Phytotaxa 584 (2): 104–114
https://www.mapress.com/pt/

Article

ISSN 1179-3155 (print edition)
PHYTOTAXA
ISSN 1179-3163 (online edition)

https://doi.org/10.11646/phytotaxa.584.2.3

Xerocomellus perezmorenoi (Boletaceae, Boletales), a new edible species from Mexico

MAGDALENA MARTÍNEZ-REYES[1,2], ANAITZI CARRERA-MARTÍNEZ[1,3], JAVIER ISAAC DE LA FUENTE[1,4], UZZIEL RÍOS-GARCÍA[1,5], IVETTE ORTIZ-LOPEZ[1,6] & OLIVIA AYALA-VÁSQUEZ[1,7]*
[1] *Colegio de Postgraduados, Km 36.5, Montecillo, Texcoco, estado de México, C.P. 56230, Mexico*
[2] *martinezreyes2012@gmail.com; https://orcid.org/0000-0003-2352-917X*
[3] *anaitzicm@gmail.com; https://orcid.org/0000-0002-8184-0217*
[4] *jdelafuenteitcv@gmail.com; https://orcid.org/0000-0003-4667-1574*
[5] *uzzielriosg@gmail.com; https://orcid.org/0000-0002-5026-1968*
[6] *ivetteortiz136@gmail.com; https://orcid.org/0000-0002-5101-9663*
[7] *yootspooj@gmail.com; https://orcid.org/0000-0002-8970-9571*
**Author for correspondence*

Abstract

Xerocomellus perezmorenoi (Boletaceae, Boletales) is described as a new species from Mexico. This species was collected under *Abies religiosa* in mixed coniferous forest located in three localities (Puebla, Tlaxcala, and State of Mexico) in central Mexico. It is morphologically characterized by its small-sized basidiomata, pileus brown at the center and cream with pink to purple tones at the margin, almost blackish at the center when young, black-brown when mature, pores lilac, peach to salmon when young, yellow citrine at mature; violet or violet-brown color reaction of the context when cut; basidiospores (12–) 15–16 (–17) × 4–5 (–6) µm. Phylogenetic analyses (Maximum likelihood and Bayesian inference) based on multi-locus sequences confirmed X. *perezmorenoi* is a new species, with biocultural importance due to edibility. Detailed a description, photographs, analyses of phylogenetics, and taxonomic discussions are presented.

Keywords: *Abies religiosa*, *boletes*, *central Mexico*, *ectomycorrhizal fungi*

Introduction

Xerocomellus Šutara, the “cracked-cap boletes”, is a genus recently separated from *Xerocomus* due to its morphological and molecular differences (Šutara 2008, Wu *et al*. 2016, Frank *et al*. 2020). Macroscopically, species of *Xerocomellus* displays red to purple red tinged pileus and stipe, dry and subtomentose pileal surface and angular and large pores. Meanwhile, the microscopic features are smooth to ornamented spores, palisadoderm pileipellis displaying sometimes incrusted hyphal elements (Smith *et al*. 2018, Wu *et al*. 2016). *Xerocomellus* has medicinal importance and edibility. Ozgur *et al*. (2021) mention that it has antimicrobial properties, anticancer activity, mainly colon cancer. Currently, eight edible species are known worldwide, Li *et al*. (2021). Around 14 species are estimated in North America, and 12 in Europe and Asia. They form ectomycorrhizal associations with *Cedrus deodara* (Hernández-Restrepo *et al*. 2016), *Quercus agrifolia* Née, *Notholithocarpus densiflorus* (Hook. & Arn.) Manos, Cannon & S. H, sometimes with *Chrysolepis chrysophylla* (Douglas ex Hook.) Hjelmq., *Betula pendula* Roth, (Frank *et al*. 2020), *Abies* sp. Mill. (Ayala-Vásquez 2021).

In Mexico, three species of the genus have been described. *Xerocomellus truncatus* (Singer, Snell & E. A. Dick) Klofac is characterized by pileus 50–105 mm, dry, tomentose, areolate surface, these areolas show the yellowish color of the context, of variable color from pale brown, brown, olive brown, grayish brown, olive gray or pinkish; distributed mainly in the Transversal Neovolcanic Axis and the Sierra Madre del Sur, associated mainly with *Abies* (Ayala-Vásquez 2021, Saldivar *et al*. 2021); *X. dryophilus* (Thiers) N. Siegel, C.F. Schwarz & J.L. Frank, is characterized by pileus 30–110 mm, rosy red, brick-red when fresh, becoming dull tan-brown with pinkish or reddish tones in dry weather, described from Baja California state associated with *Quercus agrifolia* (Ayala-Sánchez *et al*. 2015) and *X. carmeniae* (Garza-Ocañas, J. García & de la Fuente) recently described from Northeast Mexico, the species is characterized by an aberrant basidioma, basidiospores 10.5–13.6 × 5.7–7.8 µm truncate, elongate, brown in KOH and Meltzer, guttulate,

Accepted by Samantha C. Karunarathna: 9 Jan. 2023; published: 14 Feb. 2023

sometimes truncate, smooth and thick-walled, in *Pinus-Quercus* forest under *Quercus canbyi*. So far it is the only species described with molecular data (Garza-Ocaña *et al.* 2022).

In recent explorations of fungi in a mixed coniferous forest dominated from central Mexico, some interesting boletes were collected. The result of two years sampling, morphological and molecular studies confirm that collected specimens represent an undescribed species within *Xerocomellus*.

Material and methods

Sample collection and morphological study

Fresh basidiomata were collected from 2020 to 2021, especially during June to December in municipalities of Nanacamilpa, Tlaxcala (3286 m), San Juan Cuauhtemoc, Tlahuapan, Puebla (2782 m), and Ocuilan State of Mexico (2361 m). The type of vegetation in the sampling areas is a mixed coniferous forest dominated by *Abies religiosa* (Kunth) Schltdl. et Cham. Basidiomata were sampled following Lodge *et al*. (2004). Descriptions were obtained following Largent (1986). The color notations were according to Kornerup and Wanscher (1978). Hand-made cuts from the dried samples were rehydrated in 5% potassium hydroxide (KOH) and stained in Melzer's solution. Microscopic characters of 30 basidiospores, basidia, pleurocystidia, cheilocystidia, pileipellis, and stipitipellis were measured by optical microscopy (Carl Zeiss GmbH 37081, Germany). The Q index (length/width) was estimated for the basidiospores. The studied materials were deposited in the mycological herbarium MEXU (UNAM). Also, samples of parasitized specimens were taken and sent for sequencing.

