



The detection of major clades and new species of *Mallocybe* (*Inocybaceae*, *Agaricales*) from China with elongate cheilocystidia

Jian-Hua Hu¹ · Wen-Jie Yu¹ · Lun-Sha Deng¹ · Yu-Guang Fan¹ · Tolgor Bau² · Li-Ping Tang³ · Wen-Fei Lin⁴ · Chun-Ying Deng⁵

Received: 30 May 2022 / Revised: 22 November 2022 / Accepted: 24 November 2022 / Published online: 27 January 2023
© German Mycological Society and Springer-Verlag GmbH Germany, part of Springer Nature 2023

Abstract

Mallocybe, a member of the ectomycorrhizal mushroom family *Inocybaceae*, is a newly elevated genus based on *Inocybe* subg. *Mallocybe*. Although new species of *Mallocybe* have continuously been discovered worldwide during recent decades, species native to China are poorly documented. Members of the genus are frequently characterized by the presence of phaseoliform basidiospores and short, catenate cheilocystidia. Here, we describe three new *Mallocybe* species from China featuring elongate cheilocystidia that were revealed through morphological and molecular analyses: *M. pallidipes* collected from *Populus* in northeastern China, *M. aurantiodisca* discovered in subtropical evergreen broad-leaved forests dominated by *Castanopsis* in Zhejiang and Guizhou provinces, and *M. longicystis* found in fagaceous forests in tropical and subtropical China. According to a multi-gene phylogenetic analysis, which resolved the genus into three major clades, the three new species group with three North American species in a fully supported clade. Finally, we discuss the systematic position of the new species and infrageneric phylogeny of the genus.

Keywords *Inocybaceae* · Molecular phylogeny · New taxa · taxonomy · China

Introduction

Kuyper (1986) first carried out a morphological cladistic analysis to classify members of the genus *Inocybe* (Fr.) Fr. on the basis of three characters: presence or absence of pleurocystidia, the developmental source of cheilocystidia, and the presence or absence of yellow pigmentation in basidia. *Inocybe* has accordingly been divided into subg. *Mallocybe* Kuyper, subg. *Inosperma* Kühner, and subg. *Inocybe* (Fr.) Fr. (Kuyper 1986; Stangl 1989). With the discovery of diverse

new species, the genus has been continuously expanded. As a consequence, Matheny et al. (2020) recently reassigned subg. *Mallocybe* as one of seven genera under *Inocybaceae* Jülich based on a six-gene phylogeny.

Members of *Mallocybe* (Kuyper) Matheny, Vizzini & Esteve-Rav. are characterized by the presence of generally small basidiomata and an often woolly, squamulose pileus that has a noticeably dark appearance upon application of ammonium hydroxide. Other important characteristics are adnate to subdecurrent lamellae with non-reddening

Jian-Hua Hu and Wen-Jie Yu contributed equally to this work.

Section Editor: Zhu-Liang Yang

✉ Yu-Guang Fan
mycena@qq.com

✉ Tolgor Bau
junwusuo@126.com

¹ Key Laboratory of Tropical Translational Medicine of Ministry of Education, Hainan Key Laboratory for R & D of Tropical Herbs, Tropical Environment and Health Laboratory, School of Pharmacy & International School of Public Health and One Health, Hainan Medical University, Haikou 571199, China

² Engineering Research Centre of Chinese Ministry of Education for Edible and Medicinal Fungi, Jilin Agricultural University, Changchun 130118, China

³ School of Pharmaceutical Sciences and Yunnan Key Laboratory of Pharmacology for Natural Products, Kunming Medical University, Kunming 650500, China

⁴ Institute of Edible and Medicinal Fungi, Zhejiang University, Hangzhou 310030, China

⁵ Guizhou Institute of Biology, Guizhou Academy of Science, Guiyang 550009, Guizhou, China

features; phaseoliform, amygdaliform, cylindrical to elliptic spores; a small, non-distinctive apiculus; short, thin-walled cheilocystidia originating from hymenophoral trama; and necropigmented basidia (Kuyper 1986; Matheny et al. 2020). Ecologically, species of *Mallocybe* can associate with many symbiotic plants, including gymnosperms and angiosperms, and play an important role in forest ecosystems. In addition, certain species are associated with the mycoheterotrophic orchid *Epipogium aphyllum* (F. W. Schmidt) Sw. (Roy et al. 2009).

Mallocybe as currently recognized includes nearly all species previously assigned to subg. *Mallocybe*, with 64 entries present in the Index Fungorum database (www.indexfungorum.org, retrieved May 15, 2022). The elevation of *Mallocybe* to the genus rank has been followed by the discovery of new species, five of which were published in the past 2 years (Aïgnon et al. 2021; Bandini et al. 2022; Mao et al. 2022). In East Asia, species in *Mallocybe* have been poorly documented. Four species have been reported in Japan, namely, *M. gymnocarpa* (Kühner) Matheny & Esteve-Rav., *M. malenconii* (R. Heim) Matheny & Esteve-Rav., *M. leucoblema* (Kühner) Matheny & Esteve-Rav., and *M. terrigena* (Fr.) Matheny, Vizzini & Esteve-Rav. (Kobayashi 2002, 2005). One of these species, *M. malenconii*, has also been recently documented in South Korea (Cho et al. 2021). Only five species have been verified in China: *M. depressa* L. Fan, H. Zhou & N. Mao, *M. leucoblema*, *M. leucoloma* (Kühner) Matheny & Esteve-Rav., *M. piceae* L. Fan & N. Mao, and *M. terrigena* (Fan and Bau 2016; Mao et al. 2022). In addition to the scarcity of species described from Asia, relatively little attention has been paid to infrageneric relationships in *Mallocybe* (Matheny et al. 2020).

Species of *Mallocybe* usually have short cheilocystidia which appear in short, catenate, *Opuntia*-like chains. During a study of *Mallocybe* in China, however, collections with elongate-ellipsoid basidiospores and cheilocystidia attracted our attention. According to our phylogenetic and morphological analyses, these species are new to science. In this paper, we therefore describe three new species inferred from morphological studies and a multi-gene molecular analysis of combined nuclear ribosomal internal transcribed spacer region (ITS), the nuclear ribosomal large subunit (nrLSU), and the nuclear second-largest subunit of RNA polymerase II (*RPB2*) sequence data. Finally, we discuss the systematic position and infrageneric relationships of the genus.

Materials and methods

Specimens collected and microscopic observations

Fresh samples were collected from Hainan, Jilin, Yunnan, Guizhou, and Zhejiang Provinces of China. Ecological images

were photographed using a digital camera in the field, including measurement data of fruiting bodies sooner after fieldwork. Following a study by Kernerup and Wanscher (1978), color codes were subsequently assigned. Then, specimens were dried in a 45 °C electric oven overnight, sealed in plastic bags, and placed in a refrigerator for insecticidal treatment (Yu et al. 2020; Deng et al. 2021a, 2021b). After the study, the specimens were deposited at the Herbarium of the Changbai Mountain Natural Reserve (ANTU) with FCAS numbers, the Herbarium of Guizhou Academy of Sciences (HGAS), and the Mycological Herbarium of Kunming Medical University (MHKMU).

Macrofeatures were described based on field notes and digital images. Microscopic observations were conducted using a light microscope (Olympus CX23). Dried specimens were sliced and rehydrated in 5% KOH, and also 1% Congo red solution when necessary. Basidiospores, basidia, hymenophoral trama, cheilocystidia, pileipellis/pileal trama, and stiptipellis/stipe trama were examined and measured. The side views of at least 20 mature basidiospores for each specimen were measured, excluding apiculus, with the form [n/m/p], indicating the measurement of “n” basidiospores of “m” individuals from “p” collections. The measurement data were expressed in the form of (a) b–e–c (d), where “a” and “d” represent the minimum and maximum values in the measurement data, respectively, “b” and “c” represent the values when the species measurement data are arranged at 5% and 95% from small to large, and “e” represents the average value (Liu et al. 2021; Ge et al. 2021; Na et al. 2021). Additionally, the roundness of spores from a certain length (Q) conveniently distinguished different species, represented by the formula:

$$Q = \text{spore length} / \text{spore width}$$

Subsequently, Q_m , the average Q of all basidiospores (presented as basidiospores \pm sample standard deviation), was obtained (Na et al. 2022; Jean et al. 2022).

DNA extraction, PCR, and sequencing

Genomic DNA was extracted from dried samples using the NuClean Plant Genomic DNA kit (ConWin Biotech Beijing). PCR reactions were conducted using the primer pairs ITS1-F/ITS4 for ITS (Gardes and Bruns 1993), LR0R/LR7 for LSU (Vilgalys and Hester 1990), and RPB2-6F/RPB2-7.1R for *RPB2* (Matheny 2005). Specifically, the PCR amplification setup was a 25 μ L mixture comprising 10 μ L ddH₂O, 12 μ L of 2 \times Taq Plus MasterMix (Dye), 1 μ L of each primer, and 1 μ L template DNA. The PCR reaction program was set as follows: 5 min at 95 °C; 1 min at 95 °C; 30 s at 65 °C (addition of a -1 °C per cycle), then 1 min at 72 °C for 15 cycles, followed by 1 min at 95 °C; 30 s at 50 °C, and 1 min at 72 °C for 20 cycle times, finally ending with 10 min at 72 °C

(Wang et al. 2021). Amplified products were subsequently sent to BGI Biotech (Guangdong), Ltd. for purification and sequencing.

