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In this 7th contribution to the Fungal Systematics and Evolution series published by Sydowia, the authors formally describe 14 species: *Cantharomyces paschalis*, *Cryptandromyces pinguis*, *C. tricornis*, *Laboulbenia amblystomi* (Laboulbeniales); *Cortinarius squamosus*, *Entoloma brunneicoeruleum*, *E. callipygmaeum*, *E. minutigranulosum*, *E. perasprellum*, *E. pulchripes*, *E. tigrinum*, *E. timidum*, *E. violaceoserrulatum* (Agaricales); and *Suillus quercinus* (Boletales). The following new country records are reported: *Crepidotus malachioides* from Italy, *Leucoagaricus mucrocystis* from French Guiana, *Pluteus multiformis* from Turkey (Agaricales); *Herpomyces periplanetae* from Bénin, the D.R. Congo, and Togo (Herpomycetales); *Melanustilospora ari* from Pakistan (Urocystidales); *Neopestalotiopsis clavispora* causing fruit rot on *Zizyphus mauritiana* from India (Amphisphaeriales); and *Phytopythium chamaehyphon* and *Pp. litorale* from Brazil (Peronosporales). Finally, a new combination is proposed based on morphology, ecology, and phylogenetic analysis: *Rhodocollybia asema* (Agaricales).

Keywords: 14 new species, 8 new records, 1 new combination, Agaricomycetes, Entolomataceae, integrative taxonomy, Laboulbeniomycetes, Oomycota, Sordariomycetes, Ustilaginomycetes.

Materials and methods

Sample collection, isolation, and specimen examination

Most of the host insects bearing thalli of *Cantharomyces* Thaxt., *Cryptandromyces* Thaxt., and *Laboulbenia* Mont. & C.P. Robin were supplied to S. Santamaria and W. Rossi by entomologists. The host insects of *Laboulbenia amblystomi* sp. nov. from Spain and Thailand were collected in the field either by hand or by light trap. Permanent slide mounts were prepared following the method described by Rossi & Santamaria (2015) and were deposited at FI or BCB. Photomicrographs were captured with a ProgRes 10 Plus digital camera (Jenoptik, Jena, Germany) on a Leica DMR microscope (Leice Biosystems, Wetzlar, Germany) with differential interference contrast optics (DIC); images were processed with Photoshop CS5 (San Jose, California) and Dpx View Pro (Deltapix, Måløv, Denmark).

Basidiomata of *Cortinarius* (Pers.) Gray were collected in Çilekli Village, Trabzon, Turkey. Photographs were taken in the laboratory. One of the basidiomata was used for a spore print; other basidiomata were dried for further studies and vouchering purposes. Free-hand sections of pileus and lamellae were treated in 5 % NH_4OH, some of them were stained with 1 % Congo red and photographed. Microscopic structures were observed and photographed under an Axio Imager A2 trinocular microscope with Axio Imager software (ZEISS, Jena, Germany). The description follows previous literature, including Moser et al. (1995), Bidaud et al. (1997), Høiland & Holst-Jensen (2000), Moser (2002), Bidaud et al. (2006), Niskanen & Kytövuori (2008), and Niskanen et al. (2012). Specimens are deposited in the herbarium of the Fatih Education Faculty at Trabzon University (KATO).

Collections of *Entoloma* spp. were photographed in the field. Macroscopic characters were noted straight after collecting. Color codes in the descriptions follow Kornerup & Wanscher (1978), except for *Entoloma perasprellum* sp. nov. that follows Munsell Color Company (1954). Microscopic characters were studied with a Leica DMLS microscope, using a drawing tube and a Touptek Phototronics camera (Zhejiang, China); a ZEISS Axioscope A1 microscope with AxioCam 1Cc 3; and a ZEISS Axiophot microscope with DC controlled Cree XP-G3 R3 CRI 90+ LED illumination, Plan Neofluar objectives 40×/1.30 Oil, 100×/1.30 Oil (ZEISS), differential interference contrast (DIC) optics, a 12MP Touptek video camera with SONY Exmor IMX226 CMOS sensor (Tokyo, Japan), and Toupview video & image processing software (Touptek Photonics). Basidiospores, basidia, and cystidia were observed in squash preparations of small parts of the lamellae in 5 % KOH or 1 % Congo Red in concentrated NH_4OH. Pileipellis was examined on a radial section of the pileus in 5 % KOH. Stipitipellis was examined in 10 % Ammonia solution. Basidiospore dimensions are based on measuring 20 spores, dimensions of cystidia and basidia on observing at least 10 structures per collection. Basidia were measured without sterigmata, and the basidiospores without apiculus. Spore length to width ratios are reported as Q. Collections are deposited at the following herbaria: BBF, GB, L, LE, O, WU (sensu Thiers continuously updated).

For the *Suillus* Gray study, specimens were collected from moist temperate forests in Khyber Pakhtunkhwa Province, Pakistan. Basidiocarps were photographed in the field. Fresh morphological characters were recorded in the field; colors follow Munsell Color Company (1954). Field data on basidiocarps (site, habitat, association, etc.) was noted. Specimens were studied microscopically following Bessette et al. (2000). For basidiospore dimensions, the first and last values represent the range of lengths and widths, whereas the values in parentheses represent mean lengths and widths ± standard deviations; Q, length/width ratio of an individual basidiospore; Q_{av}, the mean of Q. Other measurements are given as a range with outlier values in parentheses. Voucher specimens are deposited at LAH (sensu Thiers continuously updated).

The macroscopic description of *Crepidotus malachioides* is based on observations of fresh material. Photographs were taken with a Canon EOS 80D camera (Tokyo, Japan). The micro-morphological characters are based on the study of both fresh and dried material. Dry specimens were rehydrated in distilled water or 10 % KOH before observation and mounted in aqueous Congo Red. In the notation of basidiospore dimensions, (a–)b–c(–d), 'b–c' is the range including 90 % of the measured values, with 'a' and 'd' being extreme values. Q represents the range of the length/width ratio for all measured spores. For all microscopic structures, 20 elements were measured. Voucher specimens are deposited at GDOR (sensu Thiers continuously updated).

For the *Herpomyces* Thaxt. study, *Periplaneta americana* cockroaches (Blattodea, Blattidae) were collected by hand and screened for the presence of *Herpomyces* thalli (Ascomycota, Laboulbeniomycetes) under 40–50× magnification. Antennae were dislodged from the host and embedded in cotton blue, resulting in clearly colored thalli. Next, thalli were removed from the antenna using a stainless steel No. 000 insect pin (Ento Sphinx, Pardubice, Czech Republic). Thalli were embedded in Amann solution (Benjamin 1971) with the help of a droplet of Hoyer's medium as described by De Kesel et al. (2020). Permanent slides are deposited at BR. Mounted thalli were viewed at 200–1,000× magnification using an Olympus BX51 light microscope (Tokyo, Japan) with drawing tube, digital camera, and AnalySIS software (Soft Imaging System GmbH, Münster, Germany).

For the *Leucoagaricus* Locq. ex Singer study, macromorphological features were studied on fresh collections as well as by analyzing photos taken in the field. Micromorphological data were obtained from dried material and observed under a Zeiss Axio Imager.A2 light microscope, equipped with AxioVision Release 4.8.2. software. Measurements were done with a 100× oil immersion objective (1,000× magnification). Dried basidiomata were sectioned with a razor blade, and the sections were mounted in water, stained with ammoniacal Congo red and Melzer's reagent, separately. The specimens are deposited at the Department of Plant Anatomy, Eötvös Loránd University, Budapest, Hungary (ELTE).

For the *Melanustilospora* Denchev study, infected plants of *Arum jacquemontii* (Alismatales, Araceae) were collected in Kalam, a sub-valley of Swat (Pakistan), situated at 2,085 m a.s.l. Swat valley is an important phytogeographic region in northwestern Pakistan with a very rich flora (Ali & Qaiser 1986, Ahmad et al. 2015). The genus *Arum* is native to Europe, Northern Africa, and Central and Western Asia, with the highest species diversity in the Mediterranean region (Govaerts et al. 2002). In Pakistan, only one species is currently known, *Arum jacquemontii*, found in northern areas of the country, including Swat (Stewart 1972). Spores were studied by light and scanning electron microscopy (SEM). Spores were observed under an Olympus BX40 compound microscope in lactic acid. For SEM, spores were attached to specimen holders using double-sided adhesive tape and coated with a 50-nm film of gold in a Polaron E5300 freeze dryer (Quorum Technologies, Laughton, UK). The gold-coated stubs were photographed in a 3-30BM scanning electron microscope (CamScan Inc., Cranberry Township, PA). Measurements of teliospores are presented as (a–)b–c(–d), with 'b–c' representing 90 % of the measured values, and 'a' and 'd' being extreme values. Studied materials are deposited at LAH.

The *Neopestalotiopsis* Maharachch., K.D. Hyde & Crous study was conducted in November–December 2017, with the detection of symptoms of fruit rot on ripened skins of Ber fruit, *Zizyphus mauritiana* (Rosales, Rhamnaceae). Observations were made in five different orchards in Cooch Behar District, West Bengal, India. Diseased tissue was cut into small pieces and surface-sterilized with 0.1 % $HgCl_2$ for 30 sec, then plated on potato-dextrose agar (PDA) and incubated for 10 days at 25 °C and photoperiod of 12:12 (L:D) h. To confirm pathogenicity, both mycelial plug inoculation (5 mm diam.) and conidial suspension injection (1×10^6 conidia/ml) were performed under laboratory condition (20 °C, relative humidity 90 %) on detached Ber fruit; control fruits were treated with PDA plug inoculation (5 mm diam.) and sterile water injection. Diseased plant material and cultures are preserved at the National Herbarium of Cultivated Plants, Indian Agricultural Research Institute, and at the Indian Type Culture Collection (New Delhi, India).

For the study of *Phytopythium* Abad, De Cock, Bala, Robideau, A.M. Lodhi & Lévesque in Brazil, samples of water, soil, submerged leaves, and surface sediments were collected in several areas of the Atlantic Rainforest. Soil, submerged leaves, and surface sediments were diluted in 30 ml of sterile ddH_2O and, along with water samples collected from freshwater bodies and rainbow trout farming tanks, plated and baited using the multiple baiting method (Milanez 1989). Plates were incubated for

4–7 days in an acclimatized room at ~22 °C. After this period, the baits (*Sorghum* spp. seeds, onionskin, corn leaves, and snakeskin) were observed under a Leica DMLB2 compound microscope. *Phytopythium* isolates were purified onto cornmeal agar (CMA) medium (Fuller & Jaworski 1987), with 0.5g/l streptomycin sulphate and 0.5g/l penicillin G. Species were identified morphologically based on the original descriptions using a Leica MC170 HD camera with Leica Qwin 3.1 software. Specimens were incorporated into the CCIBt culture collection (Coleção de Culturas de Algas, Cianobactérias e Fungos do Instituto de Botânica).

Collections of *Pluteus* Fr. were collected in the province of Muğla, Turkey in 2015. Morphological features were described from young to mature basidiomata. The macro-morphological descriptions and images of basidiomata were based on fresh material. For micro-morphological structures, dried basidiomata were rehydrated in 3 % KOH, and subsequently stained with Congo Red. The following abbreviations are used in the descriptions: L_m for the average length of all measured basidiospores, W_m for the average width, Q for length/width ratio, and Q_m for the average of all calculated Q values. At least thirty basidiospores from spore prints were measured. Microstructures were drawn with the help of Adobe Illustrator CS4 (San Jose, CA). Specimens are deposited in the personal fungarium of O. Kaygusuz at Isparta University of Applied Sciences (Turkey).

Collections of *Rhodocollybia* Singer were made in the framework of the Norwegian Barcode of Life project (NorBOL). Macromorphological observations are based on field notes, fresh or dried basidiomata were photographed by NorBOL staff in the laboratory as part of the standard NorBOL documentation method under a Creative Common Attribution NonCommercial ShareAlike (CC BY-SA) license. Specimens were dried in a dehydrator at 45 °C and deposited at O (sensu Thiers continuously updated).

DNA extraction, PCR amplification, and sequencing

For the *Cortinarius* study, total DNA was extracted from dried specimens following Murray & Thompson (1980). Primers ITS1F and ITS4 (White et al. 1990, Gardes & Bruns 1993) were used to amplify the internal transcribed spacer (ITS) barcode region, and LR0R and LR5 (Vilgalys & Hester 1990, Hopple 1994) were used for the large subunit (LSU) ribosomal RNA gene. Cycling conditions were as follows: initial denaturation at 95 °C for 5 min; followed by 35 cycles of denaturation at 94 °C for 45 s, annealing at 54 °C for 30 s, and extension at 72 °C for 45 s; followed by a final extension at 72 °C for 10 min (Mullis & Faloona 1987). PCR products were checked in 1% agarose gels, and positive reactions were sequenced with one or both PCR primers. Chromatograms were checked to search for putative reading errors, which were corrected manually.

For the *Entoloma* study, DNA was extracted from dried herbarium material using the NucleoSpin Plant II kit (Macherey-Nagel, Germany). Forward primers ITS1F and reverse primers ITS4 and ITS4B (White et al. 1990, Gardes & Bruns 1993) were used in both PCR and sequencing reactions for the ITS barcode region. PCR products were purified with the Fermentas Genomic DNA Purification Kit (Thermo Scientific, Pittsburg, PA). Purified PCR products were sequenced on an ABI model 3130 Genetic Analyzer (Applied Biosystems, Foster City, CA) or commercially at LGC Genomics (Berlin, Germany). Alternatively, DNA extraction, PCR, and sequencing procedures were performed through the Norwegian Barcode of Life project (NorBOL) and followed Larsson & Jacobsson (2004) and Larsson et al. (2018). Chromatograms were checked and edited with the CodonCode Aligner package (CodonCode Corporation, Centerville, MA) and MEGA X (Kumar et al. 2018). Sequence comparison with public and personal databases followed Noordeloos et al. (2017). Newly generated sequences were submitted to GenBank (Tab. 1).

Total DNA of *Suillus quercinus* sp. nov. was extracted from dried material following a modified CTAB extraction method (Lee et al. 1988). The extracted genomic DNA was evaluated using gel electrophoresis with 1 % agarose gels and a UVIpro Platinum gel documentation system (Uvitec, Cambridge, UK) with default settings. Genomic DNA was suspended in nuclease-free H_20 and stored at 20 °C. The ITS region was amplified using primers ITS1F and ITS4 (White et al. 1990, Gardes & Bruns 1993). Cycling conditions included an initial denaturation step at 94 °C for 1 min; then 35 cycles of denaturation at 94 °C for 1 min, annealing at 53 °C for 1 min, and extension at 72 °C for 1 min; and final extension at 72 °C for 8 min (Saba et al. 2020). Purification and sequencing were outsourced to Macrogen (Seoul, South Korea). Consensus sequences were generated from the obtained sequence reads in BioEdit version 7.0.9 (Hall 1999). Newly generated sequences were submitted to NCBI GenBank with accession numbers MT361744, MT361745, and MT361746.

Tab. 1. Details of sequences and isolates included in the BLAST searches and molecular analyses for the new species and interesting reports.

Species name	ID (isolate, strain^1, status^2, voucher)	Country, isolation source	SSU	ITS	LSU	Reference(s)
Agrocybe pediades	CIGYA 003	Mexico		MG817376		A.M. Montiel Gonzalez & R. Ortega Avila, unpubl.
Collybia butyracea	olrim421	Sweden		AY781251		Mata et al. (2004)
Collybia butyracea	olrim426	Sweden		AY805607		Mata et al. (2004)
Cortinarius aavae	VMS8	Canada		FJ717539		Harrower et al. (2011)
Cortinarius aciculisporus	G: 257	France		MT934844		Liimatainen et al. (2020)
Cortinarius albolens	PC:A. Bidaud 97-10-368	France		MT934855		Liimatainen et al. (2020)
Cortinarius aureifer	G:351	France		MT934893		Liimatainen et al. (2020)
Cortinarius badioflavidus	WTU:J.F. Ammirati 13668, T	USA		NR_153055		Li et al. (2016)
Cortinarius badioflavidus	WTU:M. Beug 11MWB111913	USA		KU041733		Li et al. (2016)
Cortinarius buxiolens	G:3300	France		MT934935		Liimatainen et al. (2020)
Cortinarius carcharias	G:4276	France		MT934948		Liimatainen et al. 2020
Cortinarius conicoumbonatus	KATO 3455	Turkey		MF696141		Sesli & Liimatainen (2018)
Cortinarius ferrugineifolius	IB:M. Moser 1964-0110	Sweden		MT935277		Liimatainen et al. (2020)
Cortinarius ferrugineifolius	IB:M. Moser 1991-0305	USA		MT935044		Liimatainen et al. (2020)
Cortinarius ferrugineovelatus	UBC:F17141	Canada		GQ159884		Harrower et al. (2011)
Cortinarius fulvoisabellinus	JB-8342/14	Spain		KU953939		Ballarà et al. (2016)
Cortinarius fulvoisabellinus	PC:RH1891	France		KJ206485		Dima et al. (2014)
Cortinarius griseascens	G:4263	France		MT935100		Liimatainen et al. (2020)
Cortinarius helvolus	TUB 011905	France		AY669667		Garnica et al. (2005)
Cortinarius herculinus	G:4195	France		MT935120		Liimatainen et al. (2020)
Cortinarius hinnuleoarmillatus	G: 00052098, T	France		NR_131790		Niskanen et al. (2006)
Cortinarius hinnuleoarmillatus	G:GK16160	France		DQ499464		Niskanen et al. (2006)
Cortinarius hinnuleoarmillatus	H:IK01-021	Finland		DQ499462		Niskanen et al. (2006)
Cortinarius hinnuleoarmillatus	H:TN03-093	Finland		DQ499460		Niskanen et al. (2006)
Cortinarius hinnuleoarmillatus	S:F39953	Sweden		DQ499461		Niskanen et al. (2006)
Cortinarius hinnuleocervinus	Ammirati 13502	USA		MT935133		Liimatainen et al. (2020)
Cortinarius hinnuleocervinus	Niskanen 12-175, T	USA		MG136827		Liimatainen (2017)
Cortinarius hinnuleovelatus	G:4203	France		MT935136		Liimatainen et al. (2020)
Cortinarius hinnuleus	CFP332	Sweden		DQ117926		Kytövuori et al. (2005)
Cortinarius hinnuleus	IB19960139	India		AY083183		Peintner et al. (2003)
Cortinarius cf. *hinnuleus var. minutalis*	2071876	Canada		MG786239		K. Liimatainen & J. Ammirati, unpubl.
Cortinarius hinnuloides	G:4285	France		MT935139		Liimatainen et al. (2020)
Cortinarius lepidus	G:765	France		MT935194		Liimatainen et al. (2020)
Cortinarius nauseosmus	G:4214	France		MT935240		Liimatainen et al. (2020)
Cortinarius ochraceoplicatus	G:378	France		MT935256		Liimatainen et al. (2020)
Cortinarius paraphaeochrous	IB:M. Moser 1991-0323	USA		MT935282		Liimatainen et al. (2020)
Cortinarius pseudohinnuleus	G:4224	France		MT935343		Liimatainen et al. (2020)
Cortinarius radicosissimus	G:142	France		MT935369		Liimatainen et al. (2020)
Cortinarius roseonudipes	G:37	France		MT935391		Liimatainen et al. (2020)
Cortinarius salicum	G:4479	France		MT935414		Liimatainen et al. (2020)
Cortinarius scabridipileus	H:7000550, T	Sweden		MT112168		Niskanen (2020)
Cortinarius semiodoratus	PC:R. Henry 91.6	France		MT935427		Liimatainen et al. (2020)
Cortinarius solidus	G:4253	France		MT935438		Liimatainen et al. (2020)
Cortinarius sp.	1745193	Spain		MG739379		B. McAdoo, unpubl.
Cortinarius speciosior	G:4280	France		MT935443		Liimatainen et al. (2020)

Species name	ID (isolate, strain[1], status[2], voucher)	Country, isolation source	SSU	ITS	LSU	Reference(s)
Cortinarius squamosus	KATO Fungi 3386, T	Turkey		MW314263	MW314262	This study
Cortinarius squamulifer	G:4260	France		MT935451		Liimatainen et al. (2020)
Cortinarius subfilamentosus	G:1196	France		MT935484		Liimatainen et al. (2020)
Cortinarius subhelvolus	G:470	France		MT935491		Liimatainen et al. (2020)
Cortinarius subrigidipes	IB:M. Moser 1991-0309	USA		MT935523		Liimatainen et al. (2020)
Cortinarius subulatus	G:4229	France		MT935536		Liimatainen et al. (2020)
Cortinarius tigris	G:4269	France		MT935553		Liimatainen et al. (2020)
Cortinarius umbrinolens	TUB 011918	Germany		AY669658		Garnica et al. (2005)
Crepidotus albolanatus	PDD:72865 holotype	New Zealand		KY827292		Horak (2018)
Crepidotus luteolus	16834	Italy		JF907963		Osmundson et al. (2013)
Crepidotus malachioides	303022	USA		MK607561		S.D. Russell & D. Grootmyers, unpubl.
Crepidotus malachioides	BD46	China		JQ666669		Zhiguang et al. (2016)
Crepidotus malachioides	FLAS-F-61634	USA		MH212015		B.S. Kaminsky, M.E. Smith, R. Healy & B. Spakes Richter, unpubl.
Crepidotus malachioides	GDOR5069	Italy		MW504470		This study
Crepidotus malachioides	SLO 1250, T	Slovakia		NR_132047		Jančovičová et al. (2014)
Crepidotus malachioides	WU 31421	Austria		KF879616		Jančovičová et al. (2014)
Crepidotus malachioides	WU 32709	Austria		KF879615		Jančovičová et al. (2014)
Crepidotus cf. *malachioides*	TENN 055381	Argentina		KY559326		P.B. Matheny, H.B. Korotkin & M.E. Smith, unpubl.
Crepidotus nyssicola	S.D. Russell MycoMap # 7399	USA		MN906236		S.D. Russell, unpubl.
Crepidotus nyssicola	S.D. Russell MycoMap # 7426	USA		MN906237		S.D. Russell, unpubl.
Crepidotus sp.	MushroomObserver.org/307011	USA		MH087459		A. Rockefeller, unpubl.
Crepidotus sp.	SDR NAMA 2017-156	USA		MK575449		A. Rockefeller, unpubl.
Crepidotus sphaerosporus	11253	Italy		JF907960		Osmundson et al. (2013)
Crepidotus sphaerosporus	HMAS 255466			MK966515		T.Z. Wei, unpubl.
Crepidotus sphaerosporus	HMAS 290002			MK966514		T.Z. Wei, unpubl.
Crepidotus subverrucisporus	15720	Italy		JF907961		Osmundson et al. (2013)
Entoloma anatinum [as *Entoloma longistriatum*]	TUF106928	Estonia		UDB015648*		I. Saar, unpubl.
Entoloma asprellum [as *Entoloma lividocyanulum*]	TUF106064	Estonia		UDB011486*		I. Saar, unpubl.
Entoloma atrocoeruleum [as *Entoloma poliopus* var. *parvisporigerum*]	TUF120520	Estonia		UDB031517*		UNITE
Entoloma azureosquamulosum	HKAS53408	China		JQ410334		He et al. (2012)
Entoloma brunneicoeruleum	AKS-E1-15	Norway		MZ145169		This study
Entoloma brunneicoeruleum	JL124-16	Norway		MZ145168		This study
Entoloma brunneicoeruleum	L0608198	The Netherlands		MZ145166		This study
Entoloma brunneicoeruleum	LE 302098, T	Russia		MZ145170		This study
Entoloma brunneicoeruleum	O-F-291139	Norway		MZ145167		This study
Entoloma aff. *caesiellum*	SAAS1410	China		KP329587		X.-L. He, unpubl.
Entoloma callipygmaeum	LE 253784, T	Russia		MZ145207		This study
Entoloma callipygmaeum	LE 312487	Russia		MZ145206		This study
Entoloma callipygmaeum	LE 312488	Russia		MZ145205		This study
Entoloma cf. *catalaunicum*	TU106338	Estonia		UDB011680*		I. Saar, unpubl.
Entoloma chalybaeum	TUF105760	Denmark		UDB034191*		I. Saar, unpubl.
Entoloma ekaterinae	LE312053, T	Russia		MK693215		Crous et al. (2019)

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Entoloma erhardii	LE312051, T	Russia		MK693218		Crous et al. (2019)
Entoloma exile	K(M)157760	Great Britain		MF977951		J.J. Elsey, unpubl.
Entoloma cf. *foliocontusum* [as *Leptonia* cf. *foliocontusa*]	4954SL	USA		KX574457		M. Gordon, unpubl.
Entoloma fuscosquamosum	TENN064384	USA		KY777405		P.B. Matheny, S.A. Trudell & M.G. Wood, unpubl.
Entoloma holmvassdalenense	O-F-75311, T	Norway		KM610321		Weholt et al. (2014)
Entoloma incanum	K(M)190322	Great Britain		MF977955		J.J. Elsey, unpubl.
Entoloma kauffmanii	KA13-1202	South Korea		KR673675		Kim et al. (2015)
Entoloma cf. *largentii* [as *Leptonia* cf. *convexa*]	OSC144006	USA		KX574458		M. Gordon, unpubl.
Entoloma longistriatum	TENN070451	USA		KY744164		P.B. Matheny, S.A. Trudell & M.G. Wood, unpubl.
Entoloma minutigranulosum	GB-0204540	Sweden		MZ145209		This study
Entoloma minutigranulosum	JL54-14	Norway		MZ145221		This study
Entoloma minutigranulosum	JL69-17	Norway		MZ145220		This study
Entoloma minutigranulosum	JL99-11	Norway		MZ145216		This study
Entoloma minutigranulosum	JL99-16	Norway		MZ145217		This study
Entoloma minutigranulosum	L0607681	The Netherlands		MZ145215		This study
Entoloma minutigranulosum	L0607941 / MD-2014-7	Germany		MZ145211		This study
Entoloma minutigranulosum	LE 302096, T	Russia		MZ145214		This study
Entoloma minutigranulosum	LE 312483	Russia		MZ145212		This study
Entoloma minutigranulosum	LE 312484	Russia		MZ145210		This study
Entoloma minutigranulosum	LE 312675	Russia		MZ145219		This study
Entoloma minutigranulosum	O-F-175913 / GG 3568	Norway		MZ145218		This study
Entoloma minutigranulosum	O-F-304886 / TEB 121-16	Norway		MZ145208		This study
Entoloma minutigranulosum	WU25057	Austria		MZ145213		This study
Entoloma montanum	GB-0191635, T	Sweden		MW340896		Noordeloos et al. (2021)
Entoloma mougeotii	LE254352	Russia		KC898446		Morozova et al. (2014)
Entoloma nigrovelutinum	LE295077, T	Vietnam		MF898426		Crous et al. (2017)
Entoloma nipponicum	TNS F70747, T	Japan		MK693223		Crous et al. (2019)
Entoloma nordlandicum	O-F-76176, T	Norway		MW340899		Noordeloos et al. (2021)
Entoloma ochromicaceum	TU120040	Estonia		UDB023715*		I. Saar, unpubl.
Entoloma perasprellum	GB-0204546 / EL28-19	Sweden		MZ145182		This study
Entoloma perasprellum	GB-0204547 / JBJ 19-107	Sweden		MZ145179		This study
Entoloma perasprellum	GB-0204548 / JBJ 19-122	Sweden		MZ145180		This study
Entoloma perasprellum	GB-0204549 / JBJ 19-180	Sweden		MZ145183		This study
Entoloma perasprellum	GB-0204550 / JBJ 19-119	Sweden		MZ145181		This study
Entoloma perasprellum	GC01100310, T	France		MZ145177		This study
Entoloma perasprellum	LE 312499	Russia		MZ145186		This study
Entoloma perasprellum	LE 312500	Russia		MZ145185		This study
Entoloma perasprellum	LE 312501	Russia		MZ145178		This study
Entoloma perasprellum	O-F-256732 / JBJ 18-004	Sweden		MZ145184		This study
Entoloma poliopus	G4742	Estonia		UDB0332859*		R. Pau, unpubl.
Entoloma pulchripes	LE 311808, T	Russia		MZ145188		This study
Entoloma pulchripes	LE 311809	Russia		MZ145189		This study
Entoloma pulchripes	LE 312485	Russia		MZ145187		This study

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Entoloma querquedula	18.XI.2011 TUR	Finland		LN850627		Kokkonen (2015)
Entoloma aff. *rectangulum* [as *Leptonia rectangula*]	SCL8524	USA		KU574744		M. Gordon, unpubl.
Entoloma roseotinctum	WU13070	Austria		LN850611		Kokkonen (2015)
Entoloma sarcitulum	TUR-31-VII-1967	FIN		LN850562		Kokkonen (2015)
Entoloma septentrionale	O-F-254295, T	Norway		MW340904		This study
Entoloma serrulatum	LE254361	Russia		KC898447		Morozova et al. (2014)
Entoloma sp.	CM13-233	New Caledonia		KY774214		Carriconde et al. (2019)
Entoloma sp.	MEL2382758	Australia		KP012941		G. Bonito, M. Barrett, F. Udovicic & T. Lebel, unpubl.
Entoloma sp.	MES-2627	Chile		MH930251		A.B. Mujic & M.E. Smith, unpubl.
Entoloma sp.	MES-534	Chile		KY462681		Truong et al. (2017)
Entoloma sp.	MushroomObserver.org/240552	USA		MG966312		A. Rockefeller, unpubl.
Entoloma sp.	soil sample	USA		EF619690		Parrent & Vilgalys (2007)
Entoloma sp.	soil sample	USA		KP889939		S.H.A. Guichon & S.W. Simard, unpubl.
Entoloma sp.	TRTC156923	Canada		JN021015		Dentinger et al. (2011)
Entoloma sp.	TUF120259	Estonia		UDB024650*		I. Saar, unpubl.
Entoloma sp. [as *Entoloma* cf. *sericeum*]	UBC-F14053	Canada		AF335439		M.L. Berbee, P. Inderbitzin & G. Zhang, unpubl.
Entoloma subcaesiellum	LE253776, T	Russia		MK693224		Noordeloos & Morozova (2010)
Entoloma subcaesiocinctum	SAAS2238	China		KY711234		He et al. (2017)
Entoloma subcorvinum	TENN070435	USA		KY744169		P.B. Matheny, S.A. Trudell & M.G. Wood, unpubl.
Entoloma subfarinaceum	TENN070395	USA		KY777374		P.B. Matheny, S.A. Trudell & M.G. Wood, unpubl.
Entoloma tigrinum	GB-0204535 / EL156-18	Sweden		MZ145172		This study
Entoloma tigrinum	GB-0204536 / JBJ 19-128	Sweden		MZ145171		This study
Entoloma tigrinum	GB-0204537 / JBJ 19-109	Sweden		MZ145173		This study
Entoloma tigrinum	GB-0204538	Sweden		MZ145175		This study
Entoloma tigrinum	GB-0204539	Sweden		MZ145174		This study
Entoloma tigrinum	O-F-304580, T	Norway		MZ145176		This study
Entoloma timidum	JL13-16	Norway		MZ145195		This study
Entoloma timidum	JL15-14	Norway		MZ145194		This study
Entoloma timidum	LE 311800	Russia		MZ145191		This study
Entoloma timidum	LE 312382	Russia		MZ145198		This study
Entoloma timidum	LE 312480, T	Russia		MZ145197		This study
Entoloma timidum	LE 312481	Russia		MZ145199		This study
Entoloma timidum	O-F-252355	Norway		MZ145196		This study
Entoloma timidum	O-F-75148	Norway		MZ145190		This study
Entoloma timidum	TEB73-20	Norway		MZ145193		This study
Entoloma timidum	Weholt E16-10	Norway		MZ145192		This study
Entoloma turci	MCVE3882	Italy		JF907993		Osmundson et al. (2013)
Entoloma cf. *unicolor*	TENN070383	USA		KY777373		P.B. Matheny, S.A. Trudell & M.G. Wood, unpubl.
Entoloma violaceoserrulatum	JV 8329F (TUR), T	Finland		MF476913		Morozova et al. (2018)
Entoloma violaceoserrulatum	L0607704	The Netherlands		MZ145200		This study

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Entoloma violaceoserrulatum	LE 312676	Sweden		MZ145204		This study
Entoloma violaceoserrulatum	O-F-260353 / TEB 339-15	Norway		MZ145201		This study
Entoloma violaceoserrulatum	O-F-75151	Norway		MZ145203		This study
Entoloma violaceoserrulatum	TEB128-19	Norway		MZ145202		This study
Entoloma yanacolor	QCAM 6312, T	Ecuador		MG947210		Crous et al. (2018)
Herpomyces chaetophilus	D. Haelew. 1097b	Panama, Periplaneta americana	MG438321	MG438294	MG438352	Haelewaters et al. (2019)
Herpomyces chaetophilus	D. Haelew. 1097c	Panama, Periplaneta americana	MG438322	MG438295	MG438353	Haelewaters et al. (2019)
Herpomyces chaetophilus	D. Haelew. 435b	USA Massachusetts, Periplaneta americana	MG438318	MG438292		Haelewaters et al. (2019)
Herpomyces chaetophilus	D. Haelew. 483b	USA Massachusetts, Periplaneta americana	MG438319	MG438293	MG438350	Haelewaters et al. (2019)
Herpomyces chaetophilus	D. Haelew. 483e	USA Massachusetts, Periplaneta americana	MG438320		MG438351	Haelewaters et al. (2019)
Herpomyces chaetophilus	D. Haelew. 602b	USA Massachusetts, Periplaneta americana	KT800023	KT800039	KT800009	Haelewaters et al. (2015)
Herpomyces ectobiae	MG001	Poland, Blattella germanica	KT800024	KT800040		Haelewaters et al. (2015)
Herpomyces ectobiae	TW793a	USA California, Blattella germanica		MG438296		Haelewaters et al. (2019)
Herpomyces leurolestis	2017/0199	Hungary, Phoetalia pallida		MG438299		Haelewaters et al. (2019)
Herpomyces leurolestis	D. Haelew. 1417b	Hungary, Phoetalia pallida		MG438297		Haelewaters et al. (2019)
Herpomyces leurolestis	Debr_Ppal	Hungary, Phoetalia pallida	MG438323	MG438298	MG438354	Haelewaters et al. (2019)
Herpomyces paranensis	D. Haelew. 1365a	Panama, Blaberus giganteus		MG438300		Haelewaters et al. (2019)
Herpomyces paranensis	D. Haelew. 1365b	Panama, Blaberus giganteus		MG438301		Haelewaters et al. (2019)
Herpomyces periplanetae	ADK6485	Bénin, Periplaneta americana	MZ145233	MZ145234	MZ144000	This study
Herpomyces periplanetae	D. Haelew. 1187d	USA Massachusetts, Periplaneta americana	MG438331	MG438309	MG438359	Haelewaters et al. (2019)
Herpomyces periplanetae	D. Haelew. 602a	USA Massachusetts, Periplaneta americana	MG438326	MG438304		Haelewaters et al. (2019)
Herpomyces periplanetae	D. Haelew. 602c	USA Massachusetts, Periplaneta americana	KT800025	KT800041	KT800010	Haelewaters et al. (2015)
Herpomyces periplanetae	D. Haelew. 602d	USA Massachusetts, Periplaneta americana	MG438327	MG438305	MG438357	Haelewaters et al. (2019)
Herpomyces periplanetae	D. Haelew. 620a	USA New York, Periplaneta americana	MG438328	MG438306	MG438358	Haelewaters et al. (2019)
Herpomyces periplanetae	D. Haelew. 654b	Panama, Periplaneta americana	MG438329	MG438307		Haelewaters et al. (2019)
Herpomyces periplanetae	D. Haelew. 654c	Panama, Periplaneta americana	MG438330	MG438308	MG438308	Haelewaters et al. (2019)
Herpomyces periplanetae	TW437c	USA Massachusetts, Periplaneta americana	MG438324	MG438302	MG438355	Haelewaters et al. (2019)
Herpomyces periplanetae	TW448b	USA Massachusetts, Periplaneta americana	MG438325	MG438303	MG438356	Haelewaters et al. (2019)
Herpomyces shelfordellae	Bud_Slat	Hungary, Shelfordella lateralis	MG438333	MG438312	MG438361	Haelewaters et al. (2019)
Herpomyces shelfordellae	D. Haelew. 1415a	Hungary, Shelfordella lateralis		MG438313		Haelewaters et al. (2019)
Herpomyces shelfordellae	D. Haelew. 1427a	USA Massachusetts, Shelfordella lateralis		MK299847		Haelewaters et al. (2019)