DNA extraction, amplification, sequencing, and phylogenetic analyses

Genomic DNA was obtained from 2–3 mg of dry tissue using a cetyltrimethyl ammonium bromide (CTAB) procedure according to Martínez-González *et al*. (2017). DNA quantification was performed with Nanodrop (Thermo, USA). The Internal Transcribed Spacer (ITS) and the ribosomal large subunit (LSU) loci were amplified using the pair of primers ITS5-ITS4 (White *et al*. 1990),LROR and LR5 (Vilgalys & Hester 1990), rpb1, rpb2, and tef1-α, the commonly used primer pairs RPB1-Af/fRPB1-Cr, bRPB2-6F/bRPB2-7.1R, EF1-F/EF1-R, and EF1-595F/EF1- 1160R (Matheny *et al*. 2002; Mikheyev *et al*. 2006; Wu *et al*. 2014. The PCR reaction contained the following: enzyme buffer 1 x, Taq DNA polymerase, 0.8 mM deoxynucleoside triphosphates (0.2 mM each), 100 ng DNA, 20 pmol of each primer, and 2 units of GoTaq DNA (Promega, USA), with a final volume of 15 µL. The PCR products were verified by agarose gel electrophoresis run for 1 h at 95 V cm–3 in 1.5% agarose and 1 x TAE buffer (Tris Acetate-EDTA). The products were then dyed with GelRed (Biotium, USA) and viewed in a transilluminator (Infinity 3000 Vilber, Loumat, Germany). PCR products were run on 1.5% agarose gel. Finally, the products were purified using the ExoSap Kit (Affymetrix, USA) according to the manufacturer's instructions and were prepared for the sequencing reaction using the BigDye Terminator Cycle Sequencing Kit v. 3.1 (Applied BioSystems). The sequencing of purified PCR products was carried out by Macrogen Inc, Seoul, Korea.

Sequence assembly

The sequences of both strands of each gene were analyzed, edited, and assembled using BioEdit version 7.0.5 (Hall, 1999) to generate a consensus sequence. These consensus sequences were compared with those deposited in the GenBank of the National Center for Biotechnology Information (NCBI), using the tool BLASTN 2.2.19 (Zhang *et al.* 2000).

Phylogenetic analyses

To study phylogenetic relationships, our newly produced sequences of three individuals of *Xerocomellus* were added to reference sequences of ITS, LSU, rpb1, rpb2 and tef1 deposited in the NCBI database (http://www.ncbi.nlm.nih.gov/genbank/). Each gene region was independently aligned using the online version of MAFFT v7 (Katoh *et al*. 2002; 2017; Katoh & Standley, 2013). Alignments were reviewed in PhyDE V. 10.0 (Müller *et al*., 2005), followed by minor manual adjustments to ensure character homology between taxa. The matrices were formed for ITS by 53 taxa (705 characters), for LSU by 49 taxa (592 characters), for rpb1 by 22 taxa (883 characters), for rpb2 by 21 taxa (775 characters); while *tef1* consisted of 23 taxa (895 characters). The aligned matrices were concatenated into a single matrix (78 taxa, 3850 characters) with Mesquite v3.2 (Maddison & Maddison 2021). Eight partitioning schemes were established: one for the ITS, one for the LSU, three to represent the codon positions of the gene region rpb1 and three for tef1 gene region, which were established using the option to minimize the stop codon with Mesquite v. 3.70 (Maddison & Maddison 2021). Phylogenetic inferences were estimated with maximum likelihood in Rax-ML v. 8.2.10 (Stamatakis 2014) with a GTR + G model of nucleotide substitution. To assess branch support, 1000 rapid bootstrap replicates were run with the GTRCAT model. For Bayesian posterior probability, the best evolutionary model for alignment was sought using PartitionFinder v.2 (Lanfear *et al.* 2014; 2017; Frandsen *et al*. 2015). Phylogenetic analyses were performed using MrBayes v. 3.2.6 x64 (Huelsenbeck & Ronquist 2001). The information block for the matrix included two simultaneous runs, four Montecarlo chains, temperature set to 0.2 and sampling 10 million generations (standard deviation ≤0.1) with trees sampled every 1000 generations. The first 25% of samples were discarded as burn-in, and stationarity was checked in Tracer v. 1.6 (Rambaut *et al*. 2014). Trees were visualized and optimized in FigTree v. 1.4.4 (Rambaut 2014).

TABLE 1. GenBank accession number of the ITS, LSU, RPB2, RPB1 and TEF1 sequences used in the phylogenetic analyses; the country and the references. NA refers to data not available.

Taxon	**Voucher**	**Country**	**ITS**	**LSU**	**RPB2**	**RPB1**	**TEF1**	**References**
Xerocomellus amylosporus	JLF3012	USA	KM213635	KU144742	NA	NA	NA	Frank *et al*. 2020
X. amylosporus	HDT13163	USA	KU144744	NA	NA	NA	NA	Frank *et al*. 2020
X. amylosporus	AHS70936	USA	KU144741	NA	NA	NA	NA	Frank *et al*. 2020
X. amylosporus	JLF3498	USA	NA	NA	NA	MW737514	NA	Farid *et al*. 2021
X. atropurpureus	JLF2795	USA	KM213638	KM213639	NA	NA	NA	Frank *et al*. 2020
X. atropurpureus	NY1193858	USA	NA	KF030271	NA	KF030366	KF030416	Nuhn *et al*. 2013
X. atropurpureus	NS120712	USA	KM213641	KM213642	NA	NA	NA	Frank *et al*. 2020
X. atropurpureus	JLF3620	USA	NA	NA	MW737477	MW737517	MW737495	Farid *et al*. 2021
X. atropurpureus	JLF4664	USA	KY659589	NA	NA	NA	NA	Frank *et al*. 2020
X. bolinii	JAB_133_	USA	MW675729	NA	NA	NA	NA	Farid *et al*. 2021
X. bolinii	JAB_95	USA	MW675735	MW662589	MW737472	MW737511	MW737491	Farid *et al*. 2021
X. bolinii	JAB_110	USA	MW675728	NA	NA	MW737507	NA	Farid *et al*. 2021
X. carmeniae	18219 ITCV	Mexico	ON392096	ON254917	NA	NA	NA	Garza-Ocaña *et al*. 2022
X. carmeniae	5193 ITCV	Mexico	ON392097	ON254918	NA	NA	NA	Garza-Ocaña *et al*. 2022
X. carmeniae	5194 ITCV	Mexico	ON392098	ON254919	NA	NA	NA	Garza-Ocaña *et al*. 2022
X. cisalpinus	LUGO: ECC19102906	Spain	MW376718	NA	NA	NA	NA	GenBank
X. cisalpinus	KR-M-0044831	Germany	MT006036	NA	NA	NA	NA	Genbank
X. cisalpinus	PDD94421	New Zealand	NA	JQ924322	KF112686	NA	KF112171	Wu *et al*. 2014
X. cisalpinus	AT2005034	Finland	NA	KF030354	NA	KF030367	KF030417	Nuhn *et al.*
X. communis	HKAS50467	China	NA	KT990670	KT990494	KT991008	KT990858	Wu *et al*. 2016
X. communis	HKAS68204	China	NA	KT990671	KT990495	KT991009	KT990859	Wu *et al*. 2016
X. corneri	HKAS52503	China	NA	KT990668	KT990492	KT991006	KT990856	Wu *et al*. 2016
X. corneri	HKAS90206	Philippines	NA	KT990669	KT990493	KT991007	KT990857	Wu *et al*. 2016