Phylogenetic analyses

Authentically identified sequences retrieved from previous studies (Ryberg et al. 2008; Cripps et al. 2010; Vauras and Larsson 2011; Ariyawansa et al. 2015; Horak et al. 2015; Brugaletta et al. 2017; Matheny and Bougher 2017; Matheny and Kudzma 2019; Aignon et al. 2021; Mao et al. 2022) were selected and downloaded from the NCBI database for phylogenetic analyses. Specifically, representatives from *Auritella*, *Inosperma*, and *Tubariomyces* served as outgroups (Matheny et al. 2020). After that, ITS, nrLSU, and *RPB2* sequences were aligned using the MAFFT online service (<https://mafft.cbrc.jp/alignment/server/>) (Katoh et al. 2019), then manually edited using BioEdit v.7.0.9.0 (Hall 1999). Mrmodeltest v.2.3 selected the optimal evolutionary substitution model for each gene following the Akaike information criterion (Nylander 2004), after which Mega v.5.0 concatenated the three gene sequences into a multi-locus dataset, followed by the maximum likelihood (ML) analysis using the IQ-TREE web server with 1000 duplicates (Trifinopoulos et al. 2016). Bayesian analysis (BI) was performed using MrBayes v.3.2.7a (Ronquist et al. 2012). For this analysis, a total of 2,150,000 generations were run using four Metropolis-Coupled Monte Carlo Markov chains to calculate posterior probabilities and the standard deviation of the split frequencies was terminated at 0.009975. After discarding the first quarter of all generations as the burn-in, the majority-rule consensus tree of all remaining trees was calculated.

Results

Phylogenetic analyses

Thirty-four sequences (14 ITS, 10 nrLSU, and 10 *RPB2*) from 14 collections were generated and submitted to GenBank. The final combined dataset comprised 104 samples representing 63 taxa (Table 1) and 3037 nucleotide sites (957 bp ITS, 1420 bp LSU, and 660 bp *RPB2*). For the phylogenetic analysis, the best substitution model for each of the three data partitions was GTR+I+G (Iset nst = 6, rates = invgamma; prset statefreqpr = Dirichlet [1,1,1,1]). Because phylogenetic trees inferred from ML and BI analyses were nearly identical, with only a few statistical differences, the optimal ML tree with combined support data is presented in Fig. 1.

In the tree shown in Fig. 1, all members of *Mallocybe* are divided into three major clades (A–C). Clade A, which is only weakly supported (PP = 0.71/BP = 57%), comprises 55 accessions and is divided into three subclades. In the first

subclade, 40 accessions are grouped together with strong support (PP = 0.98/BP = 90%). The second subclade, which is moderately supported (PP = 0.74/BP = 82%), contains eight accessions corresponding to *M. arenaria* (Kühner) Matheny & Esteve-Rav., *M. velutina* Saba & Khalid, *M. tomentosula* Matheny & Esteve-Rav., and *M. errata* (E. Horak, Matheny & Desjardin) Haelew. Finally, seven samples from *M. piceae* L. Fan & N. Mao, *M. arthrocytis* (Kühner) Matheny & Esteve-Rav., *M. fuscomarginata* (Kühner) Matheny & Esteve-Rav., and *M. gymnocarpa* (Kühner) Matheny & Esteve-Rav. are grouped in the third, moderately supported subclade (PP = 0.74/BP = 90%). Eleven accessions from Australia are grouped together with full support (PP = 1.0/BP = 100%) in clade B. Similarly, 20 accessions, including our three new species, are fully supported (PP = 1.0/BP = 100%) as members of clade C.

Within clade C, the Chinese materials form three independent lineages. Seven accessions from Hainan Province and one from Yunnan Province, all representing *M. longicytis*, constitute a fully supported lineage that is sister to a subclade consisting of three *M. aurantiodisca* accessions from Zhejiang Province. In addition, two accessions of *M. pallidipes* collected from Jilin Province form a fully supported lineage that is sister to the subclade comprising *M. aurantiodisca*, *M. longicytis*, *M. multisporea* (Murrill) Matheny & Esteve-Rav., and *M. unicolor* (Peck) Matheny & Esteve-Rav.

Taxonomy

Mallocybe longicytis T. Bau, Y.G. Fan, J.H. Hu & W.J. Yu, sp. nov., Figs. 2 and 3

MycoBank: MB844269

Etymology: refers to its long cheilocystidia.

Diagnosis: differs from *M. pallidipes* by the lack of reddish orange tinge in basidiomata, its erected scales in pileus, and more cylindrical cheilocystidia.

Holotype: China, Hainan Province, Wuzhishan City, Shuiman Town, Wuzhishan area of Hainan Tropical Rain Forest National Park, 18°51'53"N, 109°40'43"E, 695 m asl., 28 Jul. 2021, Y.-G. Fan & W.-J. Yu, FYG6374 (FCAS3535), GenBank accession number: ITS (OM179928), LSU (OM135611), and *RPB2* (OM835747).

Description: Basidiomata small. Pileus 16–30 mm diam. spherical to hemispherical when very young, becoming convex to broadly convex and nearly flattened when mature, sometimes turns up in a wavy shape, without umbo; margin incurved at first, then decurved for a long time, straight when mature, longer than lamellae; surface dry, covered with densely and radially arranged, thick, conical scales, erected towards center, becoming recurved outwards, nearly appressed to appressed-rimulose towards the margin; amber, burnt yellowish (4B6) to yellowish brown

Table 1 Information on taxa used in the phylogenetic analysis

Taxa	Voucher	GenBank accession number			Country	Reference
		ITS	LSU	<i>RPB2</i>		
<i>Auritella brunnescens</i>	PBM3174	KJ702344	JQ313571	KJ702349	Australia	Matheny et al. (2020)
<i>A. dolichocystis</i>	T24844		AY380371	AY337371	Australia	Matheny et al. (2020)
<i>A. foveata</i>	TBGT9631	GU062740	GU062739	GU062738	India	Matheny et al. (2020)
<i>A. fulvella</i>	AQ669492	KJ702355	KJ702352	KJ702357	Australia	Matheny et al. (2020)
<i>A. hispida</i>	TH10009	KT378203	KT378207	KT378215	Cameroon	Matheny et al. (2020)
<i>A. robusta</i>	I163	KJ702359	KJ702358	KJ702360	Tasmania	Matheny et al. (2020)
<i>A. serpentinocystis</i>	PBM3188	KJ729858	JQ313559	KJ756402	Australia	Matheny et al. (2020)
<i>A. spiculosa</i>	TH9866	KT378204	KT378206	KT378214	Cameroon	Matheny et al. (2020)
<i>Inocybe dulcamara</i>	CLC1333	GU980635	GU980635		USA	Cripps et al. (2010)
<i>Inoc. dulcamara</i>	EL59-05	GU980643	GU980643		Norway	Cripps et al. (2010)
<i>Inosperma adaequatum</i>	JV16501F	JQ801381	JQ815407	AY333771	Finland	Matheny et al. (2020)
<i>Inos. calamistratum</i>	PBM1105	JQ801386	JQ815409	JQ846466	USA	Matheny et al. (2020)
<i>Inos. calamistratum aff.</i>	SAT9826004	JQ801387	JQ815410	JQ846467	USA	Matheny et al. (2020)
<i>Inos. carnosibulbosum</i>	TBGT12047	KT329448	KT329454	KT329443	Thailand	Matheny et al. (2020)
<i>Inos. misakaense</i>	PC96234	JQ801409	EU569874	EU569873	Zambia	Matheny et al. (2020)
<i>Inos. mutatum</i>	PBM2542	MG773837	AY732212	DQ472729	USA	Matheny et al. (2020)
<i>Inos. rimosoides</i>	PBM2459	DQ404391	AY702014	DQ385884	USA	Matheny et al. (2020)
<i>Inos. virosum</i>	TBGT753	KT329452	KT329458	KT329446	India	Matheny et al. (2020)
<i>Mallochybe agardhii</i>	AB980912	HM209790	HM209790		Denmark	Vauras and Larsson (2011)
<i>M. arenaria</i>	EL25008	FN550937	FN550937		France	Ryberg et al. (2010)
<i>M. aurantiodisca</i>	2020ZD01	OM179937			China	The present study
<i>M. aurantiodisca</i>	NJ3109	OM179935	OM138834	OM835751	China	The present study
<i>M. aurantiodisca</i>	NJ3396	OM179936	OM138835	OM835752	China	The present study
<i>M. arthrocytis</i>	EL9207	FN550941	FN550941		Sweden	Ryberg et al. (2010)
<i>M. caesariata</i>	NAMA272	EU819498			USA	Palmer et al. (2008)
<i>M. caesariata</i>	JMP0105	EU819473			USA	Palmer et al. (2008)
<i>M. crassivelata</i>	MCVE29561	MN536812	MN537138		Slovenia	Crous et al. (2020)
<i>M. cf. squarrosoannulata</i>	CLC1844	GU980611	GU980611		USA	Cripps et al. (2010)
<i>M. cf. subtilior</i>	PERTH:08383081	KP641629	KP171084	KM656125	Australia	Matheny and Bougher (2017)
<i>M. depressa</i>	BJTC FM1300	OM801895	OM801900	OM780099	China	Mao et al. (2022)
<i>M. errata</i>	DED8022		EU569844		Thailand	Matheny et al. (2009)
<i>M. errata</i>	ZT10108 (SFSU)		GQ892935		Thailand	Horak et al. (2015)
<i>M. fibrillosa</i>	LVK14371	MN178498	MN178526	MN203517	USA	Matheny unpublished
<i>M. fibrillosa</i>	LVK14390	MN178499	MN178527	MN203518	USA	Matheny unpublished
<i>M. fulviceps</i>	PBM4533	MZ404928	MZ375430		USA	Matheny unpublished
<i>M. fulviceps</i>	PBM4542	MZ404929	MZ375431		USA	Matheny unpublished
<i>M. fulvipes</i>	EL3705	AM882858			Norway	Ryberg et al. (2008)
<i>M. fulvipes</i>	EL8307	FN550935	FN550935		Sweden	Ryberg unpublished
<i>M. fulvipes</i>	EL99-07	GU980600	GU980600		Sweden	Cripps et al. (2010)
<i>M. fulvoubonata</i>	PBM4537	MZ404931	MZ375433		USA	Matheny unpublished
<i>M. fuscomarginata</i>	BJ890718	GU980656	GU980656		Sweden	Cripps et al. (2010)
<i>M. fuscomarginata</i>	EL10906	FN550940	FN550940		Sweden	Ryberg et al. (2010)
<i>M. granulosa</i>	EL138-09	KR029727	KR029727		Sweden	Ariyawansa et al. (2015)
<i>M. granulosa</i>	SJ84030	KR029725	KR029725		Sweden	Ariyawansa et al. (2015)