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Herpomyces shelfordellae	DE_HerpBL1	Hungary, Shelfordella lateralis	KT800026	KT800042	KT800011	Haelewaters et al. (2015)
Herpomyces shelfordellae	MH202b, T	Poland, Shelfordella lateralis		MK299848		Haelewaters et al. (2019)
Herpomyces sp.	H77-1	USA North Carolina, Parcoblatta cf. lata	KY523239	KY293260	KY350529	Sundberg et al. (2018)
Herpomyces spegazzinii	CEPHe27-1	Argentina, Periplaneta fuliginosa		MN597427		Gutierrez et al. (2020)
Herpomyces spegazzinii	LPS:49123-2, T	Argentina, Periplaneta fuliginosa		NR_169702		Gutierrez et al. (2020)
Herpomyces stylopygae	Bud_Bori	Hungary, Blatta orientalis	MG438332	MG438310	MG438360	Haelewaters et al. (2019)
Herpomyces stylopygae	Bud_Bori_2	Hungary, Blatta orientalis		MG438311		Haelewaters et al. (2019)
Leucoagaricus americanus	BHI-F360a	USA Massachusetts		MF161229		Haelewaters et al. (2018)
Leucoagaricus americanus	S.D. Russell HRL0779	Canada		MH979431		S. Russell & R. Lebeuf, unpubl.
Leucoagaricus americanus	S.D. Russell MO #107715	USA Indiana		MW567919		S.D. Russell, unpubl.
Leucoagaricus americanus	S.J.W. Verduin (L)	USA North Carolina		AF295928		Vellinga (2000)
Leucoagaricus americanus [as *Leucoagaricus bresadolae*]	CCBAS802	Czech Republic		LN714565		Větrovský et al. (2016)
Leucoagaricus americanus [as *Leucoagaricus bresadolae*]	MCVE:756	Italy		GQ329047		Osmundson et al. (2013)
Leucoagaricus americanus [as *Leucoagaricus* sp.]	Royan 3	Iran		MT573394		Alimadadi et al. (2019)
Leucoagaricus cf. *majusculus*	MFLU 09-0164	Thailand		HM488764		Vellinga et al. (2011)
Leucoagaricus gongylophorus	MyrE002	Panama		KF572016		Kooij et al. (2015)
Leucoagaricus meleagris	AJ 542	USA Massachusetts		MN483027		Justo et al. (2021)
Leucoagaricus meleagris	E.C. Vellinga 1990	The Netherlands		AY176419		Vellinga (2004)
Leucoagaricus meleagris	E.C. Vellinga 2095	The Netherlands		AF482867		Vellinga et al. (2003)
Leucoagaricus meleagris	HAW:JKS90	USA Hawai'i		MK412590		Stallman (2019)
Leucoagaricus meleagris	iNAT:58855005	USA New York		MW031133		S. Jakob, unpubl.
Leucoagaricus meleagris	WA0000072219	Laos		MT252565		Łuczaj et al. (2021)
Leucoagaricus mucrocystis	AJ 476	USA US Virgin Islands		MN483025		Justo et al. (2021)
Leucoagaricus mucrocystis	CA 16 (JBSD)	Dominican Republic		MN483026		Justo et al. (2021)
Leucoagaricus mucrocystis	ELTE:DB-FG-167-19	French Guiana		MZ047586	MZ047585	This study
Leucoagaricus mucrocystis	ELTE:DB-FG-168-19	French Guiana		MZ047587		This study
Leucoagaricus mucrocystis [as *Lepiota besseyi*]	D.E. Hemmes deh1867	USA Hawai'i		HM488763		Vellinga et al. (2011)
Leucoagaricus mucrocystis [as *Lepiota besseyi*]	HAW:JKS109	USA Hawai'i		MK412602		Stallman (2019)
Leucocoprinus sp.	RB29	Brazil		MN473907		R. Bizarria Jr. & A. Rodrigues, unpubl.
Neopestalotiopsis clavispora	ncb01	India, Ziziphus mauritiana		MW012901		This study
Phytopythium boreale	CBS:551.88	China		AB725879	HQ665261	Robideau et al. (2011), Baten et al. (2014)
Phytopythium carbonicum	CBS:112544	France		AB725876	AB996605	Baten et al. (2014)
Phytopythium carbonicum	CBS:292.37	The Netherlands		AB690620		M.A. Baten, K. Kageyama & H. Suga, unpubl.
Phytopythium chamaehyphon	CBS:259.30	USA Hawai'i		AB690609	HQ665177	Robideau et al. (2011), Baten et al. (2014)
Phytopythium chamaehyphon	CCIBt 4338	Brazil		MT620968	MT612336	This study
Phytopythium chamaehyphon	CCIBt 4407	Brazil		MT620969	MT612337	This study

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Phytopythium chamaehyphon	CPZ68	Brazil		MT620967	MT612335	This study
Phytopythium chamaehyphon	PPRI8625	South Africa		FJ415975		McLeod et al. (2009)
Phytopythium citrinum	CBS:119171	France		AY197328	AB948195	Baten et al. (2014)
Phytopythium curcubitacearum	CBS:748.96	Japan		AB725877	AB690598	Baten et al. (2014)
Phytopythium delawarense	382B	USA Ohio		AB725875	AB690591	Baten et al. (2014)
Phytopythium dogmae	USTCMS 4101	Philippines		MF353170	MF373431	Bennett et al. (2017)
Phytopythium fagopyri	CBS:293.35	Japan		AB690617	AB690590	Baten et al. (2014)
Phytopythium fagopyri	FP1	Japan		AB690621	AB690599	Baten et al. (2014)
Phytopythium fagopyri	HonMa	Japan		AB690615	AB690588	Baten et al. (2014)
Phytopythium helicoides	CBS:286.31	USA		AB725878	MF375637	Baten et al. (2014), Bennett et al. (2017)
Phytopythium helicoides	CCIBt 4103	Brazil		KR092138		This study
Phytopythium helicoides	CCIBt 4104	Brazil		KR092137		This study
Phytopythium iriomotense	GUCC0025			AB690622	AB690600	M.A. Baten, K. Kageyama & H. Suga, unpubl.
Phytopythium iriomotense	GUCC7020			AB690629	AB690607	M.A. Baten, K. Kageyama & H. Suga, unpubl.
Phytopythium kandeliae	CBS:111.91	Taiwan		HQ643134	HQ665065	Robideau et al. (2011)
Phytopythium kandeliae	CCIBt 4023	Brazil		KJ399962	KJ399965	Marano et al. (2014)
Phytopythium leanoi	CBS:113.91	Taiwan		MF355474	KJ399963	Marano et al. (2014), Bennett et al. (2017)
Phytopythium leanoi	USTCMS 4102	Philippines		MF353169	MF373430	Bennett et al. (2017)
Phytopythium litorale	CBS:118360	Germany		HQ643386	HQ665082	Robideau et al. (2011)
Phytopythium litorale	CCIBt 4659	Brazil		MT620970	MT612338	This study
Phytopythium litorale	Dyrbkr01	Turkey		MN203107	MN197634	Derviş et al. (2020)
Phytopythium litorale	Dyrbkr02	Turkey		MN203108	MN197635	Derviş et al. (2020)
Phytopythium litorale	GUCC7167			AB690612	AB690583	Baten et al. (2014)
Phytopythium litorale	SCP82	Brazil		MT620972	MT612340	This study
Phytopythium megacarpum	CBS:112351	France		AB725881	HQ665067	Robideau et al. (2011), Baten et al. (2014)
Phytopythium mercuriale	CBS:112443	South Africa		AB725882	KF853236	de Cock et al. (2015); M.A. Baten, K. Kageyama & H. Suga, unpubl.
Phytopythium mirpurense	CBS:124524	Pakistan		KJ831614		de Cock et al. (2015)
Phytopythium montanum	ADC9762	Germany		HQ643391		Robideau et al. (2011)
Phytopythium montanum	CBS:111349	Germany		AB725883	HQ665064	Robideau et al. (2011), Baten et al. (2014)
Phytopythium nanginjense	Chen216	China		MF459636		Chen et al. (2019)
Phytopythium nanginjense	Chen218	China		MF459635		Chen et al. (2019)
Phytopythium oedochilum	CBS:292.37	USA		AB690619	HQ665191	Robideau et al. (2011), Baten et al. (2014)
Phytopythium oedochilum	CBS:738.94	South Africa		HQ643394		Robideau et al. (2011)
Phytopythium ostracodes	CBS:768.73	Spain		AB108022	HQ665295	Robideau et al. (2011); M.A. Baten, K. Kageyama & H. Suga, unpubl.
Phytopythium palingenes	CCIBt 3981	Brazil		KR092139	KR092143	This study
Phytopythium palingenes	CCIBt 4397	Brazil		MT620974	MT612342	This study
Phytopythium palingenes	CCIBt 4428	Brazil		MT620973	MT612341	This study
Phytopythium sindhum	CBS:124518	Pakistan		HM244825		Bala et al. (2010)
Phytopythium sindhum	JKI			KJ755089		König et al. (2015)

Species name	ID (isolate, strain[1], status[2], voucher)	Country, isolation source	SSU	ITS	LSU	Reference(s)
Phytopythium sp. *'amazonianum'*	WPC:8239B1845	Ecuador		GU258624		M.D. Coffey, A.K. Brar, E. Xu, E.A. Sarhan & I.M. Cunningham, unpubl.
Phytopythium sp. *'amazonianum'*	WPC:8243B519	Ecuador		GU258937		M.D. Coffey, A.K. Brar, E. Xu, E.A. Sarhan & I.M. Cunningham, unpubl.
Phytopythium vexans	CBS:119.80	Iran		AY598713	HQ665090	Lévesque & de Cock (2004), Robideau et al. (2011)
Phytopythium vexans	CCIBt 4101	Brazil		KR092141	KR092144	This study
Phytopythium vexans	CCIBt 4383	Brazil		MT620976	MT612344	This study
Phytopythium vexans	CCIBt 4398	Brazil		MT620975	MT612343	This study
Pluteus beniensis	RSPF 0299	Brazil		JQ065029		A. Justo, N. Menolli Jr. & A.M. Minnis, unpubl.
Pluteus cinereofuscus	AJ229	Portugal		HM562108		Justo et al. (2011b)
Pluteus aff. *cinereofuscus*	LE 303665	Russia		KX216324		Malysheva et al. (2016)
Pluteus eludens	MA50497	Portugal		HM562118	HM562240	Justo et al. (2011b)
Pluteus eludens	SF15	USA		HM562185		Justo et al. (2011b)
Pluteus exiguus	O-F-21721	Norway		UDB036730*		A. Molia, unpubl.
Pluteus extremiorientalis	LE 303463	Russia		KM658282		Crous et al. (2014)
Pluteus extremiorientalis, T	LE<RUS>:262872	Russia		NR_153249		Crous et al. (2014)
Pluteus floccipes	BRNM	Czech Republic		LN794642		Ševčíková & Borovička (2015)
Pluteus fluminensis	SP393710	Brazil		FJ816655		Menolli et al. (2010)
Pluteus fluminensis	SP393711	Brazil		FJ816664	FJ816650	Menolli et al. (2010)
Pluteus fuligineovenosus	SP393705	Brazil		FJ816662		Menolli et al. (2010)
Pluteus hubeiensis	HMJAU45199	China		MH167350		W. Fengjian & L. Yu, unpubl.
Pluteus hubeiensis	HMJAU45200	China		MH167353		W. Fengjian & L. Yu, unpubl.
Pluteus jamaicensis	SP393706	Brazil		FJ816657		Menolli et al. (2010)
Pluteus cf. *jamaicensis*	SP416738	Brazil		KM983709		Menolli et al. (2015)
Pluteus cf. *jamaicensis*	SP417454	Brazil		KM983711		Menolli et al. (2015)
Pluteus keselakii	BRNM 817402	Slovakia		MN250223	MN250223	Ševčíková et al. (2020)
Pluteus keselakii	LIP Mycologie 0401385	France		MN250224		Ševčíková et al. (2020)
Pluteus keselakii, T	BRNM:817402	Slovakia		NR_169977		Ševčíková et al. (2020)
Pluteus ludwigii	MCVE30136	Slovenia		MK834525	MK834527	Crous et al. (2019)
Pluteus ludwigii, T	MCVE:30136	Slovenia		NR_164496		Crous et al. (2019)
Pluteus multiformis	AC4249	Spain		HM562201	MK278503	Justo et al. (2011b), Varga et al. (2019)
Pluteus multiformis	AH 40107	Spain		MN250225	MN250225	Ševčíková et al. (2020)
Pluteus multiformis	OKA-TR1750	Turkey		MT982425	MT982429	This study
Pluteus multiformis	OKA-TR1751	Turkey		MT982426	MT982430	This study
Pluteus multiformis, T	AH:40107	Spain		NR_119877		Justo et al. (2011a)
Pluteus nanus	UC1859980	USA		KF306030		N.H. Nguyen, E.C. Vellinga, G.M. Cobian, A.J. Fernandez & T.D. Bruns, unpubl.
Pluteus nanus f. *griseopus*	NL-2546	Hungary			MK278504	Varga et al. (2019)
Pluteus pallescens	AJ214	Spain		HM562056	HM562231	Justo et al. (2011b)
Pluteus rimosoaffinis	SP394379	Brazil		HM562145		Menolli et al. (2015)
Pluteus rimosoaffinis	SP416740	Brazil		KM983706		Menolli et al. (2015)
Pluteus sapiicola	SP394382	Brazil		HM562148		Justo et al. (2011b)
Pluteus sapiicola	SP394387	Brazil		HM562146		Justo et al. (2011b)
Pluteus sp.	JLF1767	USA		MK634597		J.L. Frank, unpubl.

Species name	ID (isolate, strain[1], status[2], voucher)	Country, isolation source	SSU	ITS	LSU	Reference(s)
Pluteus sp.	PDD:106511	New Zealand		MN738653		J.A. Cooper, unpubl.
Pluteus sp.	PDD:110518	New Zealand		MN738674	MN738605	J.A. Cooper, unpubl.
Pluteus tenebromarginatus	GC17102401	France		MT079860		Corriol et al. (2020)
Pluteus terricola	PDD:107339	New Zealand		MN738665	MN738585	J.A. Cooper, unpubl.
Pythium takayamanum	CBS:122.492	Japan		HQ643853	HQ665094	Robideau et al. (2011)
Pythium takayamanum	CCIBt 4040	Brazil		KM058758	KM058755	This study
Pyxidiophora arvernensis	CBS 657.82	The Netherlands	FJ176839		FJ176894	Schoch et al. (2009)
Pyxidiophora cf. *microspora*	MG200	Poland	MG438334	MG438314	MG438362	Haelewaters et al. (2019)
Rhodocollybia asema	O-F-248185	Norway		MZ156765		This study
Rhodocollybia asema	O-F-248288	Norway		MZ156764		This study
Rhodocollybia asema	O-F-74975	Norway		MZ156766		This study
Rhodocollybia asema	O-F-75562	Norway		MZ156767		This study
Rhodocollybia butyracea	FB10726 (TENN)	Russia		AF505750		Mata et al. (2004)
Rhodocollybia butyracea	FB11456 (TENN)	Austria		AF505751		Mata et al. (2004)
Rhodocollybia butyracea	O-F-74979	Norway		MZ156768		This study
Rhodocollybia butyracea	O-F-75421	Norway		MZ156769		This study
Rhodocollybia butyracea	TENN53580	Sweden		AY313293		Mata et al. (2004)
Rhodocollybia butyracea	TU106219, UNITE RefSeq	Estonia		UDB011434*		V. Liiv, unpubl.
Rhodocollybia butyracea	TU118269	Estonia		UDB015439*		V. Liiv, unpubl.
Rhodocollybia butyracea f. *asema*	TU106218	Estonia		UDB015078*		V. Liiv, unpubl.
Rhodocollybia butyracea f. *asema*	TU106229	Estonia		UDB019799*		V. Liiv, unpubl.
Rhodocollybia butyracea f. *asema*	TU118574	Estonia		UDB017989*		V. Liiv, unpubl.
Rhodocollybia fodiens	TU106942	Estonia		UDB015266*		V. Liiv, unpubl.
Rhodocollybia maculata	BRNM699408	Italy		GU947370		Antonin & Noordeloos (2010)
Rhodocollybia maculata	BRNM714632	Czech Republic		GU947369		Antonin & Noordeloos (2010)
Rhodocollybia maculata	TU106940	Estonia		UDB015655*		V. Liiv, unpubl.
Rhodocollybia cf. *maculata*	O-F-75733	Norway		MZ156770		This study
Rhodocollybia prolixa	TU118816	Estonia		UDB019494*		V. Liiv, unpubl.
Rhodocollybia sp.	h43	Czech Republic		LN714597		Větrovský et al. (2016)
Suillus americanus	1008-NC	USA North Carolina		AF166500		Wu et al. (2000)
Suillus americanus	F1185163	USA West Virginia		KU663182		R. Zhang, X. Shi, P. Liu & G.M. Mueller, unpubl.
Suillus americanus	F1185445	USA Indiana		KU663183		R. Zhang, X. Shi, P. Liu & G.M. Mueller, unpubl.
Suillus americanus	MAV-5625	USA Ohio		AF166503		Wu et al. (2000)
Suillus americanus	TDB-581	USA Michigan		L54103		Wu et al. (2000)
Suillus americanus	TJB-7683	USA New York		AF166502		Wu et al. (2000)
Suillus cf. *americanus*	YNP:2355	USA California		KU663196		R. Zhang, X. Shi, P. Liu & G.M. Mueller, unpubl.
Suillus cothurnatus	MA-Fungi 47683	Spain		AJ419218		Martin & Raidl (2002)
Suillus cothurnatus	MA-Fungi 49403	Spain		AJ419217		Martin & Raidl (2002)
Suillus cothurnatus	NSW-4662	USA Louisiana		L54092		Kretzer et al. (1996)
Suillus decipiens	DG-1451	USA Texas		AF166508		Wu et al. (2000)
Suillus decipiens	DG-1451	USA Texas		L54079		Kretzer et al. (1996)
Suillus decipiens	DPL-5724	USA Texas		AF166510		Wu et al. (2000)
Suillus flavidus	DG66	UK		JQ888208		Jones et al. (2012)
Suillus flavidus	FFP909	Canada		JQ711962		Jones et al. (2012)

Species name	ID (isolate, strain[1], status[2], voucher)	Country, isolation source	SSU	ITS	LSU	Reference(s)
Suillus flavidus	FFP962	Canada		JQ711908		Jones et al. (2012)
Suillus granulatus	K-15-1	Russia		MK414509		O.B. Vaishlya, K.S. Karbysheva, I. Bakhtinskaya & E. Murina, unpubl.
Suillus granulatus	KA17-0554	South Korea		MN294845		Cho et al. (2020)
Suillus himalayensis	SNW-03	India		KJ472765		Verma & Reddy (2014a)
Suillus intermedius	ACAD-15271	Canada		L54074		Kretzer et al. (1996)
Suillus placidus	TDB-725	USA Michigan		L54108		Kretzer et al. (1996)
Suillus placidus	VC-1022	Nepal		L54118		Kretzer et al. (1996)
Suillus quercinus	LAH240711	Pakistan		MT361746		This study
Suillus quercinus	LAH36421, T	Pakistan		MT361745		This study
Suillus quercinus	LAH36422	Pakistan		MT361744		This study
Suillus sibiricus	EA24040	Pakistan		JN119750		Sarwar et al. (2011)
Suillus sibiricus	EA24104	Pakistan		JN119751		Sarwar et al. (2011)
Suillus sibiricus	HMAS:66061	China		AF166512		Kretzer et al. (1996)
Suillus sibiricus	QXW-2092	Austria		AF166513		Kretzer et al. (1996)
Suillus sibiricus	UC2023481	Switzerland		KX213817		Kretzer et al. (1996)
Suillus sibiricus	VC-1040	Nepal		L54117		Kretzer et al. (1996)
Suillus spraguei	GMM-5703	China		AF166518		Wu et al. (2000)
Suillus spraguei	QXW-2409	China		AF166520		Wu et al. (2000)
Suillus spraguei	QXW-2435	China		AF166522		Wu et al. (2000)
Suillus spraguei	Tissue_lib TDB-638	USA Michigan		M91617		Wu et al. (2000)
Suillus spraguei	TJB-6228	USA New York		AF166525		Wu et al. (2000)
Suillus subalutaceus	ACAD-15288	Canada		L54075		Kretzer et al. (1996)
Suillus subaureus	TDB-780	USA Massachusetts		L54109		Kretzer et al. (1996)
Suillus subluteus	IB-13-8/19/72	USA Michigan		L54088		Kretzer et al. (1996)
Suillus triacicularis	MSM 0027	Pakistan		KM677929		Sarwar et al. (2015)
Suillus triacicularis	PUN 5534	India		KF977188		Verma & Reddy (2014b)
Suillus triacicularis	PUN 5534, T	India		NR_153233		Verma & Reddy (2014b)
Uncultured Basidiomycota	4S1_A12	USA		EU489965		Hollister et al. (2010)
Uncultured Basidiomycota	A2	Australia		DQ672275		Midgley et al. (2007)
Uncultured fungus	FDBC50	Mexico		JQ247381		Romero-Olivares et al. (2013)
Uncultured fungus	4248_284	Lithuania		MT236490		Marčiulynas et al. 2020
Uncultured fungus	TUN11	UK		KM374523		Johnson et al. (2014)

[1] Herbarium abbreviations follow Index Herbariorum (Thiers continuously updated).

[2] T: ex-type strain. * from UNITE database (https://unite.ut.ee).

DNA was extracted from dried *Crepidotus malachioides* basidiomata with the CTAB protocol from Doyle & Doyle (1987). The ITS region was amplified with primers ITS1F (Gardes & Bruns 1993) and ITS4 (White et al. 1990). Cycling conditions were as in Saba et al. (2020). The generated sequence reads were assembled and edited in Geneious version 11.1.5 (Kearse et al. 2012) and then submitted to NCBI GenBank. Accession numbers are reported in Tab. 1.

Genomic DNA was isolated from 1 female thallus of *Herpomyces periplanetae* using the REPLI-g Single Cell Kit (Qiagen, Valencia, CA) following the modifications by Haelewaters et al. (2019). Amplification of the internal transcribed spacer (ITS) barcode region and the nuclear ribosomal RNA small and large subunits (SSU and LSU) was done using the following primer sets: NSL1/NSL2 for SSU (Haelewaters et al. 2015), ITS1f/ITS4 for ITS (White et al. 1990, Gardes & Bruns 1993), and LIC24R/LR3 for LSU (Vilgalys & Hester 1990, Miadlikowska & Lutzoni 2000). Amplifications were performed on a pro S Mastercycler (Eppendorf, Hauppauge, NY) in 25-µl reactions containing 12.5 µl of 2× MyTaq Mix (Bioline, Swedesboro, NJ), 9.5 µl of ddH$_2$O, 1.0 µl of each 10 mM primer, and 1.0 µl of DNA extract. Cycling conditions followed Haelewaters et al. (2019) for ITS and Liu et al. (2020) for SSU and LSU. For SSU: initial denaturation at 95 °C for 5 min; then 40 cycles of denaturation at 95 °C for 30 s, annealing at 55 °C for 45 s, and extension at 72 °C for 45 s; and final extension at 72 °C for 1 min. For ITS: initial denaturation at 94 °C for 3 min; then 35 cycles of denaturation at 94 °C for 1 min, annealing at 50 °C for 45 s, and extension at 72 °C for 90 s; and final extension at 72 °C for 10 min. For LSU: initial denaturation at 94 °C for 5 min; then 35 cycles of denaturation at 94 °C for 30 s, annealing at 50 °C for 45 s, and extension at 72 °C for 1 min; and final extension at 72 °C for 7 min. Purification and Sanger sequencing were outsourced to Genewiz (Plainfield, NJ). Raw sequence reads were assembled, trimmed, and edited in Sequencher version 5.2.3 (Gene Codes Corporation, Ann Arbor, MI).

For the *Leucoagaricus* study, the ITS and LSU regions were amplified directly from samples with the Phire Plant Direct PCR Master Mix Kit (Thermo Scientific). Amplification of the regions ITS and LSU was done using primer sets ITS1F/ITS4 (White et al. 1990, Gardes & Bruns 1993) and LR0R/LR5 (Vilgalys & Hester 1990, Hopple 1994), respectively. Sequencing of the amplicons was carried out with the primers used for amplification by LGC Genomics (Berlin, Germany). Chromatograms were checked and edited with CodonCode Aligner version 8.0.1 (CodonCode Corporation). Newly generated sequences were submitted to GenBank (Tab. 1).

Neopestalotiopsis DNA was extracted from conidia, conidiophores, and mycelium using the CTAB method from Doyle & Doyle (1990). DNA was resuspended in 100 ml of MilliQ H$_2$O and quantified using a Nanodrop 2000c spectrophotometer (Thermo Scientific) at $A_{260/280}$ and $A_{230/260}$. DNA was then diluted to 20 ng/ml and stored at –20±2 °C. Amplification of the ITS region was performed with primers ITS1 and ITS4 (White et al. 1990). PCR was done in 15-µl reactions consisting of 0.18 µl of each 10 mM primer, 0.18 µl of dNTPs, 0.90 U of GoTaqVR DNA Polymerase (Promega, Madison, WI), and 3 µl of the diluted DNA suspension. Amplified PCR products were checked by electrophoresis on 1.5 % agarose gel and cleaned with ExoSAP-IT PCR Product Cleanup Reagent (Thermo Scientific). Sequencing was done by Macrogen. The generated sequence was submitted to GenBank (accession no. MW012901).

Mycelium biomass from each *Phytopythium* specimen was grown for 3–5 days in falcon tubes containing 20 ml of MP5 (4 g of maltose, 1 g of peptone, and 1 l of ddH$_2$O) liquid medium at room temperature (~22 ºC). Biomass was transferred to Eppendorf tubes, washed with sterile water, and centrifuged at 13,000 rpm for 15 min to obtain pellets. The DNA extraction was performed according to the protocol described in the PureLink Genomic DNA kit (Invitrogen, Carlsbard, CA). The ITS and LSU regions were amplified using the primers UN–up18S42 and UN–1o28S22 (Robideau et al. 2011) and LR0R/LR6-O, respectively (Hopple 1994, Riethmüller et al. 2002). DNA was amplified with JumpStart TM Taq DNA Polymerase (Sigma-Aldrich, St. Louis, MO) for a final volume of 25 µl using the PCR conditions described by Marano et al. (2014). Amplicons were purified manually according to the protocol of Schmitz & Riesner (2006). Sanger sequencing was performed by Macrogen. Assembly of contigs and correction of ambiguous bases were manually edited using Sequencher version 4.1.4. All sequences were submitted to GenBank (Tab. 1).

Genomic DNA of *Pluteus* basidiomata was extracted using the ZR Fungal/Bacterial DNA MiniPrep kit (Zymo research, Irvine, CA). PCR amplification was performed with the following primer pairs: ITS1F and ITS4 for ITS (White et al. 1990, Gardes & Bruns 1993), and LR0R and LR5 for LSU (Vilgalys & Hester 1990, Hopple 1994). PCR procedures were after Kaygusuz et al. (2020). Purification of PCR products was done using the UltraClean PCR Clean-Up kit (MoBio Laboratories, Carlsbad, CA) following the manufacturer's instructions. Sanger sequencing of purified PCR products using the PCR primers was outsourced to Source Bioscience (Berlin, Germany). Newly generated sequences were submitted to GenBank (accession numbers in Tab. 1).

Seven *Rhodocollybia* collections from Norway were studied by molecular methods (Tab. 1). Six of them belong to the *R. butyracea* (Bull.) Lennox complex. DNA extraction and PCR amplification of the ITS region as well as Sanger sequencing were done in collaboration with the Norwegian Barcode of Life Network (NorBOL) as part of BOLD (Barcode of Life Data System). For BOLD methods, see Ratnasingham & Hebert (2007, 2013).

Phylogenetic analyses

The newly generated *Cortinarius* sequence was subjected to a BLAST search against NCBI GenBank's standard *nr/nt* nucleotide database (https://blast.ncbi.nlm.nih.gov/Blast.cgi) to select and download the most closely related sequences in *Cortinarius* subg. *Telamonia* sect. *Hinnulei* (Liimatainen et al. 2020). Sequences were aligned in MEGA5 (Tamura et al. 2011) using ClustalW and then corrected manually. The final alignment included 512 characters, of which 65 were parsimony-informative. Bayesian inference (BI) was performed in MrBayes 3.2.6 (Ronquist et al. 2012), under the following parameters: data not partitioned, GTR+G+I as substitution model, two independent runs, four chains, temperature set to 0.2, sampling every 100 generations, until convergence parameters were met after 0.74 million generations. Finally, a maximum likelihood (ML) analysis was run using RAxML version 8.2.12 (Stamatakis 2014) using the GTRGAMMA model. Bootstrapping was done with 2,000 replicates. Trees were visualized in FigTree version 1.4.3 (http://tree.bio.ed.ac.uk/software/figtree/) and then edited in Adobe Illustrator 25.1.

Entoloma sequences were aligned with MAFFT version 7 using the E-INS-i option (Katoh et al. 2019). The alignment was checked and edited in SeaView version 4 (Gouy et al. 2010). Maximum likelihood (ML) analysis was performed in PhyML version 3.0 (Guindon et al. 2010) using the non-parametric Shimodaira-Hasegawa version of the approximate likelihood-ratio test (SH-aLRT) and the GTR+I+Γ model of evolution. The final tree (Fig. 4) was edited in MEGA7 (Kumar et al. 2016) and Adobe Illustrator CS4.

For the *Suillus* study, consensus sequences were subjected to BLAST searches (https://blast.ncbi.nlm.nih.gov/Blast.cgi). ITS sequences sharing higher identity with our newly generated sequences were downloaded. All sequences were aligned using the MUSCLE alignment tool (Edgar 2004), which is available online through the European Bioinformatics Institute (https://www.ebi.ac.uk/Tools/msa/muscle/). Next, sequences in the aligned ITS dataset were trimmed at the conserved motifs 5'–(…GAT)CATTA–3' (3' end of the SSU) and 5'–GACCT(CAAA…)–3' (5' end of the LSU) (Dentinger et al. 2011). A maximum likelihood (ML) tree was inferred using RAxML-HPC2 version 8.1.11 (Stamatakis 2014) with the GTRGAMMA model of nucleotide substitution. Rapid bootstrapping was done with 1,000 replicates. Phylogenetic analysis was performed on the CIPRES Science Gateway version 3.3 (Miller et al. 2010).

Crepidotus sequences that shared >87.5% identity with the newly generated ITS sequence in BLAST were downloaded from NCBI GenBank (https://www.ncbi.nlm.nih.gov/genbank/). *Agrocybe pediades* (Fr.) Fayod), GenBank accession no. MG817376, was selected as outgroup. Sequences were aligned using MAFFT version 7.450 (Katoh & Toh 2008) with default parameters in Geneious version 11.1.5. Maximum likelihood (ML) was inferred with RAxML version 8.2.11 (Stamatakis 2014). The GTR+G model was selected, and a total of 1,000 bootstrap (MLBS) replicates were used. The average distance between clades was estimated with MEGA version 10.0.4 (Kumar et al. 2018).

All existing ribosomal DNA sequences of *Herpomyces* species were downloaded from GenBank. Sequences of two species of *Pyxidiophora* Bref. & Tavel, which served as outgroup, were also downloaded. Sequences were aligned by region (SSU, ITS, LSU) using MUSCLE version 3.7 (Edgar 2004) on the CIPRES Science Gateway (Miller et al. 2020). Aligned ITS sequences were trimmed with the conserved motifs 5'–CATTA–3' (3' end of SSU) and 5'–GACCT–3' (5' end of LSU); the alignment portion between these motifs was included in subsequent analysis (Dentinger et al. 2011). Aligned LSU sequences were trimmed with the 5'–GACCT–3' motif; the alignment portion upstream from and including this conserved motif were included in subsequent analysis. Next, aligned sequences were trimmed using TrimAl version 1.3 (Capella-Gutiérrez et al. 2009) with gap threshold (-gt) of 0.6 and minimal coverage (-cons) of 0.5. Appropriate models of nucleotide substitution were selected under the Akaike Information Criterion corrected for small sample size (AICc) using the IQ-TREE built-in ModelFinder (Kalyaanamoorthy et al. 2017). Selected models were GTR+F+R2 (SSU, -lnL=2066.978), TVM+F+G4 (ITS, -lnL=4635.696), and TIM3+F+R2 (LSU, -lnL=2729.742). The data for each region were combined using MEGA version 7.0.26 (Kumar et al. 2016). We used the command-line version of IQ-TREE to perform a maximum likelihood (ML) analysis of the concatenated SSU–ITS–LSU dataset, under multiple partitions (Nguyen et al. 2015, Chernomor et al. 2016) and with branch support calculated from 1,000 ultrafast bootstrap replicates (Hoang et al. 2018). The final tree with ML bootstrap (MLBS) support values was visualized in FigTree version 1.4.3 (http://tree.bio.ed.ac.uk/software/figtree/) and edited in Adobe Illustrator version 25.1.

Selected ITS sequences of *Leucoagaricus* spp. were aligned with MAFFT online version 7 using the E-INS-i option (Katoh et al. 2019). The alignment was checked and edited in SeaView version 4 (Gouy et al. 2010). A maximum likelihood (ML) phylogenetic analysis was performed in raxmlGUI version 1.5 (Silvestro & Michalak 2012) using the GTRGAMMA nucleotide substitution model. Branch support was evaluated using 1,000 bootstrap replicates. The best scoring tree was edited with MEGA7 (Kumar et al. 2016).

ITS and LSU datasets with sequences for 51 *Phytopythium* isolates were used for the phylogenetic analyses, with two isolates of *Pythium takayamanum* Senda & Kageyama as outgroup. The dataset was aligned using MAFFT 7 with default settings (Katoh et al. 2019) and adjusted manually in BioEdit (Hall 1999). The best-fitting model of evolution was selected using the Akaike Information Criterion in jModelTest version 0.1.1 (Posada 2008). The aligned sequences were concatenated using SequenceMatrix 1.8 (Vaidya et al. 2010), resulting in a final length of 2,140 characters. Maximum likelihood (ML) and Bayesian inference (BI) analyses were performed using RAxML 8.2.10 (Stamatakis 2014) and MrBayes 3.2.2 (Ronquist et al. 2012) in the CIPRES Science Gateway. The ML analysis was performed with 1,000 bootstraps (MLBS) replicates using the GTRGAMMAI model. The BI used the Markov Chain Monte Carlo (MCMC) methodology to calculate posterior probabilities (BIPP). Four MCMC chains were run for five million generations, with sampling every 1,000 generations, and a burn-in of 10 %. Phylogenetic trees were viewed in FigTree version 1.4.2 (http://tree.bio.ed.ac.uk/software/figtree/) and edited in Inkscape version 0.92 (https://inkscape.org/).

For the *Pluteus* study, two ITS and two LSU sequences were newly generated. Another 51 related sequences—31 ITS and 12 LSU—were downloaded from GenBank and UNITE. *Pluteus seticeps* (G.F. Atk.) Singer, GenBank accession number HM562192, was selected as the outgroup. All sequences were aligned by MAFFT version 7.110 (Katoh et al. 2019). Phylogenetic analyses were performed for the concatenated ITS–LSU dataset with both maximum likelihood (ML) and Bayesian inference (BI) methods. The ML analysis was run through the CIPRES Science Gateway online interface (Miller et al. 2010) using RAxML version 8.2.10 (Stamatakis 2014) under the GTRGAMMA model and with 1,000 bootstrap replicates. BI was performed using MrBayes version 3.2.5 (Ronquist et al. 2012). Four Markov chain Monte Carlo (MCMC) chains were run for 1 million generations, sampling trees every 100 generations. The first 25% of sampled trees were discarded as burn-in.