......continued on the next page

TABLE 1 (Continued)

Taxon	Voucher	Country	ITS	LSU	RPB2	RPB1	TEF1	References
X. cf. chrysenteron	338913	USA	ON705310	ON705310	NA	NA	NA	GenBank
X. chrysenteron	HKAS:56494	Germany	NA	KF112357	KF112685	NA	KF112172	Wu *et al*. 2014
X. chrysenteron	MICH:KUO-07271202	USA	NA	NA	MK766373	NA	MK721171	Kuo &Ortíz-Santana 2020
X. chrysenteron	DQ533981	USA	DQ533981	NA	NA	NA	NA	Frank *et al*. 2020
X. chrysenteron	MICH:KUO-09260903	USA	NA	NA	MK766374	NA	MK721172	Kuo and Ortíz-Santana 2020
X. chrysenteron	18177	Italy	JF908799	NA	NA	NA	NA	Osmundson *et al*. 2013
X. cf. chrysenteron	JLF5684	USA	MH168533	MH168533	NA	NA	NA	Frank *et al*. 2020
X. diffractus	NS120612	USA	KM213650	KM213651	NA	NA	NA	Frank *et al*. 2020
X. diffractus	JLF3554	USA	KU144769	KU144770	NA	NA	NA	Frank *et al*. 2020
X. diffractus	JLF5745	USA	MH168534	NA	NA	MW737519	NA	Farid *et al*. 2021
X. dryophilus	CFS3Nov11-2	USA	KM213645	KX534074	NA	NA	NA	Frank *et al*. 2020
X. dryophilus	JLF4134	USA	KX534076	KY659593	NA	MW737478	MW737493	Farid *et al*. 2021
X. dryophilus	CSZVM_SCI_77	USA	KM213646	NA	NA	NA	NA	Frank *et al*. 2020
X. fennicus	VP-10	Latvia	KT692929	NA	NA	NA	NA	Klavina *et al*.2016
X. fennicus	H126	Austria	NA	AF514820	NA	NA	NA	Peintner *et al*. 2003
X. fennicus	RJ126	Austria	NA	AF514821	NA	NA	NA	Peintner *et al*. 2003
X. mendocinensis	JLF2775	USA	KM213653	KM213654	NA	NA	NA	Frank *et al*. 2020
X. mendocinensis	CFS1Nov11_1	USA	KM213656	KM213657	NA	NA	NA	Frank *et al*. 2020
X. mendocinensis	CFS10Nov2012_1	USA	KM213659	KM213660	NA	NA	NA	Frank *et al*. 2020
X. mendocinensis	JLF3558	USA	KU144785	KU144786	NA	MW737476	NA	Frank *et al*. 2020
X. mendocinensis	HDT18392	USA	KM213655	NA	NA	NA	NA	
X. mendocinensis	JLF5684	USA	NA	NA	MW737480	MW737518	NA	Farid *et al*. 2021
X. perezmorenoi	**MEXU 30410**	**Mexico**	**OK350679**	**OK350681**	**OQ015646**	**OQ015753**	**OQ017656**	**In this study**
X. perezmorenoi	**MEXU 30411**	**Mexico**	**OK350680**	**OK350682**	**OQ015647**	**OQ015754**	**OQ017657**	**In this study**
X. perezmorenoi	**MEXU 30412**	**Mexico**	**OQ077193**	**OQ101206**	**OQ015648**	OQ015755	**OQ017658**	**In this study**
X. pruinatus	G.M. 2015-09-23	Germany	MW603181	MW603181	NA	NA	NA	GenBank
X. poederi	AH 44050	Spain	NR_155971	NG_060000	NA	NA	NA	Crous *et al*. 2016
X. poederi	ECC16100914	Spain	MW376719	NA	NA	NA	NA	Alonso-Diaz & Rigueiro-Rodriguez 2020
X. ripariellus	301	Spain	MN685108	NA	NA	NA	NA	GenBank
X. ripariellus	VDKO0404	Belgium	NA	NA	MH614793	NA	MH614746	Vadthanarat *et al*. 2019
X. rainisiae	JLF3523	USA	KU144789	KU144790	MW737475	MW737515	NA	Frank *et al*. 2020
X. rainisiae	OKM25915	USA	KM213664	NA	NA	NA	NA	Frank *et al*. 2020

......continued on the next page

TABLE 1 (Continued)