Table 1 (continued)

Taxa	Voucher	GenBank accession number			Country	Reference
		ITS	LSU	<i>RPB2</i>		
<i>M. gymnocarpa</i>	16413	JF908161			Italy	Osmundson et al. (2013)
<i>M. gymnocarpa</i>	SJ980707	AM882866	AM882866		Sweden	Ryberg et al. (2008)
<i>M. isabellina</i>	PERTH:07699255	KP171137	KP170915	KJ811581	Australia	Matheny and Bougher (2017)
<i>M. isabellina</i>	PERTH:08096635	KP171138	KP170916	KJ811582	Australia	Matheny and Bougher (2017)
<i>M. latispora</i>	EL190-08	KR029724	KR029724		Not given	Ariyawansa et al. (2015)
<i>M. latispora</i>	JV19640F	MN178503	MN178529	MN203520	Finland	Matheny and Kudzma (2019)
<i>M. leucoblema</i>	JV2898	HM209789	HM209789		Finland	Vauras and Larsson (2011)
<i>M. leucoblema</i>	SM2324	GU980630	GU980630		Sweden	Cripps et al. (2010)
<i>M. leucoloma</i>	Kuhner63-36Type	GU980614			Geneva	Cripps et al. (2010)
<i>M. leucoloma</i>	EL41-07	GU980622	GU980622		Sweden	Cripps et al. (2010)
<i>M. leucoloma</i>	Ohenoja 880810	HM209786	HM209786		Svalbard	Vauras and Larsson (2011)
<i>M. longicystis</i>	FYG2015407	OM179933			China	The present study
<i>M. longicystis</i>	FYG6371	OM179926	OM135609	OM835746	China	The present study
<i>M. longicystis</i>	FYG6373	OM179927	OM135610	OM747850	China	The present study
<i>M. longicystis</i>	FYG6374	OM179928	OM135611	OM835747	China	The present study
<i>M. longicystis</i>	FYG6376	OM179929	OM135612	OM835745	China	The present study
<i>M. longicystis</i>	FYG6378	OM179930	OM135613	OM835748	China	The present study
<i>M. longicystis</i>	FYG6501	OM179934			China	The present study
<i>M. longicystis</i>	FYG6880	OM179931	OM135614	OM858853	China	The present study
<i>M. longicystis</i>	HT370	OM179932	OM135615		China	The present study
<i>M. malenconii</i>	JV23101	HM209787	HM209787		Finland	Vauras and Larsson (2011)
<i>M. malenconii</i>	PAM98941302	HM209788	HM209788		France	Vauras and Larsson (2011)
<i>M. multispora</i>	CO4248	MN178509	MN178540		USA	Matheny unpublished
<i>M. myriadophylla</i>	EL121-08	HM209792	HM209792		Sweden	Vauras and Larsson (2011)
<i>M. myriadophylla</i>	JV5968	HM209794	HM209794		Finland	Vauras and Larsson (2011)
<i>M. myriadophylla</i>	JV19652	HM209791	HM209791		Finland	Vauras and Larsson (2011)
<i>M. myriadophylla</i>	JV19678	HM209793	HM209793		Finland	Vauras and Larsson (2011)
<i>M. pallidipes</i>	FYG3726	OM179924	OM137052	OM835749	China	The present study
<i>M. pallidipes</i>	FYG3727	OM179925		OM835750	China	The present study
<i>M. picea</i>	BJTC FM555	OM801896	OM801901	OM780096	China	Mao et al. (2022)
<i>M. picea</i>	BJTC FM569	OM801897	OM801903	OM780097	China	Mao et al. (2022)
<i>M. pygmaea</i>	EL48-05	GU980628	GU980628		Norway	Cripps et al. (2010)
<i>M. pygmaea</i>	J. Favre76bis Type	GU980629			Norway	Cripps et al. (2010)
<i>M. pyrhopoda</i>	TENN: 066987	KP308813	KP170983	KM406223	Australia	Matheny and Bougher (2017)
<i>M. pyrhopoda</i>	PERTH: 08383278	KP308814	KP170984	KM406224	Australia	Matheny and Bougher (2017)
<i>M. pyrhopoda</i>	PERTH: 08557764	KP308815	KP170986	KM406226	Australia	Horak et al. (2015)
<i>M. sabulosa</i>	PERTH: 07680732	KP308822	JN974916	KM406235	Australia	Matheny and Bougher (2017)
<i>M. sabulosa</i>	PERTH: 08320322	KP308821	KP170994	KM406234	Australia	Matheny and Bougher (2017)
<i>M. siciliana</i>	AMB18274	MG757417	MG757419		Italy	Brugaletta et al. (2017)
<i>M. siciliana</i>	M73	MW354997			Hungary	Csizmar et al. (2021)
<i>M. squarrosannulata</i>	K63-236 Type	HM209795			Geneva	Vauras and Larsson (2011)
<i>M. squamosodisca</i>	LVK20133	MZ404935	MZ375436		USA	Matheny unpublished
<i>M. subdecurrens</i>	REH10168	MH024850	MH024886	MH577503	USA	Matheny et al. (2020)
<i>M. subflavospora</i>	NLB1078	MN178515	MN178544	MH577504	Australia	Matheny and Bougher (2017)
<i>M. subflavospora</i>	TENN: 067023	KP641620		KM656119	Australia	Matheny and Bougher (2017)
<i>M. substraminipes</i>	EL12-08	GU980607	GU980607		USA	Cripps et al. (2010)

Table 1 (continued)

Taxa	Voucher	GenBank accession number			Country	Reference
		ITS	LSU	<i>RPB2</i>		
<i>M. substraminipes</i>	K70-148	GU980601	GU980601		USA	Cripps et al. (2010)
<i>M. subtilior</i>	PERTH: 08095388	KP641628	KP171082		Australia	Matheny and Bougher (2017)
<i>M. subtomentosa</i>	LVK17005	MN178520			USA	Matheny unpublished
<i>M. subtomentosa</i>	PBM2460	MN178521	MN178549	MN203531	USA	Matheny unpublished
<i>M. terrigena</i>	EL24-08	GU980648			USA	Cripps et al. (2010)
<i>M. terrigena</i>	EL117_04	AM882864	AM882864		Sweden	Larsson et al. (2009)
<i>M. tomentosula</i>	PBM4138	MG773814	MK421969	MH577506	USA	Matheny et al. (2020)
<i>M. umbrinofusca</i>	Kuhner70-38 Type	GU980613			Geneva	Cripps et al. (2010)
<i>M. unicolor</i>	PBM2589	EU523555			USA	Matheny unpublished
<i>M. unicolor</i>	PBM2974	MN178524	JQ313569	MN203532	USA	Matheny unpublished
<i>M. velutina</i>	MSM # 0048	MK990129	MK999927		Pakistan	Saba and Khalid (2020)
<i>M. velutina</i>	MSM # 0049	MK990130	MK999928		Pakistan	Saba and Khalid (2020)
<i>M. velutina</i>	MSM # 0050	MK990131	MK999929		Pakistan	Saba and Khalid (2020)
<i>Tubariomyces inexpectatus</i>	AH20390	GU907095	EU569855	GU907088	Spain	Matheny et al. (2020)
<i>T. sp.</i>	BB6018	MK421965	EU600887	EU600886	Zambia	Matheny et al. (2020)

(5C7) at the center, darker towards the disc and slightly paler outwards; occasionally with a thin smoky-yellowish (5B6) filamentous veil remnants layer around the disc, sometimes not distinctly. Lamellae 2–4 mm wide, adnexed, crowded, subdecurrent, alternating with 3–4 tiers of lamellulae, whitish (3A1) to grayish white (3B1) or dirty white (3B2) when young, beige (5B2), yellowish (5B4) to brownish (5C4) when mature, edges paler and fimbriate. Stipe 19–40 × 2–5 mm, solid at first, becoming fistulose with age, equal, truncate or pestle like and slightly swollen at the base; woolly or feltly from veil remnants, grayish white (3B2) to yellowish white (4C4) when young, yellowish brown (5B5) when mature, yellow to pale amber towards stipe base; partial veil present when young, fugacious. Context solid and fleshy in pileus, white (5A1) to dirty whitish (4B2), 1–2 mm thick at middle radius, 2–3 mm thick at the center, fleshy to somewhat fibrous in the stipe, whitish (5A2) to yellow whitish (3B2), with light yellowish brown (5B4) tinge near the epidermis. Odor lightly sweet, lightly earthy or not distinct.

