hyphae are wider 5–18 (up to 10  $\mu\text{m}$  in *C. colemannianus*). In addition, *C. dolomiticus* does not have a gelatinized pileipellis. There are records of *C. colemannianus* from the alpine zone with dark colours and small basidiomata that are likely to be conspecific with *C. dolomiticus* (Jamoni 2008). A species that occurs in the arctic-alpine zone and is similar in macro-morphology is *C. cinerellus*, but it is

primarily known from northern Fennoscandia and there are no confirmed records from the Alps. It is genetically distinct and differ in ecology by being restricted to nutrient poor *Vaccinium – Empetrum* lichen heath habitats (Kühner 1977, Voitk *et al.* 2020).

*Supplementary material:* doi: 10.6084/m9.figshare.28519991.v1 (alignment and tree, drawing of micro-morphological characters).



Phylogram obtained using PAUP v. 4.0a (Swofford 2003) based on ITS and LSU data showing the position of *C. dolomiticus* among its closest relatives. Heuristic searches with 1000 random-addition sequence replicates and tree bisection-reconnection (TBR) branch swapping were performed. Relative robustness of clades was assessed by the bootstrap method using 1000 heuristic search replicates with 100 random taxon addition sequence replicates and TBR branch swapping. Bootstrap support values are indicated on branches. *Cuphophyllus dolomiticus* is marked in **bold** and highlighted with a coloured block, and the holotype indicated.



*Cytospora braithwaitei*



## *Cytospora braithwaitei* Vasey & Toome, *sp. nov.*

**Etymology:** Named in honour of plant pathologist Mark Braithwaite, who isolated this fungus, for his contributions to New Zealand plant pathology and biosecurity.

**Classification:** Valsaceae, Diaporthales, Sodiariomycetes.

**Conidiomata** pycnidial, abundant and aggregated with pale yellow cirrhi in 10-d-old cultures. **Conidiophores** hyaline and unbranched. **Conidiogenous cells** hyaline, smooth, polyphialidic, enteroblastic, smooth-walled, narrowing at the apices, (8.85–)11.70(–13.77) × (1.38–)2.10(–2.95) μm (n = 20). **Conidia** hyaline, aseptate, smooth, thin-walled, allantoid, eguttulate, (5.0–)6.2(–7.5) × (1.5–)2.2(–2.5) μm (n = 20).

**Culture characteristics:** Colonies on potato dextrose agar (PDA) at 21 °C incubated under black light were round or irregular and 10–14 mm diam. after 3 d, becoming round and 80–90 mm diam. after 7 d; initially flat and white, turning pale olive grey to olive black on the surface with a grey irregular margin, older cultures olive-black on reverse. Flat, with a thick texture at the centre. Some aerial hyphae observed, but culture largely velvet or felt-like.

**Habit, habitat and distribution:** *Cytospora braithwaitei* was isolated from an apple tree branch exhibiting tip dieback and stem canker symptoms. No symptoms were observed on fruit. While internal wood discolouration was observed, the association between the fungus and the symptoms remains unknown. Numerous *Cytospora* species have been associated with apple tree diseases (Hanifeh *et al.* 2022), many of which are opportunistic pathogens infecting mainly old or weakened trees. The potential impact of *C. braithwaitei* on the orchard in New Zealand was considered low and the grower reported very low spread of the tip dieback among the trees.

**Typus:** **New Zealand**, Christchurch, Belfast, Crawford Road, on branch of *Malus domestica* (Rosaceae), Nov. 2020, R. Wards (**holotype** PDD97343, culture ex-type ICMP 23884 = CBS 151301; ITS, LSU, *act*, *rp2*, *tef1-α* and *tub2* sequences GenBank OR807325, OR808087 OR814108, OR814112, OR814116 and OR814120).

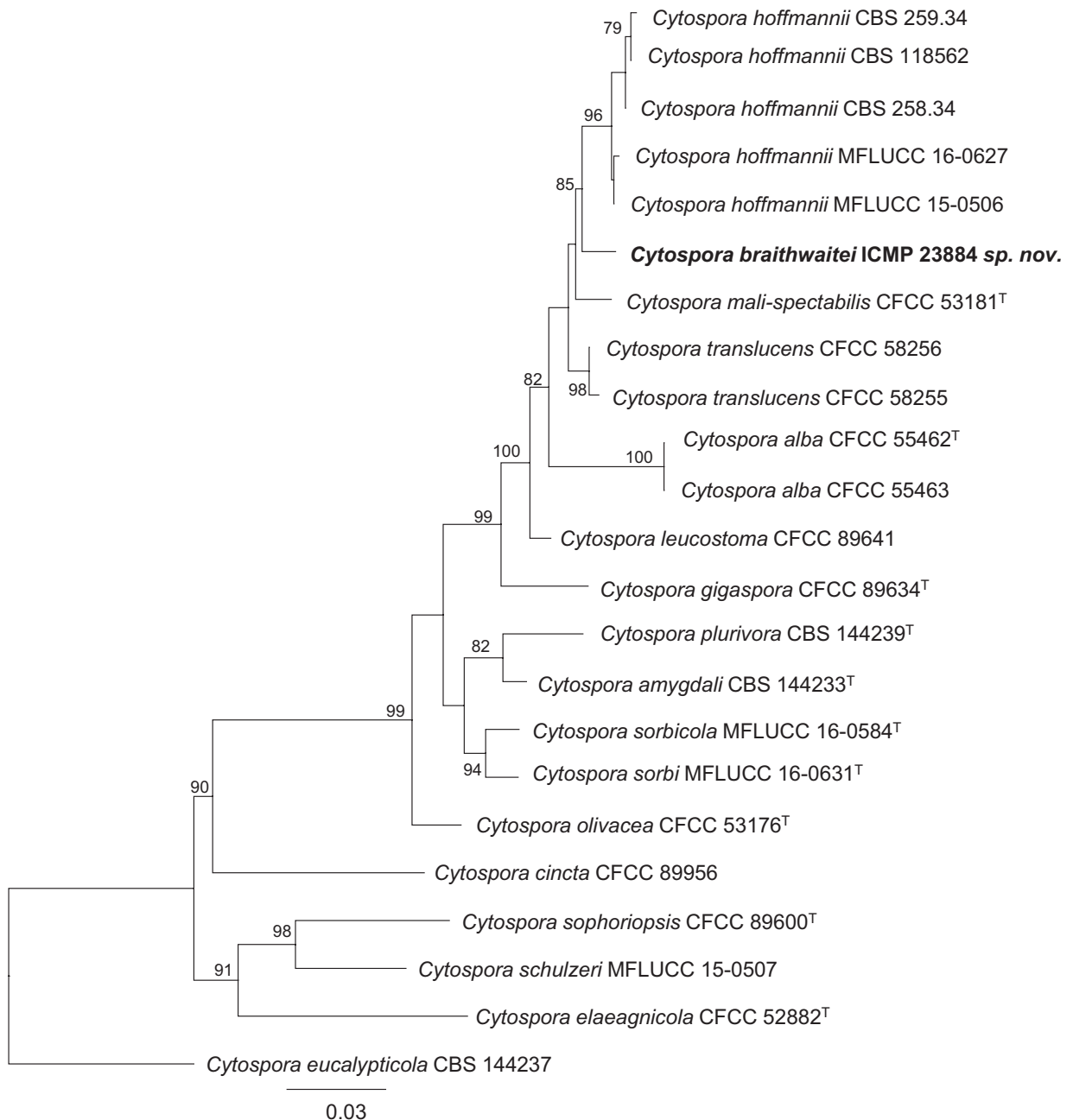
**Notes:** The variability of morphological characters of *Cytospora* are typically considered insufficient to provide distinction between species (Lin *et al.* 2024). As a result, sequence analysis has been used to delineate this new species. Sequence analysis showed that this *Cytospora* isolate is most closely related to *C. hoffmannii* (syn. *Valsa nivea*, *Leucostoma niveum*, *C. nivea*, *C. paratranslucens* as per Lin *et al.* 2024). Multi-gene phylogenetic analysis using the combined ITS, *rp2* and *act* sequences showed

that isolate ICMP 23884 is well supported as a new species closely related to *C. mali-spectabilis* and *C. hoffmannii*. The *tub2* and *tef1-α* sequences were not included in this multi-gene phylogeny as most type strains of *Cytospora* lack available sequences for these genes. Isolate ICMP 23884 is clearly distinct from *C. mali-spectabilis* and *C. hoffmannii*, showing low sequence similarity with these species across the *act*, *tef1-α* and *tub2* regions.

Based on a megablast search of NCBI's GenBank nucleotide database (blasted 26 Mar. 2025), the closest hits using the **ITS** sequence had highest similarity to *Valsa nivea* [strain CBS 259.34, GenBank MH855503; Identities = 606/607 (99 %), one gap (0 %)], *Cytospora hoffmannii* [isolate XJAU\_254, GenBank MG879497; Identities = 585/586 (99 %), no gaps], and *Cytospora hoffmannii* [isolate XJAU\_428-2, GenBank MG879496; Identities = 582/582 (100 %), no gaps]. Closest hits using the **LSU** sequence are to *Leucostoma niveum* [isolate AR3413, GenBank AF362558; Identities = 1270/1271 (99 %) no gaps], *Leucostoma niveum* [strain AR3512, GenBank AF408367; Identities = 1269/1271 (99 %), no gaps], and *Valsella salicis* [strain AR3514, GenBank AF408389; Identities = 1262/1266 (99 %), no gaps]. Closest hits using the **tef1-α** sequence are to *Cytospora* sp. [strain CFCC55462, GenBank OK303577; Identities = 282/295 (96 %), no gaps], *Cytospora* sp. [strain CFCC55462, GenBank OK303574; Identities = 282/295 (96 %), no gaps], and *Valsa nivea* [strain CFCC 89642, GenBank KP310862; Identities = 279/296 (94 %), two gaps (0 %)]. Closest hits using the **act** sequence are to *Cytospora translucens* [strain CFCC 55810, GenBank OR052757; Identities = 233/242 (96 %), no gaps], *Cytospora hoffmannii* [strain XJAU\_428-2, GenBank MH015283; Identities = 263/276 (95 %), one gap (0 %)], and *Valsella nivea* [strain N/A, GenBank KF765732; Identities = 263/276 (95 %), one gap (0 %)]. Closest hits using the **rp2** sequence are to *Cytospora* sp. [strain N/A, GenBank PQ075172; Identities = 706/714 (99 %), no gaps], *Cytospora mali-spectabilis* [strain CFCC 53181, GenBank MK673006.1; Identities = 717/726 (99 %), no gaps], and *Cytospora paratranslucens* [strain shd335, GenBank MW824362; Identities = 836/847 (99 %), no gaps]. Closest hits using the **tub2** sequence are to *Cytospora hoffmannii* [strain CXTA\_055, GenBank ON866760; Identities = 344/361 (95 %), four gaps (1 %)], *Cytospora hoffmannii* [strain CXTA\_210, GenBank ON866776; Identities = 343/360 (95 %), four gaps (1 %)], and *Cytospora hoffmannii* [strain F07, GenBank PV200209; Identities = 343/361 (95 %), four gaps (1 %)].

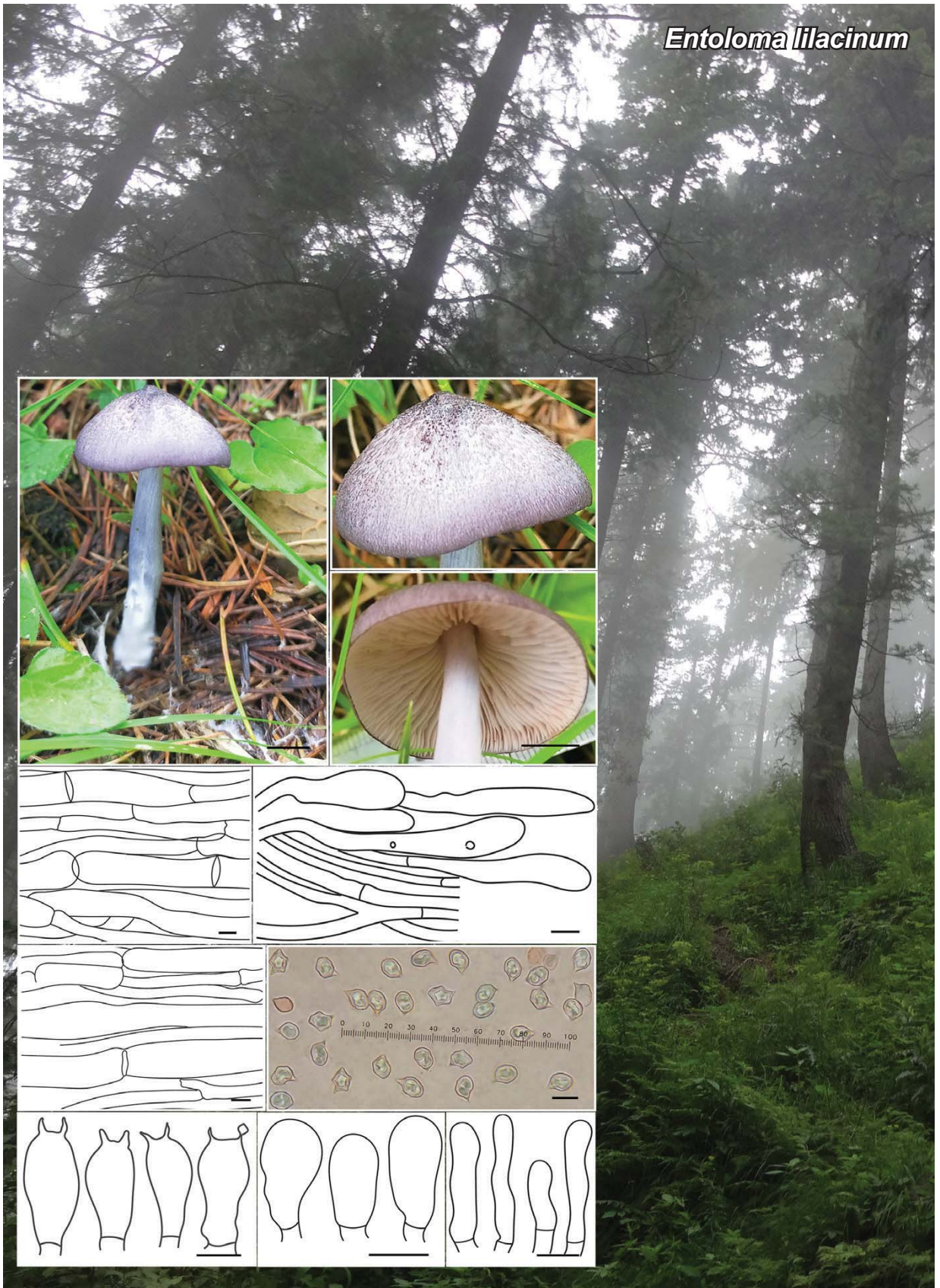
**Supplementary material:** TreeBASE study ID 32100 (alignment and tree); Figshare No: doi:10.6084/m9.figshare.28844681 (GenBank Accession numbers for sequences used in preparing alignment and tree).

**Colour illustrations:** New Zealand, Christchurch, *Malus domestica* orchard (photo credit R. Wards). Branch with tip dieback; colony on PDA agar (left = top, right = bottom); conidiogenous cells and conidia. Scale bars = 10 μm.



Maximum likelihood (GTR + G + I) tree illustrating the phylogenetic placement of the *Cytospora braithwaitei* examined here (in **bold**). This tree is based on the alignment of concatenated ITS and LSU, *act* and *rpb2* sequences. Branches are labelled with bootstrap support values  $\geq 70$  % across 1000 bootstrapping replicates, and type specimens are denoted by a superscript "T". *Cytospora eucalypticola* CBS 144237 was used as an outgroup. This tree was constructed using RAxML v. 8.2.11 (Stamatakis 2014) as provided through Geneious Prime v. 2021.1.1.

*Entoloma lilacinum*





## *Entoloma lilacinum* S. Hussain, *sp. nov.*

*Etymology*: “*lilacinum*” is derived from the Latin word “*lilacinus*”, referring to the characteristic lilac-coloured or pale violet cap.

*Classification*: *Entolomataceae*, *Agaricales*, *Agaricomycetes*.

*Pileus* small, 28–33 mm diam., convex to pulvinate or conico-convex, less concenoid, slightly umbonate at the centre and non hygrophanous. *Pileal surface* lilac to pale violet, fading with age, retaining colour at the centre, becoming greyish brown when dry, radially fibrillose, squamulose, squamules being smaller near to the margin, dense and dark towards the centre and prominently striated. *Margin* involute first then become smooth and entire. *Context* concolourous with lamellar surface. *Lamellae* emarginate, close, unequal, 0.5–1.3 mm interlamellar space, 2–3 mm wide and thin up to 0.3 mm, plane, pale to cream; edge eroded or rough, fertile; L 40–50, I 40–50; lamellulae, short and marginal. *Stipe* 50–68 × 4–6 mm, swollen, white at the base, cylindrical, fistulose, fibrillose-striate, light lilac becoming whitish with age, becoming fissured at the base. *Odour* and *taste* none. *Pileipellis* cutis to a trichoderm consisting of subparallel, thin-walled, filamentous to cylindrical, hyaline, septate hyphae, 4.4–17.6 (avg. 9.0) μm wide; inflated hyphae with subcylindrical to clavate terminal elements filled with greyish to greyish brown pigment, measuring (69–)71–89.1–96(–98) × (9.6–)11–14.2–17.4(–18.9) μm; intracellular greyish pigment observed in pileipellis. *Stipitipellis* cutis of cylindrical, hyaline, septate hyphae, 11.6–20.8 (avg. 15.4) μm wide. *Hymenophoral tramal* hyphae regular, cylindrical, thin-walled, hyaline, septate, 5.2–22.0 (avg. 11.3) μm wide. All tissues lack clamps. *Basidiospores* (8.0–)8.3–11.7–14.2(–14.5) × (6.6–)6.7–8.1–9.4(–9.8) μm, Q = 1.45–1.41–1.37, 5–6-angled in side view, with blunt angles, subsodiametrical to shortly heterodiametrical, hyaline. *Basidia* short, (18.9–)19.7–26.6–36.5(–37.1) × (10.2–)10.7–12.7–14.2(–14.8) μm, broadly clavate, bisporic, short sterigma, hyaline, clampless with basal septum. *Pleurocystidia* absent. *Cheilocystidia* (18.2–)20.3–30.2–38.3(–39.7) × (5.1–)5.3–7.5–8.6(–9.2) μm, rare, hyphoid to subclavate and septate (n = 55/2).

*Typus*: **Pakistan**, Khyber Pakhtunkhwa, district Swat, Skyland, N34°59'07", E72°11'31", 2343 m a.s.l., terrestrial grow on litter in conifer forest dominated by *Abies pindrow* and *Pinus wallichiana* (*Pinaceae*), Aug. 2020, S. Hussain, MUBS78A (**holotype** SWAT003424; ITS and LSU sequences GenBank PV257664 and PV257719).

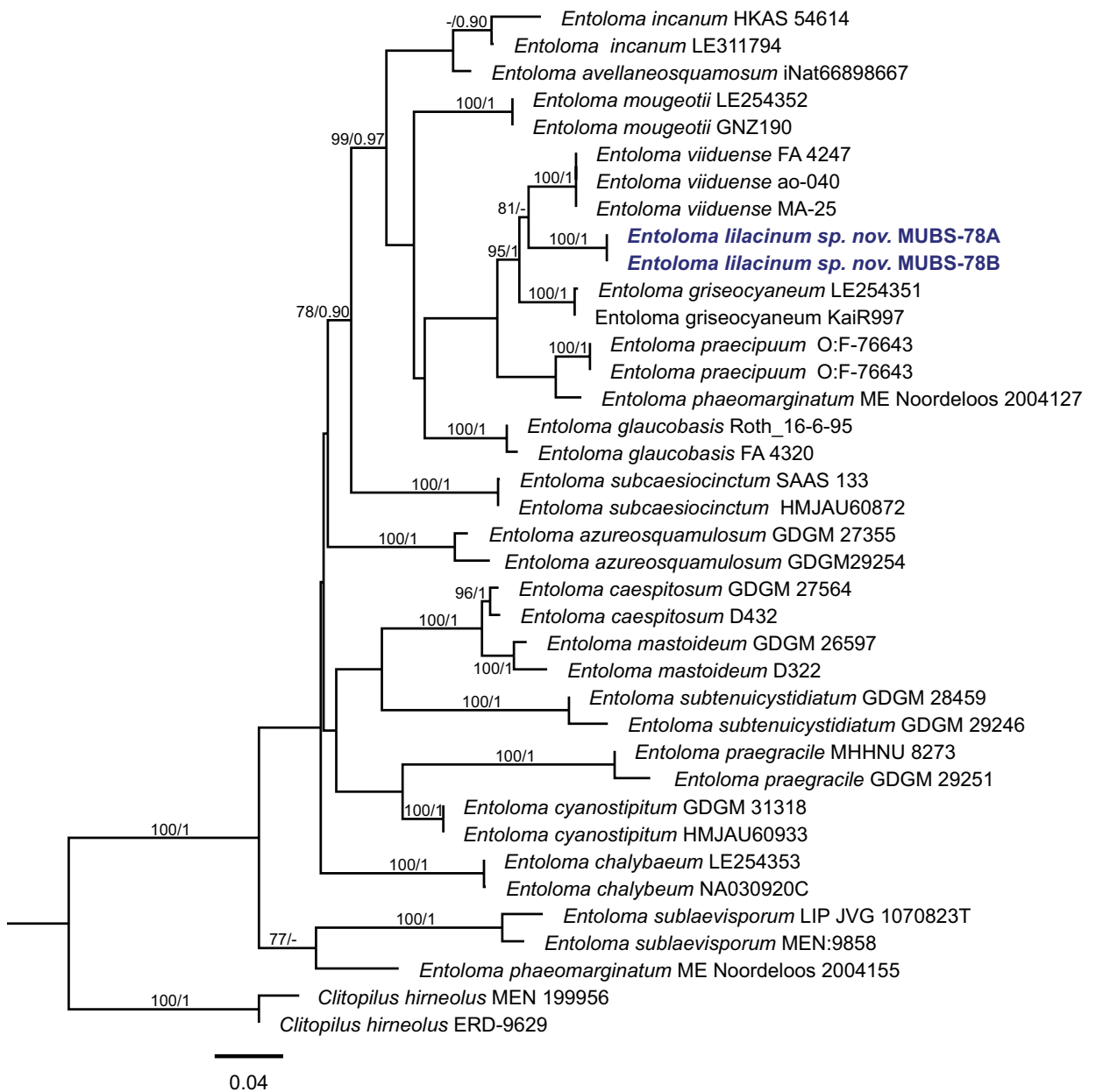
*Additional material examined*: **Pakistan**, Khyber Pakhtunkhwa, district Swat, Manai, N34°58'47", E72°12'45", 2090 m a.s.l., terrestrial grow in conifer forest dominated by *P. wallichiana*, Aug. 2020, S. Hussain, MUBS78B (SWAT003424; ITS sequence GenBank PV257665).

*Notes*: *Entoloma lilacinum* represents an independent lineage (ML 100 %, 1.00 BP) nested within *Entoloma* subgenus *Cyanula*, subsection *Griseocyaneum* (Noordeloos *et al.* 2022). Phylogenetically, *E. lilacinum* constitutes a sister clade to *E. viiduense* and *E. griseocyaneum*. However, it differs from *E. viiduense* and *E. griseocyaneum* by its distinctive pileal surface coloration, which is lilac or pale violet, in contrast to the blue grey to violaceous blue or brown pileus of *E. viiduense* and the brown to cream pileus of *E. griseocyaneum*. Additionally, *E. lilacinum* is distinguished by its broadly clavate, short, bisporic basidia (19.7–36.5 × 10.7–14.2 μm) and emarginated lamellar attachment. The species also differs from *E. viiduense*, which possesses 5–7-angled spores whereas *E. lilacinum* has predominantly 5–6-angled spores (Noordeloos 1992, Noordeloos & Liiv 1992). Among other species in subsection *Griseocyaneum*, *E. lilacinum* is differentiated by its relatively large spores (8.3–14.2 × 6.7–9.4 μm), compared to *E. phaeomarginatum* (8.5–11 × 6–7.5 μm) and *E. praecipuum* (7.5–10 × 5.0–7.0 μm). Furthermore, these species exhibit range of colour from brown to dark brown cap unlike lilac or pale violet in *E. lilacinum* (Horak 2008, Noordeloos *et al.* 2022). Morphologically, *E. lilacinum* is characterized by a convex to pulvinate, slightly umbonate pileus with a unique lilac or pale violet surface colour, emarginated lamellae, an entire margin, broadly clavate short bisporic basidia, and the presence of cheilocystidia.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had the highest similarity to *E. griseocyaneum* [strain KaiR997, GenBank MZ611684; Identities = 619/676 (92 %), 16 gaps (2 %)], *E. viiduense* [strain ao-040, GenBank PP277412; Identities = 604/660 (92 %), 25 gaps (3 %)], and *E. glaucobasis* [strain FA 4320, GenBank OR419870; Identities = 558/653 (85 %), 30 gaps (4 %)]. Closest hits using the LSU sequence had the highest similarity to *E. viiduense* [strain MA-25, GenBank PQ219014; Identities = 874/888 (98 %), three gaps (0 %)], *E. griseocyaneum* [strain G0328, GenBank MK277994; Identities = 868/889 (98 %), four gaps (0 %)], and *Entoloma* sp. [strain CME2, GenBank MZ678741; Identities = 863/890 (97 %), five gaps (0 %)].

*Supplementary materials*: doi: 10.6084/m9.figshare.28601180 (alignment and table).

*Colour illustrations*: Holotype collection locality, Swat, KP, Pakistan. Close up view cap surface; close up view lamellar surface; microscope illustrations of hyphae from stipitipellis; hyphae from pileipellis; hyphae from the pileus trama; basidiospores; basidia; basidioles; cheilocystidia. Scale bars: sporocarps = 10 mm; all other structures = 10 μm.



Maximum Likelihood (ML) tree based upon concatenated ITS+LSU sequences of *Entoloma* species depicting phylogenetic relationships. The analysis was carried out using the IQ-TREE v. 1.6.12 tool (Nguyen *et al.* 2015) and a Bayesian analysis using MrBayes v. 3.2.2 (Ronquist *et al.* 2012). Node support values (ML bootstrap / BI posterior probability) are indicated at the nodes. The novel species from this study is shown in bold and blue font.

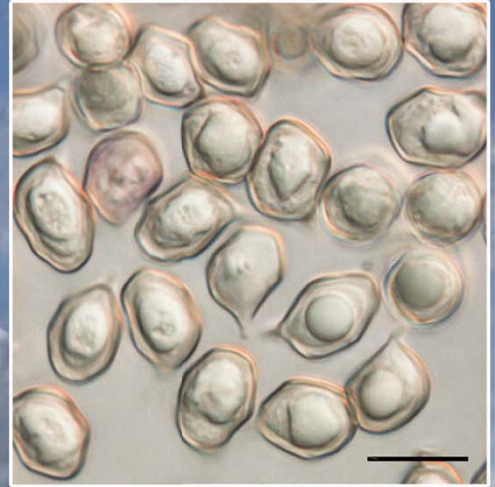
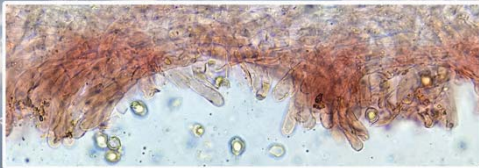
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*Entoloma daegae*



***Entoloma daegae* Rodrigues, Vila-Viçosa & Fachada, *sp. nov.***

*Etymology*: Named after João da Ega, iconic character from the novel *Os Maias* by Eça de Queirós. Known for his sharp wit and unorthodox ideas; originating from the type locality.

*Classification*: *Entolomataceae*, *Agaricales*, *Agaricomycetes*.

*Basidiomata* collybioid, in small groups. *Pileus* 7–30 mm, first hemispherical later becoming conical-hemispherical to finally plano-convex, straight margin remaining incurved until late stages, poorly hygrophanous or translucently striate, coarsely tomentose to subsquamulose especially in the centre, very dark purplish brown to nearly black when young and remaining so at the centre (7.5P 1/2, N1; Munsell 1919), fading to greyish brown (7.5P 6/2, 2.5R 3/2; Munsell 1919) near the striating margin in maturation. *Lamellae* moderately crowded (L = 30–40; I = 1–3), initially completely light greyish blue (2.5PB 5/4; Munsell 1919) sometimes remaining so near the centre and margin, edge sterile, finely serrulate or fimbriate and pigmented dark greyish purple (5P 1/2; Munsell 1919). *Stipe* 30–80 × 1–3 mm, cylindrical, straight, polished, only finely pruinose at very apex, with white mycelium at the base, light greyish brown with a purple hue (5RP 4/2, 2.5P 2/2; Munsell 1919). *Context* concolourous. *Smell and taste* indistinctive. *Basidiospores* (7.7–)8.4–9.5–10.6(–11.3) × (6.4–)7.1–7.7–8.5(–9.0) μm, Q = (1.0–)1.12–1.2–1.35(–1.55) (n = 125; N = 2), subsisdiametric, with 4–6 blunt angles. *Basidia* 25–34 × 8–10 μm, Q = 2.4–4.1 (n = 20; N = 2), clavate, 4-spored. *Cheilocystidia* (28–)32–47–70(–105) × 7–9–12 μm, Q = (2.5–)2.7–3.9–5.0(–5.3) (n = 20; N = 2), mostly of the poliopus-type, short and clavate, but sometimes in bundles of longer (uni- or di-) septate elements, resembling the carneogriseum-type, often with bluish brown intracellular pigment, rich in brilliant granules. *Pileipellis* a cutis transitioning to a trichoderm, especially at the centre, with short clavate terminal cells 50–90 × 12–23 μm, rich in brown intracellular pigment and brilliant granules. *Lamellar trama* subregular, made of hyaline cells, 6–12 μm, thick. *Clamp connections* absent.

*Habitat and distribution*: Known from Portugal's moist eutrophic and sandy soils derived from granitic bedrock, with *Plantago radicata*, *Fragaria vesca*, *Pullicaria vulgaris*, and *Echium rosulatum*. The area is characterized by temperate deciduous oak forests, where *Q. orocantabrica* transitions into thermophilic *Q. suber* formations. Additional ITS sequences were traced from Italy's volcanic landscapes with a vicariant ecotone, where *Q. robur*, *Q. pubescens*, *Castanea sativa*, and *Q. cerris* transition to evergreen *Q. ilex* formations.

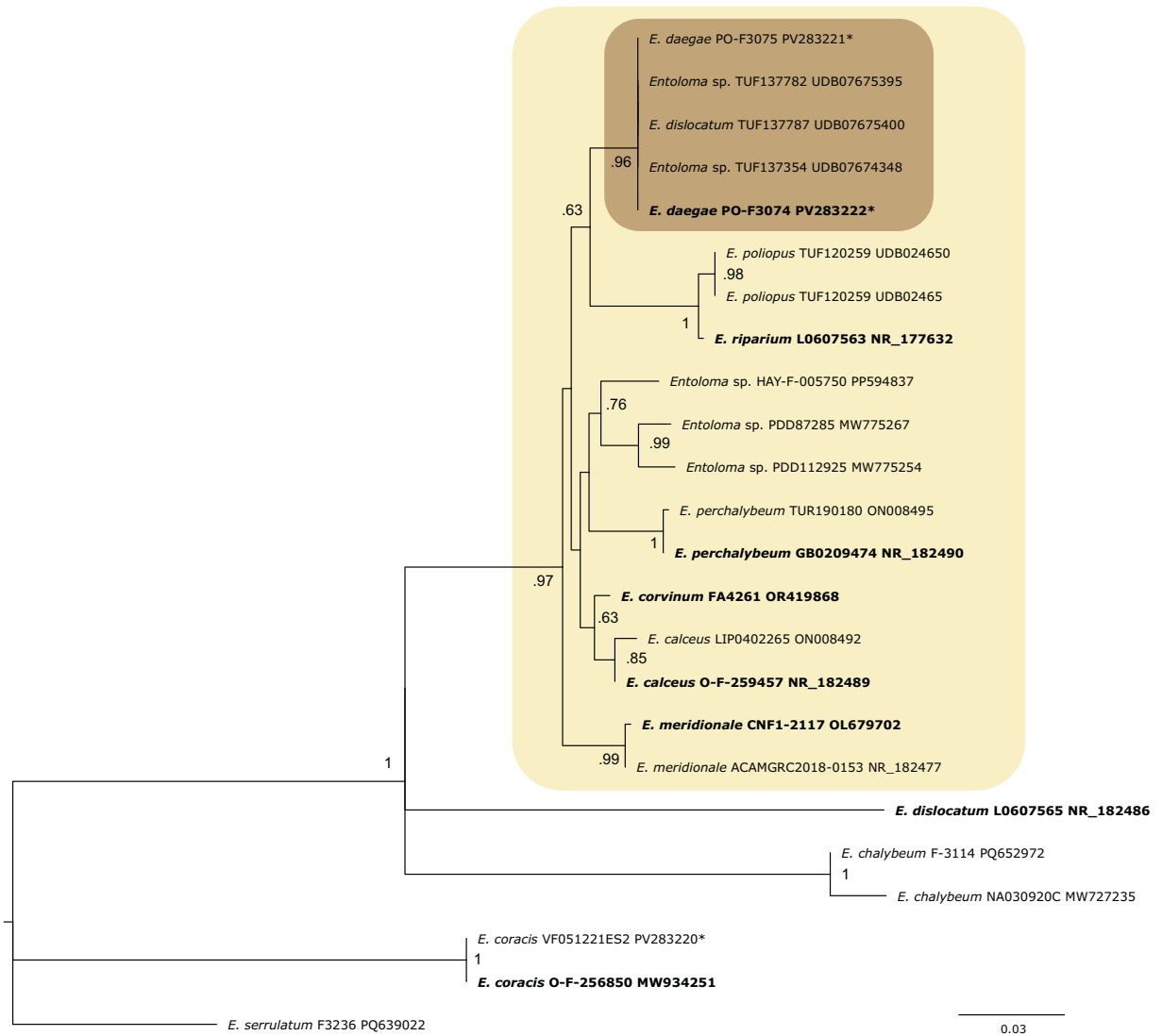
*Typus*: **Portugal**, Celorico de Basto, WGS84: 41.427277, -7.967224, 225 m a.s.l., on sandy, granitic soil, grass, near *Quercus suber* and *Fragaria vesca*, 27 Oct. 2023, H. Rodrigues, HR271023EC1 (**holotype** PO-F3074; ITS sequence GenBank PV283222).

*Additional material examined*: **Portugal**, Celorico de Basto, WGS84: 41.433217, -7.968242, 246 m a.s.l., in similar habitat as type, other *Quercus* spp. in the area, 4 Nov. 2023, H. Rodrigues, HR041123EC2, PO-F3075, ITS sequence GenBank PV283221.

*Notes*: Our ITS analysis shows that *E. daegae* has strong support (ufb = .97) within section *Poliopodes* (Noordeloos *et al.* 2022), having several *E. calceus* sequences with the highest similarity (95–96 %) when blasting in GenBank. It is likely more closely related to *E. riparium* and *E. poliopus*, although the relatively low ITS support for this node (63 %) leaves this precise relationship yet to be defined. Nevertheless, our sequences did not match any known species, except for a misidentified specimen of *E. dislocatum* (type sequence included in dendrogram). Below we discuss numerous species in section *Poliopodes* (and in subgenus *Cyanula*) with blackish blue basidiomata which can be confused with *E. daegae*, some of which having unsequenced types (Noordeloos *et al.* 2022). Fortunately, not only in the ITS sequence, but *E. daegae* stands alone in morphology as well. The striking bluish lamellae, with a finely fimbriate and dark pigmented edge, separates it from species with white gills or with an entire and concolourous gill edge, such as *E. corvinum*, *E. perchalybeum*, *E. coracis*, *E. cyanulum*, *E. dislocatum*, *E. nigroviolaceum* and *E. chalybascens*. The small, poorly angled and subsisdiametric spores are ultimately what set *E. daegae* apart more distinctly, as such an uncommon characteristic in this group of *Cyanula*, automatically discards species like *E. calceus*, *E. riparium*, *E. pseudocyanulum*, *E. meridionale*, *E. azureopallidum*, *E. poliopus* itself and the also blue-gilled *E. chalybaeum*. Finally, despite occasionally having subsisdiametric spores and serrulate lamellae edge, the distantly related *E. serrulatum*, can be readily distinguished by its fibrillose stipe surface (Noordeloos *et al.* 2022).

*Supplementary material*: TreeBASE study ID S32070 (alignment and trees).

*Colour illustrations*: Ruderal grassy habitat with shrub cultivars and *Quercus* spp., Celorico de Basto, Portugal. From top left to bottom right: Holotype representative collection; hymenophore; lamellae edge; cheilocystidia; pileus surface; basidiospores; basidiomata in natural habitat. Scale bar = 10 μm. [photo credits H. Rodrigues (background and macro); V. Fachada & H. Rodrigues (micrographs)].



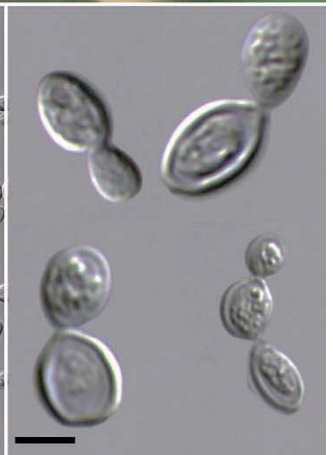
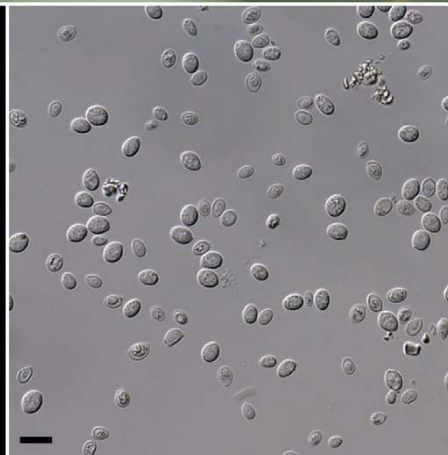
Maximum likelihood phylogenetic tree showing the ITS relationship between *E. daegae* (highlighted brown) and its neighbouring species, particularly within section *Poliopodes* (highlighted beige). The outgroup was set with *Entoloma serrulatum*. Node values represent ultrafast bootstrap (ufb) above .60, obtained with IQ-TREE v. 2.2.2.6 (Minh *et al.* 2020) by generating 2 runs of 10000 samples, using the TPM2u+F+G4 model. Names in bold represent type specimens; asterisks mark sequences produced in this study.

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*Erythrobasidium eucalypti*





# *Erythrobasidium eucalypti* R. Knop., Hammerb., M. Groenew., & T. Bose, *sp. nov.*

**Etymology:** A single isolate of this fungus was recovered from the gut of *Gonipterus* sp. n. 2, feeding on *Eucalyptus* leaves.

**Classification:** *Erythrobasidiaceae*, *Erythrobasidiales*, *Cystobasidiomycetes*.

**Thallus** unicellular, aseptate; cell surface smooth; cell wall thicker in non-budding cells measuring 0.5–1 µm while thin in actively budding cells measuring 0.1–0.3 µm; cells globose to ovate measuring 5.58–7.65(–7.87) × 3.49–6.18(–6.63) µm; 1–4 nucleate; hyphae or pseudohyphae absent; buds apical, off-axis, globose to ellipsoid in shape, 1.43–2.09(–2.34) × 1.33–3.39(–3.74) µm, *Sexual morph* was not observed after 2 mo at 25 °C on V8-juice (V8) agar, yeast extract-malt extract (YM) agar, 5 % Difco malt and yeast carbon base supplemented with 0.01 % ammonium sulphate (YCBAS) agars.

**Culture characteristics:** On potato dextrose agar (PDA), 2 % malt extract agar (MEA), and yeast peptone dextrose agar (YPD) colony coral in colour (top and reverse; Rayner 1970). Colony circular, margin entire, elevation convex. After 2 wk at 25 °C D-glucose is not fermented and carbon compounds assimilated are L-arabinose, cellobiose, D-galactose, D-gluconate, potassium-2-keto-D-gluconate, D-glucose, glucoseamine, D-glucuronate, glycerol, lactic acid, maltose, D-mannitol, melezitose, methyl-α-D-glucopyranoside (weak), L-rhamnose (weak), D-ribose (weak), D-sorbitol, L-sorbose, sucrose, α, α-trehalose and D-xylose, while growth is absent in erythritol, N-acetyl glucoseamine, inositol, lactose, melibiose, raffinose. No growth was observed for growth in the nitrogen compounds cadaverine, ethylamine, D-Glucosamine HCL, L-Lysine, nitrate, nitrate and tryptophane. Growth in peptone is positive, but it does not grow in the presence of 0.01 % cycloheximide. Growth occurred at 6 °C up to 30 °C and is absent at 33 °C.

**Typus:** **South Africa**, Gauteng Province, Pretoria, Blue Gum Valley Shooting Range, S25°57'36.855", E28°29'38.812", isolated from the gut of *Gonipterus* sp. n. 2 (*eucalyptus* snout beetle), Jan. 2024, R. Knoppersen (**holotype** CBS 19176 preserved in a metabolically inactive state in lyophilised form, culture ex-type CBS 19176; ITS, LSU and SSU sequences GenBank PV133514, PV133516 and PV133525).

**Notes:** In the BLAST pairwise sequence similarity analysis, *E. eucalypti* differs from its closest relatives, *E. hasegawianum* (GenBank EU002886) and *E. yunnanense* (GenBank JF758860), by 2 nt (no gaps) and 2 nt (1 gap), respectively, in the ITS region (541 nt). In the LSU region (979 nt), *E. eucalypti* differs from *E. hasegawianum* (GenBank DQ663696) and *E. proteacearum* (GenBank OK393710, OK393709, NG\_079572) by 2 nt (no gaps), 4 nt (no gaps), 9 nt (no gaps), and 7 nt (no gaps), respectively. In the SSU region (1024 nt), *E. eucalypti* differs from *E. hasegawianum* (GenBank DQ663697, D12803) and *E. yunnanense* (GenBank NG\_063520) by 1 gap, 1 nt (2 gaps), and two gaps, respectively.

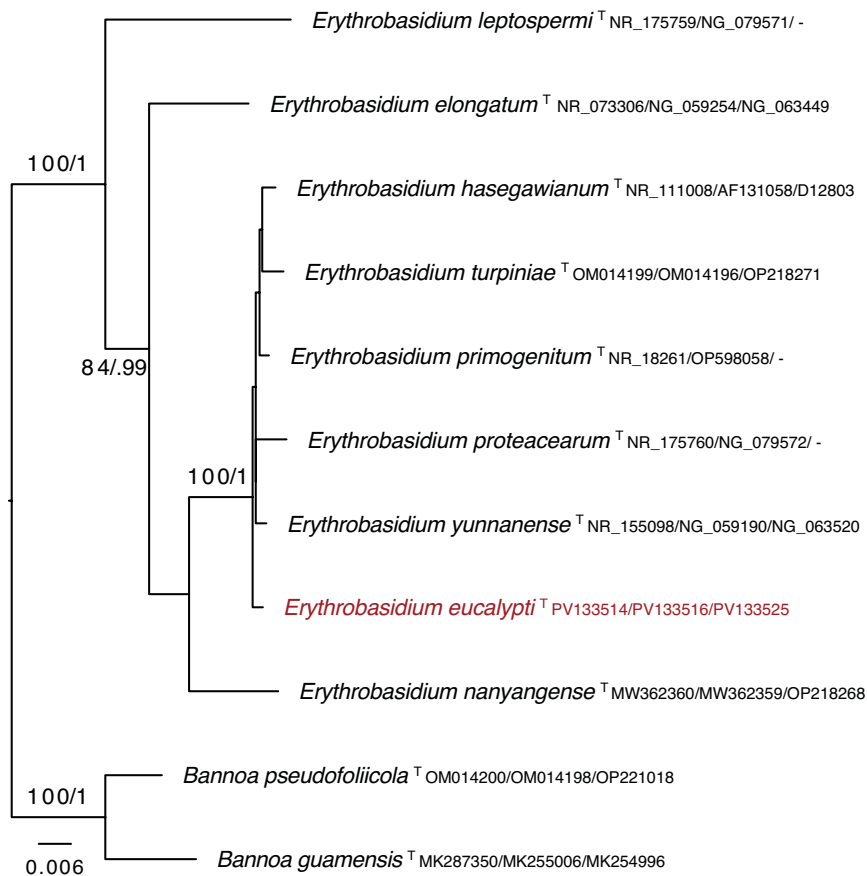
In the phylogenetic analysis using a concatenated dataset (ITS, LSU, SSU), *E. eucalypti* emerged as a sister to a clade containing *E. hasegawianum*, *E. turpiniae*, *E. primogenitum*, *E. proteacearum*, and *E. yunnanense*, with maximum branch support. Similarly, in the ITS tree, *E. eucalypti* was sister to the same clade, with 94 % bootstrap support. In the LSU tree, *E. eucalypti* and *E. turpiniae* formed a monophyletic clade with a low branch support value. In the SSU tree, *E. eucalypti* formed a monophyletic clade with *E. yunnanense* with 76 % bootstrap support (data for single gene trees not shown).

When comparing the physiological tests of *E. hasegawianum* and *E. yunnanense* (Lu *et al.* 2024) with our isolate, *E. eucalypti* tested positive for D-glucuronate and weakly positive for L-rhamnose and D-ribose. In contrast, *E. hasegawianum* was positive for D-glucuronate and D-ribose but was negative for L-rhamnose, whereas *E. yunnanense* showed no positive response for any of the three carbon substrates. For nitrogen assimilation, *E. eucalypti* tested negative for all substrates except for peptone. *Erythrobasidium hasegawianum* was positive for nitrate, nitrite, ethylamine, and L-lysine, while *E. yunnanense* was positive for nitrate and nitrite.

*Erythrobasidium eucalypti* was isolated from the gut of *Gonipterus* sp. n. 2. However, we believe this yeast species is not a native resident of the beetle's gut. Instead, it is likely a phyllosphere-inhabiting yeast, like other *Erythrobasidium* species (Lu *et al.* 2024), that entered the beetle's gut while feeding on *Eucalyptus* leaves.

**Supplementary material:** doi: [10.17632/yrvh385zsb.1](https://doi.org/10.17632/yrvh385zsb.1) (alignment and tree).

**Colour illustrations:** *Gonipterus* sp. n. 2 on *Eucalyptus* leaves. 15-d-old colonies of *Erythrobasidium eucalypti* on PDA; unicellular thalli of *E. eucalypti*; various budding cells. Scale bars = 5 µm.



The maximum likelihood (ML) tree of fungal species from the genus *Erythrobasidium* for which ITS, LSU and/or SSU sequences were available. The tree was constructed with IQ-TREE v. 1.6.12 (Minh *et al.* 2020) using the concatenated dataset (ITS, LSU, SSU) with 1000 bootstrap replicates. Bayesian analysis of the dataset was done using MrBayes v. 3.2.7a (Huelsenbeck & Ronquist 2001). *Bannoa pseudofoliicola* and *B. guamensis* served as the outgroup taxa. Branch labels indicate ML bootstrap support values / Bayesian posterior probabilities. Only bootstrap support values  $\geq 70$  % and posterior probability  $\geq 0.80$  are shown. The isolate recovered in this study is in brown font. GenBank accession numbers are listed as suffixes after each taxon (ITS/LSU/SSU). T = ex-type sequence. The alignment and tree were deposited in Mendeley Data (doi: 10.17632/yrvh385zsb.1)

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*Helicogermisita australiensis*



# *Helicogermis* *australiensis* B. Raphael, M.J. Lynch, E.J. Whiteside & Dearnaley, *sp. nov.*

*Etymology*: Named “*australiensis*” as it is the first species of the genus to be discovered in Australia.

*Classification*: Xylariaceae, Xylariales, Sordariomycetes.

*Ascomata* solitary, 1–4 mm diam., brown to black with white mycelial sheath; wall of 3–6 layers of pale brown textura angularis, superficial on substrate surface. *Paraphyses* intermingled among asci, hyphae-like, hyaline, smooth, septate, (3.3–)3.7–4.7(–5.2)  $\mu\text{m}$  diam. *Asci* 8-spored, unitunicate, cylindrical, pedicellate, apically, rounded, (147.2–)152.9–168.0(–170.2)  $\times$  (12.5–)14.5–16.1(–17.5)  $\mu\text{m}$ , with amyloid reaction of apical ring to Melzer’s reagent. *Ascospores* overlapping uniseriate, hyaline when immature, brown to dark brown when mature, spiral germ slit extending over the full length, (20.8–)21.5–24.3(–26.5)  $\times$  (8.7–)9.3–10.5(–11.2)  $\mu\text{m}$ . *Conidiomata* solitary, 1–4 mm diam., brown to black with white mycelial sheath; wall of 3–6 layers of white to pale brown textura angularis. *Conidiophores* lining inner cavity, hyaline, rough, subcylindrical with slight apical taper, (13.8–)14.0–14.6(–14.9)  $\times$  (2.3–)2.6–3.4(–3.6)  $\mu\text{m}$ . *Conidiogenous cells* hyaline, smooth, cylindrical, terminal, (6.2–)6.4–8.2(–10.06)  $\times$  (2.24–)2.4–3.4(–3.8)  $\mu\text{m}$ , *phialidic*. *Conidia* solitary, aseptate, hyaline, smooth, obovate to fusiform, (6.4–)6.8–7.2(–8.0)  $\times$  (2.2–)2.4–3.4(–3.8)  $\mu\text{m}$ .

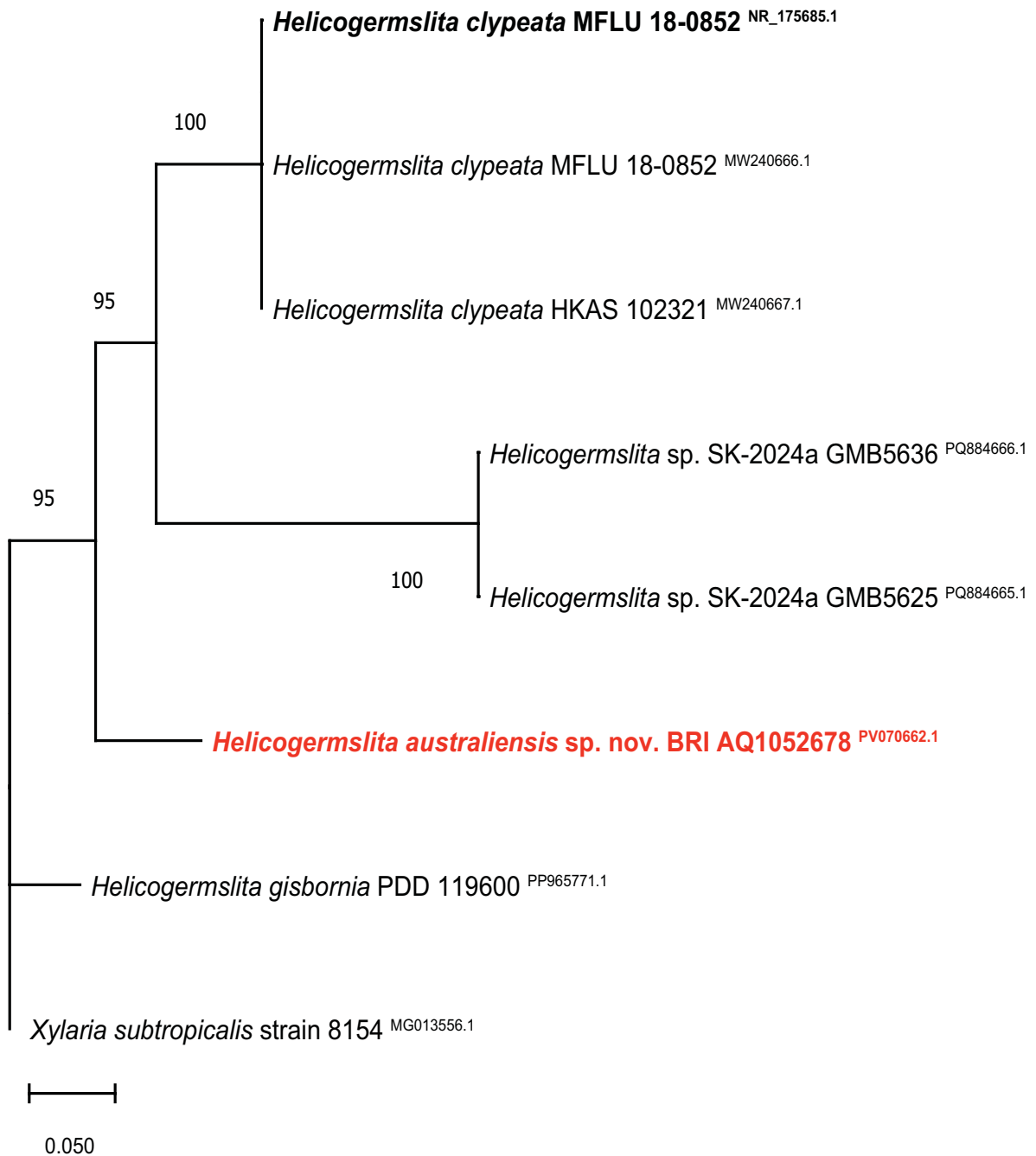
*Culture characteristics*: Colonies flat, spreading, with sparse to moderate aerial mycelium and folded surface, reaching 80 mm diam. after 2 wk at 22 °C in the dark. On potato dextrose agar (PDA), both surface and reverse are white.

*Typus*: **Australia**, Queensland, Dilkusha Nature Refuge, 26°44′13″S, 152°53′31″E, 3 m a.s.l., isolated as an endophyte from healthy leaves of *Archontophoenix cunninghamiana* (Arecaceae), 6 Dec. 2022, B. Raphael, BR002 (**holotype** stroma lodged in herbarium BRI AQ1052678, culture ex-type BRI AQ1052678 = AC1.4.1; ITS and LSU sequences GenBank PV070662.1 and PV070663.1).