Taxon	Voucher	Country	ITS	LSU	RPB2	RPB1	TEF1	References
X. salicicola	CS_5Mar2014-1	USA	KU144791	KU144792	NA	NA	NA	Frank *et al*. 2020
X. salicicola	UCSC-F-1028	USA	KU144793	KU144794	NA	NA	NA	Frank *et al*. 2020
X. salicicola	B391	USA	MW675727	MW662569	NA	MW737496	NA	Farid *et al*. 2021
X. sarnarii	ML900101XE	Italy	MH011930	MH011930	NA	NA	NA	Loizides *et al*. 2019
X. sarnarii	MCVE 28577	Italy	NR_138006	NA	NA	NA	NA	Vizzini *et al*. 2016
X. truncatus	6397	USA	NA	DQ534625	NA	NA	NA	Frank *et al*. 2020
X. truncatus	NY13856	USA	KM213665		NA	NA	NA	Genbank
X. truncatus	285192	USA	ON705300	ON705300	NA	NA	NA	Genbank
X. zelleri	JLF2977	USA	KM213666	KU144799	NA	NA	NA	Frank *et al*. 2020
X. zelleri	W.A. Murrill 105	USA	KU144803	NA	NA	NA	NA	Frank *et al*. 2020
Hortiboletus arduinus	FHMU 3323	China	NA	NG_075378	NA	NA	MT646447	Xie *et al*. 2020
H. campestris	DD614	USA	MH168538	MH203598	NA	NA	NA	Frank *et al*. 2020
H. campestris	MICH KUO-08240502	USA	NA	MK601740	MK766302	NA	MK721094	Kuo & Ortiz-Santana 2020
H. napaeus	FHMU 3326	China	NA	NG_075379	NA	NA	MT646450	Xie *et al*. 2020
H. amygdalinus	HKAS54166	China	NA	KT990581	KT990416	KT990933	KT990777	Wu *et al*. 2016
H. rubellus	MICH KUO-06081002	USA	NA	MK601741	MK766303	NA	MK721095	Kuo & Ortiz-Santana 2020
Parvixerocomus pseudoaokii	HKAS 80480	China	NA	NG_059543	KP658470	KP658472	NA	Wu *et al*. 2016
P. matheranensis	AMH 9976	India	NA		MT140889	MT140888	MT140890	Patil *et al*. 2021
Rheubarbariboletus armeniacus	AJ419221	Spain	AJ419221	AJ419221	NA	NA	NA	Martin &Raidl 2002
R. persicolor	SOMF28154	Bulgaria	MH011932	NA	NA	NA	NA	Loizides *et al*. 2019
R. armeniacus	ML41842RP	Cyprus	MH011927	MH011927	NA	NA	NA	Loizides *et al*. 2019
R. persicolor	SOMF29860	Greece	MH011931	NA	NA	NA	NA	Loizides *et al*. 2019

Results

Phylogenetic analyses

In this study, 15 sequences were generated (three ITS, three LSU, three RBP2, three RPB1, and three TEF1) and deposited in GenBank (Table 1). The *Xerocomellus* dataset is shown with 53 ITS sequences with 705 characters, 49 LSU sequences with 592 characters, 21 RPB2 sequences with 775 characters, 22 RPB1 sequences with 883 characters and 23 TEF1 with 895 characters. The Bayesian inference topology is presented with bootstrap support, having *Hortiboletus* spp., *Parvixerocomus* spp., and *Rheubarbariboletus* spp. as an outgroup. (Fig. 1). Phylogenetic analysis shows that the genus *Xerocomellus* is monophyletic and *Xerocomellus perezmorenoi* is a new species with support of 1BPP/100MLB is sister to a clade formed by *Xerocomellus salicicola*.

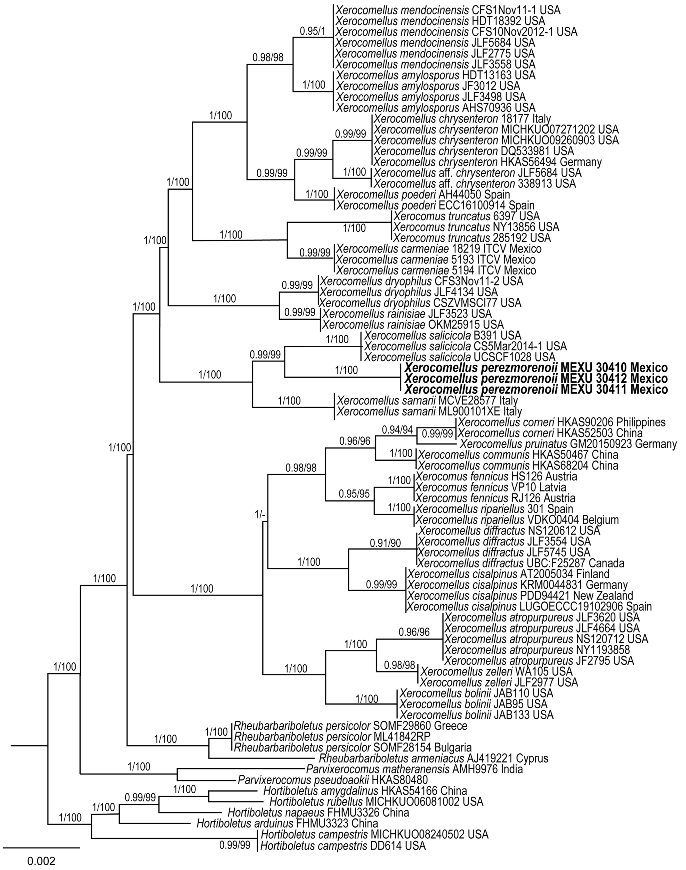

FIGURE 1. Concatenated multi-locus phylogenetic analysis (ITS, LSU, RPB1, RBP2, TEF1); The tree shows the topology of Bayesian analysis, with both MLB (≥ 90%) and BPP (≥ 0.9) clade support given, the new species is shown in bold color; having *Hortiboletus*, *Parvixerocomus* and *Rheubarbariboletus* as an outgroup.

Taxonomy

Xerocomellus perezmorenoi Ayala-Vásquez & M. Martínez-Reyes, *sp. nov*. (Fig. 2, 3)

Mycobank no. 841765. GenBank no. OK350679 (ITS), OK350681 (LSU).

Type:—MEXICO. Tlaxcala State, Nanacamilpa Municipality, San Felipe Hidalgo Town, Piedra Canteada place, 0539120 W, 2151906 N, 3285 m. a. s. l., 23 August 2021, Ayala-Vásquez (MEXU-HO 30410).

Diagnosis:—*Xerocomellus perezmorenoi* is characterized by small basidiomata; pileus brown at the center and cream with pink to purple tones at the margin, almost blackish at the center when young, black-brown when at mature, pores lilac, peach to salmon when young, yellow citrine at mature; basidiospores (12–) 15–16 (–17) × 4–5 (–6) µm, ellipsoid-fusoid.