The newly generated *Rhodocollybia* sequences were compared with those deposited in public databases (GenBank, UNITE) using the BLAST search tool (Altschul et al. 1990). Identical or most similar sequences were downloaded. Sequences belonging to the *R. maculata* (Alb. & Schwein.) Singer complex were selected as outgroup. Altogether 24 sequences were included in our final dataset. Multiple sequence alignment was done by PRANK (Löytynoja & Goldman 2005) as implemented in its graphical interface (PRANKSTER) with default settings. After manual adjustment in SeaView version 4 (Gouy et al. 2010), the alignment included 783 characters. The phylogenetically informative indels were coded following the simple indel coding algorithm (Simmons et al. 2001) with the program FastGap 1.2 (Borchsenius 2009). Adding indel characters to the nucleotide alignment of ITS sequences increases the robustness of phylogenetic analyses (Nagy et al. 2012). The final matrix including nucleotide + binary data was 829 characters in length. Bayesian inference (BI) analyses were performed with MrBayes version 3.1.2 (Ronquist & Huelsenbeck 2003). The nucleotide and indel characters were split into two partitions to which the GTR+G and two-state Markov model, respectively, were applied. Four Markov chains were run each for 5,000,000 generations, sampling every 100 generations. A burn-in of 12,500 trees was established. Sampled trees from both runs were combined in a 50 % majority rule consensus phylogram and posterior probabilities (BIPP) were calculated (Fig. 34). In addition, maximum likelihood (ML) analysis was carried out using RAxML version 7 (Stamatakis et al. 2008) in raxmlGUI (Silvestro & Michalak 2012) with 1,000 bootstrap replicates under the GTRGAMMA substitu-

Fig. 1. Laboulbeniales spp. nov. **A–C.** *Cantharomyces paschalis*, slide WR4370 (holotype). **D–E**. *Cryptandromyces pinguis*, slide SS·E534 (holotype). **F–G.** *Cryptandromyces tricornis*, slide SS·E482a (holotype). Scale bar 50 µm.

tion model for DNA and the default set for binary (indel) characters. The final tree was edited in MEGA7 (Kumar et al. 2016) and Adobe Illustrator CS4.

Taxonomy

Ascomycota, Laboulbeniomycetes, Laboulbeniales, Laboulbeniaceae

Cantharomyces paschalis W. Rossi & Santam., **sp. nov.** – Fig. 1
MycoBank no.: MB 839553

Holotypus. – CHILE. Rapa Nui Island, Maugaoa, on *Mimopaederus insularis* Cameron, 1936 (Coleoptera, Staphylinidae, Oxytelinae), 11 December 1963, *leg.* J.F.G. & T.M. Clarke, slide WR4370 (4 mature and 11 immature or incomplete thalli; holotype at FI).

Description. – Cells I and VI almost hyaline; the rest of the thallus yellowish brown, with a large, contrasting, dark spot on the upper, inner side of cell III and a second spot, lighter and smaller than the previous, on the ventral, lower angle of cell II. – Cell I obtrapezoidal in section, slightly longer than maximum width. – Cell II larger, irregularly shaped or broadly pentagonal. – Cell III quadrangular, slightly broader than long. – Appendage with the lower cell larger than cell III, irregularly quadrangular, the inner side longer than the outer, with the elongate antheridium occupying about 1/3 of the cell on the inner side; the second cell of the appendage is slightly narrower than the first but much shorter, bearing the hemispherical third cell that gives rise to two long, diverging branches, the outer of which bifurcates above its lower cell. – Stalk cell of the perithecium relatively short, slightly broader distally. – Perithecium ovoid, very slightly asymmetrical, ending in a truncate tip with almost flattened and hyaline apex. – Length from foot to perithecial apex 110–140 µm; longest branch of the appendage 125 µm; perithecium, including basal cells 50–63 × 25–30 µm.

Etymology. – From Latin *Pascha* (Easter in English, Pascua in Spanish), referring to the holotype locality, Easter Island (or Isla de Pascua).

Hosts and distribution. – Thus far only known from *Mimopaederus insularis* (Coleoptera, Staphylinidae, Oxytelinae) on Rapa Nui Island (also known as Easter Island or Isla de Pascua), Chile.

Additional material examined. – *Ibid.*, slide WR4371 (1 mature thallus; paratype at FI).

Notes. – To date, 27 species have been described in the genus *Cantharomyces*, most of which (19) are associated with Staphylinidae; the remaining species are found on riparian insects of the families Dryopidae, Limnichidae, and Hydrochidae (Picard 1912, Thaxter 1931, Haelewaters & De Kesel 2013). *Cantharomyces paschalis* might be compared with *C. chilensis* Thaxt., described from *Thinodromus signatus* (Erichson, 1834) [as *Trogophloeus signatus* Sol.] from Chilean mainland, which is more than 3,600 km away from Easter Island. The latter fungus differs from the new species mainly for the blackish color of a large portion of the thallus, for the more numerous and shorter branches of the appendage and for the distinctly larger antheridium (Thaxter 1931).

Authors: S. Santamaria & W. Rossi

Basidiomycota, Agaricomycetes, Agaricales, Cortinariaceae

Cortinarius squamosus E. Sesli, **sp. nov**. – Figs. 2, 3
Index Fungorum no.: IF 557116

Diagnosis. – Characterized by a reddish brown, quite scaly, irregular, hygrophanous, broadly umbonate pileus; adnate, distant and reddish brown lamellae; very thin content; cylindrical or clavate, curved, reddish brown and fibrous stipe, almond-like odor; and growing under *Castanea*.

Holotypus. – TURKEY. Trabzon Province, Çilekli, 40°58'01.99''N, 39°46'16.68''E, 406 m a.s.l., in forest of *Castanea sativa* (Fagales, Fagaceae), 19 September 2014, *leg.* E. Sesli (KATO Fungi 3386; holotype). Sequences ex-holotype: MW314263 (ITS), MW314262 (LSU).

Description. – Pileus conical then convex to plane, broadly umbonate, 15–30 mm in diam., margin crenate, ± incurved, reddish brown, distinctly scaly, irregular, hygrophanous, darker reddish brown when moist, lighter when dry, remaining reddish in some parts; edge lighter than the pileus surface. – Lamellae adnate, distant, reddish brown, broad, thick, edges entire to rarely crenate, L = 20–30, I = 1–4. – Context of pileus very thin, nearly as thick as a lamella except where it is attached to the pileus. – Taste indistinct. – Odor resembling almonds. – Stipe cylindrical to clavate, sometimes flattened, generally curved, 30–40 × 3–5 mm, hygrophanous, reddish brown, lighter in places, fibrous, with a mass of white mycelium at the base. – Basidiospores (7.2–)7.5–9.0(–9.6) × (4.8–)5.5–6.5(–7.2) µm, average 8 × 6 µm [n = 65], Q=1.2–1.4, light ochre or greenish-yellow; ellipsoid to subglobose, typically verrucose. – Basidia clavate, (20–)25–30(–35) × (6.3–)7.0–9.0(–10.7) µm [n = 40], with 4(2) sterigmata and clamped, some with granular contents. – Marginal cells clavate. – Epicutis composed of cylindrical, 3.3–7.6 µm hyphae. – Hypocutis composed of broadly cylindrical to enlarged, 35.5–63.7 × 13.1–18.9 µm

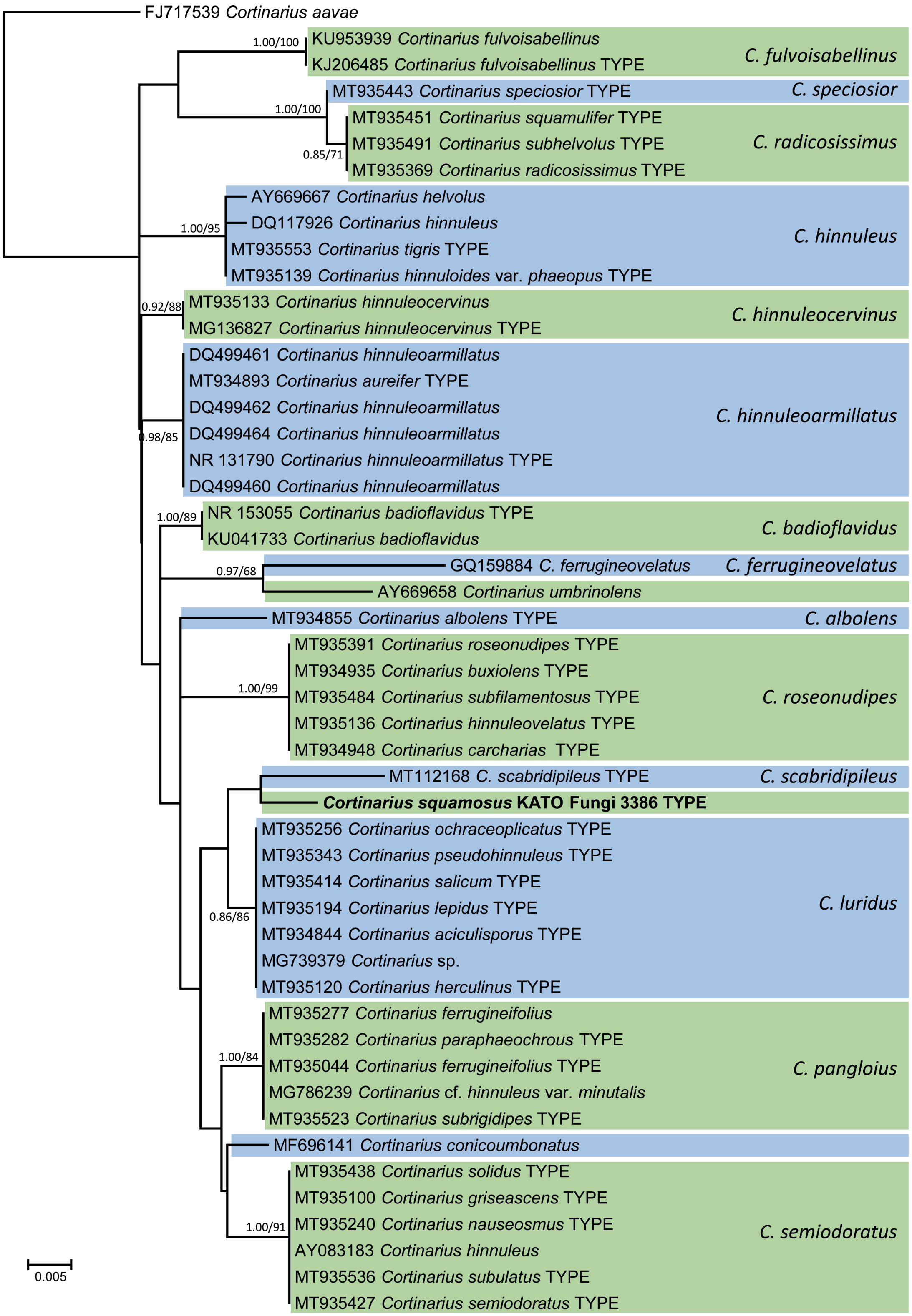

Fig. 2. Phylogeny of *Cortinarius* subgen. *Telamonia* sect. *Hinnulei*, reconstructed from an ITS dataset. The topology is the result of ML inference performed with RAxML. For each node, BIPP (if ≥0.95) and MLBS (if ≥70) are presented above the branch leading to that node. Newly generated sequence highlighted in boldface.

encrusted hyphae. – Clamp connections present.

Etymology. – from '*squamosus*' (Latin), meaning covered with or characterized by scales, referring to the distinctly scaly pileus.

Habitat and distribution. – Solitary to gregarious under *Castanea sativa*. Most probably saprotrophic, fruiting in autumn. Known only from the East Black Sea Region of Turkey so far.

Additional material examined. – TURKEY. Trabzon Province, Maçka, Sevinç neighborhood, in mixed deciduous forest under *Castanea sativa* (Fagales, Fagaceae), 2 September 2020, *leg.* E. Sesli (KATO fungi 4325; paratype).

Notes. – The ITS sequence obtained from the holotype collection KATO Fungi 3386 shared 98% identity with *C. subrigidipes* M.M. Moser (MT935523) and *C. paraphaeochrous* M.M. Moser (MT935282) of *Cortinarius* subgenus *Telamonia* section *Hinnulei*. A threshold of 99 % is sufficient to recognize species in *Cortinarius* using the ITS region (Garnica et al. 2016). Our phylogenetic analysis of selected sequences from this section (Fig. 2) placed *C. squamosus* sister to *C. scabridipileus* Kytov., Liimat. & Niskanen, with quite some evolutionary distance between both sequences. Morphologically, *C. scabridipileus* differs by the following characteristics: slightly larger, unequally plano-convex to very shallowly plano-depressed, cacao brown to hazel brown, slightly squarrose pileus; somewhat tapering or thickened, whitish silky-fibrillose stipe; and ellipsoid to obovoidly ellipsoid or subglobose basidiospores (Niskanen 2020).

Cortinarius conicoumbonatus E. Sesli, Liimat. & K. Demirel is a similar species that differs by its coniferous habitat (associated with *Picea*). Morphologically, it differs from *C. squamosus* in having a cream-colored, light ochre to beige brown, smooth pileus; a somewhat whitish stipe; light ochre-brown to rust-brown lamellae; an unpleasant and sharp odor; and broadly ellipsoid to obovoid basidiospores measuring 7.9 × 5.2 µm (Sesli & Liimatainen 2018, Sesli et al. 2020). Another close species, *C. hinnuleus* Fr., has a 25–70 mm in diam., hemispherical to conical, pale reddish to orange brown pileus; 30–120 mm, whitish fibrillose to reddish brown stipe; earthy smell; and subglobose to obovoid basidiospores measuring 7–9 × 5–6.5 µm (Breitenbach & Kränzlin 2000, Niskanen & Kytövuori 2008, Soop 2018). *Cortinarius hinnuleoarmillatus* Reumaux differs by its larger pileus (30–80 mm in diam.), raphanoid smell, longer stipe (60–100 mm), and longer basidiospores (8.5–10 µm) (Niskanen & Kytövuori 2008, Soop 2018). *Cortinarius roseonudipes* Rob. Henry & Moënne-Locc. is different from the new species by its yellowish or dark brown and larger pileus (25–60 mm in diam.), longer stipe (40–120 mm), and slightly longer basidiospores (8.5–10 µm) (Niskanen & Kytövuori 2008, Soop 2018). A *Salix*-associated species, *C. minutalis* Lamoure, also placed in sect. *Hinnulei*, has a hemispherical to conical, red brown to yellowish brown pileus, and slightly larger basidiospores (Breitenbach & Kränzlin 2000, Niskanen & Kytövuori 2008).

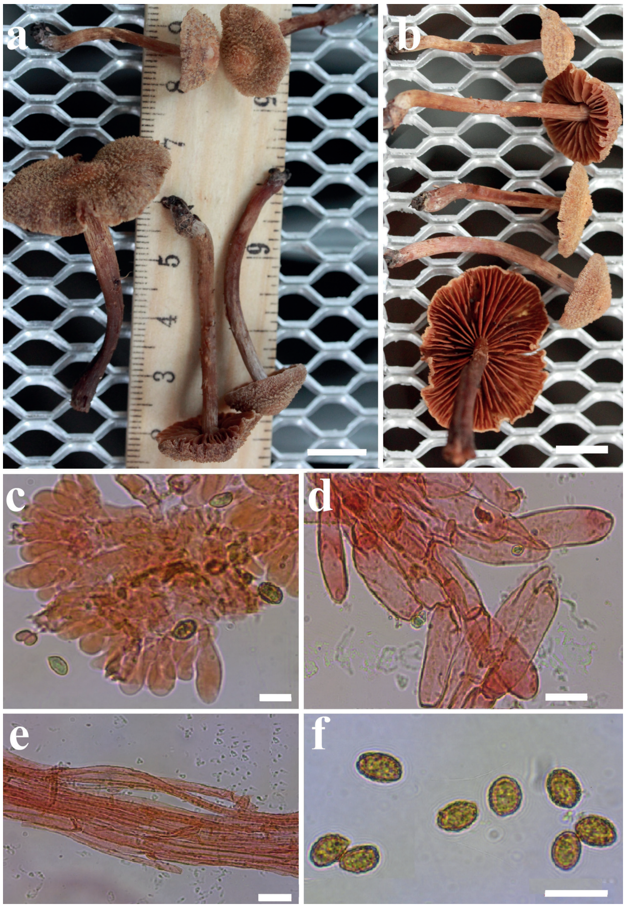

Fig. 3. *Cortinarius. squamosus*, collection KATO Fungi 3386 (holotype). **a–b.** Basidiomata. **c.** Section through the hymenium. **d.** Pileipellis. **e.** Stipitipellis. **f.** Basidiospores. Scale bars a–b 10 mm, c–f 10 µm.

A number of phylogenetically distantly related species placed in different sections (Liimatainen et al. 2020) are similar to *C. squamosus* as well. *Cortinarius safranopes* Rob. Henry (sect. *Rubricori* = sect. *Safranopedes*) differs from *C. squamosus* by its yellowish brown pileus and lamellae; longer stipe (40–110 mm); obovoid-ellipsoid to dacryoid and longer basidiospores (9–10 µm) (Niskanen & Kytövuori 2008). *Cortinarius umbrinolens* P.D. Orton is a small species with dark brown, bell-shaped to expanded pileus; yellowish or grey brown lamellae; greyish brown and fibrous stipe; and ellipsoid to amygdaloid and longer basidiospores (8–9.5 µm) (Breitenbach & Kränzlin 2000, Lindström 2012, Soop 2018). *Cortinarius aavae* Liimat. & Niskanen (sect. *Leiocastanei*), a conifer-associated species, has a reddish brown or brown pileus measuring 15–40 mm in diam., an indistinct smell, and amygdaloid basidiospores that are smaller compared to *C. squamosus* (6.5–7.5 × 4.0–4.5 µm) (Niskanen et al. 2012).

Author: E. Sesli

Ascomycota, Laboulbeniomycetes, Laboulbeniales, Laboulbeniaceae

Cryptandromyces pinguis Santam. & W. Rossi, **sp. nov.** – Fig. 1
MycoBank no.: MB 839555

Holotypus. – NICARAGUA. Departamento de Estelí, Mesas de Moropotente, on left epipleuron of *Euconnus* (*Napochus*) sp. (Coleoptera, Staphylinidae, Scydmaeninae), pitfall trap, 23–30 August 2007, *leg.* P. Andrés, slide BCB SS·E534 (holotype).

Description. – Thallus hyaline. – Lower receptacle slender and elongate, gradually enlarging from below upwards, with the suprabasal cell distinctly shorter and broader than the basal. – Appendage diverging from the perithecium, consisting of nine cells, gradually widening up to the third or the fourth cell, after which it tapers rather abruptly, never exceeding the perithecial apex. – Stalk cell of the perithecium about twice longer than broad, with the lower portion joined to inner side of the basal cell of the appendage. One of the basal cells is much larger than the others and bulges outwards. – Perithecium, including basal cells, symmetrical, broadly ovoid, slightly more than twice longer than maximum width, regularly tapering to the tip, which ends in four small, subequal lips. – Length from foot to perithecial apex 124–147 µm; length from foot to the apex of the appendage 120–144 µm; perithecium, including basal cells 58–67 × 24–29 µm.

Etymology. – From Latin *pinguis*, which means fatty, because of the stout habitus of the fungus.

Hosts and distribution. – Only known from *Euconnus* (*Napochus*) sp. (Coleoptera, Staphylinidae, Scydmaeninae) in Nicaragua.

Notes. – At present, the genus *Cryptandromyces* includes 17 species, 9 of which are found on members of subfamily Scydmaeninae (Staphylinidae). Although lacking any striking feature, except for the large and bulging secondary stalk cell, *C. pinguis* is quite different from any other *Cryptandromyces*. It may only be compared to *C. geniculatus* Thaxt., described on *Euconnus* sp. [as *Connophron*] from Argentina (Thaxter 1931) and subsequently reported from China on *Euconnus* sp. (Shen & Ye 2006), which however has a laterally bent perithecium and a much longer, slender appendage.

Authors: S. Santamaria & W. Rossi

Ascomycota, Laboulbeniomycetes, Laboulbeniales, Laboulbeniaceae

Cryptandromyces tricornis Santam. & W. Rossi, **sp. nov.** – Fig. 1
MycoBank no.: MB 839566

Holotypus. – NICARAGUA. Departamento de Estelí, Mesas de Moropotente, on elytra of *Euconnus* (*Napochus*) sp. (Coleoptera, Staphylinidae, Scydmaeninae), pitfall trap, 23–30 August 2007, *leg.* P. Andrés, slide SS·E482a (holotype at BCB).

Description. – Thallus short and hyaline. – Receptacle with the basal cell broadly trapezoidal, about one and a half times longer than broad; suprabasal cell triangular or pentagonal, distinctly shorter than the previous cell. – Appendage consisting of up to ten subequal cells including the basal, slightly tapering only near the apex. – Stalk cell of the perithecium about twice longer than broad, narrower in the middle. – Perithecium asymmetrical, with the dorsal side almost straight and the ventral distinctly convex, about twice longer than maximum width, bearing apically three elongate, straight, unequal projections, the median of which is distinctly longer than the two others. – Length from foot to the tip of the longest projection 94–114 µm; length from foot to the tip of the longest appendage 92 µm; perithecium, including basal cells but not the apical projections 42–48 × 20–25 µm; longest outgrowth 26–29 µm.

Etymology. – From Latin *tria* (= three) and *cornua* (= horns), referring to the three, long, hornlike perithecial projections.

Hosts and distribution. – Only known from *Euconnus* (*Napochus*) sp. (Coleoptera, Staphylinidae, Scydmaeninae) in Nicaragua.

Additional material examined.– *Ibid.*, SSE475 (paratype at BCB).

Notes. – The three long and erect projections of *C. tricornis* are unique among the species of the same genus and make it possible to distinguish this new species at first glance.

Authors: S. Santamaria & W. Rossi

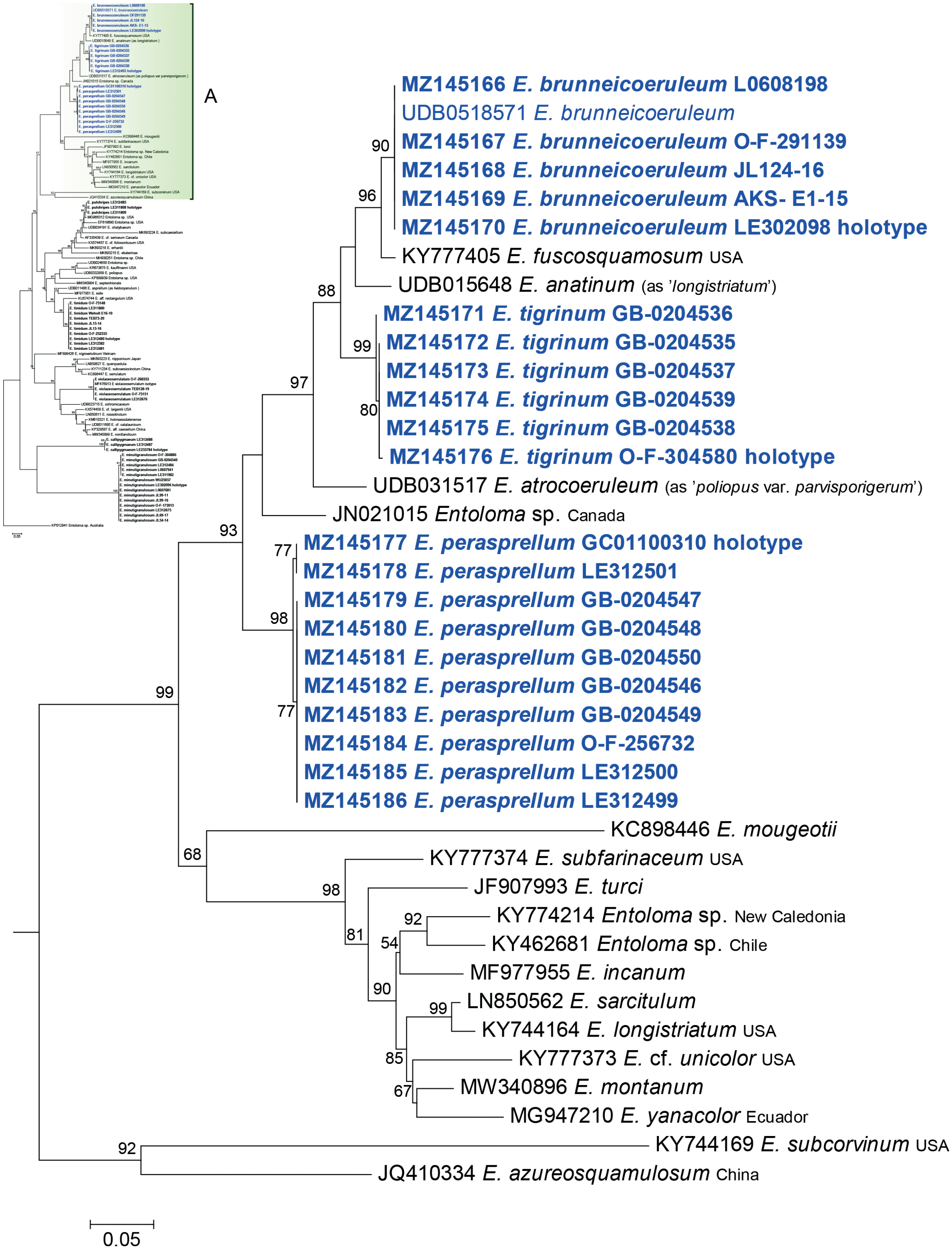

Fig. 4. Phylogeny of *Entoloma* subgen. *Cyanula*, reconstructed from an ITS dataset. The topology is the result of ML inference performed in PhyML 3.0. For each node, the SH-aLRT support value (if >50) is presented on the branch leading to that node. New species are marked in blue; newly generated sequences are highlighted in boldface; labels in smaller font size represent geographic origin except Europe. Bar indicates 0.05 expected changes per site per branch. Part A.

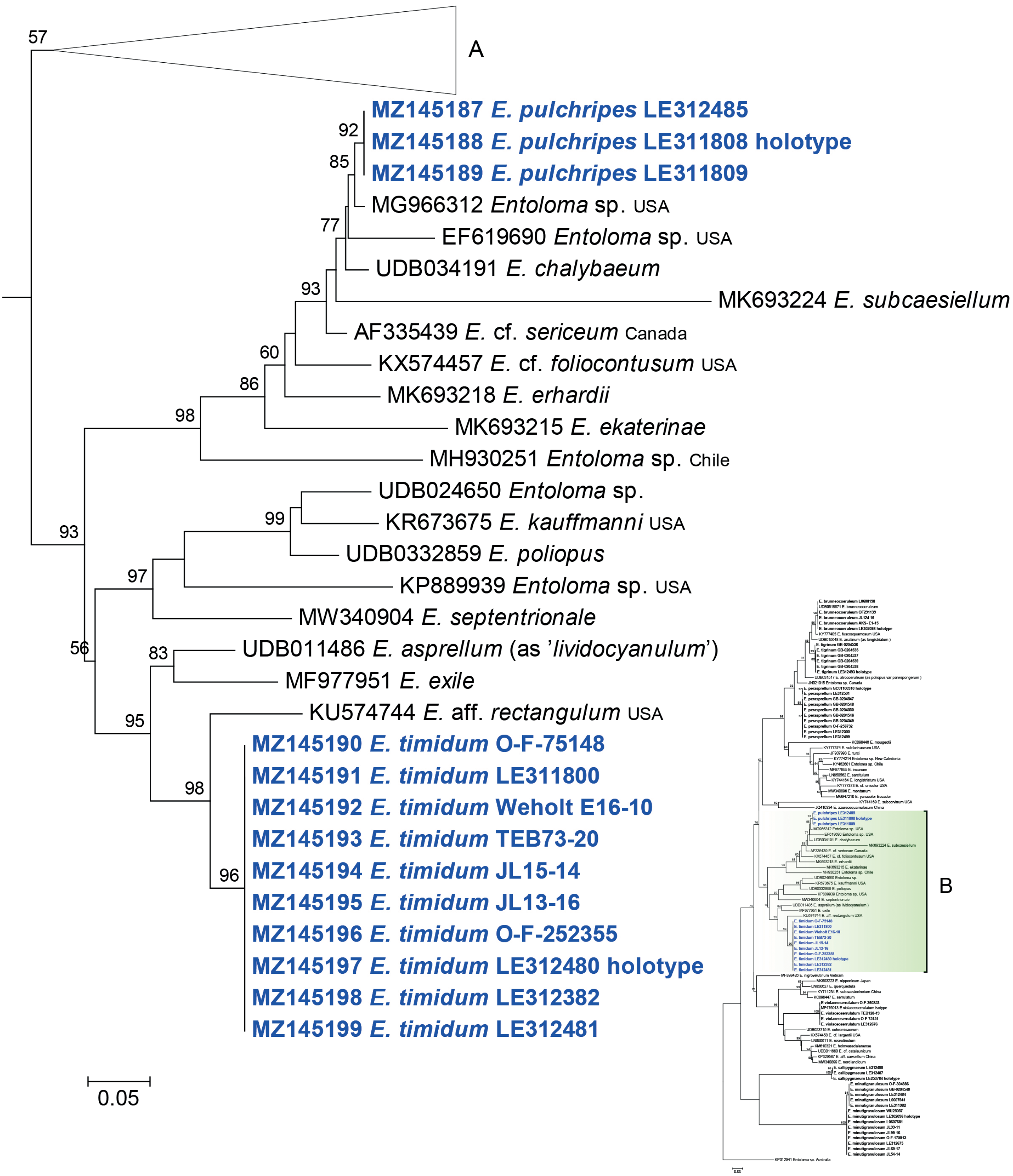

Fig. 4. *Continued.* Part B.

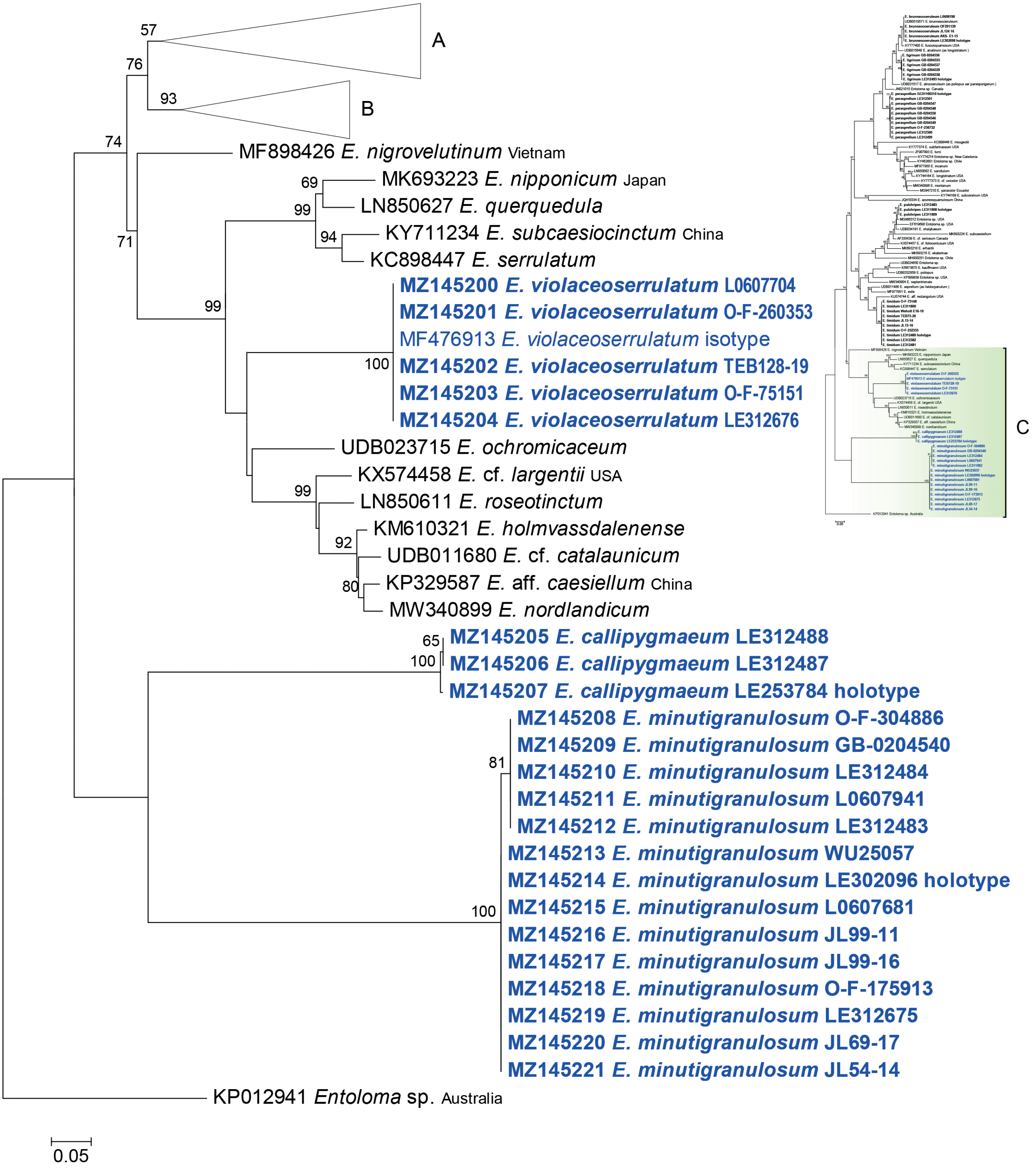

Fig. 4. *Continued.* Part C.

Fig. 5. *In situ* photos of the new *Entoloma* species. **A.** *Entoloma brunneicoeruleum*, collection LE302098 (holotype). **B.** *Entoloma callipygmaeum*, collection LE253784 (holotype). **C.** *Entoloma minutigranulosum*, collection LE 302096 (holotype). **D.** *Entoloma perasprellum*, collection GC01100310 (holotype), **E.** *Entoloma pulchripes*, collection LE311808 (holotype). **F.** *Entoloma tigrinum*, collection LE312493 (holotype). **G.** *Entoloma timidum*, collection LE312480 (holotype). **H.** *Entoloma violaceoserrulatum*, collection TEB 128-19. Photos O.V. Morozova (A–C, E–G), G. Corriol (D), B. Dima (H).

Basidiomycota, Agaricomycetes, Agaricales, Entolomataceae

Entoloma brunneicoeruleum O.V. Morozova, Noordel., Brandrud, J.B. Jordal & Dima, **sp. nov.** – Figs. 5a, 6
MycoBank no.: MB 839631

Holotypus. – RUSSIA. Pskov region, Pechorsky district, eastern shore of Lake Velje, 57°38'16"N, 27°47'35"E, 90 m a.s.l., on soil in wet *Alnus–Betula* forest, 19 July 2007, *leg.* O. Morozova (LE 302098; holotype). Sequences ex-holotype: MZ145170 (ITS).

Description. – Basidiomata medium-sized, collybioid. – Pileus 13–30 mm in diam., conico-convex or hemispherical with more or less depressed center, soon expanding to plano-convex and applanate with slightly umbilicate center, with deflexed and then straight margin, hygrophanous, translucently striate almost up to the center, minutely radially fibrillose-squamulose all over, more densely in the center, initially greyish brown with bluish or purplish tinge (17E4, 19E4–5) and only slightly darker center, then greyish-brown or yellow-brown with a darker, almost black central spot (umbilicus). – Lamellae moderately distant, emarginate or adnexed with short tooth, whitish or pale, becoming pinkish, with irregular to serrulate, concolorous edge. – Stipe 30–80 × 1.5–3 mm, cylindrical or slightly broadened towards the base, sometimes compressed with longitudinal groove, dark blue, greyish blue, steel-blue or purplish grey (20D4–5, 20E4–6, 19D3–5), initially minutely longitudinally striate(-fibrillose), but soon smooth and polished, white tomentose at base. – Context greyish. Smell indistinct, sweetish on drying, taste not reported. – Basidiospores 10.5–16 × 6.8–9.5 µm, average 12.0–13.0 × 7.5–8.7, Q=1.3–2.0 µm, Q_{av}=1.4–1.7, heterodiametrical, of two types, (*i*) with 5–8 angles in side-view, (*ii*) or almost nodulose in some collections. – Basidia 30–45 × 10.5–13.5 µm, 4-spored, narrowly clavate to clavate, clampless. – Lamella edge sterile or heterogeneous. – Cheilocystidia 20–30(–64) × 8.5–11.5 µm, cylindrical or narrowly clavate, often septate, usually intermixed with basidia. – Caulocystidia absent. – Pileipellis a cutis with transition to a trichoderm of 4–16 µm wide cylindrical hyphae, with ascending, cylindrical to fusiform terminal elements 23–80 × 11–25 µm. Pigment intracellular, sometimes agglutinate, brownish in KOH. – Clamp connections absent.