*Notes*: *Helicogermis* *australiensis* was collected as an endophyte from foliage of *Archontophoenix cunninghamiana*. The genus *Helicogermis*, was introduced to accommodate species belonging to the Xylariaceae that produced ascospores with spiral germ slits (Hawksworth & Lodha 1983). The genus was typified with *H. celastri* (Kale & Kale 1971). *Helicogermis* *australiensis* differs from *H. celastri* by having larger ascospores with 1–2 coils as opposed to 2–4. Phylogenetically, *H. australiensis* is also separate from *H. clypeata*, *H. gisbornia*, and another un-named *Helicogermis* species. Molecular data do not exist for the other species of *Helicogermis*. *Helicogermis* *australiensis* is also morphologically different from *H. clypeata*, as the ascomata of *H. clypeata* are immersed in the substrate. The ascospores of *H. australiensis* are also smaller than those of *H. gisbornia*. Based on a megablast search of NCBI’s GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Xylaria* sp. YG-2022a (strain KUNCC 22-12535, GenBank OP912879.1; Identities = 370/374, no gaps), *Xylaria* sp. [strain ATT025, GenBank HQ607803.1; Identities = 374/387, five gaps (1 %)], and *Xylariales* sp. [strain TU22, GenBank HE820889.1; Identities = 321/331, one gap (0 %)]. Closest hits using the LSU sequence are *Helicogermis* sp. YG-2024a [strain CCSG11, GenBank PQ036918.1; Identities = 614/619, no gaps (0 %)], *Xylaria curta* [strain 92092022, GenBank PP336519.1; Identities = 614/632, two gaps (0 %)], and *Helicogermis* *clypeata* [strain MFLU 18-0852, GenBank NG\_081506.1; Identities = 613/631, two gaps (0 %)].

*Supplementary material*: doi: 10.6084/m9.figshare.28520450 (alignment).

*Colour illustrations*: *Archontophoenix cunninghamiana* growing at Dilkusha Nature Refuge, Maleny, Queensland, Australia. Colony of *Helicogermis* *australiensis* growing on PDA; stroma of *H. australiensis* growing from sterilised grapevine twigs on synthetic nutrient-poor agar; conidia; ascospores; ascus containing 8 ascospores. Scale bars: colony = 1 cm, stroma = 100  $\mu\text{m}$ , and all others = 10  $\mu\text{m}$ .



Maximum Likelihood tree produced from an analysis of nrDNA ITS sequences from *H. australiensis* and related *Helicogermisliota* species in GenBank. Phylogenetic analysis was conducted in MEGA v. 11 (Tamura *et al.* 2021) using a ClustalW alignment, Kimura 2 parameters, Gamma distribution with invariant sites and 1000 bootstrap re-samplings were used to build the tree. Bootstrap support values less than 70 % are not shown, and *Xylaria subtropicalis* (*Xylariaceae*) was used as an outgroup to root the tree. The taxon described here is **bold** and in red font. Other type species in the tree are **bold** in black font. Species are also labelled with the accession numbers for the sequences used in the tree.

*Hygrocybe vulcanica*





# *Hygrocybe vulcanica* A. Mateos, De la Peña-Lastra & Illescas, *sp. nov.*

**Etymology:** The epithet refers to the volcanic origin of the collection site.

**Classification:** *Hygrophoraceae*, *Agaricales*, *Agaricomycetes*.

*Pileus* 14–48 mm wide, at first hemispherical, then with age from campanulate to spreading, sometimes flattened in the centre, at times slightly mammillate or with infract edge, surface smooth, dry, matt, somewhat hygrophanous and a little overgrown, opaque, only edge of margin slightly translucent, margin striated by transparency on one third of radius; sulphur yellow in general (Ség. 243, 244; Séguy 1936) with pinkish, orange or fleshy areas (Ség. 213, 226) in the centre or irregularly on the margin, with greyish greenish fibrillose traces on the margin. *Lamellae* distant to moderately spaced, L = 20–22, sinuous, serrate, adnate, with abundant short and long lamellulae [ $l = 1-3(-5)$ ], ventricose, whitish, whitish yellowish or usually sulphur yellow, with concolourous edge. *Stipe* 32–50 × 3–5 mm, slender, central, cylindrical, subequal, terete, straight to recurved, smooth, dry, dull, fistulous, yellow (Ség. 229), yellow orange (Ség. 226) or sometimes more or less intense orange (Ség. 211). *Context* exiguous, concolourous to surface, *odour* and *taste* indistinct. *Basidiospores* (4.9–)5.8–7.0–8.1(–9.0) × (3.7–)4.2–4.9–5.6(–6.1) μm; Q = (1.0–)1.3–1.4–1.6(–1.9); n = 100; Ve = 89 μm<sup>3</sup>, oblong, subspherical, ellipsoidal or broadly ellipsoidal, ovoid, obovoid, very rarely constricted in the centre or with a concave face in side view, sometimes constricted or mitriform in frontal view, with obvious apiculus, smooth, non-amyloid, thin-walled, hyaline, with granular/oleaginous contents and sometimes with a large guttule. *Basidia* (8.5–)24.0–25.2–30.1(–36.0) × (4.7–)5.8–6.3–6.9(–7.5) μm, predominantly tetrasporic, some bisporic, claviform, with sterigmata 3.5–7 μm high, segmented with short basal cells, with basal fibulae. *Cheilocystidia* (22.0–)22.7–31.2–41.0(–45.0) × (1.3–)4.4–7.3–10.7(–11.0) μm, polymorphic, fusiform, lecythiform, capitate, narrowly utriform, claviform with mucronate or rostrate apex, digital, with one or two vermiform excrescences, some bifurcate, abundant. *Lamellar trama* subregular, with subcylindrical or more or less inflated elements 7–13(–15) μm, 40–100 μm long, with sparse fibulae. *Pileipellis* consisting of a cutis dry with some interwoven hyphae 5–12 μm, and claviform termination 12–14(–22) μm, subcutis consisting of similar somewhat larger elements, with abundant fibulae. *Stipitipellis*, consisting of a cutis dry,

with filiform hyphae 35–80 × 2–5 μm with rare free rounded claviform, sometimes fusiform terminations, *caulotrampa* with subcylindrical or fusiform hyphae 40–90 × 10–18 μm. *Clamp connections* present in all tissues.

**Distribution:** Currently known only from island of Terceira, Azores, Portugal.

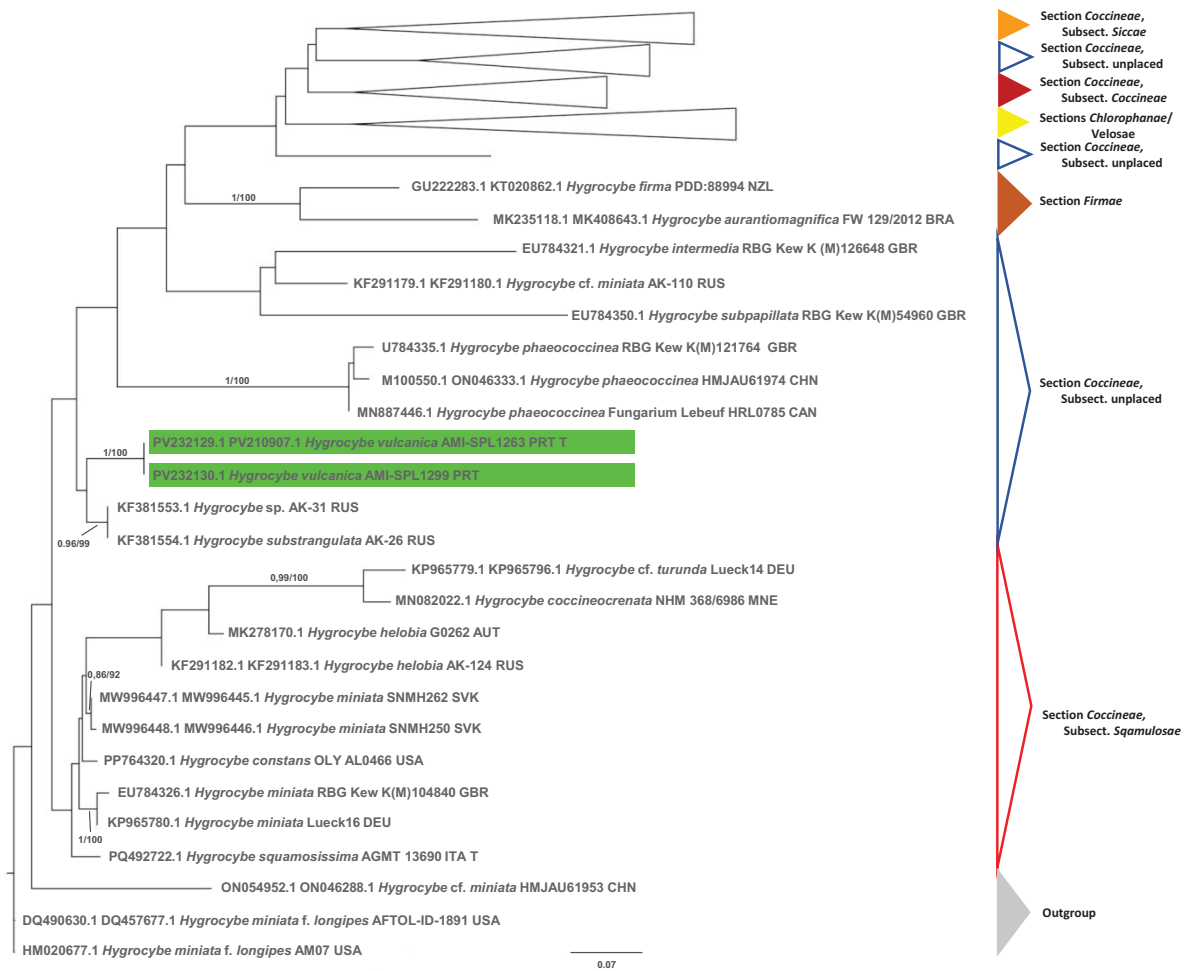
**Typus:** **Portugal**, Azores, Terceira, Angra do Heroísmo, pr. Algar do Carvão, Terra Brava, N38°44'09", W27°12'0.4", 670 m a.s.l., gregarious growing on mossy areas of laurel forest areas planted with *Cryptomeria japonica*, 14 Jan. 2022, A. Mateos & S. De la Peña-Lastra (**holotype** AMI-SPL1263; ITS and LSU sequences GenBank PV232129.1 and PV210907.1).

**Additional material examined:** **Portugal**, Azores, Terceira, Angra do Heroísmo, Mistérios Negros, N38°44'08", W27°16'54", 630 m a.s.l., gregarious in laurel forest areas planted with *Cryptomeria japonica*, 15 Jan. 2022, A. Mateos & S. De la Peña-Lastra (AMI-SPL1299; ITS sequence GenBank PV232130.1).

**Notes:** Phylogenetic analysis presents *H. vulcanica* in a fully supported subclade (1/100) located within section *Coccineae*, forming part of a small low-bearing clade between subsect. *Squamulosae* and section *Firmae* (Lodge *et al.* 2014), together with *Hygrocybe substrangulata* the phylogenetically closest species (97.4 % affinity at LSU level between the sequence extracted from the holotype of *H. vulcanica* and GenBank sequence KF381554.1). At the morphological level, there are no species in the nearby sections showing all the macro- and microscopic characteristics of the species described here: among the species with more or less yellow colourations, *H. ceracea* shows a higher percentage of constricted spores, and a mixed ixotrichodermia-ixocutis pileipellis (Boertmann 2010); *H. flavescens*, a species described from North America, has a pileipellis with ixocutis structure and larger fruitbodies (Hesler & Smith 1963); *H. subpapillata*, a small species with more orange shades, also has pileipellis in ixocutis, and longer lamellar web elements (up to 800 μm), according to Boertmann (2010). *Hygrocybe citrina*, a diversely interpreted species, differs by its slightly decurrent lamellae and spores with a Q ≥ 1.8 (Lange 1940), like *H. phaeococcinea*, which may have similar colourations, possesses pileipellis in cutis, and is the only one of the species included in this comparative to have scattered marginal cells (Boertmann 2010), although *H. vulcanica* has true, abundant and polymorphous cheilocystidia. Finally, *H. substrangulata*, with much more orange colourations and spores longer than 10 μm on average, is also distinguished by its pileipellis in trichodermia (Boertmann 2010).

**Supplementary material:** doi: 10.6084/m9.figshare.28830191 (alignment).

**Colour illustrations:** Portugal, Azores, Terceira, Terra Brava, laurel forests planted with *Cryptomeria japonica*, where the holotype of *Hygrocybe vulcanica* was collected. Top, basidiomata correspond with the holotype. Right column: upper photo corresponds with hymenophoral trama (left RC, right H<sup>2</sup>O) and hymenophore with basidia and immature basidia (on the right, RC); the bottom photo is stipitipellis (upper, H<sup>2</sup>O), and pileipellis (bottom, RC). Left column: upper photo corresponds to basidiospores (RC); the bottom photo is cheilocystidia (RC). Scale bars: hymenophoral trama (left) = 100 μm; all others = 10 μm.



The most probable maximum likelihood (ML) tree obtained from the ITS + LSU (GenBank accession numbers in supplementary table) alignment showing on the branches the ML bootstrap (ML-bs) support values and Bayesian posterior probability (BPP) values (ML-bs/BPP) considered significant (ML-bs  $\geq 80$  % and BPP values  $\geq 95$  %), calculated with IQ-TREE v. 2.1.3 (Nguyen *et al.* 2015) and MrBayes v. 3.2 (Ronquist *et al.* 2012), respectively. The novel species is highlighted in green. Sequences from type material are indicated with a T.



*Hongoboletus americanus*



# *Hongoboletus americanus* Domnauer, P.R. Miller & Dentinger, *sp. nov.*

*Etymology*: Named for this species being the only member of this genus to occur in the Americas.

*Classification*: Boletaceae, Boletales, Agaricomycetes.

*Pileus* 12 cm wide, convex when young to broadly convex in age, margin incurved and slightly overhanging, surface glabrous to slightly subtomentose, colour brick red to copper reddish orange, fading to a cream yellow near margin. *Hymenophore* adnate to centrally depressed, bright citrine yellow when young, becoming dull olive yellow in age, quickly staining deep blue where bruised, tubes 6 mm thick, 0.33 mm pore diameter. *Stipe* 7 cm length, obclavate, 1.8 cm diam. at apex, 2.3 cm diam. at base, surface glabrous, not reticulate, yellow with longitudinal red streaks and small red dots near base, vinaceous red staining on injured areas, basal mycelium white. *Context* pale yellow, immediately strongly blueing throughout, strongest blueing at stipe base, blueing fades to brownish orange red throughout all parts; flesh solid, *odour* indistinct, *taste* slightly tart. *Chemical reactions* pileus surface: KOH reddish brown, NH<sub>4</sub>OH orange yellow, FeSO<sub>4</sub> negative; pileus context: KOH ochre, NH<sub>4</sub>OH greenish yellow, FeSO<sub>4</sub> green. *Spore print* olive brown. *Basidiospores* (8.6–)9.0–11.3(–11.6) × (3.7–)3.8–4.2(–4.7) μm (n = 20), spores ellipsoid, brownish yellow in 5 % KOH, smooth. *Cystidia* ventricose, *clamp connections* absent.

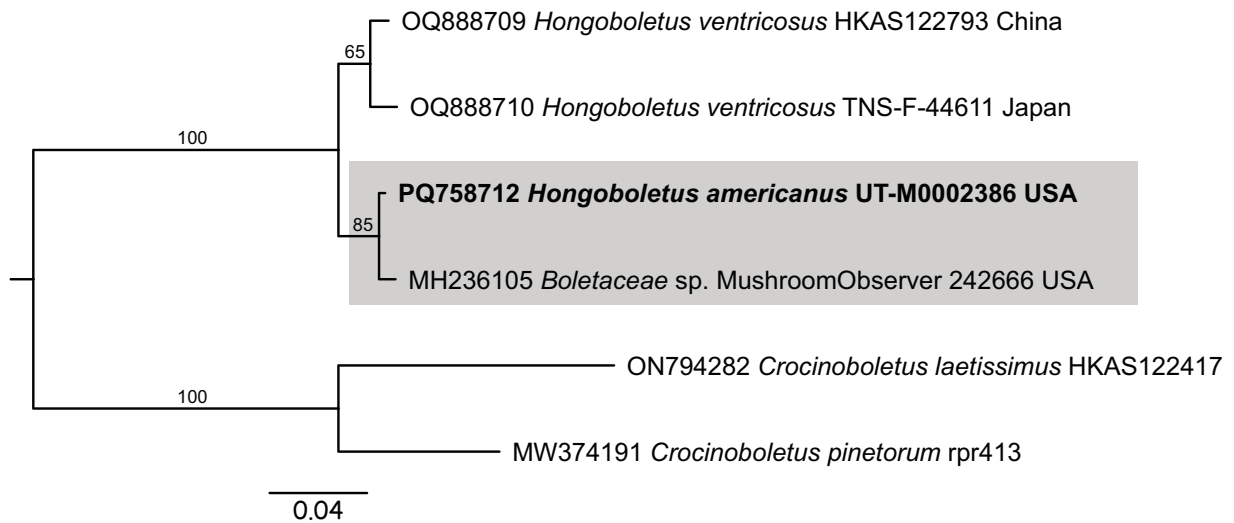
*Habit, habitat and distribution*: Solitary in mixed pine-hardwood forest, currently known only in the Eastern USA, rarely encountered.

*Typus*: USA, Mississippi, 34°21'51.0"N, 89°23'40.0"W, 177 m a.s.l., in mixed pine-hardwood forest, 15 Jul. 2021, P.R. Miller & G. Stratton, PRM2299 (**holotype** MISS0098689, **isotype** UT-M0002386; ITS sequence GenBank PQ758712).

*Notes*: *Hongoboletus americanus* can be recognized by its smooth, obclavate, yellow stipe, brick red cap, and dark blue staining throughout that fades to brown. *Lanmaoa pseudosensibilis* may be morphologically similar, also displaying a strong blue staining reaction that fades to brown (Bessette *et al.* 2024). However, *H. americanus* can be distinguished by its typically larger cap width to stipe length ratio, and the more bulbous stipe with vinaceous staining on the stipe surface. This is the second species belonging to the genus *Hongoboletus* and the first described from North America. The closest related species is *Hongoboletus ventricosus*, which is found in East Asia where it is commonly sold in markets for consumption (Wu *et al.* 2023).

*Supplementary material*: <https://mushroomobserver.org/565254> (photographs); doi: 10.6084/m9.figshare.28876139 (alignment).

*Colour illustrations*: Native habitat in mixed pine-hardwood forest (photo credit P.R. Miller). Basidiome side view (MISS0098689, type); basidiome ventral view showing hymenophore bruising blue; basidiome cross section blueing throughout; spores in KOH. Scale bars: colony = 2 cm (basidiome habits); spores = 10 μm.



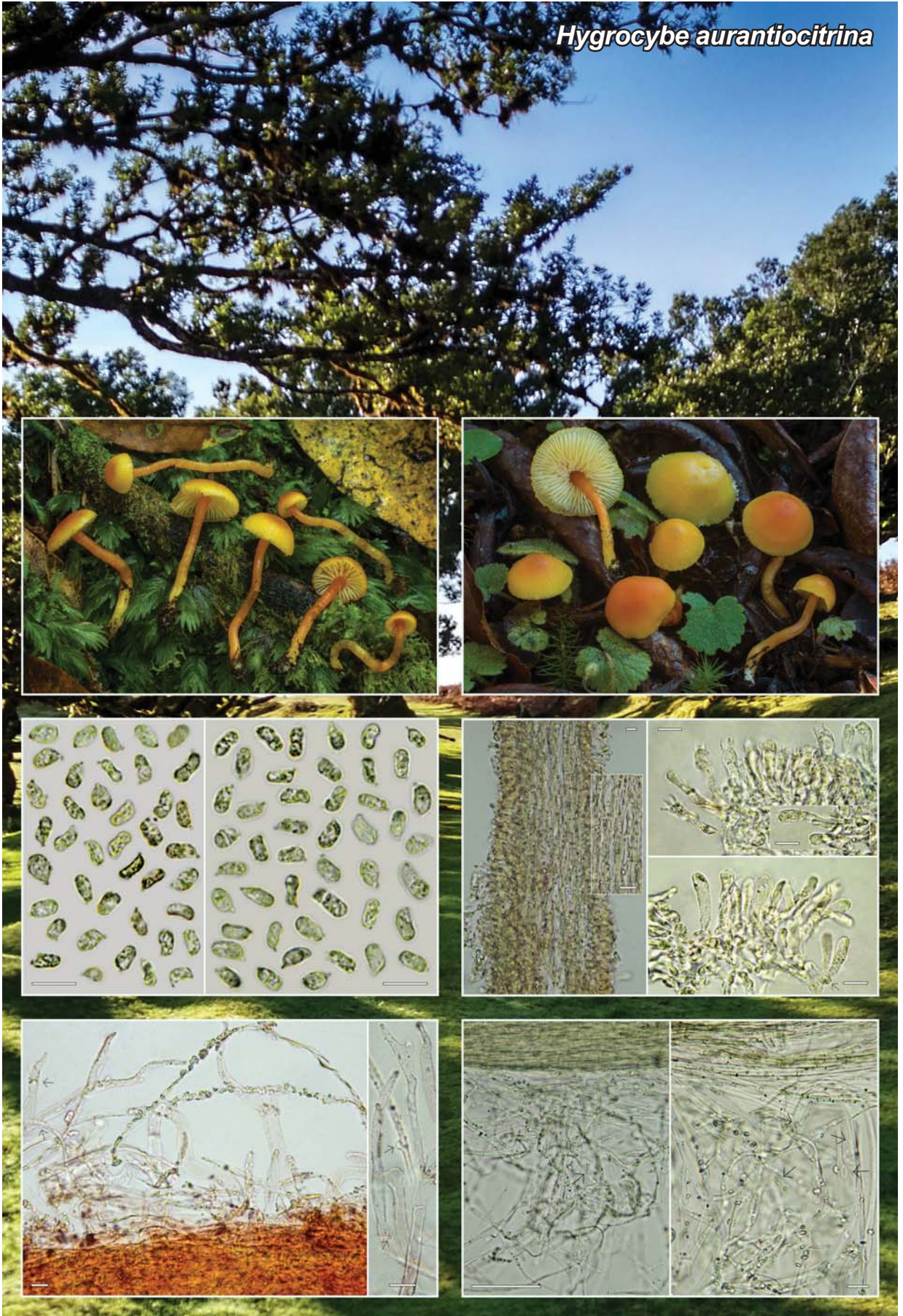
Phylogram distinguishing *Hongoboletus americanus*. The Maximum-Likelihood phylogram was obtained using IQ-TREE v. 1.6.12 and consists of available ITS sequences of known *Hongoboletus* species, with *Crocinoboletus* as an outgroup (Trifinopoulos *et al.* 2016). The support values at the nodes are based on 1000 bootstrap replicates. The novel species is shown in **bold** font. Scale bar shows substitutions per site.

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*Hygrocybe aurantiocitrina*





# *Hygrocybe aurantiocitrina* De la Peña-Lastra, A. Mateos & Illescas, *sp. nov.*

**Etymology:** The epithet refers to the orange reddish colour with yellow orange margin.

**Classification:** *Hygrophoraceae*, *Agaricales*, *Agaricomycetes*.

**Pileus** 6–18 mm wide, at first hemispherical, then campanulate, later sometimes somewhat flattened in the centre, with incurved margin when young, cuticle rugulose to magnifying glass, viscous, striated by transparency to mid-radius, margin somewhat overgrown and often crenulate; orange, to orange reddish (Ség. 196, 212; *Séguy 1936*) in the centre or entirely, usually with yellow orange margin, discolouring to yellow (Ség. 241), or sulphur yellow (Ség. 230), sometimes over the whole surface at full maturity. **Lamellae** separate, L = 24–35, adnate, slightly decurrent, with lamellulae (l = 1–3), ventricose, intervening on faces and bottom at maturity, whitish-yellowish or yellowish. **Stipe** 22–30 × 1–2 mm, slender, central, cylindrical, subequal, terete, straight to recurved or generally flexuous, smooth, translucent, very viscid, fistulous, orange reddish, orange yellowish (Ség. 246, 211) above, yellow orangish, lemon yellow (Ség. 226, 257) below. **Context** exiguous, concolourous to surface, no discernible odour and taste indistinct. **Basidiospores** (4.5–)5.7–6.4–6.8(–7.9) × (2.4–)2.8–3.4–4.1(–4.5) μm; Q = (1.3–)1.5–1.9–2.3(–2.8); n = 100; Ve = 40 μm<sup>3</sup>, oblong, ellipsoidal or broadly ellipsoidal, subcylindrical, sometimes constricted in the centre (less than 25 %), phaseoliform or rarely with a concave face in side view, smooth, non-amyloid, thin-walled, hyaline, with granular/oleaginous contents and rarely with a large guttule. **Basidia** (17.3–)22.0–25.2–29.3(–29.9) × (3.6–)4.2–5.0–6.0(–6.3) μm, tetrasporic, claviform, with sterigmas 3.7–5.0 μm high, with basal fibulae. **Lamellar trama** regular, with more or less inflated elements 2–6 μm, 50–100 μm long. **Pileipellis** mixed, consisting of an ixocutis with fibulate hyphae and very frequent rhomboidal crystals, and an ixotrichodermia 80–120(–150) high, with hyphae with rounded, claviform, narrowed or bifurcate terminations, 3–8 μm in diam. and 40–85 μm long. **Stipitipellis** mixed, consisting of an ixotrichoderm, sometimes 200–300 μm thick, with filiform hyphae 80–250 × 2–4 μm with rounded, sometimes narrowed, terminations, and areas with an ixocutis, with abundant, sometimes double, fibulae, with very frequent crystals. **Clamp connections** present in all tissues.

**Colour illustrations:** Portugal, Madeira, Ribeira da Janela, Fanal, forest of *Laurus novocanariensis*, where the holotype of *Hygrocybe aurantiocitrina* was collected. Right column: basidiomata in upper photo correspond with the holotype AMI-SPL879, in middle hymenophoral trama (left RC) and lamellar edge con basidia and immature basidia (two pictures on the right RC), and the bottom photo is stipitipellis (two pictures, H<sup>2</sup>O). Left column: upper photo corresponds AMI-SPL715, in middle basidiospores (RC, H<sup>2</sup>O); and the bottom photo is pileipellis (two pictures RC). Scale bars: hymenophoral trama (left) = 50 μm; all others = 10 μm.

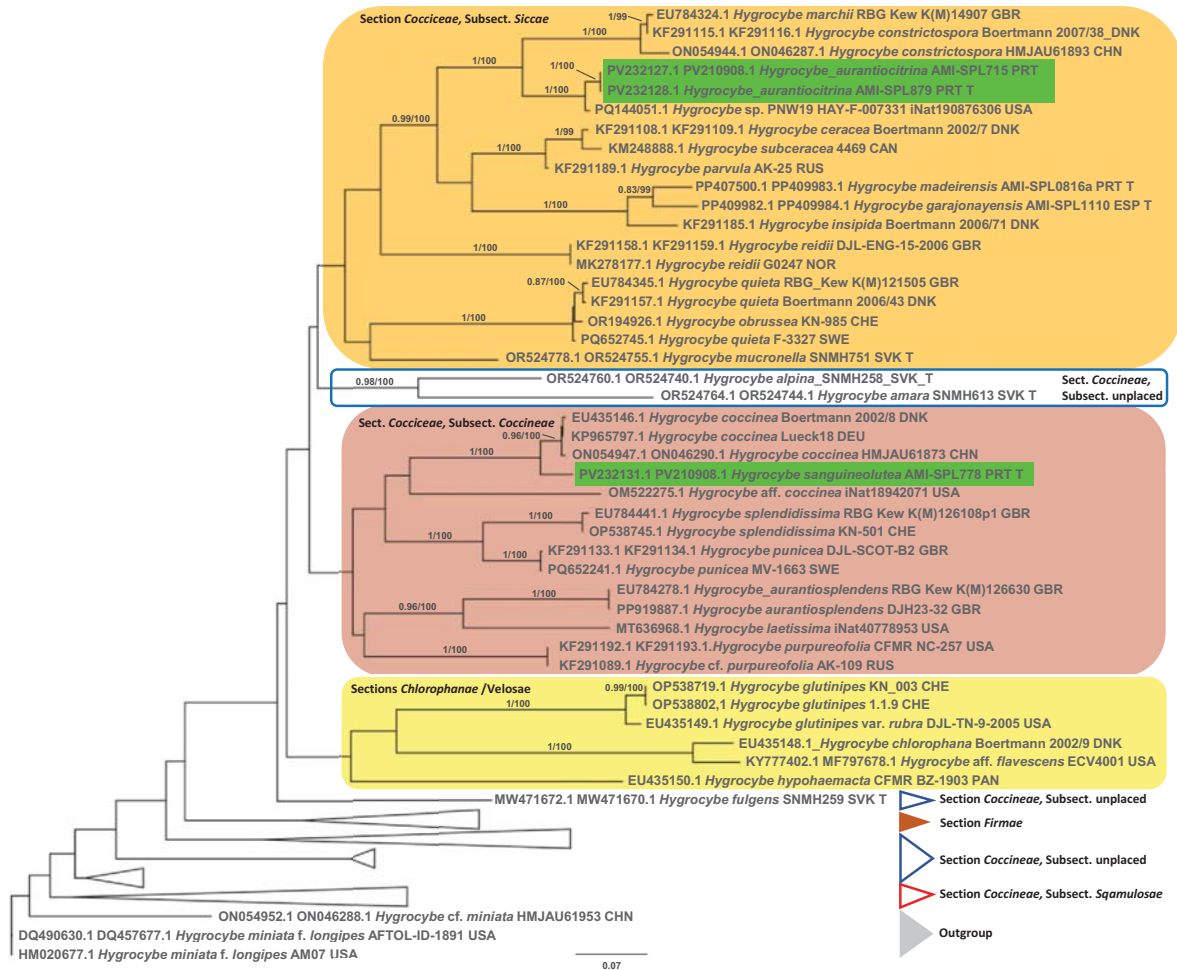
**Distribution:** Currently known only from the type location in the centre of Madeira.

**Typus:** **Portugal**, Madeira, Ribeira da Janela, Fanal, N32°48'55.9", W17°08'54.2", 1100 m a.s.l., gregarious under laurel forest, 20 Nov. 2021, A. Mateos & S. De la Peña-Lastra (**holotype** AMI-SPL879; ITS sequence GenBank PV232128.1).

**Additional material examined:** **Portugal**, Madeira, Parque Natural do Ribeiro Frio, N32°44'11.4", W16°53'11.1", 940m a.s.l., gregarious in laurel forest, 18 Nov. 2021, A. Mateos & S. De la Peña-Lastra (AMI-SPL715; ITS and LSU sequences GenBank PV232127.1 and PV210908.1).

**Notes:** In our phylogenetic analysis, *H. aurantiocitrina* clusters in a fully supported subclade (1/100) in the company of the North American species designated with the provisional name *Hygrocybe* sp. PNW19 (95.9 % identity at the ITS level with the sequence extracted from the holotype of *H. aurantiocitrina*), accompanied by the sequence attributed to *Hygrocybe marchii* (GenBank EU784324.1), and *Hygrocybe constrictospora* in a sister subclade. *Hygrocybe aurantiocitrina* clusters in subgenus *Pseudohygrocybe*, section *Coccineae*, subsect. *Sicca* (Lodge *et al.* 2014). With a similar appearance we have a whole series of small *Hygrocybe*, more or less slimy and with yellowish to reddish tones in pileus and stipe; among them we can highlight *H. parvula* and *H. minutula*, two species described in North America with small ellipsoidal spores around 6 μm long, more decurrent lamellae and a pileipellis in ixocutis with some erect elements (Hesler & Smith 1963); *H. ceracea*, with usually less intense colourations, which is further distinguished by its dry stipe and its spores on average larger than 7 μm long, constricted by more than 50 % (Boertmann 2010); *H. insipida* can be differentiated by their usually dry or at most slightly viscid stipe (Boertmann 2010); *H. garajonayensis* and *H. madeirensis* are two small species sharing laurel forest habitat with *H. aurantiocitrina*, both with pileipellis in ixotrichodermia and lamellar weft composed of articles < 70 μm long, interwoven in the case of *H. madeirensis* (Crous *et al.* 2024a). Finally, *H. reidii* and *H. constrictospora* can be separated by their pileipellis in cutis and dry stipe, by their spores on average larger than 7.5 μm long, by their typical honey odour in the first case and by their more than 75 % constricted spores in the second case. These species are phylogenetically more related to *H. aurantiocitrina*, with an identity of 90.1 % comparing the ITS-LSU matrix of the sequences corresponding to the holotype with the matching fragment of the GenBank sequences KF291115.1 and KF291116.1, extracted from the sample of *H. constrictospora* Boertmann 2007/38.

**Supplementary material:** doi: 10.6084/m9.figshare.28830191 (alignment)..

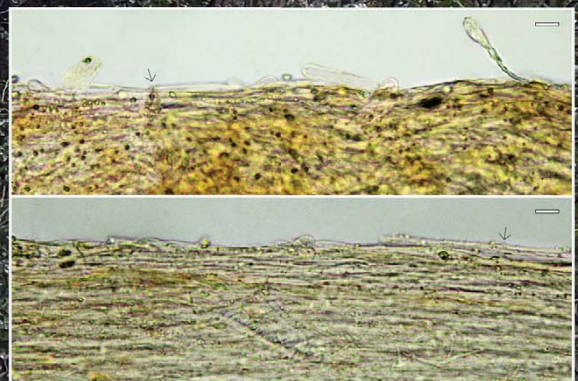
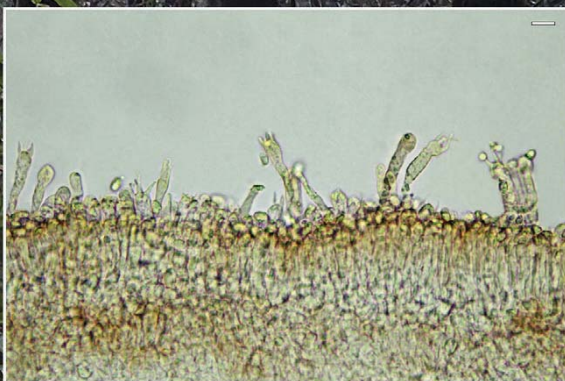
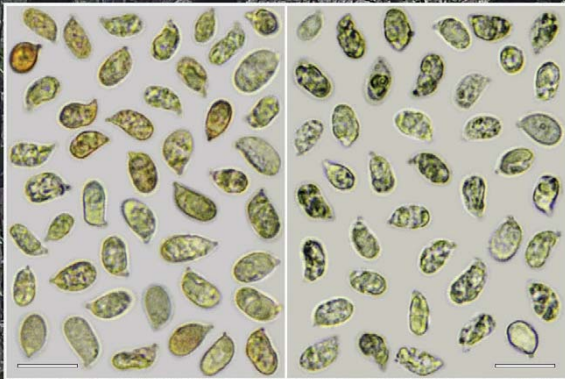


The most probable maximum likelihood (ML) tree obtained from the ITS + LSU alignment showing on the branches the ML bootstrap (ML-bs) support values and Bayesian posterior probability (BPP) values (ML-bs/BPP) considered significant (ML-bs  $\geq 80$  % and BPP values  $\geq 95$  %), calculated with IQ-TREE v. 2.1.3 (Nguyen *et al.* 2015) and MrBayes v. 3.2 (Ronquist *et al.* 2012), respectively. The novel species is highlighted in green. Sequences from type material are indicated with a T.

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*Hygrocybe sanguineolutea*



# *Hygrocybe sanguineolutea* A. Mateos, De la Peña-Lastra & Illescas, *sp. nov.*

*Etymology:* The epithet refers to the overall blood red colour of the pileus and stipe, more yellow orange on the margin of the pileus and stipe areas of the carpophore.

*Classification:* *Hygrophoraceae*, *Agaricales*, *Agaricomycetes*.

*Pileus* 26–25 mm wide, at first conical campanulate, later flat-convex or flattened, more or less mammillate in shape not very distinct, surface dry and smooth, matt, striated by transparency from one third to half of the radius, margin somewhat overgrown and often crenulate; deep scarlet red (Ség. 156; Séguy 1936), blood red, cherry red (Ség. 101, 121), discolouring at the margin to orange yellow (Ség. 168, 196), and at the edge yellow (Ség. 230, 241). *Lamellae* separate, L = 24–28, adnate, broadly adnate or slightly decurrent by one tooth, with lamellulae (l = 1–3), ventricose, intervening at the bottom at maturity, cream yellowish or sometimes entirely yellowish, reddish at the bottom, with pale arista. *Stipe* 25–35 × 3–5 mm, central, cylindrical, subequal, terete, dry, dull, somewhat ribbed as it ages, from solid to fistulous, blood red (Ség. 157) over almost the entire length, yellow (Ség. 226) in small spots and in the lower part in the area covered by the substrate, the base covered with white mycelial felt. *Context* somewhat brittle, subcoloured to surface, no perceptible *odour* and indistinct *taste*. *Basidiospores* (4.4–)5.9–6.7–7.4(–8.5) × (3.0–)3.4–3.9–4.4(–5.2) μm; Q = (1.2–)1.5–1.7–2.0(–2.5); n = 100; Ve = 55 μm<sup>3</sup>, oblong, ellipsoid, subcylindrical, rarely constricted in the centre (less than 10 %), some ovoid, sometimes amygdaliform or lacryiform, phaseoliform in side view, with apiculum often almost lateral, smooth, non-amyloid, thin-walled, hyaline, with granular/oleaginous contents and rarely with a large guttule. *Basidia* (28.1–)35.8–42.0–51.0(–63.0) × (4.3–)5.0–6.1–7.0(–7.5) μm, tetrasporic, claviform, with sterigmata 3.5–8.0 μm high, with basal fibulae, basidioles subcylindrical, claviform or subcapitate, subhymenium confused globular and with frequent ellipsoid crystals. *Lamellar trama* subregular, with more or less inflated elements 3–8(–10) μm wide, 25–60 μm long, terminally clavate. *Pileipellis* consisting of a cutis dry with hyphae 2–4

μm diam. and 30–90 μm long, with rounded or claviform terminations, with rare free elements, fibulate, subcutis with hyphae 8–10 μm diam., more shortly septate. *Stipitipellis* consisting of a cutis dry with filiform hyphae 25–100 × 2.5–3 μm in the outer layer, without free elements, and × 6–8 μm in deeper ones, sometimes interwoven. *Clamp connections* present in all tissues.

*Distribution:* Currently known only from the type location in the centre of Madeira.

*Typus:* **Portugal**, Madeira, Chão dos Louros, N32°45'37.1", W17°00'58.5", 820 m a.s.l., gregarious in laurel forest, 19 Nov. 2021, A. Mateos & S. De la Peña-Lastra (**holotype** AMI-SPL778; ITS and LSU sequences GenBank PV232131.1 and PV210908.1).

*Notes:* *Hygrocybe sanguineolutea* is phylogenetically integrated in sect. *Coccineae*, subsect. *Coccineae*, although according to the traditional morphological classification (Candusso 1997, Boertmann 2010), it should be integrated in subsect. *Siccae* considering its pileipellis in dry cutis. Morphologically similar species to *H. sanguineolutea* include: *H. phaeococcinea*, a species with the pileus and stipe with similar colouration, but different in being little or non-striated at the margin of the pileus, and with much larger spores [(8–)9–11.5(–12.5) × (5–)6–7.5 μm (Candusso 1997); (6–)7.5–10(–12.5) × (4–)4.5–5.5(–7.5) μm (Boertmann 2010)]; *H. splendidissima*, similar in colouration but with larger fructifications, free or only slightly adnate lamellae, honey odour when dry and larger spores; *H. punicea* has similarly coloured fructifications, but much larger size, slimy pileus when wet, much larger spores and epicutis in ixotrichodermia; *H. aurantiosplendens* is distinct because of its larger size, red orange colour, slimy pileus and larger spores. Finally, we have *H. coccinea*, the phylogenetically most closely related species (with an identity of 94.4 % comparing the ITS–LSU matrix of the sequences corresponding to the holotype with the matching fragment of GenBank sequence EU435146.1, obtained from the sample of *H. coccinea* Boertmann 2002/8), but with different colour, from orange to yellow, pileus with non-striated margin, not slimy, lubricated, and pileipellis in ixotrichodermia or ixocutis.

*Colour illustrations:* Portugal, Madeira, Terceira, Chão dos Louros, forest of *Laurus novocanariensis*, where the holotype of *Hygrocybe sanguineolutea* was collected. Top, basidiomata correspond with the holotype. Right column: in upper photo correspond hymenophoral trama (left RC, middle H<sup>2</sup>O), basidia (RC) and basidioles (H<sup>2</sup>O); and the bottom photo is pileipellis (upper) and stipitipellis (bottom) (RC). Left column: upper photo corresponds basidiospores (RC, H<sup>2</sup>O); and the bottom photo is hymenium with basidia and basidioles (RC). Scale bars: hymenophoral trama (left) = 50 μm; all others = 10 μm.

For phylogenetic tree, see *Hygrocybe aurantiocitrina* (FP 1835).



*Hypocrella khonsanitii*



***Hypocrella khonsanitii* Noisrip. & Luangsa-ard, *sp. nov.***

*Etymology:* Named in honour of Artit Khonsanit, who collected and studied this species and has been working on invertebrate pathogenic fungi in BIOTEC for more than 10 years.

*Classification:* Clavicipitaceae, Hypocreales, Sordariomycetes.

*Stromata* discoid, pulvinate, 0.5–1 mm diam. and 0.5 mm high, light greenish yellow to dark orange. *Conidioma pycnidial*, a conidioma per stroma, unilocular, subglobose with narrow orifices in the centre of stromata, 410–630 × 300–550 µm. *Phialides* hyaline, cylindrical, 9–22 × 1–2 µm. *Conidia* hyaline, fusoid, 11–15 × 1.5–2 µm, paraphyses present. *Perithecia* scattered, semi-embedded, numerous perithecia per stroma (≥ 10), slightly projecting, translucent, elongated flask-shaped, 250–396 × 70–100 µm. *Asci* hyaline, cylindrical, 85–170 × 4–8 µm. *Ascospores* hyaline, whole, filiform to long fusiform, 1–4-septate, 36–84 × 2–3 µm. *Colonies* on potato dextrose agar (PDA) compact, pulvinate, with a wrinkled surface, erose edge, attaining a diam of 8–11 mm after 7 wk at 25 °C, pale orange yellow mycelia, pale yellow conidial masses.

*Typus:* **Thailand**, Narathiwat Province, Waeng District, Hala Bala Wildlife Sanctuary, 500 m nature trail, on scale insects (*Coccidae*), found on underside of dicotyledonous leaves, 12 Oct. 2013, A. Khonsanit, N. Wiriyathanawudhiwong & A. Abdulrohman (**holotype** BBH 38451, culture ex-type = BCC 69112, ITS, LSU, *tef1*, and *rpb1* sequences GenBank PQ560532, PQ560534, PQ585792, and PQ585794).

*Additional materials examined:* **Thailand**, Narathiwat Province, Waeng District, Hala Bala Wildlife Sanctuary, 500 m nature trail, on scale insects (*Coccidae*), found on the underside of dicotyledonous leaves, 12 Oct. 2013, A. Khonsanit, N. Wiriyathanawudhiwong & A. Abdulrohman (SM01516); Chumphon Province, Phato District, Phato Watershed Conservation and Management Unit, on scale insects (*Coccidae*), found on the underside of dicotyledonous leaves, 23 Jan. 2014, A. Khonsanit, D. Thanakitpipattana & W. Noisripoom (SM01671: BCC 71371, ITS, LSU, *tef1*, and *rpb1* sequences GenBank PQ560533, PQ560535, PQ585793,

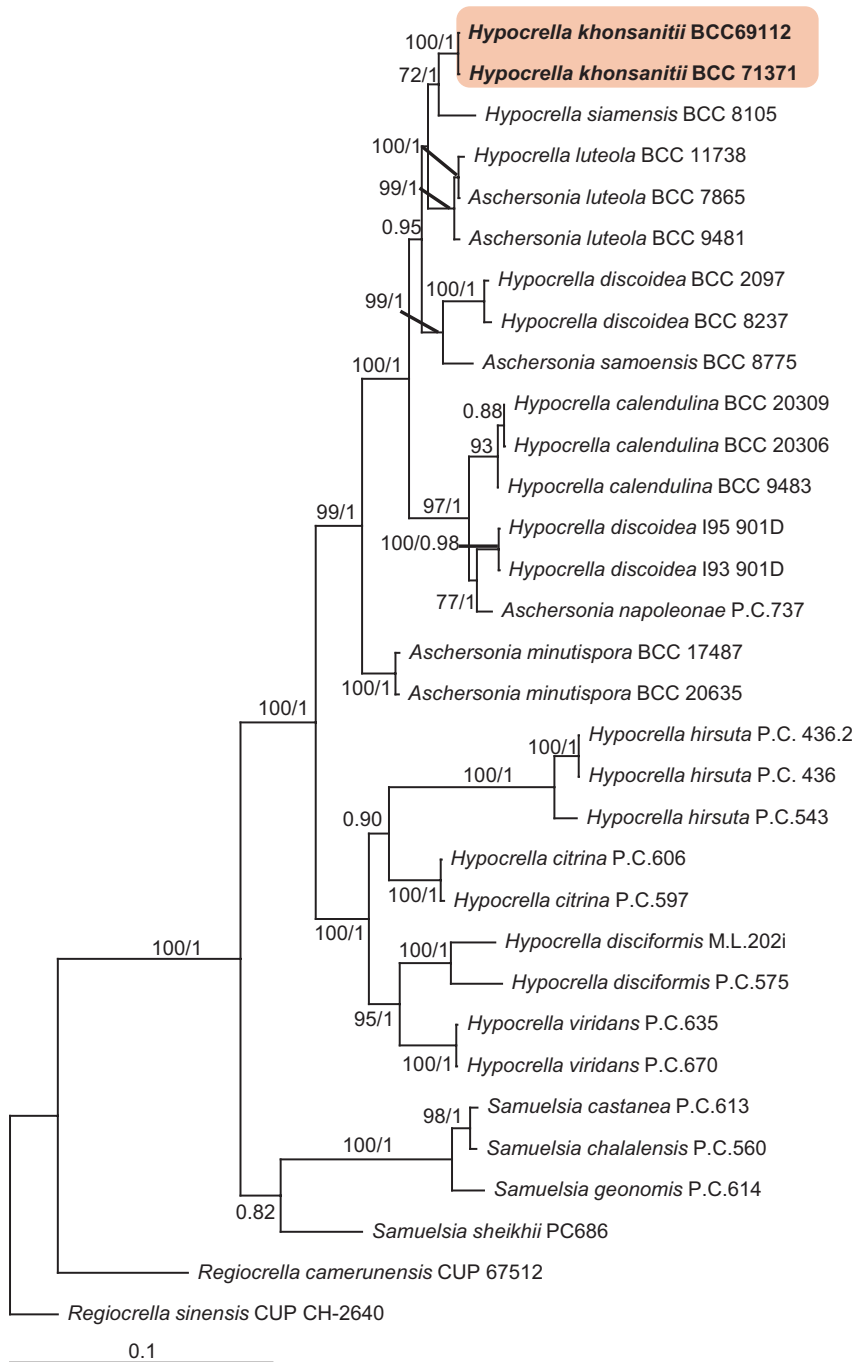
PQ585795); Narathiwat Province, Waeng District, Hala Bala Wildlife Sanctuary, 500 m nature trail, on scale insects (*Coccidae*), found on the underside of dicotyledonous leaves, 24 Nov. 2020, A. Khonsanit & K. Tasanathai (BBH 51038, BBH 51048).

*Notes:* Phylogenetically, *Hypocrella khonsanitii* is closely related to *H. siamensis* (Mongkolsamrit *et al.* 2009). However, the gross morphological characters of *H. khonsanitii* differ from *H. siamensis* in producing only one conidioma per stroma and wider ascospores, 36–84 × 2–3 µm, while *H. siamensis* produces several conidiomata per stroma (Petch 1921, Mongkolsamrit *et al.* 2009, Luangsa-ard *et al.* 2010) and narrower ascospores, 80–100 × 1–1.5 µm (Mongkolsamrit *et al.* 2009, Luangsa-ard *et al.* 2010).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence of BCC 69112 had highest similarity to *Aschersonia badia* [strain SM43, GenBank DQ365846; Identities = 617/650 (95 %), 13 gaps (2 %)], *Aschersonia badia* [strain AL23, GenBank DQ365831; Identities = 600/627 (96 %), 13 gaps (2 %)], and *Hypocrella discoidea* [strain BOKO189, GenBank EF179156; Identities = 614/650 (94 %), 20 gaps (3 %)]. Closest hits using the **LSU** sequence are *Aschersonia badia* [GenBank KC713635; Identities = 1167/1168 (99 %), no gaps], *Aschersonia* sp. [strain BCC49495, GenBank KC713633; Identities = 1162/1168 (99 %), no gaps] and *Hypocrella discoidea* [strain BCC8775, GenBank DQ384944; Identities = 1129/1137 (99 %), five gaps (0 %)]. Closest hits using the **tef1** sequence are *Aschersonia badia* [strain BCC8105, GenBank KC713630; Identities = 937/962 (97 %), no gaps], *Aschersonia* cf. *badia* [strain BCC 8407, GenBank DQ384960; Identities = 901/928 (97 %), no gaps] and *Hypocrella discoidea* [strain BCC 7865, GenBank DQ384975; Identities = 894/929 (96 %), no gaps]. Closest hits using the **rpb1** sequence are *Hypocrella discoidea* [strain MDYS2010352, GenBank KU158212; Identities = 575/590 (97 %), no gaps], *Hypocrella discoidea* [strain BCC 9481, GenBank DQ384996; Identities = 572/587 (97 %), no gaps] and *Aschersonia* cf. *badia* [strain BCC 8407, GenBank DQ384999; Identities = 572/587 (97 %), no gaps].

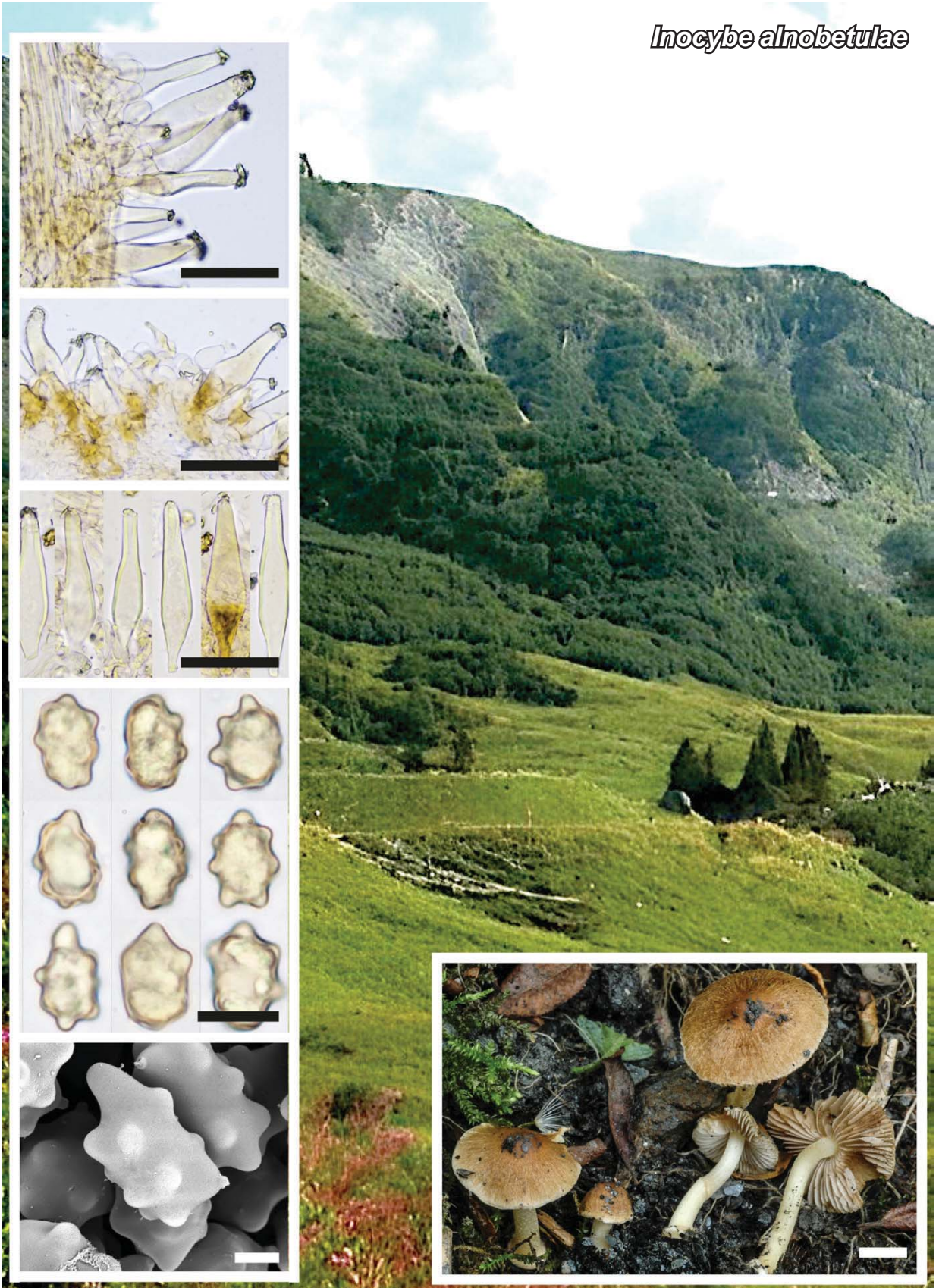
*Supplementary material:* doi: 10.6084/m9.figshare.28829255 (alignment, phylogenetic tree, table).