Basidiospores: [160/8/8] (8)8.5–9.7–10(11) × (4)4.5–5.1–5.5(8) μm, $Q = (1.52)1.59–2.20(2.64)$, $Q_m \pm SD = 1.92 \pm 0.015$, ellipsoid to oblong, smooth, thick-walled, with blunt or slightly acute apex, golden yellowish to pale yellowish in KOH, apiculus small and indistinct, with one large ellipsoid oily droplet. Basidia 24–34 × 5–9 μm, slenderly clavate to clavate, blunt or rounded at apex, nearly truncate or pestle-like at the base, colorless at the initial stage, then golden yellowish and shriveled, 4- or 2-spored, necropigmented; sterigmata acute, 3–6 μm in length. Pleurocystidia absent. Lamellae

edge sterile. Cheilocystidia 35–63 × 5–14 μm ($n = 50$), abundant, in clusters, slenderly clavate or cylindrical-clavate, less often broadly clavate or ventricose, mostly enlarged and rounded at apex, occasionally utriform or ventricose, thin-walled or slightly thick-walled, walls bright yellow. Hymenophoral trama 65–150 μm thick, regular to subregular, yellowish to golden yellowish; trama hyphae 10–30 μm wide, smooth, concave, inflated at both ends of cell, cylindrical, thin-walled or slightly thick-walled, walls bright yellow. Stipitipellis a cutis often extended with irregularly and loosely arranged hyphae, golden yellowish in mass, composed of cylindrical inflated cells, 7–15 μm wide, smooth, colorless to light yellowish. Stipe trama regularly arranged, light yellowish when aggregated, composed of smooth, cylindrical hyphae, colorless, 5–10 μm wide. Caulocystidia not observed. Pileipellis a cutis with emerged bundles of trichodermally arranged hyphae comprising scales, those bundles 93–140 μm wide, coniform, golden yellowish to yellowish brown when aggregated, composed of cylindrical to inflated encrusted, hyphae 7–18 μm wide, slightly thickened, bright yellow. Pileal trama 250–650 μm wide, subregular, yellowish in mass, composed of fleshy, cylindrical hyphae, colorless, 11–20 μm wide. Oleiferous hyphae 3–5 μm wide of two types: yellowish type often present in pileal trama, with oily inclusions, colorless type more often observed in stipe trama, smooth, with no oily inclusions. Clamp connections present in all tissues.

Habitat: gregarious, caespitose in small groups or scattered along roadsides under fagaceous trees, on sandy or lateritic soil.

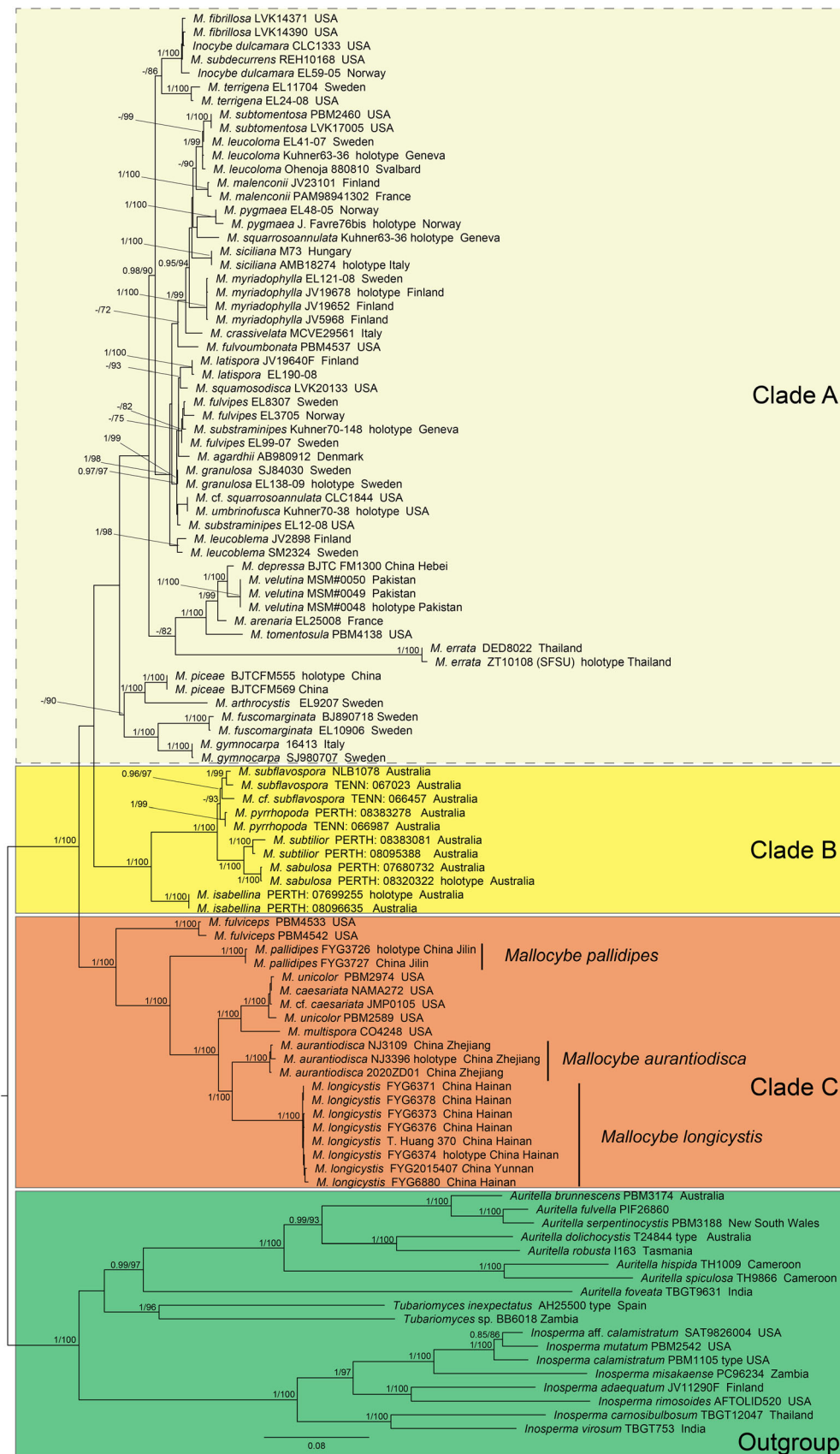


Fig. 1 Phylogram generated from the combined dataset sequence of nuclear genes (rDNA-ITS, nLSU, and *RPB2*). Bayesian inference posterior probabilities (BI-PP) ≥ 0.95 and ML bootstrap proportions ML-BP ≥ 70 are expressed by (BI-PP) / (ML-BP), respectively



Fig. 2 Basidiomata of *Mallocybe longicystis*. **a–c, e** Basidiomata. **d, h, i** Lamellae. **f** Pileus. **g, j, k** Stipe surface. **a, c, d, f, i–k** FYG6374 (holotype); **b** FYG6373; **e, g, h** FYG6378. Scale bars: **a–b, f–i, k** = 1 mm; **c–e, j** = 5 mm. Photos by Y.-G. Fan

Distribution: Known from Hainan and Yunnan Provinces, China.

Specimens examined: China. Hainan Province, Wuzhishan City, Shuiman Town, 18°51'53"N, 109°40'43"E, 695 m asl.,

under fagaceous trees, 26 May 2022, Y.-G. Fan & W.-J. Yu, FYG6972 (FCAS3583), 1 May 2022, Y.-G. Fan & W.-J. Yu, FYG6963 (FCAS3581), FYG6964 (FCAS3582); same locality, 28 Jul. 2021, Y.-G. Fan & J.-H. Hu, FYG6371 (FCAS3533),

