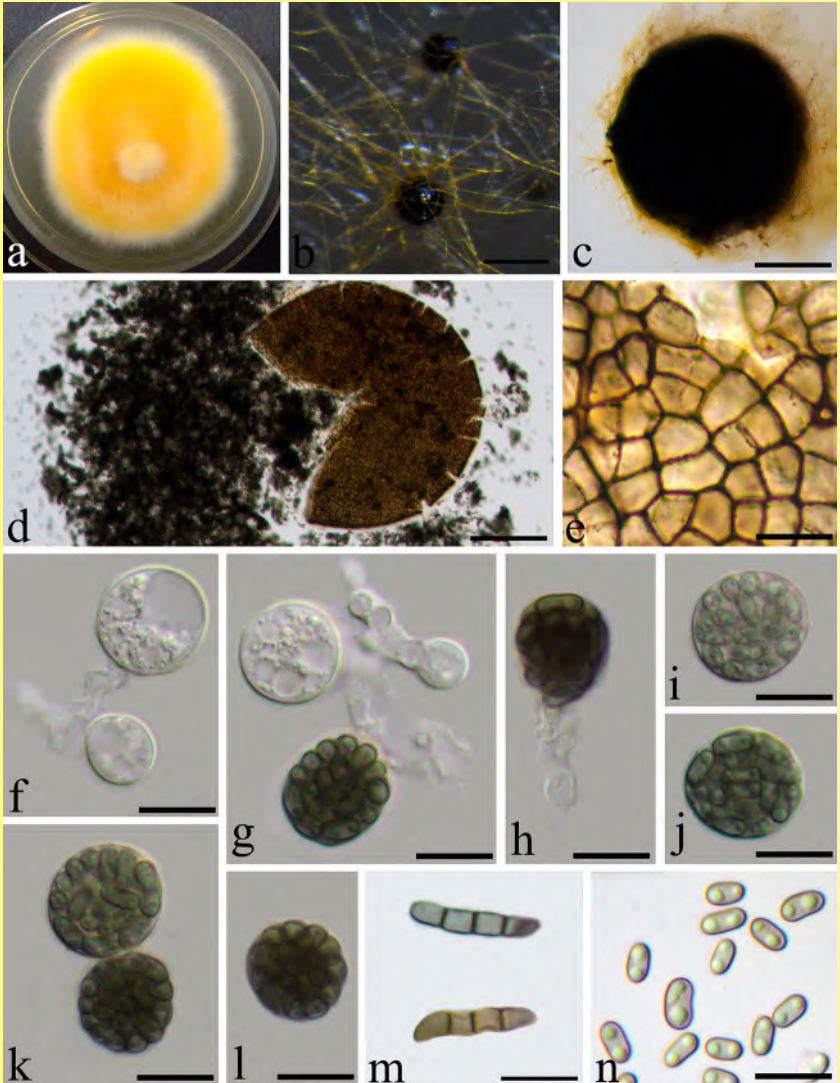


MYCOTAXON

THE INTERNATIONAL JOURNAL OF FUNGAL TAXONOMY & NOMENCLATURE

VOLUME 135 (2)

APRIL–JUNE 2020



Westerdykella aquatica sp. nov.

(Song & al.— FIG. 2, p. 289)

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READ: A. NASEER, S. KHANUM, A.R. NIAZI, A.N. KHALID 241

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READ: A. NASEER^{1*}, S. KHANUM², A.R. NIAZI², A.N. KHALID²

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The Editors express their appreciation to the following individuals who have, prior to acceptance for publication, reviewed one or more of the papers prepared for this issue.

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2020 MYCOTAXON SUBMISSION PROCEDURE

Prospective MYCOTAXON authors should download the MYCOTAXON 2020 guide, review & submission forms, and MYCOTAXON sample manuscript by clicking the 'file download page' link on our INSTRUCTIONS TO AUTHORS page before preparing their manuscript. This page briefly summarizes our '4-step' submission process.

1—PEER REVIEW: Authors first contact peer reviewers (two for journal papers; three for mycobiota/fungae) before sending them formatted text & illustration files and the appropriate 2020 MYCOTAXON journal or mycota reviewer comment form. Experts return revisions & comments to BOTH the *Editor-in-Chief* <editor@mycotaxon.com> and authors. ALL co-authors MUST correct and *proof-read* their files before submitting them to the *Nomenclature Editor*.

2—NOMENCLATURE REVIEW: Authors email all **ERROR-FREE** text & illustration files to the *Nomenclature Editor* <PennycookS@LandcareResearch.co.nz>. Place **first author surname + genus + 'MYCOTAXON'** on the subject line, and (required) attach a completed SUBMISSION FORM. The Nomenclature Editor will (i) immediately assign the accession number and (ii) after a few weeks return his notes and suggested revisions to the author(s) and *Editor-in-Chief*.

3—FINAL SUBMISSION: All coauthors thoroughly revise and proof-read files to prepare error-free text and images ready for immediate publication. Poorly formatted copy will be rejected or returned for revision. E-mail the final manuscript to the *Editor-in-Chief* <editor@mycotaxon.com>, adding the **accession number** to the message and **all** files, which include a (i) revised 2020 submission form, all (ii) text files and (iii) jpg images, and (iv) FN, IF, or MB identifier verifications for each new name or typification. The *Editor-in-Chief* acknowledges submissions within two weeks of final submission but requests authors to wait at least 14 days before sending a follow-up query (without attachments).

4—FINAL EDITORIAL REVIEW & PUBLICATION: The *Editor-in-Chief* conducts a final grammatical and scientific review and returns her editorial revisions to all expert reviewers and coauthors for final author approval. Author-approved files are placed in the publication queue.