Etymology. – From '*brunneus*' (Latin, meaning brown), and '*coeruleus*' (Latin, meaning blue), referring to the brown pileus and blue stipe.

Habitat and distribution. – In small groups on soil in damp grasslands (hayfield, pasture), *Sphagnum* bog, and damp forests with *Betula* and *Alnus*, on richer to calcareous soil. Known from Russia (European part), the Netherlands, Norway, and Estonia (from soil sample).

Additional material examined. – NORWAY. Møre og Romsdal, Fjord, Valldal, Heimsetra, 62°21'00.00"N, 7°20'51.72"E semi-natural grassland (pasture), 3 September 2008, *leg.* J.B. Jordal, O-F-291139; Nordland, Grane, Holmvassdalen Nature Reserve, 65°17'07.44"N, 13°18'48.58"E, in *Sphagnum* in old calcareous pine forest, *leg.* J. Lorås & M. Eidissen, JL 124-16; Rogaland, Strand, Strandalia, 59°02'33.36"N, 5°55'51.96"E, old wooded pasture with *Betula*, in *Sphagnum*, 26 July 2015, *leg.* A.K. Svensen, AKS E1-15. – THE NETHERLANDS. Gelderland province, Ratum, Willinks Weust, 51°57'52.93"N, 6°46'45.94"E, 19 August 2016, *leg.* G.M. Jansen (L-0608198).

Notes. – *Entoloma brunneicoeruleum* is characterized by the brown pileus, initially with a slight bluish or purplish tinge, dark blue to steel blue stipe, usually heterogeneous lamellae edge with undifferentiated, cylindrical or almost cylindrical cheilocystidia, and spores of two types, (*i*) medium sized with 5–7 normally developed angles and Q=1.5–1.7; (*ii*) large, almost nodulose with Q=1.8–2.0. *Entoloma brunneicoeruleum* belongs to a group of closely related, but phylogenetically well-separated species around *E. atrocoeruleum* Noordel., and may be considered an *E. atrocoeruleum* with more brownish pileus, hence the name. They also differ in basidiospore size. From the other species in this group, *E. anatinum* (Lasch) Donk and *E. perasprellum* and *E. tigrinum* (both described below), it differs by having by far the largest basidiospores. *Entoloma anatinum* differs additionally by the absence of cheilocystidia, a more distinctly fibrillose stipe, and a stouter habit. *Entoloma tigrinum* has ochre-tinged basidiocarps, and a very different pileus surface with small, granulose squamules, whereas *E. perasprellum* differs among other things by a completely sterile lamella edge of the serrulatum type. The poorly known *E. nigroviolaceum* (P.D. Orton) Hesler, with similar large basidiospores, has more pronounced violaceous tinges, and a strongly fibrillose stipe.

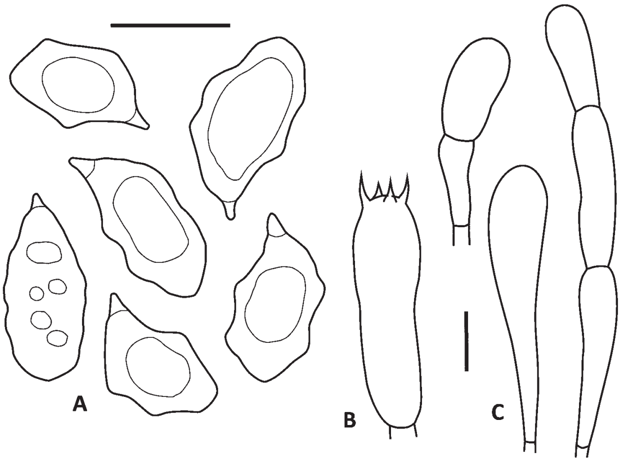

Fig. 6. *Entoloma brunneicoeruleum*, micromorphological features drawn from the holotype (LE302098). **A.** Basidiospores. **B.** Basidium. **C.** Cheilocystidia. Scale bars 10 µm, *del.* O.V. Morozova.

Authors: B. Dima, O.V. Morozova, M.E. Noordeloos, T.E. Brandrud, J.B. Jordal, G.M. Jansen & J. Lorås

Basidiomycota, Agaricomycetes, Agaricales, Entolomataceae

Entoloma callipygmaeum O.V. Morozova, Noordel. & Dima, **sp. nov.** – Figs. 5b, 7
= *Entoloma gomerense* sensu Noordeloos & Morozova *in* Mycotaxon 112: 249 (2010).
MycoBank no.: MB 839632

Holotypus. – RUSSIA. Primorsky Territory, Kedrovaya Pad Nature Reserve, right bank of Kedrovaya River, 43°05'56"N, 131°33'21"E, on soil in flood-plain forest with *Quercus mongolica*, *Tilia amurensis*, *Acer* spp., 17 August 2005, *leg.* O. Morozova (LE 253784; holotype). Sequences ex-holotype: MZ145207 (ITS).

Description. – Basidiomata small, collybioid. – Pileus 7–10 mm in diam., plano-convex with depressed center, slightly hygrophanous, deeply translucently striate, ground color rather pale bluish, blue-grey or violaceous-grey, but covered with darker squamules, more dense at center, more spread towards margin; squamules and striae greyish blue, greyish purple, or greyish brown (18E5–7, 18F5–7, 20E5–7). – Lamellae adnate-emarginate with a small decurrent tooth, whitish to greyish pink with more or less serrulate blackish purple edge. – Stipe 22–35 × 1–2 mm, cylindrical, dark greyish blue (19D4–5, 19E4–5, 20D4–5), polished, glabrous, base with white tomentum. – Context concolorous with the surface, whitish in the inner part. – Smell indistinct, taste indistinct. – Basidiospores 8.5–11 × 6.5–9.0 µm, average 10.0 × 7.5 µm, Q=1.3–1.5, Q_{av}=1.4, heterodiametrical, with 5–6 angles in side view. – Basidia 22–32 × 8–13 µm, clavate to elongate, clampless. – Lamella edge sterile. – Cheilocystidia 20–85 × 11–22 µm, broadly clavate or lageniform, including those with a rather long neck, but in some specimens, only clavate cystidia present, with dark intracellular pigment. – Pileipellis a cutis with transition to a trichoderm with inflated, narrowly clavate or elongated terminal cells 45–70 × 12–20 µm, with intracellular pigment. – Clamp connections absent.

Etymology. – From Greek 'κάλλος' (beauty) and 'πυγμαῖος' (dwarfish), referring to the nice color and small size of basidiomata.

Habitat and distribution. – Saprotrophic on soil, among living mosses and on decayed wood in floodplain forests. Thus far only been recorded from the Russian Far East (Primorski Territory).

Additional material examined. – RUSSIA. Primorski Territory, Sikhote-Alin Nature Reserve, vicinities of Maisa, on living mosses in the road in mixed forest of *Quercus mongolica*, *Acer mono*, *Tilia amurensis*, *Pinus koreana*, 45°14'19.80"N, 136°30'40.02"E, 22 August 2013, *leg.* O. Morozova (LE 312487); *Ibid.*, along stream, in flood-plain forest of *Quercus mongolica*, *Acer mono*, *Tilia amurensis*, *Pinus koreana*, 27 August 2013, *leg.* O. Morozova (LE 312488).

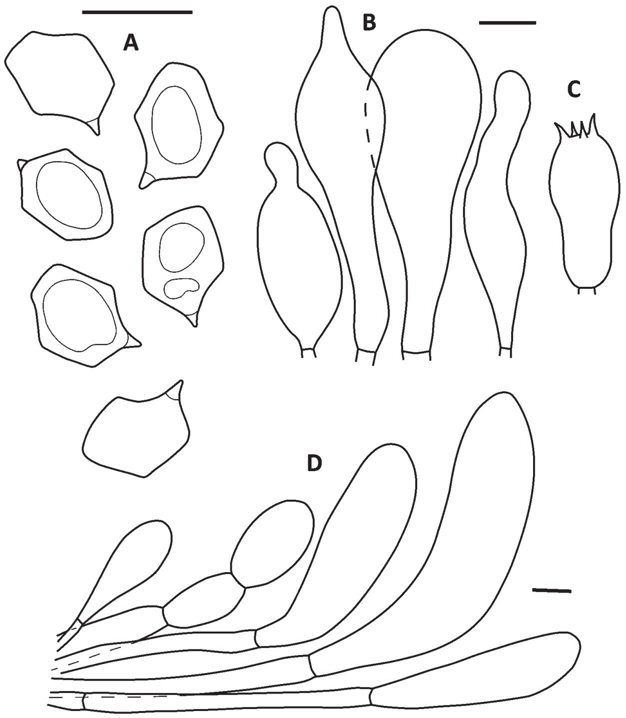

Fig. 7. *Entoloma callipygmaeum*, micromorphological features drawn from the holotype (LE253784). **A.** Basidiospores. **B.** Cheilocystidia. **C.** Basidium. **D.** Pileipellis. Scale bars 10 µm, *del.* O.V. Morozova.

Notes. – The tiny violaceous or blue basidiocarps with deeply striate pileus and purplish serrulate lamella edge are reminiscent of *E. gomerense* Wölfel & Noordel., a Mediterranean species with a slightly different pileus surface, and smaller, simple basidiospores. It is also similar to *E. cyanulum* (Lasch) Noordel., which, however, never has a blue-purple serrulate lamella edge. Phylogenetically the closest species is *E. carneogriseum* (Berk. & Broome) Noordel., another species with serrulatum-type lamellae edge, which, however, has predominantly yellow-brown colored basidiomata with only traces of blue tinge near the pileus margin and in the stipe.

Authors: B. Dima, O.V. Morozova & M.E. Noordeloos.

Basidiomycota, Agaricomycetes, Agaricales, Entolomataceae

Entoloma minutigranulosum O.V. Morozova, Noordel., Brandrud & Dima, **sp. nov.** – Figs. 5c, 8
= *Entoloma ochromicaceum* sensu Morozova et al. *in* Novosti Sist. Nizsh. Rast. 49: 196 (2015).
MycoBank no.: MB 839633

Holotypus. – RUSSIA. Pskov region, Pechorsky district, Izborsk village, Zmeinaya ravine, on calcareous grassland, 57°43’N, 27°51’E, 23 August 2011, *leg.* O. Morozova (LE 302096; holotype). Sequences ex-holotype: MZ145214 (ITS).

Description. – Basidiomata small, collybioid. – Pileus 10–20 mm in diam., hemispherical to convex, expanding to plano-convex, with blunt, slightly umbonate, or umbilicate center, with deflexed margin, not distinctly hygrophanous, dark yellow-brown to warm ochre-brown (5B4–6, 5C4–6), with darker center (up to 6D4), entirely minutely granulose or finely squamulose, sometimes glabrescent with age, initially not striate but becoming translucently striate with age. – Lamellae moderately distant, emarginate or adnate with a decurrent tooth, subventricose, white then pale pink, with minutely serrulate, (in part) brown edge. – Stipe 20–50 × 2–3 mm, cylindrical or slightly broadened towards base, pale brown with distinct metallic-grey to bluish grey tinge, particularly in the lower half, which fades with age, when very young often with distinct greyish blue tinge on the entire stipe, smooth, polished, base with some white tomentum. – Context very thin, brittle. – Smell and taste inconspicuous. – Basidiospores 7–12 × 5.5–7.5 µm, average 10.0 × 6.5 µm, Q=1.3–1.7, Q_{av}=1.5, heterodiametrical, with 5–7 distinct angles in side-view. – Basidia 31–37 × 9.5–11.5 µm, 4-spored, clavate, clampless. – Lamella edge sterile. – Cheilocystidia 35–75 × 8–14 µm, clavate or narrowly clavate, sometimes septate, sometimes with brownish intracellular pigment in KOH. – Hymenophoral trama regular, made up of cylindrical elements, 50–160 × 5–22 µm. – Pileipellis a cutis with transition to a trichoderm made up of 5–12 µm wide cylindrical hyphae, and clavate, broadly clavate or sphaeropedunculate terminal elements, 40–100 × 14–45 µm, with brown granular intracellular pigment. – Caulocystidia absent. – Clamp connections absent.

Etymology. – From Latin, ‘*minutum*’ (very small) and ‘*granulosum*’, referring to the finely granulose pileus.

Habitat and distribution. – In small groups on soil on calcareous semi-natural grasslands (pastures), once also recorded from alpine heath. Known from Austria, Denmark, France, Germany, the Netherlands, Norway, Sweden, and Russia (European part and Siberia).

Additional material examined. – RUSSIA. Altay Republic, Altaiskiy Nature Reserve, cordon Chelyush, 46°07’07.97”N, 11°06’56.76”E, grassland near farm, 28 August 2018, *leg.* O. Morozova, LE 312483; *Ibid.*, LE 312484. – AUSTRIA. Vorarlberg, Lechtal, Dalaas, Tannlägeralpe, 47°09’20.91”N, 9°54’16.98”E, August 2004, *leg.* A. Hausknecht (WU25057, as *E. glaucobasis*). – GERMANY. Bayern, Lenggries, Hohenwiesen, Hohenwiesener Berg, Hochalm, 47°36’32.29”N, 11°35’11.49”E, 2 August 2014, *leg.* M. Dondl, MD-2014-7 (L0607941). – THE NETHERLANDS. Gelderland Province, Staverden, Leemputten, 52°02’40.74”N, 6°40’12.70”E, October 2019, *leg.* Finy Salzman, L0607681. – NORWAY, Finnmark, Porsanger, Kolvik N, 70°17’33.00”N, 22°06’52.20”E, calcareous seminatural pasture, 12 August 2015, *leg.* G. Gaarder, GG 7142; Nordland, Grane, Ner-Laksfors, 65°37’47.64”N, 13°16’11.64”E, calcareous meadow along the river, 14 August 2003, *leg.* G. Gaarder, GG 3568 (O-F-175913); Nordland, Grane, Holmvassdalen Nature Reserve, 65°18’52.32”N, 13°18’08.49”E, low herb vegetation in calcareous spruce forest, 22 August 2011, *leg.* J. Lorås & S. Eidissen, JL 99-11; *Ibid.*, 65°33’19.43”N, 13°45’52.18”E, 4 September 2014, JL 54–14; *Ibid.*, 65°18’57.08”N, 13°19’12.87”E, JL 99-16; Nordland, Grane, Danielåsen Nature Reserve, 65°33’11.42”N, 13°38’26.33”E, tall herb vegetation in calcareous spruce forest, 28 August 2017, *leg.* J. Lorås & S. Eidissen, JL 69–17; Oppland, Nord-Aurdal, Øystre Slidre, Skrautvål, Jordet (Bundli Ø), 61°02’22.92”N, 9°12’25.92”E, calcareous pasture (shallow soil), 6 August 2016, *leg.* T.E. Brandrud & G. Gulden, TEB 121-16 (O-F-304886). – SWEDEN. Lule lappmark, Jokkmokk, Padjelanta, Ajajaure, 67°24’28.72”N, 16°44’40.94”E, alpine heath with *Betula nana* and *Salix* spp., 16 August 2016, *leg.* G. Gulden (GB-0204540).

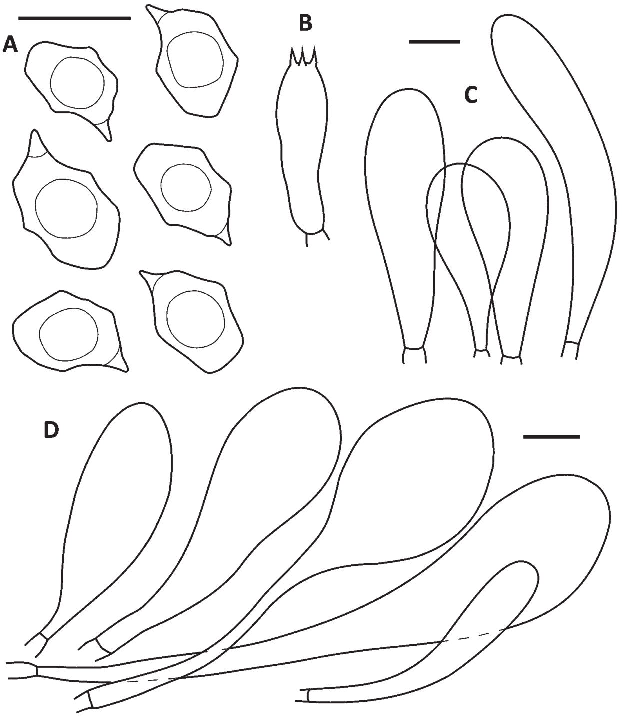

Fig. 8. *Entoloma minutigranulosum*, micromorphological features drawn from the holotype (LE 302096). **A.** Basidiospores. **B.** Basidium. **C.** Cheilocystidia. **D.** Pileipellis. Scale bars 10 µm, *del.* O.V. Morozova.

Notes. – Typically the stipe of this species appears to be bicolored: ochre-brown at the apex, and steel-grey with a glaucous-bluish tinge at the base.

This is reminiscent of *E. glaucobasis* Huijsman ex Noordel., which, however, has a distinctly fibrillose-striate stipe surface, and larger basidiospores. When very young the entire stipe can be bluish, and in such stages this species may be misidentified as *E. poliopus* var. *parvisporigerum* Noordel., but this species has a more bluish, darker pileus, and is a member of the /chalybeum clade. *Entoloma perasprellum* may appear similar, but has larger, nodulose-angled basidiospores. *Entoloma minutigranulosum* was erroneously referred to as *E. ochromicaceum* Noordel. & Liiv by Morozova et al. (2015), but the latter species lacks grey-bluish-metallic tinges in the stipe, and has larger spores (Noordeloos 1992). We note that *E. minutigranulosum* was also present in an environmental soil sample from calcareous grassland in the province of Limburg, the Netherlands (data not shown).

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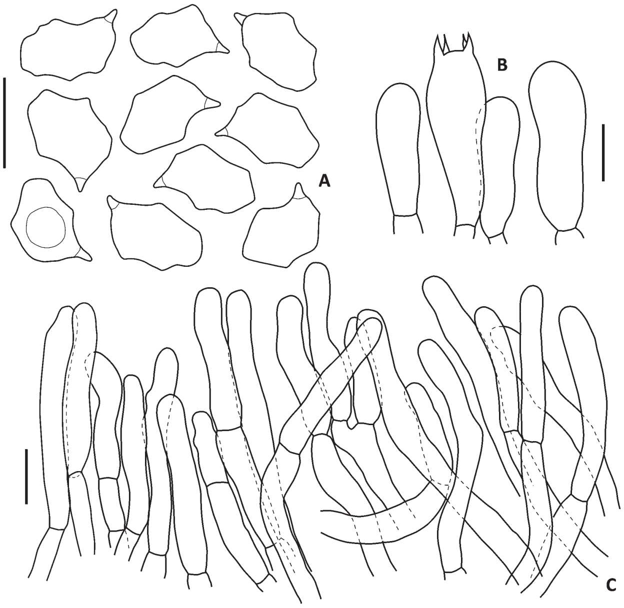

Fig. 9. *Entoloma perasprellum*, micromorphological features drawn from the holotype (GC01100310). **A.** Basidiospores. **B.** Basidium and basidioles. **C.** Lamella edge. Scale bars 10 µm, *del.* G. Corriol.

Basidiomycota, Agaricomycetes, Agaricales, Entolomataceae

Entoloma perasprellum Corriol, Dima, O.V. Morozova, J.B. Jordal & Noordel., **sp. nov.** – Figs. 5d, 9
MycoBank no.: MB 839634

Holotypus. – FRANCE. Seine-et-Marne, Fontainebleau, near the Hippodrome de la Solle, 3 October 2001, about thirty basidiomata, *leg.* G. Corriol (GC01100310; holotype in BBF). Sequences ex-holotype: MZ145177 (ITS).

Description. – Basidiomata medium-sized, collybioid. – Pileus 10–40 mm in diam., campanulate then expanding to convex or plano-convex, usually distinctly umbilicate, with deflexed margin, which is often crenulate, and sometimes undulating-lobed, opaque, not hygrophanous, indistinctly translucently striate at first, soon clearly translucently striate, grey-blue at first, but blue tinge quickly disappearing (Mu 10YR 5/4), entirely fibrillose to squamulose, then with neat, small, grey-brown (10YR 3/3) squamules on a paler yellow-brown (10YR 3/3) background. – Lamellae rather distant, adnate-emarginate, white to greyish, with an irregular edge that is often brown pigmented, but non-pigmented forms occur frequently. – Stipe 25–50 × 2–5 mm, cylindrical to compressed, glabrous, polished, or with fine pruinose-fibrillose covering, when fresh often bright blue or blue-grey, quickly pallescent to pale grey or pale greyish brown, paler than pileus, with white mycelium at base. – Context white. – Smell indistinct or somewhat sweet, like flowers. – Basidiospores (8.9–)9.4–11.0(–12.4) × (6.0–)6.4–7.6(–8.3) µm, average 10.0 × 7.0 µm; Q = (1.25–)1.30–1.60(–1.81), Q_{av}=1.45, heterodiametrical, with 6–7(–8) fairly pronounced angles, but with a tendency to be nodulose. – Basidia 28–40 × 11–12 µm, cylindrical-clavate, 4-spored, clampless. – Lamella edge sterile. – Cheilocystidia 19–38 × 3–6 µm, well-developed, subcylindrical to narrowly clavate, with brown, intracellular pigment. – Caulocystidia not observed. – Pileipellis a transition between a cutis and a trichoderm, made up of inflated-clavate terminal elements, up to 25 µm. – Pigment brown, intracellular. – Clamp connections absent.

Etymology. – Referring to the resemblance to *E. asprellum*.

Habitat and distribution. – Found mainly in calcareous alpine heaths and subalpine grasslands (pastures), but also in temperate/nemoral xerophytic grassland on base-rich sandy soil, with *Clitocybe collina* (Velen.) Klán, *C. costata* Kühner & Romagn., *Lycoperdon lividum* Pers., *Marasmius oreades* (Bolton) Fr., *Hebeloma cistophilum* Maire (holotype site). Known from France, Norway, Sweden, and Russia (Caucasus and Kamchatka).

Additional material examined. – *Ibid.* (L, isotype). – NORWAY. Trøndelag, Rennebu, Jøldalen, Bortstugusetra, 62°52'15.96"N, 9°32'52.80"E, seminatural pasture, 23 August 2018, *leg.* J.B. Jordal, JBJ 18-004 (O-F-256732). – RUS-

SIA. Karachaevo-Cherkesia Republic, Teberda Biosphere Reserve, Klukhor pass, 43°21’06.97”N, 41°41’46.22”E, ~2700 m a.s.l., on alpine grassland, 23 August 2012, *leg.* O. Morozova (LE 312501); Kamchatka Region, vicinities of Esso, near the village, 55°55’37.12”N, 158°41’04.81”E, 470 m a.s.l., in grassland, 5 August 2005, *leg.* O. Morozova (LE 312499); *Ibid.*, on hill, ~800 m a.s.l., in subalpine grassland, 5 August 2005, *leg.* O. Morozova (LE 312500). – SWEDEN. Åsele lappmark, Vilhelmina, Lasterfjället, Tjårronunjes, 65°15’27.40”N, 14°37’38.24”E, on alpine meadow on calcareous ground, 19 August 2019, *leg.* E. Larsson, EL-28-19 (GB-0204546); *Ibid.*, 65°15’27.39”N, 14°37’40.86”E, on alpine meadow on calcareous ground, 19 August 2019, *leg.* J.B. Jordal, JBJ 19-107 (GB-0204547); Åsele lappmark, Vilhelmina, Murfjället, 65°10’20.15”N, 15°08’03.97”E, on alpine heath on calcareous ground, 20 August 2019, *leg.* J.B. Jordal, JBJ 19-119 (GB-0204550); *Ibid.*, JBJ 19-122 (GB-0204548); Jämtland, Frostviken, NW slope of Raavre, 64°09’55.35”N, 17°21’17.57”E, in low alpine calcareous heath, 23 August 2019, *leg.* J.B. Jordal, JBJ 19-180 (GB-0204549).

Notes. – *Entoloma perasprellum* resembles *E. asprellum* (Fr.) Fayod, with its usually entirely finely squamulose pileus and blue-grey polished stipe. The new species differs by the almost nodulose basidiospores, and having a distinctly sterile lamella edge of the serrulatum-type. Initially, Corriol (2016) gave it the provisional name *E. cyaneoturci*, as the type specimens did have some resemblance to *E. turci* (Bres.) M.M. Moser, differing from it by the basidiospore shape and blue tinges in the basidiomata. However, now we have more collections from a rather wide geographic area, the variability appears much bigger, and the resemblance with *E. turci* is less striking. On the contrary, this new species is much more morphologically similar to *E. asprellum*, hence the name.

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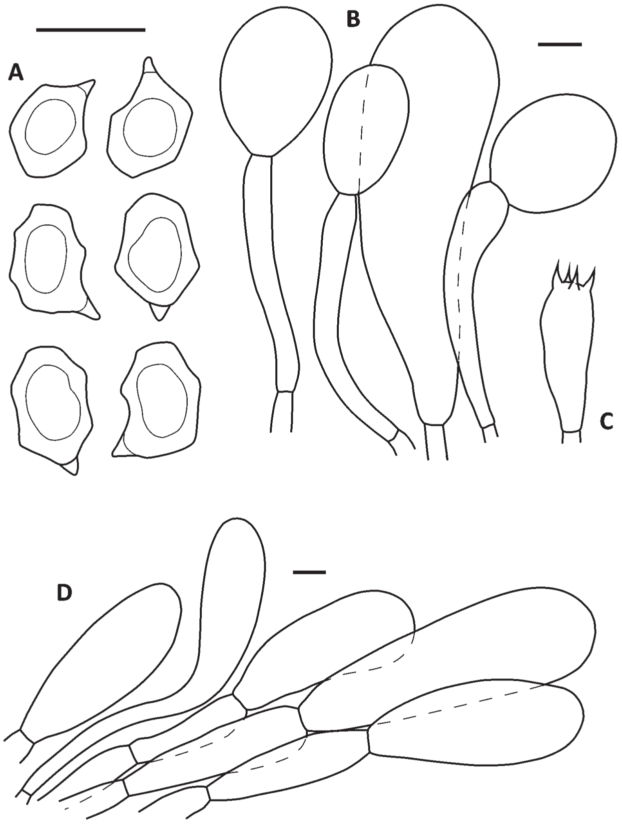

Fig. 10. *Entoloma pulchripes*, micromorphological features drawn from the holotype (LE311808). **A.** Basidiospores. **B.** Cheilocystidia. **C.** Basidium. **D.** Pileipellis. Scale bars 10 µm, *del.* O.V. Morozova.

Basidiomycota, Agaricomycetes, Agaricales, Entolomataceae

Entoloma pulchripes O.V. Morozova, Noordel., Brandrud & Dima, **sp. nov.** – Figs. 5e, 10
MycoBank no.: MB 839635

Holotypus. – RUSSIA. Tver region, Zubtsov district, 2 km SE from Mozgovo village, open place in calcareous pine forest, right bank of Derzha river, 56°12’49.90”N, 034°48’09.00”E, 11 September 2015, *leg.* O. Morozova (LE 311808; holotype). Sequences ex-holotype: MZ145188 (ITS).

Description. – Basidiomata small to medium-sized, collybioid. – Pileus 10–25 mm in diam., obtuse-conical, conico-convex or hemispherical with slightly depressed center, soon expanding to plano-convex with convex or slightly umbilicate center, with deflexed then straight margin, hygrophanous, translucently striate up to the center, minutely radially fibrillose-squamulose all over, more densely in the center, initially greyish brown (8D3, 8E3–4) with blackish-purple center, changing color with age to greyish-brown or yellowish-brown with contrasting brownish-black center, sometimes radially cracked when drying out, showing white context. – Lamellae moderately distant, adnate-emarginate, segmentiform to decurrent with short tooth, whitish, pale or greyish, becoming pinkish-grey, with irregular, more or less serrulate brown edge (sometimes almost concolor, hard to see). – Stipe 30–80 × 1.5–3 mm, cylindrical or slightly broadened towards the base, sometimes compressed with longitudinal groove, smooth, polished or minutely longitudinally striate, dark blue, greyish blue or steel-blue (20D4–5, 20E4–6), white tomentose at the base. – Context white, greyish under the surface. – Smell indistinct, sweetish on drying, taste not reported. – Basidiospores 7–11.5

× 5–7.5 µm, average 9.0 × 6.5 µm, Q=1.3–1.6, Q_{av} = 1.45, heterodiametrical, with 5–7 angles in side-view, relatively simple. – Basidia 27–34 × 10.5–11.5 µm, 4-spored, narrowly clavate to clavate, clampless. – Lamella edge sterile. – Cheilocystidia 40–90 × 16–31.5 µm, broadly clavate, vesiculose or spheropedunculate, consisting of cylindrical basal and spherical to oblong apical cells, 14–90 × 9–32 µm, often septate, with or without brown intracellular pigment in KOH. – Pileipellis a cutis with transition to a trichoderm of cylindrical 8–13 µm wide hyphae, with ascending terminal elements, 40–85 × 16–26 µm, and brownish intracellular pigment in KOH. – Caulocystidia absent. – Clamp connections absent.

Etymology. – From Latin, '*pulchrum*' (= beauty), referring to the beautifully colored stipe.

Habitat and distribution. – In small groups on soil in grasslands and calcareous pine forest. Known from Russia (European part).

Additional material examined. – RUSSIA. Tver region, Zubtsov district, 2 km SE from Mozgovo village, 56°12'49.90"N, 34°48'09.00"E, open place in calcareous pine forest, right bank of the Derzha river, 11 September 2015, *leg.* O. Morozova (LE 311809); Novgorod region, Valgay district, Valdaysky National Park, bank of Msta river, 58°16'49.19"N, 31°03'55.39"E, calcareous grassland, 23 September 2011, *leg.* O. Morozova (LE 312485).

Notes. – *Entoloma pulchripes* is characterized by the brown pileus, sometimes having a minute purplish tinge; dark blue to steel blue stipe; small basidiospores; and distinctive vesiculose or spheropedunculate cheilocystidia. It resembles *E. poliopus* (Romagn.) Noordel., from which it differs by the smaller basidiospores and the shape of cheilocystidia. Due to the brown lamella edge, *E. pulchripes* could be mistaken for *E. brunneiserrulatum* Eyssart. & Noordel., which, however, is distinguished by the brown stipe, large basidiospores, and elongate terminal cells of cheilocystidia. *Entoloma sodale* Kühner & Romagn. ex Noordel., a species with subglobose and spheropedunculate cheilocystidia, differs by the warm brown color of the pileus and lager basidiospores. According to our phylogenetic analysis (Fig. 4), the closest related species is *E. chalybaeum* (Pers.) Noordel. However, this species differs by its dark blue pileus (vs. brown pileus in *E. pulchripes*). One sequence from California, USA (GenBank accession no. MG966312, MushroomObserver.org/240552) is very close to *E. pulchripes*, sharing 99% identity. This potential conspecificity needs to be studied further.

Authors: B. Dima, O.V. Morozova, M.E. Noordeloos, T.E. Brandrud & G.M. Jansen

Basidiomycota, Agaricomycetes, Agaricales, Entolomataceae

Entoloma tigrinum Noordel., O.V. Morozova, Brandrud, J.B. Jordal & Dima**, sp. nov.** – Figs. 5f, 11
MycoBank no.: MB 839636

Holotypus. – NORWAY. Nordland, Steinkjer, Kvamsfjellet north of Lystjørna (Vesterolsenget), 64°12'46.08"N, 11°49'03.72"E, edge of rich fen, 20 August 2016, *leg.* M.E. Noordeloos, O. Morozova & J.B. Jordal (O-F-304580; holotype). Sequences ex-holotype: MZ145176 (ITS).

Description. – Basidiomata small, collybioid. – Pileus 14–20 mm, convex, expanding, umbilicate, with deflexed to straight margin, hygrophanous, background colour rather vivid ochre-brown ("golden") to brown, covered with fine, darker sepia to blackish brown dots and radially arranged squamules, densest at the center, obscurely translucently striate up to half the radius or to umbilicus, – Lamellae L=34–40, l=1–5, moderately distant, adnate, slightly emarginate with a decurrent tooth, whitish, turning pale pink, with an entire, concolorous edge. – Stipe 30–50 × 2–4 mm, cylindrical, pale ochre brown or greyish brown, much paler than the pileus, polished or innately fibrillose, with white basal mycelium, rarely slowly staining reddish at the base. – Context pale. –

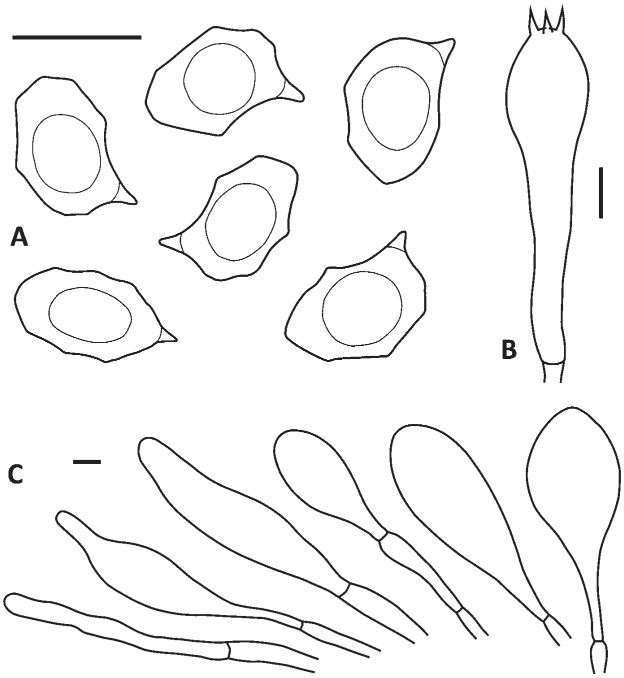

Fig. 11. *Entoloma tigrinum*, micromorphological features drawn from the holotype (LE312493). **A.** Basidiospores. **B.** Basidium **C.** Pileipellis. Scale bars 10 µm, *del.* O.V. Morozova.

Smell indistinct, taste not reported. – Basidiospores 10–13 × 7.0–8.5 µm, average 11.0 × 7.8 µm, Q=1.3–1.7, Q_{av}=1.5; heterodiametrical, 5–8-angled in side-view. – Basidia 35–52 × 10–13 µm, clavate, 4-spored, clampless. – Lamella edge fertile. – Cheilocystidia absent. – Hymenophoral trama regular, made up of cylindrical to inflated elements, up to 25 µm wide. – Pileipellis a hymeniderm of broadly clavate, broadly fusiform or ellipsoid terminal elements, 50–130 × 10–28(–50) µm. – Pigment brown, intracellular, diluted and in the form of golden brown granules. – Pileitrama of cylindrical to inflated hyphae, up to 23 µm wide with abundant brilliant granules. – Stipitipellis a cutis of cylindrical 4–8 µm wide hyphae, with a few sub-clavate terminal 7–12 µm wide endings, with brown, hyaline, intracellular pigment. – Clamp connections absent.

Etymology. – Referring to the resemblance of the pileal surface to that of *Lentinus tigrinus*.

Habitat and distribution. – Calciphilous, terrestrial in alpine meadows and heaths, but also in calcareous fen in a rather open *Picea* forest. Thus far only reported from northern Norway and Swedish Lapland.

