



Fungal diversity notes 1611–1716: taxonomic and phylogenetic contributions on fungal genera and species emphasis in south China

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Abstract

This article is the 15th contribution in the Fungal Diversity Notes series, wherein 115 taxa from three phyla, nine classes, 28 orders, 48 families, and 64 genera are treated. Fungal taxa described and illustrated in the present study include a new family, five new genera, 61 new species, five new combinations, one synonym, one new variety and 31 records on new hosts or new geographical distributions. *Ageratinicolaceae* fam. nov. is introduced and accommodated in Pleosporales. The new genera introduced in this study are *Ageratinicola*, *Kevinia*, *Pseudomultiseptospora* (Parabambusicolaceae), *Marasmiellomycena*, and *Vizzinia* (Porotheleaceae). Newly described species are *Abrothallus altoandinus*, *Ageratinicola kunmingensis*, *Allocryptovalsa aceris*, *Allophoma yuccae*, *Apiospora cannae*, *A. elliptica*, *A. pallidesporae*, *Boeremia wisteriae*, *Calycina papaeana*, *Clypeococcum lichenostigmoides*, *Coniochaeta riskali-shoyakubovii*, *Cryphonectria kunmingensis*, *Diaporthe angustiapiculata*, *D. campylandrae*, *D. longipapillata*, *Diatrypella guangdongense*, *Dothiorella franceschini*, *Endocalyx phoenicis*, *Epicoccum terminosporum*, *Fulvifomes karaiensis*, *F. pannaensis*, *Ganoderma ghatensis*, *Hysterobrevium baoshanense*, *Inocybe avellaneorosea*, *I. lucida*, *Jahnula oblonga*, *Kevinia lignicola*, *Kirschsteiniothelia guangdongensis*, *Laboulbenia caprina*, *L. clavulata*, *L. cobiae*, *L. cosmodisci*, *L. nilotica*, *L. omalii*, *L. robusta*, *L. similis*, *L. stigmatophora*, *Laccaria rubriporus*, *Lasiodiplodia morindae*, *Lyophyllum agnijum*, *Marasmiellomycena pseudoomphaliiformis*, *Melomastia beihaiensis*, *Nemania guangdongensis*, *Nigrograna thailandica*, *Nigrospora ficuum*, *Oxydothis chinensis*, *O. yunnanensis*, *Petriella thailandica*, *Phaeoacremonium chinensis*, *Phialocephala chinensis*, *Phytophthora debattistii*, *Polyposphaeria nigrospora*, *Pronectria loweniae*, *Seriascoma acutispora*, *Setoseptoria bambusae*, *Stictis anomianthi*, *Tarzetta tibetensis*, *Tarzetta urceolata*, *Tetraploa obpyriformis*, *Trichoglossum beninense*, and *Tricoderma pyrrosiae*. We provide an emendation for *Urnula ailaoshanensis* *Agaricus duplocingulatooides* var. *brevisporus* introduced as a new variety based on morphology and phylogeny.

Keywords Agaricomycetes · Ascomycota · Basidiomycota · Dothideomycetes · Eurotiomycetes · Fungal diversity · Geoglossomycetes · Geographical distribution · Host records · *Incertae sedis* · Laboulbeniomycetes · Lecanoromycetes · Leotiomycetes · Novel taxa · New combination · Oomycota · Peronosporae · Pezizomycetes · Phylogeny · Sordariomycetes · South Chinese fungi · Taxonomy

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Introduction

South China contains both tropical and subtropical areas with warm, moist to cold, dry climatic conditions and it encompasses a wide range of biodiversity (Zhao et al. 2015; Naruse et al. 2018; Niu et al. 2019). Moreover, this region has untouched, virgin ecological patches and urbanized, exploited regions (Zhao et al. 2015). There are some studies on the diversity and taxonomy of macro and microfungi in the south China region (Senanayake et al. 2020a, b, c; Jiang et al. 2022; Kularathnage et al. 2022; Liu et al. 2022a; Wang et al. 2022; Zhang et al. 2022). However, the fungal diversity in these areas is still understudied and a high number of novel taxa is expected to be recognized if studied (Hyde et al. 2018; 2020a).

Discovering novel fungal taxa is essential not only in classification or nomenclature-based studies, but also in the pharmaceutical industry, agriculture, ecological and environment management, plant disease control, epidemiology, and environmental conservation (Hyde et al. 2019b). New geographical distributions and host records are also important in taxonomy and ecology-based studies. The new records of plant pathogenic fungi reveal the disease spread or give clues on future pathogenic spreads (Chethana et al. 2021a). Several contemporary webpages and also some studies related to fungal numbers provide data on fungal taxa of different life modes, habitats and regions with descriptions, illustrations, phylogenetic trees, notes and the current number of accepted species (Pem et al. 2019; Bundhun et al. 2020; Chaiwan et al. 2021; Wijesinghe et al. 2021; Calabon et al. 2022; Phukhamsakda et al. 2022; Senanayake et al. 2022). It is therefore, necessary to reveal the host ranges of species and also their life-modes (Hyde et al. 2020d). This information predicts life-mode shifting and adaptations of fungi to new habitats. Further, new combinations can be proposed for species that not fit to the current genus and match other genera by morphology and phylogeny (Turland et al. 2018).

In this study, we revealed some novel fungal taxa mostly collected in south China and also from different geographical regions in the world and publish them in this Fungal Diversity Notes series. The Fungal Diversity Notes series have been contributed a great work on taxonomy, phylogeny and diversity of fungi in the phyla of Ascomycota, Basidiomycota and Oomycota. The series provides an outlet for publishing new species, new combinations, new records of host associations and geographical distributions. From the first to 14th series of the Fungal Diversity Notes, a total of

1610 taxa were included with 11 new families, 115 new genera and 1124 new species (Ariyawansa et al. 2015a; Liu et al. 2015; Li et al. 2016; Hyde et al. 2016, 2017a, b, 2019a, b, 2020a; Tibpromma et al. 2017, 2018; Wanasinghe et al. 2018; Phookamsak et al. 2019; Yuan et al. 2020; Boonmee et al. 2021; Jayawardena et al. 2023).

The aims of this paper are to introduce novel fungal family, genera, species, combinations and records of host and geographical distribution in Ascomycota, Basidiomycota and Oomycota based on polyphasic approaches (Chethana et al. 2021b; Maharachchikumbura et al. 2021) providing descriptions, illustrations, phylogenetic analysis and notes. We introduced several species sole based on morphology in Laboulbeniaceae, because recent studies have introduced species in this family only based on morphology (Kaishian et al. 2020; Kaishian and Weir 2021). Further, five new species combinations have been proposed here following articles in International Code of Nomenclature for Algae, Fungi, and Plants providing relevant information. There are 32 novel geographical and host records illustrated and described here providing notes. We provide descriptions of sexual morph for *Cytospora lumnitzericola* Norph. et al. and *Apiospora gaoyouensis* (C.M. Tian & N. Jiang) Pintos & P. Alvarado, for first time and *Paraphaeosphaeria verruculosa* Verkley, Göker & Stielow is synonymized under *Paraphaeosphaeria parmeliae* Crous & Trakun.