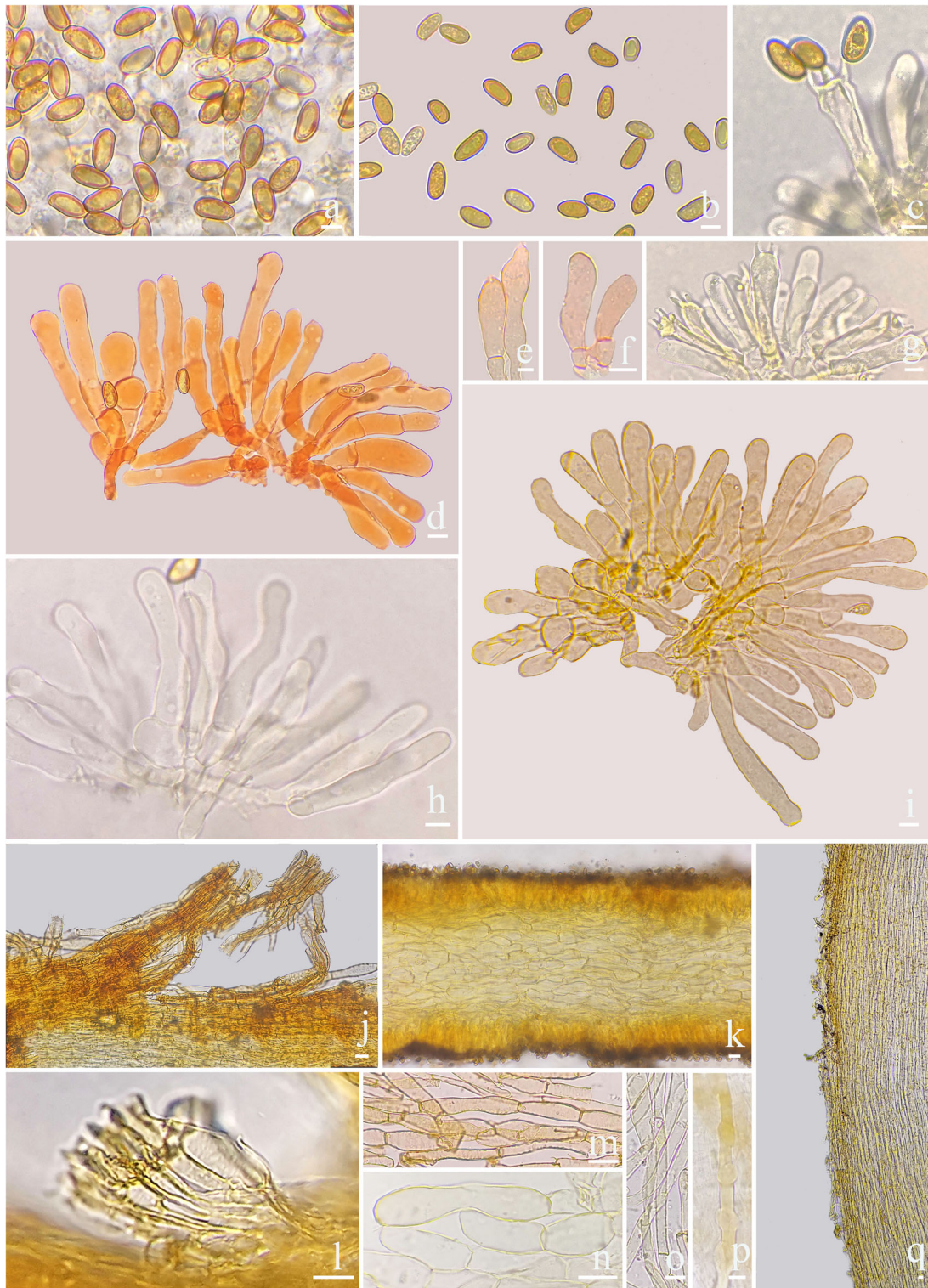


Fig. 3 Microscopic features of *Mallocybe longicystis* (FYG6374, holotype). **a–b** Basidiospores. **c, g** Basidia. **d–f, h–i** Cheilocystidia. **j** Pileipellis. **k** Transverse section of the lamella. **l** Terminal hyphae at the

pileus. **m** Pileipellis hyphae. **n** Hymenophoral trama hyphae. **o** Stipitipellis hyphae. **p** Oleiferous hyphae. **q** Stipitipellis. Scale bars: **a–i**, **p** = 5 μm ; **j–o, q** = 20 μm . Photos by J.-H. Hu

FYG6373 (FCAS3534), FYG6376 (FCAS3536), Y.-G. Fan, L.-S. Deng, L.-N. Zhao & J.-H. Hu, FYG6378 (FCAS3537), Y.-G. Fan & W.-J. Yu, FYG6880 (FCAS3538), Y.-G. Fan &

W.-J. Yu, same locality, 30 Jun 2021, T. Bau & Y.-G. Fan, FYG6501 (FCAS3541), same locality, 02 Aug 2020, MHKMU T. Huang 370 (FCAS3539); Yunnan Province,

Kunming City, Kunming Botanic Garden, 25 Sep 2015, Y.-G. Fan & W.-J. Yu, FYG2015407 (FCAS3540).

Remarks: This species fruits from late April to late September under fagaceous forests in tropical or subtropical China. The umber-colored basidiomata and erected squamules in pileus make it outstanding in the field. It usually has erected scales on the disc of the pileus, but certain individual has only appressed squamules on the disc. Microscopically, its basidiospores are mostly elongate-ellipsoid, but distinct larger basidiospores present and probably discharged from bisporic basidia measured $10.5\text{--}11.1\text{--}12.0 \times (4.0)5.0\text{--}5.2\text{--}6.0 \mu\text{m}$ ($n = 21$). The cylindrical cheilocystidia are striking and very abundant, a character that is atypical to the genus. *Mallocybe errata* (E. Horak, Matheny & Desjardin) Haelew., a tropical Asian species shares erected squamules in pileus and profile and size of basidiospores, but differs by its hazel brown to golden brown pileus, adnate to marinate-depressed lamellae, more robust stipe measured $10\text{--}35 \times (3)4\text{--}8 \text{ mm}$, and broadly clavate to vesiculose cheilocystidia (Horak et al. 2015).

Phylogenetically, *M. longicystis* is sister to another new species *M. aurantiodisca* discovered in subtropical China and shares a similar outline and size of basidiospores (see description of *M. aurantiodisca*). However, the latter species has reddish orange tinged pileus with tomentose squamules, less cylindrical cheilocystidia, and occurring in subtropical evergreen broad-leaved forests dominated by *Castanopsis*.

Mallocybe pallidipes Y.G. Fan, J.H. Hu & W.J. Yu, sp. nov., Figs. 4 and 5

Mycobank: MB844271

Etymology: refers to its pallid stipe.

Diagnosis: differs from *M. aurantiodisca* by its isabelline pileus, pallid stipes, more cylindrical basidiospores, and an association with trees of *Populus*.

Holotype: China, Jilin Province, Changchun City, in the campus of Jilin Agricultural University, $43^{\circ}48'16''\text{N}$, $125^{\circ}24'07''\text{E}$, 220 m asl., under trees of *Populus*, 26 Jul 2019, Y.-G. Fan & W.-J. Yu, FYG3726 (FCAS3542), GenBank accession number: ITS (OM179924); LSU (OM137052) and *RPB2* (OM835749).

Description: Basidiomata small. Pileus 5–17 mm diam. hemispherical when young, becoming convex to broadly convex or upon expanding, plano-convex to undulate-applanate with age, obtusely umbonate at the disc; margin initially inflexed, then depressed to straight with age; surface dry, fibrillose-tomentose to woolly tomentose with scurfy appressed squamules, not rimose; dirty-yellowish (5B3), brownish yellow (5B4), or ochraceous brown (5B6), darker around the center, paler outwards. Lamellae 3–5 mm wide, adnexed-emarginate, moderately crowded, alternated with 3–4 tiers of lamellulae; initially pale yellowish white (5A3) or pale grayish white (5B2), then yellowish brown (5B4) to brown (5B5) with age; edges pallid and fimbriate. Stipe 14–28 \times 1–3 mm, cylindrical, solid at first, then becoming fistulose, beige (5A2) or

yellowish white (5B4), sometimes concolorous with pileus, yellowish (6B5) towards the base; equal, dry, silky from veil remnants. Context dirty white (5A2) and fleshy in pileus, 1–2 mm wide at mid-radius, fleshy-fibrillose and shiny in stipe. Odor unpleasant, taste bitter.

Basidiospores $[100/4/2] (9)10\text{--}11.3\text{--}13(13.5) \times (4)4.3\text{--}5.0\text{--}5.5(6) \mu\text{m}$, $Q = (1.88)2.00\text{--}2.65(2.84)$, $Q_m \pm \text{SD} = 2.30 \pm 0.020$, smooth, thick-walled, yellowish to yellowish brown, very variable in shape, ellipsoid to subphaseoliform, sometimes phaseoliform in side view. Basidia 20–33 \times 5–9 μm , clavate to slenderly clavate, necropigmented, 4-spored, sometime 2-spored, with inner olivaceous guttulae; sterigmata 3–5 mm long. Pleurocystidia absent. Lamellae edge sterile. Cheilocystidia 38–65 \times 7–14 μm ($n = 50$), abundant, clavate to slenderly clavate, fusiform or utriform, apex rounded or slightly tapered, base truncate or tapered, colorless and hyaline, thin-walled. Hymenophoral trama 60–185 μm thick, regular to subregular, light yellowish, trama elements 11–16 μm wide, cylindrical to inflated or concave, thin-walled, smooth, hyaline. Stipitipellis a cutis often with extending hyphae, pale yellowish when aggregated, composed of cylindrical expanded hyphae, 6–10 μm wide, encrusted, hyaline. Stipe trama densely arranged, light yellowish when aggregated, composed of smooth, cylindrical hyphae, colorless, 6–11 μm wide. Caulocystidia absent. Pileipellis 90–122 μm thick, a cutis with emerging bundles of hyphae, golden yellow to yellowish brown when aggregated, composed of cylindrical to inflated and encrusted hyphae, 8–18 μm wide, slightly thick-walled, pale yellowish. Pileal trama hyaline, subregular, 300–560 μm thick, composed of several barbell cells or expanded cells of different sizes, 8–16 μm wide. Oleiferous hyphae exist in pileal and stipe trama, hyaline, 2–5 μm wide, with oval or spherical intracellular substances. Clamp connections present in all tissues.

Habitat: solitary and scattered along roadsides on clay soil under trees of *Populus* in temperate zone.

Distribution: Known only from the type locality in Jilin Province, China.

Specimen examined: China, Jilin Province, in the campus of Jilin Agricultural University, $43^{\circ}48'16''\text{N}$, $125^{\circ}24'07''\text{E}$, 220 m asl., under *Populus*, 26 Jul 2019, Y.-G. Fan & W.-J. Yu, FYG3727 (FCAS3543).

Remarks: *Mallocybe pallidipes* is a rare species collected in the Botanic Garden of Jilin Agricultural University. It occurs on the roadsides on clay soils in plantations of *Populus* and shrubs. The new species is characterized by Isabella-colored pileus with finely tomentose squamules, pallid stipe with fibrillose-fleshy context, dirty-yellowish lamellae, and a bitter smell. Microscopically, its large cylindrical basidiospores, and cylindrical to fusiform cheilocystidia are distinct. Distinct large spores probably discharged from bisporic basidia are unfrequently observed and measured $12\text{--}12.4\text{--}14 \times 4\text{--}4.8\text{--}6 \mu\text{m}$ ($n = 27$).