Description:—*Basidiomata* pileate-stipitate, epigeous. *Pileus* 14–50 mm diam, broadly convex when young, plane-convex at maturity, pink, cream to purple tones (14A3) at the margin, brown (5F5) at the center, almost blackish at the center when young, dark-brown (5F8) when at mature, *pileus surface* tomentose to areolate when young, with a cracking brown (5F4) to dark-brown (5F8) showing yellowish (4A5) flesh at mature, sterile margin incurvated. *Hymenophore* annexed, pores 0.3–1.0 mm diameter, irregular, circular to angular pale purplish (14A3) when immature, pale pink to salmon when young, yellow citrine (4A8) some pastel red (9A4–9A5) tones in the terminal pores of the apex of the stipe at maturity, when cut bruising pale-green (28A3) to olivaceus (30D5). *Tubes* 3–9 mm in length, purplish (14A3) when young, turning yellow (4A8) when mature, when bruising or when bruising or cut pale green (28A3). *Context* 2–7 mm thick, whitish to vinaceous (12D8) at immature, in a juvenile and mature stage with whitish, to the cut after two minutes is stained bluish-green (28A4); the context of the stipe, brown (5F4) at the base at immature, pale yellow (4A4) some olive-brown (30E8) at mature, the rest of the context whitish to pale yellow (4A4), to the cut it is stained bluish green (28A4). *Stipe* 28–63 × 7–8 mm, attenuated, subclavate to cylindrical; yellowish (4A5) at the apical, the rest of the salmon pink, pastel red (9A4–9A5), with purplish (14A4) tones when at immature, surface tomentose with appearance pulverulent at base, whitish to yellowish (4A3) mycelium. *Odor* and *taste* indistinct. *Chemical reaction* when applying KOH 10% on the surface pileus dark-red (9E8) to vinaceus (12D8), surface stipe ochraceous yellow(30C8), reddish tones to amber (5F8) hymenium and context.

FIGURE 2. *Xerocomellus perezmorenoi*. **A** (MEXU-HO 30411paratype), **D** (MEXU 30410-type). context of basidiomata; **B** (MEXU 30410-type), **E** (MEXU 30411 paratype). hymenophore; **C** surface of pileus (MEXU 30411 paratype); **F** basidiomata (MEXU 30412 paratype). Scale bars: 10 mm.

Basidiospores (12–) 15–16 (–17) × 4–5 (–6) µm, [Q = 2.4 ± 0.6] fusoid to subcylindrical, to cylindrical inside view, with or without distinctly suprahilar depression, smooth, yellowish-brown, multigutulate, thick wall 0.8–1.0 µm. *Basidia* 33–47 × 5–6 µm, clavate, with lipid content, hyaline to pale yellow, tetrasporic, sterigmata 3.4–5.0 × 1–2 µm. *Pleurocystidia* 35–60 (–68) × 5–6 µm, brown-yellowish, golden, some hyaline in KOH, obclavate, cylindrical, subfusoid, subclavate with visible granular content in Melzer. *Cheilocystidia* 50–55 × 9–11 µm, ventricose-fusoid, thick-walled, yellowish-brown in KOH, golden yellow in Melzer solution. *Hymenophoral trama* boletoid; with central cylindrical hyphae 7–11 µm hyaline to pale yellow, lateral hyphae 4–7 µm, cylindrical. *Pileipellis* 150–200 mm thick, trichoderm, with cylindrical, subfusoid, subclavate terminal cells, thick-walled yellow-brown in KOH, golden to yellow-brown in Melzer solution. *Caulocystidia* 13–23 × 4–8 (–12) µm, clavate, very scarce, mamillated to ovoid; *caulobasidioles* very scarce 23–27 × 8–10 µm, subclavate, hyaline in KOH to pale yellow, thin wall.