Additional material examined. – *Ibid.* (LE 312493; isotype). – SWEDEN. Lule lappmark, Jokkmokk, Padjelanta, Arranoaijvve, 66°36’19.46”N, 19°49’46.78”E, on alpine heath on calcareous ground, 11 August 2016, *leg.* J. Olsson (GB-0204539); *Ibid.*, Vielggisbakte, 66°36’19.46”N, 19°49’46.78” E, on alpine meadow on calcareous soil, 12 August 2016, *leg.* J. Olsson (GB-0204538); Åsele lappmark, Vilhelmina, Lasterfjället, Tjårronunjes, 64°09’55.47”N, 17°19’11.50”E, on alpine heath on calcareous ground, 19 August 2019, *leg.* J.B. Jordal, JBJ 19-109 (GB-0204537); *Ibid.*, Murfjället, 65°10’20.15”N, 15°08’03.97”E, on alpine heath on calcareous ground, 20 August 2019, *leg.* J.B. Jordal, JBJ 19-128 (GB-0204536); Pite lappmark, Arjeplog, NE side of Mt. Ákháris, 66°02’45.45”N, 17°50’23.73”E, on alpine heath calcareous soil, 14 August 2018, *leg.* E. Larsson, EL156-18 (GB-0204535).

Notes. – *Entoloma tigrinum* is distinctive because of the warm ochre-brown pileus with darker greyish brown center, which often has a granulose-squamulose surface alternating with lighter patches—resembling a bit the pileal surface of *Lentinus tigrinus* (Bull.) Fr., and the fertile lamella edge. It is reminiscent of *E. leochromus* Noordel. & Liiv, a more or less similarly colored species with fertile lamella edge. However, this species is phylogenetically distant. *Entoloma minutigranulosum* has a similarly colored pileus, but differs in having glaucous to blue tinges in the stipe and a sterile lamella edge.

Authors: B. Dima, O.V. Morozova, M.E. Noordeloos, T.E. Brandrud, J.B. Jordal, G.M. Jansen & E. Larsson

Basidiomycota, Agaricomycetes, Agaricales, Entolomataceae

Entoloma timidum O.V. Morozova, Noordel., Brandrud, J.B. Jordal & Dima, **sp. nov.** – Figs. 5g, 12
MycoBank no.: MB 839637

Holotypus. – RUSSIA. Karachaevo-Cherkesia Republic, Teberda Nature Reserve, near Teberda town, on grassland in broad-leaved forest, 43°26’19.92”N, 41°43’52.20”E, 1350 m a.s.l., 21 August 2012, *leg.* O. Morozova (LE 312480; holotype). Sequences ex-holotype: MZ145197 (ITS).

Description. – Basidiomata small, collybioid. – Pileus 15–35 mm in diam., abruptly conical or hemispherical, then expanding to conico-convex, convex, and plano-convex with slightly depressed center, with deflexed then straight margin, hygrophanous, translucently striate up to the center, minutely squamulose, more densely in center, typically pallid; pale beige, yellowish brown, or pale grey with a darker central spot (4A2–3, 5B3–4, 5C3–4), initially often almost whitish towards margin. – Lamellae moderately distant, adnate-emarginate, decurrent with a tooth or arcuate, white, becoming pale or pinkish, with a concolorous entire edge. – Stipe 20–70 × 1.5–3 mm, cylindrical or slightly broadened towards the base, sometimes compressed with longitudinal groove, smooth, polished, either entirely pale beige or greyish, or with distinct greyish blue tinge, then often discoloring to

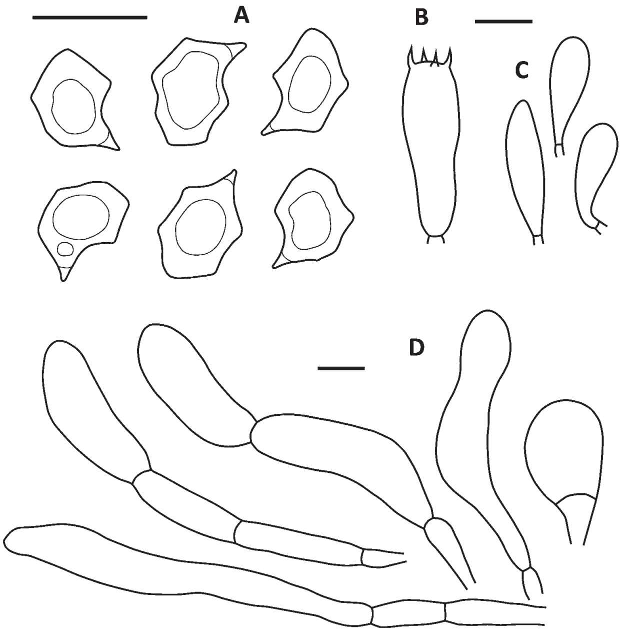

Fig. 12. *Entoloma timidum*, micromorphological features drawn from the holotype (LE312480). **A.** Basidiospores. **B.** Basidium. **C.** Cheilocystidia. **D.** Pileipellis. Scale bars 10 µm, *del.* O.V. Morozova.

beige with age, especially in upper part, white tomentose at the base. – Context white, under the surface beige. – Smell indistinct, taste not reported. – Basidiospores 8–11 × 5.5–8 µm, average 9.5 × 6.5 µm, Q=1.2–1.6, Q_{av}=1.4, heterodiametrical, with 5–7 angles in side-view. – Basidia 30–39 × 9–10.5 µm, 4-spored, narrowly clavate to clavate, clampless. – Lamella edge fertile. – Cheilocystidia absent. – Hymenophoral trama regular, made up of 4–15 µm wide, cylindrical hyphae. – Pileipellis a cutis of cylindrical 5–10 µm wide hyphae, with transition in the center to a trichoderm of chains of inflated cells with cylindrical, inflated or clavate terminal elements, 30–75 × 10–17 µm, and yellow-brown intracellular pigment in KOH. – Caulocystidia as ascending bundled cylindrical to slightly inflated cells, 23–28 × 5–7 µm. – Clamp connections absent.

Etymology. – From Latin, '*timidus*' meaning modesty, referring to the tender habitus and expressionless colors of basidiomata, especially the greyish-beige stem.

Habitat and distribution. – In small groups in semi-natural grasslands and margins of rich to calcareous *Tilia–Fraxinus–Corylus* and *Picea* forests. Known from Norway and Russia (European part and Caucasus).

Additional material examined. – RUSSIA. Tver region, Staritsa district, vicinities of the Krutitsy village, bank of Volga River, 56°34'22.49"N, 33°36'25.48"E, in grassland, 10 September 2015, *leg.* O. Morozova (LE 311800); Karachaevo-Cherkesia Republic, Teberda Nature Reserve, near Teberda town, 43°26'19.92"N, 41°43'52.20"E, in grassland in broad-leaved forest, 1350 m a.s.l., 6 August 2009, *leg.* O. Morozova (LE 312481); *Ibid.*, foot of a waterfall on the western slope of Mount Kelbashi, 56°52'03.71"N, 35°54'56.47"E, in grassland, 1450 m a.s.l., 25 August 2012, *leg.* O. Morozova (LE 312482). – NORWAY. Nordland, Grane. Holmvassdalen Nature Reserve, 65°31'57.59"N, 13°43'33.64"E, tall herb vegetation in calcareous spruce forest, 14 August 2004, *leg.* J. Lorås, JL 15-14; Nordland, Grane, Danielåsen Nature Reserve, 65°33'11.42"N, 13°38'26.33"E, tall herb vegetation in calcareous spruce forest, 9 August 2016, *leg.* J. Erlandsen & M. Eidissen, JL 13–16; Oppland, Lunner, S. Oppdalen, Amundrud, 60°17'39.84"N, 10°40'48.72"E, ~450 m a.s.l., on calcareous, semi-natural (mown) meadow, 19 August 2014, *leg.* T.E. Brandrud (O-F-75148); Troms, Senja, Lenvik, Senja familiepark, Gressmyrbotn, 69°17'07.08"N, 17°53'43.44"E, 80 m a.s.l., in base rich semi-natural pasture, 31 August 2011, *leg.* J.B. Jordal (O-F-252355); Telemark, Kragerø, Grønnåsliane, 58°52'19.39"N, 9°19'48.47"E, 8 August 2020, rich *Tilia–Fraxinus* forest, near ditch, *leg.* T.E. Brandrud, TEB 73-20; Trøndelag, Steinkjer, Egge church, 64°01'26.04"N, 11°28'26.76"E, rich lawn of churchyard, 23 August 2016, *leg.* Ø. Weholt, OW E10-16.

Notes. – *Entoloma timidum* is characterized by the rather anonymous pale yellowish-brown to beige pileus, greyish-beige polished stipe, rather small basidiospores with 5–7 distinct angles, and the lack of cheilocystidia. Some collections have a bluish-grey tinge in the stipe, particularly when young, at which time the species can be confused with the phylogenetically distant *E. lividocyanulum* (Kühner) Noordel. It is very likely that this species has been described by Ludwig (2007) as *E. mutabilipes* f. *acystidiatum* E. Ludw. *Entoloma mutabilipes* Noordel. & Liiv differs by the (partly) sterile lamella edge and slightly smaller basidiospores (Noordeloos 1992). *Entoloma timidum* might also in certain stages resemble *E. ochromicaceum* Noordel. & Liiv, but this species has a sterile lamellar edge with well-developed cheilocystidia.

Authors: B. Dima, O.V. Morozova, M.E. Noordeloos, T.E. Brandrud, J.B. Jordal, G.M. Jansen & E. Larsson

Basidiomycota, Agaricomycetes, Agaricales, Entolomataceae

Entoloma violaceoserrulatum Noordel., Brandrud, O.V. Morozova & Dima, **sp. nov.** – Figs. 5h, 13
MycoBank no.: MB 839638

= *Entoloma violaceoserrulatum* Noordel. in *Entoloma* s.l., Fungi Europaei vol. 5a: 1038 (2004), *nom. inval.*, Art. 40.7 (Melbourne).

Holotypus. – FINLAND. Varsinais-Suomi, Archipelago National Park, Berghamn, Island of Böskar, Lönöholmen, 60°03'00.07"N, 21°46'56.97"E, 25 August 1993, *leg.* J. Vauras, JV 8329F (L; holotype).

Description. – Basidiomata medium-sized, collybioid. – Pileus 12–50 mm in diam., convex to plano-convex with slightly depressed center, with subinvolute then deflexed margin, not hygrophanous, not translucently striate, entirely velutinous or tomentose, then minutely squamulose, initially dark violet to almost violaceous black, the bluish tinges very soon fades, and then almost blackish and soon discoloring to grey-brown. – Lamellae L = 30–40, l = 3–5, moderately crowded, adnate-emarginate with decurrent tooth, ventricose, initially pure white, then pink, lamellae edge fimbriate to serrulate, usually concolorous, but sometimes developing bluish black, spots. – Stipe 20–45 × 2–5 mm, cylindrical, initially silvery violaceous-grey, then discoloring more brownish grey, strongly fibrillose striate lengthwise with darker fibrils and often also minute squamules towards the apex, base with abundant white mycelium. – Context whitish to pale grey. – Smell indistinct ("leptonioid"), taste not recorded. – Basidiospores 8.5–11 × 6.0–7.5 µm, average 8.7 × 7.2 µm, Q = 1.25–1.45, Q_{av} = 1.35,

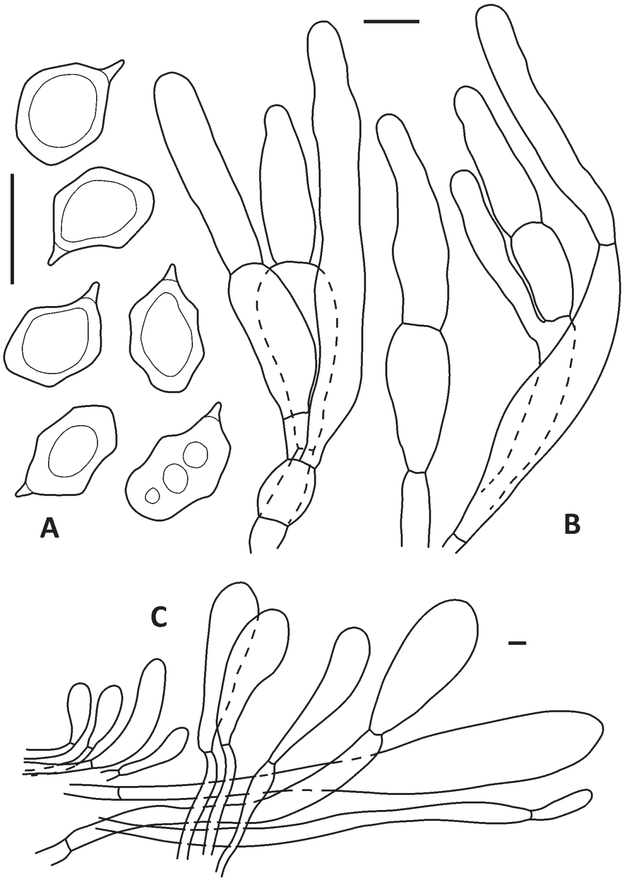

Fig. 13. *Entoloma violaceoserrulatum*, micromorphological features drawn from collection LE312676. **A.** Basidiospores. **B.** Cheilocystidia. **C.** Pileipellis. Scale bars 10 µm, *del.* O.V. Morozova.

5–6-angled in side-view, rather regularly, relatively thin-walled. – Basidia 28–40 × 4.0–10 µm, 4-spored, clampless. – Lamella edge sterile, of serrulatum-type, with dense clusters of cylindrical cheilocystidia (pseudocystidia), 20–50 × 2.5–7.0 µm, thin-walled, filled with brilliant, diffractive-hyaline granules, very rarely with bluish pigment. – Hymenophoral trama regular, made up of cylindrical elements; brilliant granules very abundant in trama and in the lamellar edge. – Pileipellis a trichoderm of very broadly clavate to vesiculose elements, 40–100 × 10–30 µm, with brown, intracellular pigment. – Stipitipellis a cutis of loosely arranged, cylindrical hyphae, 3.0–10 µm wide, without caulocystidia. – Clamp connections not seen with certainty.

Etymology – The name refers to the violaceous, serrulate lamellar edge, seen in the type material. Based on study of more material, this, however, appears to be a rare feature of the species.

Habitat and distribution. – Mainly recorded in calcareous grasslands, both natural and semi-natural (grazed or mown), but sometimes also in rather open, calcareous *Picea–Pinus–Betula* forests. This species seems to be northern, widely distributed in calcareous districts of Norway (north to Troms), and recorded also in Finland and Sweden. One recent record from the Netherlands was from a semi-natural grassland on calcareous, loamy-sandy soil.

Additional material examined. – *Ibid.* (TUR; isotype). Sequences ex-isoype: MF476913 (ITS). – NORWAY, Telemark, Porsgrunn, Åsstranda brygge, 59°05'36.96"N, 9°38'49.56"E, near-shore, open, dry, calcareous grassland, 10 September, *leg.* T.E. Brandrud & B. Dima, TEB 339-15 (O-F-260353); Oppland, Lunner, S. Oppdalen, Amundrud nordre, 60°17'39.84"N, 10°40'48.72"E, calcareous hayfield, 19 August 2014, *leg.* T.E. Brandrud (O-F-75151); *Ibid.*, 9 August 2019, *leg.* T.E. Brandrud & B. Dima, TEB 128-19 (O). – SWEDEN. Jämtland, Östersund, Torvalla, Ängsmoen västra, 63°08'45.24"N, 14°45'19.08"E, calcareous semi-natural formerly grazed/mown grassland, 28 August 2016, *leg.* T.E. Brandrud, LE312676. – THE NETHERLANDS. Gelderland Province, Staverden, Leemputten, 52°02'40.74"N, 6°40'12.70"E, 22 October 2019, *leg.* F. & R. Salzmann (L0607704).

Notes. – Noordeloos (2004) indicated a holotype specimen for this species in both L and TUR. This is against the rules of the International Code of Nomenclature for algae, fungi, and plants (Turland et al. 2018). Therefore this *nomen invalidum* is here corrected, with a holotype specimen in L, an isotype specimen in TUR, and an emended description. *Entoloma violaceoserrulatum* phylogenetically belongs to the /serrulatum clade. Within this group, it has some aberrant characters that make it quite different from related taxa; the very dark violaceous pileus when young, which is entirely tomentose-squamulose, not translucently striate; the initially pure white lamellae; and the stipe with the same shade of color as the pileus but lighter, and distinctly fibrillose striate. Other *E. corvinum* (Kühner) Noordel. lookalikes have a completely different structure of the lamellar edge, without brilliant granules. *Entoloma mougeotii* (Fr.) Hesler has some resemblance, but it differs by the tender, grey-violaceous color, the often brown lamellar edge, without brilliant granules, and slightly larger basidiospores.

Authors: B. Dima, O.V. Morozova, M.E. Noordeloos & T.E. Brandrud

Ascomycota, Laboulbeniomycetes, Laboulbeniales, Laboulbeniaceae

Laboulbenia amblystomi W. Rossi & Santam., **sp. nov.** – Fig. 14

MycoBank no.: MB 839568

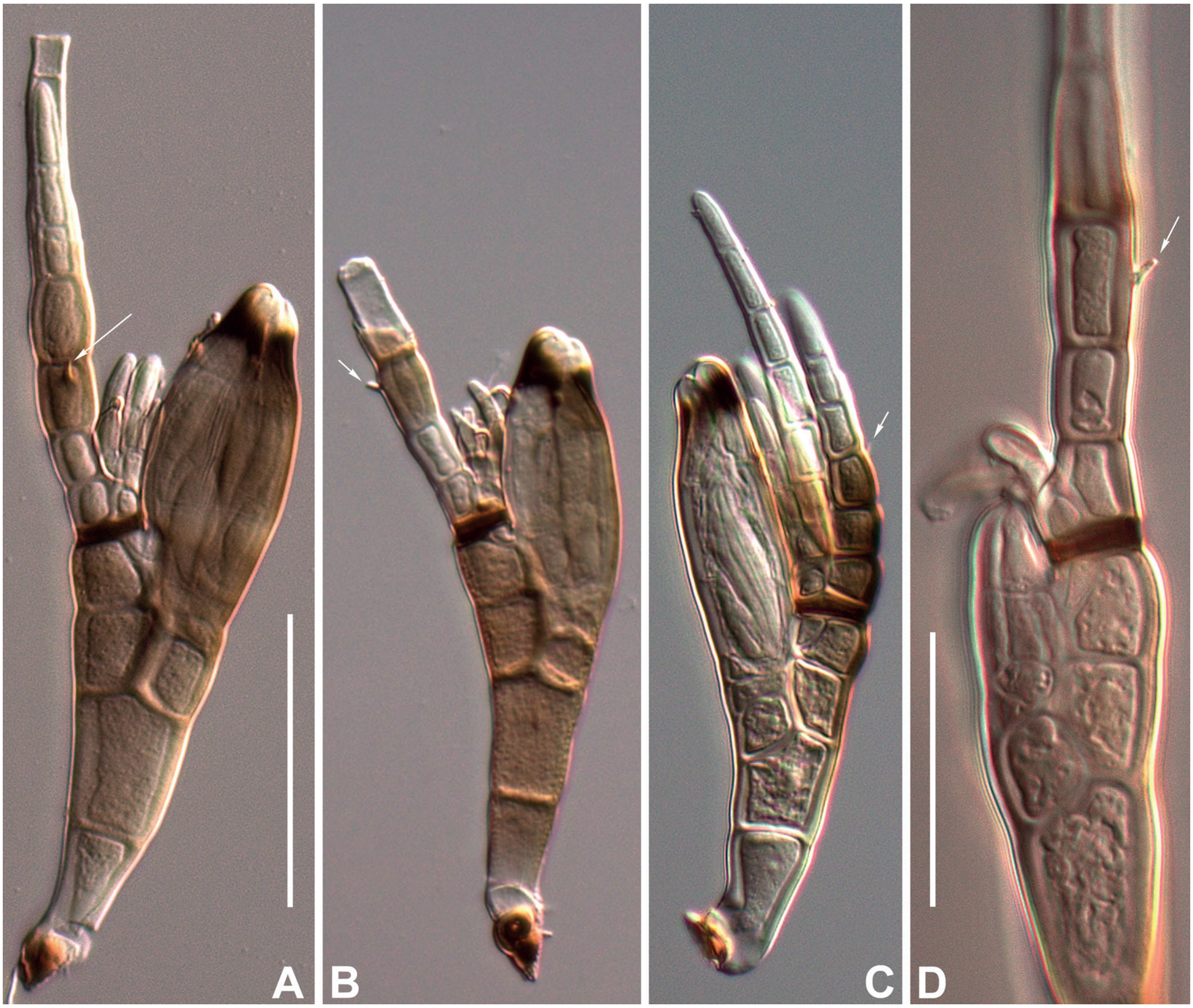

Fig. 14. *Laboulbenia amblystomi*. **A.** Mature thallus from elytra of *Amblystomus notabilis*, slide WR4173. **B.** Mature thallus from elytra of *A. femoralis*, slide WR4185 (holotype). **C**. Thallus from the abdominal tip of *A. similis*, slide WR4229. **D.** Detail of immature thallus, slide WR4229. Arrows in all figures point to the remains of the spore apex. Scale bars A–C 50 µm, D 25 µm.

Holotypus. – THAILAND. Lamphun Province, Ban San Ka Yom, on elytra of *Amblystomus femoralis* (Motschulsky, 1858) (Coleoptera, Carabidae, Harpalinae), light trap, 30 October 2016, *leg.* W. Rossi, slide WR4185 (holotype at FI).

Description. – Thallus brownish gray, with paler cell V and lower portion of cell I, and with the surface of the cells of the receptacle finely dotted. – Cell I about twice longer than broad, gradually enlarging upwards. – Cell II slightly longer and distinctly broader than cell I, divided from cell III and cell VI by oblique septa, the latter of which is usually longer and more concave. – Cell III slightly broader than long. – Cell IV similar to cell III. – Cell V small and wedge-shaped. – Outer appendage simple and very long when unbroken, consisting of a basal cell isodiametric in outline, followed by gradually longer cells that start tapering from the fourth cell, and with the third and fourth cells usually darker; the upper, outer portion of the third cell shows a very small spinous process, the remnant of the ascospore apex; additional branches can be produced if the main branch has been broken (Fig. 14C). – Inner appendage with the basal cell much smaller than the outer one, bearing two short cells, each apically producing a short, simple branch and two grayish antheridia, the latter replaced by short branchlets in older thalli. – Cell VI from isodiametric to distinctly broader than long. – Perithecium oblong, about twice longer than broad, with a broad, blackish tip not well distinguished except by its color, the hyaline apex obliquely directed outwards consisting of rounded, hardly protruding, hyaline lips. – Length from foot to perithecial apex 115–120 µm; length from foot to tip of longest appendage 295 µm; perithecium 49–50 × 22–24 µm.

Etymology. – Referring to the host genus, *Amblystomus*.

Hosts and distribution. – On species of *Amblystomus* (Coleoptera, Carabidae, Harpalinae) in Italy, Spain, and Thailand.

Additional material examined. – THAILAND. Lamphun Province, Ban Lam Chan, Tambon Pratu Pa, on elytra of *Amblystomus notabilis* Landin, 1955 (Coleoptera, Carabidae, Harpalinae), light trap, 23 October 2016, *leg.* W. Rossi, slide WR4173 (paratype at FI); Lamphun Province, Mueang Lamphun District, harvested rice fields near Umong, on various body parts of *A. similis* Landin, 1955, 13 February 2017, *leg.* M. Bernardi & W. Rossi, slide WR4229 (paratype at FI). ITALY, Sassari Province, near Romana, on *A. sardous* Baudi di Selve, 1864, 5 December 1975, *leg.* G. Franzini, slide WR1115 (paratype at FI); *Ibid.*, slides WR1116, WR1117, WR1118 (paratypes at FI); Oristano Province, near Abbasanta, on *A. melonii* Wrase & Magrini, 2012, 6 January 2000, *leg.* P. Magrini, slide WR4274 (paratype at FI); *Ibid.*, slide WR4275 (paratype at FI); Roma Province, near Fiumicino, on *A. algirinus* Reitter, 1887, 22 December 1975, *leg.* G. Franzini, slide WR1119 (paratype at FI). SPAIN, Catalonia, Barcelona, Gualba, Gualba de Baix, riera de Gualba, on *A. metallescens* (Dejean, 1829), 17 April 1992, *leg.* S. Santamaria, slide SS1459 (paratype at BCB).

Notes. – The description is based on the thalli occurring on *A. femoralis* (holotype). The thalli found on the pro- and mesothorax of *A. similis* are larger (up to 250 µm), but this is not unusual when thalli of *Laboulbenia* grow on these parts of the body; the thalli found on the elytra of the same insect are identical with the parasites observed on the elytra of *A. femoralis* and *A. notabilis*. The parasites occurring on European species of *Amblystomus* (*A. algirinus*, *A. melonii*, *A. metallescens*, and *A. sardous*) have more or less the same length of the type series (120–140 µm), but have a stockier habitus. This is caused by the shape of the suprabasal cell, which is broader than long in the European thalli vs. longer than broad in the Asian ones. All other features are practically identical, including obviously the remains of the spore apex. Our caution is also due to the lack of information from the huge geographical gap between Europe and Thailand. Any doubt can be eliminated only by the study of the fungi occurring on the species of *Amblystomus* from this large intermediate area.

At first sight, new species displays no striking feature. However, the remains of the ascospore apex have never been observed before in any of the more than 650 species of *Laboulbenia* described so far. This feature was also not detected in the detailed studies on the development of *Laboulbenia* published by Tavares (1985) and De Kesel (1989).

Laboulbenia amblystomi seems to be related to *L. polyphaga*, but is distinguished from it by several features: in the new species the perithecium is freer from the receptacle, the perithecial tip is broader, the antheridia are darker and fewer in number, the appendage is made of much shorter cells, of which the 3rd and 4th are darker. The fungus reported as *L. polyphaga* Thaxt. on *Amblystomus* sp. from Bali Island (Indonesia) most likely belongs to *L. amblystomi*; the photo accompanying this record (Sugiyama & Majewski 1985: Fig. 5) leave very little doubts.

Authors: S. Santamaria & W. Rossi

Basidiomycota, Agaricomycetes, Boletales, Suillaceae

Suillus quercinus Sarwar, Naseer & Khalid, **sp. nov.** – Figs. 15–17
MycoBank no.: MB 835423

Holotype. – PAKISTAN. Khyber Pakhtunkhwa Province, Swat District, Toa Valley, 2100 m a.s.l., under *Quercus incana* (Fagales, Fagaceae), 1 August 2018, *leg.* A. Naseer & A.N. Khalid, ANK356 (LAH36421; holotype). Sequences ex-holotype: MT361745 (ITS).

Description. – Basidiomata medium-sized, length 5.5–10 cm. – Pileus 4.0–9.5 cm in diam., convex when young, broadly convex or flat with age; margins smooth, acute, entire, regular. – Pileus surface dry, not viscid or slightly viscid only when wet, brownish-yellow to yellow, discoloring to pale yellow with age, brownish-red to reddish-brown appressed fibrillose throughout the pileal surface, which becomes prominent with age. – Pileus context thick in the center and thin towards margins, soft, pale yellow to yellowish in age, unchanging when exposed. – Taste and odor not recorded. – Hymenium tubes up to 10 mm deep, adnate to sub-decurrent, fully peeling, yellow when young, yellowish-brown with age, slowly changing to dark brown when exposed. – Pores irregular, 1–3 mm broad, concolorous with the tubes. – Stipe central, equal, curved, length 5.0–9.5 cm, 1.3–1.5 cm in diam., concolorous with the tubes but white at the base; brown glandular dots all over the surface that are prominent towards the apex, annulus absent, basal mycelia white. –

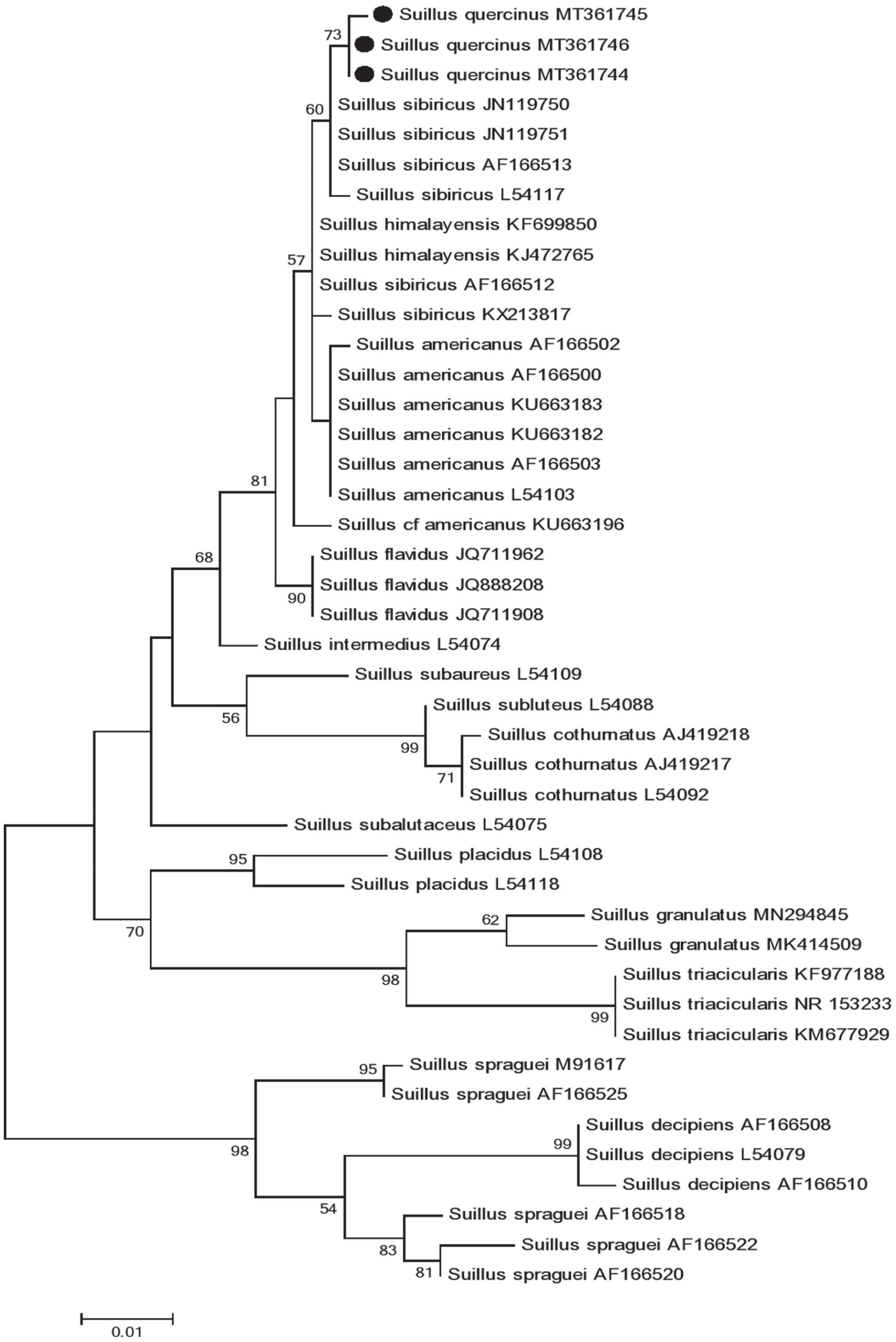

Fig. 15. Phylogeny of *Suillus* reconstructed from an ITS dataset. The topology is the result of ML inference performed with RAxML. For each node, MLBS (if >50) is presented above/below the branch leading to that node. Labels consist of species names followed by GenBank accession numbers. • indicates the new species.

Fig. 16. *Suillus quercinus*. **A, C, D, F.** Fresh basidiomata in the field showing distinct pileal features. **B, E, G.** Hymenium and stipe surface. Scale bars A–C 1.5 cm, D–E 1.2 cm, F–G 1 cm.

Stipe context solid, whitish to slightly pale yellow with no color change when exposed. – Basidiospores (8.2–)8.9–10.9(–11.2) × (3.2–) 3.5–4.1(–4.3) µm, average 9.8 × 3.9 µm, Q=2.2–2.9, Q_{av} = 2.5, ellipsoid or oblong, yellowish brown in 5 % KOH, thick-walled. – Basidia 19.9–39.3 × 6.3–9.9 µm, average 28.4 × 8.0 µm, narrowly utriform to clavate, four-spored, hyaline to brown in 5 % KOH, thin-walled. – Pleurocystidia 47.7–85.5 × 4.9–6.7 µm, average 62.4 × 5.9 µm, cylindrical to sub-clavate, pseudocystidium, hyaline to brown in 5% KOH, thin-walled. – Cheilocystidia 11.9–25.7 × 3.9–9.1 µm, average 16.4 × 6.5 µm, clavate to mucronate, hyaline in 5 % KOH, thin-walled. – Pileipellis 6.1–19.7 µm, average width 11.4 µm, septate, branched, hyaline in 5 % KOH, thin-walled. – Stipitipellis 5.9–17.6 µm, average width 9.9 µm, septate, branched, hyaline in 5 % KOH, clamp connections present, thick-walled.

Etymology. – Referring to the *Quercus* forests in which this species was found, alluding to a strict mycorrhizal association.

Habitat and distribution. – Thus far only reported from Pakistan in temperate moist forests of *Quercus incana*.

Additional material examined. – PAKISTAN. Khyber Pakhtunkhwa Province, Shangla/ Swat boundary, Toa, Solitary, under *Quercus incana* rhizosphere, 1 August 2019, *leg.* M. Usman, A. Naseer & Ab.N. Khalid, ANK328 (LAH36422); Khanspur, Ayubia, in forest of *Q. incana,* 24 July 2011, *leg.* S. Sarwar & A.N. Khalid, B102 (LAH240711).

Notes. – *Suillus* is an ectomycorrhizal genus of currently some 60 described species (Wijayawardene et al. 2020), characterized by fleshy, pored basidiomata, sometimes a ring, wide pore openings, and smooth spores (Bessette et al. 2000, Kuo 2004). Most of the species of this genus are found in association with Pinaceae and they are widely distributed with reports from all continents, including Asia (Kirk et al. 2008, Sarwar et al. 2018). In their preliminary checklist of the Boletales in Pakistan, Sarwar & Khalid (2012) reported 9 species of *Suillus*: *S. bovinus* (L.) Roussel, *S. collinitus* (Fr.) Kuntze, *S. granulatus* (L.) Roussel, *S. grevillei* (Klotzsch) Singer, *S. luteus* (L.) Roussel, *S. placidus* (Bonord.) Singer, *S. sibiricus* (Singer) Singer, *S. tomentosus* Singer, and *S. viscidus* (L.) Roussel. Since then, *S. brevipes* (Peck) Kuntze (Sarwar et al. 2011), *S. flavidus* (Fr.) J. Presl (Sarwar et al. 2012), *S. marginielevatus* S. Sarwar, Khalid & Dentinger (Sarwar et al. 2015), and *S. himalayensis* B. Verma & M.S. Reddy (Sarwar et al. 2018) were added to the funga of Pakistan. With *S. quercinus*, 15 species in the genus are known from the country.