Materials and methods

Fresh specimens were collected mainly from south China and additional specimens were obtained from Africa, America, Asia and Europe (i.e. Australia, Benin, Bolivia, Canada, France, India, Indonesia, Iran, Italy, Mongolia, Norway, Russia, Spain, Sri Lanka, Sweden, Thailand, Uganda, USA, Uruguay and Uzbekistan). Materials and methods discussed in Senanayake et al. (2020d) were followed for isolation and sporulation. Illustrations of macro and microscopic characters and molecular phylogenetic analyses were performed following recent FDN issues (Phookamsak et al. 2019; Boonmee et al. 2021; Jayawardena et al. 2023). New species were introduced based on guidelines in Maharachchikumbura et al. (2021).

Taxonomy

Ascomycota Caval.-Sm.

The latest updated account of Ascomycota followed in Wijayawardene et al. (2020).

Dothideomycetes O.E. Erikss & Winka.

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

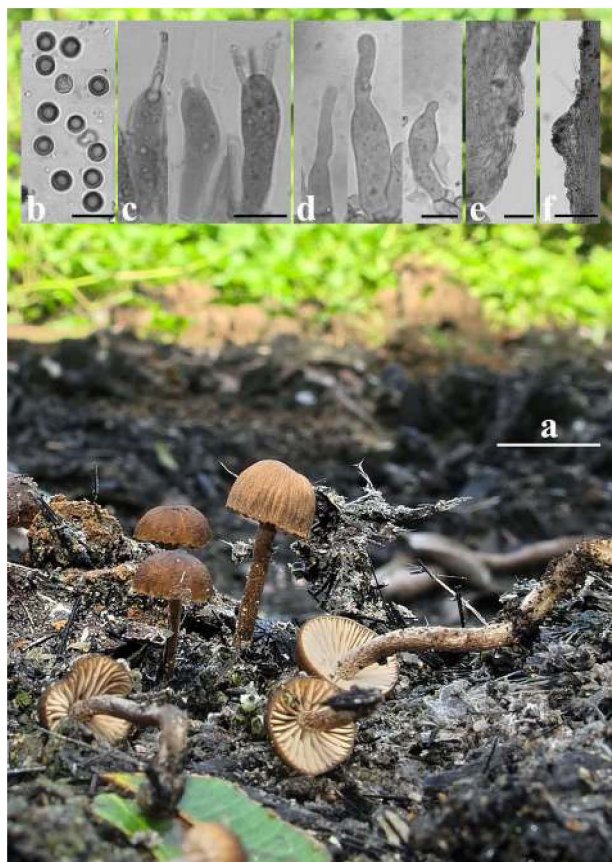


Fig. 150. *Lyophyllum agnijum* (CAL 1388, holotype). **a** Basidiocarps in their natural habitat. **b** Basidiospores. **c** Basidia. **d** Marginal cells. **e** Pileipellis. **f** Stipitipellis towards the apex of the stipe. Scale bars: a = 10 mm, b–d = 10 μ m, e–f = 20 μ m

basidiospores, a lamella-edge without cystidia and the absence of clamp connections (Moser 1983; Breitenbach and Kränzlin 1991a). *Lyophyllum anthracophilum* (Lasch) M. Lange & Sivertsen, a carbonicolous species reported from Europe, North America, Africa and Asia, is similar to *L. agnijum* in having brown-tinted basidiocarps with a striate, hygrophanous pileus, a longitudinally fibrillose stipe which is furfuraceous at the apex, globose to subglobose basidiospores, a pileipellis composed of parallel hyphae, the presence of clamp connections and a gregarious habit. *Lyophyllum anthracophilum*, however, is distinguished from *L. agnijum* by its larger basidiocarps (pileus up to 30 mm diam., stipe 30–50 \times 1.5–2 mm) with black-brown pileus and stipe, a non-umbonate pileus which becomes applanate with age, broadly adnate to subdecurrent, grey-white lamellae with a smooth edge, smaller basidiospores (4.8–5.7 \times 4.5–5.5 μ m) and lamellae devoid of cystidia (Moser 1983; Breitenbach and Kränzlin 1991b).

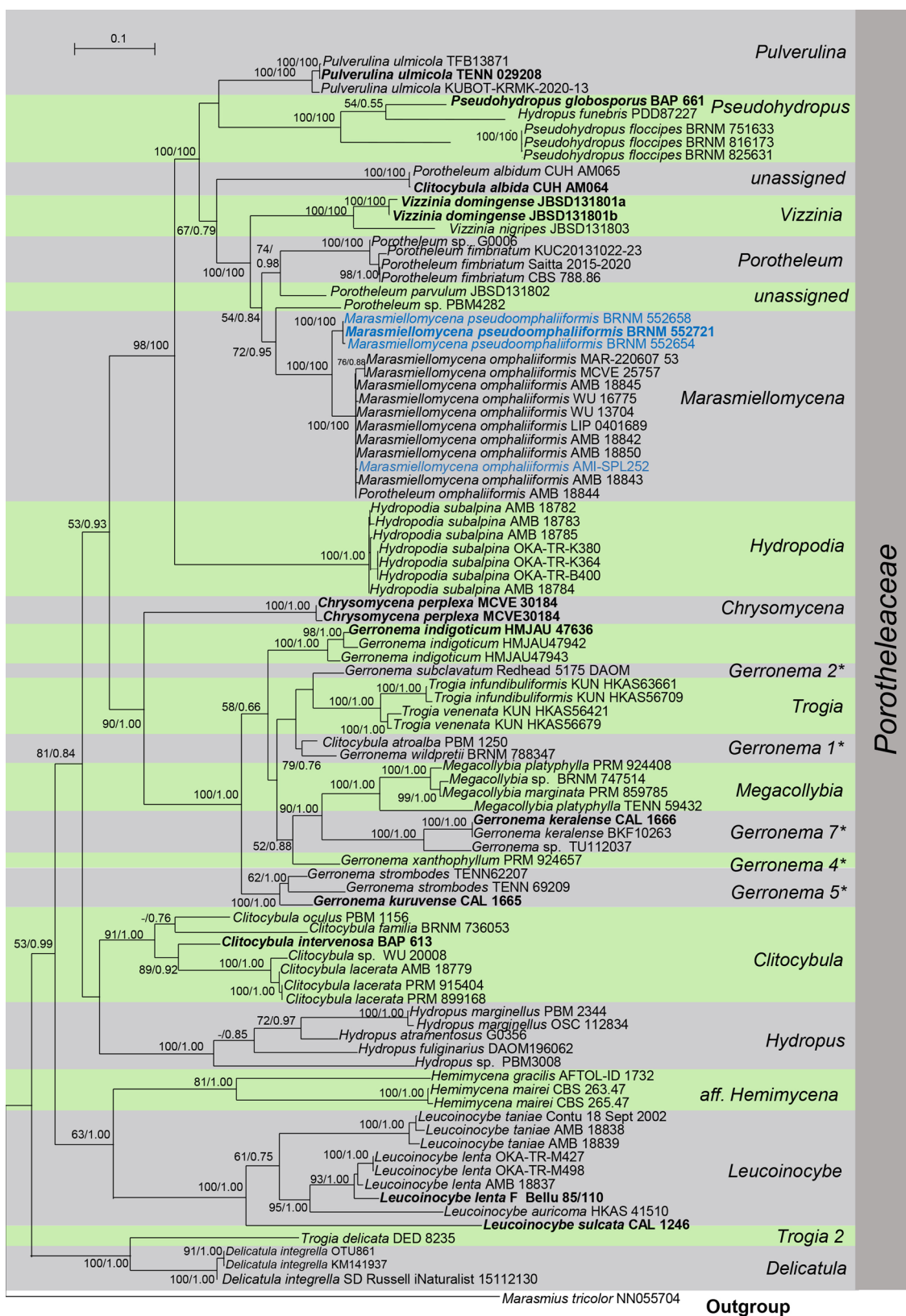
The closest hit of our collection in the Blastn search was *Lyophyllum decastes*. *Lyophyllum decastes* is a species complex that includes several lineages and this has