Mallocybe aurantiodisca is similar in having finely squamules in pileus, pallid stipes, cylindrical basidiospore



Fig. 4 Basidiomata of *Mallocybe pallidipes*. **a** Basidiomata. **b** Pileus. **c** Lamellae. **d–e** Stipe surface. **a–c** FYG3727 (holotype); **d–e** FYG3726. Scale bars: **a, d** = 5 mm; **b–c, e** = 2.5 mm. Photos by Y.-G. Fan

outlines, and elongate cheilocystidia, but differs by its reddish orange tinged basidiomata, narrower lamellae, smaller basidiospores, and ecology in subtropical forest. *Mallocybe unicolor*, originally described from New York, shares

fibrillose-fleshy context in stipes, elongate-ellipsoid basidiospores, and long cheilocystidia, but differs in most cylindrical to cylindrical-flexuose cheilocystidia (Kuo 2017). *Mallocybe pallidotomentosa* E. Ludw., a species described from

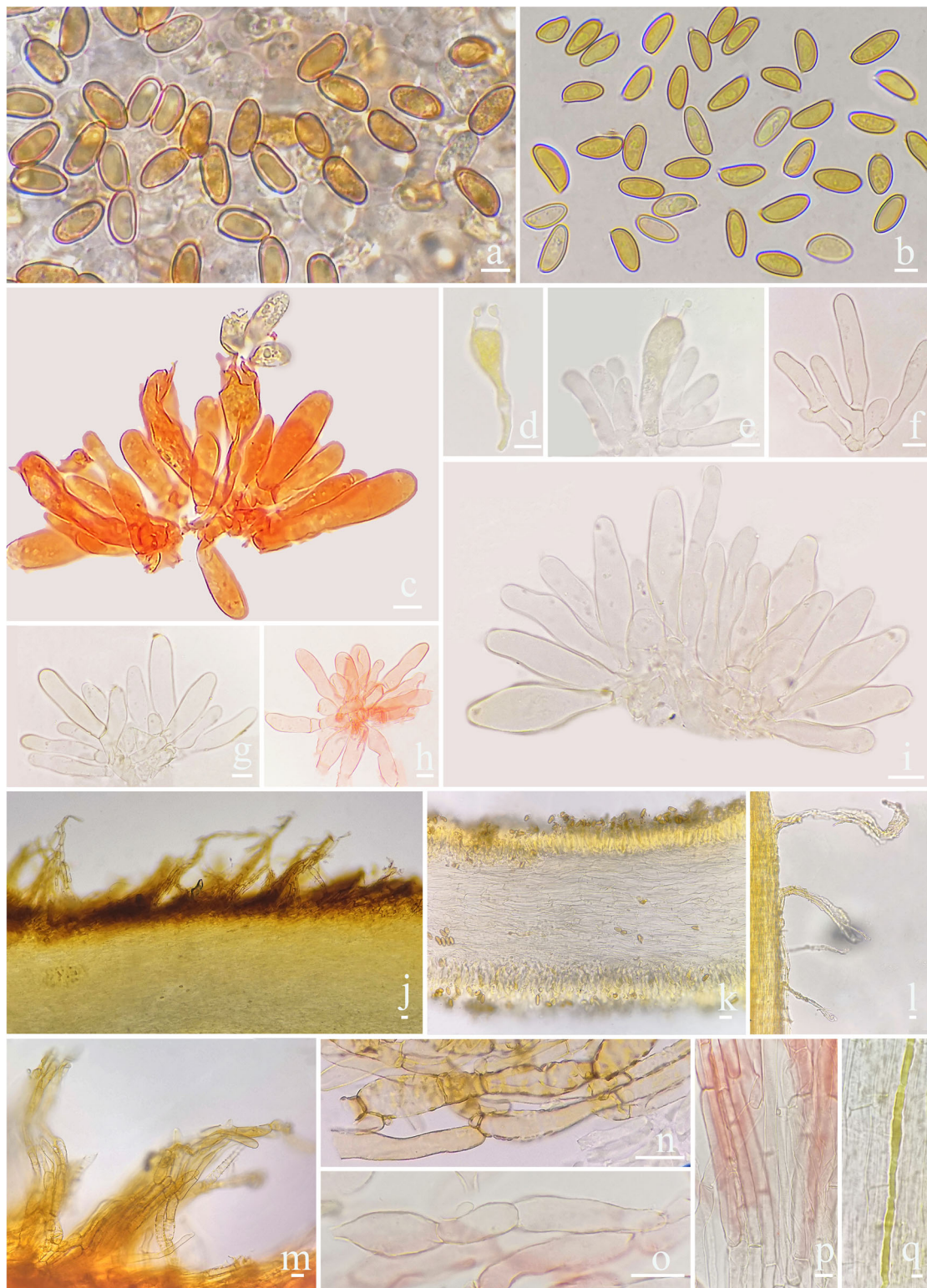


Fig. 5 Microscopic features of *Mallocybe pallidipes* (FYG3727, holotype). **a–b** Basidiospores. **c–e** Basidia. **f–i** Cheilocystidia. **j** Pileipellis and pileal trama. **k** Transverse section of the lamella. **l** Stipitipellis. **m** Terminal hyphae at the pileus. **n** Pileipellis hyphae. **o**

Hymenophoral trama hyphae. **p** Stipitipellis hyphae. **q** Oleiferous hyphae. Scale bars: **a–f, q** = 5 μm ; **g–i** = 10 μm ; **j–p** = 20 μm . Photos by J.-H. Hu

Germany, is similar in outwards appearance and occurs under *Populus* and *Betula*, but it differs in smaller and often

phaseoliform basidiospores measuring $6.5\text{--}9.5 \times 4\text{--}5 \mu\text{m}$ and mostly catenate cheilocystidia (Ludwig 2017).

Mallocybe aurantiodisca Y.G. Fan, Y.P. Ge, J.H. Hu & W.J. Yu, sp. nov., Figs. 6 and 7

Mycobank: MB844273

Etymology: refers to the orange tinge on the disc of the pileus.

Diagnosis: differs from *M. longicystis* by its reddish orange pileus with finely tomentose squamules and shorter cheilocystidia.

Holotype: China, Zhejiang Province, Lishui City, Liandu District, 28°26'9"N, 119°54'14"E, 59 m asl., Under forest dominated by *Pinus*, 3 Jun. 2020. Y.-P. Ge & Q. Na, NJ3396 (FCAS3545), GenBank accession number: ITS (OM179936); LSU (OM138835) and *RPB2* (OM835752).

Description: Basidiomata small. Pileus 13–25 mm diam. convex when young, becoming plano-convex to broadly convex or upon expanding, becoming plano-convex to undulate-applanate with age, obtusely umbonate at the disc, margin initially inflexed, then deflexed, fibrillose-tomentose to woolly tomentose with scurfy appressed squamules, not rimose; initially brownish with orange tinge (6B4) or orange (6B5) to reddish brown (6B6), becoming pale yellow brown (6C6) or pale ochraceous yellow with orange tinge (6C7) at least around the disc. Lamellae 1–3 mm wide, adnate, narrow, initially pale grayish white (6B2), becoming yellowish white (6B4) to ochraceous brown (6C5), edge whitish (6B3) and fimbriate. Stipe 24–30 × 2–3 mm, cylindrical or slightly tapering towards base, solid at first, then becoming fistulose, dirty white (6A2) to pale orange (6B5), surface fibrillose with appressed velar remnants, yellowish (5B5) to pale orange (5B7) towards the base, whitish (6A1) cortina present in young basidiomes. Context creamy white (6B2) or pale yellowish white (6A2) in pileus, 1–2 mm thick, concolorous in stipe. Odor indistinct.

Basidiospores [100/5/3] 8–9.1–10(12) × 4–5.0–5.5(6) μm, $Q = (1.52)1.58–2.13(2.29)$, $Q_m \pm SD = 1.85 \pm 0.016$, smooth, thick-walled, yellowish, thick-walled, ellipsoid, elongate ellipsoid to subphaseoliform. Basidia 27–38 × 6–10 μm, clavate to narrowly clavate, 4-spored, sometimes 2-spored, necropigmented, sterigmata up to 3–4 mm long. Pleurocystidia absent. Lamellae sterile. Cheilocystidia 28–62 × 6–18 μm ($n = 52$), mean 41 × 11 μm, abundant, subfusiform, subclavate, clavate to slenderly clavate, sometimes fusiform or cylindrical, septate and often constricted at septa, hyaline, thin-walled, Hymenophoral trama 92–141 μm, regular to subregular, colorless or somewhat yellowish, trama elements 13–20 μm wide, inflated or concave, cylindrical, thin-walled, hyaline. Stipitipellis a cutis often with extending hyphae, yellowish when aggregated, composed of cylindrical expanded hyphae, 4–8 μm wide, encrusted, yellowish. Stipe trama densely arranged, light yellowish when aggregated, composed of smooth cylindrical hyphae, colorless, 5–8 μm wide. Caulocystidia absent. Pileipellis a cutis often with emerging bundles of hyphae, 98–225 μm thick, brownish to yellowish brown when aggregated, composed of cylindrical to expanded shell hyphae, 9–18 μm wide, slightly thickened, pale yellowish. Pileal

trama 246–425 μm thick, hyaline, composed of several barbell-shaped cells or expanded cells of different sizes. Oleiferous hyphae 3–5 μm wide, hyaline, present in the epidermis of pileus and the stipe trama, exist oval or spherical substances. Clamp connections present in all tissues.

Habitat: solitary or scattered on clay soils in subtropical evergreen broad-leaved forests dominated by *Castanopsis* in subtropical zone.

Distribution: Known from the two localities in Zhejiang Province and one locality in Guizhou Province, China.