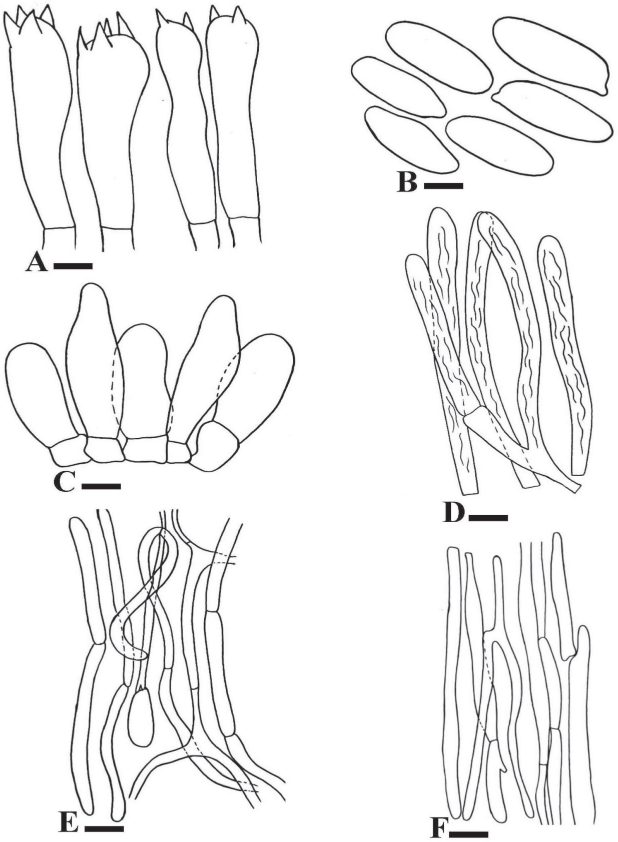

Fig. 17. *Suillus quercinus*, line drawings of micromorphological structures. **A.** Basidia. **B.** Basidipospores. **C.** Cheliocystidia. **D.** Pleurocystidia. **E.** Pileipellis. **F.** Stipitepellis. Scale bars A, C 3 µm; B 4.5 µm; D 4 µm; E–F 9.5 µm, *del.* M. Usman.

Our ITS dataset for the phylogenetic analysis included 43 sequences and 670 characters, of which 487 were constant and 142 were parsimony-informative. The sequences from the Pakistani collections formed a well-supported (MLBS=73) monophyletic clade within the *S. sibiricus* group (Fig. 15). Morphologically, *S. quercinus* is similar to *S. sibiricus* due to its yellowish pileus surface and brownish squamules. However, *S. sibiricus* has a white pileal veil, which is absent in *S. quercinus* (Sarwar et al. 2018). *Suillus himalayensis* is also a phylogenetically closely related species. The new species can be distinguished from *S. himalayensis* due to its thin stipe, and prominent fibrillose pileus surface. In addition, the pileus context of *S. himalayensis* changes color after bruising (Verma & Reddy 2014a); this is not the case for *S. quercinus*. Ecologically, *S. quercinus* is likely associated with *Quercus incana*—as it was only observed in oak forests. Both *S. himalayensis* and *S. sibiricus* are mostly associated with conifers (Sarwar & Kahlid 2014; Sarwar et al.

2015, 2018). Some other *Suillus* species have been found in association with oak trees but these are not phylogenetically closely related with *S. quercinus* and mostly they were reported from mixed forests so their mycorrhizal associations are as yet uncertain (Sarwar et al. 2011, 2018; Sarwar & Khalid 2012).

Authors: A. Naseer, S. Sarwar, M. Usman & A.N. Khalid

Interesting taxonomical notes, new hosts, and geographical records

Basidiomycota, Agaricomycetes, Agaricales, Crepidotaceae

Crepidotus malachioides Consiglio, Prydiuk & Setti, Il genere *Crepidotus* in Europa, p. 303 (2008). – Figs. 18, 19

Material examined. – ITALY. Friuli Venezia Giulia, Farra d'Isonzo, Isonzo (Soca) river, on trunks of broadleaved trees on the ground, 13 June 2019, *leg.* G. Ferisin (GDOR5069).

Description. – Basidiomata gregarious in large groups with reduced, lateral stem. – Pileus 4–15 × 4–14 mm, convex to slightly applanate, spathuliform, reniform, rounded flabelliform to mostly flabelliform, hygrophanous, margin inflexed to straight, surface initially pubescent, later glabrous, generally with dense white villosity near the point of attachment, from whitish to pale orange in early stage, becoming ochraceous to light brown when matured. – Stipe up to 3 mm, only visible in very young stage, whitish, slightly pubescent. – Context up to 1 mm thick, whitish to orange-white, taste not recorded, smell indistinct. – Lamellae L = 5–20, l = 3–5, up to 2 mm wide, ventricose, adnexed, pale cream when young, then ochraceous orange to light brown when matured, edge fimbriate and paler than surface. – Basidiospores (4.7–)4.8–5.5(–5.6) × (4.4–)4.5–5.4(–5.5) µm, Q = (1.00–)1.00–1.11(–1.13), globose to subglobose, yellowish in KOH, generally with one large vacuole, moderately echinulate. – Basidia 19–30 × 6–7 µm, 4-sterigmate, clavate. – Cheilocystidia (20–)25–35(–40) × (6–)8–10(–11) µm, from clavate to cylindrical or flexuose with subcapitate terminal part, hyaline, thin-walled. – Pileipellis a hymeniderm with pileocystidia [(20–)21–30(–44) × (4–)4–7(–9) µm] similar to cheilocystidia, non-gelatinized, hyaline. – Trama composed of parallel hyphae up to 8 µm wide, hyaline to yellowish in KOH, thin-walled. – Clamp connections present in all parts.

Habitat and distribution. – On hardwood and conifer. Described from Ukraine, also reported from some other European countries (Austria, Italy, Slovakia) and in China.

Notes. – *Crepidotus malachioides* Consiglio, Prydiuk & Setti belongs to section *Sphaerula* sensu Hesler & Smith (1965) due to its globose to subglobose basidiospores. This species is mainly characterized by its small-sized basidiomata with whitish to light brown tinge, globose to subglobose basidiospores with "spore wall formed of rod-shaped warts with truncate apex" under SEM (Jančovičová et al. 2014) that appear as being finely echinulate under the light microscope, and a hymenidermic pileipellis with capitate pileocystidia similar to cheilocstidia that are sometimes covered with mucus. Our Italian collection (voucher GDOR5069) has smaller basidiospores compared to the type material [(4.7–)4.8–5.5(–5.6) × (4.4–)4.5–5.4(–5.5) µm vs. 5.2–6.2 × 5.1–5.8 µm] and Austrian and Slovakian collections (5.1–5.9 × 4.7–5.6 µm); and cheilocystia are shorter than those of the type (32.1–43.3 × 8.1–11.1 µm) and Austrian and Slovakian collections (33.9–47.2 × 7.5–10.1 µm) (Jančovičová et al. 2014). In our observations, no mucus was found on cheilocystia or pileocystidia, highlighting that this character is not constant among collections of this species.

The Italian ITS sequence of *C. malachioides* shares 100% (636/636 bp) identity with the ex-epitype sequence of *C. malachioides* (GenBank accession no. NR_132047). In the ML tree (Fig. 18), four sequences of *C. malachioides* from Europe and a sequence named "uncultured soil fungus" from China clustered in a strongly supported clade (MLBS = 87), highlighting the fact that *C. malachioides* has a thus far Eurasian distribution. Eurasian sequences of *C. malachioides* are retrieved as a sister clade (MLBS = 98) of *Crepidotus* cf. *malachioides* from the USA and Argentina. In our ITS analysis, the average distance between the Eurasian and American clades is 3.7 %; and further studies are needed to evaluate whether or not collections from North and South America represent *C. malachioides*.

Authors: F. Dovana & G. Ferisin

Ascomycota, Laboulbeniomycetes, Herpomycetales, Herpomycetaceae

Herpomyces periplanetae Thaxt., Proc. Am. Acad. Arts Sci. 38(2): 13 (1902). – Fig. 20

Material examined. – BÉNIN. Atacora Province, Natitingou, Auberge de la Montagne, bedroom, 10°12'40.80"N, 1°26'16.38"E, on antennae of *Periplaneta americana* Linnaeus, 1758 (Blattodea, Blattidae, Blattinae), ADK2088 [host

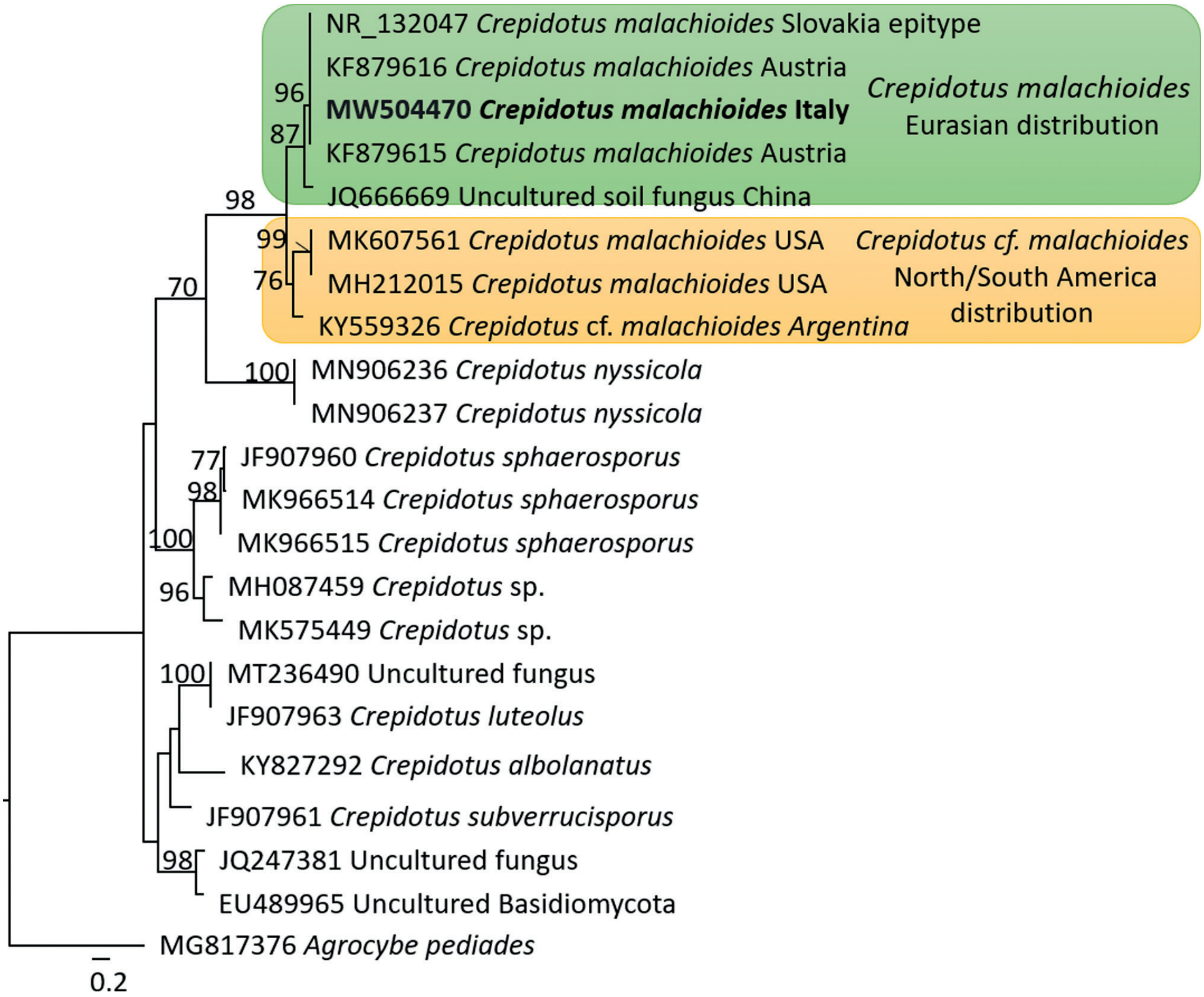

Fig. 18. Phylogeny of *Crepidotus* reconstructed from an ITS dataset. The topology is the result of ML inference performed with RAxML. For each node, MLBS (if ≥70) is presented above the branch leading to that node. Newly generated sequence highlighted in bold.

label], 8 September 1997, *leg.* A. De Kesel, slide BR5020195036610V; Atlantique Province, Calavi, house of N.S. Yorou, near kitchen, on antennae of *P. americana*, ADK6351 [host label], 3 June 2018, *leg.* A. De Kesel, slide BR5020195041478V; Atlantique Province, Cotonou, Cadjehoun, Hotel Chant d'Oiseau, corridor near kitchen, 6°21'25.60"N, 2°24'14.72"E, on antennae of *P. americana*, ADK6485 [host label], 17 September 2019, *leg.* A. De Kesel, slide BR5020195035583V. – DEMOCRATIC REPUBLIC OF THE CONGO. Haut-Katanga Province, Lubumbashi, University guesthouse at Boulevard M'siri, on antennae of a nymph of *P. americana*, ADK6326 [host label], 3 February 2018, *leg.* A. De Kesel, slide BR5020195040440V. – TOGO. Maritime Region, Lomé, Maison Guelly, city garden, on antennae of *P. americana*, ADK4870 [host label], 17 November 2010, *leg.* A. Guelly & A. De Kesel, slide BR5020195039703V; *Ibid.*, ADK4909 [host label], 12 June 2011, *leg.* A. De Kesel, slides BR5020195044561V, BR5020195043533V, BR5020195042505V; Centrale Region, Fazao Malfakassa National Park, kitchen of abandoned Hotel de Fazao, 8°41'41.08"N, 0°46'31.40"E, on antennae of *P. americana*, ADK4943 [host label], 17 June 2011, *leg.* A. De Kesel, slide BR5020195038676V, reported as "*Herpomyces*" in De Kesel et al. (2011).

Hosts and distribution. – Known from *Periplaneta* spp. in North, Central, and South American, Europe, Africa, and Asia (Thaxter 1908, 1931; Wang et al. 2016). On the African continent thus far reported from Algeria (Maire 1916), Morocco (González Fragoso 1916), and Somalia (Spegazzini 1915).

Notes. *Herpomyces* is the only genus in the recently established order Herpomycetales. Both Herpomycetales and Laboulbeniales include the "thal-

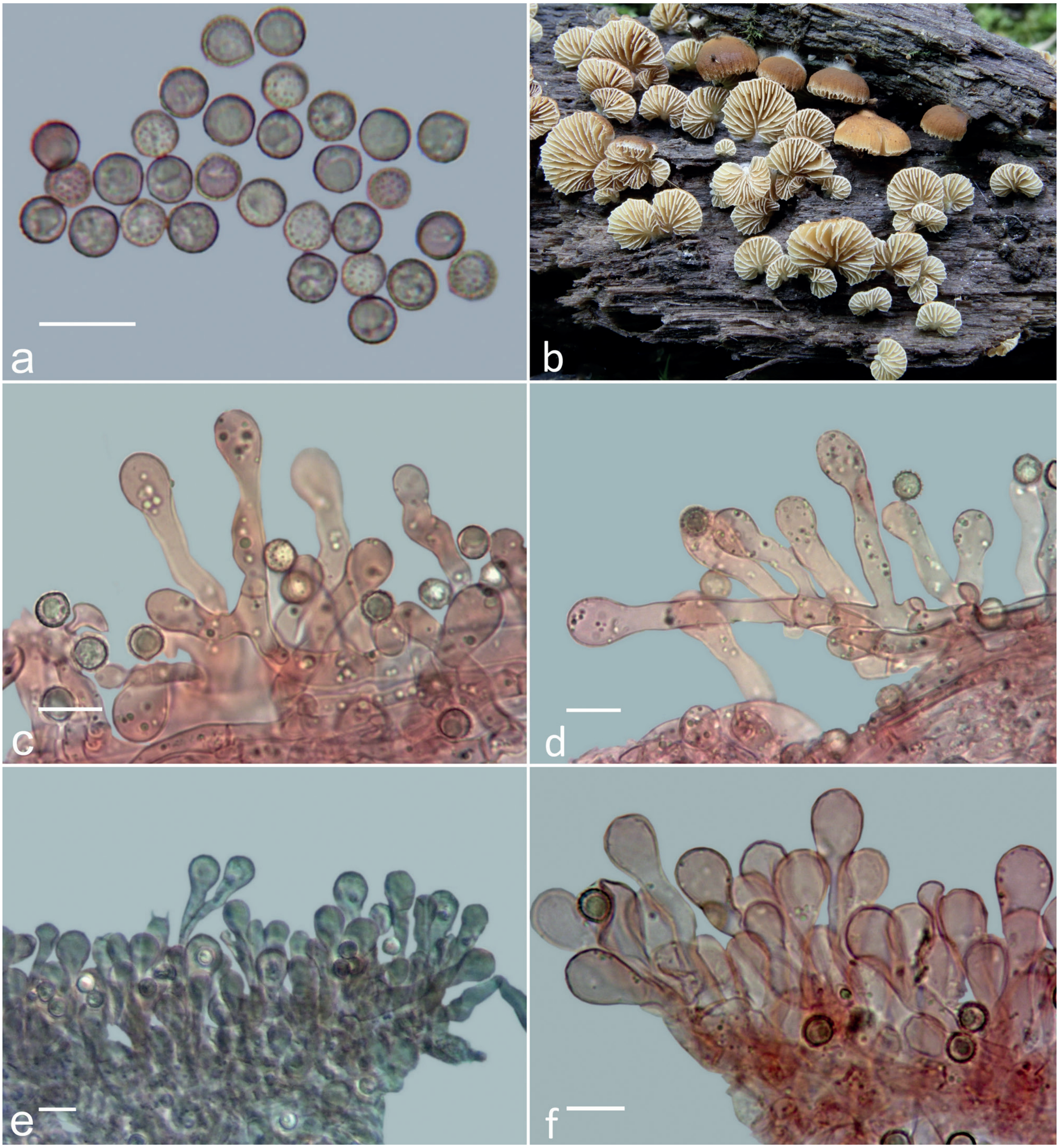

Fig. 19. *Crepidotus malachioides*, collection GDOR5069. **A.** Basidiospores. **B.** Basidiomata. **C–D.** Pileipellis. **E–F.** Cheilocystidia. Photos: G. Ferisin. Scale bars 10 µm.

lus-forming" representatives of class Laboulbeniomycetes (Haelewaters et al. 2019, 2021). Both orders produce 3-dimensional thalli resulting from determinate mitotic divisions from a single, bicellular ascospore (Blackwell et al. 2020). However, compared to Herpomycetales with its single genus and 27 described species (Gutierrez et al. 2020), Laboulbeniales are much more diverse with 2,325 described species in 145 genera (Kirk 2019, Haelewaters et al. 2020). *Herpomyces periplanetae* is a widespread species, with reports in all continents except Oceania. Our records of *H. periplanetae* from Bénin, D.R. Congo, and Togo are the first African ones in over a hundred years. One of us (A. De Kesel) also observed *H. periplanetae* on *P. americana* in a basement at the University of Nairobi, Kenya in August 1998 but we were unable to trace back the slides left at the university. The whole African continent is largely unexplored for both Herpomycetales and Laboulbeniales. Efforts are being undertaken to fill this distributional knowledge gap, with fieldwork planned in Bénin and Mozambique.

Our three-locus dataset consisted of 33 *Herpomyces* isolates, representing 9 species, and 2,251 characters (SSU: 822, ITS: 603, LSU: 826) of which 599 were parsimony-informative (SSU: 67, ITS: 366, LSU: 155). The ML analysis resulted in a *H. periplanetae* clade (MLBS=100) consisting of 10 isolates—all removed from *P. americana* collected in different localities: Massachusetts and New York in the USA, Panama, and Bénin (Fig. 20). It may be that the One Host One Parasite model sensu Haelewaters & De Kesel (2020) is also applicable to species of *Herpomyces*, which all form haustoria. This hypothetical model postulates that the intertwined interactions of Herpomycetales and haustorial Laboulbeniales, such as species of *Hesperomyces* Thaxt., with their hosts lead to an evolutionary arms race, resulting in specialization and ultimately speciation. More data are needed to find support

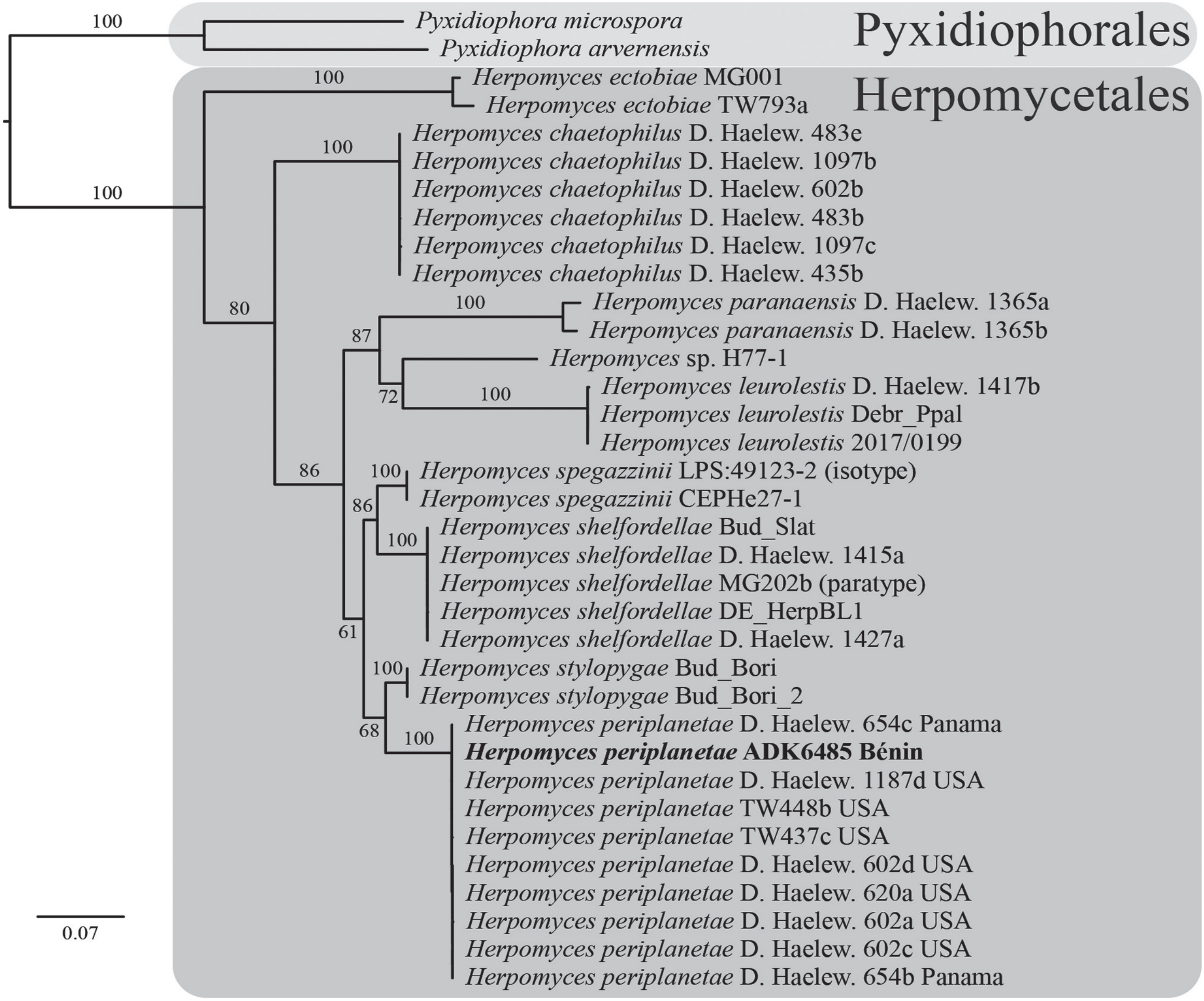

Fig. 20. Phylogeny of *Herpomyces* reconstructed from a three-locus dataset (SSU–ITS–LSU). The topology is the result of ML inference performed with IQ-TREE. *Pyxidiophora arvernensis* and *P. microspora* (Pyxidiophorales) serve as outgroup taxa. For each node, MLBS >60 is presented above or below the branch leading to that node. New isolate highlighted in bold.

for this model. One additional finding from the tree is that *Herpomyces* sp. isolate H77-1 from *Parcoblatta* cf. *lata* (Brunner von Wattenwyl, 1865) (Blattodea, Ectobiidae, Blattellinae) represents an undescribed species.

Authors: A. De Kesel & D. Haelewaters

Basidiomycota, Agaricomycetes, Agaricales, Agaricaceae

Leucoagaricus mucrocystis (Pegler) Justo, Bizzi & Angelini, Mycologia 113(2): 380 (2021) – Figs. 21–23

Basionym. – *Lepiota mucrocystis* Pegler, Kew Bull., Addit. Ser. 9: 387 (1983).

Synonym. – *Lepiota besseyi* H.V. Sm. & N.S. Weber, Contr. Univ. Mich. Herb. 16: 212 (1987).

Material examined. – FRENCH GUIANA. Kaw Mountain, 4°29'58.4"N, 52°02'35.5"W, on decayed dead standing trunk of an unknown angiosperm tree, 26 December 2019, *leg.* B. Dima & V. Papp, agaricoid form (ELTE:DB-FG-167-19) and corticioid form (ELTE:DB-FG-168-19).

Description. – Pileus 25–50 mm in diam., obtusely conical to paraboloid at first, then plano-convex to applanate/umbonate, velvety, brown when young, cracking into small scales towards margin, center remaining brown, whitish towards margin, turning reddish brown when touched; margin not striate. – Lamellae medium spaced, lamellulae present, ventricose, free, whitish then turning orange or reddish brown when touched, becoming dark brown on drying. – Stipe 30–70 mm long, cylindrical, with clavate to bulbous base, lower part covered by brownish granules, whitish at the upper part, rapidly turning orange or reddish brown when touched; membranaceous ring present, white on the upper surface, reddish brown on the lower surface. – Context thin, hollow in the stipe, white, turning reddish brown when cut. – Basidiospores (9.1–)9.2–9.8(–10.2) × (6.2–)6.6–7.0(–7.2) µm, L=9.5 µm, W=6.8 µm, Q=1.43 (n=30), ellipsoid, dextrinoid, metachromatic in chresyl blue. – Basidia clavate, thin-walled, 4-spored, 21–29 × 9–12 µm. – Cheilocystidia up to 70 µm long, clavate, mucronate. – Pleurocystidia similar to cheilocystida. – Pileipellis trichoderm, with lageniform and mucronate terminal elements, hyphae with brownish vacuolar pigmentation. – Hyphae of corticoid mycelia cylindrical, 2.5–3.5 µm in diam. – Clamp connections present.

Habitat and distribution. – Growing both on litter and on decayed angiosperm wood. Reported from the Dominican Republic, Dominica, Hawaii, Nigeria, Trinidad, U.S. Virgin Islands, the USA (Texas and Louisiana), and French Guiana (this study).

Notes. – Our specimen (DB-FG-167-19) collected in French Guiana shows similar macro- and microscopic characteristics as *Leucoagaricus mucrocystis* by Justo et al. (2021). Based on our ITS phylogeny (Fig. 21), the examined samples from French Guiana (DB-FG-167-19, DB-FG-168-19) clustered together with other *La. mucrocystis* (syn. *Lepiota besseyi* H.V. Sm. & N.S. Weber) specimens in a strongly supported clade (MLBS=100). Since only ITS sequence data is available from this species in public databases, the closest species using the LSU sequence were *Lepiota brunneoincarnata* Chodat & C. Martín (GenBank accession no. EU416303, identities 1339/1361, 98 % similarity), *Leucoagaricus barssii* (Zeller) Vellinga (GenBank accession no. DQ911601, identities 1341/1364, 98 % similarity), and *Leucoagaricus nympharum* (Kalchbr.) Bon (GenBank accession no. EU416311, identities 1335/1358, 3 gaps, 98 % similarity).

Leucoagaricus mucrocystis was described by Pegler (1983) from Dominica under the name *Lepiota mucrocystis* Pegler. Based on morphological and molecular examinations of the specimens collected from the Dominican Republic and U.S. Virgin Islands, Justo et al. (2021) transferred *Lepiota mucrocystis* to the genus *Leucoagaricus* and showed that this species is identical with *Lepiota besseyi*, which was reported from Hawai'i, Louisiana, and Texas (Smith & Weber 1987, Stallman 2019). Furthermore, they found that *Lepiota biornata* (Berk. & Broome) Sacc. sensu Dennis (1952) also corresponds to *La. mucrocystis*. The new locality of *La. mucrocystis* was discovered in French Guiana, representing the first record of this species in South America. In the absence of detailed morphological studies and available sequences, confirmation of the occurrence of this species in Africa (see Adedokun et al. 2016) requires further investigation.

The type of *La. mucrocystis* was found on a rotten termite mound (Pegler 1983). Justo et al. (2021) characterized this species as terrestrial, growing both on litter of broadleaf woods and on wood on the ground. In French Guiana, the examined specimens were growing on a dead standing broadleaf tree at a height of several meters (Fig. 22). Close to the basidiomata, we also found a whitish mycelium structure (corticioid form, Figs. 22B, E), which was also produced by *La. mucrocystis*, verified by ITS sequencing (Fig. 21). In the existing body of literature, we were unable to find any reference to this corticioid form.

In the Amazon, and in particular in French Guiana, the distribution of the lepiotoid fungi is not

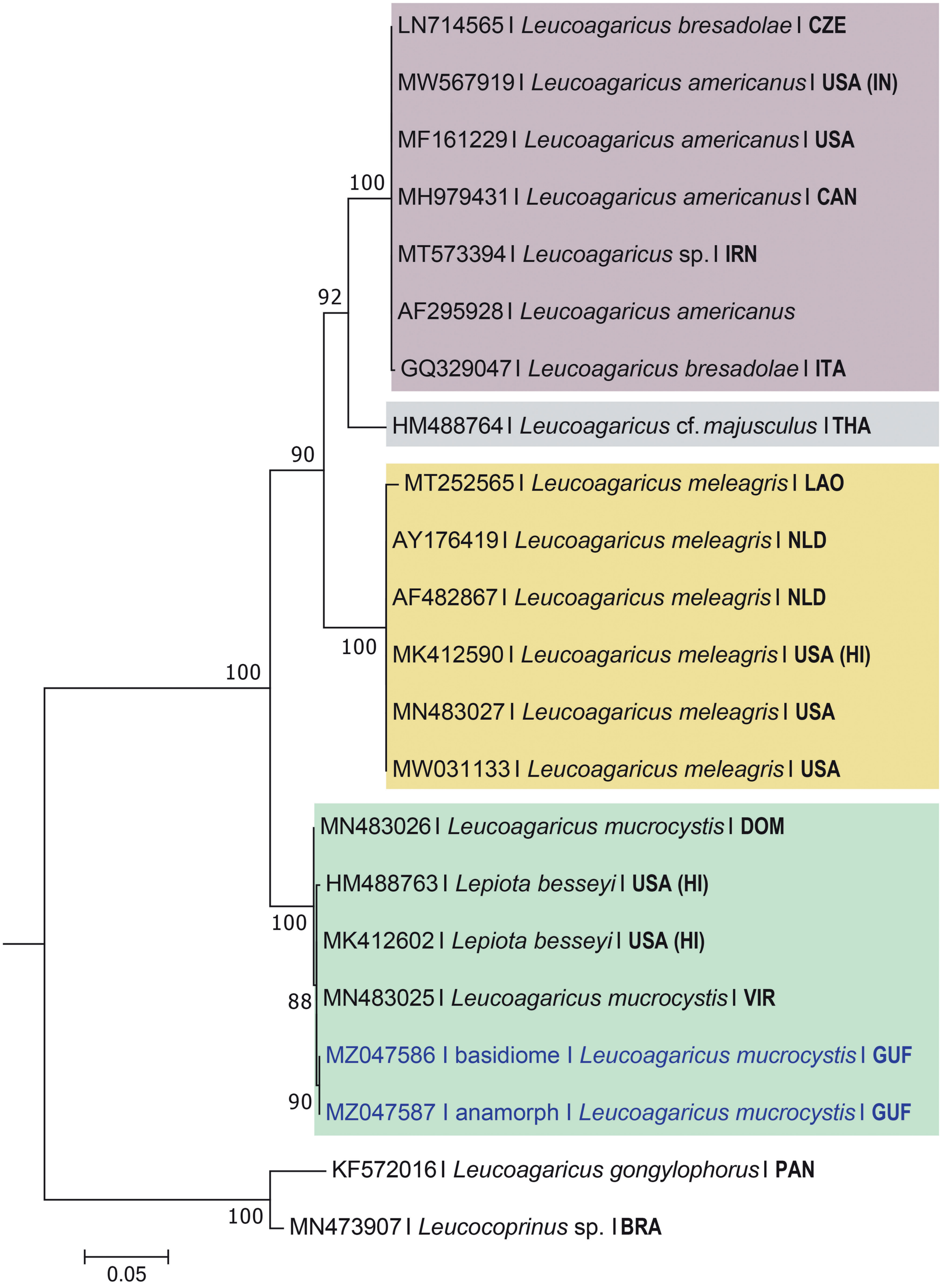

Fig. 21. Phylogeny of *Leucoagaricus* reconstructed from an ITS dataset. The topology is the result of ML inference performed with RAxML. MLBS >70 are shown at the branches. Newly generated sequences highlighted in blue.

Fig. 22. Habitat and in-situ photo documentations of *Leucoagaricus mucrocystis*. **A–C.** Basidiomata on the substratum. **D.** Fresh basidiomata, collection DB-FG-167-19. **E.** Corticioid form, collection DB-FG-168-19. Photos B. Dima (A, C–E), V. Papp (B).

well documented (e.g., Courtecuisse et al. 1996, Jaouen et al. 2019). Jaouen et al. (2019) generated and analyzed sequences of more than 5,000 specimens of fungi in French Guiana, thus establishing a vast amount of new data. Among them, the lepiotoid fungi were represented by only two species of *Lepiota* (*L. roseolamellata* Dennis and *L. atrodisca* Zeller), three *Leucocoprinus* [*Lc. fragilissimus* (Ravenel ex Berk. & M.A. Curtis) Pat., *Lc. birnbaumii* (Corda) Singer, and *Lc. tenellus* (Boud.) Locq.] and two *Leucoagaricus* [*La. sulphurellus* (Pegler) B.P. Akers and *La. subcretaceus* Bon] species, in addition to unidentified species in all three genera as well. Their work and our own experiences and unpublished sequences show that lepiotoid taxa are much more diverse in French Guiana, and further morphological and molecular phylogenetic studies are needed to clarify the many

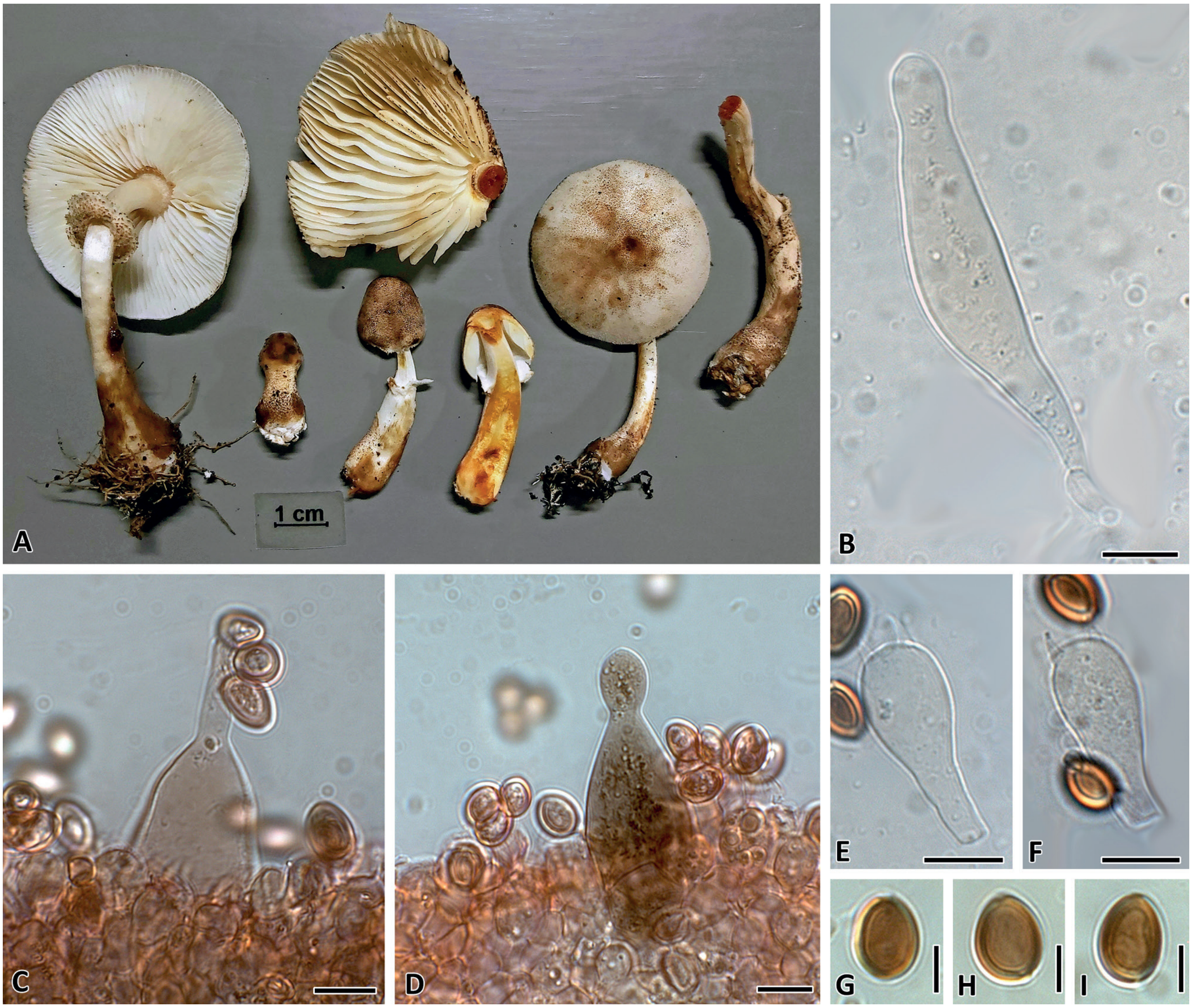

Fig. 23. Macro- and microscopic features of *Leucoagaricus mucrocystis*, collection DB-FG-167-19. **A.** Basidiomata. **B.** Pileocystidium. **C–D.** Cheilocystidia. **E–F.** Basidia. **G–I.** Basidiospores. Photos B. Dima (A), Á. Radnóti (B–I).

unidentified species expected to occur in the Amazonian forests.