caused considerable taxonomic confusion in the past (Larsson and Sundberg 2011). Therefore, a morphology-based comparison of *L. decastes* is not useful. In our ML analyses (Fig. 151), our collection was grouped with *L. littorale* (ML = 66%) representing a well-differentiated clade from *L. decastes* species complex with ML = 98% bootstrap support. *Lyophyllum littorale* (Ballero & Contu) Contu, a species described from Sardinia in Italy, shares some characters such as close, decurrent lamellae, a fibrillose stipe with pruina restricted to the apex, globose to subglobose basidiospores (4.5–6.3 \times 4.5–5.7 μ m), clamped hyphae and a gregarious habitat. However, *L. littorale* is distinguished from our collection in having large (pileus 15–65 mm diam., stipe 20–60 \times 4–8 mm), grayish basidiocarps fruiting on calcareous soil, a non-hygrophanous pileus with a depressed centre and pruinose surface devoid of striations, a stipe which is tapered towards the apex and an orange-yellow base, 4-spored basidia and slightly gelatinized pileipellis (Ballero and Contu 1990). *Lyophyllum atratum*, *L. anthracophilum*, *L. ambustum*, and the other carbonicolous species treated in the present phylogenetic analyses, seem to be phylogenetically unrelated with our collection and hence we introduce our collection as *L. agnijum*.

Porotheleaceae Murrill

The family Porotheleaceae was phylogenetically revised and 14 genera were accepted (Antonín et al. 2019; He et al. 2019; Vizzini et al. 2019; Kalichman et al. 2020; Matheny et al. 2020). These studies indicated that taxonomic placements of some genera are still doubtful. Consiglio et al. (2022) mentioned that there are no obvious morphological or ecological synapomorphies shared by all members of the pale-spored Porotheleaceae *s. stricto*, with the exception of their lignicolous habit and the presence of clamp connections. Unfortunately, the same situation within the genus *Porotheleum* is amended by Consiglio et al. (2022). Moreover, their phylogenetic trees (Consiglio et al. 2022, p. 104, 106 and 107), as well as our tree (Fig. 152) support that *Porotheleum* sensu Consiglio et al. contains more genera. All specimens classified by Consiglio et al. (2022) under the genus *Porotheleum* formed a clade with ML/BI = 72%/0.95 statistical support (Fig. 152). We identified several well-separated lineages as, (1) *Clitocybula albida* (*P. albidum*), (2) *P. domingense* and *P. nigripes* (3) *P. fimbriatum* and *Porotheleum* sp. G0006 (4) *P. parvulum*, (5) *Porotheleum* sp. PBM4282, and a lineage of (6) *Marasmiellomyces pseudoomphaliiformis* and *M. omphaliiformis*.

Porotheleum fimbriatum (Pers.) Fr. is the type species of *Porotheleum* Fr. Thus, lineage 3) *P. fimbriatum* and *Porotheleum* sp. G0006 represents *Porotheleum* sensu *stricto*. *Clitocybula albida* A.K. Dutta, K. Acharya & Antonín clustered with *Porotheleum* in the phylogenetic analysis of Consiglio et al. (2022). Phylogenetic analysis in this study



◀**Fig. 152** Phylogram generated from maximum likelihood analysis based on combined ITS and LSU sequence data. Maximum likelihood bootstrap supports ($\geq 60\%$) followed by Bayesian posterior probabilities (≥ 0.70) followed by supports are indicated. The dataset was compiled using data from previous studies of *Clitocybula*, *Gerronema*, *Hydropus* and *Megacollybia* (Matheny et al. 2006; Antonín et al. 2019; Kaygusuz et al. 2020; Consiglio et al. 2022) and the most similar sequences ($> 91\%$ sequence similarity in LSU rDNA) were selected from GenBank using BlastN similarity search tool. The ITS and LSU sequences originating from the single voucher or strain were concatenated (93 sequence pairs). Sequence alignment generated in MAFFT 6 (Kato and Toh 2008) was curated manually to remove hypervariable regions. Bayesian searches were conducted in MrBayes 3.0 (MB) with 10 million replicates. Maximum likelihood searches were conducted in IQ-TREE multicore version 1.4.1. in IQ-TREE including standard automated model selection (“-m TEST”) as well as FreeRate (+R) model, and standard nonparametric bootstrap approximation (“-b 1000”). The dataset had 1872 columns, 1225 distinct patterns, 735 parsimony-informative characters, 249 singleton sites, 888 constant sites. The substitution models for MB (TPM2+F+I+G4 for both partitions) were estimated in jModeltest 0.1.1. Two data partitions (one for each subunit) were recognized in the rDNA concatenated dataset. For each terminal, the species name and the voucher/herbarium code are indicated, and the type strains are in bold and new isolates are in blue bold. **Gerronema* genera sensu (Vizzini et al. 2019)

(Fig. 152) also showed that, *Clitocybula albida* (= *Porotheleum albidum*) forms a separate clade and however, further studies are required to confirm its generic position using additional materials and more genes, since only ITS data for *C. albida* are available (Dutta et al. 2018). *Porotheleum domingense* and *P. nigripes* form well-separated lineage and clearly represent a new genus, described here as *Vizzinia*.

Marasmiellomycena De la Peña-Lastra, Mateos, Kolařík, Ševčíková & Antonín, **gen. nov.**

MycoBank number: MB839731; *Facesoffungi* number: FoF 14222

Etymology: Epithet reflects its similarity to *Marasmiellus* and (Hemi) mycenoid genera.

Diagnosis: *Basidiomata* omphaloid or marasmiod, non-fragile. *Pileus* thin-fleshed, minutely tomentose, pubescent, granulose to subsquamulose. *Lamellae* well-developed, frequently forked, anastomose, adnate, sub-decurrent or decurrent, triangular or arcuate. *Stipe* central, filiform, entirely pruinose or pruinose-floccose, flesh thin. *Basal tomentum* present. *Spores* smooth, inamyloid. *Basidia* mostly tetrasporic. *Cheilocystidia* less distinct. *Pleurocystidia* absent. *Pileipellis* a cutis or with transitions to a trichoderm, terminal elements cylindrical, fusiform, lageniform or mucronate with or without excrescences or long rostrum (pileocystidioid structures). *Clamp connections* present. *Chemical reactions* metachromatic in cresyl blue or not, no other part of basidiomata dextrinoid or amyloid. *Ecology* saprotrophic, on dead wood and decayin leaves.

Type species: *Marasmiellomycena pseudoomphaliiformis* Antonín & Ševčíková.