*Colour illustrations.* Background photo of Hala Bala Wildlife Sanctuary, 500 m nature trail, Waeng District, Narathiwat Province, Thailand. Asexual stromata and sexual stroma on scale insects (*Coccidae*); section of stroma showing conidioma; section of stroma showing perithecia; colonies obverse on PDA; phialides and conidia at the tips with paraphyses; conidia; asci; whole ascospores. Scale bars: asexual stromata on scale insects = 5 mm; sexual stroma on scale insect = 1 mm; section of stroma showing perithecia = 200 µm; section of stroma showing conidioma = 100 µm; phialides and conidia at the tips with paraphyses = 50 µm; asci = 20 µm; conidia, whole ascospores = 10 µm.



Maximum likelihood tree of *H. khonsantii* and phylogenetically closely related species based on a 2464 bp combined dataset comprising LSU, *tef1* and *rpb1* sequences. Analyses were performed using RAxML v. 8.2.12 (Stamatakis 2014) and MrBayes v. 3.2.7a (Huelsenbeck & Ronquist 2001) with 5 M generations and MrModeltest v. 2.2 (Nylander 2004) under the SYM+G model. RAxML bootstrap values > 70 % and Bayesian posterior probabilities > 0.7 are represented on the nodes. The new species proposed in the present study is highlighted and indicated in **bold** text.

*Inocybe alnobetulae*





# *Inocybe alnobetulae* P.-A. Moreau, Esteve-Rav. & Pancorbo, *sp. nov.*

**Etymology:** The name is derived from the species *Alnus alnobetula* (*Betulaceae*), due to its apparently exclusive ectomycorrhizal relationship with this plant.

**Classification:** *Inocybaceae*, *Agaricales*, *Agaricomycetes*.

**Basidiomata** agaricoid and stipitate. **Pileus** 1.2–2.8(–3.5) mm, initially hemispherical to paraboloid, then convex to plano-convex, finally applanate or shallowly and broadly umbonate; margin straight to hardly inflexed, entire to irregularly lobate; generally uniform in colour or slightly darker towards the umbo, fulvous, yellow ochraceous or orange ochraceous, especially in young specimens (Mu 7.5YR 6/6–8, 10YR 6/6–8) (Munsell 1994); surface dry, finely smooth fibrillose, centre smooth, usually radially lacerated in some specimens, not hygrophanous. **Velipellis** conspicuous in young basidiomes, whitish, lanose-arachnoid, especially at the margin. **Lamellae** moderately distant ( $L = 30\text{--}36$ );  $l = 1\text{--}2(-3)$ , 3–5 mm wide, adnexed, ventricose, long-time pale, initially white, becoming pale grey, then pale brown ochraceous, finally pale brown; edge white or paler, fimbriate to finely crenulate. **Stipe** 2.5–4.5 × 0.3–0.5 mm, firm, often curved to sinuose, abruptly bulbous to marginate bulbous; colour initially white to pale yellow-ochraceous; surface uniform, finely and densely floccose along the entire length. **Cortina** not seen. **Context** firm, fibrous, whitish at pileus, white to pale ochraceous at the stipe. **Smell** faintly spermiatic when cut. **Spores** (8.8–)9.4–11.0–12.7(–13.9) × (6.4–)7.2–8.2–9.3(–10.7) μm,  $Q = (1.06\text{--})1.19\text{--}1.30\text{--}1.53(-1.64)$  ( $n = 242 / N = 4$ ), mostly subheterodiametric, distinctly nodulose under the optical microscope, provided with 9–15 distinct obtuse knobs variable in height (0.9–1.7 μm high). **Basidia** (26.2–)28.9–33.4–39.0(–41.1) × (8.2–)10.0–12.6–15.8(–18.6) μm;  $Q = (2.03\text{--})2.12\text{--}2.60\text{--}3.55(-4.32)$  ( $n = 76 / N = 2$ ), 4-spored (sterigmata 4–7 μm long), not rarely 2-spored (sterigmata 11–15 μm long), clavate. **Lamellar edge** sterile, composed of abundant, protruding cheilocystidia mixed with hyaline, slightly thin-walled claviform paracystidia. **Pleurocystidia** (60.0–)66.4–78.0–92.9(–97.5) × (12.5–)14.1–18.9–24.8(–32.5) μm,  $Q = (2.21\text{--})3.07\text{--}4.20\text{--}5.62(-6.48)$ , ( $n = 76 / N = 4$ ), subfusiform, sublageniform, often provided with a short pedicel, crystalliferous, sometimes with microcrystals covering the apical portion of the neck, hyaline or with yellowish ochre content; walls (1.35–)1.64–2.00–2.40(–2.57) μm thick, widening slightly at the apex, yellowish in aqueous ammonia solutions. **Cheilocystidia** (39.5–)46.1–62.2–81.0(–85.4) × (9.8–)12.1–16.9–23.6(–28.5) μm,  $Q = (2.24\text{--})2.53\text{--}3.70\text{--}4.88(-5.38)$  ( $n = 51 / N = 3$ ), similar in morphology to pleurocystidia. **Lamellar trama** pale yellowish, composed of

septate parallel hyphae, with more or less widened and short elements thinned at the septa, 5–10 μm wide. **Stipitipellis** a cutis of parallel hyphae 3.6–11 μm wide, with parietal brownish pigment. **Caulocystidia** abundant and present along the entire length of the stipe, similar in size and shape to hymenial cystidia in clusters with cauloparacystidia. **Clamp connections** abundant. **Colour in exsiccata** dark brown.

**Habitat and distribution:** Sporulating in small groups in wet, mineral-rich places within subalpine thickets of *Alnus alnobetula* (green alder, *Betulaceae*), with sparsed megaphorb plants such as *Adenostyles alliariae*, *Petasites* spp. and *Prenanthes purpurea*. So far it has only been reported from two localities in France and one in Switzerland; discreet and scarce, but likely widespread throughout the host's range (Alps, Carpathians, etc.); it should be specifically looked for during surveys in its habitat.

**Typus:** **France**, 73, Arêches-Beaufort, Arêches, below Cornet d'Arêches, 45°37'20.15"N, 6°36'37.71"W, 2180 m a.s.l., in subalpine green alder stands (*Alnus alnobetula*) on schists, 24 Aug. 2011, *M. Durand & P.-A. Moreau* (**holotype** LIP 0404660, coll. PAM10082305; ITS and LSU sequences GenBank KP641653 and KP171101).

**Additional materials examined:** **France**, 73, Arêches-Beaufort, Arêches, below Cornet d'Arêches, 45°37'20.15"N, 6°36'37.71"W, 2180 m a.s.l., in subalpine green alder stand, on schists, 28 Aug. 2010, *M. Durand & P.-A. Moreau* (LIP 0404662, coll. PAM11082807; ITS and LSU sequences GenBank KP641651 and KP171099); *ibid.*, (LIP 0404661, coll. PAM11082808; ITS and LSU sequences GenBank KP641652 and KP171100). **Switzerland**, Graubünden, Lower Engadin, Scuol, S-charl, road to Alp Sesvenna, 1800–2000 m a.s.l., in coniferous forest of the subalpine zone, in small stand of *Alnus alnobetula*, in silicate soil (gneiss, granite), 15 Sep 1995, *E. Horak, G. Moreno & F. Esteve-Raventós* (AH 26871; ITS sequence GenBank PQ773489).

**Notes:** Terminology follows Vellinga (1988) and Kuyper (1986). *Inocybe alnobetulae* is a very characteristic species growing under *Alnus alnobetula* in the subalpine areas of central Europe. *Inocybe alnea* (= *I. ochracea*) and *I. undinea* are also species associated with *Alnus* in Europe, but in more continental and warmer areas, and found with *A. glutinosa* or *A. incana* (although one paratype collection of *I. undinea* comes from *Alnus alnobetula* subsp. *suaveolens* in Corsica; Bandini *et al.* 2019a). *Inocybe alnea* and its synonymous *I. ochracea* (Stangl 1979, Vauras & Kokkonen 2009) have a more robust appearance, and are clearly distinguished by the somewhat shorter, ventricose, fusiform cystidia and wider subsodiametric spores with low and obtuse knobs. *Inocybe undinea* (Bandini *et al.* 2019a, Esteve-Raventós *et al.* 2022b) shows characteristic ventricose cystidia with a long, well-defined neck, often rostrate, and asteriform spores with very prominent nodules. Typical of *I. alnobetulae* is not only its habitat, but also its characteristic very elongate subfusiform

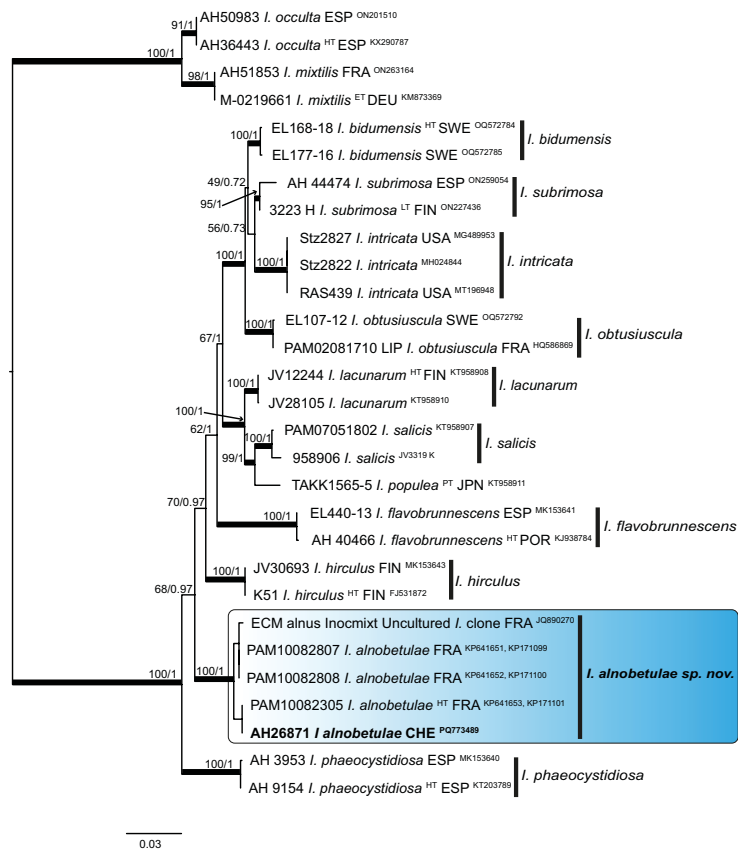
**Colour illustrations.** *Inocybe alnobetulae* habitat in green alder grove at Cornet d'Arêches, the type locality. *In situ* basidiomata of the holotype (PAM10082305); from bottom to top: photos of basidiospores SEM; basidiospores OM; pleurocystidia; cheilocystidia; caulocystidia in the upper part of the stipe. Scale bars: basidiomata = 10 mm; cystidia = 50 μm; spores MO = 10 μm; spores SEM = 2 μm.

cystidia and (sub)heterodiametric spores with lower, obtuse nodules. *Inocybe alnobetulae* is known so far from France and Switzerland.

According to our study, *I. alnobetulae* belongs phylogenetically to the Xanthomelas group (*Inocybe* section *Marginatae*), which species show a marked tendency to darken (dark brownish to blackish) on drying. Although it appears to be in a rather isolated position here, the species (see phylogram) belongs to the group or clade Phaeocystidiosa. *Inocybe phaeocystidiosa* (= *I. salicis-herbaceae*), which is a more robust species that can occur up to the alpine zone, grows under conifers and also *Salix herbacea* in acidic soils, and has remarkable macro- and microscopic differences

(Esteve-Raventós & Moreno 1987, Kühner 1988, Armada *et al.* 2024). Both *I. alnea* and *I. undinea* also belong to this group within the Xanthomelas clade. The sequence GenBank JQ890270 (Roy *et al.* 2013) was generated from a single ectomycorrhizal root samplings of *A. alnobetula*, proving the ectomycorrhizal relationship between both organisms, as well as the rarity of *I. alnobetulae* compared to other *A. alnobetula*-specific ECM species detected in this study. The sampling site is quite distant from the above-mentioned locality (col de la Croix-de-Fer, Saint-Sorlin-d'Arve, 100 km south from Arêches).

*Supplementary material:* doi: 10.6084/m9.figshare.28184501 (alignments).



Most likely tree of the Maximum Likelihood analysis of nodulose-spored species of Xanthomelas group inferred from the ITS and LSU regions generated by IQ-TREE v. 1.6.12 (Trifinopoulos *et al.* 2016) using 1000 bootstrap replicates. Maximum Likelihood bootstrap values (ML-BS)  $\geq 70\%$  and Bayesian posterior probabilities (BPP)  $\geq 0.95$  are shown on the thick branches and ordered as ML-BS/BPP. The BI analysis was performed with MrBayes v. 3.2.7a (Ronquist & Huelsenbeck 2003). Voucher numbers and the nucleotide accession numbers are indicated for all species retrieved from GenBank and generated in this study, as well as country ISO alpha3 code abbreviations. Type collections are indicated in superscript by their initials: HT = holotype, ET = epitype, IT = isotype, LT = lectotype and PT = paratype. The tree was rooted with collections of *Inocybe mixtilis* and *I. occulta*. The new species described here is embedded in the coloured rectangle. The sequences generated in this study are highlighted in **bold**. The scale bar represents the expected number of nucleotide changes per site.

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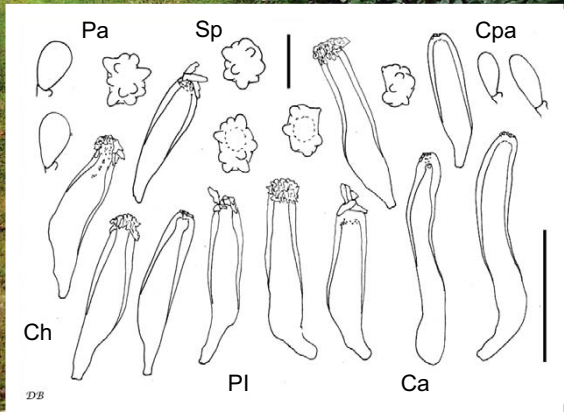
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*Inocybe canicularis*



*Inocybe canicularis* Bandini & U. Eberh., *sp. nov.*

*Etymology*: refers to dogs' days, because all collections were gathered in summer and in honour of Hündchen.

*Classification*: *Inocybaceae*, *Agaricales*, *Agaricomycetes*.

*Pileus* 15–50 mm wide, (sub)conical to (sub)campanulate, later conico-convex to expanded, without or with only low large umbo, margin at first slightly incurved to decurved, later straight; young basidiomata with remnants of a whitish velipellis; colour pale yellowish to yellowish-ochraceous, ochraceous-brownish or light brown (Mu 10YR 7/6, 6/6–6/8, 5/6–5/8) (Munsell 2009), sometimes a little speckled, and some basidiomata much darker brown at the centre with age, and therefore strongly bicoloured; surface smooth and glabrous, towards the margin sometimes minutely rim(ul)ose; no remnants of a cortina observed. *Lamellae* moderately crowded to crowded (ca 50–70), almost free to narrowly adnate, (sub)ventricose, at first whitish, with or without greyish hue, then greyish brownish with or without faint pinkish hue; edge fimbriate, whitish to almost concolourous. *Stipe* 20–80 × 2–6 mm, straight or slightly curved, base thickened to marginate bulbous, glabrous, whitish to faintly brownish; pruinose on the entire length of the stipe. *Context* whitish in the pileus, and faintly pinkish in the stipe. *Smell* (sub)spermatric. *Colour of exsiccata* pileus nut- brown (Mu 7/5YR 5/4–5/6, 4/4–4/6), lamellae and stipe concolourous or a little lighter in colour, no darkening or blackening on drying. *Basidiospores* 8.4–12.9 µm (av. 10.2 µm, SD 0.7 µm) × 6.2–9.8 µm (av. 7.7 µm, SD 0.7 µm); Q = 1.1–1.7 (av. 1.3, SD 0.1) (n = 120 of 3 coll.), nodulose, 8–13 often strongly pronounced nodules with (sub)obtusate apex. *Basidia* 24–31 × 9–13 µm, generally 4-spored, rarely also 2-spored. *Pleurocystidia* 30–81 µm (av. 61 µm, SD 10 µm) × 11–20 µm (av. 15 µm, SD 2 µm); Q = 2.0–6.5 (av. 4.2, SD 0.8) (n = 45 of 3 coll.), mostly (sub)cylindrical to (sub)fusiform, sometimes also (sub)utriform or (sub)clavate, without or with short or longer neck, in each collection often cystidia with a distinct bend near the pedicel, with short or longer pedicel, apex usually crystalliferous, walls up 3.5(–4.5) µm near the apex, often strongly thickening towards the apex, pale yellowish-greenish with 3 % KOH. *Cheilocystidia* similar in size, but somewhat more variable in shape; intermixed with numerous colourless, (sub)clavate, thin-walled cheiloparacystidia. *Caulocystidia* on entire length of the stipe, 30–90 × 10–20 µm, typically long, undate, subcylindrical, intermixed with much shorter (sub)fusiform, (sub)cylindrical, (sub)utriform or even (sub)clavate cystidia, without, with short or longer neck, without or with only short pedicel, apex usually crystalliferous, walls up 3.5(–4.5) µm near the apex, pale yellowish greenish with 3 % KOH; intermixed with some colourless, (sub)clavate to (sub)ovoid, thin-walled cauloparacystidia.

*Habitat and distribution*: *Inocybe canicularis* was found on calcareous to more acidic soil with conifers or both conifers and frondose trees. Europe.

*Typus*: **Germany**, Brandenburg, Uckermark, Milmersdorf, Ahlimbsmühle, TK25 2947/2, 67 m a.s.l., *Quercus robur*, *Pinus sylvestris*, *Fagus sylvatica*, 27 Jul. 2024, D. Bandini, DB27-7-24-2 (**holotype** STU SMNS-STU-F-0901907, **isotype** personal collection D. Bandini; ITS-LSU sequence GenBank PV245925).

*Additional material examined*: **France**, Sarthe, Saint-Calais, Lavaré, on calcareous sandy soil, *Quercus* sp. among other frondose trees and conifers, 20 Jun. 2018, F.-X. Boutard (STU SMNS-STU-F-0901910, double personal collection DB20-6-18-2-Boutard). **Germany**, Bayern, Rottal-Inn, Simbach, TK25 7744/1, alt. 335 m, *Picea abies*, 12 Aug. 2014, D. Bandini, J. Christan & L. Quecke, DB12-8-14-16 (STU SMNS-STU-F-0901909, double personal collection D. Bandini; ITS sequence GenBank PV245927); Brandenburg, Uckermark, Milmersdorf, Ahlimbsmühle, TK25 2947/2, alt. 67 m, at some distance from holotype collection, *Quercus robur*, *Pinus sylvestris*, *Fagus sylvatica*, 27 Jul. 2024, D. Bandini, DB27-7-24-4 (STU SMNS-STU-F-0901908, double personal collection D. Bandini; ITS-LSU sequence GenBank PV245926).

*Notes*: *Inocybe canicularis* differs from *I. margaritispora*: e.g. by more mottled and more distinctly speckled pileus colour, without distinctly darker centre with age, smaller spores, and on av. shorter hymenial cystidia without typical bend near the pedicel; from *I. nobilis*: e.g. by often almost beige pileus colour, often (sub)utriform hymenial cystidia not typically bent towards the pedicel, and shorter, not long undate subcylindrical caulocystidia. *Inocybe phaeosticta* can be distinguished, e.g. by smaller spores, and larger, mostly ventricose (sub)utriform pleurocystidia not typically bent towards the pedicel and *I. pseudohiulca* e.g. by darker, up to chestnut-brown pileus colour, greyish velipellis, larger spores, and usually not (sub)cylindrical hymenial cystidia typically bent near the pedicel.

Based on a megablast search of NCBI's GenBank nucleotide database accessed 4 Mar. 2025, the closest ITS sequence hits and ordered by Max Score were from *I. pseudohiulca* and *I. kohistanensis* and showed similarities from 85.2–83.7 %. For the LSU, the closest hits were 96.2 % and lower for species from the *I. nobilis* clade (see Fig. 1) and from 94.6 % or lower for species from other clades, starting with members of the *I. praetervisa* group. The BLAST results show clearly that *I. canicularis* is different from all sequenced species.

To further explore the position of *I. canicularis* within the genus, for BLAST matches from described taxa, ITS-LSU sequences were selected that were either from types, > 99 % matches to type ITS sequences or stemmed from collections morphologically verified by us. For most species included in the analysis, either type material was available or, judging from GenBank sequence identifications, taxonomists agreed on the interpretation of species names. The concept of *I.*

*Colour illustrations*: Germany, Brandenburg, Uckermark, Milmersdorf, Ahlimbsmühle, mixed forest. Type collection in situ; Drawing: spores (Sp), caulocystidia (Ca), cheilocystidia (Ch), cauloparacystidia (Cpa), cheiloparacystidia (Pa) and pleurocystidia (Pl) (photos and drawing credit: D. Bandini). Scale bars: all others = 50 µm; spores = 10 µm.

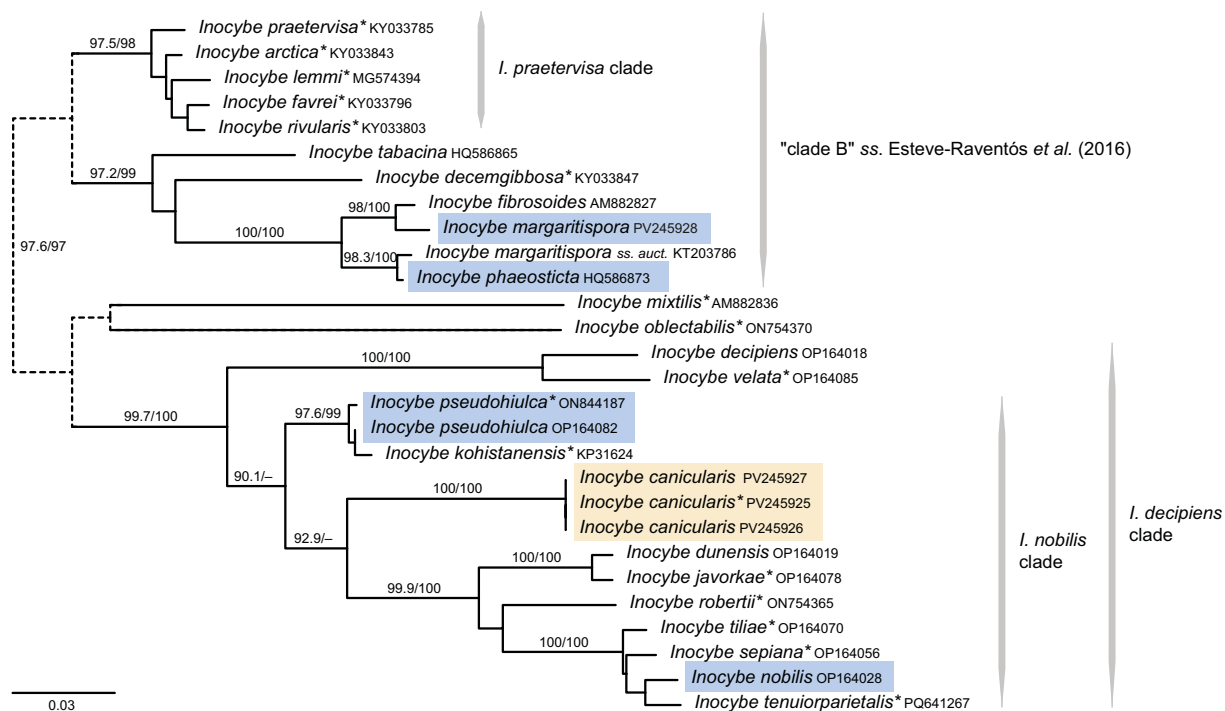


*margaritispora* s. str. GenBank accession number PV245928 adopted here was based on the morphological study of the holotype (K!). We (Bandini *et al.* 2022a, but see Esteve-Raventós *et al.* 2022a) consider *I. piceae* as a synonym of *I. pseudohiulca*.

The selected sequences were analysed together with different combinations of taxa and outgroups. As these analyses did not converge towards a consensus on infrageneric relationships, the phylogenetic tree presented here shows the parts of the tree close to the backbone for which various tree building attempts had contradictory results as dashed lines, irrespective of support values in the analysis selected for this figure. The tree is unrooted, using the longest path between any two tips as backbone. However,

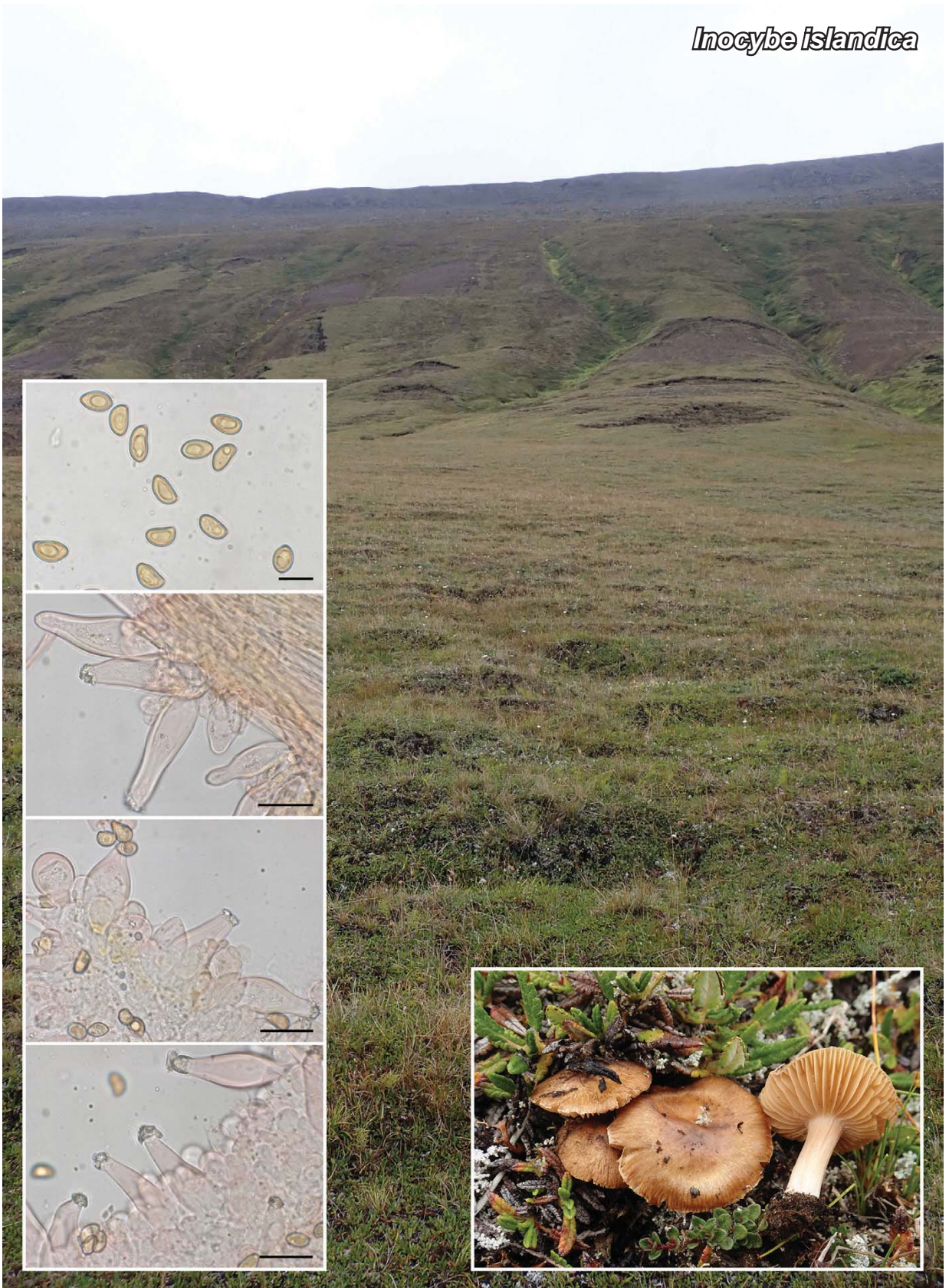
all of the analyses supported a species clade for *I. canicularis* with (close to) 100 % support for both support methods, as part of a "*I. decipiens* clade" (see phylogenetic tree), with support of (close to) 100 %. Likewise, both subclades from what is termed "clade B" in the tree were retrieved with (near) 100 % support in all analyses, but not "clade B" itself. In summary, for *I. nobilis* and *I. pseudohiulca*, the morphological similarities with *I. canicularis* could be explained by common (infrageneric) phylogenetic descent. The overall similarity between *I. canicularis* and *I. margaritispora* and *I. phaeosticta* is not readily explained phylogenetically.

*Supplementary material:* doi: [10.57754/FDAT.dc6m3-yhx67](https://doi.org/10.57754/FDAT.dc6m3-yhx67) (Sequence table, alignments and additional ML tree results).



Maximum Likelihood phylogram obtained from a MAFFT (v. 7.526, Katoh *et al.* 2019) alignment and analysed by IQ-TREE v. 1.6.12 (Trifinopoulos *et al.* 2016, Kalyaanamoorthy *et al.* 2017, Hoang *et al.* 2018) based on ITS and LSU data, showing the position of *Inocybe canicularis* within the *I. decipiens* clade. Sequences are identified by GenBank accession numbers. Support values were obtained from 1000 replicates of SH-like approximate likelihood ratio tests (SH-aLRT) and ultrafast bootstrap (ufb). Support values  $\geq 80$  % were given for SH-aLRT and  $\geq 95$  % for ufb; \* indicate type sequences or sequences that matched the respective type sequence with  $\geq 99$  % similarity BLAST searches. For species names without \* we were not aware of published type sequences. The clade of the new species is indicated in yellow. Names of species discussed as similar are indicated in blue.

*Inocybe islandica*





## *Inocybe islandica* E. Larss., *sp. nov.*

*Etymology:* Refers to Iceland where the type was collected.

*Classification:* *Inocybaceae*, *Agaricales*, *Agaricomycetes*.

*Pileus* 8–28 mm diam, hemispherical to convex, sometimes with an obtuse and broad umbo, later plano-convex to plane with or without a broad umbo, as young with slightly incurved margin, later plane to decurved, sometimes with uplifted and somewhat undulate margin, dry, rather uniformly coloured yellowish ochraceous brown to brown, smooth to finely fibrillose, radially rimulose-subrimose, margin with age rimose and breaking up, velipellis frosty whitish, fugascious. *Lamellae* up to 3.5 mm broad, moderately crowded, interspersed with lamellulae,  $L = 30\text{--}45$ , adnate to adnexed, first buff white with a yellowish tint, later pale ochraceous brown to brown, edge concolourous. *Stipe* 15–30 × 2–4 mm, cylindrical with submarginately to marginately bulbous base, first pale white buff, longitudinally striate, with age yellowish ochraceous brown with white stipe base, pruinose over the entire length, more dens at apex. *Cortina* not observed. *Smell* indistinct to weakly spermatic. *Basidiospores* (8.2–)9.0–9.4–9.6(–11.0) × (4.9–)5.5–5.6–5.7(–6.2) μm,  $n = 58$ ,  $Q = 1.52\text{--}1.78$ ,  $Q\text{ av.} = 1.66$ , smooth, ovoid to subamygdaliform, often with suprahilar depression, some with obtuse apical papilla, small distinct apiculus, pale ochraceous brown. *Basidia* 27–31–34 × 9–10–11 μm,  $n = 25$ , clavate, 4-spored, a few 2-spored, hyaline, sterigmata 4.6–5.8 μm long. *Pleurocystidia* 50–59–70 × 11–14–18 μm,  $Q\text{ mean} = 4.3$ ,  $n = 60$ , lageniform, utriform to fusiform, with truncate base or pedicel, thick-walled, wall up to 3.7 μm thick, hyaline to pale yellowish in KOH solution. *Cheilocystidia* 36–47–62 × 9–14–20 μm,  $n = 47$ , similar to pleurocystidia but more variable and on average shorter, with rounded base truncate-variable to pedicellate, paracystidia rather abundant, pyriform to subglobose 19–25–32 × 10–14–17 μm,  $n = 17$ . *Caulocystidia* over the entire length, similar to pleurocystidia, 31–54–71 × 9–15–18 μm,  $n = 60$ , hyaline to pale yellowish in KOH solution. *Cauloparacystidia* pyriform to subglobose 17–23–34 × 8–11–16 μm,  $n = 44$ . *Stiptipellis* a cutis of parallel interwoven hyphae 3.5–7.4 μm wide. *Pileipellis* a cutis formed of parallel interwoven hyphae 5–17 μm wide, constricted at septa, with yellowish ochraceous brown pigments. *Clamp connections* frequent.

*Ecology and distribution:* The species is found in the arctic-alpine zone growing associated with *Dryas octopetala* in more rich habitats and seems to be favoured by calcareous ground. The two collections were both sporulating in mid-August. Known from Iceland and Sweden. Blast search of NCBI's GenBank and the UNITE database recovered no additional data, suggesting the species to be rare.

*Colour illustrations:* *Inocybe islandica* in subarctic habitat from the type locality in Hrafnkelsdal, Aðalból, Iceland. In situ basidiomata of the holotype (GB-0207713); photos of the hymenium with pleurocystidia, cheilocystidia, caulocystidia and basidiospores. Scale bars: pleuro-, caulo- and cheilocystidia = 20 μm; spores = 10 μm.

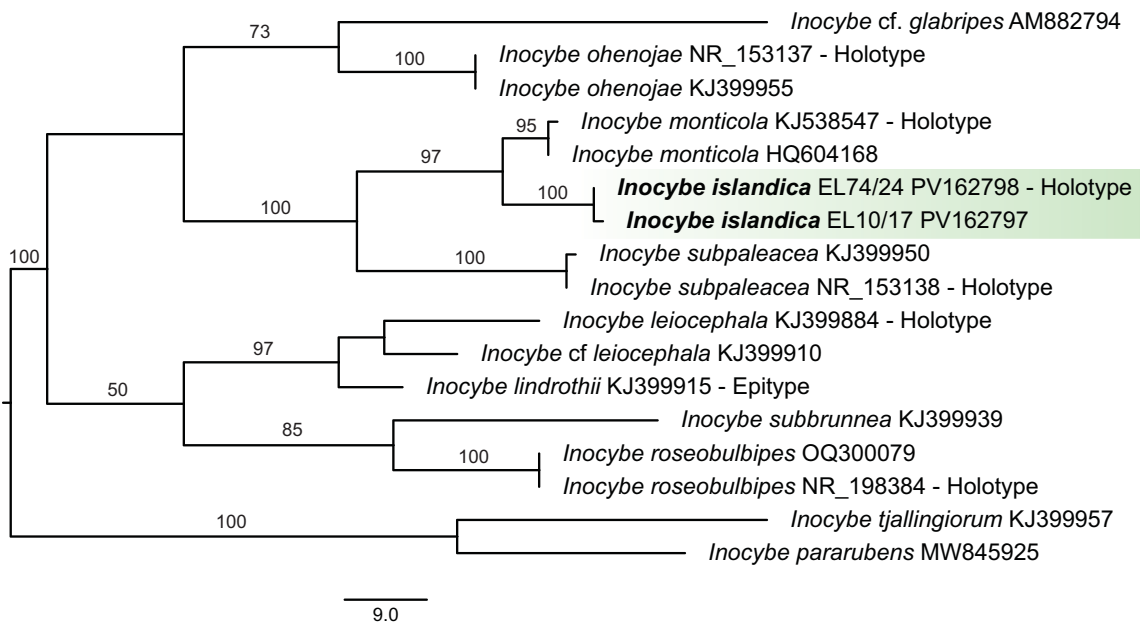
*Typus:* Iceland, Austurland, Jökuldalsvegur, Hrafnkelsdal, Aðalból, 65.01428 N, 15.58148 E, subarctic vegetation grazed by sheep, in matt of *Dryas octopetala*, 21 Aug. 2024, E. Larsson & M. Jeppson, EL74-24 (**holotype** GB-0207713; ITS-LSU sequence GenBank PV162798); *ibid.*, **isotype** AMNH, FA-19820).

*Additional materials examined:* **Sweden**, Torne lappmark, Jukkasjärvi, about 2 km WSW of Jiebrenjokk, alpine area on calcareous ground, associated with *Dryas octopetala* and *Salix reticulata*, 10 Aug. 2017, E. Larsson, EL10-17 (GB-0207714; ITS sequence GenBank PV162797). *Collection studied for comparison:* *Inocybe monticola*. **USA**, Utha, Cache Co., Cache National Forest, Beaver Mountain ski area, on ground in a subalpine fir, lodgepole pine and aspen community, 28 Jun. 1998, B.R. Kropp (UTC-00248120 **holotype**; ITS-LSU sequence GenBank KJ538547). *Inocybe ohenojae*. **Canada**, Northwest Territories, District of Franklin, Melville Peninsula, Repulse Bay, on hummock in *Dryas integrifolia* and *Salix* sp. Vegetation, 2 Aug. 1974, E. & M. Ohenoja (OULU **holotype**; ITS-LSU sequence GenBank NR\_153137). **Svalbard and Jan Mayen**, Svalbard, Nordenskiöld Land, Revneset, arctic tundra with *Salix polaris*, 12 Aug. 2015, E. Larsson, EL72-15 (ITS-LSU sequence GenBank PV167069). *Inocybe subpaleacea*. **France**, Savoie, Parc National de la Vanoise, plan de Bellecombe, with *Helianthemum*, *Dryas* and *Salix serpyllifolia*, 30 Aug. 1973, Kühner, 73-346 (G-0052223 **type**; ITS sequence GenBank NR\_153138). **Sweden**, Lule lappmark, Jokkmokk, Padjelanta National Park, Svátinjunjes, alpine area on calcareous ground with *Dryas octopetala*, 19 Aug. 2016, E. Larsson, EL266-16 (ITS-LSU sequence GenBank PV167070).

*Notes:* *Inocybe islandica* is a small yellowish to ochraceous brown species with smooth to finely rimulose pileus, complete pruinose stipe and submarginately bulbous base. It has smooth spores, metuloids and lacks a cortina which places it in the supersection *Marginatae* and with the group that has smooth spores, section *Splendentes* (Stangl 1989). The closest match when blasting the ITS sequence in GenBank is with *I. monticola* (97.3 % similarity; GenBank KJ538547), and it also comes out as the sister species in the phylogeny. *Inocybe monticola* was described by Kropp *et al.* (2010) from a subalpine fir, lodgepole pine and aspen community in Utha. It is similar in habitus and morphological characters but has a more reddish-brown pileus and based on available data it seems to be restricted to North America. Another closely related species is *I. ohenojae* described by Larsson *et al.* (2014) based on a specimen from the arctic tundra in Canada, Northwest Territories, associated with *Dryas*. Later it has also been found on Svalbard associated with *Salix polaris* (GenBank PV162797) but is so far not found on Iceland or in Fennoscandia. It differs from *I. islandica* by having dirty grey brown pileus and significantly thick-walled and larger spores. *Inocybe subpaleacea* is a species that is found in the alpine zone in Europe and often growing associated with *Dryas* on calcareous ground (Kühner 1988, Larsson *et al.* 2014). It can cooccur with *I. islandica* and is similar in morphological characters, but the pileus is usually more umbonate and

has a darker ochraceous brown colour, and the spores are somewhat larger. All the discussed species must be regarded as rare or may be overlooked as they are living in arctic alpine environments.

*Supplementary material:* doi: 10.6084/m9.figshare.28519847.v1 (alignment and tree).



Phylogram obtained using PAUP v. 4.0a (Swofford 2003) based on ITS and LSU data showing the position of *I. islandica* among its closest relatives. Heuristic searches with 1000 random-addition sequence replicates and tree bisection-reconnection (TBR) branch swapping were performed. Relative robustness of clades was assessed by the bootstrap method using 1000 heuristic search replicates with 100 random taxon addition sequence replicates and TBR branch swapping. Bootstrap support values are indicated on branches. *Inocybe islandica* is marked in **bold** and a coloured block, the holotype is indicated.



*Inocybe minata*



# *Inocybe minata* Bandini, Ayer, I. Saar, Vauras & E. Larss., *sp. nov.*

*Etymology:* From Latin *minata* = threatened, endangered, because the species is rare, and its habitat is endangered.

*Classification:* *Inocybaceae*, *Agaricales*, *Agaricomycetes*.

*Pileus* 8–17 mm diam., first conical to convex, later plano-convex to applanate, without or with an obtuse and low umbo, margin deflexed, straight to uplifted, later often slightly depressed around the umbo, as young rather uniformly brown to dark brown, with age often blackish brown at centre and paler brown at margin, first smooth to finely fibrillose with age subquarrose to depressed scaly, outwards radially fibrillose to rimose, when young with whitish velipellis at margin, cortina not observed. *Lamellae* up to 3 mm broad, distant to moderately crowded, interspersed with lamellulae, adnexed, some with decurrent tooth, ventricose, first pale beige, later pale brown to brown, edge uneven, concolourous or somewhat paler. *Stipe* 24–45 × 1.5–2.5 mm, equal cylindrical, often bending, slightly boubous base, pale reddish-brown to ochraceous-brown, with age even blackish brown, stipe base pale whitish, pruinose over the entire length, longitudinally white-fibrillose, glabrous. Context whitish in pileus and stipe. *Smell* acidulous. *Basidiospores* (8.0–)8.6–9.2–10.0(–10.6) × (5.2–)5.5–5.8–6.3(–6.4) µm, on average 9.0–9.7 × 5.7–6.0 µm, Q = 1.4–1.75, Q av. = 1.59, smooth (n = 80 / N = 4), subamygdaliform, apex subobtuse, pale ochraceous brown. *Basidia* 20–24–30 × 8–9–11 µm (n = 47 / N = 3), clavate, mainly 4-spored, hyaline. *Pleurocystidia* (46–)50–58–67(–81) × (12–)13–17–21(–24) µm, on average 52–61 × 14–19 µm, Q mean = 3.5 (n = 100 / N = 4), fusiform to subutriform, without or with only short pedicel, with crystals and microcrystals under the crown of crystals, thick-walled, up to 5 µm, pale yellow to yellow in NH<sub>4</sub>OH. *Cheilocystidia* (34–)39–45–51(–57) × (10–)12–15–18(–21) µm (n = 60 / N = 3), similar to pleurocystidia but more variable and on average shorter, mixed with hyaline, pyriform to clavate paracystidia 13–19–25 × 9–11–15 µm (n = 20 / N = 2). *Caulocystidia* over the entire length, similar to pleurocystidia but more variable, 40–53–66 × 13–15–21(–22) µm (n = 51 / N = 2), hyaline. *Cauloparacystidia* 14–19–24 × 10–12–14 µm (n = 26 / N = 2), subsphaerical to pyriform. *Clamp connections* frequent.

*Ecology and distribution:* *Inocybe minata* occurs in mixed moist forests, growing solitary or gregarious, on both acid and more rich soils associated with *Alnus incana*, *Betula*, *Salix* and *Picea abies*, sporulating from late August to September. So far specimens only known from Finland and Switzerland. Blast search of NCBI's GenBank and the UNITE database recovered only one ITS from Estonia based on soil DNA (UDB0321575), suggesting the species to be rare or overlooked.

*Colour illustrations:* Collection site of the holotype of *Inocybe minata*, Switzerland. Holotype in situ; basidiospores (Sp), caulopara- (Cpa), cheilo- (Ch), para- (Pa) and pleurocystidia (Pl) in KOH. Scale bars: basidiomata = 10 mm; cystidia = 50 µm; basidiospores = 10 µm.

*Typus:* **Switzerland**, Fribourg/Freiburg, La Verrerie, Le Crêt, Tourbière du Crêt, 46.60882781°N, 6.92805722°E, *Salix* sp. and *Betula* sp., bog, peat soil, very wet, 16 Sep. 2019, *F. Ayer* (**holotype** TUF140825, ITS sequence GenBank PV562313, UNITE UDB07676405; **isotype** DB16-9-19-Ayer).

*Additional material examined:* **Finland**, Kainuu, Paltamo, Melalahti, Nature Reserve Ellukanlahden lehto, near the end of Ellukka bay, 64.39406N, 27.67443E, 123 m a.s.l., middle boreal zone in forest close to lake shore, on moist somewhat calcareous soil, near *Salix* bushes, *Salix caprea*, *Alnus incana*, *Picea abies*, *Pinus sylvestris* and *Betula*, 1 Sep. 2018, *J. Vauras*, JV32664 (TUR-A 208003; ITS-LSU sequence GenBank PV147300); Etelä-Häme, Orivesi, Yröskulma, S side of the river Yrösjoki, 61.7563N, 24.3046E, 120 m a.s.l., N slope in moist, fairly rich spring-fed forest with *Betula*, *Alnus incana*, *Picea abies*, *Salix* spp. and *Populus tremula*, 15 Sep. 1999, *J. Vauras*, JV15556 (TUR 178213; ITS sequence GenBank PV147301); Etelä-Häme, Ruovesi, Nature Reserve Runeberginlähde, 61.9904N, 24.0663E, 99 m a.s.l., 8 Sep. 2005, *E. Larsson*, EL108-05 (GB-0248104; ITS-LSU sequence GenBank AM882794; TUR-A 208299); Kainuu, Paltamo, Melalahti, Nature Reserve Ellukanlahden lehto, near the end of Ellukka bay, 64.39406N, 27.67443E, 123 m a.s.l., 26 Aug. 2011, *J. Vauras*, JV28393 (TUR-A195577; ITS sequence GenBank PV147302). **Switzerland**, Fribourg/Freiburg, La Verrerie, Le Crêt, Tourbière du Crêt, 46.60913754°N, 6.92691865°E, *Salix* sp. and *Betula* sp., bog, peat soil, very wet, 26 Sep. 2019, *F. Ayer* (TUF140826, ITS sequence UNITE UDB07676406; DB26-9-19-Ayer).

*Collections studied for comparison:* *Inocybe ohenojae*. **Canada**, Northwest Territories, District of Franklin, Melville Peninsula, Repulse Bay, on hummock in *Dryas integrifolia* and *Salix* sp. vegetation, 2 Aug. 1974, *E. & M. Ohenoja* (OULU **holotype**; ITS-LSU sequence GenBank NR\_153137). **Svalbard and Jan Mayen**, Svalbard, Nordenskiöld Land, Revneset, arctic tundra with *Salix polaris*, 12 Aug. 2015, *E. Larsson*, EL72-15 (ITS-LSU sequence GenBank PV167069).

*Notes:* *Inocybe minata* is a small brown species with a complete pruinose stipe, smooth spores, thick-walled pleurocystidia with microcrystals under the crown of crystals, suggesting it belongs in Sect. *Splendentes*. Having microcrystals is a common feature within the *I. leioccephala* group with which *I. minata* is related (Larsson *et al.* 2014). Most species of this group are found and seem to be favoured by more calcareous soils. However, the most common species in the group, *I. lindrothii* is not strongly calciphilous. It is a larger species than *I. minata* but also found in similar moist to wet habitats associated with *Salix* and *Betula*. The closest match with a described species, when blasting the ITS sequence in GenBank is with *I. ohenojae* (88.3 % similarity; GenBank NR\_153137). *Inocybe ohenojae* was described by Larsson *et al.* (2014) based on a specimen from the arctic tundra in

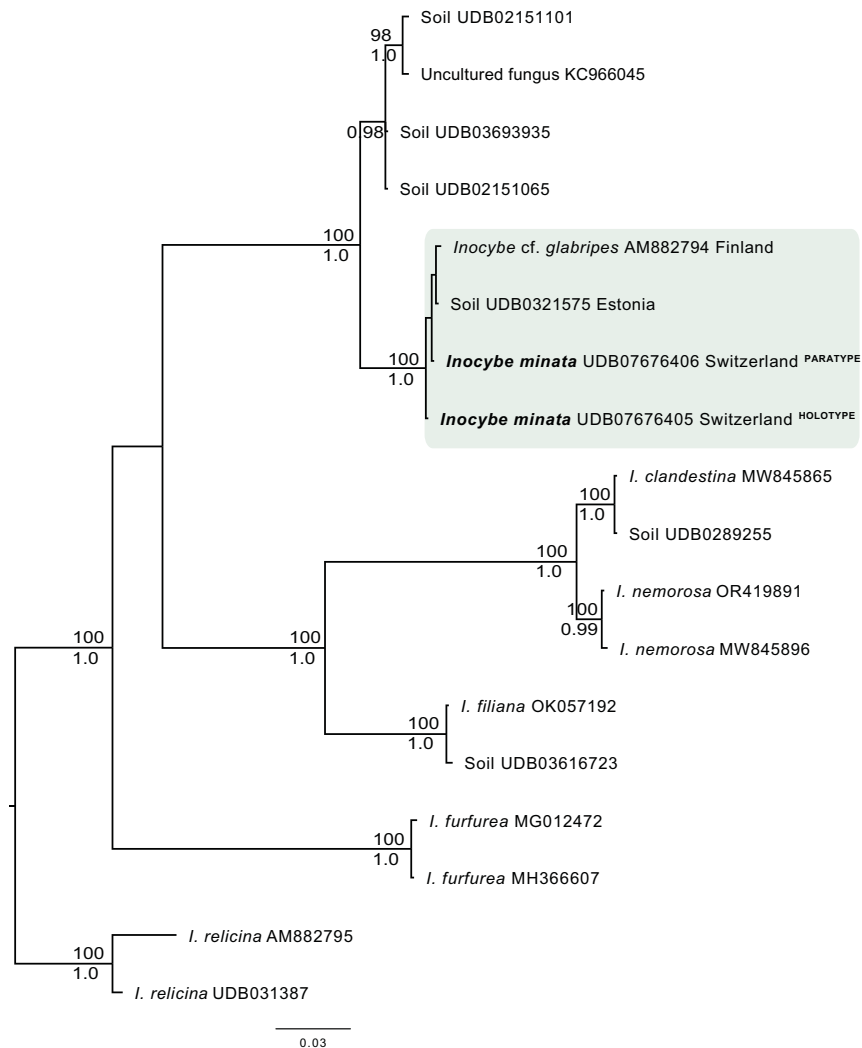


Canada, Northwest Territories. It differs from *I. minata* by having dirty grey brown pileus and significantly thick-walled spores.

*Inocybe clandestina* differs by not having a hygrophanous pileus surface, larger spores, on av. shorter hymenial cystidia with thinner walls and weaker reaction to KOH, and growth with conifers in dryer locations (Bandini *et al.* 2021). *Inocybe filiana* has a whitish velipellis, with age up to (sub) squamulose-sublanose pileus surface, larger spores, on av. shorter hymenial cystidia with thinner walls, and it grows on dryer ground with conifers (Bandini *et al.* 2022b). *Inocybe*

*furfurea* has a paler, often more or less ochraceous pileus colour, less smooth pileus surface with age, on av. shorter but wider spores, shorter hymenial cystidia, and growth on dryer calcareous soil (Kühner 1955, Bandini *et al.* 2019b), and *I. nemorosa* differs by usually paler pileus colour, whitish velipellis, not hygrophanous pileus surface, larger spores, and on av. shorter hymenial cystidia (Grund & Stuntz 1968).

*Supplementary material:* doi: 10.6084/m9.figshare.28218044.v1 (alignment and phylogenetic tree).



Bayesian inference (BI) analysis of the ITS alignment was performed with MrBayes v. 3.2.6 (Ronquist *et al.* 2012), applying default values of prior settings, the first 100 K generations without a stable likelihood score were discarded. Maximum Likelihood (ML) analysis was performed with RAxML (Stamatakis 2014) using raxmlGUI v. 2.0 (Edler *et al.* 2020). The best-fit model estimated in raxmlGUI v. 2.0 using ModelTest-NG (Darriba *et al.* 2019) was TPM2uf. The best tree of the BI analysis is presented. The novel species is highlighted in a light green box, types are in **bold**. Bootstrap support values from 1000 bootstrap replicates are shown above (≥ 70 %) and Bayesian posterior probabilities (≥ 0.95) below nodes. The tree was rooted to the sequences of *Inocybe relicina*, the type of the genus.

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*Inocybe pini-halepensis*





# *Inocybe pini-halepensis* Esteve-Rav. & Pancorbo, *sp. nov.*

**Etymology:** The name is derived from the species *Pinus halepensis*, due to its ectomycorrhizal relationship with this host.