Specimen examined: China, Zhejiang Province, Lishui City, Liandu District, 28°30'5"N, 119°42'35"E, 166.4 m asl., in evergreen broad-leaved forests dominated by Fagaceae trees, 4 Aug 2021, Q. Na, NJ3109 (FCAS3544); Hangzhou City, Yutang District, 866 Hangtang Road, Campus of Zhejiang University, 30°18'33"N, 120°5'27"E, 666 m asl., under mixed broad-leaved forest, 3 Jun. 2020, W.-F. Lin, 2020ZD01 (FCAS3546); Guizhou Province, Tongren City, Jiangkou County, Fanjing Mountain Scenic Area, 27°53'49"N, 108°43'21'E, 1118 m asl., under fagaceous trees, 2 July 2020, C.Y. Deng, J. Zhang & H. Gao, D2663 (HGAS MF01-9312); Tongren City, Jiangkou County, Taiping Town, Fanjingshan Village, 27°53'49"N, 108°43'21"E, 1110 m asl., under fagaceous trees, 30 July 2020, C.Y. Deng, J. Zhang & H. Gao, D3188 (HGAS MF01-9582).

Remarks: The new species is known so far from Zhejiang and GuiZhou Provinces of China. It occurs on clay soils in a subtropical evergreen broad-leaved forest dominated by *Castanopsis* and on the campus of Zhejiang University. *Mallocybe aurantiodisca* is characterized by its reddish orange tinged basidiomata, tomentose-squamulose pileus, elongate-ellipsoid basidiospores, utriform, ventricose to cylindrical cheilocystidia that is usually flexuous.

Phylogenetically, it is sister to *M. longicystis*. Both the two species share similar-sized basidiospores. However, the latter has umber-colored pileus with erected squamules and more elongate cheilocystidia (see descriptions of *M. longicystis* above).

Discussion

Major clades in *Mallocybe*

Kuyper (1986) established the subgenus *Mallocybe* to accommodate species having necropigmented basidia and thin-walled cheilocystidia that originate from hymenial hyphae. Molecular phylogenetic studies have confirmed the monophyletic status of *Mallocybe* and supported its assignment as one of seven major clades in *Inocybaceae* (Matheny 2005; Matheny et al. 2009, 2020). Other recent studies on *Mallocybe* have mainly focused on new species discovery or on ectomycorrhizal associations of this genus with plants (Saba and Khalid 2020; Aignon et al. 2021; Daskalopoulos et al. 2021). Although molecular studies have uncovered some



Fig. 6 Basidiomata of *Mallocybe aurantiodisca*. **a** Basidiomata. **b** Pileus. **c** Lamellae. **d–e** Stipe surface. **a–d** NJ3396 (holotype); **e** NJ3109. Scale bars: **a–e** = 5 mm. Photos by Y.-P. Ge

specific clades, infrageneric relationships in *Mallocybe* have not been investigated in depth and require further clarification.

In the multi-gene phylogenetic analysis of *Mallocybe* described in this paper, we identified two strongly supported clades

and one weakly supported one. Clade A, which is weakly supported (BP = 0.71/BI = 57) in the tree in Fig. 1, comprises 55 accessions belonging to at least 29 taxa, all from the Northern Hemisphere. We thus consider this clade to be the most diverse in



Fig. 7 Microscopic features of *Mallocybe aurantioidisca* (NJ3396, holotype). **a–b** Basidiospores. **d–f** Basidia. **c, g, h** Cheilocystidia. **i** Pileipellis and pileal trama. **j** Transverse section of the lamella. **k** Stipitipellis hyphae. **l** Terminal hyphae at the pileus. **m** Pileipellis

hyphae. **n** Hymenophoral trama hyphae. **o–p** Oleiferous hyphae. **q** Stipe trama. Scale bars: **a–b, e–g, o–p** = 5 μm; **c–d, h** = 10 μm; **i–n, q** = 20 μm. Photos by J.-H. Hu

terms of major *Mallocybe* taxa. We also observed that the taxa in this clade are associated with a diverse range of plants, including

angiosperms and gymnosperms. To date, most taxa in this clade have been described from Europe and North America. Few taxa

have yet been described from East Asia. Interestingly, clade B (PP = 1/BP = 100%) comprises 11 accessions corresponding to at least five known species from Australia. These five species have been reported to have associations with *Eucalyptus*, *Allocasuarina*, and *Acacia* in temperate/tropical Australia (Matheny and Bougher 2017). Clade C, which includes the three new species described in the present paper, is also strongly supported (PP = 1/BP = 100%) in our phylogenetic tree.

Species with elongate-ellipsoid basidiospores and long cheilocystidia

Mallocybe species usually have catenate, thin-walled cheilocystidia. In this paper, we described three new *Mallocybe* species with elongate, thin-walled cheilocystidia. Our phylogenetic analysis placed these species in clade C along with three interesting North American species. The first species, *Mallocybe unicolor*, originally described from New York, is common under *Quercus* and widely distributed in eastern North America (Matheny 2014). Second, *M. multispora* (Murrill) Matheny & Esteve-Rav., first described from Florida (USA), occurs in open and mixed woods and is sister to *M. unicolor* in the phylogenetic tree. The species has oblong-ellipsoid basidiospores measuring 10–13 × 4–6 μm (Murrill 1945). Two unpublished sequences (MZ404934 and MN178509) of *M. multispora* identified by Dr. Matheny were collected in Florida and Oklahoma (USA), respectively, reflecting the subtropical to temperate distribution of this species in North America. Finally, *M. fulviceps* (Murrill) Matheny & Esteve-Rav., originally described from Florida, likewise has elongate-ellipsoid basidiospores measuring 10–12 × 5–6 μm, but detailed morphological features were not provided in the original description (Murrill 1945).

Acknowledgements We thank Dr. Yu-Peng Ge and Dr. Qin Na (Ludong University) for providing valuable specimens and valuable references, and Mr. Chuang-Teng Huang (Hainan Academy of Forestry & Hainan Academy of Mangrove) for his kind help in the identification of host plants.

Author contribution Conceptualization: Y-G.F. and T.B. Methodology: Y-G.F. Performing the experiment: J-H.H. Formal analysis: J-H.H., W-J.Y., and L-S.D. Resources: Y-G.F., L-P.T., C-Y. D., W-F.L., and T.B. Writing—original draft preparation: J-H.H. and W-J.Y. Writing—review and editing: Y-G.F. and T.B. Supervision: Y-G.F. and T.B. Project administration: Y-G.F. Funding acquisition: Y-G.F., C-Y.D., and L-S.D. All authors have read and agreed to the published version of the manuscript.

Funding This study was supported by the National Natural Science Foundation of China (Nos. 31860009 & 32260005), the Hainan Basic and applied research project for cultivating high-level talents (No. 2019RC230), the Project of Science and Technology Programs of Guizhou province [(2019)2451-2], and the Innovative Research Projects for Graduate Students in Hainan Province, China (No. HYYB2022A29).

Data availability The sequence data generated in this study are deposited in NCBI GenBank. The final alignment was included in Supplemental Material.

Declarations

Ethics approval and consent to participate Not applicable.

Conflict of interest The authors declare that no competing interests.

References

- Aignon HL, Naseer A, Matheny BP, Yorou NS, Ryberg M (2021) *Mallocybe africana* (Inocybaceae, Fungi), the first species of *Mallocybe* described from Africa. *Phytotaxa* 478(1):49–60. <https://doi.org/10.11646/phytotaxa.478.1.3>
- Ariyawansa HA, Hyde KD, Jayasiri SC, Buyck B, Chethana KWT, Dai DQ, Dai YC, Daranagama DA, Jayawardena RS, Lücking R, Ghobad-Nejhad M, Niskanen T, Thambugala KM, Voigt K, Zhao RL, Li G-J, Doilom M, Boonmee S, Yang ZL et al (2015) Fungal diversity notes 111–252—taxonomic and phylogenetic contributions to fungal taxa. *Fungal Divers* 75(1):27–274. <https://doi.org/10.1007/s13225-015-0346-5>
- Bandini D, Oertel B, Eberhardt U (2022) Noch mehr Risspilze (3): Einundzwanzig neue Arten der Familie Inocybaceae. *Mycologia Bavarica* 22:31–138
- Brugaletta E, Consiglio G, Marchetti M (2017) *Inocybe siciliana*, una nuova specie del Sottogenere *Mallocybe*. *Riv Micol* 60(3):195–209
- Cho SE, Kwag YN, Han SK, Kim CS (2021) Seven newly recorded macrofungi of Inocybaceae (Agaricales, Basidiomycota) in Korea. *Kor J Mycol* 49(2):139–153
- Cripps CL, Larsson E, Horak E (2010) Subgenus *Mallocybe* (*Inocybe*) in the Rocky Mountain alpine zone with molecular reference to European arctic-alpine material. *N Am Fungi* 5(5):97–126
- Crous PW, Wingfield MJ, Chooi Y-H, Gilchrist CLM, Lacey E, Pitt JJ, Roets F, Swart WJ, Cano-Lira JF, Valenzuela-Lopez N, Hubka V, Shivas RG, Stehlig AM, Holdom DG, Jurjević Ž, Kachalkin AV, Lebel T, Lock C, Martín MP et al (2020) Fungal planet description sheets: 1042–1111. *Persoonia* 44:301–459. <https://doi.org/10.3767/persoonia.2020.44.11>
- Csizmar M, Cseh P, Dima B, Orlóci L, Bratek Z (2021) Macrofungi of urban *Tilia* avenues and gardens in Hungary. *Glob Ecol Conserv* 28: e01672
- Daskalopoulos V, Polemis E, Fryssouli V, Kottis L, Bandini D, Dima B, Zervakis GI (2021) *Mallocybe heimii* ectomycorrhizae with *Cistus creticus* and *Pinus halepensis* in Mediterranean littoral sand dunes—assessment of phylogenetic relationships to *M. arenaria* and *M. agaradhii*. *Mycorrhiza* 31(4):497–510. <https://doi.org/10.1007/s00572-021-01038-1>
- Deng LS, Yu WJ, Zeng NK, Liu LJ, Liu LY, Fan YG (2021a) *Inosperma subsphaerosporum* (Inocybaceae), a new species from Hainan, tropical China. *Phytotaxa* 502(2):169–178. <https://doi.org/10.11646/phytotaxa.502.2.5>
- Deng LS, Kang R, Zeng NK, Yu WJ, Chang C, Xu F, Deng WQ, Qi LL, Zhou YL, Fan YG (2021b) Two new *Inosperma* (Inocybaceae) species with unexpected muscarine contents from tropical China. *MycKeys* 85:87–108. <https://doi.org/10.3897/mycokeys.85.71957>
- Fan YG, Bau T (2016) Taxonomy in *Inocybe* subgen. *Mallocybe* from China. *J Fungal Res* 14:129–141
- Gardes M, Bruns TD (1993) ITS primers with enhanced specificity for basidiomycetes—application to the identification of mycorrhizae and rusts. *Mol Ecol* 2(2):113–118. <https://doi.org/10.1111/j.1365-294X.1993.tb00005.x>