Notes: Our three new collections (BRNM 552658, BRNM 552721, BRNM 552654) are morphologically identical and they shares many similar characters with *Porotheleum omphaliiforme*. Therefore, this well-supported clade herein introduce as *Marasmiellomycena* gen. nov. Vu et al. (2018) predicted that optimal thresholds for fungi (at least for filamentous) at the genus level of 98.2% based on LSU barcodes and 94.3% based on ITS barcodes. The genetic similarity of the genus *Marasmiellomycena* to neighboring genera, expressed by the similarity of *M. pseudoomphaliiformis* (type collection) to *P. parvulum* and (sequences identified as) *P. fimbriatum*, is 97.8% for LSU, and 88.9% for ITS. *Marasmiellomycena* has morphological affinities with *Marasmiellus*, *Hemimycena*, *Pulverulina*, and several mycenoid genera in Mycenaceae (Redhead and Singer 1981; Moncalvo et al. 2002; Matheny et al. 2006, 2020; Redhead 2012; See discussion under *M. pseudoomphaliiformis* for detailed comparison with the most similar species).

The phylogenetically closely related genus, *Pseudohydropus* Vizzini & Consiglio differs from *Marasmiellomycena* by a mycenoid habit, sinuate, adnexed to adnate lamellae, globose to broadly ellipsoid basidiospores and the presence of pileocystidia (Consiglio et al. 2022). *Vizzinia* (see below) differs by basidiomata turning brown on handling, a distinctly squamulose pileus, a floccose or floccose-fibrillose stipe, weakly amyloid spores, and the absence of cheilocystidia (Consiglio et al. 2022). *Pulverulina ulmicola* (H.E. Bigelow) Matheny & K.W. Hughes, the only species of the genus *Pulverulina* Matheny & K.W. Hughes, differs by clitocyboid basidiomata, a white stipe, a pileipellis in the form of a regular cutis and constantly cylindrical caulocystidia (Matheny et al. 2020).

Marasmiellomycena pseudoomphaliiformis Antonín & Ševčíková, **sp. nov.**

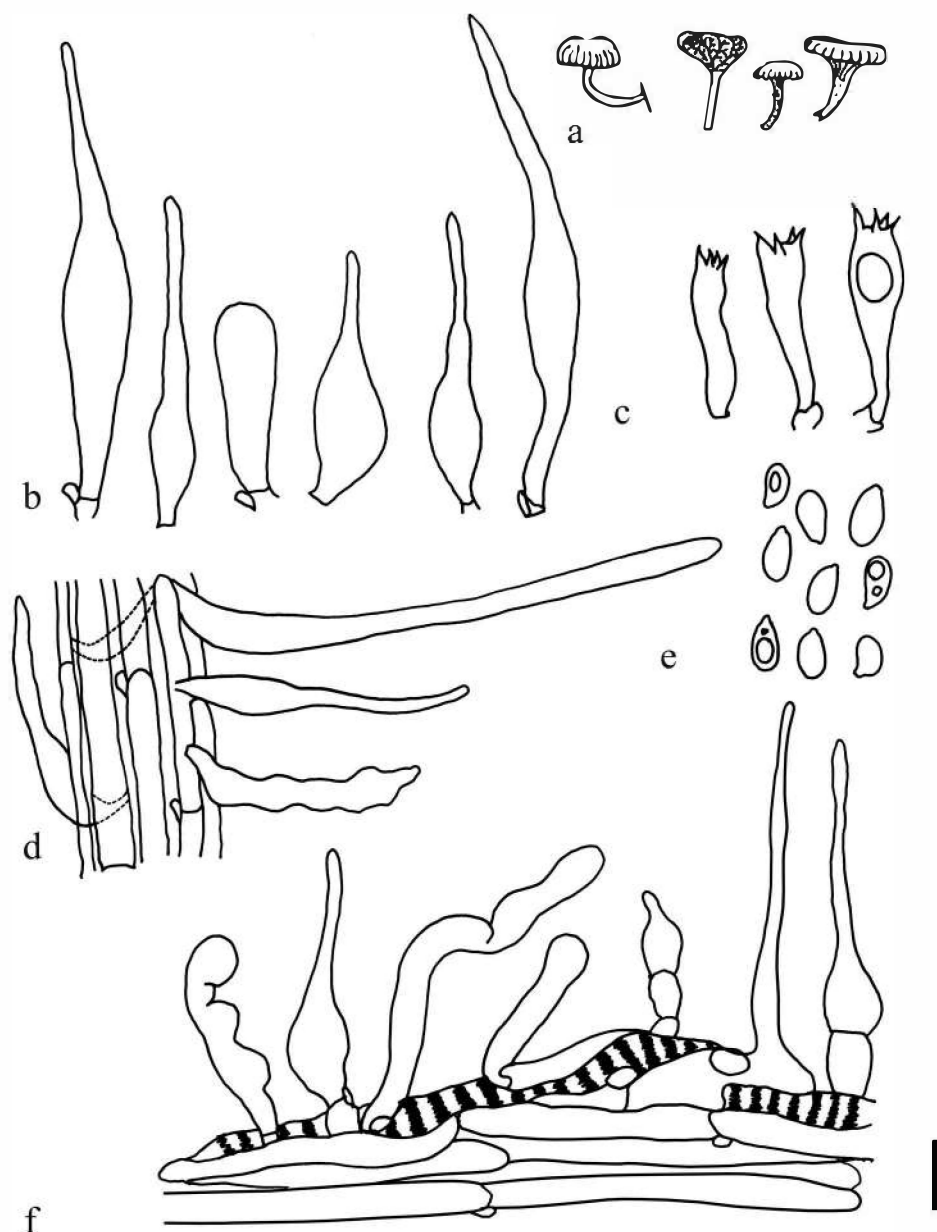
Index Fungorum number: IF900584; *Facesoffungi* number: FoF 14223; Fig. 153

Etymology: species epithet refers to the close resemblance of this species to *M. omphaliiformis*.

Diagnosis: differs from *M. omphaliiformis* by distinct ITS and LSU sequences and by the geographic distribution in North America.

Macromorphology: *Pileus* 4–16 mm, convex with plane, slightly papillate or slightly depressed centre when young, then \pm applanate and omphaloid, funnel-shaped at the end, with small central umbilicus, with involute to straight, finally uplifted, slightly undulate margin, entirely finely tomentose to pubescent when young, partly glabrescent when old, but with constantly pubescent margin, hygrophamous, slightly translucently striate in older basidiomata, distinctly radially grooved at margin when old, with small brown radial

Fig. 153 *Marasmiellomyces pseudoomphaliiformis* (Drawing based on BRNM 552721). **a** Basidiomata. **b** Cheilocystidia. **c** Basidia. **d** Stipitipellis with caulocystidia. **e** Basidiospores. **f** Pileipellis with pileocystidia. Scale bar = 10 μm



fibrils, most close and suberect at centre, less frequent and adpressed at margin, dark watery brown (up to 8E7) when moist and very young then whitish to pale beige (c. 5B2–3) with darker centre, in mature basidiomata watery beige to greyish (slightly paler than 5B2–4), or greyish (between 6B3 and 6C3), sometimes brownish or brown (c. 7D6, 7E8) when moist, drying-up to whitish. *Lamellae* distant, $L = 14\text{--}17$, $l = 1\text{--}2(-3)$, broadly adnexed when young, almost triangular and shortly decurrent when old, intervenose and sometimes forked especially when old, white to cream-white or beige (c. 6B3), with concolorous, finely pubescent edge. *Stipe* $5\text{--}11 \times 0.6\text{--}1.3$ mm, central to slightly eccentric, subsinistitious, cylindrical when very young, then tapering towards base, broadened into a small disc at base, entirely white

pubescent, finely longitudinally fibrillose in lower part, basal hairs brown, slightly carnosous tinged (paler than 8B2) when very young, then whitish to pale brownish at apex and dark brown to black-brown (7F6–7, 9F5, 9F8) at base and sometimes entirely dark brown when old. *Context* without distinct smell and taste, very thin, in pileus whitish and greyish under pileipellis, in stipe hollow, cortex concolorous with the colour of stipe surface.