**Classification:** *Inocybaceae*, *Agaricales*, *Agaricomycetes*.

*Basidiomata* agaricoid and stipitate. *Pileus* 25–35(–40) mm, initially hemispherical to paraboloid, then convex to plano-convex, finally applanate or shallowly and broadly umbonate; margin straight to hardly inflexed, often wavy, not or exceptionally reflexed with age; colour darker in young or wet specimens such as umber brown or chestnut brown, but often becoming bay, fulvous to snuff or greyish brown in old or dehydrated specimens, range (Mu 7.5YR 4/3–6, 5/4–8; Munsell 1994); surface dry, finely smooth fibrillose to subtomtose, occasionally broken or lacerated in old or sunlight exposed specimens, slightly but clearly hygrophane. *Velipellis* very distinct in young specimens, especially in the centre, often rather persistent as an arachnoid appressed, silky dirty white to greyish patch, more rarely broken into small patches, in some cases agglutinating soil debris or sand grains. *Lamellae* moderately crowded to crowded (L = 44–50); l = 1–2(–3), 4–6 mm wide, adnexed to narrowly adnate, ventricose, long-time pale, initially whitish, becoming pale grey, then pale brown ochraceous, finally pale brown; edge white or paler, fimbriate to finely crenulate. *Stipe* 25–40(–50) × 4–7(–8) mm, firm, straight or sometimes curved towards the base, cylindrical to hardly enlarged towards the base, but also elongated and rooting when growing in pure sand or in dunes; colour initially white to dirty white, often in some specimens or collections with pale pink ochraceous tones or reflections, especially towards the apex; surface uniform, finely white fibrillose longitudinally, subfloccose-fibrillose at the extreme apex. *Cortina* present in very young specimens only, very ephemeral. *Context* firm, fibrous, whitish to pale ochraceous at pileus and stipe base, sometimes pale pinkish ochraceous to orange pink at the upper stipe cortex. *Smell* spermatric when cut. *Spores* (7.6–)8.5–9.7–11.1(–11.8) × (4.8–)5.1–5.9–6.6(–7.0) μm, Q = (1.31–)1.43–1.60–1.82(–1.96) (n = 288 / N = 4), smooth, ovoid to amygdaliform; apex with acute to papillate tendency, sometimes showing a pseudopore or callus and then slightly thick walled (~ 0.5 μm). *Basidia* (23.5–)25.9–29.7–35.0(–38.9) × (7.2–)7.9–9.4–11.2(–12.6) μm; Q = (2.40–)2.62–3.10–3.78(–4.57) (n = 76 / N = 3), 4-spored (sterigmata 4–6 μm long), clavate. *Lamellar edge* whitish, crenulate, with numerous transitions between cheilocystidia and thin-walled clavate paracystidia. *Pleurocystidia* (30.6–)37.6–46.8–55.6(–73.2) × (9.5–)11.5–15.1–19.4(–24.2) μm, Q = (1.60–)2.33–3.10–4.07(–4.91), (n = 155 / N = 4), narrowly utriform to subclavate, sometimes subcapitate, crystalliferous at apex, hyaline or with a pale brownish content; walls even 0.91–1.00–1.25(–1.38) μm

thick, yellowish in aqueous ammonia solutions. *Cheilocystidia* (32.5–)37.2–46.4–54.9(–61.8) × (11.0–)12.9–16.4–22.0(–24.3) μm, Q = (2.20–)2.33–3.00–3.72(–4.45) (n = 128 / N = 3), similar to pleurocystidia. *Lamellar trama* pale yellowish, reddish brown when old, composed of septate parallel hyphae, 3.6–7.1 μm wide. *Stipitipellis* a cutis of parallel hyphae, 3.8–6.9 μm wide, with intracellular yellowish ochre pigment. *Caulocystidia* only present at the extreme apex of the stipe, cylindrical top sublageniform, with rounded apex and sometimes septate, (30.8–)35.5–51.6–69.0(–83.0) × (6.7–)8.3–11.5–15.1(–18.7) μm, Q: (2.53–)2.97–4.60–7.3(–7.84) (n = 34 / N = 4) becoming caulocystidioid thin-walled hairs downwards. *Clamp connections* abundant.

**Habitat and distribution:** Both *Inocybe pini-halepensis* and *I. complutensis* are sometimes found in the same places and habitats. They establish mycorrhizae with the Aleppo pine, commonly in ruralised and eutrophicated areas such as parks, roadsides and gardens, and very often also in coastal areas near the sea; it has been found so far in limestone sandy soils, and it seems very common in the Balearic Islands.

**Typus:** **Spain**, Community of Madrid, Alcalá de Henares, Campus Universitario externo, Faculty of Science Building, 40°30'17.53"N, 3°20'14.95"W, 597 m a.s.l., among grass and fallen leaves of *Pinus halepensis* (*Pinaceae*) in garden, in calcareous loamy soil, 7 Nov. 2023, *F. Esteve-Raventós* & *A. Altés* (**holotype** AH 56245; ITS-LSU sequence GenBank PQ773494).

**Additional materials examined:** **Spain**, Balearic Islands, Cabrera, Comellar des Caló des Macs, 39°8'59.60"N, 2°57'45.44"E, 20 m a.s.l., under *P. halepensis*, 23 Nov. 1994, *J.L. Siquier* & *X. Lillo* (AH 26899, duplo in JLS C-98B); Eivissa, Sant Josep de sa Talaia, platja de Ses Salines, 38°50'29.58"N, 1°23'36.85"E, 5 m a.s.l., in coastal dunes under *P. halepensis*, 14 Nov. 1994, *J.L. Siquier* & *C. Lado* (AH 25428, duplo JLS I-123B; ITS sequence GenBank PQ773493); Eivissa, Sant Josep de sa Talaia, platja des Cavallet, 38°50'49.80"N, 1°24'4.09"E, 5 m a.s.l., in coastal dunes with *P. halepensis* and *Juniperus phoenicea* (*Cupressaceae*), 4 Dec. 2009, *F. Esteve-Raventós* & *J. Llistosella* (AH40225; ITS sequence GenBank PQ773886); idem., (AH 40232; ITS sequence GenBank PQ773887); Mallorca, Muro, Parc Natural de s'Albufera, Es Comú, 39°46'43.52"N, 3°8'9.66"E, 3 m a.s.l., in coastal dunes under *P. halepensis*, 2 Nov. 1994, *J.L. Siquier* (AH 25298, duplo JLS 732B); Menorca, Maó, Parc Natural de Es Grau, Cala Sa Torreta, 39°57'48"N, 4°15'17"E, 13 m a.s.l., in coastal dunes under *P. halepensis* and *Pistacia lentiscus* (*Anacardiaceae*), 25 Nov. 2023, *J.C. Salom*, *M.A. Ribes* & *F. Pancorbo* (AH 58638, FP23112504; ITS sequence GenBank PQ773888).

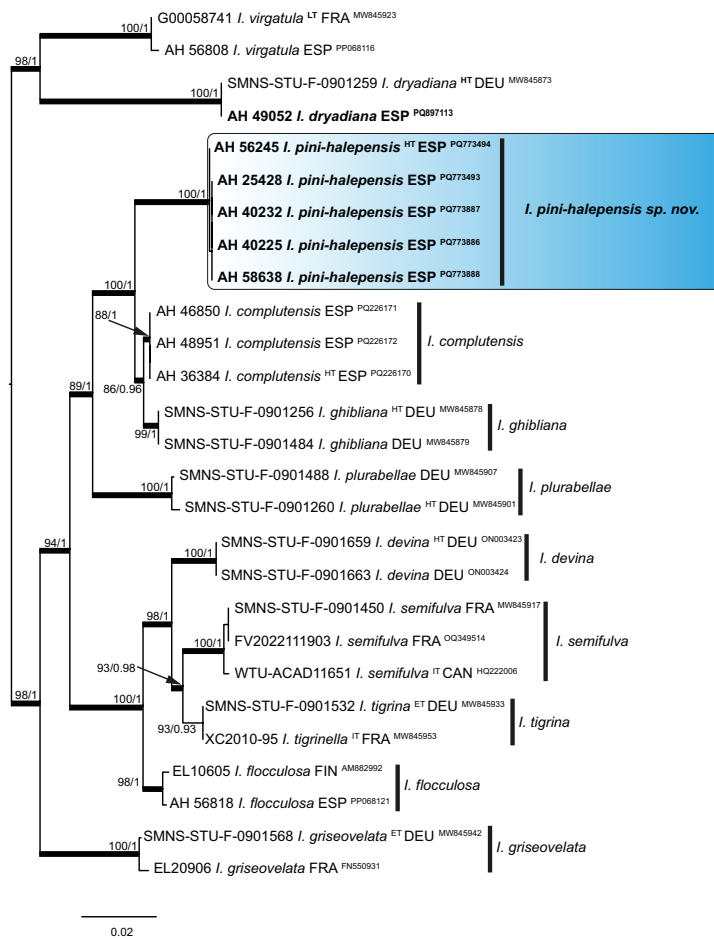
**Colour illustrations.** *Inocybe pini-halepensis* habitat in *Pinus halepensis* gardens surrounding the Faculty of Sciences Building, Alcalá de Henares University, the type locality. *In situ* basidiomata of the holotype (AH 56245); from bottom to top: photos of spores SEM, spores OM, pleurocystidia, cheilocystidia, caulocystidia at the extreme apex of stipe. Scale bars: basidiomata = 10 mm; cystidia = 50 μm; spores MO = 10 μm; spores SEM = 5 μm.

**Notes:** Terminology follows Vellinga (1988) and Kuyper (1986). *Inocybe pini-halepensis*, *I. complutensis* and *I. ghibliana* are all part of a phylogenetically well-supported clade, but with some genetic, morphological and ecological differences. The first two are species with a marked sabulicolous character and strictly linked to Aleppo pine and, presumably, with

a distribution linked to that of their host. *Inocybe ghibliana* shows in general a more continental distribution, although it is a thermotolerant species that can also occur in areas with a Mediterranean climate, linked to plants such as the *Cistaceae*. *Inocybe pini-halepensis* shows a marked hygrophaneity in the pileus colour, and its cystidia are rather short (< 50 µm on average) and mostly claviform or sub-utriform, with an obtuse apex devoid of a neck. The spores have a marked tendency to show a conical and often papillate apex, with the presence of a pseudo-pore. *Inocybe complutensis* is a phylogenetically close species (Crous *et al.* 2024b), occurring in the same environments due to its characteristic relationship with Aleppo pine, although the latter shows slightly longer cystidia with a

sublageniform to subfusiform tendency, with a more delimited but not very prominent neck. Both species show molecular differences (see phylogram) and seem to be well separated from *I. ghibliana* (Bandini *et al.* 2021, 2023). In terms of macromorphology, *I. pini-halepensis* is characterised by the presence of a rather persistent veil on the pileus and the soft orange-pinkish tones of the stipe with development and age; these characters could lead to confusion with *Inocybe griseovelata* (Kühner 1955, Bandini *et al.* 2023), which is phylogenetically very distant, and inhabits deciduous forests in preferentially ruderalised areas and parks.

*Supplementary material:* doi: 10.6084/m9.figshare.28189016 (alignments).



Most likely tree of the Maximum Likelihood analysis of smooth-spored species of *Inocybe* inferred from the ITS and LSU regions generated by IQ-TREE v. 1.6.12 (Trifinopoulos *et al.* 2016) using 1000 bootstrap replicates. Maximum Likelihood bootstrap values (ML-BS)  $\geq 70$  % and Bayesian posterior probabilities (BPP)  $\geq 0.95$  are shown on the thick branches and ordered as ML-BS/BPP. The BI analysis was performed with MrBayes v. 3.2.7a (Ronquist & Huelsenbeck 2003). Voucher numbers and the nucleotide accession numbers are indicated for all species retrieved from GenBank and generated in this study, as well as country ISO alpha3 code abbreviations. Type collections are indicated in superscript by their initials: HT = holotype, ET = epitype, IT = isotype and LT = lectotype. The tree was rooted with sequences of *Inocybe virgatula* and *I. dryadiana*. The new species described here is embedded in the coloured rectangle. The sequences generated in this study are highlighted in **bold**. The scale bar represents the expected number of nucleotide changes per site.

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# *Inocybe subentolomospora*



# *Inocybe subentolomospora* Poli, Maraia, Bandini, Tacconi, Dovana F. & Vizzini, *sp. nov.*

**Etymology:** The species epithet “subentolomospora” refers to the often entoloma-like spores of the species.

**Classification:** *Inocybaceae*, *Agaricales*, *Agaricomycetes*.

**Pileus** 8–20(–25) mm diam., at first almost subglobose to campanulate or (sub)conical, later conical-convex to hemispherical, with rounded umbonate apex when young, later almost flat with low large umbo. Margin at first incurved, later decurved; young basidiomata covered with abundant radially scattered whitish remnants of a velipellis, cracked at the centre and radially scattered, and often pending from or rimming the margin; surface uniformly dark brown, somewhat paler in young basidiomata; when young finely to thickly tomentose, later sometimes finely lanose or due to the velipellis almost scaly without diverging fibres even at the margin or innately fibrillose with slightly diverging fibres, sometimes areolate-diffracted at the centre. No remnants of a cortina observed. **Lamellae** subdistant (24–30,  $l = 1–3$ ), almost free to narrowly adnate, broad, ventricose, at first dingy beige, with age dark brown with faint reddish hues or concolourous to the pileus, edge whitish, eroded due to cheilocystidia presence. **Stipe** 30–45 × 3–5 mm, cylindrical or somewhat curved, solid, base even to subbulbous, but without a marginate bulb, at first covered with rough whitish tomentum, later longitudinally striate to subflocculose, sometimes glabrous with age, brownish to concolourous to the pileus; mostly stuck almost completely in the moss. **Context** thin, hygrophanous, fibrous in the stipe, dark brown in the pileus, dark reddish brown in the stipe. **Smell** indistinct. **Basidiospores** 8.8–11.8–15.0 (SD 0.2  $\mu\text{m}$ ) × 6.2–7.8–9.4  $\mu\text{m}$  (SD 0.8  $\mu\text{m}$ );  $Q = 1.0–1.5–2.0$  (SD 0.2) (160 spores from 4 basidiomata of two collections), almost entolomoid to nodulose with 6–10 obtuse nodules, one of them often strongly protruding. **Basidia** 23–35 × 10–14  $\mu\text{m}$ , clavate, apices rounded or obtuse, four-spored, rarely two-spored, sterigmata up to 6  $\mu\text{m}$  long. **Pleurocystidia** 55–70–84 (SD 7  $\mu\text{m}$ ) × 10–14–21  $\mu\text{m}$  (SD 3  $\mu\text{m}$ );  $Q = 2.9–5.2–6.9$  (SD 1.0), (sub)cylindrical, subfusiform, seldom subutriform, without or with only a short neck, often subcapitate, with short pedicel, apex crystalliferous, walls up to 2.0(–3.0)  $\mu\text{m}$  thick at the apex, pale yellowish greenish with 3 % KOH. **Cheilocystidia** similar to pleurocystidia in shape and size, intermixed with (sub)clavate thin-walled paracystidia. **Caulocystidia** present only near the extreme apex of the stipe, in size and shape

similar to the hymenial cystidia, but usually somewhat narrower and with slightly undulate walls, with only few small apical crystals, walls up to 0.5 (only rarely up to 1.0)  $\mu\text{m}$  thick at the apex, pale yellowish greenish with 3 % KOH. **Pileipellis** a cutis, composed of regular to sub-regular, 4–8  $\mu\text{m}$  wide subcylindrical hyphae, slightly gelatinized, featuring brownish intracellular and extracellular encrusting pigment, hyphae of the subpellis subcylindrical to irregular, up to 34  $\mu\text{m}$  wide. **Clamp connections** present in all tissues.

**Habit, habitat and distribution:** Gregarious, sometimes loosely cespitose, at the edge of a stream bed, on moss with the presence of *Alnus incana*, *Populus nigra* and *Salix* spp. So far known only from the type locality, Lombardia (Italy) and probably also present in China based on an ITS sequence present in GenBank.

**Typus:** **Italy**, Lombardia, Novate Mezzola (SO), in the proximity of the Codera River, on moss with the presence of *Alnus incana*, *Populus nigra* and *Salix* spp., 12 May 2019, *L. Poli* (**holotype** GDOR 5779, ITS and *RPB2* sequences GenBank PV253001 and PV261927).

**Additional material examined:** **Italy**, Lombardia, Novate Mezzola (SO), in the proximity of the Codera River, on moss with the presence of *Alnus incana*, *Populus nigra* and *Salix* spp., 1 May 2010, *L. Poli*, (GDOR 5780, ITS and *RPB2* sequences GenBank PV253000 and PV261928).

**Notes:** *Inocybe subentolomospora* is characterized by rather small-sized basidiomata, copious whitish velipellis, dark brown, thickly tomentose to appressed scaly pileus, only near the apex pruinose stipe, rather long mostly (sub) cylindrical to subfusiform usually rather slender hymenial cystidia and large almost entolomoid to nodulose spores. In our phylogenetic analysis, the two sequences of *I. subentolomospora* grouped with *Inocybe* sp. (voucher: FYG1146b) in a well-supported clade (SH-aLRT test = 97, ML-UBS = 97). The voucher FYG1146b corresponds to an *Inocybe* sp. collected in China and described by Gao *et al.* (2024); however, the authors did not propose a valid name for this species due to the existence of only a single collection. The morphological description of the collection FYG1146b is quite comparable to that of *I. subentolomospora*, as is the habitat associated with *Salicaceae*. The nrITS sequence differs by eight nucleotides from the ITS sequence of the holotype of *I. subentolomospora*, and the *RPB2* sequence exhibits differences at three positions. Although it is likely that the collection FYG1146b belongs to the same species, the description of *I. subentolomospora* is based solely on the Italian collections that we have analysed. Further studies will be necessary to clarify the actual status of the Chinese collection. *Inocybe subentolomospora* belongs to *I. pseudoasterospora* subclade that includes *Inocybe peppa*, *Inocybe perlucida* and *Inocybe pseudoasterospora*. *Inocybe peppa* is sister of *I. subentolomospora* (SH-aLRT test=100, ML-UBS = 98) and differs mainly by wider pleurocystidia

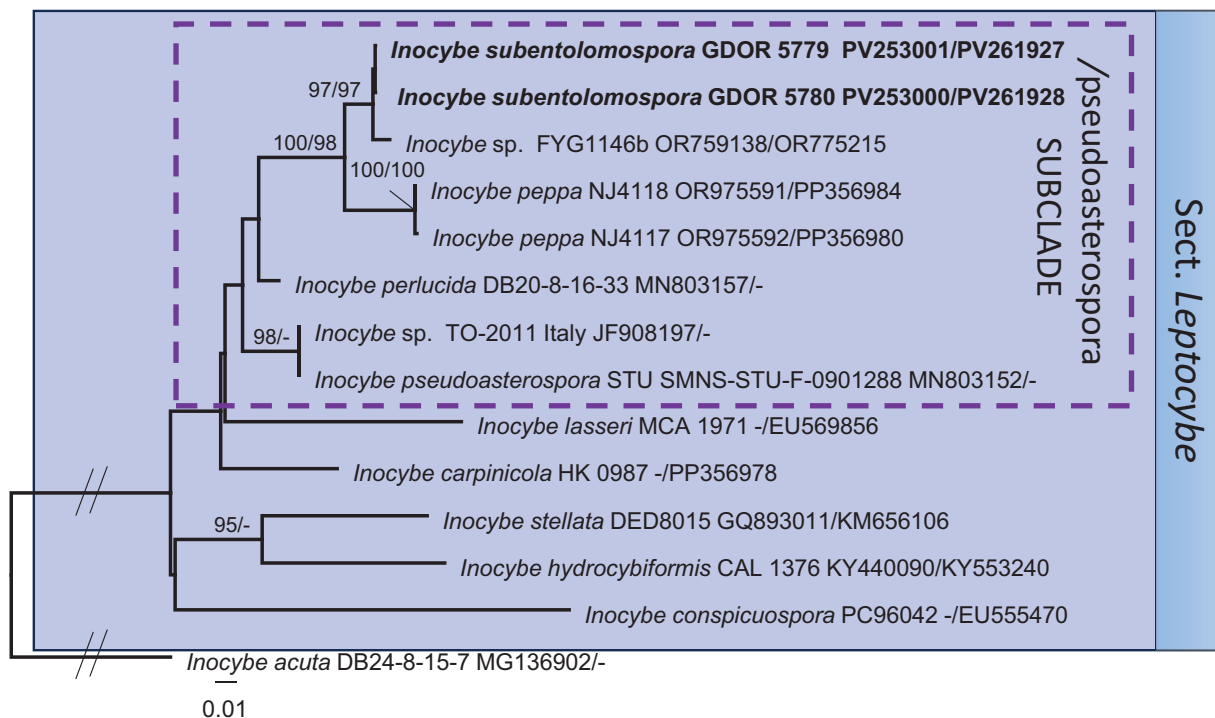
**Colour illustrations:** Novate Mezzola, Italy, The Codera Valley. *Inocybe subentolomospora* basidiomata in habitat. Microscopy drawing: basidiospores (Sp), caulocystidia (Ca), cheilocystidia (Ch), pleurocystidia (Pl), paracystidia (Pa), cauloparacystidia (Cpa) in KOH. Microscopy pictures from top to bottom: cheilocystidia and basidiospores (holotype GDOR 5779). Scale bars: bar positioned at the bottom of the drawing = 50  $\mu\text{m}$ ; all others = 10  $\mu\text{m}$ .



(42–70 × 20–32 μm) of different shape and nodulose, angular-stellate with 7–9 prominent conical projections basidiospores (Gao *et al.* 2024). On first few the species might be mistaken for *I. pseudoasterospora*. However, the spores of this species are always clearly nodulose, and they are wider on average, thus have a smaller Q-value. Furthermore, the pileus of *I. pseudoasterospora* often shows an almost blackish centre with only very faint remnants of a velipellis, its surface is generally smoother, and it is to be

found in a different habitat, often park-like terrain (Kühner & Boursier 1932, Esteve-Raventós & Caballero 2009). *Inocybe perlucida*, the former *I. pseudoasterospora* var. *mycenoides* can easily be distinguished from *I. subentolomospora* by its almost translucent pileus surface which reminds those of most *Mycena* species, wider angular-stellate basidiospores [9–13(–14) × 7–11(–12) μm], slightly shorter hymenial cystidia (50–70 μm) and growth in association with *Picea abies* (Ferrari 2006, Bandini *et al.* 2020).

Supplementary material: TreeBASE study S32061 (alignment and tree).



Most likely tree of the Maximum Likelihood (ML) analysis of *Inocybe* sect. *Leptocybe* species (sequences retrieved from the dataset used in Gao *et al.* 2024) inferred from the ITS/*RPB2* regions generated by IQ-TREE v. 1.6.12 (Trifinopoulos *et al.* 2016). The reliability of the clades was evaluated using the SH-like approximate likelihood ratio test (with 1000 replicates) (Guindon *et al.* 2010) and the ultrafast bootstrap approximation (UFB) (also with 1000 replicates) (Hoang *et al.* 2018). SH-like approximate likelihood ratio test (SH-aLRT) ≥ 80 % and ML ultrafast bootstrap support (ML-UBS) ≥ 95 % are shown above branches. Voucher numbers and GenBank accession numbers are indicated in the tree ITS/*RPB2*. The tree was rooted to *Inocybe acuta* (DB24-8-15-7) and *Inocybe subentolomospora* is highlighted with **bold** font.

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*Inocybe subporcorum*





## *Inocybe subporcorum* Esteve-Rav. & Pancorbo, *sp. nov.*

**Etymology:** Named after *Inocybe porcorum* due to its morphological similarity.

**Classification:** *Inocybaceae*, *Agaricales*, *Agaricomycetes*.

*Basidiomata* agaricoid and stipitate. *Pileus* 15–25 mm, initially convex to plano-convex, becoming applanate or shallowly and broadly umbonate; margin straight to irregular or wavy when extended; colour generally uniform, tobacco-brown, deer-brown to snuff brown or avellaneous (Mu 7.5YR 4/3–6, 5/3–4; Munsell 1994); surface dry, but often slimy or sticky in wet weather and agglutinating soil debris, smooth, occasionally lacerated towards the centre, radially fibrillose, margin sometimes subrimulose, not or hardly hygrophanous. *Velipellis* white, not very conspicuous, but present in young specimens, especially on the margin of the pileus, fleeting in rainy weather and on old specimens. *Lamellae* moderately distant (L = 36–40); l = 1–2, 4–6 mm wide, adnexed to narrowly adnate, rather ventricose, initially pale grey, then beige to ochraceous, finally pale brown; edge white or paler, fimbriate to finely crenulate. *Stipe* 23–40 × 3–8 mm, firm, straight or sometimes curved towards the base, cylindrical to hardly enlarged towards the base, rarely attenuated; colour initially white to dirty white or pale ochraceous, in some specimens with a pale pink tone or reflection especially towards the apex; surface uniform, smooth to finely or sparsely white fibrillose longitudinally, fibrillose to hardly flocconose at the very extreme apex. *Cortina* present in very young specimens, ephemeral. *Context* firm, fibrous, whitish to pale ochraceous at pileus and stipe base, sometimes pale pinkish ochraceous at the upper stipe cortex. *Smell* subspermiatic when cut. *Spores* (8.8–)9.5–10.8–12.1(–13.7) × (6.2–)6.6–7.4–8.4(–9.5) μm, Q = (1.08–)1.24–1.40–1.68(–1.99) (n = 360 / N = 3), angular-polygonal outline or with few small, low nodules. *Basidia* (28.4–)30.2–38.1–44.1(–46.0) × (8.8–)9.3–11.5–13.5(–15.1) μm, Q = (2.40–)2.76–3.30–4.04(–4.99) (n = 86 / N = 2), 4-spored, some 2-spored, clavate, sterigmata 4–9 μm long. *Lamellar edge* almost sterile, with abundant, hyaline cheilocystidia mixed with sparse, thin-walled claviform paracystidia. *Pleurocystidia* (49.6–)54.3–71.2–86.6(–93.2) × (6.7–)10.7–16.0–20.0(–23.2) μm, Q = (2.96–)3.28–4.50–5.91(–9.95), (n = 124 / N = 3), elongated metuloid, usually subcylindrical, subutriform, subfusiform, asymmetric, flexuose in outline, mostly with a crystalliferous apex, thin-walled (0.64–)0.71–0.90–1.24(–1.25) μm thick, weakly yellowish in aqueous ammonia solutions. *Cheilocystidia* (44.5–)49.9–65.8–83.2(–91.7) × (10.0–)11.2–14.8–19.1(–21.4) μm, Q = (2.61–)3.26–4.50–6.31(–7.09) (n = 129 / N = 2), similar in morphology and size to pleurocystidia. *Stipitipellis* a cutis of parallel hyphae 3–7 μm wide, with brownish intracellular

and epiparietal pigment. *Caulocystidia* only present at the apex of the stipe, subcylindrical, some curved at the top, mostly with corpuscular intracellular pigmentation (28.8–)40.2–57.0–82.9(–100.1) × (6.3–)7.0–9.4–12.2(–17.0) μm, Q: (3.59–)4.00–6.10–9.57(–10.57) (n = 66 / N = 3) becoming caulocystidioid hairs downwards. *Clamp connections* abundant.

**Habitat and distribution:** All the collections studied come from the Iberian Peninsula and have been found in supra-Mediterranean forests, always with oaks (*Quercus ilex* subsp. *ballota*, *Q. faginea*, *Fagaceae*), very often with the presence of various species of *Cistaceae* (*Cistus*, *Halimium*, *Helianthemum*) and *Juniperus thurifera* (*Cupressaceae*) in the high “parameras”; it inhabits clay soils in areas with slightly acidic pH. These data suggest that it is a species with a markedly Mediterranean character, probably confused with other similar taxa.

**Typus:** Spain, Aragón, Teruel, Mora de Rubielos, El Casal, 40°12'30"N, 0°43'40"W, 1050 m a.s.l., in sandy soils under *Quercus ilex* subsp. *ballota* (*Fagaceae*) and *Pinus pinaster* (*Pinaceae*), 22 Dec. 2022, E. Suárez (**holotype** AH 56244, **isotype** HHTSG 1860; ITS-LSU sequence GenBank PQ773490).

**Additional materials examined:** Spain, Basque Country, Álava, Oriso, 42°41'59"N, 2°20'15"W, 598 m a.s.l., grassy sandy area between *Quercus ilex* subsp. *ballota* with *Cistus salviifolius* (*Cistaceae*) and Mediterranean scrub in siliceous soil, 10 Nov. 2011, A. Caballero (AH 40305; ITS-LSU sequence GenBank PQ773491); Castilla-La Mancha, Guadalajara, Maranchón, Codes, 41°4'28.93"N, 2°5'54.41"W, 1300 m a.s.l., in *Juniper* grove moorland (“paramera”), slightly acidic soils containing an open bushland with *Thymus vulgaris* (*Lamiaceae*) and diverse *Cistaceae* (*Helianthemum* sp., *Fumana* sp.) and some sparse Portuguese oaks (*Quercus faginea*, *Fagaceae*) and Spanish junipers (*Juniperus thurifera*, *Cupressaceae*) nearby, 18 Nov. 1990, V. González & F. Esteve-Raventós (AH 24480; ITS-LSU sequence GenBank PQ773492).

**Notes:** Terminology follows Vellinga (1988) and Kuyper (1986). *Inocybe subporcorum* is a Mediterranean species, taxonomically placed in the *Giacomi* and *Proximella* group (section *Cortinatae*, subsection *Cortinatae*, lineage *Boltonii*, according to Bon 1998). It is phylogenetically close to *I. subdeciens*, *I. proximella*, *I. giacomii* and *I. halimiphila*. Due to its close macro- and microscopic characters, it could be confused mainly with *I. subdeciens*, an earlier species that was proposed but not validated by Bresadola (1934), but whose name now takes preference over the more recent *I. porcorum* (Kokkonen & Vauras 2012), according to recent taxonomic-phylogenetic studies by Cervini *et al.* (2024). The latter authors have also shown that *I. hypervelata* (Cervini & Bizio 2005), is a later synonym of *I. subdeciens*.

*Inocybe subporcorum* is characterised by its small to medium size, the uniform brownish colour of the pileus, contrasting with the whitish (sometimes pinkish on top) of

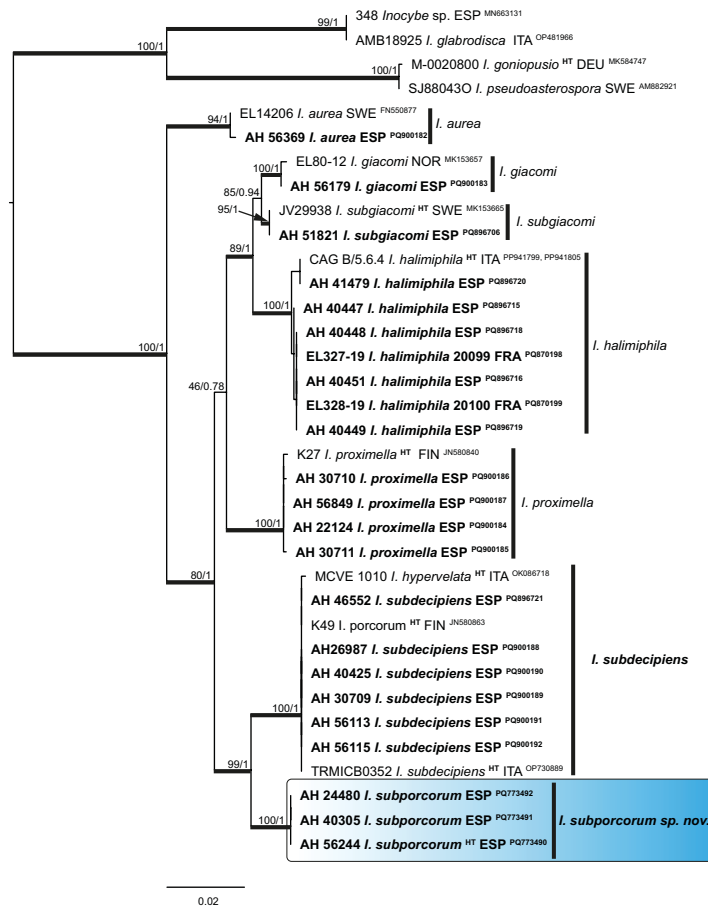
**Colour illustrations:** Habitat of *Inocybe subporcorum* on siliceous soil in the proximity of *Quercus ilex* and *Pinus pinaster* in Mora de Rubielos, Spain at 1050 m altitude, the type locality. *In situ* basidiomata of the holotype (AH 56244); from bottom to top: photos of SEM basidiospores (AH 24480); OM basidiospores; pleurocystidia; cheilocystidia; caulocystidia in the upper part of the stipe. Scale bars: basidiomata = 10 mm; cystidia = 50 μm; OM spores = 10 μm; SEM spores = 2 μm.

the stipe and, above all, microscopically by its somewhat variable cystidia, generally subcylindrical to fusiform with rounded apex, often long pedicellate and, especially, by the very thin walls that are barely more than 1 µm thick. This last characteristic, together with the very light pinkish tones on the stem and its habitat in Mediterranean ecosystems, makes it recognisable, growing in forests of the evergreen species *Quercus ilex* (*Fagaceae*) in washed and slightly acid soils. In our phylogenetic study, *Inocybe subdeciapiens* (= *I. porcorum*) share 96.8 % ITS similarity with *I. subporcorum*.

With respect to its spores, *I. subporcorum* shows a polygonal and subrectangular outline with the presence of small, low and obtuse nodules (7–12), hardly exceeding

1–1.2 microns in height. *Inocybe subdeciapiens* and *I. giacomii* have very similar spores, but different from those of *Inocybe proximella* and *I. halimiphila* (Sanna *et al.* 2024), the latter being fusiform in appearance, without nodules, and sharing similar habitats under *Cistaceae* in Mediterranean ecosystems. *Inocybe giacomii*, with similar heterodiametrical spores to *I. subporcorum*, differs in the different morphology of its cystidia, with thicker cystidial walls, spores with fewer and less distinct nodules or even with a subangulose outline, and prefers more continental to colder habitats, also reaching the boreal and alpine levels (Kokkonen & Vauras 2012).

*Supplementary material:* doi: 10.6084/m9.figshare.28254275 (alignment).



Most likely tree of the Maximum Likelihood (ML) analysis of nodulose-spored species of Giacomi and Proximella group inferred from the ITS and LSU regions generated by IQ-TREE v. 1.6.12 (Trifinopoulos *et al.* 2016) using 1000 bootstrap replicates. Maximum Likelihood bootstrap values (ML-BS)  $\geq 70$  % and Bayesian posterior probabilities (BPP)  $\geq 0.95$  are shown on the thick branches and ordered as ML-BS/BPP. The BI analysis was performed with MrBayes v. 3.2.7a (Ronquist & Huelsenbeck 2003). Voucher numbers and the nucleotide accession numbers are indicated for all species retrieved from GenBank and generated in this study, as well as country ISO alpha3 code abbreviations. Type collections are indicated in superscript: HT = holotype. The tree was rooted with sequences of *Inocybe glabrodisca*, *I. goniopusio* and *I. pseudoasterospora*. The new species described here is embedded in the coloured rectangle. The sequences generated in this study are highlighted in **bold**. The scale bar represents the expected number of nucleotide changes per site.

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*Laccaria decolorans*



## *Laccaria decolorans* S. Hussain, *sp. nov.*

*Etymology*: The specific epithet “*decolorans*” is from Latin verb *decolorare*, meaning “to fade or lose colour” which signifies that the species undergoes significant colour changes over time.

*Classification*: *Hydnangiaceae*, *Agaricales*, *Agaricomycetes*.

*Pileus* 18–32 mm diam., plano-convex, centrally depressed, reddish brown (10R 4/6) to dark red (10R 3/6) coloured (Munsell, 1975), hygrophanous, turning to pale cream (5Y 9/1) or light beige coloured retaining reddish tint at the margin. *Pileal surface* glabrous to finely fuzzy, prominently sulcated extending from the margin towards the centre, gradually fading out. *Margin* decurved later become flattened, prominently crenate. *Context* pale white (10YR 9/1). *Lamellae* reddish brown (10R 4/6) to pale white (10YR 9/1), subdecurrent, distant, 2–5 mm wide and thin less than 0.4 mm, initially plane later becoming undulated, L 16–30, l 2–3 × of L range. *Lamellulae* attenuate, marginal. *Stipe* 50–65 × 4–8 mm, brick red (10R 4/6) becoming light beige (2.5Y 9/2) or whitish (10YR 9/1), cylindrical, swollen at the base and insertion, solid, becoming hollow, glabrous, striate, striation continuous with lamellae. *Odour* and *taste* indistinct. *Pileipellis* consisting of interwoven, thin-walled, cylindrical, hyaline, septate and clamped hyphae, 4.4–16.2 (avg. 9.1) µm wide. *Stipitipellis* consisting of parallel, cylindrical, hyaline, thin-walled, septate hyphae, with frequent clamps, 3.9–17.5 (avg. 9.6) µm wide. *Caulocystidia* were not found. *Subhymenium* undifferentiated. Lamellar tramal hyphae subparallel to parallel, thin-walled, hyaline, septate, 3.1–11.8 (avg. 6.6) µm wide. *Basidiospores* (8.1–)8.5–9.2–10.7(–10.8) × (7.9–)8.4–9.0–10.1(–10.8) µm (without ornamentation), Q = 0.99–1.00–1.02, globose, hyaline, echinulate, spines 1.8–3.8 (avg. 2.3) µm in length, up to 1 µm wide at base, sparse, uniguttulate. *Basidia* (35.2–)34.4–43.7–56.7(–57.8) × (9.9–)9.0–13.3–17.1(–17.9) µm, frequently tetrasporic sometimes bisporic, with longer sterigma 9.0–15.0 (avg. 12.0) µm in length, with rounded tip, clavate, hyaline with granular content. *Pleurocystidia* (25.1–)27.4–35.0–40.7(–50.8) × (4.0–)4.1–6.5–7.3(–8.9) µm, filamentous, narrowly clavate, flexuous, thin-walled, hyaline. *Cheilocystidia* (28.2–)30.4–40.3–50.3(–56.8) × (5.0–)5.8–7.0–8.2(–9.4) µm filamentous, subclavate to somewhat irregular shaped, thin-walled (n = 55/2).

*Typus*: **Pakistan**, Khyber Pakhtunkhwa, district Swat, Chinar Jambil, N34°41'26", E72°27'23", 1731 m a.s.l., terrestrial growth on litter in broad-leaved subtropical forest dominated by *Quercus* sp. and *Acer* sp., Sep. 2020, S. Hussain, MUC-90A (**holotype** SWAT003425; ITS and LSU sequences GenBank PV257657 and PV257662).

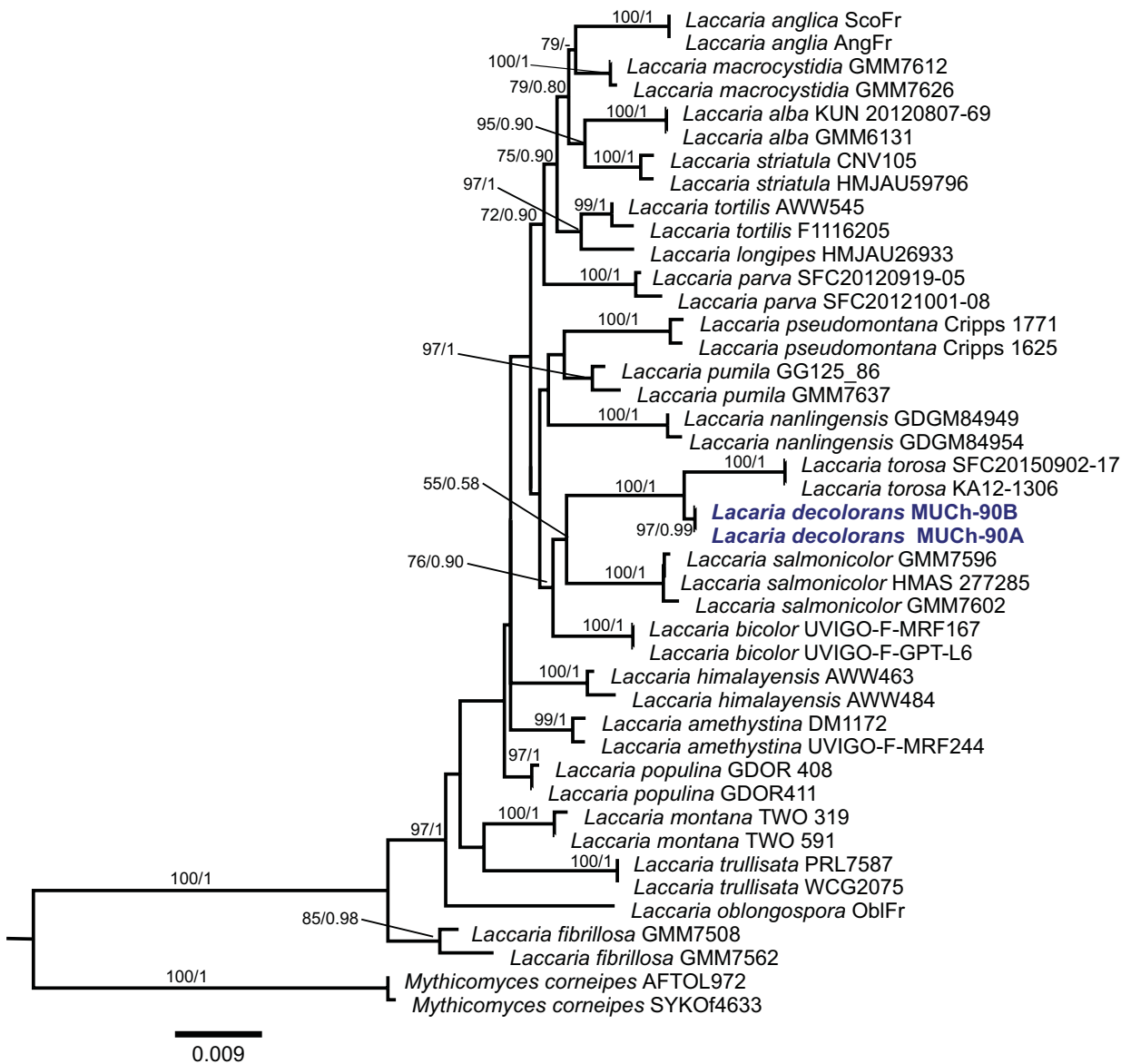
*Colour illustrations*: Holotype collection locality, Swat, KP, Pakistan. Habitat; basidiomes collection at the habitat showing variation in colour; young basidiomes at the habitat: close-up view pileal and gill surface; basidiospores; microscope illustrations of hyphae from pileipellis; hyphae from the pileus trama; hyphae from stipitipellis; cheilocystidia; basidioles; basidia. Scale bars: sporocarps = 10 mm; all other structures = 10 µm.

*Additional material examined*: **Pakistan**, Khyber Pakhtunkhwa, district Swat, Parona Jambil, N34°42'25", E72°28'07", 1755 m a.s.l., terrestrial growth on soil of broad-leaved subtropical forest dominated by *Quercus* sp., Sep. 2020, S. Hussain, MUC-90B (SWAT003425; ITS sequence GenBank PV257660).

*Notes*: *Laccaria decolorans* is distinguished by its reddish brown to darker red pileus with a crenate margin, reddish brown to pale white lamellae, and relatively larger, ornamented basidiospores measuring (8.5–)9.2(–10.7) × (8.4–)9.0(–10.1) µm. The spores bear prominent echinulae measuring 1.8–3.8 µm in length. Additionally, the species is characterized by its longer sterigmata, reaching up to 10 µm in length. This combination of morphological features, along with its genetic distinctiveness, clearly differentiates it from previously described species within the genus *Laccaria* and supports its recognition as a novel species. Phylogenetically, *L. decolorans* forms an independent lineage with strong support (ML = 97 %, BPP = 0.99), constituting a sister clade to *L. torosa* and showing morphological resemblance to *L. salmonicolor* and *L. bicolor*. However, it can be distinguished from these taxa based on several key macromorphological characters. *L. decolorans* possesses a darker red pileus that fades to pale cream, whereas *L. torosa* exhibits an orange brown pileus (Cho *et al.* 2018), *L. salmonicolor* has a salmon-pink to orange-brown pileus (Wilson *et al.* 2013), and *L. bicolor* has a purple brown pileus that fades to buff or tan (Orton, 1960). Additionally, the lamellar coloration of *L. decolorans*, which ranges from reddish brown to pale white, differs from the consistently orange-brown lamellae in *L. torosa*, the salmon pink lamellae in *L. salmonicolor*, and the lilac to buff coloured lamellae in *L. bicolor*. Ecologically, *L. decolorans* is found in broad-leaved subtropical forests, whereas its closest relatives are typically associated with temperate coniferous forests.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence had the highest similarity to *L. montana* [strain AWW446, GenBank JX504097; Identities = 640/657 (97 %), six gaps (0 %)], *L. pumila* [strain OMDL K. Canan, GenBank OR945069; Identities = 637/653 (98 %), six gaps (0 %)], *L. pumila* [strain GG126\_86, GenBank GU234157; Identities = 639/657 (97 %), six gaps (0 %)], *L. amethystina* [strain LaAM-08-1, GenBank OM238141; Identities = 639/657 (97 %), seven gaps (1 %)], *L. amethystina* [strain UVIGO-F-MRF244, GenBank OR037567; Identities = 638/657 (97 %), seven gaps (1 %)], and *L. macrocystidia* [strain GMM7601, GenBank KM067841; Identities = 636/657 (97 %), seven gaps (1 %)]. The closest hits using the LSU sequence had the highest similarity to *L. parva* [strain SFC20150902-17, GenBank MG519598; Identities = 860/867 (99 %), two gaps (0 %)], *L. ohioensis* [strain KH\_07192006\_1, GenBank KU685871; Identities = 874/890 (98 %), two gaps (0 %)], and *L. bicolor* [strain UVIGO-F-AMR241, GenBank OR037632; Identities = 873/890 (98 %), two gaps (0 %)].

*Supplementary materials*: doi: 10.6084/m9.figshare.28601306 (alignment and table).



Maximum Likelihood (ML) tree based on the concatenated ITS+LSU sequences of *Laccaria* species depicting phylogenetic relationships. The analysis was carried out using IQ-TREE v. 1.6.12 (Nguyen *et al.* 2015) and Bayesian analysis using MrBayes v. 3.2.2 (Ronquist *et al.* 2012). Support values at each branch (ML bootstrap / BI posterior probability) are indicated at the nodes. Sequences from this study are shown in **bold** and blue font.

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*Lichenohendersonia cetrariae*





## *Lichenohendersonia cetrariae* Darmostuk, *sp. nov.*

*Etymology:* Named after the host genus, *Cetraria*.

*Classification:* Phaeosphaeriaceae, Pleosporales, Dothideomycetes.

*Sexual morph* not observed. *Asexual morph* pycnidial, globose, dull brown, scattered or in groups, semi-immersed to superficial on the host thallus, 170–200 µm diam. Conidiomatal wall relatively thin, 15–20 µm, composed by several layers of cells, inner region of hyaline flattened cells, 5–7 × 3–4 µm; an outer region of brown, broadly elongate to irregular cell, 5–10 × 3–5 µm; the pigment of conidiomatal wall changed to olive-brown in KOH. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* lining the inner cavity, ampulliform, smooth-walled, holoblastic, 3.5–4.5 µm. *Conidia* solitary, 3-euseptate, golden brown, became darker in KOH, smooth-walled, narrowly ellipsoid to fusiform, not constricted at the septa, apical part round, base truncate, smooth-walled, (16.6–)17.2–18.6(–19.8) × (3.0–)3.2–3.6(–4.0) µm, length/width ratio (4.6–)4.9–5.4(–5.7) (n = 30).

*Habit, habitat and distribution:* *Lichenohendersonia cetrariae* is known only from its type locality in the Mykolaiv region of Ukraine, where it was found growing on the terricolous lichen *Cetraria aculeata*. The infected host was discovered on a dry petrophytic steppe slope near the Inhulets river.

*Typus:* Ukraine, Mykolaiv region, Snihurivskiy district, near Yasna Poliana village, 46.98133°N, 32.83878°E, 16 m a.s.l., dry steppe slope with limestone pebbles, on thallus of terricolous *Cetraria aculeata* (Parmeliaceae), 30 Apr. 2021, V. Darmostuk 413 (**holotype** KRAM L-75118; ITS, LSU and *tef1* sequences GenBank PV273879, PV273881 and PV289755); *ibid.*, V. Darmostuk 1158 (KRAM L-75119; ITS and LSU sequences GenBank PV273880 and PV500578).

*Notes:* The genus *Lichenohendersonia* was introduced by Calatayud & Etayo (2001) to accommodate species with pycnidial conidiomata, ampulliform conidiogenous cells, holoblastic conidiogenesis, and brown, ellipsoidal or oblong, 1–3-euseptate conidia. The genus currently comprises four lichenicolous species (Calatayud & Etayo 2001, Berger &

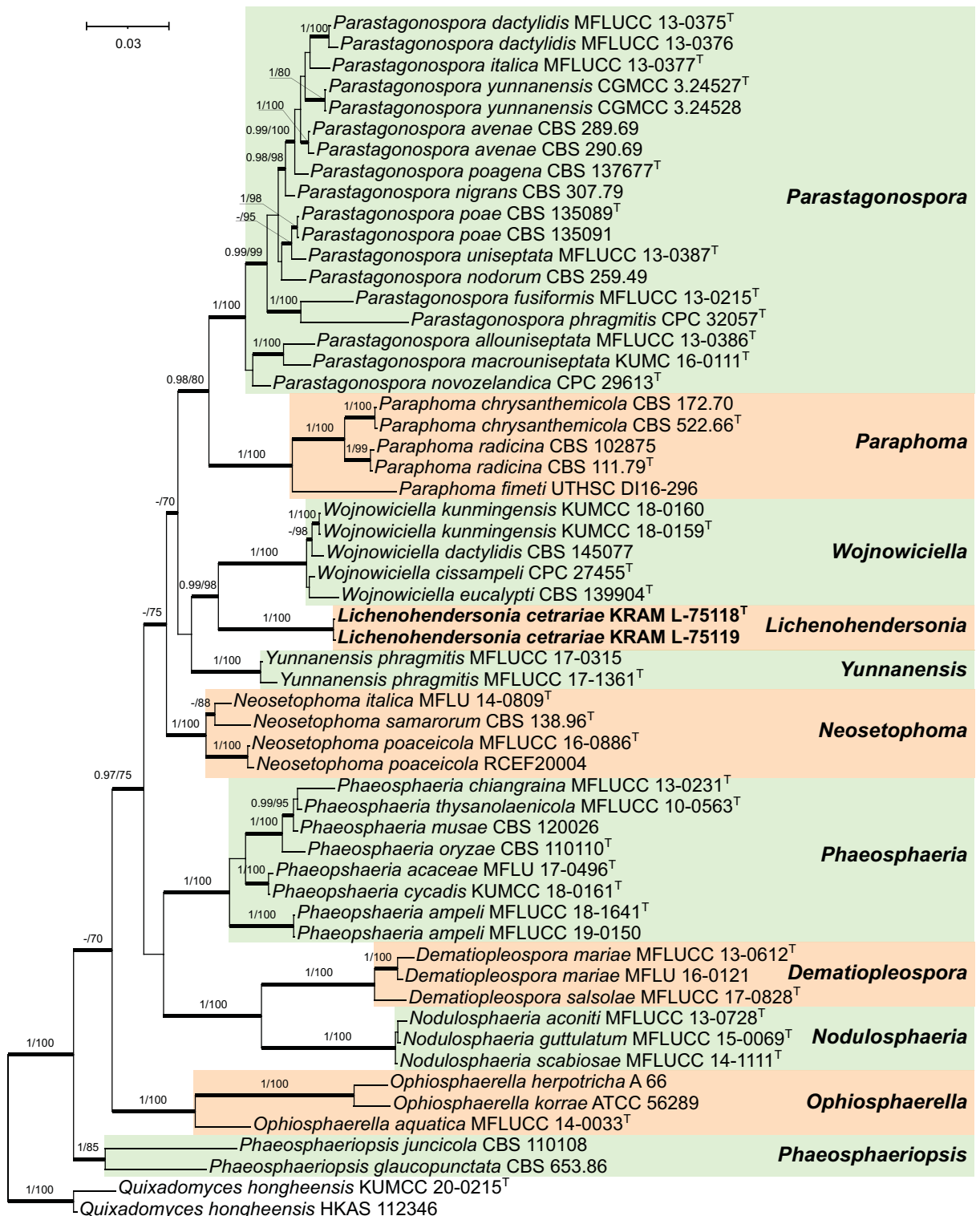
Brackel 2021). *Lichenohendersonia cetrariae* is similar to *L. squamarinae*, which was described on *Squamarina lentigera* from Spain (Calatayud & Etayo 2001), and later reported from Ukraine (Darmostuk *et al.* 2018). The latter species can be distinguished from *L. cetrariae* by its immersed pycnidia, 80–150 µm diam. (vs superficial pycnidia, 170–200 µm in *L. cetrariae*), wider conidia, 4–4.5(–5) µm [vs (3.0–)3.2–3.6(–4.0) µm in *L. cetrariae*], and different lichen host. Another morphologically similar species is *Phaeoseptoria peltigerae*, described on *Peltigera horizontalis* from Norway (Punithalingam & Spooner 1997). It differs from *L. cetrariae* by having immersed pycnidia, 128–160 µm diam. (vs superficial pycnidia, 170–200 µm in *L. cetrariae*), somewhat shorter conidia, 13–19 µm [vs (16.6–)17.2–18.6(–19.8) µm in *L. cetrariae*] and different lichen host. However, molecular data are unavailable for *Lichenohendersonia squamarinae* and *Phaeoseptoria peltigerae*, making it impossible to test their conspecificity with the new species.

Multigene phylogenetic analyses of Phaeosphaeriaceae resolved two specimens of *Lichenohendersonia cetrariae* in a well-supported clade, forming a sister relationship with the genus *Wojnowiciella*. The genus *Wojnowiciella* (type species *Wojnowiciella eucalypti*) was established by Crous *et al.* (2015b) to accommodate species with non-papillate conidiomata lacking setae, as well as septate, verruculose, dark brown conidia intermixed with hyaline microconidia. *Lichenohendersonia cetrariae* can be distinguished by its smooth-walled, golden brown, 3-septate conidia.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Phaeosphaeria pontiformis* [isolate C113-35F, GenBank PP171721; Identities = 94.64 %, five gaps]. Closest hits using the LSU sequence are *Phaeosphaeria musae* (strain CBS 120026, GenBank DQ885894; Identities = 98.77 %, two gaps), and *Tintelnotia destructans* (strain CBS 125924, GenBank KY090665; Identities = 98.76 %, two gaps). Closest hits using the *tef1* sequence are *Paraphoma radicina* (strain UTHSC: D116-209, GenBank LT797075; Identities = 96.70 %, no gaps), and *Neostagonospora arrhenatheri* (strain MFLUCC 15-0464, GenBank MG520901; Identities = 96.70 %, no gaps).

*Supplementary material:* doi: 10.6084/m9.figshare.28601156 (alignment and tree); doi: 10.6084/m9.figshare.28601141 (table).