- Ge YP, Liu Z, Zeng H, Cheng X, Na Q (2021) Updated description of *Atheniella* (*Mycenaceae*, *Agaricales*), including three new species with brightly coloured pilei from Yunnan Province, southwest China. *MycKeys* 81(3):139–164. <https://doi.org/10.3897/mycokeys.139.67773>
- Hall TA (1999) BioEdit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. *Nucleic Acids Symp Ser (Oxf)* 41(41):95–98
- Horak E, Matheny PB, Desjardin DE, Soyong K (2015) The genus *Inocybe* (*Inocybaceae*, *Agaricales*, *Basidiomycota*) in Thailand and Malaysia. *Phytotaxa* 230(3):201–238. <https://doi.org/10.11646/phytotaxa.230.3.1>
- Jean EC, Wang PM, Martin R, Nourou SY, Yang ZL (2022) *Amanita* sect. *Phalloideae*: two interesting non-lethal species from West Africa. *Mycol Prog* 21(3):39. <https://doi.org/10.1007/s11557-022-01778-0>
- Katoh K, Rozewicki J, Yamada KD (2019) MAFFT online service: multiple sequence alignment, interactive sequence choice and visualization. *Brief Bioinform* 20(4):1160–1166. <https://doi.org/10.1093/bib/bbx108>
- Kobayashi T (2002) Notes on the genus *Inocybe* of Japan: I. *Mycoscience*. 43(3):207–211
- Kobayashi T (2005) Notes on the genus *Inocybe* of Japan: III. *Mycoscience* 46(3):184–191
- Kornerup A, Wanscher JH (1978) *The methuen handbook of colour*, 3rd edn. Eyre Methuen, London
- Kuo M (2017) *Inocybe unicolor*. Retrieved from the MushroomExpert. Com Web site: http://www.mushroomexpert.com/inocybe_unicolor.html. Accessed 15 May 2022
- Kuyper TW (1986) A revision of the genus *Inocybe* in Europe 1. Subgenus *Inosperma* and the smooth-spored species of subgenus *Inocybe*. *Persoonia* 3:1–247
- Liu Z, Qin NA, Cheng X, Wu XM, Ge YP (2021) *Mycena yuezhui* sp. nov. (*Mycenaceae*, *Agaricales*), a purple species from the peninsula areas of China. *Phytotaxa* 511(2):148–162. <https://doi.org/10.11646/phytotaxa.511.2.3>
- Ludwig E (2017) *Pilzkompodium*. Band 4 (two parts). Fungicon Verlag, Berlin
- Mao N, Xu YY, Zhao TY, Lv JC, Fan L (2022) New species of *Mallocybe* and *Pseudosperma* from North China. *J Fungi (Basel)* 8(3):256. <https://doi.org/10.3390/jof8030256>
- Matheny PB (2005) Improving phylogenetic inference of mushrooms with RPB1 and RPB2 nucleotide sequences (*Inocybe*, *Agaricales*). *Mol Phylogenet Evol* 35(1):1–20. <https://doi.org/10.1016/j.ympev.2004.11.014>
- Matheny PB (2014) *Mallocybe unicolor* and other *Inocybes* in North America. The mycophile: newsletter of the North American Mycological Association. 52(2):6–13. <https://namyco.org/docs/MycophileMar-Apr2014.pdf>. Accessed 12 May 2022
- Matheny PB, Bougher NL (2017) *Fungi of Australia: Inocybaceae*. CSIRO Publishing, Canberra
- Matheny PB, Kudzma LV (2019) New species of *Inocybe* (*Inocybaceae*) from eastern North America. *J Torrey Bot Soc* 146(3):213–235. <https://doi.org/10.3159/TORREY-D-18-00060.1>
- Matheny PB, Aime MC, Bougher NL, Buyck B, Desjardin DE, Horak E, Kropp BR, Lodge DL, Soyong K, Trappe JM, Hibbett DS (2009) Out of the Palaeotropics? Historical biogeography and diversification of the cosmopolitan ectomycorrhizal mushroom family *Inocybaceae*. *J Biogeogr* 36(4):577–592
- Matheny PB, Hobbs AM, Esteve-Raventós F (2020) Genera of *Inocybaceae*: new skin for the old ceremony. *Mycologia* 112(1):83–120. <https://doi.org/10.1080/00275514.2019.1668906>
- Murrill WA (1945) New Florida fungi. *Q J Fla Acad Sci* 8(2):175–198
- Na Q, Liu Z, Zeng H, Cheng X, Ge YP (2021) *Crepidotus yuanchui* sp. nov. and *C. caspari* found in subalpine areas of China. *Mycoscience* 63:1–11. <https://doi.org/10.47371/mycosci.2021.10.004>
- Na Q, Hu YP, Zeng H, Song ZZ, Ding H, Cheng XH, Ge YP (2022) Updated taxonomy on *Gerronema* (*Porothelaeaceae*, *Agaricales*) with three new taxa and one new record from China. *MycKeys* 89:87–120. <https://doi.org/10.3897/mycokeys.89.79864>
- Nylander J (2004) MrModeltest V2. Program distributed by the author. *Bioinformatics* 24:581–583
- Osmundson TW, Robert VA, Schoch CL, Baker LJ, Smith A, Robich G, Mizzan L, Garbelotto MM (2013) Filling gaps in biodiversity knowledge for macrofungi: contributions and assessment of an herbarium collection DNA barcode sequencing project. *PLoS One* 8(4):e62419
- Palmer JM, Lindner DL, Volk TJ (2008) Ectomycorrhizal characterization of an American chestnut (*Castanea dentata*)-dominated community in Western Wisconsin. *Mycorrhiza* 19(1):27–36
- Ronquist F, Teslenko M, van der Mark P, Ayres DL, Darling A, Höhna S, Larget B, Liu L, Suchard MA, Huelsenbeck JP (2012) MrBayes 3.2: efficient Bayesian phylogenetic inference and model choice across a large model space. *Syst Biol* 61:539–542
- Roy M, Yagame T, Yamato M, Iwase K, Heinz C, Faccio A, Bonfante P, Selosse M-A (2009) Ectomycorrhizal *Inocybe* species associate with the mycoheterotrophic orchid *Epipogium aphyllum* but not its asexual propagules. *Ann Bot* 104:595–610
- Ryberg M, Nilsson RH, Kristiansson E, Töpel M, Jacobsson S, Larsson E (2008) Mining metadata from unidentified ITS sequences in GenBank: a case study in *Inocybe* (*Basidiomycota*). *BMC Evol Biol* 8(1):50
- Ryberg M, Larsson E, Jacobsson S (2010) An evolutionary perspective on morphological and ecological characters in the mushroom family *Inocybaceae* (*Agaricomycotina*, *Fungi*). *Mol Phylogenet Evol* 55(2):431–442
- Saba M, Khalid AN (2020) *Mallocybe velutina* (*Agaricales*, *Inocybaceae*), a new species from Pakistan. *Mycoscience* 61(6):348–352. <https://doi.org/10.1016/j.myc.2020.06.006>
- Stangl J (1989) Die Gattung *Inocybe* in Bayern. *Hoppea* 46:1–409
- Trifinopoulos J, Nguyen LT, von Haeseler A, Minh BQ (2016) W-IQ-TREE: a fast online phylogenetic tool for maximum likelihood analysis. *Nucleic Acids Res* 44(W1):W232–W235. <https://doi.org/10.1093/nar/gkw256>
- Vauras J, Larsson E (2011) *Inocybe myriadophylla*, a new species from Finland and Sweden. *Karstenia* 51(2):31–36
- Vilgalys R, Hester M (1990) Rapid genetic identification and mapping of enzymatically amplified ribosomal DNA from several *Cryptococcus* species. *J Bacteriol* 172(8):4238–4246. <https://doi.org/10.1128/JB.172.8.4238-4246.1990>
- Wang SN, Hu YP, Chen JL, Qi LL, Zeng H, Ding H, Huo GH, Zhang LP, Chen FS, Yan JQ (2021) First record of the rare genus *Typhrasa* (*Psathyrellaceae*, *Agaricales*) from China with description of two new species. *MycKeys* 79:119–128. <https://doi.org/10.3897/mycokeys.79.63700>
- Yu WJ, Chang C, Qin LW, Zeng NK, Wang SX, Fan YG (2020) *Pseudosperma citrinostipes* (*Inocybaceae*), a new species associated with *Keteleeria* from southwestern China. *Phytotaxa* 450(1):8–16. <https://doi.org/10.11646/phytotaxa.450.1.2>

Publisher's note Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.

Springer Nature or its licensor (e.g. a society or other partner) holds exclusive rights to this article under a publishing agreement with the author(s) or other rightsholder(s); author self-archiving of the accepted manuscript version of this article is solely governed by the terms of such publishing agreement and applicable law.