Micromorphology: *Basidiospores* $(6.5\text{--})7.0\text{--}9.0(-9.5) \times 4.0\text{--}5.5$ μm , average 7.93×4.64 μm , $E = 1.55\text{--}1.88(-2.0)$, $Q = 1.69\text{--}1.75$, ellipsoid, ellipsoid-fusiform, smooth, inamyloid, non-dextrinoid. *Basidia* $(21.5\text{--})29\text{--}33 \times 6.1\text{--}9.0$ μm , 4-spored. *Basidioles* $15\text{--}34 \times 3.5\text{--}8.0$ μm , clavate, subfusiform or cylindrical. *Cheilocystidia* $25\text{--}87 \times 9.0\text{--}18$ μm ,

sometimes indistinct, (irregularly) clavate, fusiform to lageniform, sometimes with up to 40 µm long, tapering neck. Trama hyphae ± cylindrical, colourless, thin-walled, up to 17 µm wide. *Pileipellis* a cutis composed of cylindrical, smooth or incrustated, sometimes with brown walls, 3.0–9.2(–14) µm wide hyphae; terminal cells in groups (especially towards margin), (7.2–)20–88 × (3.2–)4.8–12.3 µm, irregularly cylindrical to narrowly clavate or clavate, often with coloured walls; awl-shaped cells (pileocystidia) present especially towards centre. *Stipitipellis* a cutis of cylindrical, ± slightly thick-walled, 2.5–8.5 µm wide hyphae. *Caulocystidia* (17.8–)20–50 × 5.2–12 µm, fusiform, clavate, sometimes rostrate, thin- to slightly thick-walled. Trama and cystidia metachromatic in Cresyl blue. *Clamps* present in all studied tissues.

Hosts and geographical distribution: On decaying wood of a broad-leaved tree and leaves veins in amixed forest (*Acer*, *Carya*, *Pinus*, *Quercus*, *Rhododendron*, *Tsuga*); USA, Tennessee and North Carolina.

Holotype: USA, Tennessee, Blount Co., Great Smoky Mts. Nat. Park, Parsons Branch Road, Gregory Ridge Trail, 29 July 1991 leg. V. Antonín 91/277 (BRNM 552721).

Additional material examined: USA, Tennessee, Blount Co., Great Smoky Mts. Nat. Park, Parsons Branch Road, 31 July 1991 leg. et det. V. Antonín 91/297 (BRNM 552653). USA, Tennessee, Blount Co., Great Smoky Mts. Nat. Park, Cades Cove, Crib Gap, 22 July 1991 leg. et det. V. Antonín 91/242 (BRNM 552654). USA, North Carolina, Swain Co., Great Smoky Mts. Nat. Park, Kephart Prong Trail, 25 July 1991 leg. et det. V. Antonín 91/258 (BRNM 552658).

Notes: Our collections (BRNM 552721, BRNM 552653, BRNM 552654, BRNM 552658) are morphologically identical and they are characterized by an omphalinoid habit, a small, mostly pale coloured pileus, broadly adnexed to (shortly) decurrent, white, cream-white, or beige lamellae, a short, central to slightly eccentric, subsinistitious, entirely white pubescent stipe, ellipsoid, ellipsoid-fusiform Basidiospores, (irregularly) clavate, fusiform to lageniform cheilocystidia, a pileipellis a cutis with irregularly cylindrical to narrowly clavate, clavate or awl-shaped terminal cells, and fusiform, clavate, sometimes rostrate caulocystidia. Our collections formed a well-supported clade with strains of *Porothelium omphaliiforme* (Fig. 152). The blastn searches with NCBI revealed most similar species to our collection as *P. omphaliiforme* (OM422782) with 97.1% (ITS) respective *P. omphaliiforme* (OM423656) with 99.5% sequence similarity (LSU). However, our collections are morphologically different from *P. omphaliiforme*. Consiglio et al. (2022) mentioned that *Hydropus omphaliiformis* (PBM4282, ITS: MT196987), collected in the USA is phylogenetically distant from *Hydropus* sensu stricto, representing an undescribed species. Therefore, our collections together with *P. omphaliiforme* represent a generic lineage and herein introduce as

Marasmiellomyцена. Our collections represent a distinct lineage which is sister to *P. omphaliiforme* and we introduce this clade as *Marasmiellomyцена pseudomphaliiformis*.

Hemimycena mairei belongs to the undescribed “hemimycenoid genus 1” in the Dima’s tree (Lehmann and Lüderitz 2018), while sequences of *H. gracilis* (Quél.) Singer (DQ457671) and (DQ490623) probably represent the “hemimycenoid genus 2” together with *H. ochrogaleata* (J. Favre) M.M. Moser. Both of these genera are distinct from *Marasmiellomyцена*.

Marasmiellomyцена pseudomphaliiformis is macro- and micromorphologically very similar to *M. omphaliiformis*. The description of *Porothelium omphaliiforme* by Antonín and Noordeloos (2010) is based on both European and North-American collections, and therefore, represents a mixed description of these vicariants. The morphological comparison of *Marasmiellomyцена pseudomphaliiformis* with similar taxa listed in Table 7.

Marasmiellomyцена omphaliiformis (Kühner) Mateos, Kolařík, De la Peña-Lastra, Ševčíková & Antonín, *comb. nov.*

Index Fungorum number: IF900585; ***Facesoffungi number:*** FoF 14224; ***Figs.*** 154, 155.

Basionym: *Marasmius omphaliiformis* Kühner, in Kühner & Romagnesi, *Bull. Soc. nat. Oyonnax* 8: 75, 1954

Synonym: *Porothelium omphaliiforme* (Kühner) Vizzini, *Consiglio & M. Marchetti, Rivista di Micologia* 64: 110. (2021) 2022;

Marasmiellus omphaliiformis (Kühner) Noordel., [as ‘*omphaliiformis*’], *Persoonia* 12 (1): 35. 1983;

Hydropus omphaliiformis (Kühner) Honrubia, [as ‘*omphaliiformis*’], *Cryptog. Mycol.* 5 (1): 57. 1984;

Mycena lapalmaensis Dähncke & Robich, *Bol. Soc. Micol. Madrid* 34: 99. 2010

Holotype: France, Charente Maritime, Corniche de Nauzan pres Royan, 2 September 1935, R. Kühner (fragm. in PC).