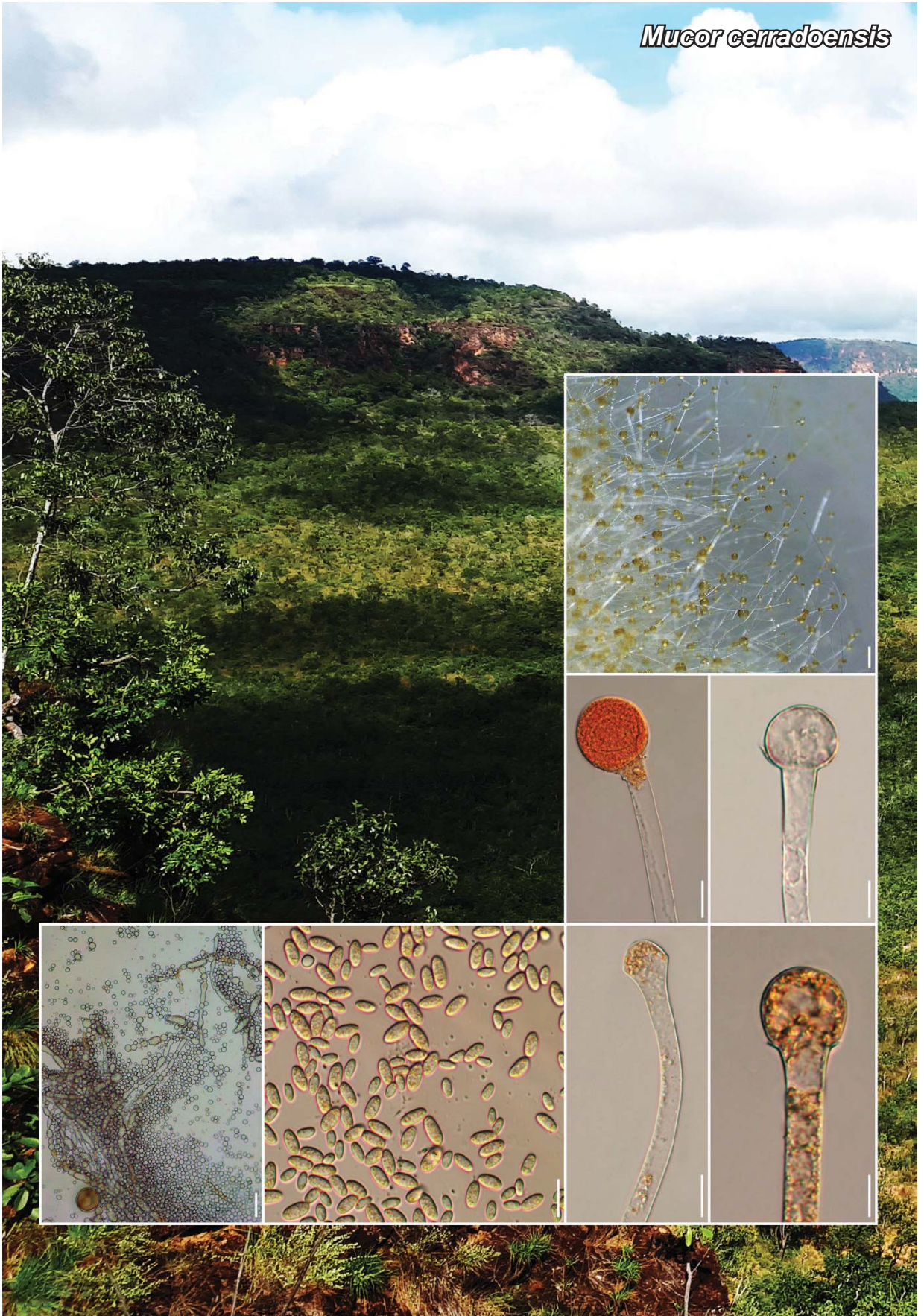
*Colour illustrations:* Ukraine, Mykolaiv region, dry petrophytic steppe. Habits of the conidiomata (mature and young); conidiomatal wall with conidiogenous cells; conidia (upper row in lactophenol cotton blue, lower row in water). Scale bars: habits = 250 µm; all others = 10 µm.



Phylogenetic relationships of *Lichenohendersonia* (highlighted with **bold** font) inferred from Bayesian Inference analysis (BI) of a combined ITS, LSU and *tef1* data set. Two specimens of *Quixadomyces hongheensis* were used as the outgroup. Thickened branches represent either Bayesian posterior probabilities  $\geq 0.97$  and/or bootstrap support values  $\geq 70$  %. Maximum likelihood analyses were carried out using a heuristic search as implemented in IQ-TREE v. 2.1.2 on XSEDE (Nguyen *et al.* 2015) and 100 bootstrap interactions on 1000 replicates to estimate branch support. Bayesian inference of the phylogenetic relationships was calculated using the Markov chain Monte Carlo (MCMC) approach as implemented in MrBayes v. 3.2.6 on XSEDE (Ronquist *et al.* 2012). Sequences from material with a type status are indicated by superscript T.



*Mucor cerradoensis*



# *Mucor cerradoensis* L.S.W Freitas, T.R.L. Cordeiro & A.L. Santiago, *sp. nov.*

**Etymology:** Referring to the Brazilian biome Cerrado (or “Brazilian Savanna”) where the species was first isolated.

**Classification:** *Mucoromycota*, *Mucoromycetes*, *Mucorales*, *Mucoraceae*.

*Mycelium* orange with oil contents. *Colony* floccose, orange on verse and reverse, with citrus odour. *Rhizoids* rare, turnip-like in morphology. *Stolons* not formed. *Sporangiophores* orange, 1.5–8.5 mm in height, with a septum below the sporangium, rarely with two septa, commonly monopodially and sympodially branched (up to 4 times), short, 15–45 × 2.4–5.5 µm or long, 150–400(–580) × (2.5–)4.5–10.5(–25) µm, smooth or encrusted-walled. *Sporangia* orange, globose, 15–40 µm in diam., leaving a collar; wall smooth with vitreous aspect. *Columellae* hyaline or orange, subglobose to hemispherical, rarely irregularly-shaped, 7–35 × 5–30 µm. *Sporangiospores* ellipsoidal with granular contents, 5–18 × 2.5–7.5 µm. *Chlamydospores* common in substrate hyphae, hyaline, terminally or intercalary, single or in long chains, globose to subglobose, ellipsoidal or irregularly-shaped, 3.5–6.5 × 2.5–6 µm. This species presents a dimorphic state, partially changing into yeast state at temperature of 25 °C, after 10 d, becoming completely yeast-like at a temperature of 35 °C, after 10 d. *Yeast cells* globose, subglobose or elongated, 2.5–45 µm diam. *Zygosporangia* not seen.

**Culture characteristics:** Colonies floccose, orange; reverse with regular margin, orange on potato dextrose agar (PDA) and malt extract agar (MEA). On PDA: at 10 °C – lack of growth. At 15 °C – 5.1 cm diam. after 10 d, with poor sporulation; at 20 °C – 6 cm diam. after 7 d, with sporulation; at 25 °C – 7.5 cm diam. after 5 d, with sporulation; at 30 °C – 8 cm diam. in 4 d, with sporulation; at 35 °C – no growth; appearance of yeast cells after 10 d. Yeast cells appear at 25 up to 30 °C, but at 35 °C only yeast cells are observed. On MEA: at 10 °C – no growth; at 15 °C – 7 cm diam. after 10 d, and poor sporulation; at 20 °C – 7 cm. diam after 7 d, with sporulation; at 25 °C – 8.5 cm diam. in 5 d, with excellent sporulation; at 30 °C – 8.5 cm diam. after 4 d, with sporulation; at 35 °C – Absence of filamentous growth; appearance of yeast cells after 10 d.

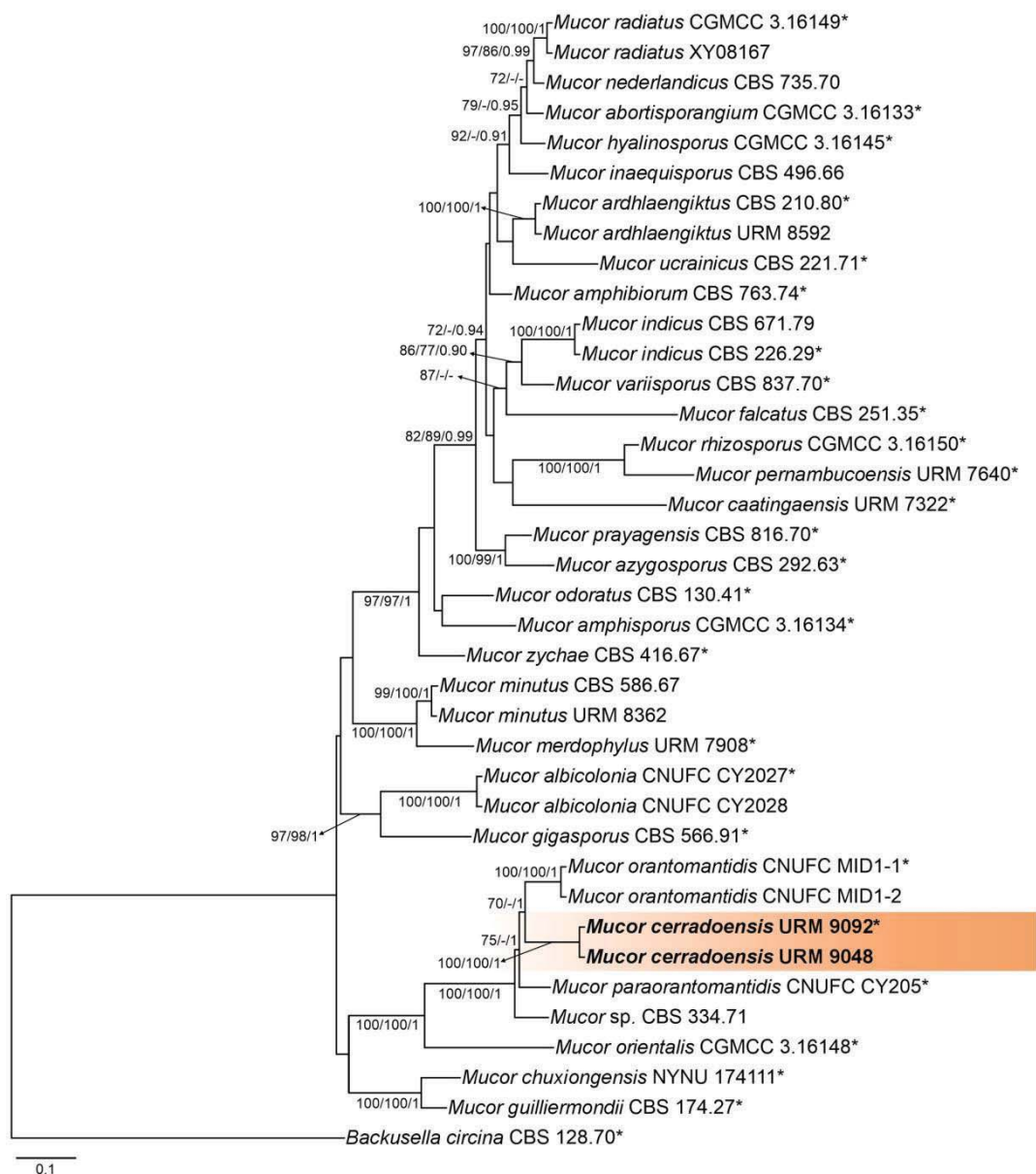
**Colour illustrations:** Brazil, Maranhão, Chapada das Mesas (type locality). Sporangiphores with sporangia; sporangiphore with orange sporangium; sporangiphore with subglobose columella; sporangiphore with subglobose columella; sporangiphore with subglobose to hemispherical columella; yeast cells; sporangiospores. Scale bars: sporangiphores with sporangia = 100 µm; sporangiphore with sporangium and sporangiphore with subglobose columella = 15 µm; other microscopic structures = 10 µm.

**Typus:** **Brazil**, Maranhão State, Carolina, Poço Azul, 7°08'32.7"S, 47°08'41.5"W, isolated from soil samples, coll. 15 Mar. 2023, T.B. Gibertoni, isol. 25 Jul. 2023, L.W. S de Freitas (**holotype** URMH 95808), cultures ex-type URM 9092 (ITS and LSU sequences GenBank PQ741862 and PQ757921), URM 9048 (ITS and LSU sequences GenBank PQ742164, and PQ757929).

**Notes:** During a survey on the diversity of *Mucoromycota* from the Cerrado biome in the State of Maranhão, Brazil, we isolated one species belonging to *Mucor* that is morphologically and genetically [internal transcribed spacer (ITS) and large subunit (LSU) rDNA] distinct from other species. The two isolates formed a fully supported clade, close to *M. orantomantidis*, but also close to *M. paraorantomantidis*. *Mucor orantomantidis* shares morphological characteristics with *M. cerradoensis*, e.g. the formation of sporangiphores with short or long branches and subglobose columellae (Phookamsak *et al.* 2019). However, *M. cerradoensis* differs from *M. orantomantidis* by the dimorphic state, partially changing into the yeast-like state at 25 to 35 °C, after 10 d. In addition, *M. orantomantidis* forms globose to subglobose sporangia, initially light yellow, later becoming yellow brown, 28.5–58.5 µm diam, bigger than the ones of *M. cerradoensis* (15–35 µm in diam), which are orange instead. Columellae are subglobose, globose and ellipsoidal, while the ones of the new species are subglobose, subglobose to hemispherical, and rarely irregularly shaped. Furthermore, sporangiospores of *M. orantomantidis* are ellipsoidal, some with one side slightly fattened, 8–11.5 × 4.5–6 µm, whereas the ones of the new species are constantly ellipsoidal with granular contents and larger (5–18 × 2.5–7.5 µm) (Phookamsak *et al.* 2019). *Mucor paraorantomantidis* differs from the new species mostly by the formation of unbranched sporangiphores and by not showing dimorphism. The columellae of *M. paraorantomantidis* are subglobose to ellipsoid, and sporangiospores are hyaline to greyish green, elliptical to fusiform and some elliptical flattened on one side, (5.5–)7–11.5 × 3–5 µm (Nguyen *et al.* 2024), thus differing from the columellae and sporangiospores of *M. cerradoensis*.

Based on a megablast search of NCBI's GenBank nucleotide database, *M. orantomantidis* and *M. paraorantomantidis* are also the closest hits using ITS [*M. orantomantidis* strain STM1, GenBank OQ380842, Identities = 314/354 (89 %), five gaps (1 %); *M. orantomantidis* CNUFC MID1-1, GenBank NR\_164587, Identities = 498/589 (85 %), 26 gaps (4 %); *M. paraorantomantidis* strain CNUFC CY205, GenBank PP844901, Identities = 510/589 (87 %), 27 gaps (4 %)] and LSU [*M. orantomantidis* strain CNUFC-MID1-2, GenBank MH591458, Identities = 607/624 (97 %), one gap (0 %); *M. orantomantidis* strain CNUFC MID1-1, GenBank MH591458, Identities = 607/624 (97 %), one gap (0 %)].

**Supplementary material:** doi: 10.6084/m9.figshare.28017233 (alignment and table).



Maximum Likelihood tree based on ITS and LSU sequences of *Mucor* were conducted in RAxML v. 8.2.12, in the CIPRES science gateway (Miller *et al.* 2010). Bayesian inference (BI) was conducted in MrBayes on XSEDE v. 3.2.7a (Ronquist *et al.* 2012). The substitution model GTR+G+I was used for the alignment in the ML and GTR+G in the BI analyses. Confidence values for ML-BS  $\geq 70$  % (UFboot2/RAxML) and BPP  $\geq 0.95$  are included near the nodes and the "-" indicates statistical support below the threshold values (Trifinopoulos *et al.* 2016). The scale bar represents the expected number of changes per site. The species obtained in this study is in **bold**, orange. Ex-type strains are marked with an asterisk (\*) and GenBank accession numbers (superscript; ITS/LSU) are indicated for all species in supplementary material. The tree was rooted to *Backusella circina* (CBS 128.70).





# *Mycena morenoi* M. Villarreal & Couceiro, *sp. nov.*

**Etymology.** Dedicated to Gabriel Moreno Horcajada for his contributions to the Spanish mycobiota.

**Classification:** *Mycenaceae*, *Agaricales*, *Agaricomycetes*.

**Primordia** 0.5–1 mm diam., hemispherical, entirely covered with white detersile powder. **Pileus** 0.8–3.7 mm diam., initially conic, then convex to plano-convex without umbo, slightly depressed at the centre, sulcate-striate almost to the centre, margin crenulate, membranaceous, surface dry, velvety at centre, pallid, purely white when young, after light greyish brown, somewhat darker at centre, turning greyish white to greyish when dry. **Lamellae** narrowly adnatae to subfree, moderately spaced (10–13 reach to the stipe), with 1–2 series of lamellulæ, thin, whitish to pale greyish, edge convex and concolourous. **Stipe** up to 38 × 0.15–0.25 mm, cylindrical, slightly tapering towards apex, dry, shiny, watery white, arising from a white strigose basal disc of –0.45 mm diam. **Context** thin, concolourous with cap and stipe surfaces, **odour** and **taste** not recorded. **Basidiospores** (6.2–)6.7–7.5(–8.2) × (3.3–)3.6–4.2(–4.5) µm; Q = (1.6–)1.7–2.0(–2.2); N = 100; Me = 7.2 × 4 µm; Qe = 1.8, narrowly ellipsoid to subcylindrical with small apiculus, smooth, hyaline, amyloid. **Basidia** 13.2–17.5(–19.6) × 5–6(–8) µm, subclavate, 2- or 4-spored in the same carpophore, clamped. **Basidiolae** 13–17 × 3–5 µm, subclavate or subfusoid. **Cheilocystidia** 15.2–19.8 × 7.62–12.46 µm, mostly clavate to obpyriform, thin-walled, apically covered with short warts and 0–9 slender necks, (3.3–)8.4–17.6(–18.5) × (0.6–)0.8–1.2(–1.5) µm, clamped. **Lamellar edge** sterile. **Pleurocystidia** absent. **Hymenophoral trama** made of cylindrical, smooth, hyaline, dextrinoid hyphae 1.9–2.7(–3.5) µm diam. **Pileus trama** subregular, hyphae 10–17 µm wide, dextrinoid. **Pileipellis** of primordia a hymenoderm to subhymenoderm layer of acanthocysts; in mature basidiomata a cutis with terminal detersile acanthocysts and broad terminal cells. **Hyphae of the pileipellis** 3–12 µm wide, densely covered with simple warts 0.5–1.5 × 0.4–0.8 µm, hyaline, not embedded in a gelatinous matrix. Detersile acanthocysts over the pileus, (16.9–)17.1–23.3(–24.4) × (10.7–)12.6–16.9(–17.7) µm, globose-pedicellate to broadly clavate, hyaline, thin to thick-walled (–2 µm), densely covered with simple, conical or cylindrical excrescences. **Pileus marginal cells**, clavate to ellipsoid, 23.8–47.6 × 9.6–12.9 µm with simple cylindrical warts, 0.5–2.5 × 0.5–1 µm. **Stipitipellis** made of parallel hyphae, 2–3(–3.5) µm diam., cylindrical, smooth, with abundant caulocystidia all over the stipe. **Caulocystidia** 16.8–30.2(–54.5) × 4.8–9.2(–11.8) µm, scattered to clustered, cylindrical-acuminate to lanceolate, sometimes septate, smooth, frequently with 1–3 lateral or apical projections. Basal disc cystidia similar to caulocystidia, but typically shorter and forming a trichodermium. **Clamp connections** present in all tissues.

**Colour illustrations:** *Mycena morenoi* habitat in the atlantic forest (fragas) from the type locality, Rego, Quente, Lugo, Spain. In situ basidiomata of the holotype (AH56031) and primordium; basidiospores, cheilocystidia, acanthocysts, hyphae of the pileipellis, caulocystidia. Scale bars: basidiomata = 1 cm and 1 mm, respectively; all others = 10 µm.

**Habitat and distribution:** Gregarious, on fallen leaves and logs of *Betula pubescens*, *Salix atrocinerea* (*Salicaceae*) or *Quercus robur* (*Fagaceae*) and rachis of the fern *Woodwardia radicans* (*Blechnaceae*). Known from three localities in the northwest of the Iberian Peninsula.

**Typus:** **Spain**, Lugo, Rego, Quente, 43°28'49.6"N, 7°38'30.8"W, 785 m a.s.l., on dead leaves of *Betula pubescens* and *Salix atrocinerea*, 4 Aug. 2022, A. Couceiro, M. Saavedra & M. Villarreal (**holotype** AH56031; ITS sequence GenBank OP453345).

**Additional materials examined:** **Spain**, A Coruña, Ortigueira, Playa de Morouzos, 43°41'51"N, 7°50'47"W; 9 m a.s.l., on dead leaves of *Salix atrocinerea*, 15 Apr. 2022, A. Couceiro, M. Saavedra & M. Villarreal (AH56027; ITS sequences GenBank OP453346); *ibid.*, 14 m a.s.l., on dead leaves of *Salix atrocinerea* (cultivated on moist chamber), harvested 10 May 2022, M. Villarreal, AH56028; *ibid.*, 6 Dec. 2022, A. Couceiro, A. Jurado, J. Mateos, C. Sos & M. Villarreal, dead log of *Salix atrocinerea*, AH60376; Lugo, Rego, Quente, 43°28'49"N, 7°38'30"W, 785 m a.s.l., 7 Apr. 2022, A. Couceiro, A. Jurado & M. Villarreal, dead leaves of *Quercus robur* and *Salix atrocinerea*, AH60374, *ibid.*, 4 Sep. 2022, on dead leaves of *Salix atrocinerea*, A. Couceiro, AH60377; Fraga dos Casas, San Xoan dos Casas, Cerdido, A Coruña, 43°35'57"N, 7°54'26"W, 127 m a.s.l., 1 Apr. 2022, A. Couceiro, raquis of *Woodwardia radicans* (AH56032, ITS sequence GenBank OP453347).

**Notes:** *Mycena morenoi* could not be assigned to any of the sections described by Maas Geesteranus (1992a, b) for the Northern Hemisphere. The new species forms a sister clade with *M. discogena* and *M. loginqua*, both erroneously assigned to sections *Sacchariferae* and *Polyadelphia* respectively (Desjardin 1995, Cooper *et al.* 2018). This clade is grouped with two other species, *M. illuminans* and *M. indigotica*, both grouping in a well-supported clade (BS = 93 %, BPP = 1) which have also not been assigned to any known *Mycena* section. All these species appear to be closely related to *M. sect. Exornatae*, which forms a monophyletic group (BS = 90 %, BPP = 0.99) and the only one sequenced species of *M. sect. Granuliferae*, *M. antennae*. The latter species shares many characters with *M. morenoi* and *M. discogena*, but its placement in *M. sect. Granuliferae* is based on the presence of inamyloid spores and a non-dextrinoid hymenophoral trama, according to Maas Geesteranus & de Meijer (1997). The closest species to *M. morenoi* is *M. discogena*, which was originally described from Juan Fernandez Islands (Singer 1959), and is also found in Hawaii (Desjardin 1995) and Sao Tomé (Cooper *et al.* 2018) but phylogenetically this relationship is unsupported, and *M. morenoi* stands in a comparatively long branch, indicating a considerable sequence dissimilarity. In terms of raw sequence similarity, based on a blastn search of the NCBI GenBank nucleotide database, the resulting aligned ITS sequences had moderate similarity to *M. discogena* [BAP 649 (SFSU), GenBank MH414556; Identities = 500/593 (84.32 % homology), 44 gaps (7 %)]. Microscopically, *M. discogena* differs from

*M. morenoi* by having wider spores (4–6 µm), as well as cheilocystidia with shorter outgrowths, basal disc cystidia of two types, as well as a different habitat.

**Supplementary material:** doi: 10.6084/m9.figshare.28602104 (alignment and phylogenetic trees).



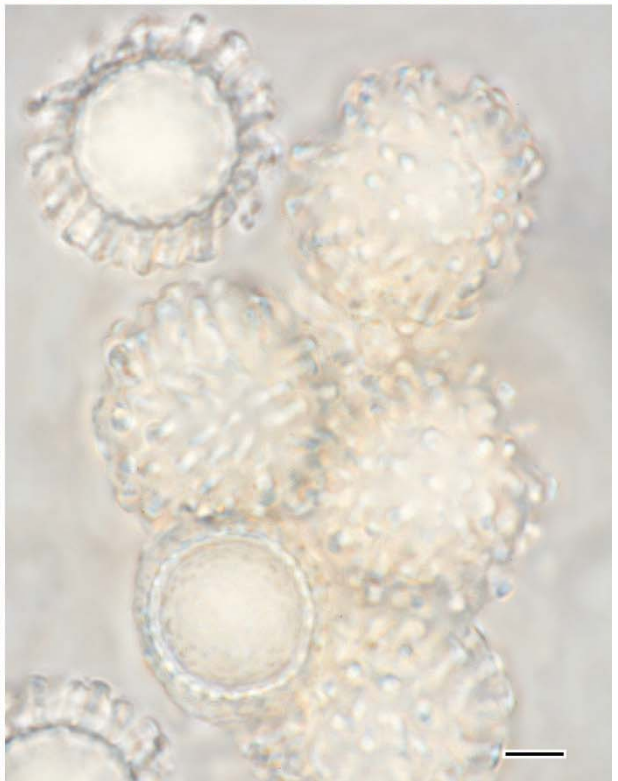
Phylogenetic relationships of *M. morenoi* reconstructed from an unpartitioned ITS dataset. The Maximum Likelihood (ML) analyses were performed using IQ-TREE v. 2.2.0 (Nguyen *et al.* 2015). Branch support was assessed through 1000 replicates of standard non-parametric bootstrapping (Felsenstein 1985). The Bayesian Inference (BI) analyses were carried out in MrBayes v. 3.2.7 (Ronquist *et al.* 2012) and included two runs that will stop automatically when the standard deviation falls below 0.01 or the generation number reaches  $10^6$ , with a sample frequency of 100 and a burn-in value of 25 %. Alignment statistics: 40 strains including the outgroup; 700 characters including alignment gaps analysed: 232 parsimony-informative, 394 singleton sites, 330 constant sites. The best-fit model identified for the entire alignment in IQ-TREE according to BIC scores was: HKY+F+G4. In the BI analysis, substitution models were sampled within the HKY space allowing a gamma distributed rate heterogeneity across sites and a proportion of invariant sites (rates = invgamma) to be estimated. The ML bootstrap support values and Bayesian posterior probabilities are indicated around the branches. Tree was displayed with FigTree v. 1.4.4 (Rambaut 2018) and edited with Inkscape v. 1.1. All tips are labelled with database accession number, taxon name and collection number. *Mycena morenoi* is marked in **bold** and the holotypes are indicated. Scale bar on the tree indicates the expected number of changes per site. The tree was rooted to *M. pura*.

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*Pachyphlodes algarvensis*



***Pachyphlodes algarvensis* L. Möller & A. Paz., sp. nov.**

*Etymology*: The epithet *algarvensis* is dedicated to the Algarve region in Portugal, where the holotype was collected.

*Classification*: Pezizaceae, Pezizales, Pezizomycetidae, Pezizomycetes, Pezizomycotina.

*Ascoma* subglobose to oval, with basal cavity, 1 × 2.2 cm diam., reddish brown surface, with compound, irregular, angular warts, covered with a thin layer of young yellowish mycelium. Marbled *gleba*, compact with yellow and pink tones, with slight bluish oxidation when cut, darker when ripe, with light bifurcated sterile veins, cream in colour. No noticeable *odour*. *Peridium* between 420–455 µm thick, composed of two layers. Exoperidium or ectal excipulum measures an average of 120–274 µm thick, with warts that measure an average of 171.48 (high) × 401.24 (base) µm, formed by angular cells, very irregular in size, measuring between 5.13–50.52 × 9.67–41.25 µm, with walls 1 µm thick and yellowish brown in the outermost part and hyaline in the inner part with the thinner cell walls. Endoperidium or internal excipulum that measures between 42.11–181.33 µm thick, composed of an intricate texture, with thin and hyaline walls. *Paraphyses* not seen. *Asci* irregularly distributed between intertwined hyphae in the gleba, generally subglobose or slightly pyriform 70.40–120.86 × 48.85–130.83 µm, excluding the pedicel, this measures between 30–50 × 16–20 µm, which widens to a generally forked base, indicative of their origin from a baculum, the asci have walls 1 µm thick and contain between 6 to 8 spores, with evidence of disintegration of spores into asci with fewer, irregularly arranged and the walls do not react in Melzer's reagent. The ascospores are globose, measuring on average 20.5 µm diam. with a range of 19 to 22 µm (including ornamentation), decorated with capitate spines, measuring between 3.68–4.24 µm (high) × 1.12–1.65 µm (base), light yellow in colour, agglutinating at the tips to form a perisporium covering.

*Habitat and distribution*: Solitary among plant remains, under *Pinus* with presence of *Quercus* and *Cistus*, sandy soil, occurring in spring. Species so far only known from the type locality in Portugal.

*Typus*: **Portugal**, Algarve, Carvoeiro, 37°06'12.9"N, 08°25'38.4"W, 70 m a.s.l., under *Cistus salvifolius*, *Quercus suber* and *Pinus pinea*, on sandy soil, 10 Mar. 2024, E. Muche (dog Joe) & L. Möller (dog Figo) (**holotype** BCN-Myc 3670, **isotype** IC10032415; ITS sequences GenBank PV345761).

*Additional material studied*: **Portugal**, Algarve, Carvoeiro, 37°06'12.9"N, 08°25'38.4"W, 70 m a.s.l., under *Cistus salvifolius*, *Quercus suber* and *Pinus pinea*, on sandy soil, 12 Mar. 2024, E. Muche (dog Joe) & L. Möller (dog Figo) (**paratype** BCN-Myc 3671, IC12032402 copy; ITS sequences GenBank PV345762).

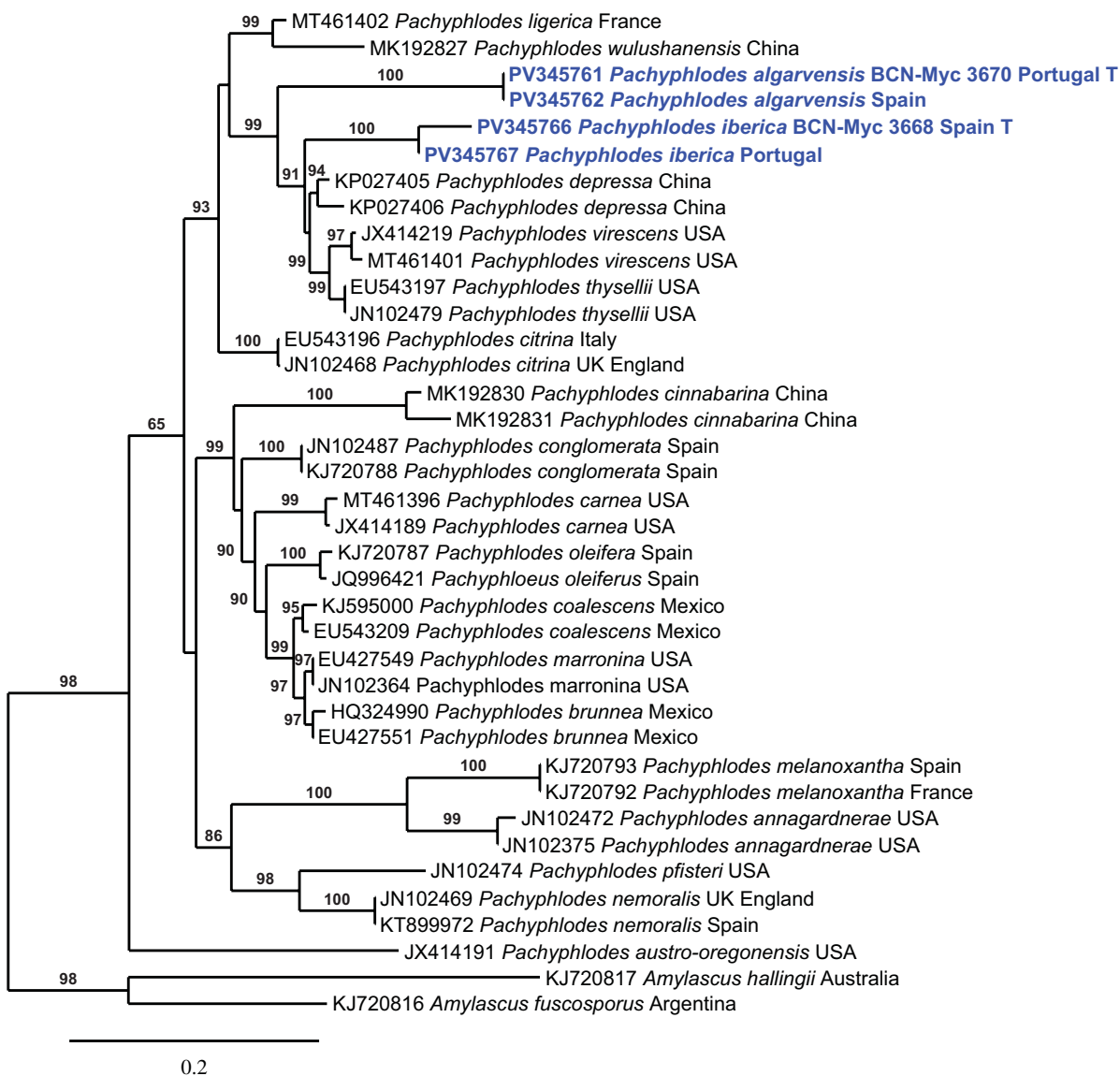
*Notes*: Phylogenetic studies reveal that *Pachyphlodes algarvensis* clusters in the same clade as *P. citrina* from Italy, *P. wulushanensis* from China, *P. ligerica* from France, and has as sister species *P. depressa* from China, *P. iberica* sp. nov. from the Iberian Peninsula, *P. virescens* and *P. thysellii* from the USA.

*Pachyphlodes citrina* has clavate asci and ascospores ornamented with spines that are rounded or truncated at the apex; *P. wulushanensis* has its ascospores ornamented with spines that are partially fused at the apex (Ting 2019); *P. ligerica* has spores with short, cylindrical spines (Tulasne & Tulasne 1851); *P. depressa* is distinguished by the smooth surface of the ascumata, which is almost absent in warts (Fan & Cai 2015); *P. iberica* has ascumata with compound warts, small spores with sharp or capitate spines, *P. virescens* has olive yellow ascumata, with conical warts, olive grey gleba and spores with blunt spines; *P. thysellii* has spores with very fine spines > 2 × 0.7–1 µm tall (Doweld 2013a, b).

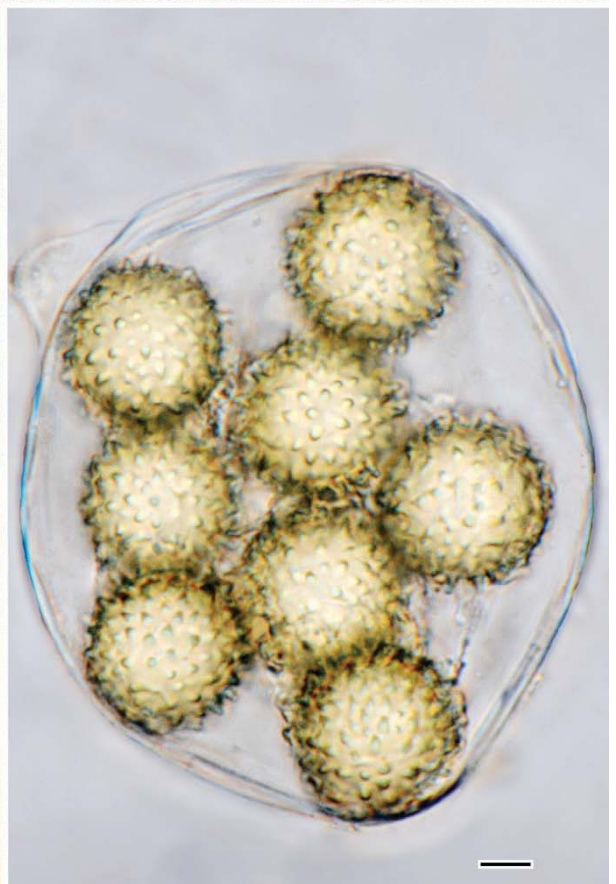
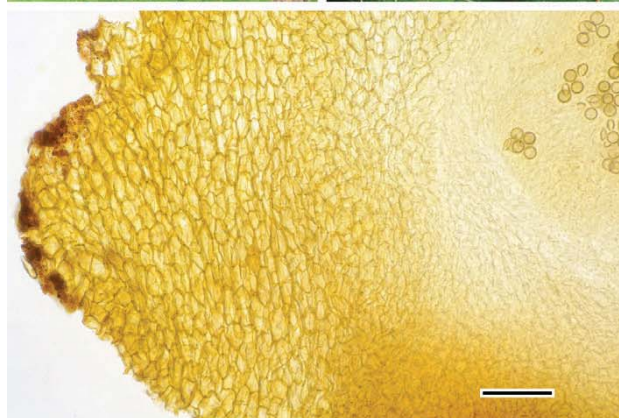
Based on a Blast analysis of the ITS region for *P. algarvensis*, the following similarities were observed: *P. citrina* EU543196: 94.16 %; *P. wulushanensis* MK192827: 93.97 %; *P. ligerica* MT461402: 94.06 %; *P. depressa* KP027405: 98.15 %; *P. iberica* PV345766: 96.14 %; *P. virescens* JX414219: 96.46 %; *P. thysellii* EU543196: 94.16 %

*Supplementary material*: doi: [10.11646/phytotaxa.411.2.2](https://doi.org/10.11646/phytotaxa.411.2.2) (alignment and tree).

*Colour illustrations*: Portugal, Algarve, Carvoeiro, where the type specimens were collected. Mature ascumata; organisation of peridium hyphae (exoperidium and endoperidium) and gleba; ascospores under light microscope. All images are from the holotype. Scale bars: peridium = 100 µm; ascospores = 5 µm.



*Pachyphloides* phylogeny based on an ITS alignment. The alignment was done with ClustalW and checked in BioEdit Sequence Alignment Editor v. 7.2.5 (12/11/2013) and then analysed at "Méthodes et Algorithmes pour la Bio informatique LIRMM", phylogeny.fr. One click mode. Phylogenetic tree obtained from the maximum likelihood (ML) analysis. Numbers above branches are maximum likelihood bootstrap (MLbs), bootstrap support values ( $\geq 50\%$ ) are given above the branches. Adobe Acrobat Pro software was used to edit the final tree. New species are in shaded boxes, Terminals contain GenBank accession number, and country/state of collection. T = denote sequences from holotypes. *Amylascus fuscusporus* and *A. hallingii* were included as an outgroup.





## *Pachyphlodes iberica* A. Paz & L. Möller., *sp. nov.*

**Etymology:** The epithet *iberica* is dedicated to the Iberian Peninsula, where the species was collected.

**Classification:** *Pezizaceae*, *Pezizales*, *Pezizomycetidae*, *Pezizomycetes*, *Pezizomycotina*.

*Ascoma* subglobose to oval, with basal cavity, 0.5 cm × 1.6 cm diam., reddish brown surface, with compound, irregular, angular warts, covered with a thin layer of young yellowish mycelium. Marbled *gleba*, compact with yellow and pink tones, with slight bluish oxidation when cut, darker when ripe, with light bifurcated sterile veins, cream in colour. No noticeable *odour*. *Peridium* between 380–425 µm thick, composed of two layers. Exoperidium or ectal excipulum measures an average of 130–244 µm thick, with warts that measure an average of 160.20 (high) × 380.17 (base) µm, formed by angular cells, very irregular in size, measuring between 4.99–42.52 × 9.26–40.12 µm, with walls 1 µm thick and yellowish brown in the outermost part and hyaline in the inner part with the thinner cell walls. Endoperidium or internal excipulum that measures between 38.25–162.21 µm thick, composed of an intricate texture, with thin and hyaline walls. *Paraphyses* not seen. *Asci* irregularly distributed between intertwined hyphae in the *gleba*, generally subglobose or slightly pyriform 68.54–122.13 × 49.17–128.13 µm, excluding the pedicel, this measures between 29–48 × 16–21 µm, which widens to a generally forked base, indicative of their origin from a baculum, the *asci* have walls 1 µm thick and contain between 6 to 8 spores, with evidence of disintegration of spores into *asci* with fewer, irregularly arranged and the walls do not react in Melzer's reagent. The *ascospores* are globose, measuring on average 17.50 µm diam. with a range of 16.69 to 18.19 µm (including ornamentation), decorated with sharp or capitate spines, measuring between 1.94–2.25 µm (high) × 0.9–1.58 µm (base), light yellow in colour, without clumping together at the tips to form a perisporium cover.

**Habitat and distribution:** Solitary among plant remains, under *Quercus*, on clayey and silty soils. In late spring, early summer. Until now, this species has only been collected in the Iberian Peninsula.

**Typus:** Spain, Cataluña, Girona, Aiguaviva, 41°57'33.14"N, 2°45'16.94"E, 166 m a.s.l., under *Quercus ilex* and *Quercus rotundifolia*, on clayey and loamy soil, 3 Jul. 2023, A. Paz (dog Skotty) & C. Lavoise (dog Mimis) (**holotype** BCN-Myc 3668, **isotype** IC03072335; ITS sequences GenBank PV345766).

**Additional material studied:** Portugal, Algarve, Salir, 37°13'09.2"N, 08°00'31.9"W, 180 m a.s.l., under *Quercus ilex*, *Quercus rotundifolia* with *Arbustus unedo*, on clayey and loamy soil, 19 May. 2024, L. Möller (dog Figo) & N. Eleonore dos Santos (dog Nala) (**paratype** IC19052407; ITS sequences GenBank PV345767).

**Notes:** Phylogenetic studies reveal that *Pachyphlodes iberica* is placed in the same clade as *P. citrina* from Italy, *P. wulushanensis* from China, *P. ligerica* from France, and has as sister species *P. depressa* from China, *P. algarvensis sp. nov.* from Portugal, *P. virescens* from the USA and *P. thysellii* from the USA.

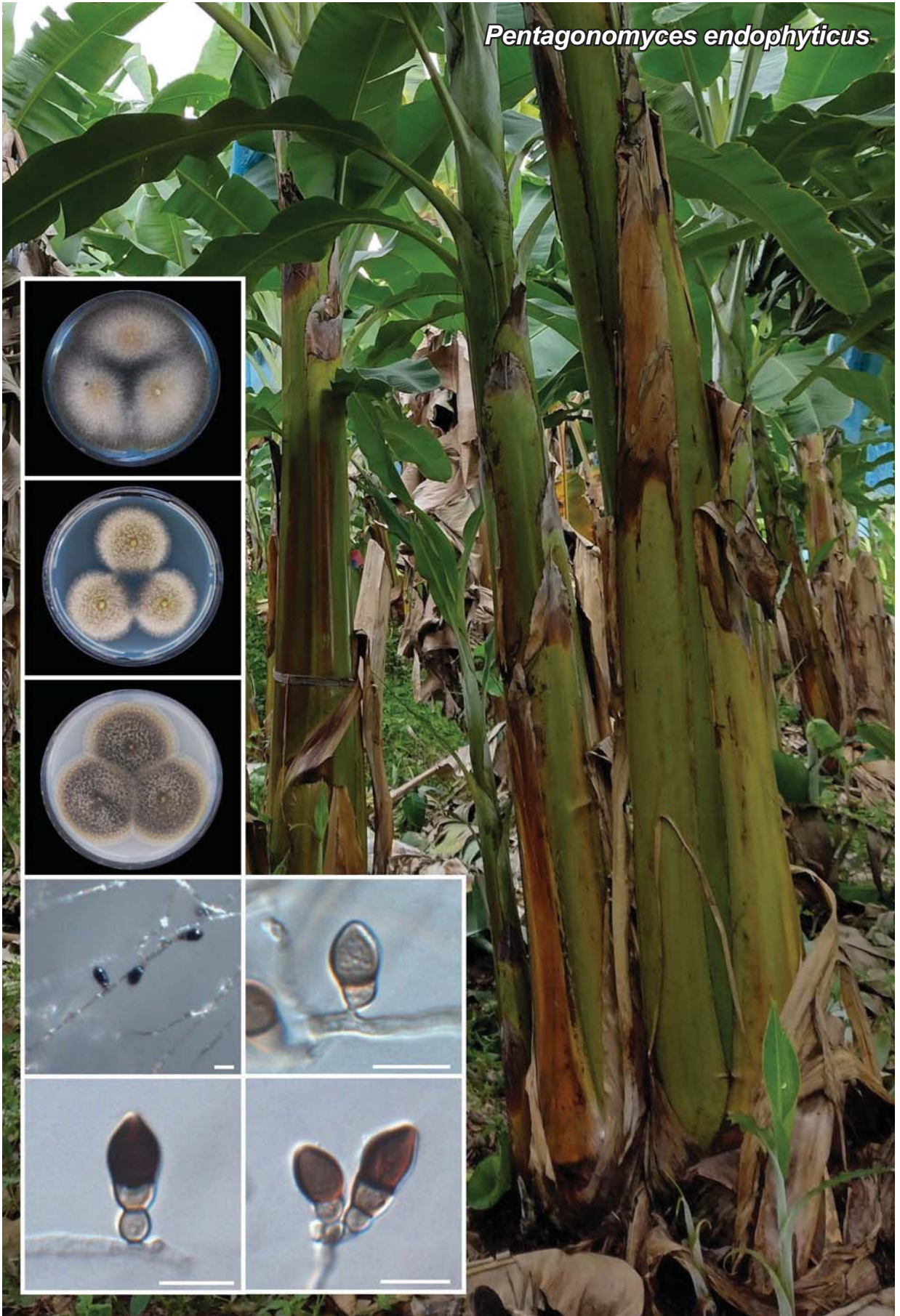
*Pachyphlodes citrina* has clavate *asci* and *ascospores* ornamented with spines that are rounded or truncated at the apex; *P. wulushanensis* has its *ascospores* ornamented with spines that are partially fused at the apex (Ting 2019); *P. ligerica* has spores with short, cylindrical spines (Tulasne & Tulasne 1851); *P. depressa* is distinguished by the smooth surface of the *ascomata*, which almost lacks warts (Fan & Cai 2015); *P. algarvensis* has larger spores decorated with long capitate spines; *P. virescens* has olive yellow *ascomata*, with conical warts, olive grey *gleba* and spores with blunt spines; *P. thysellii* has spores with very fine spines > 2 × 0.7–1 µm tall (Doweld 2013a, b).

Based on a Blast analysis of the ITS region for *P. iberica*, the following similarities were observed: *P. citrina* EU543196: 88.60 %; *P. wulushanensis* MK192827: 92.20 %; *P. ligerica* MT461402: 91.30 %; *P. depressa* KP027405: 92.55 %; *P. algarvensis* PV345761: 96.14 %; *P. virescens* JX414219: 90.61 %; *P. thysellii* EU543196: 92.88 %.

For phylogenetic tree, see *Pachyphlodes algarvensis* (FP 1849).

**Colour illustrations:** Spain, Cataluña, Girona, Aiguaviva, where the type specimens were collected. Mature *ascomata*; organisation of *peridium* hyphae (exoperidium and endoperidium) and *gleba*; *ascospores* under light microscope. All images are from the holotype. Scale bars: *peridium* = 100 µm; *ascospores* = 5 µm.

*Pentagonomyces endophyiticus*





## *Pentagonomyces* J.S. Santana, F.A. Custódio & O.L. Pereira, *gen. nov.*

*Etymology:* Name refers to shape of the terminal cell of the aleurioconidium.

*Classification:* *Neoschizotheciaceae*, *Sordariales*, *Sordariomycetes*.

*Mycelium* septate, branched, subhyaline to pale brown, smooth-walled, sometimes in fascicles in aerial mycelium. *Conidiogenous cells* hyaline, reduced to a single denticle, arising laterally or terminally from the hyphae. *Aleuriconidia* initially 2-celled, often 3-celled, solitary, or formed in clusters

of two, emerging directly from the conidiogenous cells and delimited by a basal septum, thin- and smooth-walled, released rhexolytically. Basal cell obconical or cupulate, sometimes irregular, subhyaline to pale brown, paler than the terminal cell. Terminal cell pentagonal, initially subhyaline to pale brown becoming dark brown with age. *Sexual morph* not observed.

*Type species:* *Pentagonomyces endophyticus* J.S. Santana, F.A. Custódio & O.L. Pereira

MB 857713

## *Pentagonomyces endophyticus* J.S. Santana, F.A. Custódio & O.L. Pereira, *sp. nov.*

*Etymology:* Name refers to the endophytic lifestyle of the fungus.

*Mycelium* septate, branched, subhyaline to pale brown, smooth-walled, (2.1–)2.5–5.0(–5.5)  $\mu\text{m}$  diam. hyphae. *Conidiogenous cells* hyaline, reduced to a single little denticle, arising laterally or terminally from the hyphae, measuring (1.1–)1.7–3.0(–3.9)  $\mu\text{m}$  wide. *Aleuriconidia* solitary, initially 2-celled, often 3-celled, rarely 4-celled, thin- and smooth-walled, emerged directly from the conidiogenous cells and delimited by a basal septum, (9.2–)9.5–19.8(–23.0)  $\times$  (6.1–)6.5–9.9(–12.3)  $\mu\text{m}$ . Basal cell obconical or cupulate, subhyaline to pale brown, paler than the terminal cell, smooth-walled, (2.8–)2.9–5.0  $\times$  3.6–5.9  $\mu\text{m}$ . Terminal cell pentagonal, at first subhyaline like the basal cell, becoming pale brown to dark brown, measuring at the base (4.7–)5.0–7.1(–9.6)  $\mu\text{m}$  diam, smooth-walled, 7.4–14.4  $\times$  (6.1–)6.5–9.9(–12.3)  $\mu\text{m}$ . Conidial secession rhexolytic, with the rupture occurring at any point in the basal cell, but usually very close to the bottom. *Sexual morph* not observed.

*Culture characteristics:* Colonies on corn meal agar (CMA) flat, entire edge, sporulation aerial, moderate aerial mycelium, surface yellowish brown (5F4) to greyish brown (5E3) (Kornerup & Wanscher 1978) and reverse brownish grey (4F2) in the centre to olive brown (4E4) on the edge, reaching 56 mm diam. after 2 wk at 25 °C under photoperiod of 12

h. Colonies on potato dextrose agar (PDA) flat, spreading, entire edge, with aerial sporulation, sparse to moderate aerial mycelium, surface olive brown (4E3) to medium grey (4E1) and reverse dark blue (23F4) in the centre to dark grey (23F1) on the edge, reaching 63 mm diam. after 2 wk at 25 °C under photoperiod of 12 h. Colonies on oatmeal agar (OA) flat, entire edge, moderate aerial mycelium, surface yellowish brown (5F4) in the centre to greyish brown (5D3) on the edge, reverse dark blue (23F4) in the centre to medium grey (23E1) on the edge, reaching 45 mm diam. after 2 wk at 25 °C under photoperiod of 12 h.

*Habit, habitat and distribution:* *Pentagonomyces endophyticus* was isolated as an endophytic fungus from roots of *Musa acuminata* (Dwarf Cavendish) in Itinga do Maranhão, Maranhão, Brazil.

*Typus:* **Brazil**, Maranhão, Itinga do Maranhão, 52°03'N, 05°10'E, 1.5 m a.s.l., isolated as endophytic from roots of *Musa acuminata* (*Musaceae*), 14 Dec. 2021, F.A. Custódio (**holotype** VIC 49608; culture ex-type COAD 3971; ITS, LSU and *rpb2* sequences GenBank PV155404, PV155405 and PV159346).

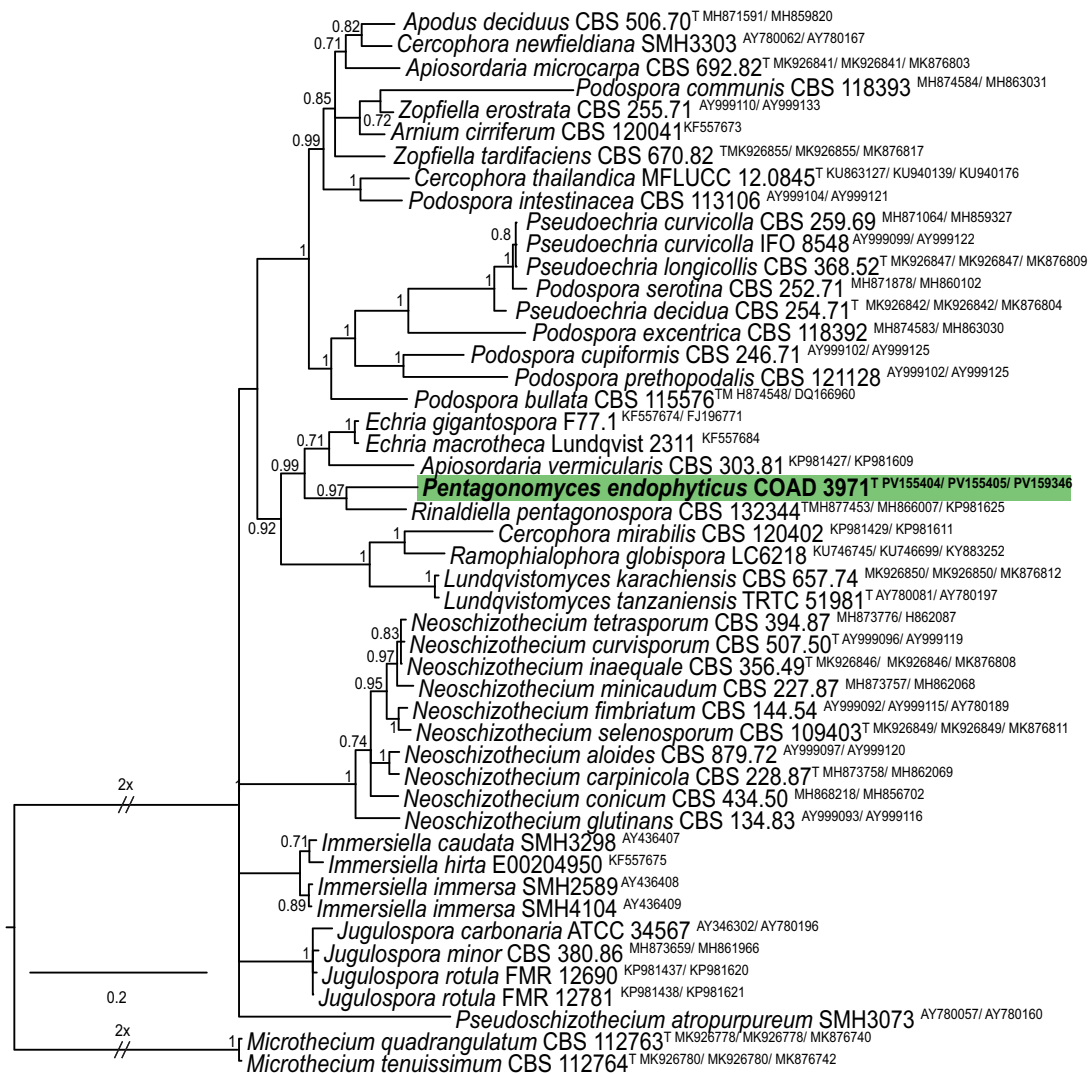
*Notes:* *Pentagonomyces* represents a new genus of dark septate endophytes belonging to *Neoschizotheciaceae* and differs phylogenetically from other genera in this family. *Pentagonomyces* is closely related to the monotypic genus *Rinaldiella*, typified *Rinaldiella pentagonospora* (Crous *et al.* 2014), and differs from this genus by producing aleuroconidia, and its endophytic habit. *Rinaldiella pentagonospora* was isolated from a contaminated human lesion, and represents a sexual morph with ostiolata, pyriform to subglobose ascospores, producing clavate, hyaline and aseptate when young, becoming brown and transversely 1-septate ascospores (Crous *et al.* 2014). Most of the genera belonging to the family *Neoschizotheciaceae* are known from their sexual morphs (Huang *et al.* 2021). However, no sexual morph was observed in *Pentagonomyces*.