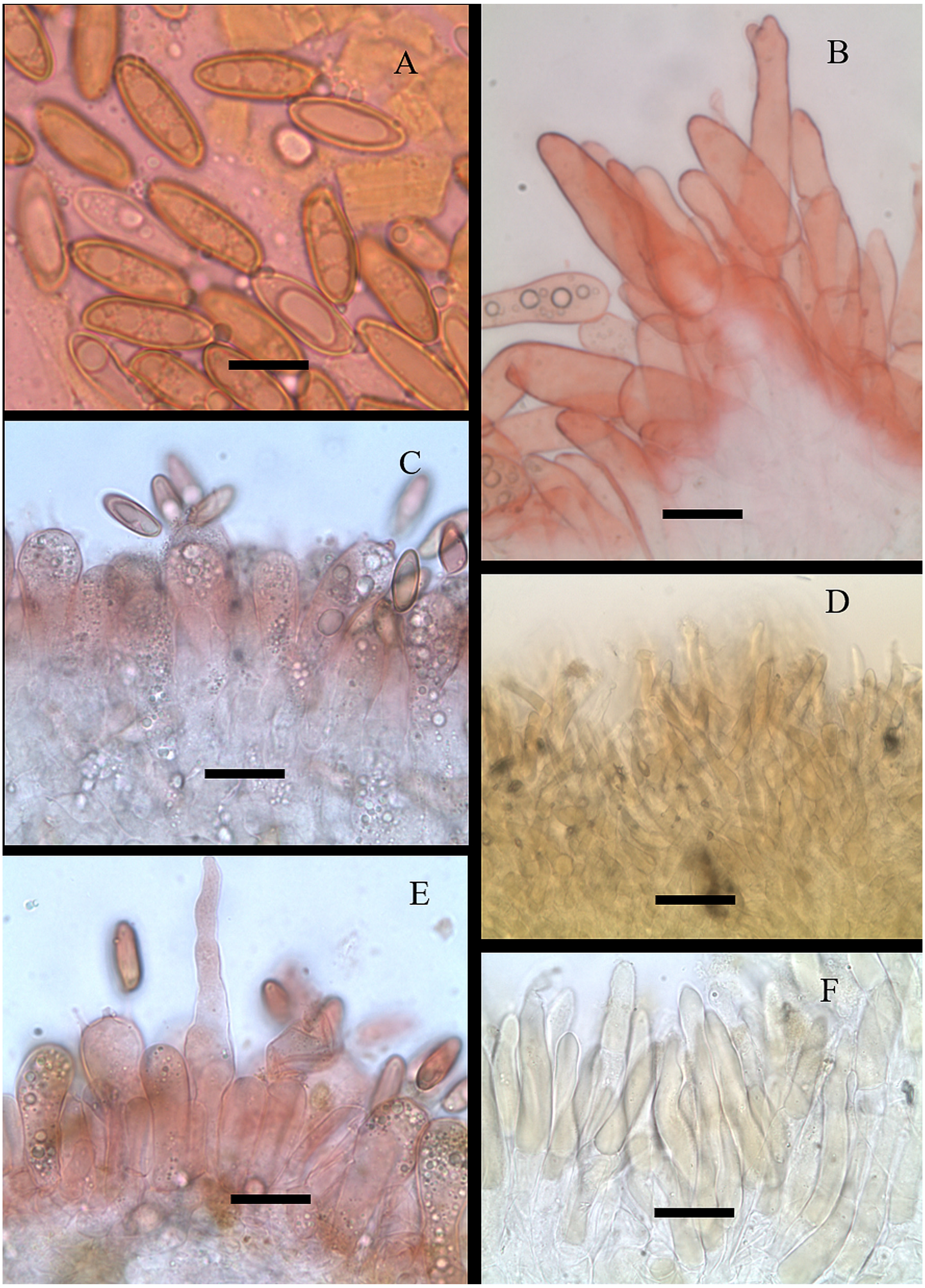

FIGURE 3. A basidiospores; **B** pleurocystidia; **C** basidia**; D** pileipellis; **E** cheilocystidia; **F** pileipellis**.** Scale bars: 10 µm. (MEXU 30410-type).

Etymology:—Dedicated to the eminent Mexican mycologist Prof. Jesús Pérez Moreno who is a pioneer in biotechnology of ectomycorrhizal fungi with biocultural importance in Mexico mainly Boletales and Agaricales, with more than 30 years of experience.

Distribution:—Epigeous, in mixed coniferous forest under *Abies religiosa*. Recorded from the Mexican state of Tlaxcala, State of Mexico and Puebla.

Additional material examined:—MEXICO. Tlaxcala State, Nanacamilpa Municipality, San Felipe Hidalgo Town, Piedra Canteada Place, 0539151W, 2151881N, 3286 m. a. s. l.,15 September 2021, Ayala-Vásquez, Ríos-García

(MEXU-HO 30411); Piedra Canteada Place, 0539151 W, 2151881N, 3286 m. a. s. l., 27 September 2021, Ayala-Vásquez (MEXU-HO 30450), Estado de Mexico State, Ocuilan Municipality, San Juan Atzingo Town, mixed forest Place, 18 September 2021, Martínez-Reyes M, (MEXU-HO 30412), Puebla, Santa Rita Tlahuapan Municipality, San Juan Cuauhtémoc Town, 28 September 2021, Ayala-Vásquez, O. Martínez-Reyes, (MEXU-HO 30449).

Dichotomous key of species the genus *Xerocomellus* described in Mexico

1a	Basidiomata epigeous to aberrant	*X. carmeniae*
1b	Basidiomata only epigeous	2
2a	pileus pink-red to vinaceous red, rosy red or brick-red, associated with *Quercus agrifolia*	*X. dryophilus*
2b	Pileus typically pale brown, brown, black brown to black	3
3a	Pores lilac, peach to salmon when young, yellow citrine at mature	*X. perezmorenoi*
3b	Pores yellow to yellow-olivaceous	*X. truncatus*

Comments:—*Xerocomellus perezmorenoi* differs from the rest of the species by Hymenophore pale lilac when immature, pale pink to salmon when young, yellow citrine some reddish tones, when cutting bruising green to olivaceus. Phylogenetically *Xerocomellus perezmorenoi* is related to *Xerocomellus salicicola*, however, the second species differs by the pileus dull red to brown, hymenophore dull yellow staining dingy blue, stipe nearly entirely red, often with obscure coarse reticulum at apex, associated with *Salix* spp., and in one case with *Populus trichocarpa*, occasionally in landscaped areas under *Betula pendula* from USA (Frank *et al*. 2020), while *Xerocomellus perezmorenoi* is associated with *Abies religiosa* from Transverse Neovolcanic Axis, Mexico. *Xerocomellus perezmorenoi* is relevant due to its biocultural importance, since some people from San Felipe Hidalgo, Tlaxcala, Mexico consume it, in addition, four of the six authors of this article confirmed its edibility. Also, a dichotomous key for the known species of *Xerocomellus* from Mexico is presented.

Acknowledgments

The authors thank the community members of Piedra Canteada for allowing us to carry out the research on their property. AVO thanks thank to CONACyT financial support, Id project:3129307, César Martínez-González, and Mariana Herrera. All authors thank the project CONACyT-PRONACES FOP07-2021-03 316198 for research support.

References

Alonso-Diaz, J. & Rigueiro-Rodriguez, A. (2020) *Catalogo da Macromicobiota das montanas do courel (Galicia, no Espana). Monografias do ibader. serie cuadernos da estacion cientifica do courel ibader*. Universidade de Santiago de Compostela. Spain.

Ayala-Sánchez, N., Soria-Mercado, I.E., Romero-Bautista, L., López-Herrera, M., Rico-Mora, R. & Portillo-López, A. (2015) *Los hongos Agaricales de las áreas de encino del estado de Baja California, México*. Estudios en Biodiversidad. 19. University of Nebraska, 315 pp.

Ayala-Vásquez, O. (2021) *Taxonomía, biogeografía y filogenia de los hongos del orden Boletales en la Sierra Norte de Oaxaca, México. Tesis de doctorado en Ciencias de la Biología*. Instituto Tecnológico de Ciudad Victoria, Tamaulipas, Mexico, 303 pp.