Macromorphology: *Pileus* 1–5 mm, hemispherical, convex, plano-convex and/or with umbilicate, sometimes somewhat depressed centre when mature, with involute, not translucently striate, not hygrophanous, not radially grooved margin, *Pileipellis* distinctly pruinose, whitish pubescent, with innate conglomerated fibrils and also granulate appearance; cream-coloured in the background and reddish-brown fibres when young (Ség. 250), turning greyish or sordid with age (Ség. 694), especially in the center. *Lamellae* distant, L = 14–16, l = 0–1, arcuate-decurrent, sometimes forked, and somewhat intervened in the background, larger, cream-white to pale ochre with a slightly darker edge, with whitish abundant hairs on the lamellar edge. *Stipe* 5–10 × 0.6–1 mm, cylindrical, sometimes broadened towards the base, sometimes bulbous, pale ochre at the top, ochre in the middle part

Table 7 Differences between *Marasmiellomycena pseudoomphaliiformis* and morphologically similar species

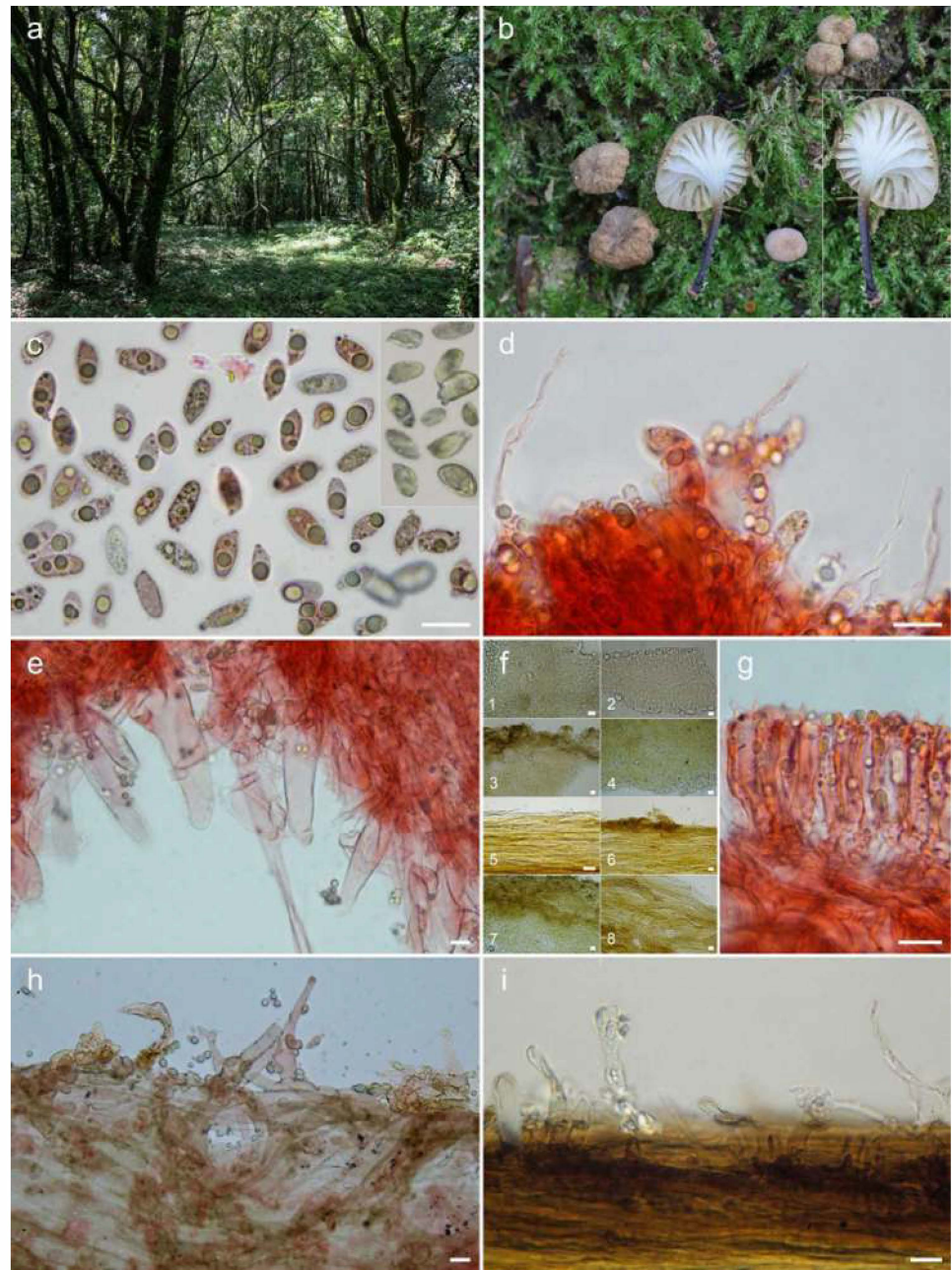
Species	Difference	References
<i>Marasmiellus candidus</i> (Bolton) Singer	Distinctly larger basidiospores	Antonín and Noordeloos (2010)
<i>Marasmiellus celebanticus</i> Pérez-De-Greg., Vizzini, Contu & Roqué	A constantly darker, light brown, caramel then brown, dark brown pileus, distinctly larger basidiospores, smaller and differently shaped cheilocystidia and caulocystidia and pileipellis terminal cells (pileocystidia) without flabelliform elements	Pérez-De-Gregorio et al. (2011)
<i>Porotheleum albodescendens</i> J.A. Cooper	A constantly pale pileus, slightly narrower basidiospores, absence of cheilocystidia and pleurocystidia, and longer, differently shaped pleurocystidia	Consiglio et al. (2022)
<i>Porotheleum parvulum</i> Angelini, Vizzini, Consiglio & M. Marchetti	A sparse, minutely darkly squamulate pileus, ochre-brown in the center, fading to pale ochre-yellow outside, slightly smaller basidiospores, absence of cheilocystidia and pileocystidia and different pileipellis	Consiglio et al. (2022)
<i>Clitocybula albida</i> A.K. Dutta, K. Acharya & Antonín	A pileus with a brownish orange to light brown, later pale orange to light orange or light brown center, slightly larger weakly amyloid basidiospores, 2-spored basidia, cheilocystidia and pileocystidia without a flabelliform tapering neck	Dutta et al. (2018)
<i>Marasmiellus tricolor</i> (Alb. & Schwein.) Singer	A pileus with a conical papilla, larger spores (except f. <i>americanum</i> Singer), Rameales-structure of pileipellis and cystidia and occurs in Herbaceae and grasses	Antonín and Noordeloos (2010)
<i>Hemimycena mairei</i> (E.-J. Gilbert) Singer	smell resembles <i>Clitopilus prunulus</i> , smaller cheilocystidia, the absence of pileocystidia, only cylindrical to clavate caulocystidia and growing among mosses and grasses	Singer (1943); Antonín and Noordeloos (2004)
<i>Hemimycena sordida</i> Noordel. & Antonín	Clavate or irregular corralloid cheilocystidia and a pileipellis without pileocystidia and growing on soil together with mosses and grass	Antonín and Noordeloos (2004)
<i>Atheniella delectabilis</i> (Peck) Lüderitz & H. Lehmann	A hygrophanous pileus, cheilocystidia usually with subcapitate apex and a different pileipellis	Peck (1875); Antonín and Noordeloos (2004); Lehmann and Lüderitz (2018)

(Ség. 250) and turning dark brown (Ség. 701) to blackish in the lower part (Ség. 706), pubescent, formed by whitish hairs distributed along its entire length, non-insititious, with basal hairs. Species thin-fleshed, often with elastic, cartilaginous or leathery flesh and which generally dry out without rotting, reviscent appearance.