*Colour illustrations:* Banana plants growing in a farm located at the Itinga do Maranhão, Maranhão state, Brazil. Colonies after 2 wk at 25 °C (top to bottom on PDA, CMA and OA); aleurioconidia arising laterally from the hyphae; aleurioconidium 2-celled; aleurioconidium 3-celled; aleurioconidia arising terminally from hyphae in cluster. Scale bars = 10  $\mu\text{m}$ .

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Sordariomycetes* sp. [strain PS5975 GenBank MW530209; Identities = 635/635 (100 %), no gaps], "*Uncultured fungus*" [strain gbCTA56\_060, GenBank DQ900979; Identities = 574/575 (99 %), no gaps], and "Fungal sp." [strain ARIZ AZ0830, GenBank HM123519; Identities = 619/635 (97 %), no gaps]. Closest hits using the LSU sequence are *Echria macrotheca* [strain SMH3253, GenBank KF557686; Identities = 798/815 (98 %), five gaps (0 %)], *Neomorinagamyces pyriformis* [strain CGMCC 3.22317, GenBank NG\_243254; Identities = 796/814 (98 %),

four gaps (0 %)], and *Neomorinagamyces pyriformis* [strain CGMCC 3.22326, GenBank OQ758142; Identities = 796/817 (97 %), seven gaps (0 %)]. Closest hits using the *rpb2* sequence are *Apiosordaria microcarpa* [strain CBS 692.82, GenBank MK876803; Identities = 389/470 (83 %), no gaps], *Zopfiella tardifaciens* [strain CBS 670.82 T, GenBank MK876817; Identities = 372/453 (82 %), two gaps (0 %)], and *Jugulospora rotula* [strain FMR 12428, GenBank KP981619; Identities = 384/480 (80 %), two gaps (0 %)].

*Supplementary material:* doi: 10.6084/m9.figshare.28462148 (alignment and tree).



Bayesian phylogenetic tree based on a dataset of ITS, LSU and *rpb2* sequences conducted in MrBayes v. 3.2.7a (Ronquist *et al.* 2012) on XSEDE in the CIPRES science gateway (Miller *et al.* 2015). Taxa obtained from banana roots in Brazil are highlighted in **bold**. Ex-type isolates are marked a superscript "T". Posterior probabilities (pp)  $\geq 0.70$  are shown at the branches. The tree is rooted with *Microthecium quadrangulatum* CBS 112763 and *Microthecium tenuissimum* CBS 112764

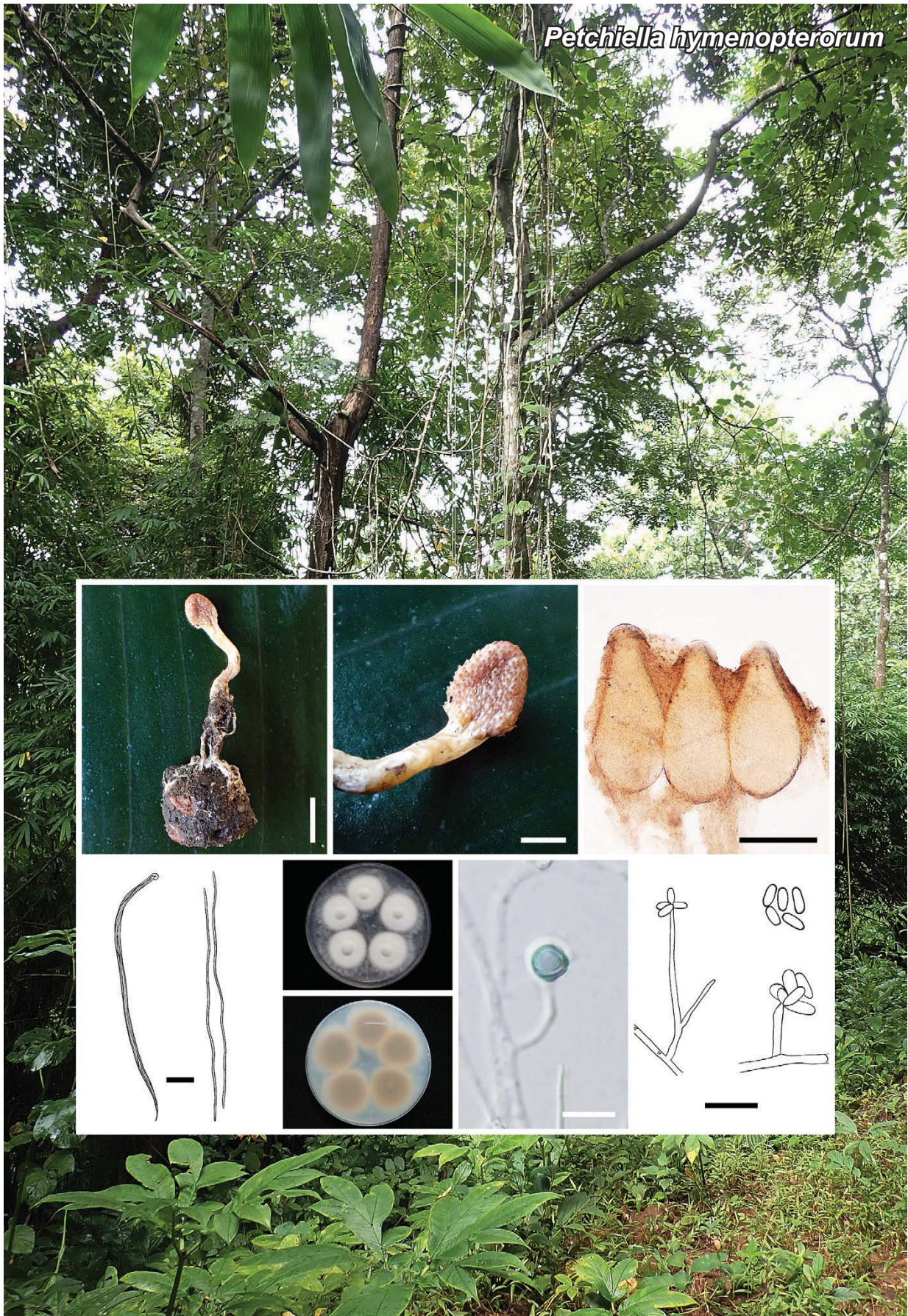
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*Petchiella hymenopterorum*



The composite figure illustrates the morphology and development of *Petchiella hymenopterorum*. It includes:

- Photographs of the fungus on a host, showing a dark, sclerotized base and a long, slender, reddish-brown stalk with a rounded, textured tip.
- Micrographs of the apical region of the stalk, showing a cluster of four large, rounded, brownish structures.
- Line drawings of the long, slender, slightly curved hyphae.
- Micrographs of circular structures, likely spores or developing stages, showing four distinct, rounded, light-colored units.
- A micrograph of a single, large, greenish, spherical structure, possibly a spore or a developing stage.
- Line drawings of the reproductive structures, showing a long, slender stalk with a branched, multi-lobed tip.

# *Petchiella hymenopterorum* Mongkols., Noisripoom, Jangsantear & Luangsa-ard, *sp. nov.*

*Etymology:* Named after the order of the insect host, *Hymenoptera*.

*Classification:* *Clavicipitaceae*, *Hypocreales*, *Sordariomycetes*.

*Stromata* solitary, unbranched, clavate, cream, 12–20 mm long, 1–1.5 mm broad. *Rhizoids* flexuous arising from the head region of hymenopteran pupal nest buried ca 5–10 mm underground. *Fertile part* occurs at the terminal end of stroma, subovoid, pale yellow, slightly flattened, tough, 5–8 mm long, 2–4 mm broad. *Perithecia* pseudo-immersed, oblique, narrowly ovoid, 310–430 × 150–220 µm. *Asci* cylindrical, 8-spored, up to 270 µm long, 4–5 µm wide, with cap 2–3 µm thick. *Ascospores* hyaline, whole, filiform, septate, extending to the length of ascus.

*Culture characteristics:* Colonies on potato dextrose agar (PDA), 10–12 mm diam. in 14 d at 25 °C, white, cottony, with high mycelial density, reverse pale brown. *Vegetative hyphae* smooth, septate, hyaline, 2–3 µm wide. *Phialides* arising from vegetative hyphae, solitary, cylindrical or acromonium-like, up to 85 µm long, 2–5 µm wide. *Chlamydospores* present, solitary, subglobose, (3–)4.5–7(–10) × (2–)3–5.5(–7) µm. *Conidia* aggregated at the apex of phialides, hyaline, ellipsoidal to cylindrical with round the ends, 1-celled, (6–)7.5–10.5(–12.5) × 2–5 µm.

*Typus:* **Thailand**, Kamphaeng Phet Province, Khlong Wang Chao Waterfall, Khlong Wang Chao National Park, on hymenopteran pupae in the nest (*Hymenoptera*), soil, 8 Jun. 2022, *B. Sakolrak & P. Jangsantear* (**holotype** BBH51230; culture ex-type MY12858 = BCC 97167; ITS, LSU, *tef1* and *rpb1* sequences GenBank PP446721, PP446807, PP453599 and PP4453601).

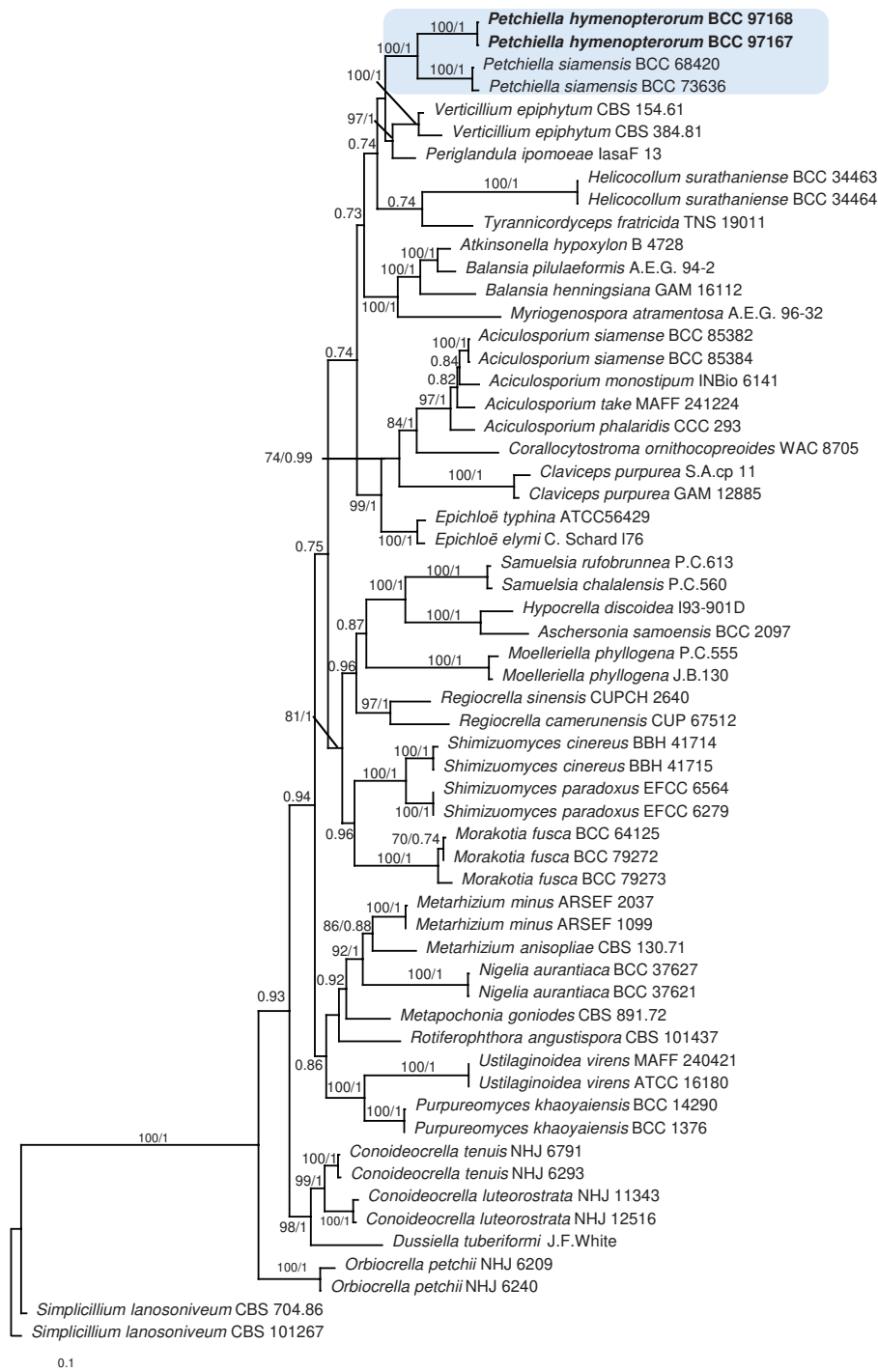
*Additional material examined:* **Thailand**, Kamphaeng Phet Province, Khlong Wang Chao Waterfall, Khlong Wang Chao National Park, hymenopteran pupae in the nest (*Hymenoptera*), soil, 8 Jun. 2022, *B. Sakolrak & P. Jangsantear*, BBH51231, culture MY12860 = BCC 97168, ITS, LSU and *tef1* sequences GenBank PP446722, PP446808 and PP453600.

*Notes:* *Petchiella* (syn. *Petchia*), a genus introduced by Thanakitpipattana *et al.* (2020), currently comprises two recognized species: *P. siamensis* and *P. mantidicola*, as listed in MycoBank ([www.mycobank.org](http://www.mycobank.org), accessed 28 Feb. 2025). These species were originally described from Thailand and Japan, respectively, and are found on the oothecae of praying mantis (*Mantidae*). Both *P. siamensis* and *P. mantidicola* produce cream, terminal, obovoid perithecial heads. In contrast, *P. hymenopterorum*, which occurs on hymenopteran pupal nests, produces slightly flattened perithecial heads. The ascospores of *P. hymenopterorum* and *P. siamensis* remain whole, whereas those of *P. mantidicola* disarticulate into part-spores (Kobayasi & Shimizu 1983). Additionally, the arrangement of perithecia in *P. hymenopterorum* is oblique, differing from the ordinal arrangement observed in *P. siamensis* and *P. mantidicola*. On PDA, conidia and reproductive structures in *P. hymenopterorum* are produced sparingly.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Periglandula* sp. WB-2014 [strain llepGRIN, GenBank KP235251; Identities = 473/513 (92 %), 16 gaps (3 %)], *Periglandula* sp. 1 WB-2014 [strain llep13D, GenBank KP235253; Identities = 473/513 (92 %), 16 gaps (3 %)] and *Periglandula* sp. 3 WB-2014 [strain largGRIN, GenBank KP235245; Identities = 470/510 (92 %), 18 gaps (3 %)]. Closest hits using the **LSU** sequence are *Periglandula* sp. 1 WB-2014 [strain llepGRIN, GenBank KP235253; Identities = 473/513 (92 %), 16 gaps (3 %)], *Periglandula* sp. 1 WB-2014 [strain llep13D, GenBank KP235245; Identities = 470/510 (92 %), 16 gaps (3 %)] and *Periglandula* sp. 3 WB-2014 [strain largGRIN, GenBank KP235245; Identities = 470/510 (92 %), 18 gaps, (3 %)]. Closest hits using the **tef1** sequence are *Periglandula ipomoeae* [strain lasaF13, GenBank KP689568; Identities = 892/985 (91 %), 0 no gaps], *Metarhizium flavoviride* [strain ARSEF 2025, GenBank KJ398804; Identities = 891/988 (90 %), six gaps (0 %)] and *Metarhizium flavoviride* var. *flavoviride* [strain ARSEF 1184, GenBank DQ463997; Identities = 884/980 (90 %), six gaps, (0 %)]. Closest hits using the **rpb1** sequence are *Petchia siamensis* [strain BCC68420, GenBank MK632163; Identities = 520/563 (92 %), no gaps], *Clavicipitaceae* sp. [strain TCF01, GenBank HQ702610; Identities = 515/563 (91 %), no gaps] and *Clavicipitaceae* sp. [strain lasaredF01, GenBank HQ702612; Identities = 515/564 (91 %), no gaps].

*Supplementary material:* doi: 10.6084/m9.figshare.28829147 (alignment, phylogenetic tree and table).

*Colour illustrations:* Background photo of National Park in Thailand. Fungi on hosts; perithecia part; perithecia; ascus (left), ascospores (right); culture on PDA (obverse and reverse); chlamydospores on PDA; phialides with conidia (acromonium-like) on PDA, conidia on PDA; Scale bars: fungi on insect host = 5 mm; perithecia part = 2 mm; perithecia = 150 µm; ascus; ascospores = 25 µm; chlamydospores = 10 µm; phialides; conidia = 20 µm.



Phylogenetic tree derived from a Maximum Likelihood (ML) analysis based on a combined dataset comprising LSU, *tef1* and *rpb1* sequences. The data was analysed using Maximum likelihood (ML) and Bayesian inference (BI). The ML analysis was run with RAxML-VI-HPC2 v. 8.2.12 (Stamatakis 2014) on XSEDE in the CIPRES portal ([www.phylo.org](http://www.phylo.org)). Bayesian inference was calculated with MrBayes v. 3.2 (Ronquist *et al.* 2012), with 5 M generations and MrModeltest v. 2.2 (Nylander 2004) under the GTR+I+G model. Numbers at the significant nodes represent maximum likelihood bootstrap (MLB) and Bayesian posterior probabilities (BPP), MLB/BPP. The new species proposed in the present study is highlighted and indicated in **bold** text.

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*Polyschema endophytica*





# *Polyschema endophytica* J.A. Oliveira, L.N.P. Silva & O.L. Pereira, *sp. nov.*

**Etymology:** The epithet refers to the endophytic habitat associated with coffee plant roots.

**Classification:** *Polyschema*, *Latoruaceae*, *Pleosporales*, *Dothideomycetes*.

Dark septate endophyte (DSE) isolated on culture media from surface-disinfested healthy roots of a coffee plant. *Mycelium* superficial, composed of branched, septate, hyaline to dark brown, predominantly dark brown, thin-walled to verruculose *hyphae*, 2–3 µm wide. *Conidiophores* hyaline, septate, unbranched, up to 45 µm tall, 3–5 µm wide, macronematous or micronematous. *Conidiogenous cells* monoblastic, hemispherical, subspherical, or cylindrical, 6–8.5 × 2–7 µm, and sometimes inconspicuous. *Conidia* solitary, aseptate, globose, subglobose to ellipsoidal, smooth-walled, dark brown, sometimes formed directly on hyphae or in the apical cells of the conidiophore. *Chlamydospores* not observed.

**Culture characteristics:** Colonies on potato carrot agar (PCA) flat with undulate edge, aerial mycelium profuse, cottony, smoke grey colour in the centre to olivaceous buff periphery on surface, reverse umber colour in the centre to olivaceous buff periphery (Rayner 1970), reaching 26 mm diam. after 2 wk at 25 °C in the dark. Colonies on potato dextrose agar (PDA) raised with undulate edge, aerial mycelium profuse, cottony, greyish sepia colour in the centre to lavender buff periphery surface, reverse umber colour in the centre to honey on periphery, reaching 27 mm diam. after 2 wk at 25 °C in the dark. Colonies on malt extract agar (MEA) flat with entire edge, aerial mycelium profuse, mouse grey colour in the surface, reverse iron grey, reaching 37 mm diam. after 2 wk at 25 °C in the dark. Colonies on oatmeal agar (OA) flat with entire edge, aerial mycelium profuse, fuscous black colour in the centre to greenish olivaceous surface, reverse ochreous buff, reaching 38 mm diam. after 2 wk at 25 °C in the dark.

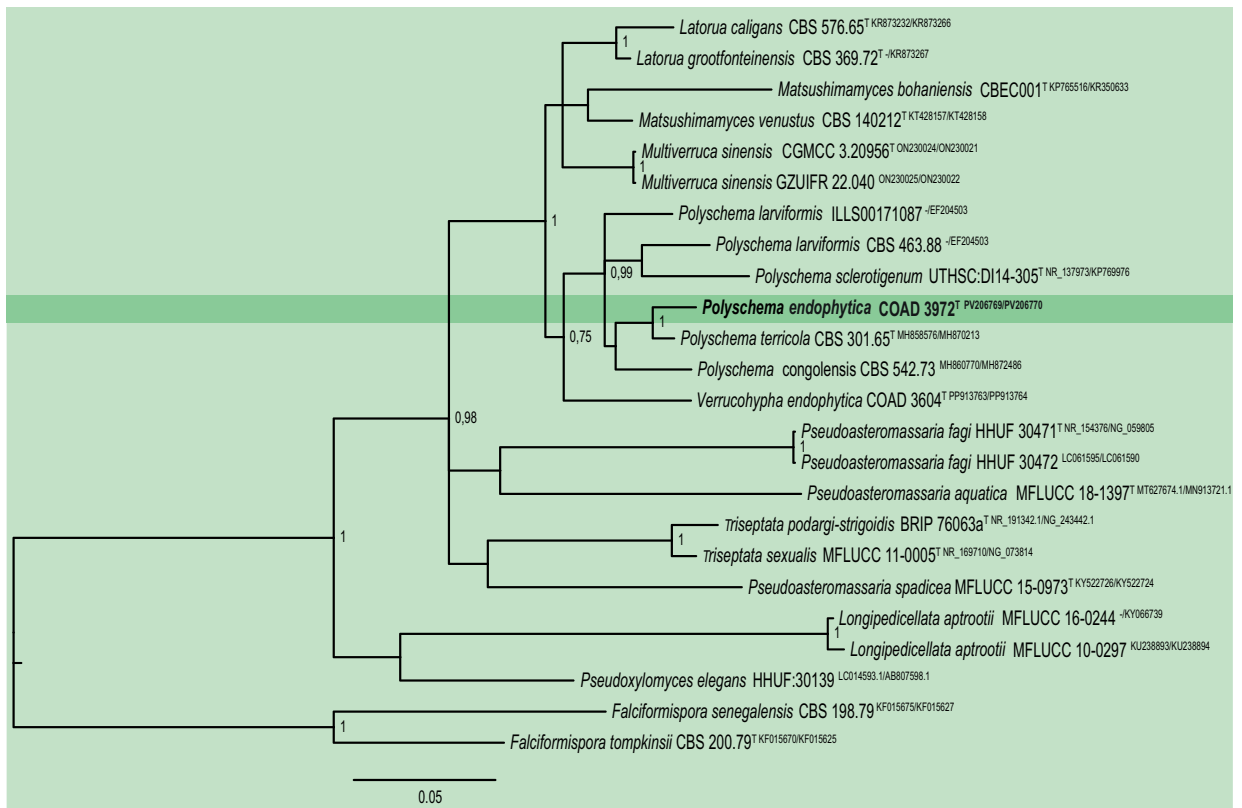
**Typus:** **Brazil**, Minas Gerais, Viçosa, 20°41'20"S, 42°49'36"W, isolated from healthy roots of coffee plant, Oct. 2024, O.L. Pereira & J.A. Oliveira (**holotype** VIC 49616, culture ex-type COAD 3972; ITS and LSU sequences GenBank PV206769 and PV206770).

**Notes:** *Polyschema* was introduced by Upadhyay (1966) and included in *Latoruaceae* by Crous *et al.* (2015a). *Polyschema* consisted of 21 species already described from soils, lake sediments, decaying plant materials, and human clinical specimens (Castañeda-Ruiz *et al.* 2000, Crous *et al.* 2015b). To our knowledge, this is the first report of a *Polyschema* species as a root endophyte. *Polyschema endophytica* is a root endophyte with dark septate hyphae, commonly referred to as dark septate endophytes (DSE). and the first DSE reported in *Polyschema* and the second in *Latoruaceae* (Crous *et al.* 2024b). *Polyschema endophytica* is phylogenetically close to *Polyschema terricola*, the type species of the genus. Compared to the *P. terricola*, *P. endophytica* has 95.34 % identity and 23 polymorphisms, including gaps for the ITS region, and 98.63 % identity with LSU and 12 polymorphisms, including gaps. Additionally, the two species are morphologically distinct. *Polyschema endophytica* produces solitary, smooth-walled, globose, subglobose to ellipsoidal asexual conidia, with micronematous and macronematous conidiophores. In contrast, *P. terricola* produces subglobose to pyriform or clavate, 1–4-septate conidia with verruculose walls, with micronematous conidiophores (Castañeda-Ruiz *et al.* 2000, Seifert *et al.* 2011). A distinctive feature of *P. endophytica* is its asexual conidia, which has never been reported before for *Polyschema*.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had the highest similarity to *Dothideomycetes* sp. isolate from the seed of *Cecropia longipes* in Panama [PS2959, GenBank MW529343.1; Identities = 557/583 (96 %), nine gaps (1 %)], *Polyschema terricola* isolate from soil in Brazil [CBS 301.65, GenBank MH858576.1; Identities = 471/494 (95 %), 11 gaps (2 %)], and Fungal sp. isolate from the seed of *Ficus insipida* [PS3050, GenBank KY776225.1; Identities = 582/611 (95 %), nine gaps (1 %)]. Closest hits using the **LSU** sequence are *Polyschema terricola* isolate from soil in Brazil [CBS 301.65, GenBank MH858576.1; Identities = 866/878 (99 %), three gaps (0 %)], *Polyschema larviformis* from lake sediments in the USA [ILLS00171087, GenBank MH472659.1; Identities = 970/991 (98 %), four gaps (0 %)], and *Pseudoasteromassaria fagi* from Japan [HHUF 30471, GenBank NG\_059805.1; Identities = 930/966 (96 %), 10 gaps (1 %)].

**Supplementary material:** <https://figshare.com/s/f8546f3ac4ee02e5d16b> (alignment and tree).

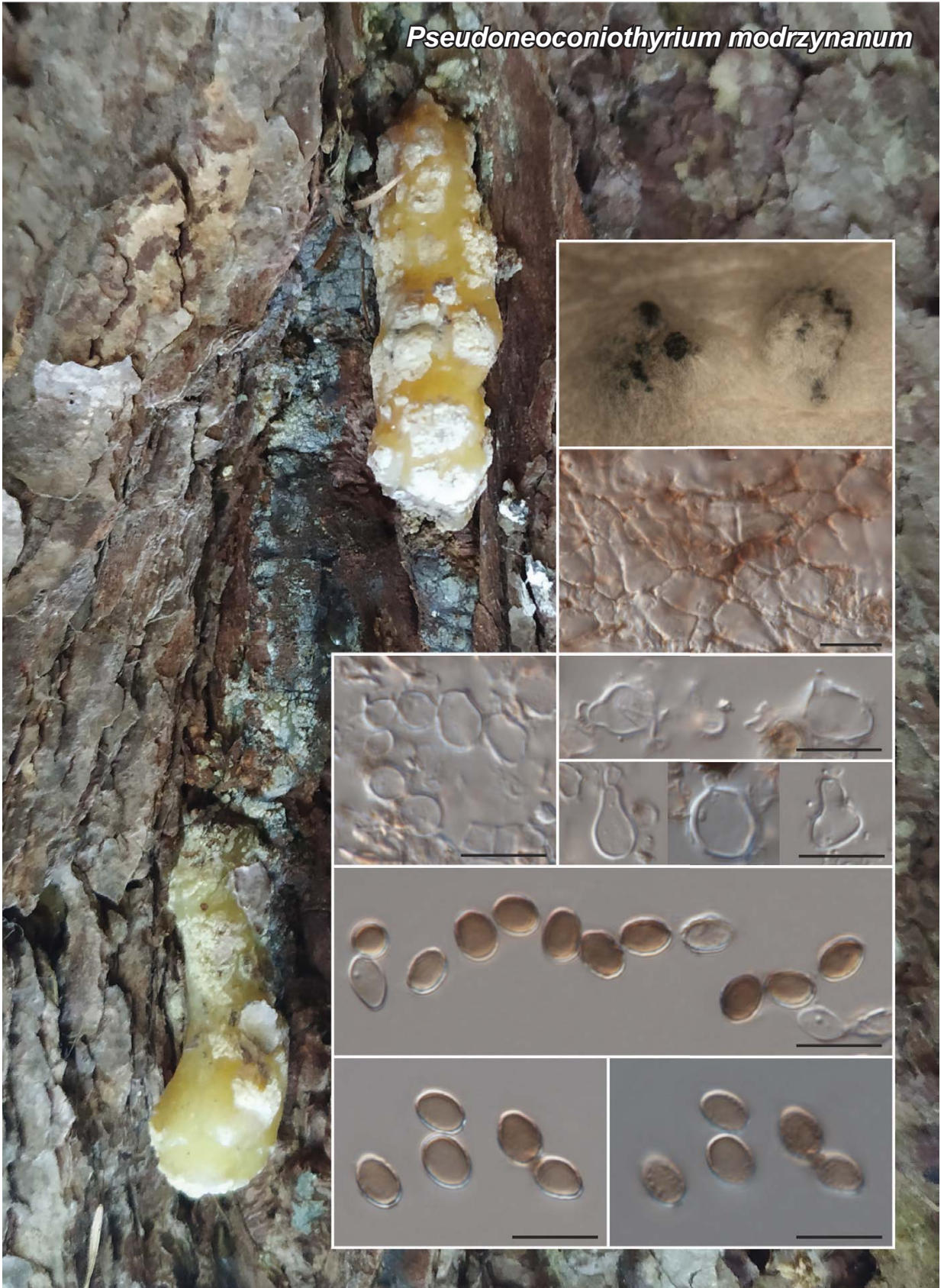
**Colour illustrations:** Young coffee plant growing in the undergrowth of a forest reserve called Mata do Paraíso at Universidade Federal de Viçosa, Viçosa, Minas Gerais state, Brazil. Top to bottom: conidia and conidiophores reduced to conidiogenous cells, conidia formed directly on hyphae, conidia, colony on PCA. Scale bars = 20 µm.



Bayesian inference tree obtained by phylogenetic analyses of ITS and LSU sequences conducted in MrBayes v. 3.2.7a on XSEDE in the CIPRES science gateway. Bayesian posterior probability values > 0.70 are indicated at the nodes. Strains with an ex-type status are indicated with a superscript 'T'. The new species is shown in **bold** and colour face. *Falciformispora tompkinsii* (CBS 200.79) and *Falciformispora senegalensis* (CBS 198.79) were used as outgroups.



*Pseudoneoconiothyrium modrzyanum*



# *Pseudoneoconiothyrium modrzynanum* Piątek & Czachura, *sp. nov.*

*Etymology:* Named after the Modrzyna Reserve in the Beskid Niski Mts in Poland, where the fungus was collected.

*Classification:* Roussoellaceae, Pleosporales, Dothideomycetes.

*Mycelium* composed of branched, septate, hyaline or brown, smooth or finely verrucose, thin-walled hyphae, 1–4 µm wide. *Conidiomata* semi-immersed, erumpent, pycnidial, globose, up to 250 µm diam., with a central ostiole, exuding a black conidial mass, enclosed by a wall of brown textura angularis. *Conidiophores* reduced to conidiogenous cells, lining the inner cavity, discrete, ampulliform, rarely doliiform, hyaline, smooth, phialidic, mostly without neck, 4–8 × 4–7.5 µm. *Conidia* solitary, ellipsoid, rarely subglobose, golden brown, rarely subhyaline or pale brown, finely verruculose, aseptate, thick-walled, 4.5–7.5 × (3.5–)4–5 µm; wall ca 0.5 µm thick. [Description based on malt extract agar (MEA)].

*Culture characteristics:* Colonies on MEA convex, slightly radially folded from the colony centre toward the margin, pale grey at the centre becoming whitish toward the margin, reaching 23 mm diam. after 2 wk at 15 °C and 9 mm diam. after 2 wk at 25 °C, margin undulate, reverse pale green at the centre becoming pale buff toward the margin. Colonies on potato dextrose agar (PDA) slightly convex, pale buff, with pale grey aerial hyphae, reaching 23 mm diam. after 2 wk at 15 °C and 8 mm diam. after 2 wk at 25 °C, margin slightly undulate, reverse pale green at the centre becoming pale buff toward the margin.

*Typus:* **Poland**, Podkarpackie Province, Krosno County, Modrzyna Reserve, ca 13 km south of Dukla city, isolated from the resin of *Larix decidua* ssp. *polonica* (Pinaceae), 22 Oct. 2020, *P. Czachura* (**holotype** KRAM F-60025, culture ex-type PLM7 = CBS 153696; ITS, LSU, *rpb2* and *tub2* sequences GenBank PV264893, PV264894, PV275093 and PV275094).

*Pseudoneoconiothyrium rosae* (Phukhams. *et al.*) Phukhams. *et al.*, *Index Fungorum* **357**: 1. 2018.

*Basionym:* *Neoconiothyrium rosae* Phukhams. *et al.*, *Fungal Diversity* **89**: 165. 2018. [Effectively published: 13 March 2018].

*New synonyms:* *Roussoella euonymi* Crous & Akulov, *Fungal Syst. Evol.* **1**: 204. 2018. [Effectively published: 18 April 2018]. *Pseudoneoconiothyrium euonymi* (Crous & Akulov) Phukhams. & K.D. Hyde, *Fungal Diversity* **102**: 112. 2020.

*Notes:* The genus *Pseudoneoconiothyrium* (replaced synonym: *Neoconiothyrium*, *nom. illeg.*) includes two species *P. euonymi* and *P. rosae* that produce coniothyrium-like asexual morphs with pycnidial conidiomata, annellidic conidiogenous cells and golden brown to orange brown, globose to ellipsoid, aseptate, verruculose conidia (Wanasinghe & Hyde 2018, Wanasinghe *et al.* 2018, Phukhamsakda *et al.* 2020). The type species *P. rosae* was described from dead spines of *Rosa canina* collected in Italy (Wanasinghe & Hyde 2018, Wanasinghe *et al.* 2018) and also found on dead hanging stem of *Galium* sp. and living stem of *Lonicera* sp. in Italy (Hyde *et al.* 2020). The second described species *P. euonymi* (syn. *Roussoella euonymi*) is known from fallen branches of *Euonymus europaeus* in the Ukraine, branches of *Prunus avium* in Germany and paper in the Slovak Republic (Crous *et al.* 2018b, Bien & Damm 2020, Phukhamsakda *et al.* 2020, Pavlović *et al.* 2023). *Pseudoneoconiothyrium rosae* and *P. euonymi* are close morphologically, ecologically and phylogenetically. Based on a megablast search of NCBI's GenBank nucleotide database sequence similarity between different strains analysed in this study is 99–100 % (0–4 bp differences) in ITS, 100 % (no differences) in LSU, 99 % (1 bp difference) in *rpb2*. The latter name is therefore included in synonymy with *P. rosae*.

*Pseudoneoconiothyrium modrzynanum* is different from *P. rosae* (incl. *P. euonymi*) in that its conidiogenous cells usually lack elongated necks with percurrent proliferations and conidia are smaller (6–8 × 3–7 µm in *P. rosae*; Crous *et al.* 2018b, Wanasinghe *et al.* 2018). *Pseudoneoconiothyrium modrzynanum* is also different phylogenetically and ecologically as it inhabits gymnosperm exudates (resin).

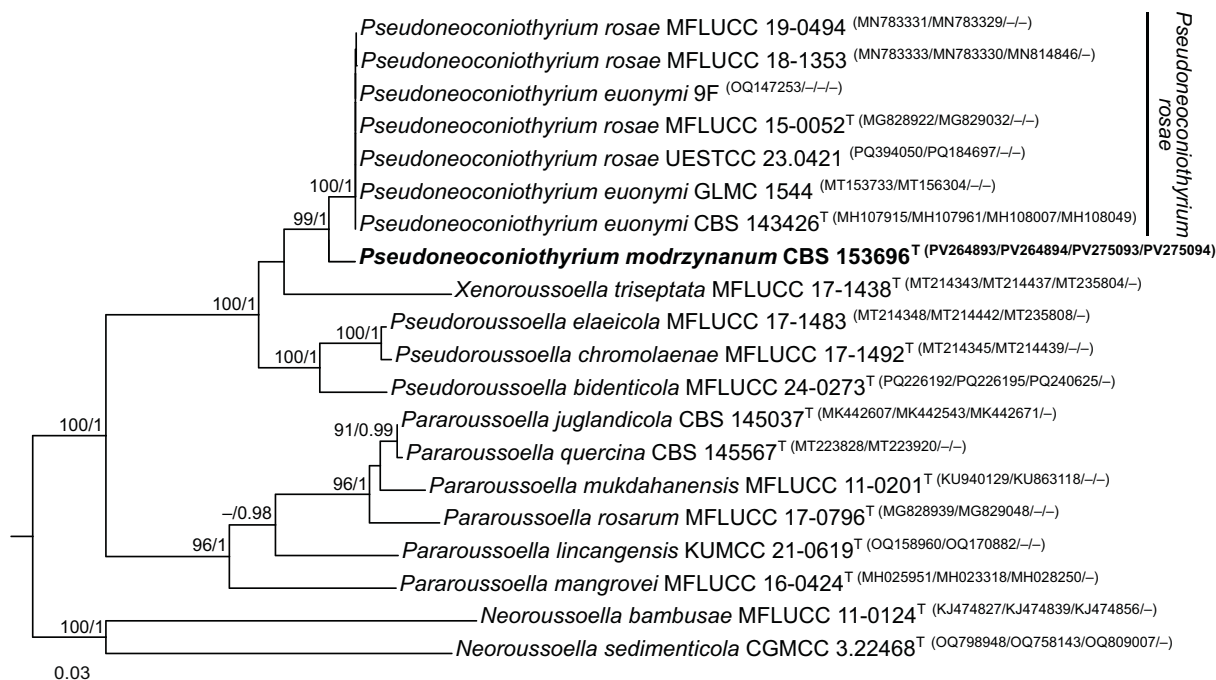
Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence are *Pseudoneoconiothyrium euonymi* [culture GLMC 1544, GenBank MT153733; Identities = 480/485 (99 %), no gaps], *Pseudoneoconiothyrium rosae* [culture UESTCC 23.0421, GenBank PQ394050; Identities = 513/519 (99 %), no gaps] and *Xenorousoella triseptata* [culture KNUF-20-NI009, GenBank LC719282; Identities = 522/546 (96 %), one gap (0 %)]. The closest hits using the **LSU** sequence are *Pseudoneoconiothyrium rosae* [culture MFLUCC 15-0052, GenBank NG\_059868; Identities = 861/866 (99 %), one gap (0 %)], *Pseudoneoconiothyrium euonymi* [culture CBS 143426, GenBank MH107961; Identities = 847/852 (99 %), one gap (0 %)] and *Xenorousoella triseptata* [culture XY24\_2, GenBank OR887099; Identities = 846/852 (99 %), one gap (0 %)]. The closest hits using the **rpb2** sequence are *Pseudoneoconiothyrium euonymi* [culture CBS 143426, GenBank MH108007; Identities = 712/738 (96 %), no gaps], *Pseudoneoconiothyrium rosae* [culture IT3796, GenBank MN814846; Identities = 764/795 (96 %), no gaps] and *Pseudorousoella elaeicola* [culture MFLUCC 17-1483, GenBank MT235808; Identities = 935/1034 (90 %), no gaps]. The closest hits using the **tub2** sequence are *Pseudoneoconiothyrium euonymi* [culture CBS 143426, GenBank MH108049; Identities = 340/352 (97 %), no gaps],

*Colour illustrations:* Resin on the bark of *Larix decidua* ssp. *polonica*, Poland. Conidiomata on MEA; wall of textura angularis; conidiogenous cells; conidia, median and surface view. Scale bars = 10 µm.



*Thelebolus microsporus* [culture CBS 109799, GenBank AY957544; Identities = 173/201 (86 %), seven gaps (3 %)] and *Thelebolus ellipsoideus* [culture CBS 113937, GenBank AY957542; Identities = 173/201 (86 %), seven gaps (3 %)].

Supplementary material: <https://doi.org/10.6084/m9.figshare.28589795.v1> (alignment).



Phylogenetic tree of selected members of the family Roussoellaceae obtained from a maximum likelihood analysis of the combined multi-locus alignment (2666 characters, including gaps: ITS/LSU/*rpb2/tub2*). The maximum likelihood analysis was performed using RAxML-NG v. 1.1.0 (Kozlov *et al.* 2019) and the Bayesian inference was performed using MrBayes v. 3.2.6 (Ronquist *et al.* 2012). The position of *Pseudoneoconiothyrium modrzyanum* is indicated in bold and marked by coloured block. Ex-type cultures are indicated with superscript T. Numbers above branches indicate maximum likelihood (MLB) support values  $\geq 70$  % and Bayesian posterior probabilities (BPP)  $\geq 0.9$ , respectively (MLB/BPP). *Neorousoella bambusae* and *Neorousoella sedimenticola* were used as an outgroup. The scale bar represents the expected number of changes per site.

*Puccinia clemensiorum*

*Puccinia scleriae-rugosae*





## *Puccinia clemensiorum* Y.P. Tan & R.G. Shivas, *sp. nov.*

**Etymology:** Named after Mary Strong Clemens (1873–1965) and her husband Joseph Clemens (1862–1936), who from about 1922 to 1936 worked together in south-east Asia as professional, full-time plant collectors.

**Classification:** Pucciniaceae, Pucciniales, Pucciniomycetes.

**Uredinia** on culms of *Eleocharis ochrostachys*, scattered on pale brown lesions, linear up to 5 mm long, bullate, reddish brown. **Urediniospores** subglobose to broadly ellipsoidal or obovoid, 21–28 × 17–22 µm, golden brown; wall 1.5–3(–4) µm wide, uneven, with two conspicuous superequatorial or scattered germ pores ca 2 µm diam., sparsely and minutely echinulate. **Telia** not seen.

**Typus:** **Australia**, Queensland, Cairns, rust on culms of *Eleocharis ochrostachys* (Cyperaceae), Oct. 2013, R.G. Shivas, T.S. Marney & T. Denchev (**holotype** specimen BRIP 59686a; ITS, LSU and CO3 sequence GenBank PQ416769, KX999881 and KX999922).

**Additional materials examined:** **Australia**, Queensland, Innisfail, uredinia on culms of *E. equisetina*, 30 Nov. 1941, R.F.N. Langdon (BRIP 3579a, IMI 58161); Queensland, Brisbane, uredinia on culms of *E. equisetina*, 16 Feb. 1943, R.F.N. Langdon (BRIP 3580a, IMI 58180); Queensland, Brisbane, uredinia on culms of *E. philippinensis*, 5 Apr. 1943, M.S. Clemens (BRIP 3581a, IMI 58171); Queensland, Mackay, uredinia on culms of *E. dulcis*, 18 Mar. 1996, G. Gunning (BRIP 23202a); Queensland, Tully, uredinia on culms of *E. dulcis*, L.I. Forsberg & M. Ottone (BRIP 27975a); Northern Territory, Adelaide River, uredinia on culms of *E. dulcis*, 3 Jun. 2016, R.S. James (BRIP 65231a).

**Notes:** *Puccinia clemensiorum* infects culms of some *Eleocharis* spp. native to Australia and Southeast Asia. Five rust species, *Puccinia eleocharidis*, *P. incomposita*, *P. liberta*, *Uredo eleocharidicola*, and *Uromyces eleocharidis* have been described on *Eleocharis* spp. in the American continents (Kern 1919); and one, *Uredo eleocharidis-variegatae*, from Africa (Gjærum *et al.* 2003). There are little publicly available sequence data for the rusts on *Eleocharis* spp., and no barcode sequences are available from type specimens for the names listed above. Léveillé & Bourret *et al.* (2021) included sequence data for specimens identified as *P. liberta* (on *E. albibracteata*; specimen voucher DAOM 172613, GenBank MW009485) and *Uromyces eleocharidis* (on *E. palustris*; specimen voucher DAOM 90854; GenBank MW009450)

from South and North America, respectively. The sequences provided by Léveillé & Bourret *et al.* (2021) differ from the those we obtained from *P. clemensiorum* [compared with *P. liberta* GenBank MW009485, Identities 210/224 (94 %), seven gaps (3 %); and *U. eleocharidis* GenBank MW009450, Identities 254/288 (88 %), 20 gaps (6 %)].

Based on a megablast search of the NCBI GenBank nucleotide database, the closest relevant hits with the **LSU** sequence of *P. clemensiorum* were *P. caricis-shepherdiae* [specimen voucher DAOM 181319; GenBank MW009426; Identities 1018/1034 (98 %), two gaps (0 %)], *P. cyperi* [specimen voucher BRIP 60997; GenBank KU296885; Identities 1022/1035 (99 %), one gap (0 %)], *P. emiliae* [specimen voucher BPI 910237; GenBank KY764120; Identities 1017/1035 (98 %), three gaps (0 %)], *P. granularis* [specimen voucher U443; GenBank OQ215047; Identities 1016/1034 (98 %)], *P. merrilliana* [specimen voucher BRIP 56913; GenBank KX999885; Identities 1021/1035 (99 %), one gap (0 %)], *P. thunbergiae* [specimen voucher U260; GenBank OQ215074; Identities 1016/1034 (98 %)], *P. xanthii* [specimen voucher BRIP 56946; GenBank KX999896; Identities 1017/1037 (98 %), three gaps (0 %)], and *Uromyces silphii* [specimen voucher DAOM 182148; GenBank MW009483; Identities 1016/1035 (98 %), four gaps (0 %)]. The closest relevant hits with the **ITS** region of *P. clemensiorum* were *P. canaliculata* [strain TA436; GenBank OL437017; Identities 503/530 (95 %), 17 gaps (3 %)], *P. doidgeae* [strain TA430; GenBank OL437018; Identities 502/528 (95 %), 11 gaps (2 %)], *P. obscura* [specimen voucher KR14322; Identities 584/641 (91 %), 21 gaps (3 %)], *P. tenuis* [specimen voucher DAOM 2618; GenBank MW009562; Identities 516/545 (95 %), 10 gaps (1 %)]. The closest relevant hits with the **CO3** sequence of *P. clemensiorum* were *Endophyllum mpenjatiense* [specimen voucher U1708; GenBank OR789138; Identities 591/591 (100 %)], *P. canaliculata* [specimen voucher BRIP 57789; GenBank MW139656; Identities 556/556 (100 %)], *P. caricina* [specimen voucher BRIP 57951; GenBank KX999912; Identities 502/503 (99 %)], *P. dimidipes* [holotype specimen ZT Myc58917; GenBank MH144380; Identities 512/548 (93 %)], *P. lagenophorae* [specimen voucher BRIP 57563; GenBank KT199417; Identities 552/554 (99 %)], *P. muehlenbeckiae* [specimen voucher BRIP 57718; GenBank KX999925; Identities 605/607 (99 %)], *P. scirpi* [specimen voucher BRIP 61027; GenBank KX999929; Identities 606/609 (99 %)], and *P. ursiniae* [specimen voucher BRIP 57993; GenBank KT199421; Identities 509/513 (99 %)].

**Colour illustrations:** Cape York, Queensland, Australia. Uredinia and urediniospores of *Puccinia clemensiorum* on culms of *Eleocharis ochrostachys* (left), *Puccinia scleriae-rugosae* on leaves of *Scleria rugosa* (right), and urediniospores (equatorial view and surface view). Scale bars: *S. rugosa* (right) = 0.5 mm; *E. ochrostachys* (left) = 1 mm; (urediniospores) = 10 µm.

## *Puccinia scleriae-rugosae* Y.P. Tan & R.G. Shivas, *sp. nov.*

*Etymology*: Named after the host *Scleria rugosa*.

*Classification*: Pucciniaceae, Pucciniales, Pucciniomycetes.

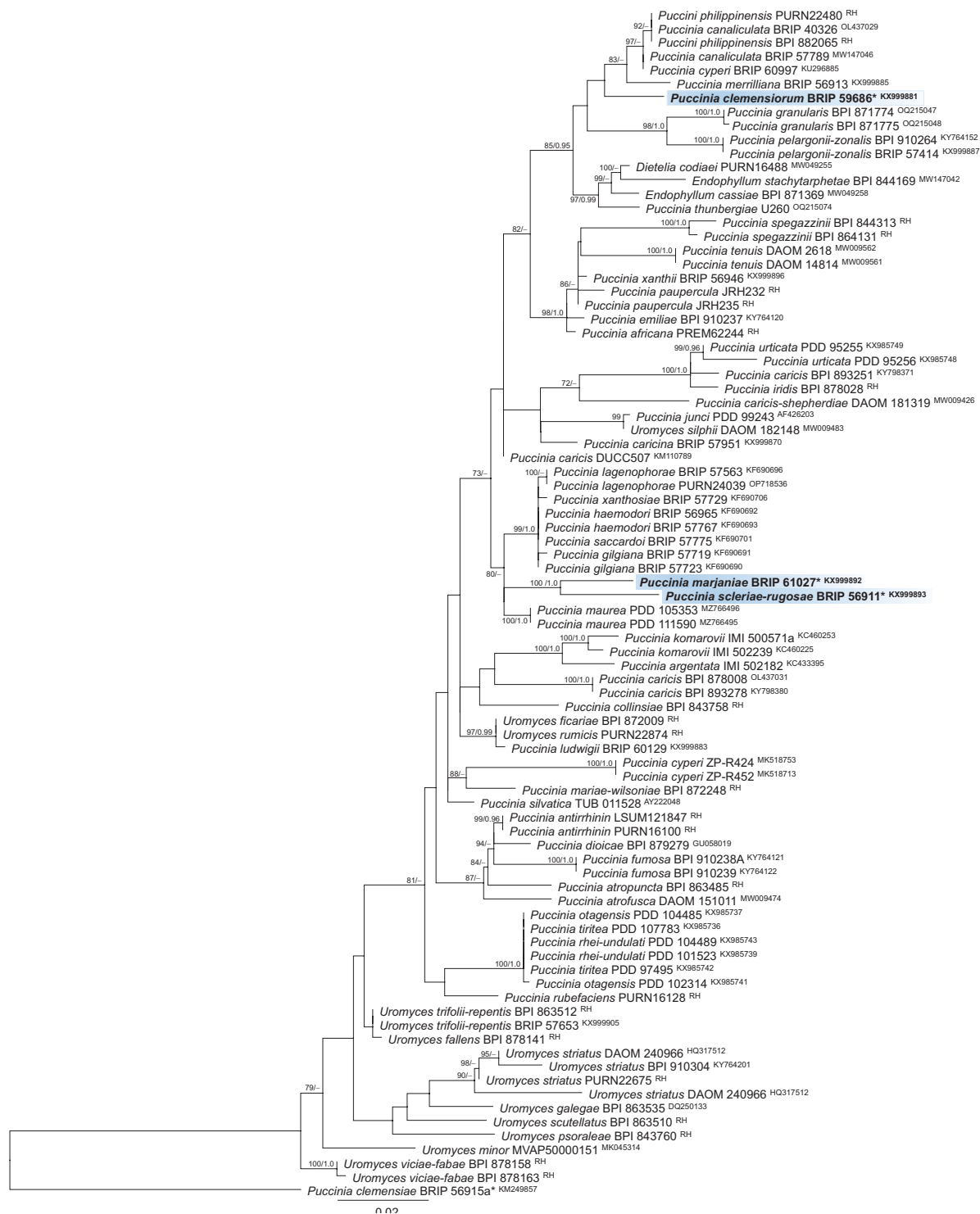
*Uredinia* on leaves of *Scleria rugosa*, scattered on reddish brown lesions, up to 1 mm long, bullate, reddish brown. *Urediniospores* subglobose to broadly ellipsoidal, 21–20 × 18–28 µm, reddish to golden brown; wall 1.5–3 µm wide, with (2–)3 equatorial or scattered germ pores ca 2 µm diam., sparsely and minutely echinulate. *Telia* not seen.

*Typus*: **Australia**, Western Australia, Lake Argyle, rust on leaves of *Scleria rugosa* (Cyperaceae), 17 Apr. 2012, V. Andjic, M. Butt, K. Ireland, C. Doungsa-ard, A.R. McTaggart, R. Berndt, V. Faust-Berndt, M.D.E. Shivas & R.G. Shivas (**holotype** specimen BRIP 56911a; LSU sequence GenBank KX999893).