Authors: Á. Radnóti, B. Dima & V. Papp

Basidiomycota, Ustilaginomycetes, Urocystidales, Urocystidaceae

Melanustilospora ari (Cooke) Denchev, Mycotaxon 87: 476 (2003). – Figs. 24, 25

Basionym. – *Protomyces ari* Cooke, Grevillea 1(1): 7 (1872).

Synonym. – *Melanotaenium ari* (Cooke) Lagerh., Bull. Soc. Mycol. Fr. 15: 98 (1899).

Material examined. – PAKISTAN. Khyber Pakhtunkhwa Province, Swat District, Kalam valley, Kargilo, 2085 m a.s.l., on leaves, petioles, and sheath of *Arum jacquemontii* (Alismatales, Araceae), 2 May 2015, *leg.* A. Naseer & S. Hussain (LAH SH-S02).

Description. – Sori in leaves, petioles, and sheaths of petioles as irregular, lead-colored pustules, clustered in rows or scattered along midrib covered by epidermis. In abaxial surface, sori looking as aggregation of black dots, aggregations mostly in rows. – Teliospores (11.5–)13.5–17.0(–20.5) × (16.0–)16.5–23.0(–26.0) µm, average 15.3 × 19.1 µm (n = 50); mostly globose to ovoid, sometimes irregular, ellipsoid to angular; yellowish brown to strong brown; wall 2.0–6.8 µm thick, two-layered. – Endospores dark brown, evenly ca. 2 µm thick. – Exospores light olive brown, unevenly 0.9–

Fig. 24. *Arum jacquemontii*, the host plant for *Melanustilospora ari* in Pakistan, with both healthy and diseased leaves (arrowheads). *Inset*, close-up of a *M. ari*-infected leaf (arrows indicate places of sori).

4.8 µm thick, often pierced by one or two protuberances of the endospore.

Hosts and distribution. – Reported from various European countries—Bulgaria, Denmark, Germany, the UK, and Ukraine (Vánky 1994, 2012; Denchev 2003; Bauer et al. 2007; Savchenko et al. 2010). In Asia, only known from Israel (Savchenko et al. 2015) and Pakistan (this study). Thus far found on *Arum* spp. and *Biarum tenuifolium* (Alismatales, Araceae) (Ellis 2019).

Notes. – *Melanustilospora ari* is characterized by dark color, single-celled, non-powdery spores, which are embedded in the host tissue (Denchev 2003). The studied Pakistani collection was found on a new host species, *A. jacquemontii*. The observed symptoms resemble other specimens of *M. ari* on *A. maculatum*; lead-colored pustules on the adaxial side, scattered on both side of the midrib; sori as aggregations of black dots, often in rows covered by host epidermis (Vánky 2012). Spores of the specimens on *A. jacquemontii* were similar to specimens on *A. maculatum* in shape, color, and wall thickness. However, the spores of the Pakistani

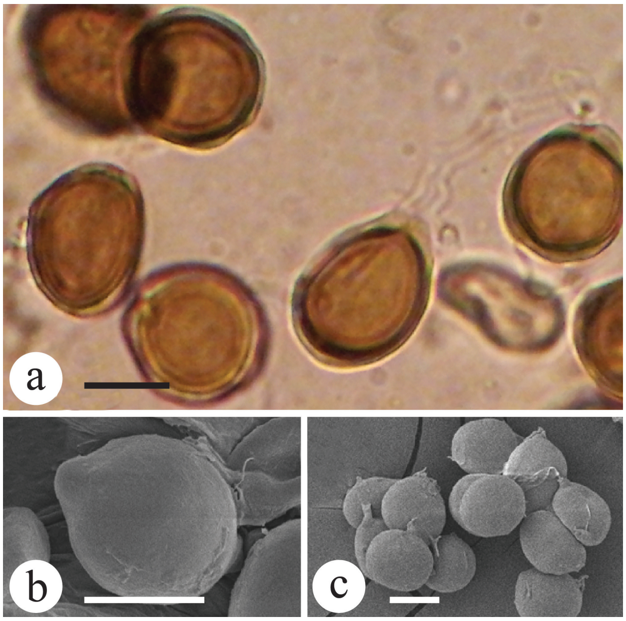

Fig. 25. *Melanustilospora ari*. **a.** Light microscopic image of teliospores. **b–c.** Scanning electron micrographs of teliospores. Scale bars 10 µm.

collection are larger in size [(11.5–)13.5–17.0(–20.5) × (16.0–)16.5–23.0(–26.0) µm] compared to previous records of *M. ari* from Bulgaria (11–14 × 13–17 µm, Denchev 2003), Denmark and the UK (12–15 × 12–20 µm, Vánky 2012), Ukraine (10–15 × 12–20 µm, Savchenko et al. 2020), and Israel (12–16 ×13–21 µm, Savchenko et al. 2015). In Asia, *M. ari* was thus far only reported from Israel infecting *Arum elongatum* (Savchenko et al. 2015). This study resulted in an extension of the geographic distribution of *M. ari* to Pakistan, South Asia, as well as the discovery of a new host species, *A. jacquemontii*.

Authors: S. Hussain, A. Naseer, I. Ahmad, N.S. Afshan, A.N. Khalid & S. Mahammad

Ascomycota, Sordariomycetes, Amphisphaeriales, Pestalotiopsidaceae

Neopestalotiopsis clavispora (G.F. Atk.) Maharachch., K.D. Hyde & Crous, in Maharachchikumbura et al., Studies in Mycology 79: 138 (2014). – Fig. 26

Basionym. – *Pestalotia clavispora* G.F. Atk., Bulletin of Cornell University 3(1): 37 (1897).

Synonym. – *Pestalotiopsis clavispora* (G.F. Atk.) Steyaert, Bulletin du Jardin Botanique de l'État, Bruxelles 19: 335 (1949).

Material examined. – INDIA. West Bengal, Cooch Behar District, 26°20'08.52"N, 89°26'45.24"E, causing fruit rot of *Zizyphus mauritiana* (Rosales, Rhamnaceae), 28 November 2017, *leg.* R. Saha; *Ibid.*, 15 December 2017, *leg.* R. Saha.

Description. – Colonies on PDA wooly-cottony, white. – Acervuli appearing after 12 days throughout entire plate, black, distributed as ink-like masses. – Conidia 11.9–24.5 × 5.2–9.6 µm, average 18.8 × 7.2 µm (n=50), clavate to fusiform, four-septate, straight or slightly curved; basal and apical cells hyaline, median cells (3) dark brown; with a single basal appendage, 3.5–7.4 µm long (n=50), and 2–3 apical appendages, 15.0–27.3 µm long (n=50).

Habitat and distribution. – Known from USA (holotype), China (epitype), Sri Lanka (Maharachchikumbura et al. 2012), Argentina (Obregón et al. 2018), Uruguay (González et al. 2012), Italy (Gilardi et al. 2019), Spain (Borrero et al. 2018), India (Banerjee & Rana 2020), South Korea (Lee et al. 2019), and Australia (Prasannath et al. 2020). Plant pathogenic, also isolated as endophyte.

Notes. – Our ITS sequence shared 99.49% identity with the sequence obtained from the ex-epitype culture of *N clavispora* (MFLUCC 12-0281).

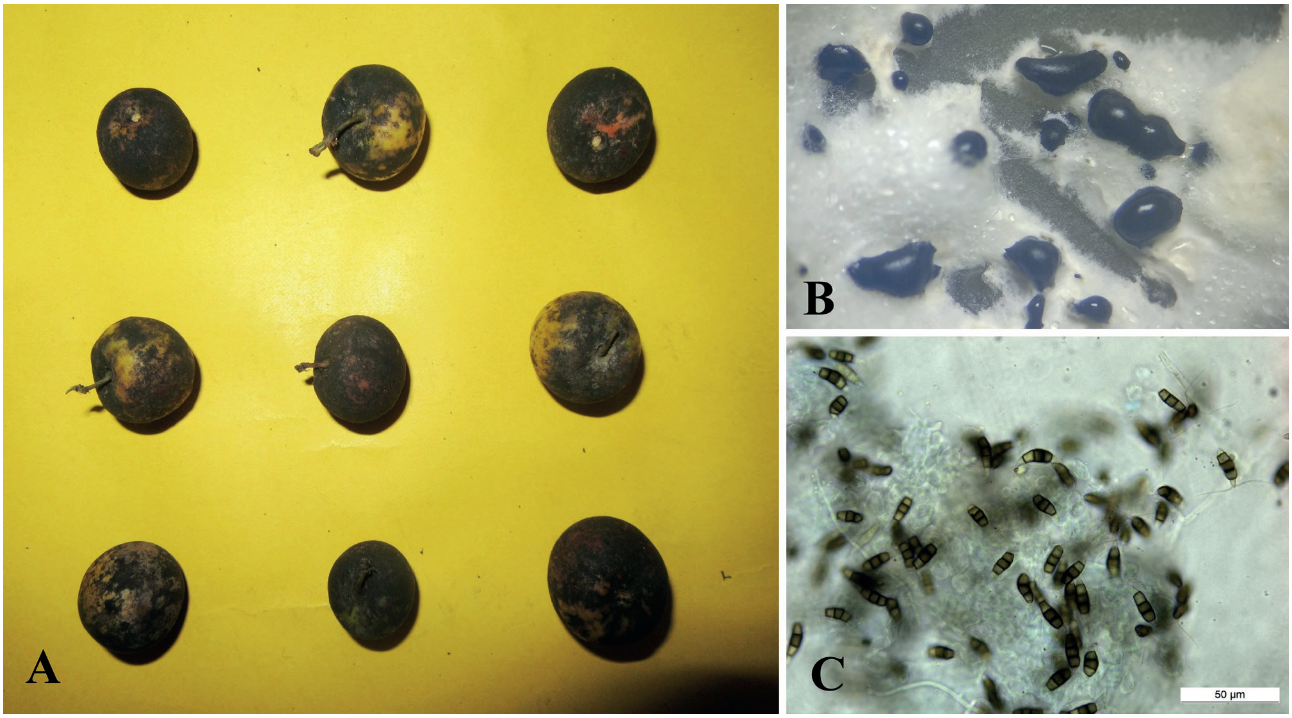

Fig. 26. *Neopestalotiopsis clavispora* on *Zizyphus mauritiana*. **A.** Fruit rot symptoms of *Z. mauritiana*. **B.** Ink-like acervuli of *N. clavispora* formed on PDA, 12 days after inoculation. **C.** Conidia of *N. clavispora*. Scale bar 50 µm.

Also the morphological features are consistent with this species (Maharachchikumbura et al. 2014). The pathogenicity assay resulted in lesions of 1.08 cm length, 1.2 cm width, and 0.4 cm depth on injured Ber fruits inoculated with mycelial plug; and of 1.34 cm length, 1.4 cm width, and 0.4 cm depth on Ber fruits inoculated with *N. clavispora* spore suspension. Control fruits were asymptomatic. *Neopestalotiopsis clavispora* was reisolated from symptomatic tissues, fulfilling Koch's postulates.

Neopestalotiopsis clavispora is here reported for the second time in India; the first report by Banerjee & Rana (2020) was on *Syzygium cumini* (Myrtales, Myrtaceae). Mahapatra et al. (2018) found a species of *Neopestalotiopsis* on strawberry, *Fragaria* × *ananassa* (Rosales, Rosaceae), in India. The authors had reported it as *N. clavispora* but this is incorrect based on BLAST results: 97.05% shared similarity with *N. rosae* Maharachch., K.D. Hyde & Crous CBS:101057 (ex-holotype culture), between 96.23 and 96.85% with 16 species of *Neopestalotiopsis* (ex-type cultures), while only 96.07% with *N. clavispora* MFLUCC12-0281 (ex-epitype culture). More study is needed to identify this material, but it is possible that it is an undescribed species.

On the same host, *Z. mauritiana*, Gupta & Razdan (2010) also reported *Pestalotiopsis funerea* (Desm.) Steyaert. This study represents the first report of *N. clavispora* causing fruit rot on *Z. mauritiana* in India.

Authors: A. Banerjee, K. Banerjee, R, Saha, D. Rana, S. Islam, D.K. Mishra, B.N. Panja & P.S. Nath

Oomycota, Peronosporomycetes, Peronosporales, Peronosporaceae

Phytopythium chamaehyphon (Sideris) Abad, de Cock, Bala, Robideau, A.M. Lodhi & Lévesque, Persoonia 34: 36 (2014). – Figs. 27, 28

Basionym. – *Pythium chamaehyphon* Sideris, Mycologia 24(1): 33 (1932).

Synonym. – *Ovatisporangium chamaehyphon* (Sideris) Uzuhashi, Tojo & Kakish., Mycoscience 51(5): 360 (2010).

Material examined. – BRAZIL. São Paulo, Iguape, nature preserve Mosaico de Unidades de Conservação Juréia-Itatins, isolated from sediment, on *Sorghum* spp. seeds used as bait, 27 June 2017, C.L.A. Pires-Zottarelli & A.L. Jesus, culture CCIBt 4338; *Ibid.*, isolated from sediment, on *Sorghum* spp. seeds used as bait, 13 February 2017, *leg.* C.L.A. Pires-Zottarelli & A.L. Jesus, culture CPZ68; *Ibid.*, isolated from sediment, on *Sorghum* spp. seeds used as bait, 27 June 2017, *leg.* C.L.A. Pires-Zottarelli & A.L. Jesus, culture CCIBt 4407; isolated from water, on corn leaves (1 specimen) and *Sorghum* spp. seeds (1 specimen) used as bait, 13 February 2017, *leg.* C.L.A. Pires-Zottarelli & A.L. Jesus; *Ibid.*, isolated from submerged leaves (1 specimen), 13 February 2017, *leg.* C.L.A. Pires-Zottarelli & A.L. Jesus; *Ibid.*, isolated from sediment, on corn leaves (1 specimen), 27 June 2017, *leg.* C.L.A. Pires-Zottarelli & A.L. Jesus.

Description. – Mycelium well-developed on cornmeal agar with low aerial mycelium. – Appressoria sickle-shaped. – Sporangia globose, 17–36 µm diameter, sometimes subglobose; lateral and intercalary; proliferating internally. – Encysted zoospores spherical, 10 µm diam., discharge tubes differentiated into an evanescent vesicle. – Sexual structures not observed.

Habitat and distribution. – Isolated from water and plants in many countries in North and South America, Europe, Africa, and Asia (Abdelzaher et al. 2020). Recently reported in Italy from roots of *Actinidia chinensis* var. *deliciosa* (Ericales, Actinidiaceae) (Savian et al. 2021), and in South Korea from a decaying leaf in freshwater bodies (Nam & Choi 2019).

Notes. – *Phytopythium* and *Pp. sindhum* A.M. Lodhi, Shahzad & Lévesque were described by Bala et al. (2010) based on an LSU-based phylogenetic analysis. *Phytopythium* species were previously classified within "clade K" of *Pythium* Pringsh. (sensu Lévesque & de Cock 2004) and de Cock et al. (2015) formally transferred these species to *Phytopythium*, based on the phylogenetic analysis of SSU, LSU, and the mitochondrial DNA cytochrome oxidase subunit 1 (COI). The genus comprises 25 species (Wijayawardene et al. 2020) distributed among three clades. Morphological features include ovoid to globose sporangia, papillate or non-papillate, internal zoosporangial proliferation similar to *Phytophthora* de Bary, and a typical *Pythium*-type zoospore discharge. *Phytopythium kandeliae* (H.H. Ho, H.S. Chang & S.Y. Hsieh) Thines is morphologically exceptional; the zoospores develop in both the sporangium and the external vesicle simultaneously and are released after vesicle rupture (Marano et al. 2014, Baten et al. 2015, Jesus et al. 2016, Bennett et al. 2017).

Phytopythium includes saprophytes in various substrates as well as pathogens of plant roots in aquatic and terrestrial ecosystems, some of them being economically important (Baten et al. 2015, Bouket et al. 2016, Jesus et al. 2016, Benfradj et al. 2017, Gonçalves et al. 2017, Tkaczyk 2020). In Brazil, five species of *Phytopythium* have been recorded to date: *Pp. helicoides* (Drechsler) Abad, de Cock, Bala, Robideau, A.M. Lodhi & Lévesque, *Pp. indigoferae* (E.J. Butler) P.M. Kirk, *Pp. kandeliae*, *Pp. palingenes*, and *Pp. vexans* (Milanez et al. 2007, Marano et al. 2014, Jesus et al. 2016, Gonçalves et al. 2017). In this study, 21 *Phytopythium* isolates representing 4 species were isolated from samples of soil, water, surface sediments, and submerged leaves collected in Brazilian Atlantic Rainforest areas.

We retrieved 3 Brazilian isolates CPZ68, CCIBt 4338, CCIBt 4407 in Clade II with other sequences of *Pp. chamaehyphon* (Fig. 27), allowing their identification since no sexual reproduction not observed. This species was described as a pathogen of *Carica papaya* (Brassicales, Caricaceae) (Sideris 1932), and sexual reproduction has only been observed in the original host. Our isolates were found as decomposers on cellulosic substrates. This is the first record of *Pp. chamaehyphon* in Brazil.

Authors: S.C.O. da Paixão, A.L. Jesus, D.R.S. Colombo & C.L.A. Pires-Zottarelli

Oomycota, Peronosporomycetes, Peronosporales, Peronosporaceae

Phytopythium litorale (Nechw.) Abad, de Cock, Bala, Robideau, Lodhi & Lévesque, Persoonia 34: 37 (2014). – Figs. 27, 29

Basionym. – *Pythium litorale* Nechw., in Nechwatal & Mendgen, FEMS Microbiology Letters 255(1): 99 (2006).

Synonym. – *Ovatisporangium litorale* (Nechw.) Uzuhashi, Tojo & Kakish., Mycoscience 51(5): 360 (2010).

Material examined. BRAZIL. São Paulo, Campos do Jordão, trout farm, isolated from freshwater samples collected at the outflow of the tank system, on *Sorghum* spp. seeds used as bait, 29 November 2016, *leg.* S.C.O. da Paixão & C.L.A. Pires-Zottarelli, culture CCIBt 4659; isolated from freshwater samples collected in a tank with juvenile fishes, on *Sorghum* spp. seeds used as bait, 7 March 2017, *leg.* S.C.O. da Paixão & C.L.A. Pires-Zottarelli, culture SCP82.

Description. – Mycelium well-developed on cornmeal agar, delicate hyaline hyphae with septa present in old cultures. – Sporangia terminal, sometimes intercalary, subglobose, and ovoid, 22.0–42.0 × 14.0–28.0 µm, sometimes catenulate up to seven sporangia; proliferating internally. – Encysted zoospores spherical, 7.5–12.5 µm diameter, discharge tubes apical, differentiated into an evanescent vesicle. – Sexual structures not observed.

Habitat and distribution. – Described from rhizosphere soils of *Phragmites australis* (Poales, Poaceae) in Germany (Nechwatal & Mendgen 2006) and since then isolated from water and plants in several countries in North America, Europe, Africa, and Asia (Mcleod et al. 2009, Bouket et al. 2016, Abdelzaher et al. 2020). Recently reported in the USA from recycled irrigation water system at a horticultural nursery (Redekar et al. 2020), in Turkey from roots and stained branch parts and shoots of *Platanus orientalis* (Proteales, Platanaceae) (Derviş et al. 2020) and from roots of *Malus domestica* (Rosales, Rosaceae) (Mert et al. 2020), and in South Korea from a decaying leaf and an alga in freshwater bodies (Nam & Choi 2019).

Notes. – Two isolates of *Pp. litorale* were recorded in this study. Our isolates of *Pp. litorale* are retrieved in a maximum-supported clade with other sequences of this species (Fig. 27). The Brazilian isolates only developed asexual structures. Derviş et al. (2020) observed, for the first time, sexual structures for this species in a pathogenic isolate from *Platanus orientalis* in Turkey. Our isolates represent the first report of *Pp. litorale* in Brazil.

Authors: S.C.O. da Paixão, A.L. Jesus, D.R.S. Colombo & C.L.A. Pires-Zottarelli

Oomycota, Peronosporomycetes, Peronosporales, Peronosporaceae

Phytopythium palingenes (Drechsler) Abad, de Cock, Bala, Robideau, Lohdi & Lévesque, Persoonia 34: 37 (2014). – Figs. 27, 30

Basionym. – *Pythium palingenes* Drechsler, Journal of the Washington Academy of Sciences 20: 416 (1930).

Material examined. BRAZIL. São Paulo, Iguape, nature preserve Mosaico de Unidades de Conservação Juréia-Itatins, isolated from soil samples, on *Sorghum* seed, 31 October 2017, *leg.* C.L.A. Pires-Zottarelli & A.L. Jesus, culture CCIBt 4397; *Ibid.*, isolated from water samples, on *Sorghum* seed, 31 October 2017, *leg.* C.L.A. Pires-Zottarelli & A.L. Jesus, culture CCIBt 4428; *Ibid.*, isolated from water samples, on *Sorghum* seeds (4 specimens), onion skin (1 specimen), and snake skin (1 specimen) used as bait, 31 October 2017, *leg.* C.L.A. Pires-Zottarelli & A.L. Jesus.

Habitat and distribution. – Described from discolored roots of *Ambrosia trifida* (Asterales, Asteraceae) in the USA (Drechsler 1930, 1941) and since then isolated from water and plants in the USA, Brazil, Poland, and Taiwan (Abdelzaher et al. 2020). Recently reported in Brazil from water and soil samples (Machado & Rocha 2019), and Iran from rhizosphere soil and plant debris of ornamented trees (Salmaninezhad & Mostowfizadeh-Ghalamfarsa 2019).

Notes. – The characteristics of our *Pp. palingenes* isolates are in agreement with the original description of Drechsler (1930, 1941). The main features of *Pp. palingenes* include an oogonium with antheridia wrapping around the oogonial stalk, and cylindrical and irregular antheridium cells longitudinally or apically applied to the oogonium (van der Plaats-Niterink 1981). Recently, Jesus et al. (2016) isolated this species from freshwater and soil samples in Parque Estadual da Ilha do

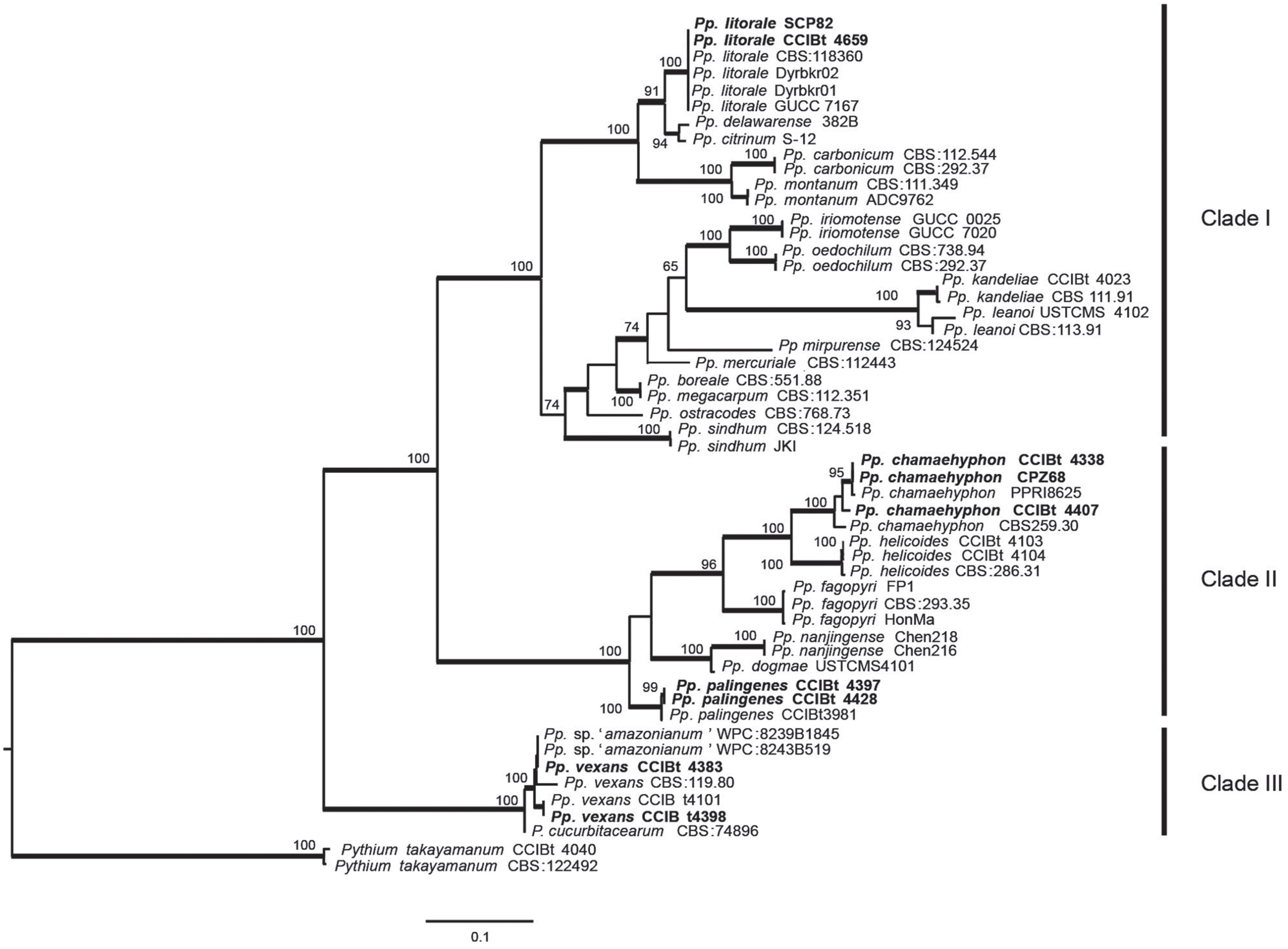

Fig. 27. Phylogeny of *Phytopythium* reconstructed from a concatenated ITS–LSU dataset. The topology is the result of ML inference performed with RAxML. MLBS (if >60) are presented at the nodes. Thick branches indicate nodes with BIPP >0.95. Isolates from this study are highlighted in bold.

Cardoso, situated in the Atlantic Rainforest biome in Brazil.

Authors: S.C.O. da Paixão, A.L. Jesus, D.R.S. Colombo & C.L.A. Pires-Zottarelli

Oomycota, Peronosporomycetes, Peronosporales, Peronosporaceae

Phytopythium vexans (de Bary) Abad, de Cock, Bala, Robideau, A.M. Lodhi & Lévesque, Persoonia 34: 37 (2014). – Figs. 27, 29

Basionym. – *Pythium vexans* de Bary, Journal of the Royal Agricultural Society of England 12: 255 (1876).

Synonyms. – *Ovatisporangium vexans* (de Bary) Uzuhashi, Tojo & Kakish., Mycoscience 51(5): 360 (2010).

Pythium complectens M. Braun, Journal of Agricultural Research 29: 415 (1924).

Pythium allantocladon Sideris, Mycologia 24(1): 27 (1932).

Pythium ascophallon Sideris, Mycologia 24(1): 29 (1932).

Pythium polycladon Sideris, Mycologia 24(1): 32 (1932).

Pythium euthyhyphon Sideris, Mycologia 24(1): 34 (1932).

Pythium piperinum Dastur, Proceedings of the Indian Academy of Sciences B 1(11): 803 (1935).

Material examined. BRAZIL. São Paulo, Iguape, nature preserve Mosaico de Unidades de Conservação Juréia-Itatins, isolated from soil samples, on onion skin used as bait, 31 October 2017, *leg.* C.L.A. Pires-Zottarelli & A.L. Jesus, culture CCIBt 4383; *Ibid.*, isolated from soil samples, on snake skin used as bait, 27 June 2017, C.L.A. Pires-Zottarelli & A.L. Jesus, culture CCIBt 4398; *Ibid.*, isolated from soil samples, on *Sorghum* spp. seeds (1 specimen) used as bait, 27 June 2017, *leg.* C.L.A. Pires-Zottarelli & A.L. Jesus; *Ibid.*, isolated from soil samples, on snake skin (1 specimen) used as bait, 31 October 2017, *leg.* C.L.A. Pires-Zottarelli & A.L. Jesus.

Habitat and distribution. – Isolated from water, soil, and plants in many countries in North and South America, Europe, Africa, Asia (including the Middle East), and Oceania (van der Plaats-Niterink 1981, Abdelzaher et al. 2020, Rezaei et al. 2021).

Notes. – In Brazil, *Pp. vexans* is commonly found both as a saprophyte in aquatic and terres-

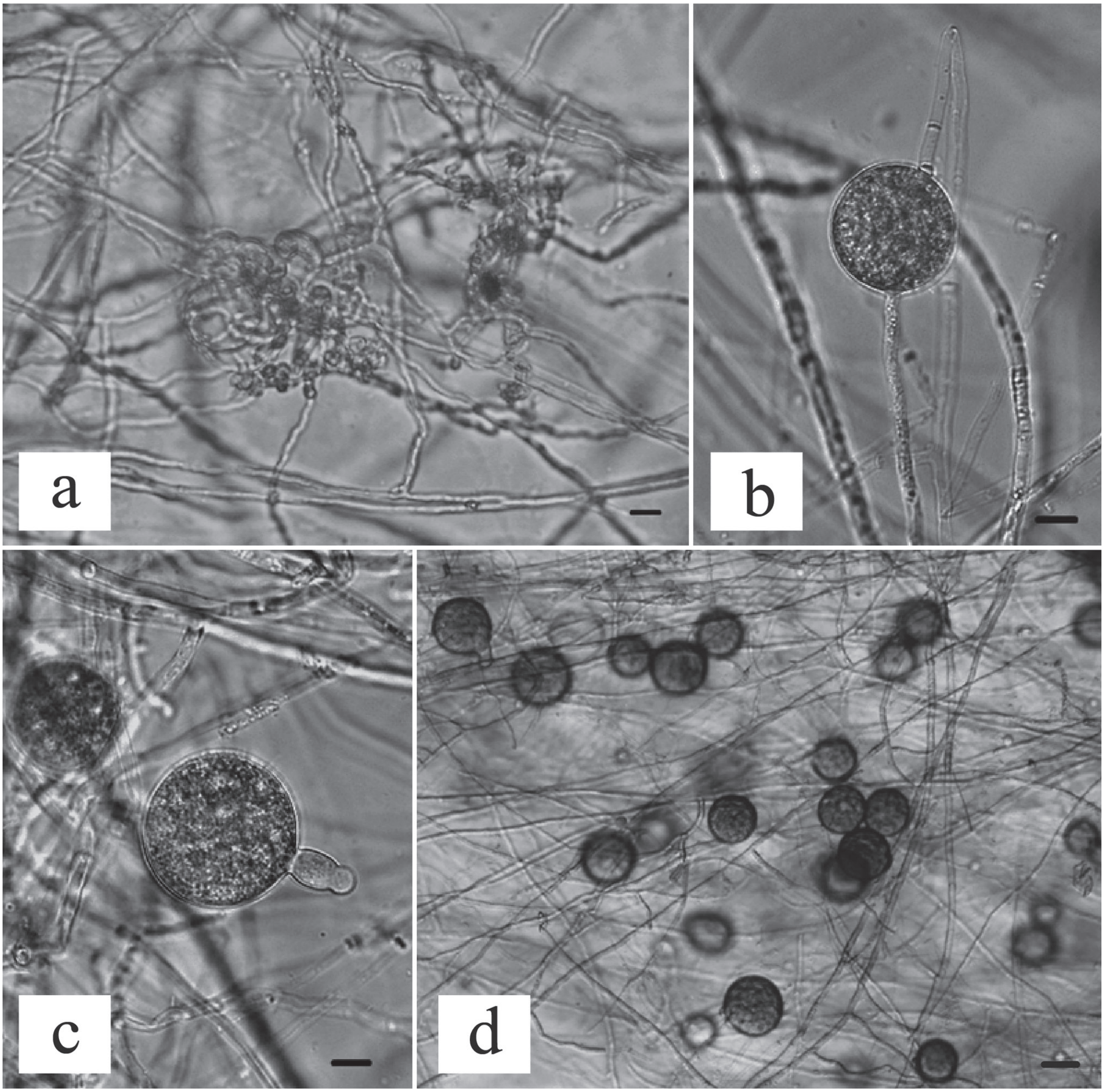

Fig. 28. *Phytopythium chamaehyphon*. **a.** Appressoria. **b.** Intercalary sporangia. **c.** Sporangium with discharge tube. **d.** General aspect of the mycelium and sporangia. Scale bars a–c 10 µm, d 20 µm.

trial environments and as a phytopathogen (Carvalho 1965, Pires-Zottarelli 1999, Baptista et al. 2004, Jesus et al. 2016, Gonçalves et al. 2017). In this study, *Pp. vexans* isolates were recovered from soil samples and showed characteristics that are in agreement with the description by van der Plaats-Niterink (1981), as well as with previously reported material for this species in Brazil (Jesus et al. 2016, Gonçalves et al. 2017).

Phytopythium vexans is commonly isolated around the world as a saprophyte or plant pathogen (e.g., Carvalho 1965, van der Plaats-Niterink 1981, Spies et al. 2011, Gonçalves et al. 2017, Rodriguez-Padrón et al. 2018, Thao et al. 2020). Our isolates (CCIBt 4383 and CCIBt 4398) were grouped with sequences of other isolates of *Pp. vexans* and *Pp.* sp. '*amazonianum*', arranged in two subclades (Fig. 27). Spies et al. (2011) mentioned the complexity of

Clade III, with strains of *Pp. vexans* distributed among several subclades, together with *Pp. cucurbitacearum* P.M. Kirk (invalid taxon), *Pp.* sp. '*amazonianum*', and *Pp. indigoferae*. *Phytopythium* sp. '*amazonianum*' (not formally described) is pathogenic on avocado, *Persea americana* (Laurales, Lauraceae), in Mexico (Robideau et al. 2011, Ochoa et al. 2018) and Ecuador (M.D. Coffey et al. unpublished). The sequences of *Pp. indigoferae*, is a species with filamentous zoosporangia (de Cock et al. 2015), seem to be misidentified and, therefore, were excluded from our analysis.

Authors: S.C.O. da Paixão, A.L. Jesus, D.R.S. Colombo & C.L.A. Pires-Zottarelli

Fig. 29. *Phytopythium litorale* (a–b) and *Pp. vexans* (c–d). **a.** Internal proliferation of the sporangia. **b.** Sporangium with discharged zoospores. **c.** Sporangium with discharged zoospores. **d.** Oogonia and antheridia. Scale bars 10 µm.