Micromorphology: Spores (6.3–)7.5–8.6–9.9(–10.3) × (3.7–)3.8–4.1–4.6(–4.9) μm; Q = (1.5–)1.8–2.1–2.3(–2.6); n = 32; V_m = 78 μm³, smooth, narrowly ellipsoid or subcylindrical, ellipsoid, sublacrymoid or sometimes fusiform, with thick apiculum, usually with one, two or more oily guttules. Basidia 20–37 × 4–7 μm, claviform, with sterigmata 3–3.5 μm high, tetrasporic. Basidioles

claviform or subcylindrical, 18–35 × 4–6.5 μm. Lamellar edge low fertile and heterogeneous, cheilocystidia numerous, 37–58 × 5.7–7.6 μm, sublageniform, with slightly broadened base and flagelliform neck (1.7–3.5 μm). Pleurocystidia absent. Hymenophoral trama subregular, 2.5–6.0 μm wide hyphae, trama elements 99–120 × 15–31 μm, abundant, fusiform, sometimes thick-walled. Pileipellis an irregular cutis with transitions to a trichoderm, made up of 3–10 μm wide cylindrical hyphae, with scattered suberect or erect fusiform, sublageniform or flagelliform, thin-walled, weakly diverticulate terminal elements, very polymorphous, 30–56 × 6–10.3 μm; with brown intracellular pigment. Stipitipellis a cutis of parallel, cylindrical, smooth, 2–6.0 μm

Fig. 154 *Marasmiellomyces omphaliiformis* (AMI-SPL252). **a** Habitat. **b** Basidiomata (RC, MLZ). **c** Basidiospores (RC, MLZ). **d** Cheilocystidia (RC). **e** Hymenophoral trama elements (RC). **f** Chemical reactions: 1–2, trama of lamellae (MLZ, KOH); 3–4, trama subpellis (MLZ, KOH); 5–6, trama stipitipellis (MLZ, KOH); 7 trama subpellis (BC); 8, trama stipitipellis (BC). **g** Hymenium (RC). **h** Pileipellis (RC). **i** Caulocystidia and stipitipellis. Scale bars: c–i = 10 μ m



wide hyphae, with dark brown intracellular pigment. *Caulocystidia* numerous along the entire length of the stipe, (15.1–)30.8–62.6(–65.8) × (2–)2.4–11, 6(–15.5) μ m, fusiform, subclavate, sublageniform, sometimes with digital projections, usually narrowed at the apex or large rostrum. *Clamps* present in all tissues. *Chemical reactions* no part of the basidiocarp dextrinoid or amyloid, except the spores which are slightly amyloid. Cresyl blue negative in all tissues. KOH 10% slightly yellowish in the subpellis.

Material examined: Spain, Galicia, Pontevedra, Vilagarcía de Arousa, Parque Nacional das Illas Atlánticas de Galicia, Illa de Cortegada, N42° 37' 1.29" W8° 47' 10.97",

10 m a.s.l., growing on the lower part of a living trunk of *Quercus robur* L., 22 August 2020, S. De la Peña-Lastra, AMI-SPL252.

GenBank numbers: ITS: MZ542542, LSU: MZ542546.

Hosts and geographical distribution: Saprobic on a woody trunk of *Quercus robur*; northwestern Spain.

Notes: Our collection (AMI-SPL252) and another unpublished collection (AMI-SPL250) were consistently showed negative Cresyl blue reaction in all tissues, in many preparations at various temperatures (up to 70 °C). Noordeloos (1983) mentioned the metachromatic reaction of the trama in Cresyl blue as one of the crucial features of this species

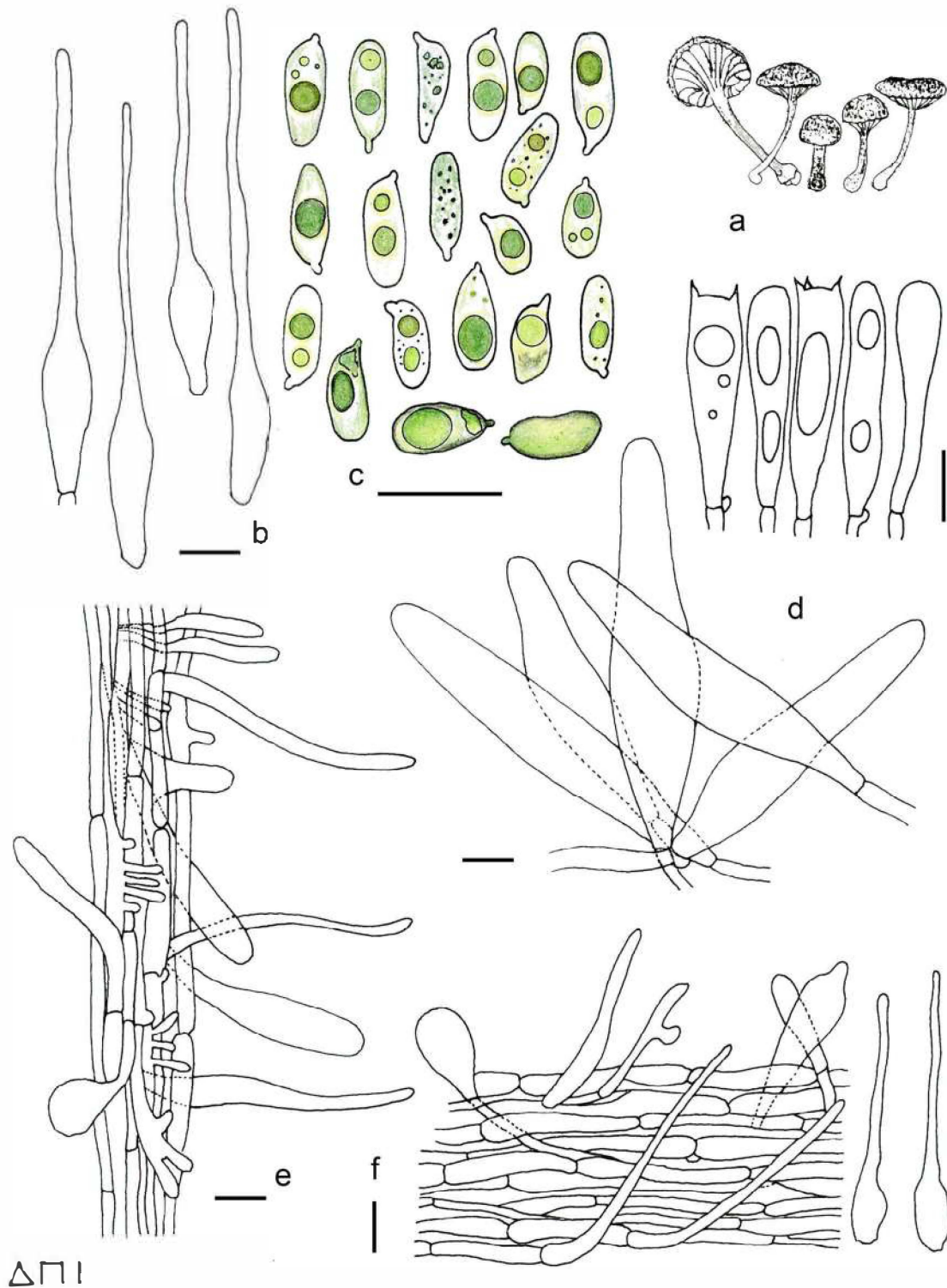


Fig. 155 Line drawing of *Marasmiellomycena omphaliiformis* (AMI-SPL252). **a** Basidiomata. **b** Cheilocystidia. **c** Basidiospores. **d** Hymenophore with basidia, basidioles and trama elements. **e** Stipitipellis and caulocystidia. **f** Pileipellis. Scale bars: b–f = 10 μ m

together with its trichodermal pileipellis and almost setiform/flagelliform elements. Consiglio et al. (2022) also emphasized this feature as stable within this very variable

species. Also caulocystidia with digital projections are atypical for *Marasmiellomycena omphaliiformis*. However, collection AMI-SPL252 clustered and is identical to

M. omphaliiformis. Thus, its variability is larger than these authors expected. *Marasmiellomyces omphaliiformis* is a morphologically variable species (Antonín and Noordeloos 1993, 2010; Consiglio et al. 2022) (Figs. 154, 155).