*Additional material examined*: **Australia**, Northern Territory, Hayes Creek, rust on leaves of *Scleria rugosa* (Cyperaceae), 21 Apr. 2012, V. Andjic, M. Butt, K. Ireland, C. Doungsa-ard, A.R. McTaggart, R. Berndt, V. Faust-Berndt, M.D.E. Shivas & R.G. Shivas (specimen BRIP 57593a).

*Notes*: *Puccinia scleriae-rugosae* infects leaves of *Scleria rugosa* in Australia. *Scleria rugosa* is widely distributed across India, Australasia, and the Pacific Islands (Zich *et al.* 2020). *Puccinia scleriae-rugosae* has larger urediniospores than given in the type descriptions for three species on *Scleria* sp. in the Americas, namely *P. scleriae* [20–27 × 16–20 µm, as *Rostrupia scleriae* in Prantl (1892)], *Uromyces scleriae* [20–28 × 18–22 µm in Hennings (1899)] and *P. scleriicola* [19–26 × 15–22 µm in Arthur (1915)]. Lèveillé-Bourret *et al.* (2021) included sequence data for two specimens of rust identified as *P. scleriae*, one from South America (on *S. latifolia*; specimen voucher DAOM 78611; GenBank MW009525) and the other from West Africa (on *S. naumanniana*; specimen voucher DAOM 19401; GenBank MW009524) as well as one specimen of rust identified as *Uromyces scleriae* from South America (on *S. gaertheri*; specimen voucher DAOM 79554; GenBank MW009535).

Based on a megablast search of the NCBI GenBank nucleotide database, the closest relevant hits with the **LSU** sequence of *P. scleriae-rugosae* were *P. caricis-ribicola* [holotype specimen HMJAU8873; GenBank MW414415; Identities 584/602 (97 %), five gaps (0 %)], *P. maurea* [specimen voucher PDD 111590 GenBank MZ766495; Identities 950/972 (98 %), five gaps (0 %), *P. maureanui* [holotype specimen PDD 102954; GenBank MZ766494; Identities 947/969 (98 %), four gaps (0 %)], *P. scirpi* [specimen voucher BRIP 61027; GenBank KX999892; Identities 953/970 (98 %), two gaps (0 %)], *P. thunbergiae* [specimen voucher U260; Identities 947/969 (98 %); two gaps (0 %)], *Uromyces silphii* [specimen voucher DAOM 182148; GenBank MW009483; Identities 948/969 (98 %), four gaps (0 %)].



Phylogenetic tree of selected *Puccinia* species based on maximum likelihood (ML) analysis of the LSU region. The ML analysis was performed with the IQ-TREE web server (Trifinopoulos *et al.* 2016) based on the GTR substitution model with gamma-distribution rate variation (1 000 bootstrap replicates). Bootstrap support values greater than 70 % are shown at the nodes. *Puccinia clemensiae* (type specimen BRIP 56915a) was used as the outgroup. GenBank accession numbers are indicated (superscript LSU). Sequences obtained from Rust HUBB are indicated (superscript RH; Kaishian *et al.* 2024). Novel taxa are shown in coloured bold. Type specimens are marked by an asterisk (\*). The alignment and phylogeny are publicly available in Zenodo (doi: 10.5281/zenodo.14257461).

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# *Puccinia geethae* Y.P. Tan, Bishop-Hurley, Dhileepan & R.G. Shivas, *sp. nov.*

*Etymology:* Named after Geetha Dhileepan, a medical practitioner whose interests include women's and children's health.

*Classification:* Pucciniaceae, Pucciniales, Pucciniomycetes.

*Uredinia* on leaves of *Cyperus brevifolius*, amphigenous on necrotic lesions up to 2 mm long, scattered, erumpent, pulverulent, circular to linear, reddish brown. *Urediniospores* subglobose to broadly ellipsoidal or obovoid, 18–27 × 14–21 µm, pale to medium reddish brown; wall 1–2.5(–3) µm wide, with (1–)2(–3) germ pores mostly equatorial to superequatorial or scattered, sparsely and finely echinulate. *Telia* amphigenous, black, linear, up to 1 mm long. *Teliospores* clavate, straight or apical cell curved, 32–43 × 12–15 µm, (1–)2-celled, pale yellowish brown, medially septate, slightly constricted at septum, apically rounded or conically rounded and slightly curved; wall 2–5 µm thick at apex, 1–2 µm thick at sides; pedicels ca 10 × 6 µm, pale brown, not persistent.

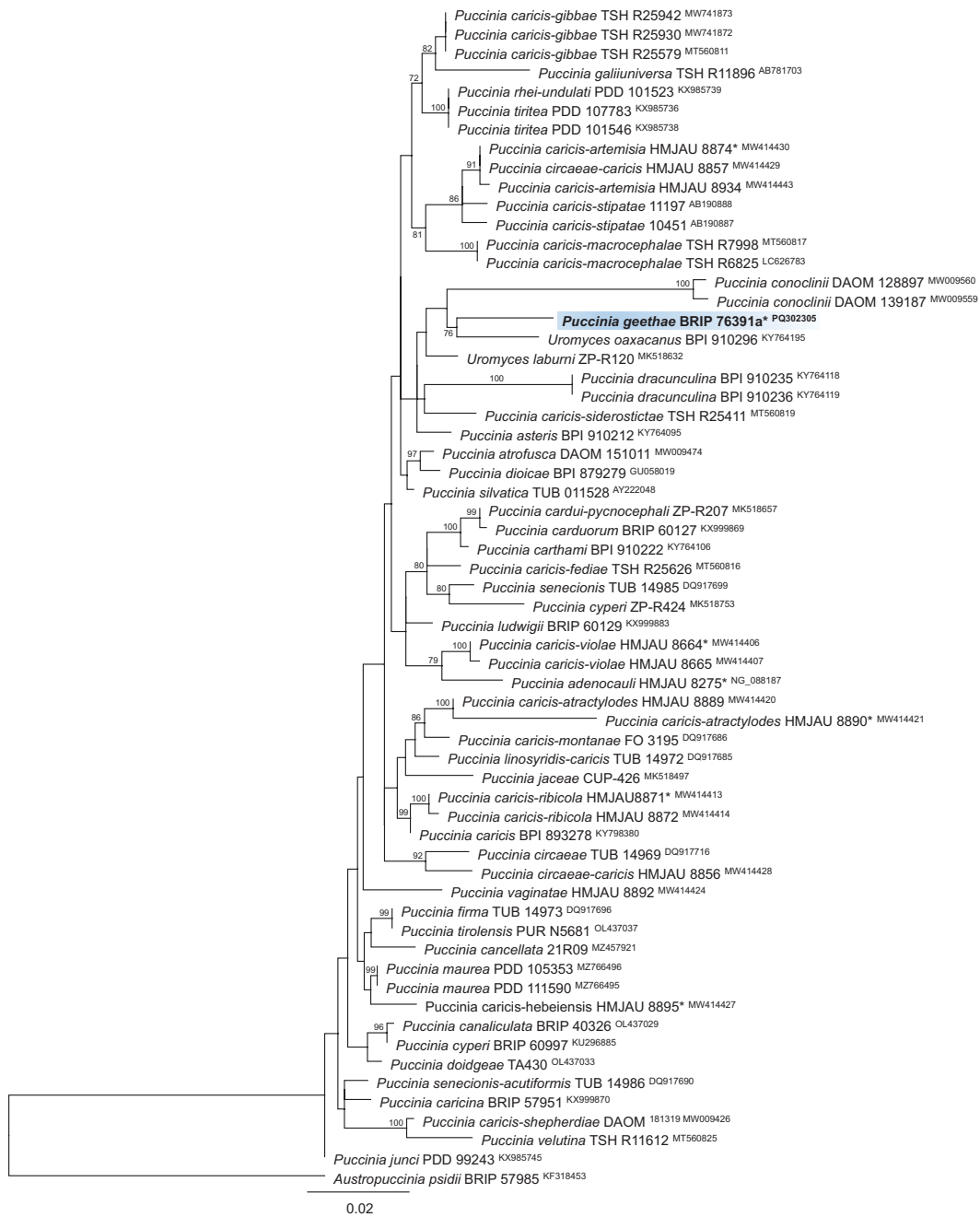
*Typus:* **Australia**, Queensland, Topaz, leaf rust on *Cyperus brevifolius* (Cyperaceae), 19 Feb. 2024, R.G. Shivas, M.D.E. Shivas, B. Shi & K. Dhileepan (**holotype** specimen BRIP 76391a; LSU sequence GenBank PQ302305).

*Additional materials examined:* **Australia**, Queensland, Gordonvale, leaf rust on *C. brevifolius*, 1 Sep. 2020, R.G. Shivas, M.D.E. Shivas & K. Dhileepan (BRIP 72802a); Wongabel, leaf rust on *C. brevifolius*, 19 Feb. 2024, R.G. Shivas, M.D.E. Shivas, B. Shi & K. Dhileepan (BRIP 76393a). **China**, Hong Kong, Sai Kung, leaf rust on *C. brevifolius*, 30 Aug. 1999, R.G. Shivas, C.S. Tong (BRIP 64150a). **Nigeria**, Ogun State, Ijebu-Imushin, leaf rust on *C. brevifolius*, 13 Jun. 2019, K. Dhileepan, P.R.O. Edogbanya, E.C. Chukwuma, M.D.E. Shivas & R.G. Shivas (BRIP 71080a).

*Notes:* *Puccinia geethae* infects leaves of *Cyperus brevifolius*, which is native to tropical Asia and the warm temperate regions of China and Japan (Anon. 2016). In Australia, *C. brevifolius* has become widely naturalised in the eastern and northern coastal regions. This rust was collected and identified as part of a biological control project to determine the identity of rust fungi on *Cyperus* spp. in the immediate vicinity of *C. aromaticus* infected with *Puccinia kyllingae-erectae* (Dhileepan *et al.* 2021, Tan & Shivas 2024). The rust fungi on *Cyperus* spp. and many other sedges need taxonomic revision by molecular phylogenetic methods.

Based on a megablast search of the NCBI GenBank nucleotide database, the closest relevant hits with the LSU region of *P. geethae* were *P. caricis* [specimen voucher BPI 893278; GenBank KY798380; Identities 911/936 (97 %), three gaps], *P. atrofusca* [specimen voucher DAOM 151011; GenBank MW009474; Identities 910/935 (97 %), four gaps], *P. ludwigii* [specimen voucher BRIP 60129; GenBank KX999883; Identities 895/920 (97 %), four gaps], *P. carthami* [specimen voucher BPI 910222; GenBank KY764106; Identities 908/936 (97 %), five gaps;], and *P. asteris* [specimen voucher BPI 910212; GenBank KY764095; Identities 908/936 (97 %), eight gaps].

*Supplementary material:* <https://doi.org/10.5281/zenodo.13739355> (alignment and tree).

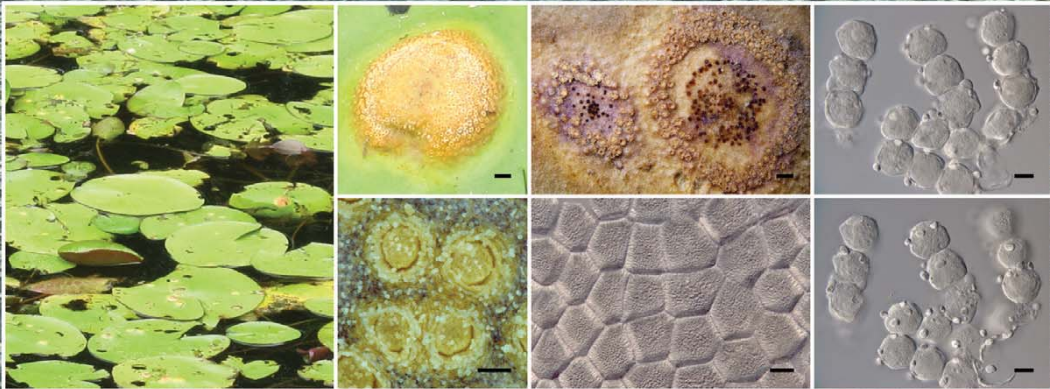


Phylogenetic tree of selected *Puccinia* species based on maximum likelihood (ML) analysis of the LSU region. The ML analysis was performed on the IQ-TREE web server (1000 bootstrap replicates; Trifinopoulos *et al.* 2016) and Bayesian analysis was performed on the Geneious Prime 2024 platform with MrBayes v. 3.2.6 (Huselsenbeck & Ronquist 2001), both based on the GTR substitution model with gamma-distribution rate variation. Bootstrap support (bs) values > 70 % and Bayesian posterior probabilities (pp) > 0.95 are given at the nodes (bs/pp). *Austropuccinia psidii* (specimen BRIP 57985) was used as the outgroup. GenBank accession numbers are indicated (superscript LSU). Novel taxon is shown in **bold**. Type specimens are marked by an asterisk (\*).

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*Puccinia marjaniae*



***Puccinia marjaniae* R.G. Shivas, *sp. nov.***

*Etymology*: Named after Marjan Doris Ellen Shivas (née Tellegen), who collected the type specimen.

*Classification*: *Pucciniaceae*, *Pucciniales*, *Pucciniomycetes*.

On scattered bullate lesions on the upper surface of leaves of *Nymphoides indica*, mostly near the centre of circular lesions 4–15 mm diam., with chlorotic haloes up to 1–2 mm wide. *Spermogonia* in the central part of lesions, in groups of up to 100 in larger lesions, globose, 150–250 µm diam., reddish brown. *Spermatia* subglobose to cylindrical, hyaline, 2.5–5.5 µm diam. *Aecia* on upper leaf surface, surrounding spermogonia, scattered or in concentric rings, cupulate, 150–250 µm diam., yellow; peridial cells irregularly polyhedral with (4–)5(–6) curved or straight sides and rounded corners in surface view, 20–35 × 10–24 µm; wall 2–4 µm thick, hyaline, outer surface densely and coarsely verrucose, inner surface densely and finely verruculose. *Aeciospores* catenulate, subglobose to irregular with curved sides and rounded corners, 15–22 µm, subhyaline; wall 1–1.5 µm wide, finely verruculose, with 2–5 inconspicuous scattered germ pores.

*Typus*: **Australia**, Queensland, Maleny, rust on leaves of *Nymphoides indica* (*Menyanthaceae*), 8 May 2014, *M.D.E. Shivas* (**holotype** specimen BRIP 61027a; LSU and CO3 sequences GenBank KX999892 and KX999929).

*Notes*: *Puccinia marjaniae* infects leaves of *Nymphoides indica*, an aquatic species native to tropical regions in Africa, Asia, Australia and extending to the Pacific Islands, but not native to South and Central America (Thayer & Pfungsten 2024). Globally, there are 52 accepted species

of *Nymphoides* (Govaerts *et al.* 2021). The aecidial rusts (*Aecidium limnanthemii*, *A. nymphoidis*, *Dicaeoma scirpi*) reported on *Nymphoides* spp. (Saccardo 1888, Arthur & Kern 1920, Soares *et al.* 2006) have often been referred to *P. scirpi* based on morphology (e.g. see tabulation in Lee *et al.* 2024) although this identification is not supported by sequence data. Lee *et al.* (2024) recognised that there was sequence variation between an aecidial rust they identified as *Puccinia* sp. on *N. peltata* in Korea and the sequences obtained from the specimen that we have proposed as the type of *P. marjaniae* on *N. indica* (McTaggart & Shivas in Marin-Felix *et al.* 2017). Taxonomic resolution of the cryptic aecial rusts on *Nymphoides* will depend on phylogenetic analysis of sequence data.

Based on a megablast search of the NCBI GenBank core nucleotide database, the closest relevant hits with the LSU sequence of *P. marjaniae* were *P. cyperi* [specimen voucher BRIP 60997; GenBank KU296885; Identities 1338/1380 (97 %), seven gaps (0 %)], *P. junci* [specimen voucher PDD 99243; GenBank KX985745; Identities 1343/1389 (97 %), 16 gaps (1 %)], *P. ocimi* [specimen voucher BPI 910262; GenBank KY764149; Identities 1354/1403 (97 %), 12 gaps (0 %)], *P. otagensis* [specimen voucher PDD 104485; GenBank KX985737; Identities 1325/1375 (96 %), 17 gaps (1 %)], *P. rhei-undulati* [specimen voucher PDD 101523; GenBank KX985739; Identities 1320/1370 (96 %), 17 gaps (1 %)], *Uromyces silphii* [specimen voucher DAOM 182148; GenBank MW009483; Identities 1320/1364 (97 %); 15 gaps (1 %)].

For phylogenetic tree, see *Puccinia scleriae-rugosae* (FP 1856).

*Colour illustrations*: Fruit Bat Falls, Queensland, Australia. *Nymphoides indica* infected by *Puccinia marjaniae* (left), aecium, aecia, aecia surrounding spermatia, aecial wall, aeciospores (equatorial view and surface view). Scale bars: aecia = 1 mm and 100 µm; aecia surrounding spermatia = 1 mm; all others = 10 µm.

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*Purimyces endophyticus*



***Purimyces endophyticus* D.O. Ramos & O.L. Pereira, *sp. nov.***

*Etymology:* Name refers to the endophytic lifestyle of the fungus.

*Classification:* *Hyphodiscaceae*, *Helotiales*, *Leotiomyces*.

*Mycelium* septate, branched, smooth-walled, sometimes verrucose, hyaline to pale brown, forming mycelial strands covered by a slime exudate with spiral hyphae pattern, 1.5–3 µm diam. hyphae, produce swollen hyphal cells that resemble chlamydospore-like structures. *Colonies* sterile.

*Culture characteristics:* Colonies on potato dextrose agar (PDA) circular, with entire margin, white aerial mycelium moderate with hyphal tufts cover in a slime exudate, low convex, surface cinnamon to rosy buff colour (61) at the centre and buff (45) at the margin of the colony, buff (45) colour on reverse (Rayner 1970), reaching 67 mm diam. after 4 wk at 25 °C in the dark. Colonies on malt extract agar (MEA) circular to irregular, with lobate edge, flat, white aerial mycelium moderate at the centre cover in a slime exudate and sparse to absent at the margins of the colony, buff (45) colour surface, reverse buff (45), reaching 64 mm diam. after 4 wk at 25 °C in the dark. Colonies on Czapek yeast agar (CYA) circular, with entire margin, aerial mycelium moderate, flat, smoke grey colour (105) in the centre to white on the periphery surface, reverse rosy buff (61), reaching 48 mm diam. after 4 wk at 25 °C in the dark.

*Habit, habitat and distribution:* Root endophyte of *Cattleya locatellii*. Known so far from Brazil.

*Typus:* **Brazil**, Minas Gerais, Araponga city, isolated as root endophyte of *Cattleya locatellii* (*Orchidaceae*), 21 Nov. 2021, O.L. Pereira (**holotype** VIC 49583, dried culture, ex-type living culture COAD 3876; ITS and LSU sequences GenBank PQ323564 and PQ323566).

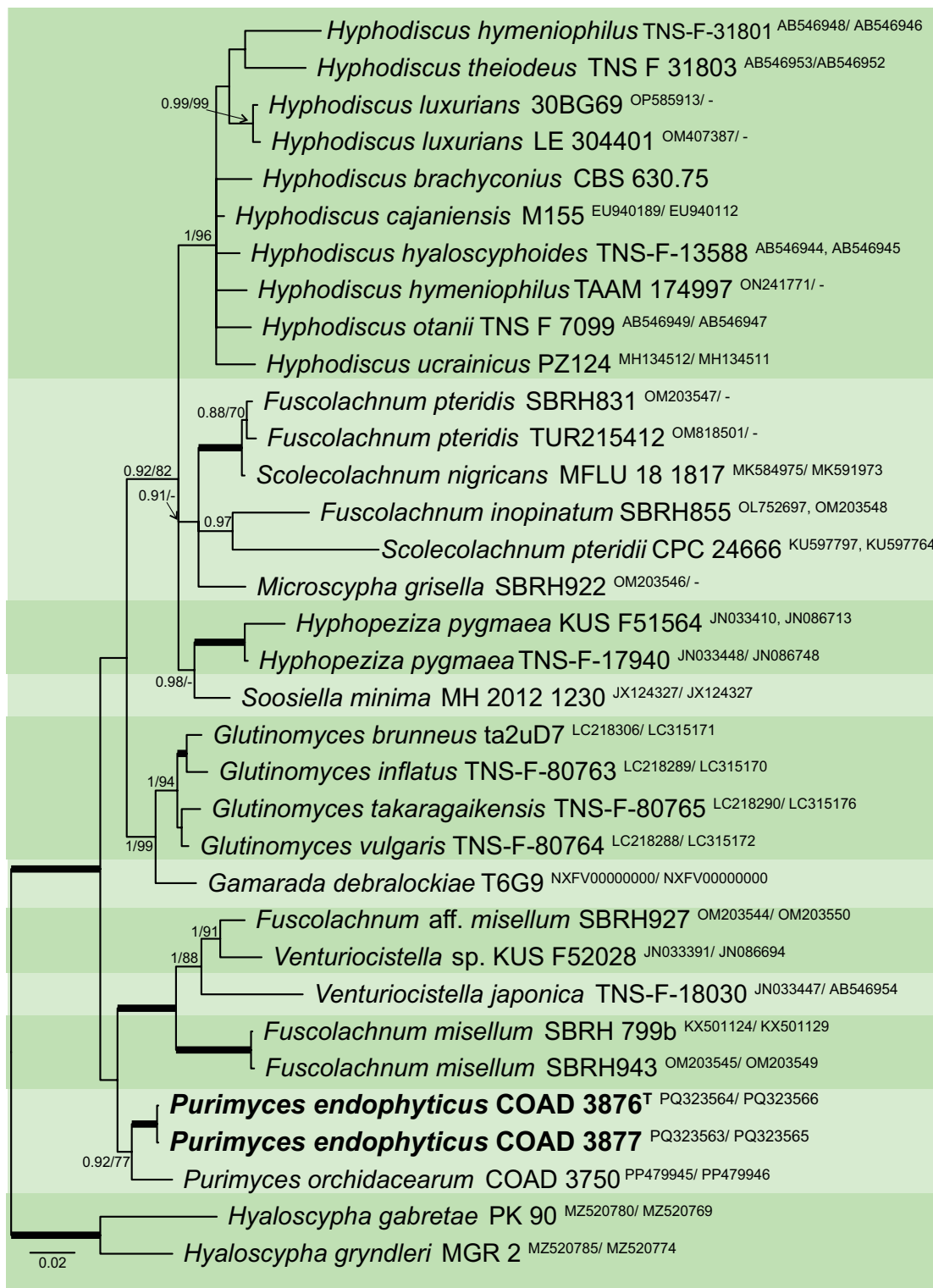
*Additional material examined:* **Brazil**, Minas Gerais, Araponga city, isolated as root endophyte of *Cattleya locatellii* (*Orchidaceae*), 21 Nov. 2021, O.L. Pereira (living culture COAD 3877; ITS and LSU sequences GenBank PQ323563 and PQ323565).

*Notes:* *Purimyces endophyticus* is phylogenetically related to *Purimyces orchidacearum* (Crous *et al.* 2024a), forming a distinct clade from the rest of the family. Morphologically, *P. endophyticus* resembles *P. orchidacearum* due to the brown colour of colonies, becoming darker with the age. The species also differs from *P. orchidacearum* by producing swelled hyphae similar to chlamydospore-like structures, coiled hyphae and melanized mycelium strands. The genus *Purimyces* comprises root endophytic species isolated from *Orchidaceae* that lacks any reproductive structures, producing sterile colonies (Crous *et al.* 2024a).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to the sequence of an "Uncultured *Helotiales*" [clone 50.C4.1, GenBank: JX898957.1, Identities = 520/522 (99 %), no gaps], "Uncultured *Leotiomyces*" [clone NMF-OTU-60, GenBank: MG707532.1, Identities = 517/522 (99 %), no gaps], "Fungal sp." [R5, GenBank: AY699668.1, Identities = 511/515 (99 %), no gaps], "Uncultured *Helotiales*" [clone FM090.2, GenBank: JF691173.1, Identities = 510/515 (99 %), no gaps]. Closest hits using the **LSU** sequence are "Uncultured fungus" [isolate H38\_L3703, GenBank: FN298719.1; Identities = 838/842 (99 %), no gaps], "Uncultured fungus" [isolate H038y\_L3258, GenBank: FN298722.1; Identities = 838/842 (99 %), no gaps], "Uncultured fungus" [isolate H038x\_L3637, GenBank: FN298721.1, Identities = 838/842 (99 %), no gaps], "Fungal sp." [strain CBS 255.35, GenBank: MH867184.1, Identities = 840/849 (99 %), one gap (0 %)], and *Cistella spicicola* [strain CBS 731.97, GenBank: GU727553.1, Identities = 839/848 (99 %), no gaps].

*Supplementary material:* doi: 10.6084/m9.figshare.28473203 (alignment and tree).

*Colour illustrations:* Flower of *Cattleya locatellii* (*Orchidaceae*). From top to bottom, colony on PDA after 4 wk at 25 °C; colony on MEA after 4 wk at 25 °C; colony on CYA after 4 wk at 25 °C; from bottom left to right, aggregated hyphae growing on PDA; mycelial strands; chlamydospore-like swellings. Scale bars = 20 µm.



Phylogenetic tree based on concatenated dataset of ITS and LSU sequences conducted using RAxML-HPC2 v. 8.1.11 and MrBayes v. 3.2.7a on XSEDE, both in the CIPRES science gateway (Stamatakis 2014; Ronquist *et al.* 2012). Only bootstrap support values (BS) and Bayesian posterior probability (pp) values > 75 and 0.80 are indicated at the nodes, respectively. The branches that presented full statistical support (BS = 100 % and pp = 1) are thickened. The new species is indicated in bold face. *Hyaloscypha gabretae* PK-90 and *Hyaloscypha gryndleri* MGR-2 were used as outgroup.

*Ramariopsis coronata*





# *Ramariopsis coronata* De la Peña-Lastra, A. Mateos & Olariaga, *sp. nov.*

*Etymology:* The epithet refers to the crown-shaped apex.

*Classification:* *Clavariaceae*, *Agaricales*, *Agaricomycetes*.

*Basidiomata* clavarioid, reminiscent of craterelloid basidiomata, 4–10 mm, width 1 mm at the base and up to 2.5 mm at the apex, obconical, and trumpet-like, with the apex truncate, concave, and a margin that appears crowned by 2–5 short branches, dichotomously branched, sometimes absent in young basidiomata. Branch apices generally rounded, some pointed, with V-shaped angles between branches and U-shaped ones at the bifurcations of each branch. *Stipe* 1–1.5 mm broad, often curved, gradually widening upwards, terete, with the lower sterile part occupying one third to half of the height, smooth, with the upper fertile part pruinose, with white basal tomentum. Colour white, translucent in high humidity conditions, more evidently on the stipe, turning pale ochre with age or upon drying. *Context* white, fragile, hygrophanous. *Smell* and *odour* indistinct. *Basidiospores* (2.5–)2.7–3.5–4.2(–4.5) × (2.1–)2.3–3.1–4.1(–4.5) μm; Q = 1–1.1–1.3; n = 50, Ve = 20 μm<sup>3</sup>, globose to subglobose, sometimes broadly ellipsoid, with a prominent apiculus 0.5–1 long, with a greenish, central large guttule, surface ornamented with scattered warts, small and irregular, difficult to observe in a light microscope, hyaline, inamyloid, congophilous. *Basidia* 20–23.8–30.8 × 4–5.6–7.7 μm, 4-spored, clavate, with sterigmata up to 6 μm long, septate and basally clamped. *Hymenium* and *subhymenium* with abundant polymorphous crystallized deposits among hyphae, sometimes bipyramidal or rhomboid. *Hyphal system* monomitic, formed by parallel arranged to interwoven hyphae. *Paracystidia* present in the hymenium, (18.5–)19.5–29.9(–32.1) × (3.1–)3.14–7.1(–7.3) μm, narrowly clavate to cylindrical, frequently septate, immersed in the hymenium. *Context* hyphae short-celled. *Basal tomentum* white, composed of sparse hyphae, cylindrical, slightly thick-walled, hyaline, clamped, 1.7–2.4 μm wide. *Clamp connections* present in all tissues.

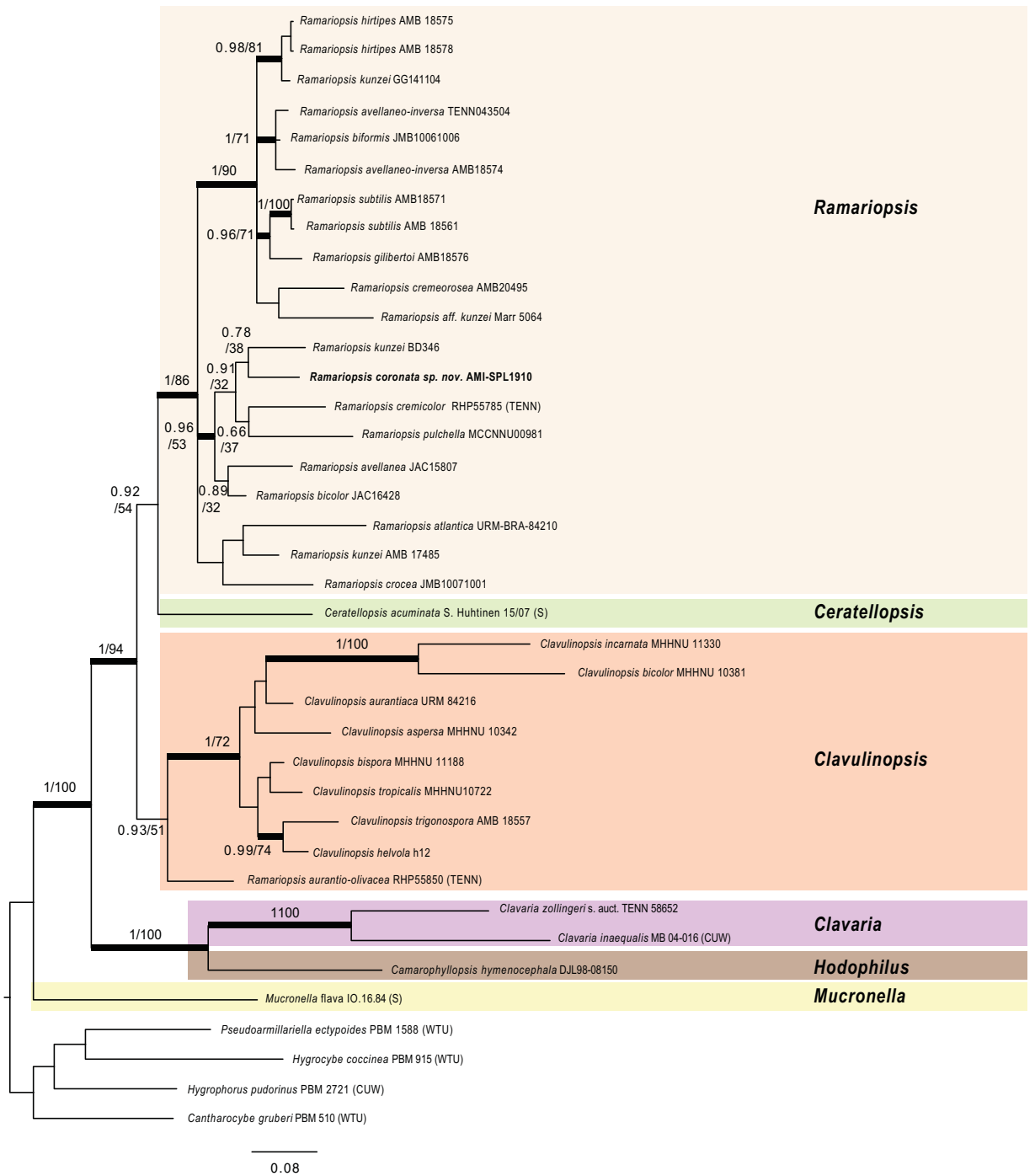
*Distribution:* Currently known only from the type location in northwestern Spain.

*Typus:* **Spain**, Galicia, Pontevedra, Parque Nacional de las Islas Atlánticas de Galicia, Illa de Cortegada, N42°36'56.3", W8°47'06.9", 1 m a.s.l., gregarious in laurel forest, 6 Dec. 2023, A. Mateos & S. De la Peña-Lastra (**holotype** AMI-SPL1910; ITS, LSU, SSU and *RPB2* sequences GenBank PV211423, PV211427, PV211428 and PV231442).

*Notes:* *Ramariopsis coronata* is characterized by its unique, small-sized clavarioid basidiomata reminiscent of *Clavicornia* or *Craterellus* in basidiomatal configuration, which are simple and furnished with a crowned margin. Microscopically, the globose to subglobose ornamented spores and the presence of crystallized polymorphic deposits are characteristic. *Ramariopsis coronata* nests within the monophyletic *Ramariopsis* clade in our multigenic analyses. The monomitic hyphal system with clamp connections on hyphae and subglobose ornamented basidiospores, present in *R. coronata*, are typical of *Ramariopsis* (Olariaga 2009, Franchi & Marchetti 2021). Species of *Clavicornia* differ in the smooth spores and lack of clamps on the context hyphae (Requejo *et al.* 2024). Within *Ramariopsis*, *R. coronata* nests in a well-supported clade containing sequences assigned to – some probably misidentified – *R. avellanea*, *R. bicolor*, *R. cremicolor*, *R. kunzei*, and *R. pulchella*, but all of them differ in having more robust and branched basidiomata. No species with the basidiomatal configuration of *R. coronata* could be traced in *Ramariopsis* after consulting monographic treatments (Olariaga 2009, Franchi & Marchetti 2021). Blast results based on the ITS region of *R. coronata* retrieve as closer hits several sequences assigned to *Ramariopsis*, all with a similarity below 90 %. Therefore, we conclude that *R. coronata* merits recognition at the species level and we hence propose it as new.

*Supplementary material:* doi: 10.6084/m9.figshare.28870313 (Alignment); 10.6084/m9.figshare.28870436 (Table).

*Colour illustrations:* Spain, Pontevedra, P. Nacional Illas Atlánticas de Galicia, Illa de Cortegada, forest of *Laurus nobilis*, where the holotype of *Ramariopsis coronata* was collected. Basidiospores; hymenophore, with basidia, basidioles, and probasidia. Scale bars = 10 μm.

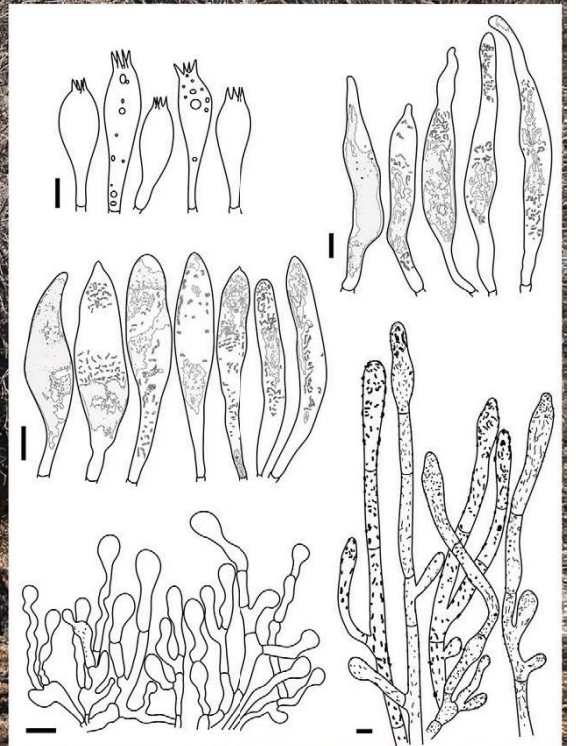
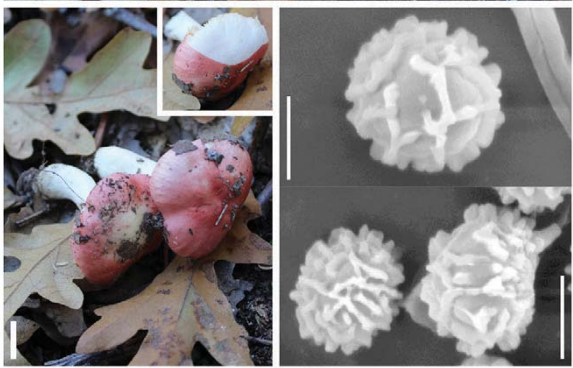


Best tree of the Maximum Likelihood analysis of selected sequences of *Clavariales* in IQ-TREE 1.16.12 (Nguyen *et al.* 2015) from a concatenated dataset of the 5.8S-28S-18S-*RPB1*-*RPB2*-*TEF1*-regions. Maximum Likelihood standard bootstrap support values (ML-Boot)/Bayesian posterior probabilities (PP) are shown on branches, ordered as ML-Boot/PP. Thickened branches received support in both analyses (ML-Boot ≥ 70 % and/or PP ≥ 0.95). Values are provided for nodes supported at least in one analysis. Genera are indicated by coloured blocks.

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*Russula anatolica*



***Russula anatolica* Çolak & Kaygusuz, *sp. nov.***

*Etymology:* From *anatolica* (Latin), referring to Anatolia, the Turkish Peninsula where this species was collected.

*Classification:* Russulaceae, Russulales, Agaricomycetes.

*Basidiomata* small to medium-sized. *Pileus* 25–35 mm diam., initially hemispherical, then becoming plano-convex to nearly applanate, sometimes slightly depressed at the centre when mature; margin even, obtuse, not striate when young, becoming slightly striate up to 10 mm when old; surface dry, smooth, matt, with the cuticle peeling readily to half of the radius, revealing a chalky white beneath the cuticle; pink rose to pastel pink or pale violet red, becoming darker towards the pileus centre, and sometimes discolouring to pinkish white, with the margin being pale pink. *Lamellae* 3–6 mm wide, free, thin, moderately crowded to crowded, with scattered lamellulae, fragile, light yellow ochre to light orange, with entire, concolourous edges that remain unchanged when cut or bruised. *Stipe* 40–50 × 8–15 mm, central, cylindrical, tapering towards the apex, entirely longitudinally striate, curved, dry, smooth, with a white surface; stipe context chalky white, hollow, unchanging when cut or bruised. *Context* white to cream, fragile, unchanging when damaged, 1–2 mm thick at half of the pileus diameter. *Macrochemical reactions* pale pink with 10 % iron sulphate (FeSO<sub>4</sub>), yellow with 10 % potassium hydroxide (KOH), and almost negative with sulfo-vanillin (SV). *Taste* mild. *Odour* rose-like, especially when mature. *Spore print* deep yellow. *Basidiospores* (6.5–)7.1–8.9(–9.5) × (5.8–)6.1–7.8(–9.0) μm (n = 125 of 3 coll.), L<sup>m</sup> × W<sup>m</sup> = 8.0 × 6.9 μm, Q = (1.0–)1.1–1.2(–1.3), Q<sup>m</sup> = 1.2, subglobose to broadly ellipsoid, with ornamentation consisting of relatively small, moderately distant, somewhat dense to dense, amyloid warts up to 1.3 μm high, composed mostly of minute warts and ridges and forming an incomplete reticulum, occasionally to frequently fused in pairs, short-branched chains, suprahilar spot distinct, amyloid. *Basidia* 35–47 × 12.5–15.0 μm, mostly 4-spored, clavate, hyaline, thin-walled; *basidiola* 5–9 μm wide, clavate, thin-walled. *Hymenial cystidia on lamellae sides* dispersed to moderately numerous, approximately 400–600/mm<sup>2</sup>, 75–115 × 8.5–12 μm, narrowly fusiform to fusiform, usually narrowed at both the base and apex, often with a mucronate or obtuse apex, thin-walled, with heteromorphous or granulose contents mainly in the middle part, turning greyish in SV. *Hymenial*

*cystidia near the lamellae edges* moderately numerous, 55–65 × 7.5–15 μm, clavate, narrowly cylindrical, or lanceolate, with an apex that is mainly obtuse to acute, sometimes mucronate, thin-walled, heteromorphous with granulose contents, turning greyish in SV. *Pileipellis* composed of two layers; *epipellis* an irregular trichoderm, approximately 50–110 μm deep, made up of cylindrical hyphae 4–6 μm wide, usually branched, hyaline; *terminal cells* mainly narrowly clavate or clavate, often inflated at the apex and up to 8 μm wide, usually moniliform to flexuous, generally branched, hyaline in SV; *primordial hyphae* abundant, larger, up to 15 μm wide, and regularly septate, mainly narrowly clavate with an obtuse apex, sometimes narrowly utriform, with surface distinct acid-resistant incrustations; *subpellis* composed of repent subparallel hyphae, 3–6 μm wide, very flexuous, sometimes branched, septate, hyaline in SV. *Cystidioid or oleiferous hyphae* not observed.

*Habitat and distribution:* Solitary or scattered on humus-rich, calcareous soil in deciduous forests dominated by the endemic *Quercus vulcanica*, which is limited to a few locations in west and south-central Türkiye, mostly present at elev. 1400–1500 m, during October.

*Typus:* Türkiye, Isparta Province, Eğirdir District, Yukarıgökdere town, in Kasnak Oak Forest Nature Reserve, under *Quercus vulcanica*, 1450 m a.s.l., 20 Oct. 2013, O.F. Çolak (**holotype** OFC-961; ITS, LSU and SSU sequences GenBank PV226180, PV226183 and PV226186).

*Additional materials examined:* *Russula anatolica*. Türkiye, Eğirdir District, Yukarıgökdere town, in Kasnak Oak Forest Nature Reserve, under *Quercus vulcanica*, 1500 m a.s.l., 15 Oct. 2014, O.F. Çolak (OFC-962; ITS, LSU and SSU sequences GenBank PV226181, PV226184, and PV226187); *ibid.*, 1470 m a.s.l., 19 Oct. 2015, O.F. Çolak (OFC-963; ITS, LSU and SSU sequences GenBank PV226182, PV226185 and PV226188).

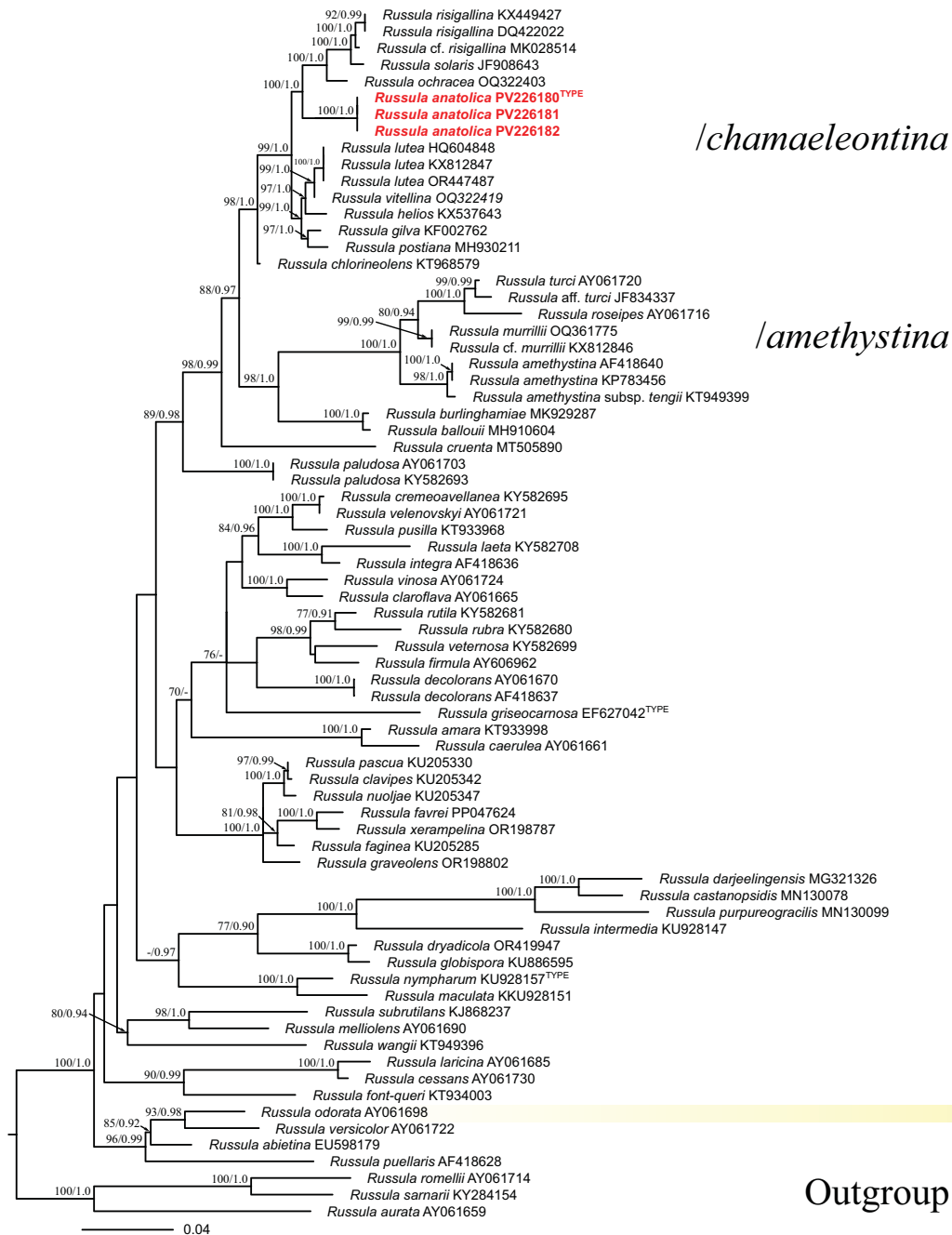
*Notes:* *Russula anatolica* is characterised by a pink rose pileus, distinctive cristate basidiospores, narrowly clavate to clavate epicuticular hairs that are frequently inflated at the apex, and branched primordial hyphae that are larger and regularly septate, as well as its growth under the endemic *Quercus vulcanica*. In addition to these morphological features, phylogenetic analyses indicate that *R. anatolica* belongs to the *Russula* subsection *Chamaeleontinae*. The molecular analyses reveal that *Russula anatolica* clusters with *R. ochracea*, *R. risigallina*, and *R. solaris*, and is a sister clade to *R. gilva*, *R. helios*, *R. lutea*, *R. postiana*, and *R. vitellina*. However, the newly presented species forms a genetically distinct terminal lineage from all these species, with high statistical support (MLB = 100 %, BPP = 1.0). Morphologically, *Russula gilva*, *R. lutea*, *R. ochracea*, *R. postiana*, *R. risigallina*, and *R. vitellina* are easily distinguished from *Russula anatolica* by their non-cristate basidiospores (Saccardo 1915, Melzer & Zvára 1927, Romagnesi 1985, Sarnari 1998, 2005). In *R.* subsect. *Chamaeleontinae*,

*Colour illustrations:* *Quercus vulcanica* forest in the Kasnak Oak Forest Nature Reserve, located in Türkiye (Isparta Province). *Basidiomata* in situ, holotype collection (OFC-961, top left panel) and coll. OFC-961 (bottom left panel); basidiospores under SEM (left panel); drawing of basidia, hymenial cystidia on lamellae sides, hymenial cystidia near the lamellae edges, epicuticular hairs, and primordial hyphae (holotype OFC-961) (right panel). Scale bars: basidiomata = 10 mm; SEM images of basidiospores = 5 μm; all other microscopic structures = 10 μm.



*Russula helios* also has cristate basidiospores but differs from *R. anatolica* by its bright yellow pileus (Romagnesi 1985, Samari 2005). The sequence labelled as *R. solaris* (JF908643) in the phylogenetic analyses was likely

misidentified. *Russula solaris*, a member of *R. sect. Russula*, exhibits distinctive morphological and microscopic features that are significantly different from those of *R. subsect. Chamaeleontinae*.



A Maximum Likelihood (ML) phylogenetic analysis of selected representatives of the genus *Russula* was performed using RAxML v. 8.2.10 (Stamatakis 2014) on the CIPRES Science Gateway v. 3.3 (Miller *et al.* 2010), based on an alignment of ITS nuclear rDNA sequences. *Russula aurata* (GenBank AY061659), *R. romellii* (GenBank AY061714), and *R. sarnarii* (GenBank KY284154) were used as the outgroup. Maximum likelihood bootstrap (MLB) support values of  $\geq 70\%$  and Bayesian posterior probability (BPP) values of  $\geq 0.90$  are indicated above the branches (MLB/BPP). The new species is highlighted in **bold red font** with a coloured box. The scale bar represents the estimated number of changes per site. Bayesian inference (PP) was performed using MrBayes v. 3.2.6, running for 1 M generations with the software estimating the evolutionary model (Ronquist *et al.* 2012). As the overall topology was identical in both ML and Bayesian analyses, only the ML tree is presented.

*Septoria reinamora*





## *Septoria reinamora* G.H. Ramirez, *sp. nov.*

**Etymology:** The species name is derived from the Spanish common name of its host plant, reina mora (*Mutisia spinosa*), from which the fungus was isolated.

**Classification:** *Mycosphaerellaceae*, *Capnodiales*, *Dothideomycetes*.

**Leaf spots** amphigenous, subcircular, 2–3 mm diam., white to grey in the centre with dark purple border and diffuse margin. **Conidiomata** pycnidial, hypophyllous, subglobose, immersed, dark brown, up to 150 µm diam., unilocular, ostiolum central, circular, 15–30 µm diam.; wall of 2–4 layers of brown textura angularis to epidermoidea, pale brown. **Conidiogenous cells** formed from the inner cells of the pycnidial wall, mainly at the base and also from the lateral walls, narrowly to broadly ampulliform with a relatively wide and sometimes elongated neck, hyaline, smooth, holoblastic, proliferating percurrently, 8–12.5(–13.5) × (3–)3.5–5.5(–6) µm. **Conidia** cylindrical, straight to slightly curved, narrowly to broadly rounded at the apex, narrowing slightly to a truncate base, 3–5(–7)-septate, slightly constricted around the septa, hyaline, smooth, 25–45(–47) × 3.5–4.5(–5) µm. **Sexual morph** unknown.

**Culture characteristics** (12 h photoperiod, 20 °C, 14 d): Colonies slow-growing, irregular and spreading, raised, verrucose, velvety, with irregular margins, reaching 9 mm diam. On PDA surface pale purplish grey, reverse dark brick. On MEA surface pale rosy buff, reverse rosy buff. On OA surface dark brick showing sparse aerial mycelium, reverse rosy buff. Conidia in mass salmon.

**Typus:** **Argentina**, Neuquén Province, Villa la Angostura, 40°41'2.78"S, 71°42'18.50"W, on leaf spots of *Mutisia spinosa* (*Asteraceae*), 15 Jan. 2024, G.H. Ramirez (**holotype** BBB: GR-MUT-02, culture ex-type BBB:GR-SE-02; ITS, LSU and *tub2* sequences GenBank PQ329535, PQ329536 and PQ787289).

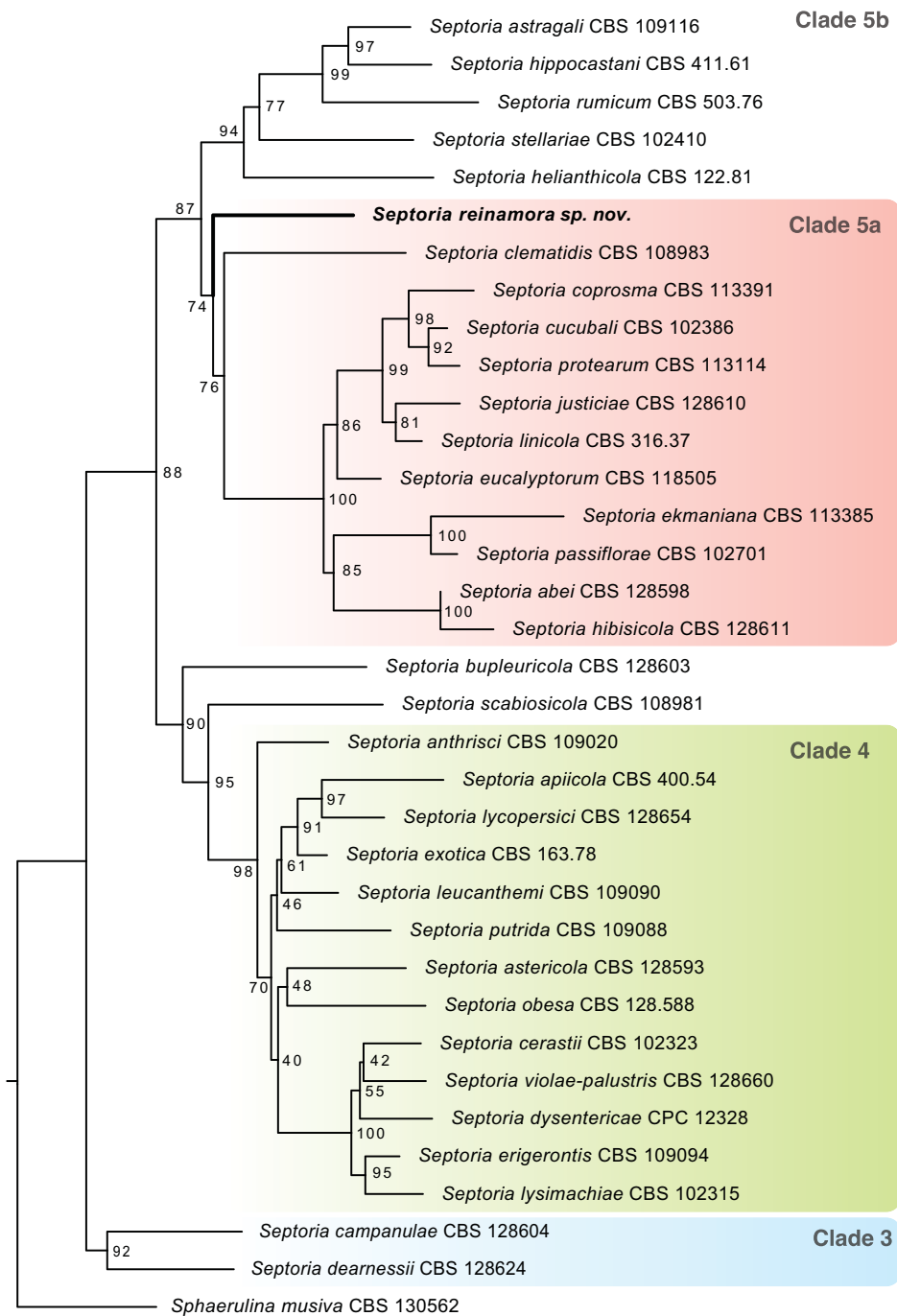
**Notes:** There are two recorded species of *Septoria* associated with *Mutisia* from which *S. reinamora* can be distinguished. *Septoria mutisiae*, described on *M. subspinosa* (a species closely related to *M. spinosa* but with little geographical overlap), differs notably from *S. reinamora* in both morphological and symptomatological characteristics. While *S. reinamora* induces well-defined, amphigenous leaf spots, *S. mutisiae* is associated with generalised leaf wilting and discolouration rather than distinct necrotic lesions. Their conidial characteristics are also markedly different, since *S. mutisiae* produces larger conidia (50–60 × 4–5 µm) that are 1–3-septate. Another species, *S. jaffuelii*, described on *M. latifolia* in Chile, differs from *S. reinamora* in both conidial morphology and host association. *Septoria jaffuelii* produces shorter conidia (20–35 × 2.5–4 µm) that are only 1–3-septate, compared to the longer, more septate conidia of *S. reinamora*. Although molecular data for *S. mutisiae* and *S. jaffuelii* are currently unavailable, these clear distinctions in symptomatology, morphology, and host range support the recognition of *S. reinamora* as a distinct species.