Crous, P.W., Wingfield, M.J., Richardson, D.M., Leroux, J.J., Strasberg, D., Edwards, J., Roets, F., Hubka, V., Taylor, P.W.J., Heykoop, M., Martín, M.P., Moreno, G., Sutton, D.A., Wiederhold, N.P., Barnes, C.W., Carlavilla, J.R., Gené, J., Giraldo, A., Guarnaccia, V., Guarro, J., Hernández-Restrepo, M., Kolařík, M., Manjón, J.L., Pascoe, I.G., Popov, E.S., Sandoval-Denis, M., Woudenberg, J.H.C., Acharya, K., Alexandrova, A.V., Alvarado, P., Barbosa, R.N., Baseia, I.G., Blanchette, R.A., Boekhout, T., Burgess, T.I., Cano-Lira, J.F., Čmoková, A., Dimitrov, R.A., Dyakov, M.Yu., Dueñas, M., Dutta, A.K., Esteve-Raventós, F., Fedosova, A.G., Fournier, J., Gamboa, P., Gouliamova, D.E., Grebenc, T., Groenewald, M., Hanse, B., Hardy, G.E.ST.J., Held, B.W., Jurjević, Ž, Kaewgrajang, T., Latha, K.P.D., Lombard, L., Luangsa-ard, J.J., Lysková, P., Mallátová, N., Manimohan, P., Miller, A.N., Mirabolfathy, M., Morozova, O.V., Obodai, M., Oliveira, N.T., Ordóñez, M.E., Otto, E.C., Paloi, S., Peterson, S.W., Phosri, C., Roux, J., Salazar, W.A., Sánchez, A., Sarria, G.A., Shin, H.-D., Silva, B.D.B., Silva, G.A., Smith, M.TH., Souza-Motta, C.M., Stchigel, A.M., Stoilova-Disheva, M.M., Sulzbacher, M.A., Telleria, M.T., Toapanta, C., Traba, J.M., Valenzuela-Lopez, N., Watling, R. & Groenewald, J.Z. (2016) Fungal Planet description sheets: 400-468. Persoonia- *Molecular Phylogeny and Evolution of Fungi* 36: 316–458. https://doi.org/10.3767/003158516X692185

Farid, A., Bessette, A.E., Bessette, A.R., Bolin, J.A., Kudzma, L.V., Franck, A.R. & Garey, J.R. (2021) Investigations in the boletes

(Boletaceae) of southeastern USA: four novel species, and three novel combinations. *Mycosphere* 12: 1038–1076. https://doi.org/10.5943/mycosphere/12/1/12

Frandsen, P.B., Calcott, B., Mayer, C. & Lanfear, R. (2015) Automatic selection of partitioning schemes for phylogenetic analyses using iterative k-means clustering of site rates. *BMC Evolutionary Biology* 15: 1–17. https://doi.org/10.1186/s12862-015-0283-7

Frank, J.L., Siegel, N., Schwarz, C.F., Araki, B. & Vellinga, E.C. (2020) *Xerocomellus* (Boletaceae) in western North America. *Fungal Systematics and Evolution* 6: 265–288. https://doi.org/10.3114/fuse.2020.06.13

García-Jiménez, J. & Garza-Ocañas, F. (2001) Conocimiento de los hongos de la familia Boletaceae en México. *Ciencia Universidad Autónoma de Nuevo León* 4: 336–434.

Garza-Ocañas, F., García Jiménez, J., Guevara-Guerrero, G., Martínez-González, C.R., Ayala-Vásquez, O. & de la Fuente, J.I. (2022) *Xerocomellus carmeniae* (Boletales, Basidiomycota), a new fungus from northeastern Mexico. *Acta Botanica Mexicana* 129: e2039. https://doi.org/10.21829/abm129.2022.2039

Hall, T.A. (1999) BioEdit: a user-friendly biological sequence alignment editor and analysis program for windows 95/98/NT. *Nucleic Acids Symposium Series* 41: 95–98.

Hernández-Restrepo, M., Schumacher, R.K., Wingfield, M.J., Ahmad, I., Cai, L., Duong, T.A., Edwards, J., Gené, J., Groenewald, J.Z., Jabeen, S., Khalid, A.N., Lombard, L., Madrid, H., Marin-Felix, Y., Marincowitz, S., Miller, A.N., Rajeshkumar, K.C., Rashid, A., Sarwar, S., Stchigel, A.M., Taylor, P.W.J., Zhou, N. & Crous, P.W. (2016) Fungal Systematics and Evolution: FUSE 2. *Sydowia* 68: 193–230.

Huelsenbeck, J.P. & Ronquist, F. (2001) MrBayes: Bayesian inference of phylogeny. *Bioinformatics* 17: 754–755. https://doi.org/10.1093/bioinformatics/17.8.754

Katoh, K. & Standley, D.M. (2013) MAFFT multiple sequence alignment software version 7: improvements in performance and usability. *Molecular Biology and Evolution* 30: 772–780. https://doi.org/10.1093/molbev/mst010

Katoh, K., Misawa, K., Kuma, K. & Miyata, T. (2002) MAFFT: a novel method for rapid multiple sequence alignment based on fast Fourier transform. *Nucleic Acids Research* 30: 3059–3066. https://doi.org/10.1093/nar/gkf436

Katoh, K., Rozewicki, J. & Yamada, K.D. (2017) MAFFT online service: multiple sequence alignment, interactive sequence choice and visualization. *Briefings in Bioinformatics* 20: 1160–1166. https://doi.org/10.1093/bib/bbx108

Kďaviňa, D., Lazdiňđ, A., Bârdule A., Nikolajeva, V., Okmanis, M., Skranda, I., Gaitnieks T., & Menkis A. (2016) Fine root development and mycorrhization in Norway spruce stands one year after fertilization with potassium sulphate and wood ash. *Journal of Forensic Sciences* 62: 17–23. https://doi.org/10.17221/93/2015-JFS

Kornerup, A. & Wanscher, J.H. (1978) *Methuen handbook of colours*. 3rd ed. Eyre Methuen, London, UK.

Lanfear, R., Calcott, B., Kainer, D., Mayer, C. & Stamatakis, A. (2014) Selecting optimal partitioning schemes for phylogenomic datasets. *BMC Evolutionary Biology* 14: 1–14. https://doi.org/10.1186/1471-2148-14-82

Lanfear, R., Frandsen, P.B., Wright, A.M., Senfeld, T. & Calcott, B. (2016) Partition Finder 2: New methods for selecting partitioned models of evolution for molecular and morphological phylogenetic analyses. *Molecular Biology and Evolution* 34: 772–773. https://doi:10.1093/molbev/msw260

Largent, D.L., Johnson, D. & Watling, R. (1977) *How identify mushrooms to genus III: Microscopic features*. Mad River Press, Eureka. 148 pp.