***Vizzinia* Ševčíková & Kolařík, gen. nov.**

Index Fungorum number: IF900586; *Facesoffungi number*: FoF 14225

Etymology: in honor of the mycologist Alfredo Vizzini for his excellent contribution to mycology.

Diagnosis: Genus *Vizzinia* (see below) differs from *Marasmiellomyces* by basidiomata turning brownish on handling, distinctly squamulose pileus, floccose or floccose-fibrillose stipe, weakly amyloid spores, and absence of cheilocystidia (Consiglio et al. 2022).

Basidiomata strongly omphalinoid to omphalinoid-clitocyboid-marasmioid. *Pileus* small, squamulose, translucently radially striate-furrowed. *Lamellae* often whitish, thick, distant, intervenose, adnate-decurrent to long-decurrent, with lamellulae of various length. *Stipe* cylindrical, fistulous, covered with floccose fibrils, often darker on the lower part, strigose at the lowest part of the base. *Context* thin, turning brownish on handling. *Odour* non-distinctive. *Basidiospores* colourless, thin-walled, smooth, congophilic, cyanophilic, weakly amyloid. *Basidia* slightly amyloid at apex. *Hymenial cystidia* absent. Subhymenium filamentous, consisting of intertwined short elements. *Hymenophoral trama* metachromatic. *Pileipellis* a cutis with frequent or rare pileocystidioid elements. *Caulocystidia* present. Thromboplerous hyphae and clamp connections present.

Type species: *Vizzinia nigripes* (Angelini, Vizzini, Consiglio & M. Marchetti) Ševčíková & Kolařík

Notes: The genus *Vizzinia* contains two species viz. *V. domingense* and *V. nigripes* and it forms a well-supported lineage clearly represents a new genus. This genus matches optimal thresholds at the genus level according to Vu et al. (2018); which is 98.2% based on LSU barcodes and 94.3% based on ITS barcodes. The closest matches with NCBI were *P. fimbriatum* with 96.64–96.37% (*Vizzinia nigripes* type) and 97.59%–97.36% (*V. domingense* type) based on LSU; *P. omphaliiforme* reference species with 84.28% (*V. nigripes* type) and 90.19% (*V. domingense* type) based on ITS. Consiglio et al. (2022) mentioned that “these groups of species will probably be considered as independent genera, especially the *P. albodescendens*/*P. omphaliiforme* and *P. domingense*/*P. nigripes* pairs”. In spite of these claims, they preferred to describe these species as *Porotheleum domingense* and *P. nigripes*. We could not avoid solving this new genus, if we want to justify the existence of the genus *Marasmiellomyces* and we believe that our new species *M. pseudoomphaliiformis* makes clear enough the relationship between *P. omphaliiforme* and *P. domingense*/*P. nigripes* lineages.

Vizzinia nigripes (Angelini, Vizzini, Consiglio & M. Marchetti) Ševčíková & Kolařík **comb. nov.**

Index Fungorum number: IF900587; *Facesoffungi number*: FoF 14226

Basionym: *Porotheleum nigripes* Angelini, Vizzini, Consiglio & M. Marchetti, in Consiglio et al., *Micologia* 64 (2): 165, 2022.

Holotype: Dominican Republic, Sosúa (Puerto Plata Province), Puerto Chiquito, 20. December 2016, leg. C. Angelini (JBSD 131803).

Vizzinia domingense (Angelini, Vizzini, Consiglio & M. Marchetti) Kolařík & Ševčíková **comb. nov.**

Index Fungorum number: IF900588; *Facesoffungi number*: FoF 14227

Basionym: *Porotheleum domingense* Angelini, Vizzini, Consiglio & M. Marchetti, in Consiglio et al., *Micologia* 64 (2): 163, 2022.

Holotype: Dominican Republic, Sosúa (Puerto Plata Province), Puerto Chiquito, 8 December 2013, leg. C. Angelini (JBSD 131801).

Notes: Both species share a lot of similarities to identical morphological features. However, *Vizzinia domingense* seems to possess a strictly omphalinoid shape of basidiomata, while appearance of *V. nigripes* was described as omphalinoid-clitocyboid-marasmioid (Consiglio et al. 2022). Phylogenetically, *V. nigripes* is relatively distant from *V. domingense*. More collections need to explain the taxonomical position and limitation of the genus *Vizzinia*.

***Pleurella* E. Horak**

Members of *Pleurella* are commonly characterized by smooth, strongly amyloid, elliptical or subcylindrical spores, conspicuous cheilocystidia, form of the carpophores and habitat (Horak 1971). Currently, this genus includes two species, viz. *Pleurella ardesiaca* and *P. microspora* (Alessio & Nonis) Vizzini, Consiglio & E. Campo (Horak 1971; Vizzini et al. 2022). In this study, we provide a new geographical record for *Pleurella ardesiaca* from China.

Pleurella ardesiaca (G. Stev. & G.M. Taylor) E. Horak, N.Z. *Jl Bot.* 9(3): 477 (1971)

Index Fungorum number: IF320667; *Facesoffungi number*: FoF 14228; Fig. 156

Macromorphology: On rotten wood and bark of unidentified host. *Pileus* 13–40 mm diam., convex to plano-convex at first, then becoming umbellate to plane, margin smooth; white (5A1), grayish orange (5B4–7), brownish orange (5C5–6), brown (5E6–7); *Lamellae* adnate, emarginated or subdecurrent, regular, very crowded, white (1A1) at the beginning, later turning cream coloured (18B1), pale orange (5A5) when maturity or after bruising; gill edge even. *Stipe*

Notes: Our phytophthora-like isolates phylogenetically close to the species in the sub-clade 6b (Fig. 162) and they grouped with *Phytophthora megasperma* forming a sister clade with ML = 100 statistical support. However, nucleotide differences in ITS, β -*tubulin* and *cox1* loci of our isolates and *P. megasperma* revealed 0.12%, 0.61%, and 0.18% respectively. Our collection morphologically differs from *P. megasperma* by sporangia shape and sizes, colony growth and formation, a lower minimum temperature for growth, apleurotic oospores and antheridia mostly amphigynous. Further, our collection is phylogenetically closed to *P. crassamura* that have 0.49%, 0.73%, and 2.97% nucleotide differences in ITS, β -*tubulin* and *cox1* loci respectively. *Phytophthora crassamura* produces sporangia similar in shape to our collection, but significantly smaller in size ($\bar{x} = 60.3 \pm 6.0 \times 37.4 \pm 3.6 \mu\text{m}$, with a length/breadth ratio of 1.6). Therefore, we introduce our collection as *P. debattistii* sp. nov.

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Declarations

Conflict of interest The authors declare that they have no conflict of interest.

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