Basidiomycota, Agaricomycetes, Agaricales, Pluteaceae

Pluteus multiformis Justo, A. Caball. & G. Muñoz, in Justo et al., Mycologia 103(3): 647 (2011). – Figs. 31–33

Material examined. – TURKEY. Muğla Province, Fethiye district, near Yanıklar town, 15 m a.s.l., forest *of Liquidambar orientalis* (Saxifragales, Altingiaceae), 5 April 2015, *leg.* O. Kaygusuz, OKA-TR1750; Muğla Province, Köyceğiz district, near Dögüşbelen town, 5 m a.s.l., forest of *L. orientalis*, 5 April 2015, *leg.* O. Kaygusuz, OKA-TR1751.

Description. – Pileus 15–20 mm in diam., at first convex to plano-convex, then concave, slightly depressed at center, without umbo, surface smooth or at or around center slightly rugose-venose, with smooth margin, not hygrophanous, dark olive-brown to dark ochraceous brown at center and paler to light olive-green at edge, margin translucently striate up to half of radius, undulate and crenulate with age. – Lamellae moderately crowded, free, ventricose, up to 4 mm broad, thin, whitish when young, later pink to pinkish white, with undulate-crenate, light brown edges. – Stipe 30–35 × 2.0–3.5 mm, cylindrical, slender, narrow at the center, widening towards the apex and base, surface white with light olive-yellow. – Context white to whitish. – Smell and taste not distinctive. – Basidiospores (5.8–) 6.0–7.5(–7.8) × (5.3–)5.5–6.5(–7.0) µm, $L_m \times W_m$=6.5 × 5.8 µm, Q = (1.0–)1.1–1.2, Q_m=1.1, globose or subglobose, rarely broadly ellipsoid, hyaline, smooth, thin-walled, inamyloid. – Basidia 20–32 × 8.0–12 µm, clavate to narrowly utriform, four-spored, hyaline, with granular contents, thin-walled. – Pleurocystidia (39–)46–60(–66) × (11.5–)13–15(–16.5) µm, scattered, scarce to moderately abundant, mostly narrowly lageniform or narrowly utriform with short neck and rounded apex, fusiform to clavate, thin-walled, hyaline in 3 % KOH or sometimes with evenly dissolved brown intracellular pigment. – Lamellar margin sterile. – Cheilocystidia (20–)27–62(–65) × (9–)10–21 (–24) µm, numerous, in clusters, most frequently narrowly to broadly clavate, a few narrowly utriform, thin-walled, mostly with evenly dissolved brown intracellular pigment in 3% KOH or sometimes hyaline in 3% KOH. – Pileipellis a euhymeniderm, composed of clavate, pyriform to spheropedunculate or utriform elements, (17–)26–49(–55) × (8.5–) 10–25 µm, thin-walled, with evenly dissolved brown intracellular pigment in 3% KOH. – Caulocystidia (26–)32–66 × (9.5–)11–19(–21) µm, narrowly clavate to clavate, fusiform or obovoid, in clusters, distinctly more abundant toward the apex, thin-walled, with brown intracellular pigment in 3 % KOH. – Stipitipellis a cutis of hyphae, 5–12 µm wide, cylindrical, thin-walled, hyaline in 3 % KOH. – Clamp connections absent.

Habitat and distribution. – Thus far only known from Spain (Justo et al. 2011a) and Turkey (this study). Collected in forest dominated by *Liquidambar orientalis* (Saxifragales, Altingiaceae), Turkish sweetgum, or *Quercus ilex* (Fagales, Fagaceae) with *Cistus* (Malvales, Cistaceae).

Notes. – Justo et al. (2011a) reported that *P. multiformis* is characterized by scarce pleurocystidia, clavate cheilocystidia and caulocystidia, and highly polymorphic elements of the pileipellis. In our phylogenetic tree, *P. multiformis* is placed within the *cinereofuscus* clade of *Pluteus* sect. *Celluloderma*, together with *P. hubeiensis* Y. Li & F.J. Wang (invalid name), *P. keselakii* Ševčíková, P.-A. Moreau & Borovička, and several unnamed and undescribed taxa (Fig. 31). The closest phylogenetic relative of *P. multiformis* in our reconstruction of an ITS–LSU concatenated dataset is *P. keselakii*, with high support (MLBS=80, BIPP=0.92). However, *P. keselakii*, described from Slovakia, can be morphologically distinguished from *P. multiformis* by the whitish stipe covered entirely by distinct brown floccules, slightly larger basidiospores measuring 5.5–9.0 × 5.0–8.0 µm, mostly narrowly utriform or fusiform pleurocystidia with obtuse apex, and longer caulocystidia up to 110 µm long (Ševčíková et al. 2020). *Pluteus hubeiensis* from China is another close relative although placed on a branch separate from both *P. keselakii* and *P. multiformis* with high support. Its ITS shares 96% identity with *P. multiformis*, but no morphological data of *P. hubeiensis* are available for comparison.

Morphologically, *P. multiformis* is close to *P. eludens* E.F. Malysheva, Minnis & Justo, *P. eugraptus* (Berk. & Broome) Sacc., *P. minutissimus* Maire, *P. phlebophorus* (Ditmar) P. Kumm., and *P. podospileus* Sacc. & Cub. *Pluteus eludens* can be distinguished from *P. multiformis* by having predominantly utriform pleurocystidia, while *P. eugraptus* differs mainly by its narrowly lageniform or fusiform pleurocystidia (Justo et al. 2011a). *Pluteus minutissimus* can be separated from *P. multiformis* by its pilose-tomentose to velvety pileus, snuff-brown scaly stipe, and slightly smaller basidiospores (4.5–7.0 × 4.8–6.0 µm) (Orton 1986, Pradeep & Vrinda 2006). *Pluteus phlebophorus* differs by the more venose and darker brown pileus color, larger basidiospores (5.5–9.5 × 4.5–7.0 µm), and smaller pileipellis elements (25–85 × 18–45 µm) (Vellinga

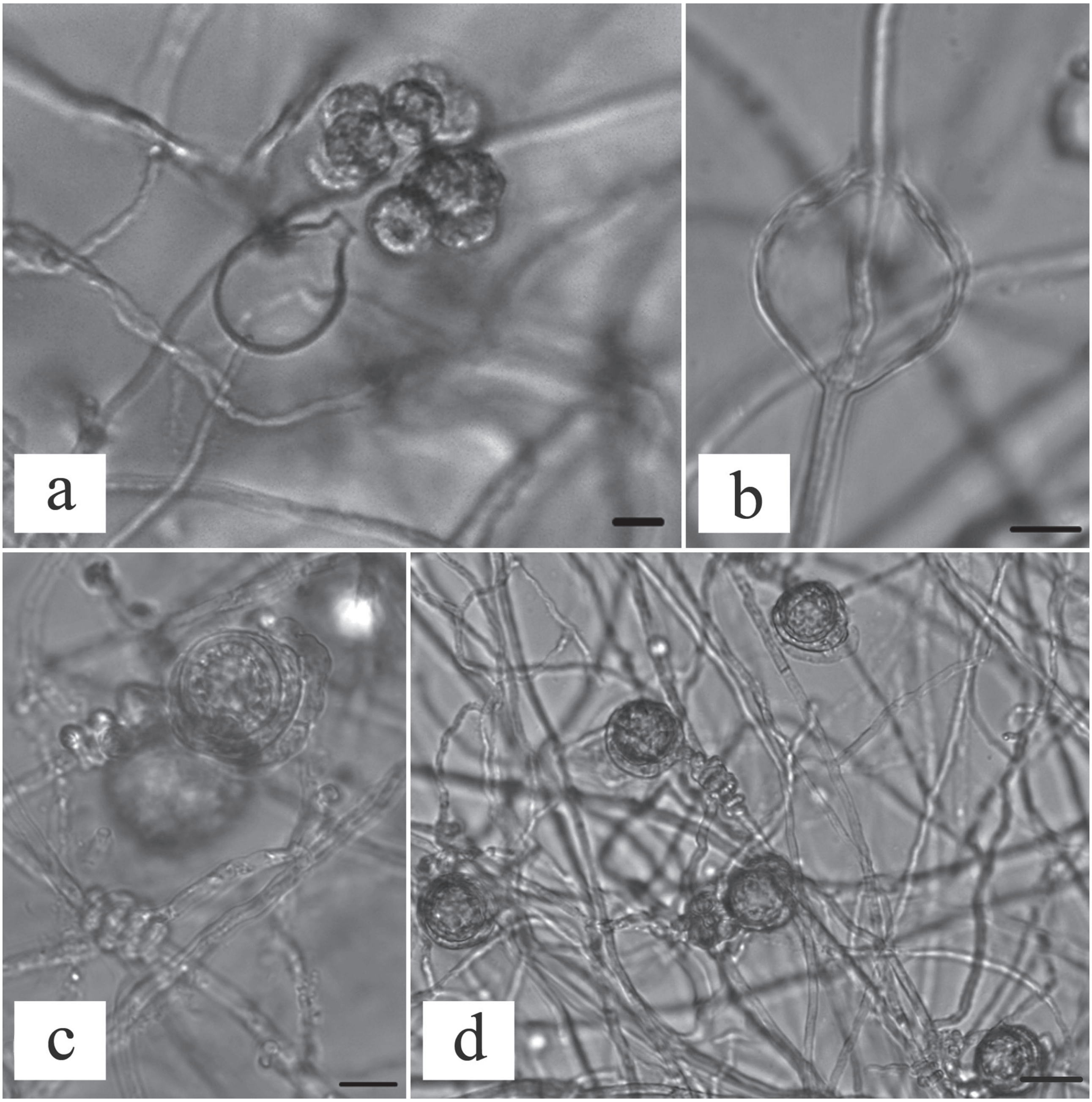

Fig. 30. *Phytopythium palingenes*. **a.** Sporangium with discharged zoospores. **b.** Spherical sporangia with internal proliferation. **c.** Oogonium with antheridium applied lengthwise to the oogonium over its entire length, wrapping around the oogonial stalk and hyphae. **d.** General aspect of the mycelium with oogonia and antheridia. Scale bars a–c 10 µm, d 20 µm.

1990). Finally, *P. podospileus* is different in its subtomentose to squamulose (at the center) pileus and longer pileipellis elements (up to 200 µm) (Vellinga 1990).

Pluteus multiformis was described by Justo et al. (2011a) from Spain. In this study it is reported for the first time from Turkey, which is only the second locality for this species in the world. Justo et al. (2011a) found *P. multiformis* during autumn (November) in a forest of *Quercus ilex* with *Cistus* sp. In our study, it was found in spring (April) in an endemic *Liquidambar orientalis*-dominated forest, representing a new habitat for *P. multiformis*. In Turkey, it grows in a shady microclimate near the

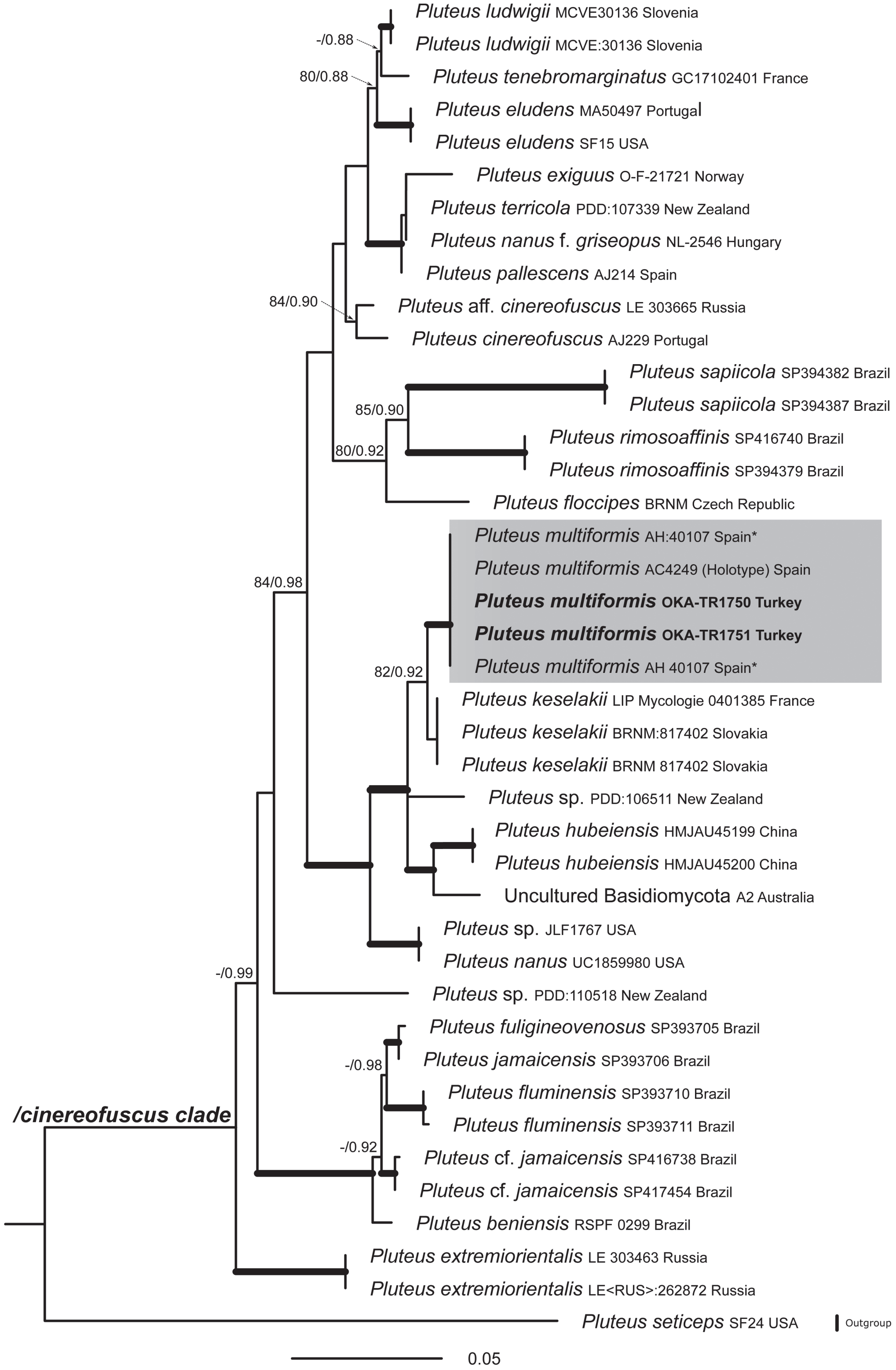

Fig. 31. Phylogeny of *Pluteus* section *Celluloderma* reconstructed from a concatenated ITS–LSU dataset. The topology is the result of ML inference performed with RAxML. For each node, support values (MLBS ≥80/BIPP ≥0.85) are presented above the branch leading to that node. Branches in bold have MLBS ≥90 and BIPP ≥0.95. Newly generated sequences from Turkey are highlighted in bold. Asterisks (*) indicate ex-holotype sequences.

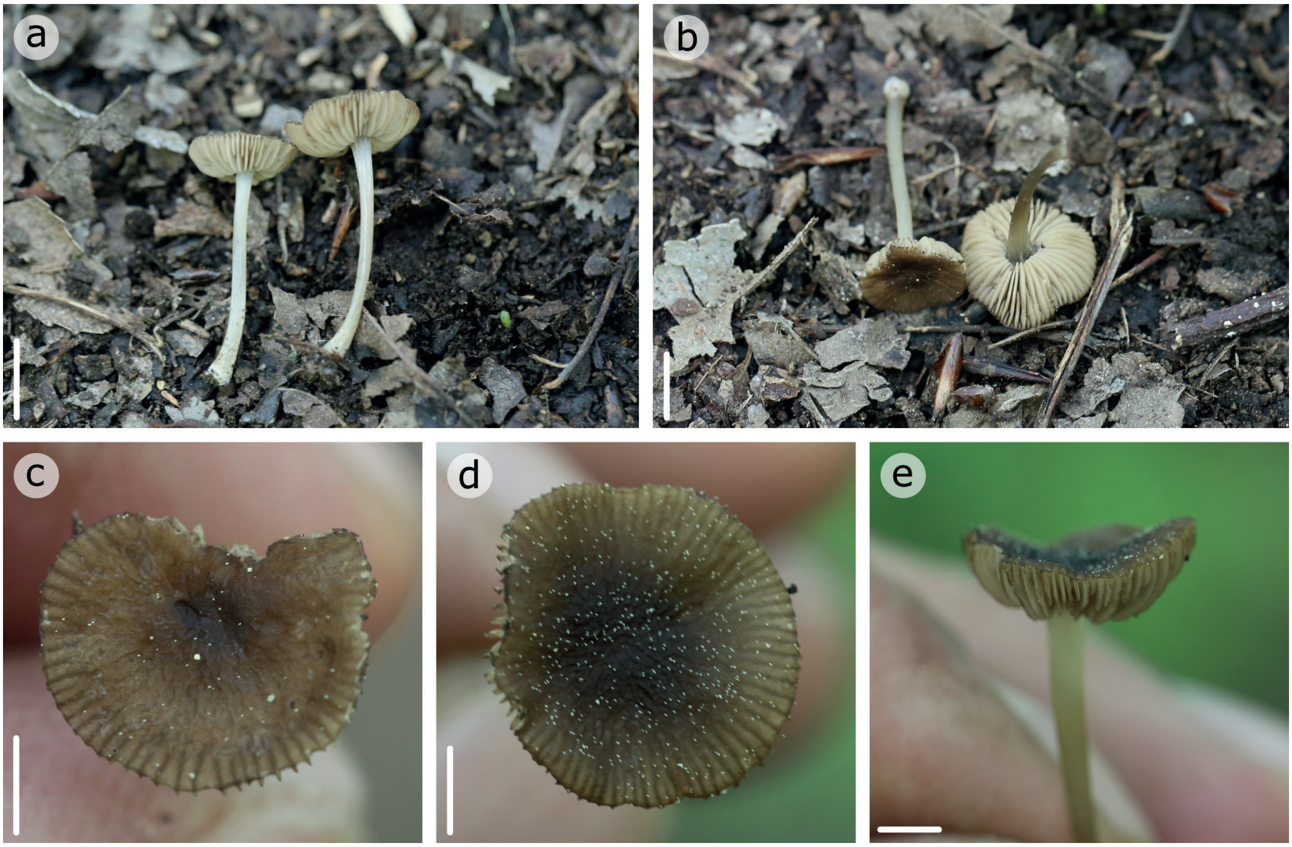

Fig. 32. *Pluteus multiformis*, fresh basidiomata in their natural habitat. **a–b.** Basidiomata in side view. **c–d.** Close-up of the pileus surface. **e.** Lamellae view. Scale bars a–b 10 mm, c–e 5 mm.

coast where the soil is always wet and rich in humus, sandy-loam, with a pH of 7.0–7.5.

As a final note, our observation about the olive color tones in the pileus expands the morphological variability of *P. multiformis*. The holotype from Spain was described as having much darker tones in its pileus.

Authors: O. Kaygusuz & İ. Türkekul

Basidiomycota, Agaricomycetes, Agaricales, Omphalotaceae

Rhodocollybia asema (Fr.) Bendiksen & Dima, comb. & stat. nov. – Figs. 34, 35
MycoBank no.: MB 839703

Basionym. – *Agaricus butyraceus* var. *asemus* Fr., Observ. mycol. (Havniae) 2: 124 (1818).

Material examined. – *Rhodocollybia asema*. – NORWAY. Akershus, Lørenskog, Østmarka, Liseterkollen E, 14 October 2013, *leg.* E. Bendiksen, EB 503/13 (O-F-74975); Akershus, Nesodden, Røerskogen, 18 September 2014, *leg.* K. Bendiksen (O-F248185); Oppland, Lunner, S. Oppdalen, Mørkomdalen, Olstadskogen, 12 October 2014, *leg.* E. Bendiksen & K. Bendiksen (O-F248288); Oslo, Sandbakken, 12 September 2014, *leg.* S. Moen, E. Grytøyr, P. Karlsen & S. Weseth (O-F-75562).

– *Rhodocollybia butyracea*. – NORWAY. ; Buskerud, Sigdal, Hagavollsetra 10 September 2014, *leg.* A. Borge (O-F-75421); Finnmark, Alta, Storelvdalen, Vatnheim E, Nature Type locality BN 00062755, Tvestraumen, 17 August 2013, *leg.* E. Bendiksen (O-F-74979).

Notes. – Two common European taxa are currently normally called *Rhodocollybia butyracea* f. *asema* (Fr.) Antonín, Halling & Noordel. and *R. butyracea* f. *butyracea* (Bull.) Lennox. Throughout mycological history, these two taxa have alternately been separated on the levels of different species, varieties or only forma. Even Fries (1821) operated with the two different species *Agaricus asemus* (Fr.) Fr. and *A. butyraceus* Bull. Later, the first one was for a long period partly called *Collybia asema* (Fr.) Gillet (Gillet 1876) and partly *C. butyracea* f. *asema* (Fr.) Singer (Singer 1951), or *C. butyracea* var. *asema* (Fr.) Quél. (Quélet 1888). After taxonomic revisions and splitting of the old large genus *Collybia* into several smaller genera, the names normally

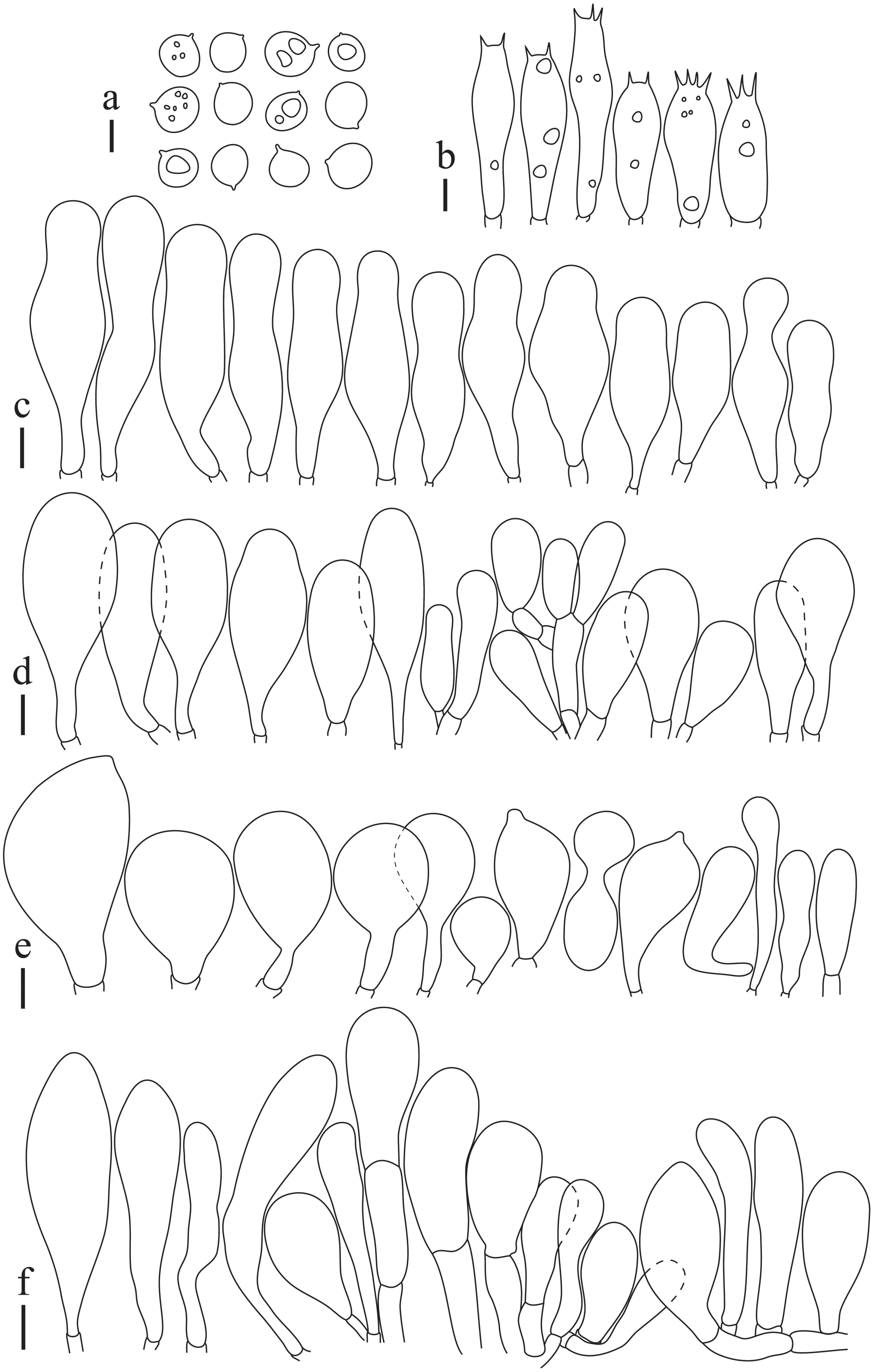

Fig. 33. *Pluteus multiformis*, micromorphological structures drawn from collection OKA-TR1750. **a.** Basidiospores. **b.** Basidia. **c.** Pleurocystidia. **d.** Cheilocystidia. **e.** Pileipellis elements. **f.** Caulocystidia. Scale bars a–b 5 µm, c–f 10 µm, *del.* O. Kaygusuz.

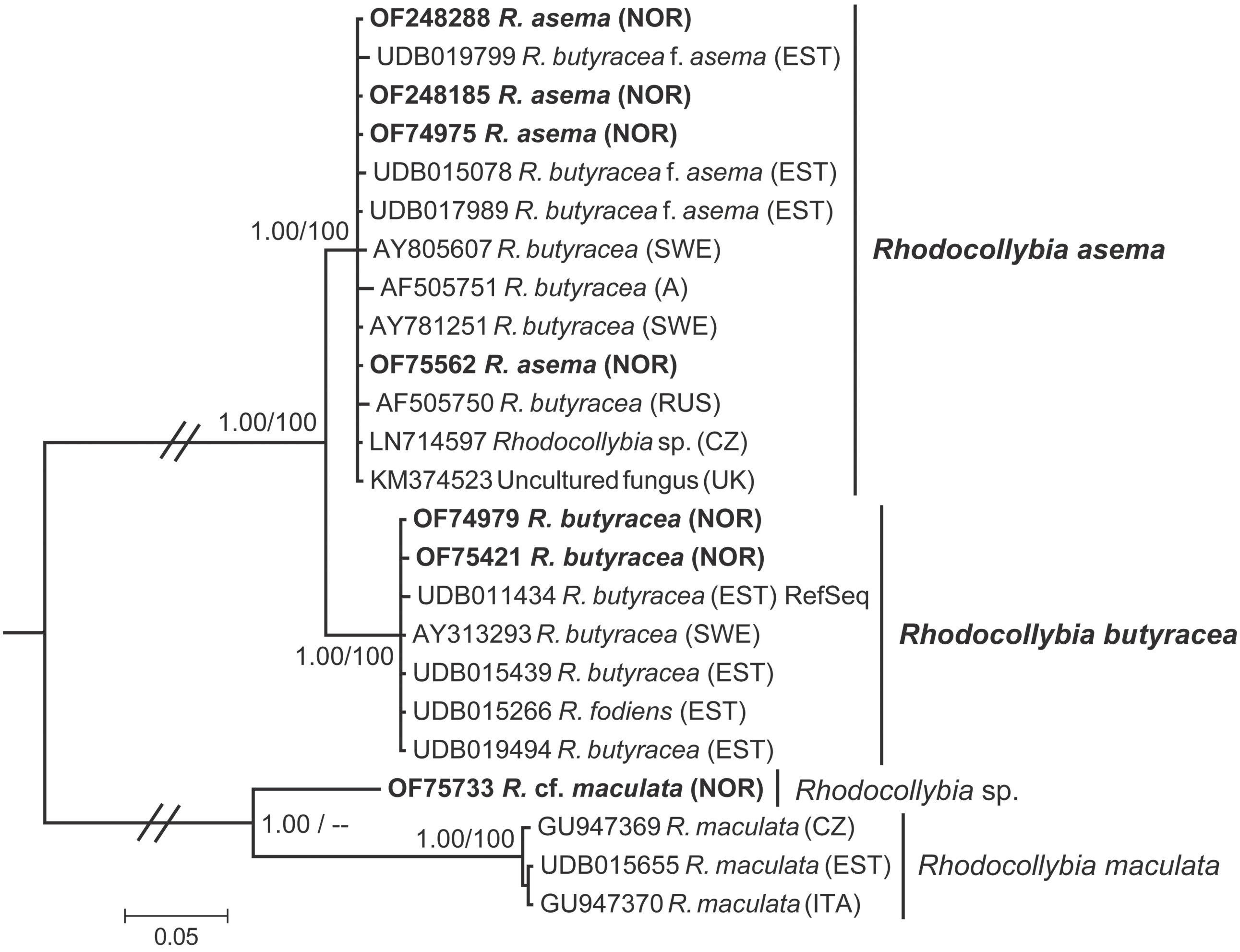

Fig. 34. Phylogeny of *Rhodocollybia* showing the relationship between *R. asema* and *R. butyracea*, reconstructed from an ITS dataset. The topology is the result of Bayesian inference performed with MrBayes. BIPP followed by MLBS values are indicated at the nodes. Newly generated sequences are highlighted in bold. Countries abbreviated as follows: A, Austria; CZ, Czech Republic; EST, Estonia; ITA, Italy; NOR, Norway; RUS, Russia; SWE, Sweden; UK, United Kingdom. Bar indicates 0.05 expected changes per site per branch.

used today for these two taxa are *Rhodocollybia butyracea* and *R. butyracea* f. *asema* (e.g., Antonín & Noordeloos 1997, 2010; Knudsen & Vesterholt 2012). Recently, Günther et al. (2019) elevated f. *asema* to variety level (*R. butyracea* var. *asema* Gminder).

According to Antonín & Noordeloos (2010), f. *asema* differs from f. *butyracea* especially by having a (pale) grey, yellow-brown or grey-brown pileus with darker center, and the basidiomata are somewhat more thin-fleshed and slender than the typical variety. However, the authors did not find microscopical differences between the two taxa. The separating macrocharacters mentioned by Antonín & Noordeloos (2010) fit very well with our observations (Fig. 35). The "main" form, *R. butyracea* f. *butyracea*, is a dark red brown or sometimes dark yellow brown species with a more convex pileus. In contrast to the very distinctly hygrophanous *R. butyracea* f. *asema*, its pileus is not or indistinctly hygrophanous.

These two common taxa are very rarely confused in the field when in good condition. Even if the two taxa may sometimes grow together, they have also distinct differences in their ecology and partly in their distribution. *Rhodocollybia butyracea* is common and widely distributed, but most often locally rather scattered and with rather few basidiomata in each locality. It has a wide ecological amplitude, from coniferous to deciduous forests and from nutrient-rich to poor soils. In Baltoscandian coniferous forests, it may grow in the most acid *Picea* for-

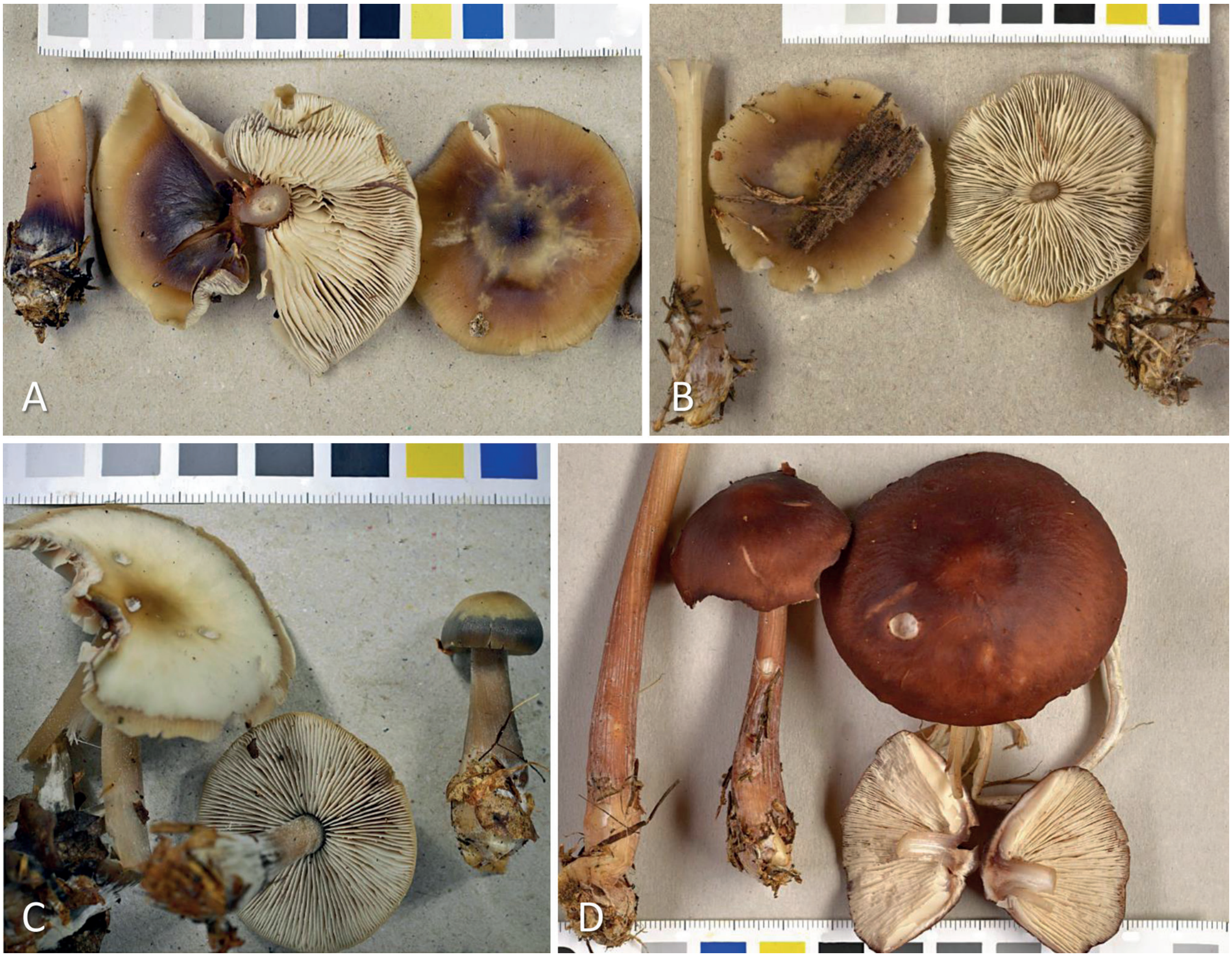

Fig. 35. Basidiomata of *Rhodocollybia* spp. **A–C.** *Rhodocollybia asema* (A, O-F-248288; B, O-F-75562; C, O-F-248185). **D.** *Rhodocollybia butyracea* (O-F-75421).

ests with pH below 4.0 and in companion with *Vaccinium* species, *Avenella flexuosa*, and mosses on a deep raw humus soil. It has also been found in the dense *Cladonia*-carpet in dry lichen pine forest. *Rhodocollybia asema* never occurs in these habitats. This species is more common in the South; it demands more nutrients and is typical in, e.g., low herb and calcareous forests. It is far more common in Central Europe and The Netherlands compared to *R. butyracea* (Antonín & Noordeloos 2010). The results of our molecular analysis also showed a distinct difference between the two taxa (Fig. 34). According to pairwise comparison of the ITS region of *R. asema* and *R. butyracea* sequences, they differ from each other by 12 nucleotide positions. Furthermore, there are two remarkable gap regions (deletions of 14 and 11 positions) observed in the ITS1 of *R. asema* where *R. butyracea* has an insertion in these parts. Thus, the difference between the two species in terms of nucleotide and indel positions is 5.5 %. Both our BI and ML analyses indicate that the sequences of *R. butyracea* and *R. asema* form two distinct and phylogenetically strongly supported clades (BIPP=1.00, MLBS=100). Based on these morphological, ecological, and molecular phylogenetic data, we propose to elevate the variety "*asema*" to species level in the genus *Rhodocollybia*.

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