Li, H., Yang, T., Menolli, Jr N., Ye, L., Samantha, C., Karunarathna, S.C., Perez-Moreno, J., Rahman, M.M., Rashid, M.R., Phengsintham, P., Rizal, L., Kasuyal, T., Lim, Y.W., Arun Kumar Dutta, A.K., Khalid, A.N., Huyen, L.T., Balolong, M.P., Baruah, G., Madawala, S., klang, N.T., Hyde, K.D., Kirk, P.M., Xu, J., Sheng, J., Boa, E. & Mortimer, P.E. (2020) Reviewing the world's edible mushroom species: A new evidence based classification system. *Comprehensive Reviews in Food Science and Food Safety* 20: 1982–2014. https://doi.org/10.1111/1541-4337.12708

Lodge, D.J., Ammirati, J.F., Dell, T.O. & Mueller, G.M. (2004) Terrestrial and Lignicolous Macrofungi: Colecting and describing macrofungi. *In*: Mueller, G., Bills, G.F. & Foster, M.S. (Eds.) *Biodiversity of Fungi. Inventary and Monitoring Methods*. Elsevier Academic Press, pp. 128–158. https://doi.org/10.1016/B978-012509551-8/50011-8

Martin, M.P. & Raidl, S. (2002) The taxonomic position of *Rhizopogon melanogastroides* (Boletales). *Mycotaxon* 84: 221–228.

Matheny, P.B., Liu, Y.J., Ammirati, J.F. & Hall, B.D. (2002) Using RPB1 sequences to improve phylogenetic inference among mushrooms

(*Inocybe*, Agaricales). *American Journal of Botany* 89: 688–698.

Martínez-González, C.R., Ramírez-Mendoza, R., Jiménez-Ramírez, J., Gallegos-Vázquez, C. & Luna-Vega, I. (2017) Improved method for genomic DNA extraction for *Opuntia* Mill. (Cactaceae). *Plant Methods* 13: 1–10.
https://doi.org/10.1186/s13007-017-0234-y

Mikheyev, A.S., Mueller, U.G. & Abbot, P. (2006) Cryptic sex and many-to-one colevolution in the fungus-growing ant symbiosis. *Proceedings of the National Academy of Sciences* 103: 10702–10706.
https://doi.org/10.1073/pnas.0601441103

Müller, K., Quandt, D., Müller, J. & Neinhuis, C. (2005) PhyDE®-Phylogenetic data editor. Program distributed by the authors, versión 10.0. Available from: https://www.phyde.de (accessed 30 September 2021)

Nuhn, M.E., Binder, M., Taylor, A.F., Halling, R.E. & Hibbett, D.S. (2013) Phylogenetic overview of the Boletineae. *Fungal Biology* 117: 479–511.

Osmundson, T.W., Robert, V.A., Schoch, C.L., Baker, L.J., Smith, A., Robich, G., Mizzan, L. & Garbelotto, M.M. (2013) Filling gaps in biodiversity knowledge for macrofungi: contributions and assessment of an herbarium collection DNA barcode sequencing project *PLoS ONE* 8: 4.
https://doi.org/10.1371/journal.pone.0062419

Ozgur, A., Gökşen, T.N., Ozlem, K. & Isa, G. (2021) *Green Synthesis of Silver Nanoparticles Using Armillaria mellea and Xerocomellus chrysenteron Extracts and Evaluation of Their Antimicrobial and Anticancer Potentials*. 3rd Eurasia Biochemical Approaches & Technologies Congress (EBAT)At: Antalya, Turkey.

Patil, B.P., Gunasekaran, S., Singh, K.S. & Vaidya, S. (2021) *Parvixerocomus matheranensis* (Boletaceae), a new species from India. *Mycoscience* 62: 244–249.
https://doi.org/10.47371/mycosci.2021.03.007

Peintner, U., Ladurner, H. & Simonini, G. (2003) *Xerocomus cisalpinus* sp. nov., and the delimitation of species in the *X. chrysenteron* complex based on morphology and rDNA-LSU sequences. *Mycological Research* 107: 659–679.
https://doi.org/10.1017/S0953756203007901

Rambaut, A., Suchard, M.A., Xie, D. & Drummond, A.J. (2014) Tracer v1.6. Available from: http://beast.bio.ed.ac.uk/Tracer (accessed 30 September 2021)

Saldivar, Á.E., García-Jiménez, J., Herrera-Fonseca, M.J. & Rodríguez-Alcántar, O. (2021) updated checklist and new records of Boletaceae (fungi, Basidiomycota, Boletales) from Jalisco, Mexico. *Polibotanica* 52: 25–49.
https://doi.org/10.18387/polibotanica.52.3

Snell, W.H. & Dick, E.A. (1970) *The Boleti of Northeastern North America*. Cramer, Lehre.

Stamatakis, A. (2014) RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. *Bioinformatics* 30: 1312–1313.
https://doi.org/10.1093/bioinformatics/btu033

Šutara, J. (2008) Xerocomus s.l. in the light of the present state of knowledge. *Czech Mycology* 60: 29–62.
https://doi.org/10.33585/cmy.60104

Vilgalys, R. & Hester, M. (1990) Rapid genetic identification and mapping of enzymatically amplified ribosomal DNA from several *Cryptococcus* species. *Journal of Bacteriology* 172: 4238–4246.
https://doi.org/10.1128/jb.172.8.4238-4246.1990

White, T.J., Bruns, T.D., Lee, S. & Taylor, J.W. (1990) Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenies. *In*: Innis, M.A., Gelfand, D.H., Sninsky, J.J. & White, T. (Eds.) *PCR Protocols: a guide to methods and applications*. Academic Press. pp. 135–322.
https://doi.org/10.1016/B978-0-12-372180-8.50042-1

Wu, G., Feng, B., Xu, J., Zhu, X.T., Li, Y.C., Zeng, N.K., Hosen, M.I. & Yang, Z.L. (2014) Molecular phylogenetic analyses redefine seven major clades and reveal 22 new generic clades in the fungal family Boletaceae. *Fungal Diversity* 69: 93–115.
https://doi.org/10.1007/s13225-014-0283-8

Wu, G., Li, Y.C., Zhu, X.T., Zhao, K., Han, L.H., Cui, Y.Y. & Yang, Z.L. (2016) One hundred noteworthy boletes from China. *Fungal Diversity* 81: 25–188.
https://doi.org/10.1007/s13225-016-0375-8

Xie, H.-J., Lin, W.-F., Jiang, S., Xue, R., Wu, L.-L., Zhang, Y.-Z., Liang, Z.-Q., Zeng, N.-K. & Su, M.S. (2020) Two new species of *Hortiboletus* (Boletaceae, Boletales) from China. *Mycological Progress* 19: 1377–1386.
https://doi.org/10.1007/s11557-020-01634-z

Zhang, Z., Schwartz, S., Wagner, L. & Miller, W. (2000) A greedy algorithm for aligning DNA sequences. *Journal of Computational Biology* 7: 203–214.
https://doi.org/10.1089/10665270050081478