Molecular phylogenetic analysis places *S. reinamora* within the Clade 5, *sensu* Verkley *et al.*, (2013), near species from Subclade 5a, which includes *Septoria* species isolated from a diverse range of hosts that are not closely related.

Based on a search in GenBank database, the closest hits using the **ITS** sequence had highest similarity to *Septoria scabiosicola* [CBS 102334, GenBank KF251532; Identities = 495/495 (100 %), no gaps], *S. anthrisci* [CBS 109019, GenBank KF251338; Identities = 494/495 (99 %), no gaps] and *S. cirsii* [TCM-10, GenBank KC874680; Identities = 494/495 (99 %), no gaps]; closest hits using the **LSU** sequence had highest similarity to *Apseudocercospora trigonotidis* [CBS 131890, GenBank JQ324972; Identities = 823/825 (99 %), no gaps], *S. helianthicola* [CBS 122.81, GenBank KF251936; Identities = 823/825 (99 %), no gaps] and *S. stellariae* [CBS 102378, GenBank KF252080; Identities = 823/825 (99 %), no gaps]; closest hits using the **tub2** sequence had highest similarity to *S. justiciae* [CBS 128610, GenBank KF252908; Identities = 216/250 (86 %), one gap], *S. linicola* [CBS 316.37, GenBank MZ073925; Identities = 294/342 (86 %), 5 gaps] and *S. clematidis* [CBS 108983, GenBank KF252855; Identities = 207/241 (86 %), 2 gaps].

**Supplementary material:** doi: 10.6084/m9.figshare.28840508 (Sequence alignments and table).

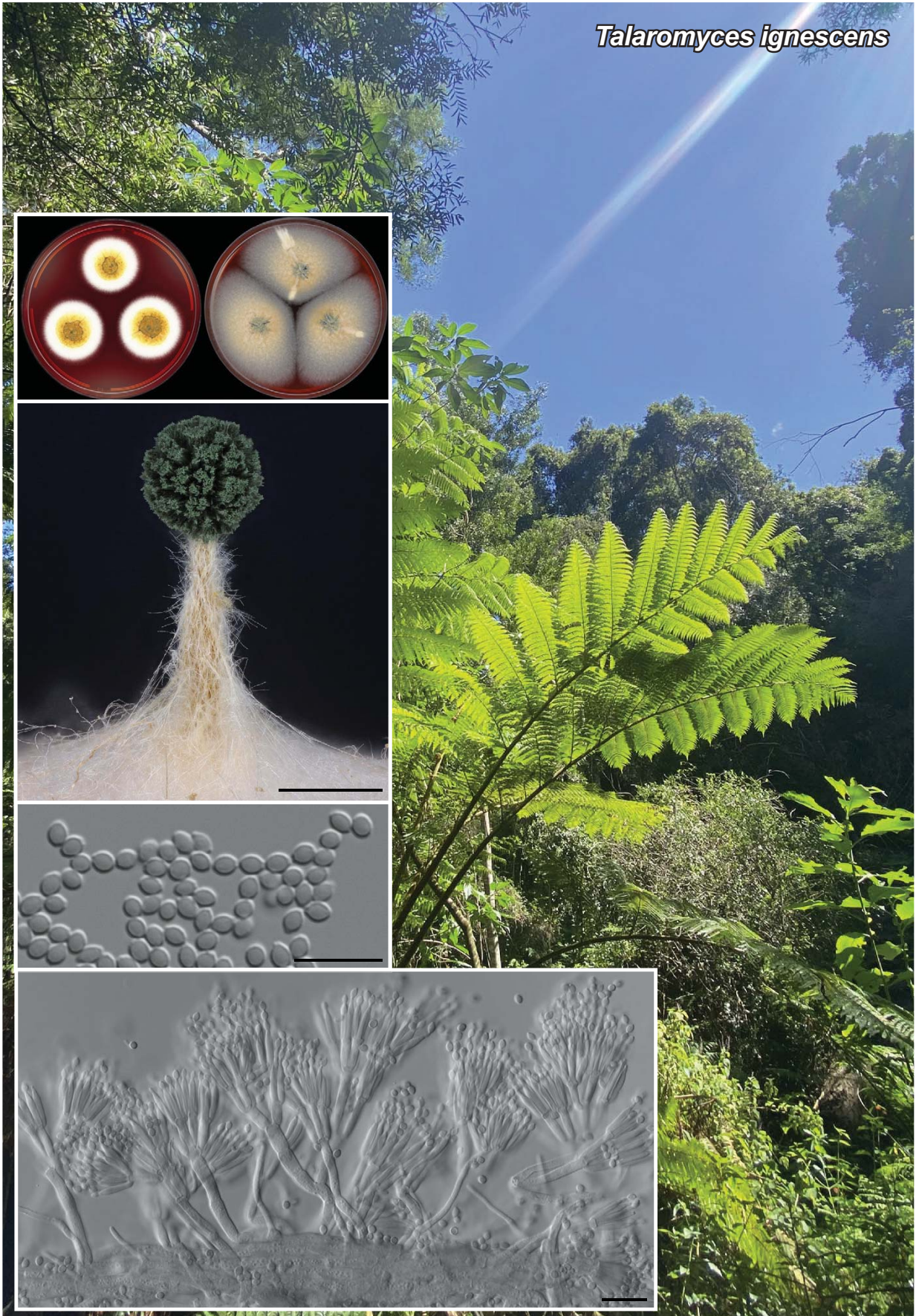
**Colour illustrations:** Reina mora (*Mutisia spinosa*) in Villa la Angostura, Argentina. Foliar symptoms; lower side of leaf symptom with semi-immersed pycnidia; pycnidia; conidiogenous cells; conidia. Scale bars = 10 µm.



Maximum likelihood (ML) phylogenetic tree constructed with the concatenated ITS, LSU and *tub2* sequences using IQ-TREE v. 1.6.12 (Nguyen *et al.* 2015), performing an ultrafast bootstrap with 1000 replicates (Hoang *et al.* 2018). The species included in this analysis belong predominantly to clades 4 and 5 sensu Verkley *et al.* (2013). *Sphaerulina musiva* was used as outgroup. The ML bootstrap support values are indicated on the branches. The novel species is indicated in **bold**.



*Talaromyces ignescens*



***Talaromyces ignescens* Van Vuuren, Harms & Visagie, *sp. nov.***

*Etymology*: Latin, *ignescens*, meaning red. Named after the striking red soluble pigments produced on growth media.

*Classification*: *Trichocomaceae*, *Eurotiales*, *Eurotiomycetes*.

*Conidiophores* biverticillate, subterminal branching common; *stipes* smooth, minor proportion appears finely roughened, 20–80 × 2.5–4 µm; *branches* 12–26 µm; *metulae* 3–4 per stipe or branch, appressed, 10–13(–14) × 2.5–4 µm; *phialides* acerose, 3–6 per metula, 10–13(–14) × 2–3 µm; *conidia* smooth, fusiform, (2–)2.5–3.5 × 2–3 µm (2.98 ± 0.23 × 2.5 ± 0.37), av. width/length = 0.82, n = 100. Synnemata inconsistently produced after prolonged incubation, determinate, 970–2000 µm long, stalk yellowish, 74–250 µm wide, head apex width 115–600 µm.

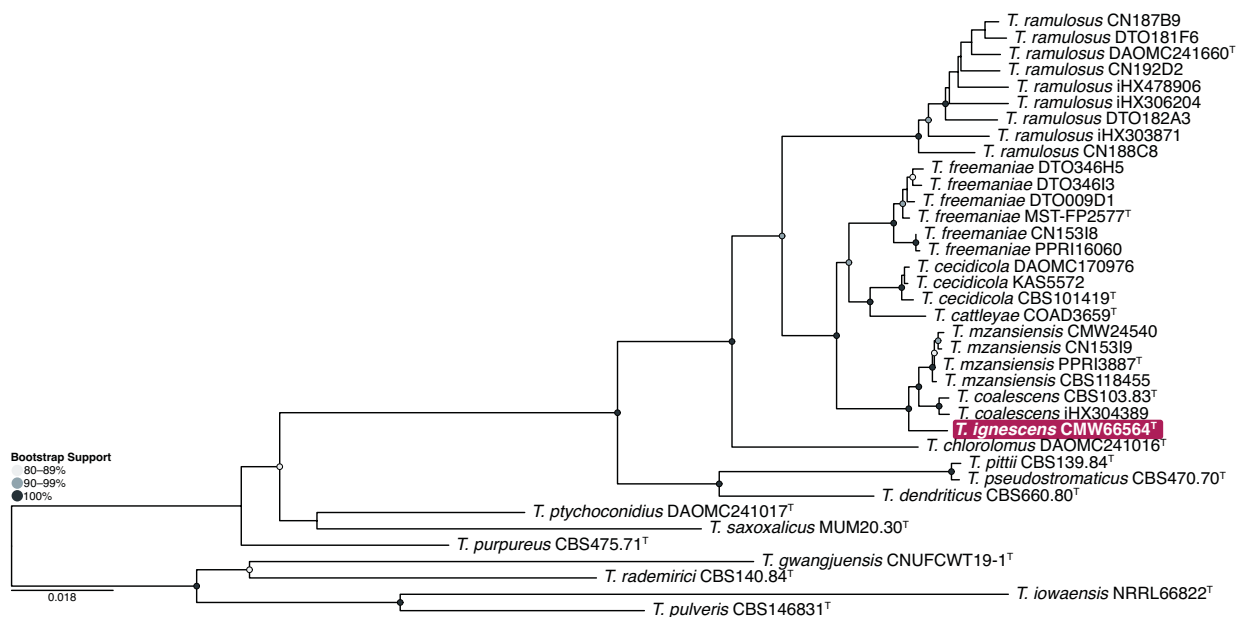
*Culture characteristics* (25 °C, 7 d): On Czapek yeast autolysate agar (CYA): Colonies moderately deep, sulcate, synnemata inconsistently produced after prolonged incubation, determinate; margins low, wide, entire; mycelia white and yellow; texture floccose, strongly funiculose; sporulation sparse, conidia en masse dark green [26F5; colour codes based on (Kornerup & Wanscher 1967)]; soluble pigments red; exudates absent; reverse dark to violet brown (8F8–10F8). On malt extract agar (MEA): Colonies moderately deep, plane, sulcate, synnemata inconsistently produced after prolonged incubation, determinate; margins low, wide, entire; mycelia white and yellow; texture floccose, strongly funiculose; sporulation moderately dense, conidia en masse dark green (26F5); soluble pigments red; exudates clear; reverse dark to violet brown (8F8–10F8). On yeast extract sucrose agar (YES): Colonies similar to those on CYA. On dichloran 18 % glycerol agar (DG18): Colonies moderately deep, plane, slightly sulcate; margins low, wide, entire; mycelia white; texture floccose, strongly funiculose; sporulation moderately dense, conidia en masse dark green (26F5); soluble pigments red; exudates clear to inconspicuously brown; reverse dark brown (7F8). On oatmeal agar (OA): Colonies low, plane, granular in appearance, synnemata inconsistently produced after prolonged incubation, determinate; margins subsurface, wide, entire; mycelia white; texture velutinous, strongly funiculose; sporulation moderately dense, conidia en masse dark green (26F5); soluble pigments inconspicuous, orange to brown; exudates clear to light orange. On creatine sucrose agar (CREA): Growth weak, no acid produced.

*Colony diam.* (in mm): CYA 29–34; CYA 10 °C 4–5; CYA 15 °C 9–14; CYA 20 °C 20–23; CYA 30 °C 30–33; CYA 37 °C 14–18; CYAS 7–8; MEA 35–40; DG18 14–17; YES 32–37; OA 38–44; CREA microcolonies.

*Typus*: **South Africa**, Western Cape Province, George, Outeniqua Nature Reserve, -33.93361, 22.42533, from soil, 9 Mar. 2023, coll. C.M. Visagie, isol. J. Spraker (**holotype** PRU(M):4626, culture ex-type CMW-IA 007111 = CMW 066564 = CBS 153397 = CN231B7 = iHX305259; ITS, *BenA*, *CaM*, *RPB2*, *ACT*, *Cct8*, *MCM7*, *RPB1* and *Tsr1* sequences GenBank MH281565, PV550672, PV550673, PV550674, PV550677, PV550688, PV550699, PV550710 and PV550721).

*Notes*: The multigene phylogeny resolves *T. ignescens* in section *Purpurei* as a close relative of *T. coalescens* and *T. mzansiensis*. Pairwise comparisons revealed that the new species has at least 27 (*ACT*), 16 (*BenA*), 14 (*CaM*), 19 (*Cct8*), 29 (*MCM7*), 8 (*RPB1*), 9 (*RPB2*) and 12 (*Tsr1*) bp differences from all other species. It shares identical ITS sequences with some *T. freemaniae* and *T. mzansiensis* strains. Morphologically, the new species are very similar to *T. coalescens*; both have colonies producing bright red soluble pigments, which are not produced by *T. mzansiensis* (Yilmaz *et al.* 2014, Visagie *et al.* 2024). Minor differences are noted regarding colony growth rates: on CYA at 37 °C the new species grows faster than *T. coalescens* (14–18 vs 2–4 mm), but a bit slower on CYA at 30 °C (30–33 vs 40–41 mm). *Talaromyces ignescens* produces synnemata 970–2000 µm long, while those of *T. mzansiensis* are up to 2700 µm long and *T. coalescens* are 400–1200 µm long (Yilmaz *et al.* 2014, Visagie *et al.* 2024).

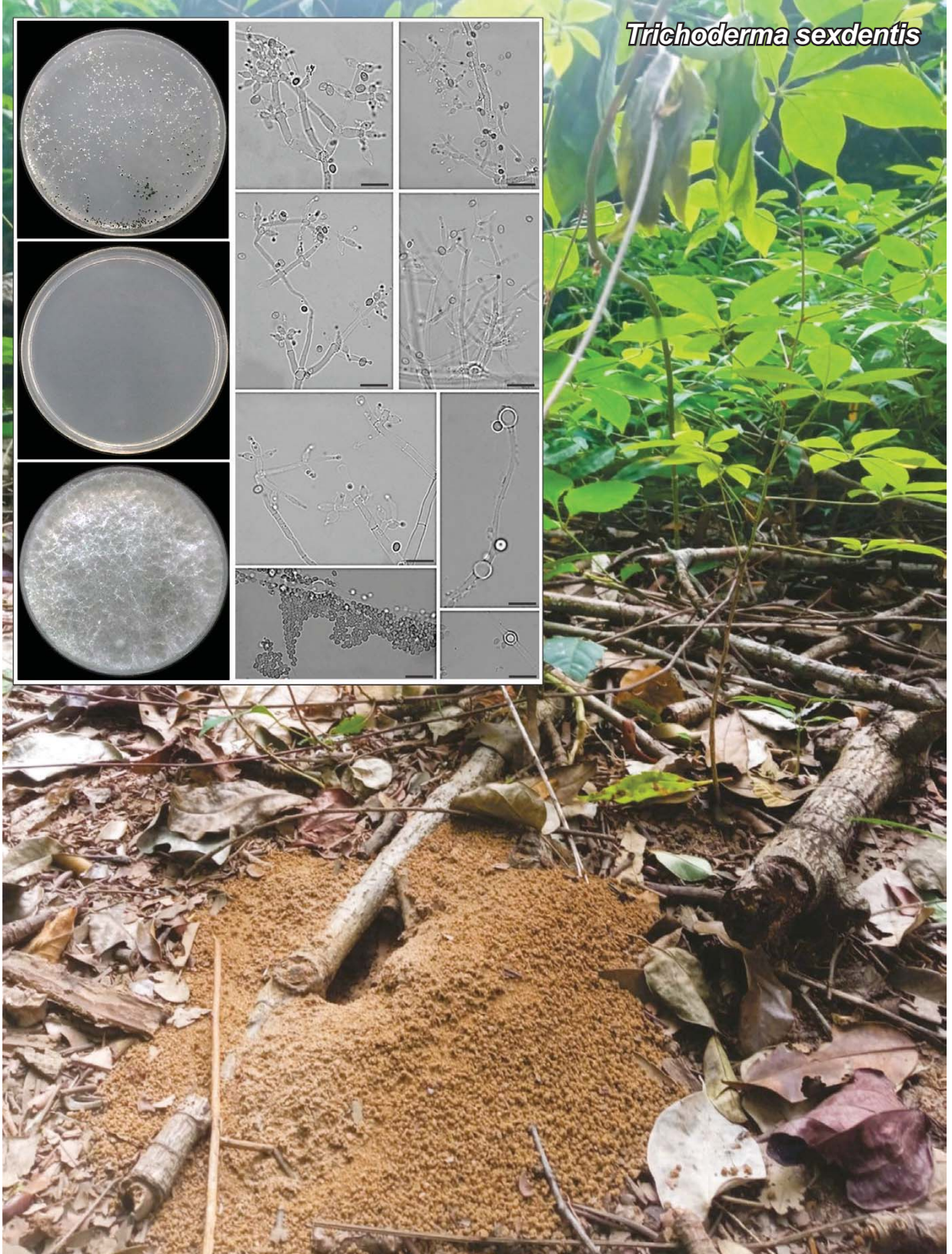
*Supplementary information*: <https://doi.org/10.5281/zenodo.15279204>.



Combined phylogeny of *Talaromyces ignescens* and its close relatives based on ITS, *BenA*, *CaM*, *RPB2*, *ACT*, *Cct8*, *MCM7*, *RPB1* and *Tsr1* (see Suppl. Table for GenBank accession numbers). Each gene region was aligned in MAFFT v. 7.526 (Kato & Standley 2013). These were concatenated, and a Maximum likelihood tree was calculated in IQ-TREE v. 2.3.4 (Minh *et al.* 2013). Each gene region was treated as a separate partition, and the most appropriate nucleotide substitution model was selected using ModelFinder (Kalyaanamoorthy *et al.* 2017) built into IQ-TREE. A bootstrap analysis was run with 1000 replicates. The new species is indicated by **bold** text inside a coloured box, <sup>T</sup> = ex-type strain.

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*Trichoderma sexdentis*





# *Trichoderma sexdentis* L.S. Sales, J.T. De Souza & P.A.S Marbach, *sp. nov.*

**Etymology:** The epithet *sexdentis* is related to the collection and isolation source, leaves inside a nest of the leaf-cutting ant *Atta sexdens rubropilosa*.

**Classification:** *Hypocreaceae*, *Hypocreales*, *Hypocreomycetidae*, *Sordariomycetes*.

**Mycelium** on cornmeal dextrose agar (CMD) with hyaline aerial hyphae. **Pustules** are solitary and aggregated, initially appearing on the margins of the plate, later becoming dark green, measured in 14-d-old cultures, 0.2–0.8 × 0.2–0.5 µm (n = 30). **Conidiophores** trichoderma-like to verticillium-like. **Phialides** loosely disposed, solitary or paired, ampulliform and terminal, lageniform 4–10 × 2–4 µm, L/w (1.3–)2.0–3.3(–5.0), 1–3 µm wide at the base (n = 60), arising from a cell (7–)9–12(–14) × 2–4 µm (n = 30). **Conidia** green, smooth, oblong, ellipsoidal to ovoid, 2–5 × 2–3 µm, L/w 1–2 (n = 60). **Chlamydospores** abundant, intercalary and terminal, globose to subglobose (4–)6–10(–13) × 4–11 µm, L/w (0.8–)1.0–1.3(–1.6) (n = 30).

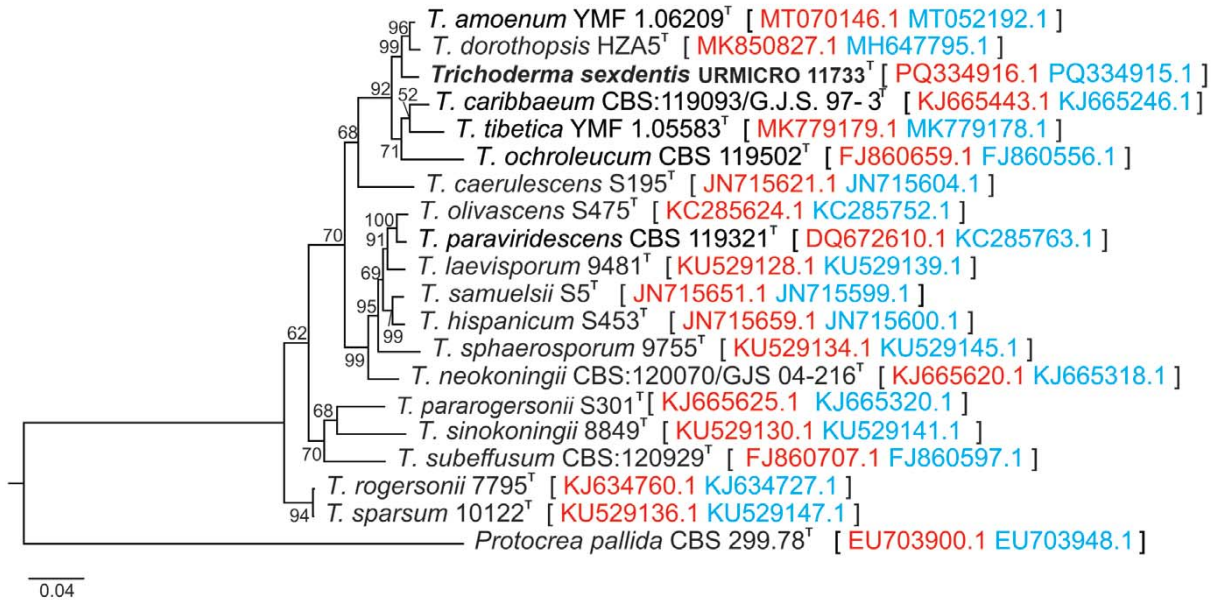
**Culture characteristics:** On CMD after 72 h, colony radius 17–21 mm at 20 °C, mycelium covering plate after 7 d at 20 °C. Colony with sparse aerial mycelium, hyaline-white colour. Conidiation starting after 6 d, formed on aerial hyphae and on white and green pustules. No distinct odour observed. No pigment noted. On SNA after 72 h, colony radius 8–13 mm at 20 °C, mycelium covering plate after 10 d at 20 °C. Colony hyaline, with mycelium formed on aerial hyphae. Conidiation starting after 10 d, formed on aerial hyphae and on infrequent, solitary or aggregated pustules, that are white and green. No distinct odour observed. Pigment sulphur yellow noted. On PDA after 72 h, colony radius 24 mm at 20 °C, mycelium covering plate after 7 d at 20 °C. Colony dense, initially white, turning dark green. Conidiation beginning after 5 d, formed on dense aerial hyphae, pustules white and green formed on the periphery of the plate. No distinct odour observed. No pigment noted.

**Typus:** **Brazil**, Zona da Mata de Minas Gerais, Viçosa, remnant of the Atlantic Forest: a seasonal, subtropical, semideciduous, montane forest 'Mata do Seu Nico' (Fazenda Bonsucesso), -20.750000°S, -42.916667°W, from leaves inside a nest of the leaf-cutting ant *Atta sexdens rubropilosa*, Feb. 2010, S.L. Rocha [**holotype** preserved as metabolically inactive culture URMicro 11733, preserved in the culture collection URMicro (Microbiological Resources Unity) at Federal University of Lavras (UFLA), Lavras, Brazil; *tef1*, *rpb2*, *cal1*, and LSU sequences GenBank PQ334916, PQ334915, PQ334914 and PQ321306.1]; ex-type culture also preserved at the Department of Forestry, Federal University of Viçosa (UFV) under number TR17.

**Notes:** *Trichoderma sexdentis* is morphologically similar and shares an evolutionary history with *T. amoenum* and *T. dorothisopsis*. The conidia of *T. sexdentis* (2–5 × 2–3 µm) are narrower than the conidia of the species *T. amoenum* (3–5 × 3.2–3.9 µm) and *T. dorothisopsis* (3.2–4.2 × 2.9–3.6 µm) (Tomah *et al.* 2020, Zheng *et al.* 2021). Based on a megablast search, the closest hits using the LSU sequence were *T. caribbaeum* var. *caribbaeum* (GenBank MH874605.1, identity 99.76 %) and *T. caribbaeum* var. *aequatoriale* (GenBank NG\_069883.1, identity 99.64 %). The sequence of *tef1* was closest to *T. amoenum* (GenBank MT070146.1, identity 98.55 %) and *T. dorothisopsis* (GenBank MK850827.1, identity 98.13 %). The closest hits with the *rpb2* sequence were *T. amoenum* (GenBank MT052192.1, identity 96.69 %) and *T. dorothisopsis* (GenBank MH647795.1, identity 97.44 %) and the *cal1* sequence was closest to *T. ovalisporum* (GenBank DQ379005.1, identity 96.42 %) and *T. koningii* (GenBank DQ367686.1, identity 96.01 %).

**Supplementary material:** [doi: 10.5281/zenodo.13931632](https://doi.org/10.5281/zenodo.13931632) (alignment and tree).

**Colour illustrations:** Nest of the leaf-cutting ant *Atta sexdens rubropilosa*. Plates show cultures of *T. sexdentis* on different media incubated for 7 d at 20 °C (top CMD, middle SNA and bottom PDA); conidiophores; phialides; conidia; chlamydospores. Scale bars = 5 µm.



Maximum likelihood tree obtained with the combined *tef1* and *rpb2* sequences of phylogenetically related species of the clades *Koningii*, *Rogersonii* and *Viridences* performed in RAXML-HPC v. 8 (Stamatakis 2014) employing the GTR+G model with 1000 bootstrap re-samplings. *Protocrea pallida* strain CBS 299.78 was used as an outgroup. The new species is presented in **bold** font (<sup>T</sup> = ex-type). GenBank accession numbers are given after each strain (*tef1* = red and *rpb2* = blue).

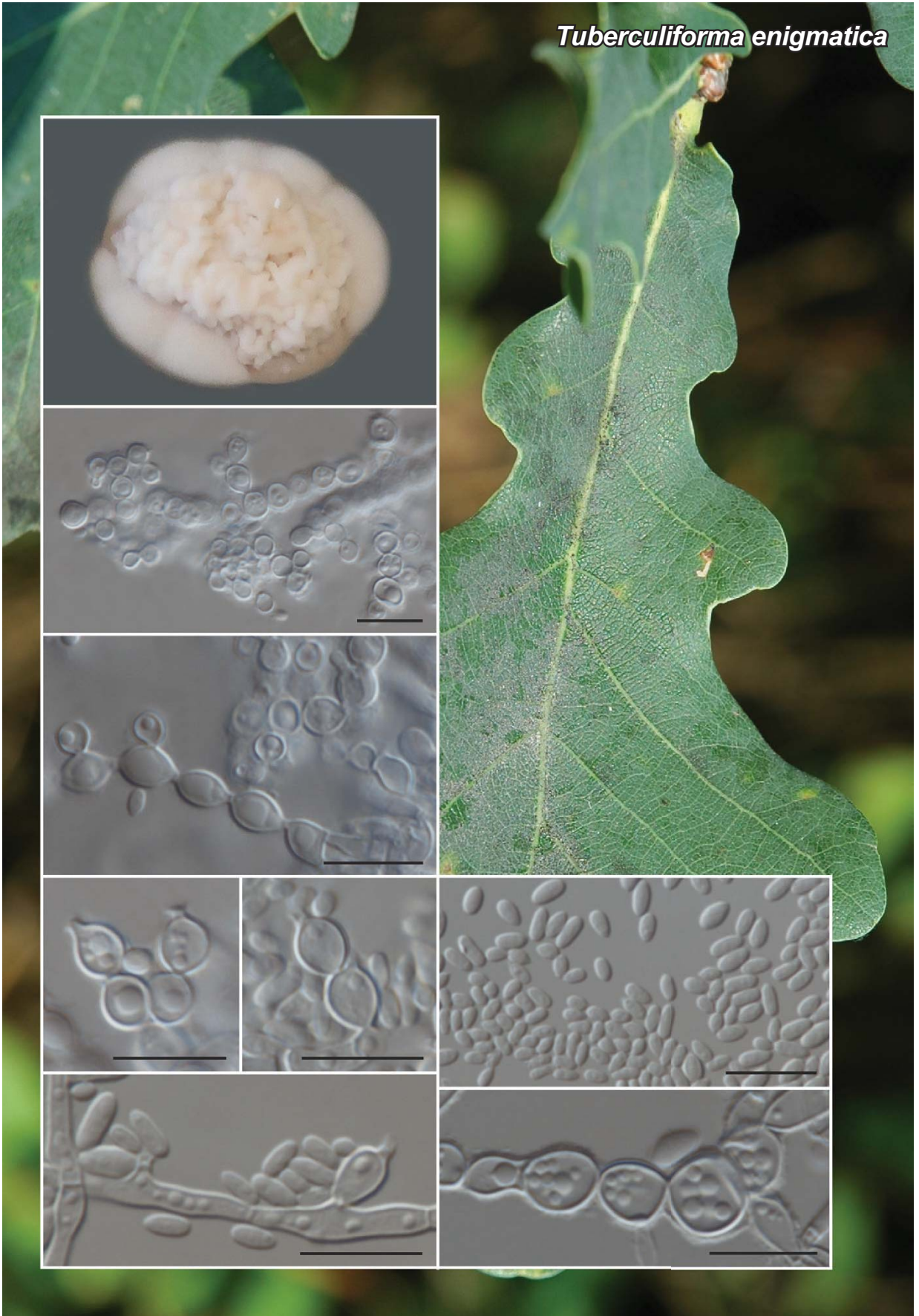
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*Tuberculiforma enigmatica*



# *Tuberculiforma enigmatica* Piątek, Stryjak-Bogacka & Czachura, *sp. nov.*

**Etymology:** Name refers to the enigmatic generic placement of the fungus after initial molecular analyses.

**Classification:** *Tuberculiformaceae*, *Tuberculiformales*, *Eurotiomycetes*.

**Mycelium** composed of branched, septate, hyaline, straight, smooth, 2–5 µm wide hyphae, sometimes with inflations and intercalary chlamydospore-like cells. **Conidiophores** reduced to conidiogenous cells. **Conidiogenous cells** obovoid to ampulliform, formed on subglobose cells (3–7 × 3–6.5 µm) arising in dense clusters, or scattered on hyphae, hyaline, smooth, aseptate, phialidic, 5–7.5 × 3–4 µm; conidiogenous cells rarely undifferentiated, intercalary on hyphae, forming conidia from short denticles, phialidic. **Conidia** cylindrical or ellipsoidal, rarely subglobose, hyaline, smooth, aseptate, thin-walled, 2–8 × 1.5–2.5(–3) µm, sometimes budding at polar areas. **Chlamydospore-like cells** globose or subglobose, hyaline, smooth, aseptate, 5–9.5 × 5–8.5 µm. [Description based on malt extract agar (MEA)].

**Culture characteristics:** Colonies on MEA erumpent, spreading, umbonate, white to pale cream, reaching 6 mm diam. after 2 wk and 12 mm diam. after 4 wk at 15 °C and 8 mm diam. after 2 wk and 14 mm diam. after 4 wk at 25 °C, surface wrinkled-cerebriform at the centre, with weak aerial mycelium, margin lobate. Reverse cream-coloured. Colonies on potato dextrose agar (PDA) erumpent, spreading, umbonate, white to pale cream, reaching 5 mm diam. after 2 wk and 10 mm diam. after 4 wk at 15 °C and 8 mm diam. after 2 wk and 15 mm diam. after 4 wk at 25 °C, surface wrinkled-cerebriform at the centre, with weak aerial mycelium, margin lobate. Reverse cream-coloured.

**Typus:** **Poland**, Podkarpackie Province, Rzeszów County: Rzeszów-Nowe Miasto, municipal greenery, isolated from sooty mould community on *Quercus robur* leaves, 17 Sep. 2018, *M. Piątek*, *W. Bartoszek* & *P. Czachura* (**holotype** KRAM F-60034; culture ex-type G105 = CBS 153697; ITS, LSU and mtSSU sequences GenBank PV242217, PV242258 and PV247098).

***Tuberculiforma catenata*** (Oorschot *et al.*) Piątek, Stryjak-Bogacka & Czachura, **comb. nov.** MB 858816.

**Basionym:** *Anthopsis catenata* Oorschot *et al.*, *Antonie van Leeuwenhoek* **48**: 63. 1982.

**Synonym:** *Tuberculiforma catenata* (Oorschot *et al.*) Zhi Yuan Zhang & Y.F. Han (as '*catenatus*'), *Mycosphere* **15**: 694. 2024, nom. inval., Art. F.5.1 (Shenzhen).

**Notes:** The genus *Tuberculiforma* was recently described for two species: the type species *Tuberculiforma sinensis* isolated from soil in China and an additional species, *T. catenata* that was originally described as *Anthopsis catenata* from the roots of *Abies alba* in Germany (van Oorschot *et al.* 1982, Zhang *et al.* 2024). The combination *T. catenata* was invalidly published (Zhang *et al.* 2024) and it is therefore validated here. *Tuberculiforma* resides in a clade that in many studies was resolved as basal lineage within the order *Sclerococcales* and included unnamed beetle-associated fungi and unnamed *Sclerococcus* species (Réblová *et al.* 2017, 2020, Olariaga *et al.* 2019, Dong *et al.* 2020a, Ma *et al.* 2023, Diederich *et al.* 2024). However, morphologically *Tuberculiforma* is a distinct genus in having hyaline hyphae with short lateral branches consisting of subglobose cells and conidiophores reduced to conidiogenous cells arising in clusters, intercalary or terminal on hyphae (van Oorschot *et al.* 1982, Zhang *et al.* 2024). It therefore differs from the asexual morphs of the remaining *Sclerococcales* that are chalara-like or sporodochial dematiaceous hyphomycetes (Réblová *et al.* 2017, 2020, Olariaga *et al.* 2019). The genus *Tuberculiforma* is accommodated in a distinct family *Tuberculiformaceae* and order *Tuberculiformales* (Zhang *et al.* 2024).

*Tuberculiforma enigmatica* is phylogenetically well separated from the two previously described *Tuberculiforma* species. It is also different morphologically in having cylindrical or ellipsoidal, rarely subglobose conidia, sometimes budding at polar areas. The megablast search of NCBI's GenBank nucleotide database resulted in some sequences not assigned to species, including sequences of unnamed "*Dactylospora*" sp., with about 97–99 % threshold similarity with the ITS sequence of *T. enigmatica*. It is not clear whether they belong to *T. enigmatica* or to closely related undescribed species.

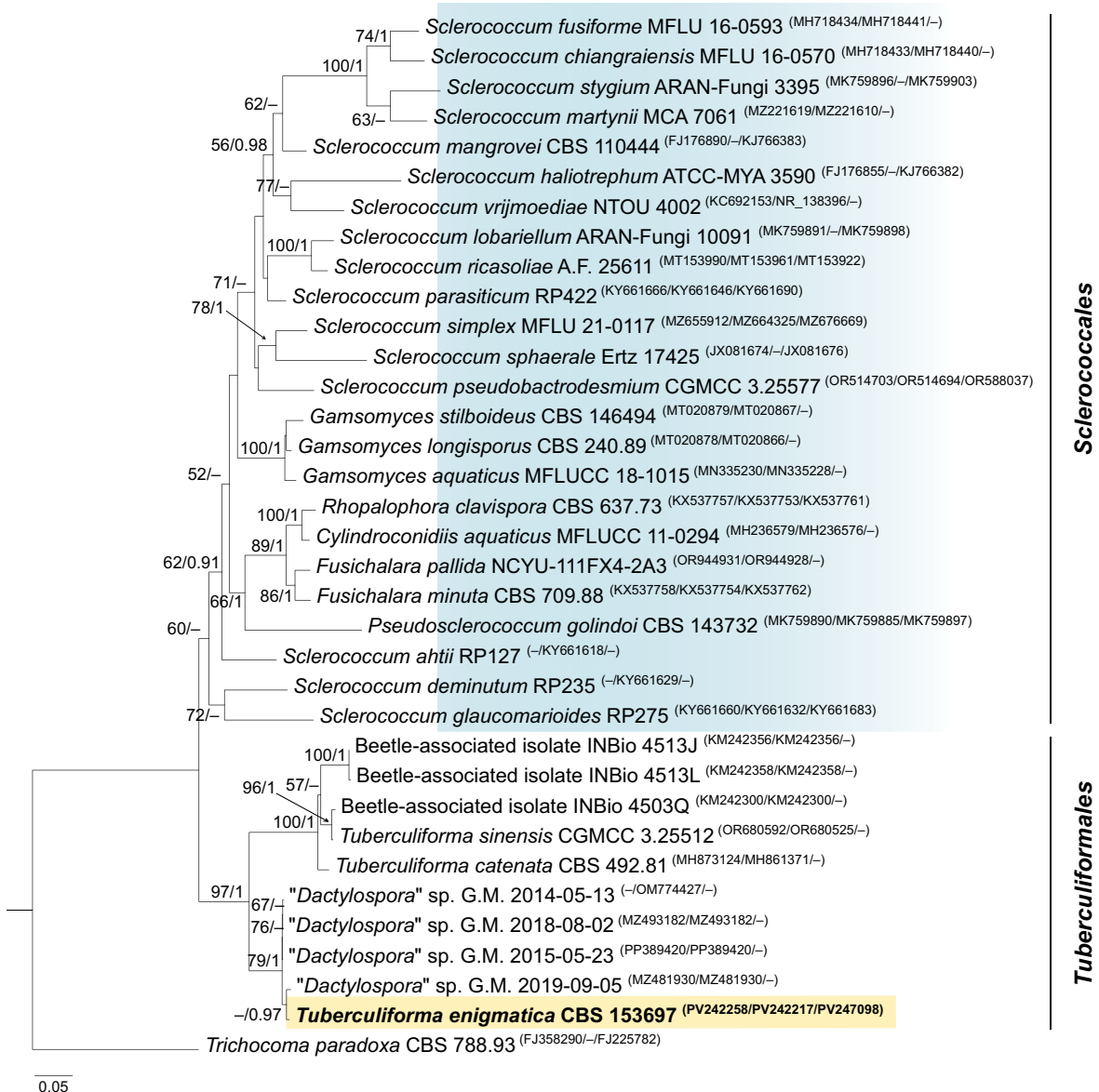
Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits of the named species using the **ITS** sequence are *Sclerococcum tardum* [voucher PDD 105454, GenBank MK432753; Identities = 392/451 (87 %), 17 gaps (3 %)], *Sclerococcum parasiticum* [isolate PRA-JV24261, GenBank OK332927; Identities = 389/449 (87 %), 16 gaps (3 %)] and *Sclerococcum ahtii* [voucher Talbot CHI017-63a (H), GenBank NR\_166387; Identities = 387/449 (86 %), 14 gaps (3 %)]. The closest hits of the named species using the **LSU** sequence are "*Coenogonium pineti*" [voucher Spribille 39097 (GZU), GenBank KR017237; Identities = 697/716 (97 %), four gaps (0 %)], *Tuberculiforma sinensis* [strain ZY 22.046, GenBank OR680592; Identities = 765/804 (95 %), two gaps (0 %)] and *Pseudosclerococcum golindoi* [voucher ARAN-Fungi 6619, GenBank NG\_073673; Identities = 834/893 (93 %), eight gaps (0 %)]. The closest hits of the named species using the **mtSSU** sequence are *Rhopalophora clavispora* [culture CBS 281.75, GenBank KX537760; Identities = 502/554 (91 %), one gap (0 %)], *Sclerococcum parasiticum* [voucher J. Pykala 39145 (H), GenBank KY661692; Identities = 501/557 (90 %), three gaps (0 %)] and *Sclerococcum ricasoliae* [voucher A.F.

**Colour illustrations:** Leaves of *Quercus robur* with patches of sooty mould communities, Poland. Colony on MEA; clusters of subglobose cells with conidiogenous cells; conidiogenous cells; conidia; chlamydospore-like cells. Scale bars = 10 µm.



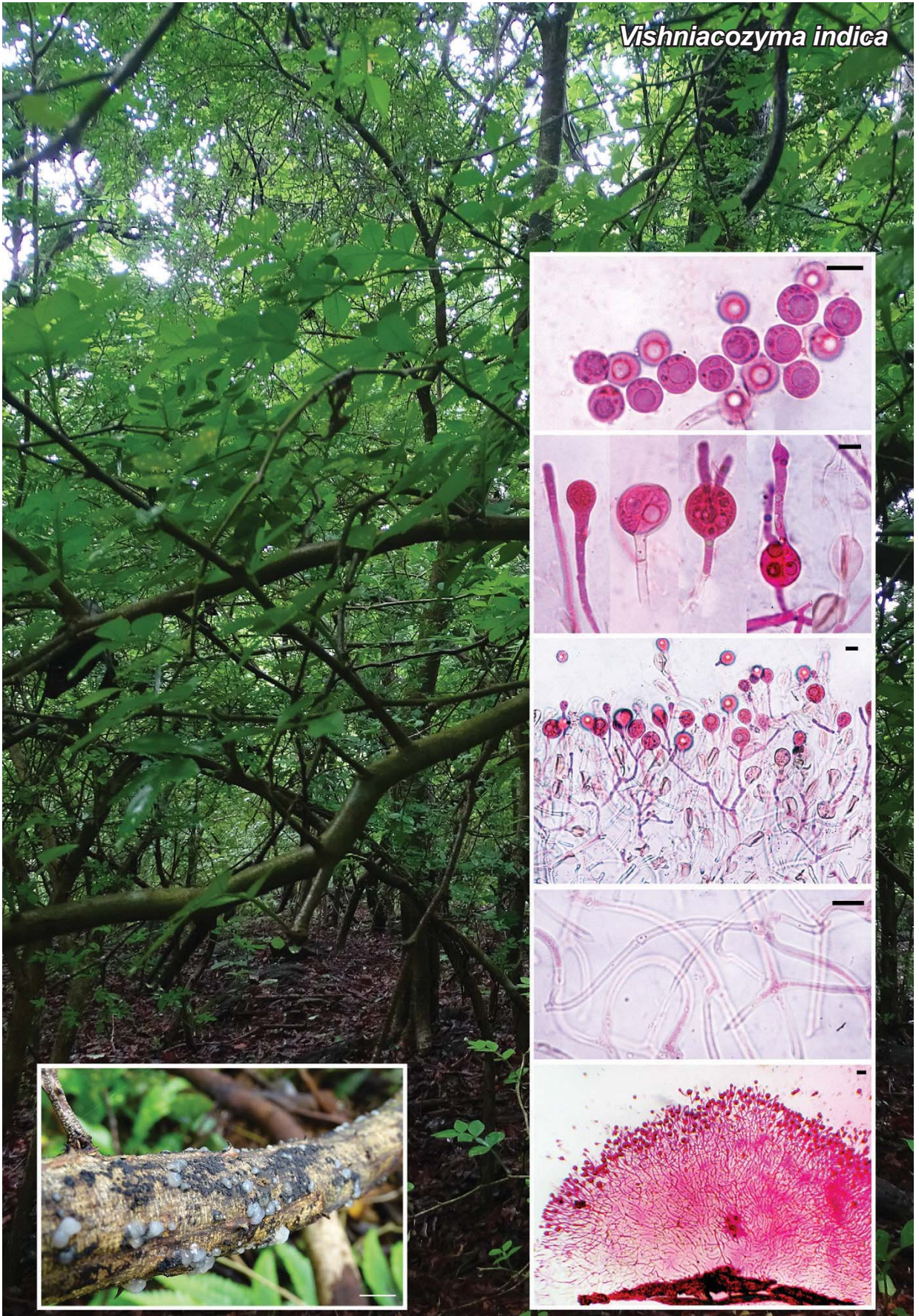
29132, GenBank MT153924; Identities = 528/593 (89 %), three gaps (0 %)].

Supplementary material: <https://doi.org/10.6084/m9.figshare.28595516.v1> (alignment).



Phylogenetic tree of representatives of the orders *Sclerococcales* and *Tuberculiformales* obtained from a maximum likelihood analysis of the combined multi-locus alignment (2041 characters, including gaps: LSU, ITS, mtSSU). The maximum likelihood analysis was performed using RAxML-NG v. 1.1.0 (Kozlov *et al.* 2019) and the Bayesian inference was performed using MrBayes v. 3.2.6 (Ronquist *et al.* 2012). The position of *Tuberculiforma enigmatica* is indicated in **bold** and highlighted with a coloured block. Numbers above branches indicate maximum likelihood bootstrap (MLB) support values > 50 % and Bayesian posterior probabilities (BPP) > 0.9, respectively (MLB/BPP). *Trichocoma paradoxa* was used as an outgroup. The scale bar represents the expected number of changes per site.

*Vishniacozyma indica*





## *Vishniacozyma indica* A. Thomas & T.K.A. Kumar, *sp. nov.*

**Etymology:** Named after the country where it was collected, India.

**Classification:** *Bulleribasidiaceae*, *Tremellales*, *Tremellomycetes*.

**Basidiocarps** 3–8 × 2–3 mm, soft gelatinous, pustular, discrete, occasionally coalescing, translucent, off-white to white when fresh turning to thin film adhered on the substratum when dry. **Spore print** whitish. **Hymenium** limited to the upper surface. **Hyphidia** absent. **Basidia** 20–34 × 17–19 μm, globose, sphaeropedunculate, 2–4-celled, longitudinally or obliquely septate, thin-walled, guttulate, hyaline. **Basidiospores** 8–12 × 8–12 μm (Q = 0.88–1.04 μm, Qm = 0.97 μm), subglobose to globose, hyaline, thin-walled, smooth, guttulate, apiculate. Secondary spore production from basidiospores observed. **Zygoconidia** not observed. **Tramal hyphae** 3–9 μm wide, thick-walled towards base, branched, smooth, hyaline, frequently anastomosing, gelatinous, without clamp connections. **Haustoria** not observed.

**Habit and distribution:** On dead twigs, known only from the type collection site.

**Typus:** **India**, Kerala State, Kozhikode District, Kakkad, 11°28'29.712"N, 75°57'58.572"E, 150 m a.s.l., on dead twigs, 13 Dec. 2023, A. Thomas (**holotype** ZGCAT354; LSU sequence GenBank PP724435).

**Additional material examined:** **India**, Kerala State, Kozhikode District, Kakkad, on dead twigs, 13 Dec. 2023, A. Thomas, ZGCAT359; LSU sequence GenBank PP724719.

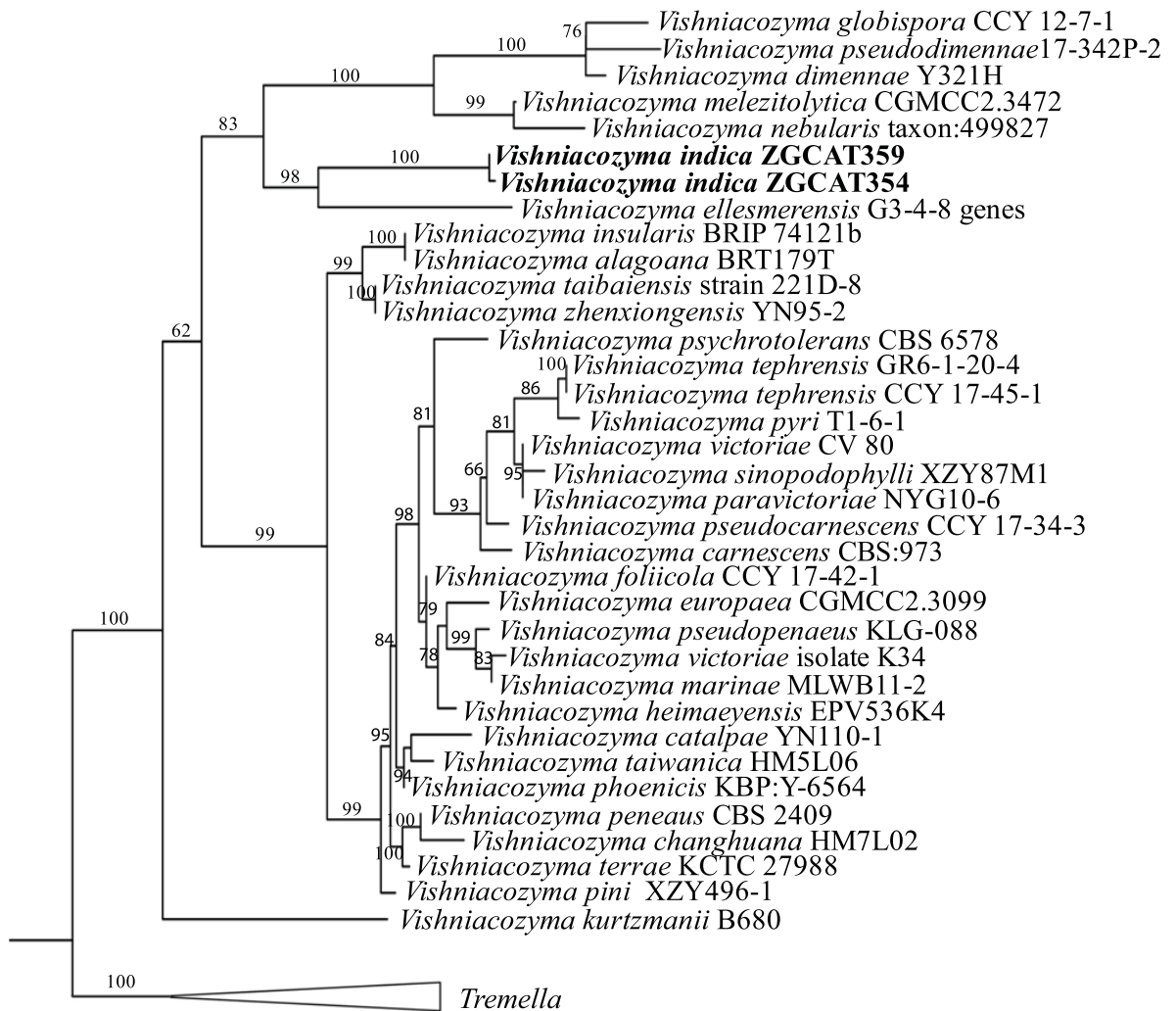
**Notes:** *Vishniacozyma* was established by Liu *et al.* (2015a) in *Bulleribasidiaceae* to accommodate 11 species belonging to the *victoriae* (sensu Fonseca *et al.* 2011) and *dimennae* clades recognised in Boekhout *et al.* (2011), and Liu *et al.* (2015b). Thirty-two species have been reported in the genus so far (Index Fungorum accessed on 23 Jan. 2025). Except for *V. nebularis*, all other members of *Vishniacozyma* are known only by their yeast stage. This is the second time a species of the genus with a basidiocarp has been reported. *Vishniacozyma indica* is characterised by the presence of gelatinous pustular basidiocarps; longitudinally septate, globose, sphaeropedunculate basidia; subglobose to globose basidiospores, secondary spore formation from basidiospores, and hyphae without clamp connections.

Although *V. indica* shows similarity with *V. nebularis* in having pustular gelatinous basidiocarps, it differs by the absence of H-shaped zygoconidia, and clamp connections. In our molecular phylogenetic analysis of *Tremellomycetes*, the Kerala collections clustered along with species of *Vishniacozyma*, as sister to *Tremella*. *Vishniacozyma indica* settled as sister clade with *V. ellesmerensis*, which is a psychrophilic basidiomycetous yeast species isolated from the glacier on the Canadian Arctic (Tsuji *et al.* 2019).

Morphological and molecular evidence prove that the collections from Kerala represent a so far undescribed *Vishniacozyma* species. This is the first report of *Vishniacozyma* species with the absence of clamp connections. There are no reports of this genus from India to date.

**Supplementary material:** doi: 10.6084/m9.figshare.28267136 (table, alignment and phylogram).

**Colour illustrations:** India, Kerala state, Kozhikode district, Kakkad, type locality. Left inset shows fresh basidiocarps; right insets show cross section of basidiocarp; tramal hyphae; hymenium with basidia and basidiospores. Scale bars: basidiocarp = 10 mm; right insets = 10 μm.



Maximum Likelihood tree generated from the nrLSU sequences of *Vishniacozyma* and *Tremella* members. IQ-TREE v. 1 (IQ-TREE Web Server: Fast and accurate phylogenetic trees under maximum likelihood; univie.ac.at) (Trifinopoulos *et al.* 2016) was used to generate the phylogenetic tree. Parameters such as autodetecting the substitution model, ultrafast bootstrap analysis with 1000 bootstrap alignments, and Shimodaira-Hasegawa (SH)-like approximate likelihood-ratio test (SHaLRT) were set for constructing the phylogram (Nguyen *et al.* 2015, Kalyaanamoorthy *et al.* 2017, Hoang *et al.* 2018). The new species and its voucher numbers are indicated in **bold** black letters.



**Conflict of interest:** The authors declare that there is no conflict of interest.

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