The PDF proof and bibliographic & nomenclatural index entries are sent to all coauthors for final inspection. After PDF processing, the *Editor-in-Chief* corrects ONLY PDF editorial/conversion and index entry errors; corrections of all other errors are listed in the ERRATA of a subsequent issue for no charge. Authors will pay fees for mycobiota uploads, optional open access, and correction of major author errors to the *Business Manager* <subscriptions@mycotaxon.com> at this time.

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FROM THE EDITOR-IN-CHIEF

COLLABORATION & THE MULTI-AUTHORED PAPER—Mycological taxonomic research is no longer a simple matter of reaching down, plucking a fungus from its substrate, seeing something REALLY different, checking the microscopical characters, reading the one or two papers ever written on aforesaid fungal family, and then writing a paper. Current fungal taxonomy encompasses a great many disciplines, including (but not limited to) microscopy, ecology, physiology, mating studies, ultrastructure, systematics, DNA extractions, sequence analyses, and evolutionary relationships. Yet we somehow expect students injected into this bewildering maelstrom of disciplines to be able (eventually) to present their research in the form of a published paper.

As only a limited number of geniuses can master all modern disciplines, there are now relatively few solo-authored papers. Most research papers are crafted by an agreeable consortium of individuals, each of whom contributes one or two expert pieces that flesh out the final manuscript. The individual who bears the greatest responsibility (and gets—however little deserved—most of the credit) is the first author. All students must oversee all stages of each manuscript submission to ensure that they master the scientific publication process. The first named author bears the responsibility for ensuring that a manuscript meets all journal requirements and seeing that all facts are coherently written and correct. Generally it is that author who discusses the research with all whose names will stand on the final publication. It is also generally the first author who gathers all contributors together to work out a complication and perfect the final text whenever an error or oversight is detected.

Nonetheless, a multi-authored paper is NOT a work by one author. Journals such as MYCOTAXON expect ALL contributing authors to read and revise numerous drafts thoroughly, to check all drawings, tables, and data, and communicate with the first author throughout the research process and prior to submission. Editors expect to receive papers that have been—by *all* authors—thoroughly proofed and that contain no scientific, grammatical, or visual errors. Only through rigorous oversight by all collaborators, particularly the more experienced and knowledgeable among them, is it possible for a beginning scientist to publish in a well-established international scientific journal.

We heartily urge all of our authors to discuss their research among themselves and with their lab mates. That way lies progress!

DEAR READERS (PLUS PREMATURE THANKS TO THE MYCOTAXON EDITORIAL BOARD)—Your editors are currently swamped with submissions—the expected result of discontinuing required page charges in 2018. For sixteen years, Dr. Pennycook has tirelessly accessioned and examined manuscripts, gradually adding scientific and grammatical oversight to his already heavy nomenclatural duties. In the process, he has nomenclaturally accepted almost 2000 manuscripts, rejected ~100, and is currently reviewing 105 more. In its search for scientifically rigorous and nomenclaturally correct papers produced by dedicated authors and their expert

reviewers, MYCOTAXON still needs Shaun's nomenclatural knowledge because so few mycologists fully understand the rules of the International Code of Nomenclature.

Needless to say, both authors and editors are unhappy with the current lengthy time between manuscript accession and return of the nomenclatural review.

However, it now appears that all too often, author-selected experts do not devote the time needed for rigorous review, so that Dr. Pennycook frequently accesses manuscripts that require much more work. With many problems not detected by a quick scan of accessioned files, frequently only after Shaun has begun a review does he discover that the unsatisfactory files must be returned to authors for more work. Not surprisingly, this further lengthens the time between accession and nomenclatural approval.

Three months ago we decided that Shaun could work through his backlog more quickly by focusing only on nomenclature and by returning all other grammatical and scientific edits to the Editor-in-Chief (me). Unfortunately after encountering far too many scientific errors or inaccurate citations, I now must also double-check GenBank, herbarium records, and – yes – even scale bars for accuracy and consistency.

Fortunately, learning in June that your two volunteer editors needed at least one extra pair of eyes, editorial board member Else Vellinga volunteered to serve as MYCOTAXON's first 'official' PRELIMINARY READER. She offered to glance through still unreviewed manuscripts to determine which authors properly implemented expert suggestions, formatted grammatically correct text files, and presented no scientific contradictions as well as flag those papers needing additional work. Dr. Vellinga surveyed several manuscripts—happily finding one in excellent shape and less happily finding several in need of considerable repair or additional research prior to nomenclatural review.

In our estimation, Else, who delivered thorough reviews forwarded to the authors, has been a rousing success. We now plan to contact other board members to help us determine which other accessions are ready for nomenclatural review, which need additional research, and which should be rejected. Authors able to make any suggested changes and return them before Shaun begins his review will not lose their place in the nomenclatural 'queue.'

We sincerely hope this will help shorten our review turn-around time and give your volunteer editors much needed assistance in their currently overwhelming editorial duties. We both dearly desire returning to a time when all submissions were so well prepared that all we need do is to rubber-stamp "approved" after the first read-through. 'Tis a consummation devoutly to be wished.

MYCOTAXON 135(2) provides 22 papers and announces three mycobiota by 88 authors (from 23 countries) reviewed by 54 experts.

The 2020 April–June MYCOTAXON sets forth ONE new genus (*Ramiphialis* from Brazil) and EIGHT species new to science representing *Acarospora* & *Sarcogyne* from

the US & CANADA; *Armillaria*, *Haematomma*, *Vanderbylia*, and *Westerdykella* from CHINA; *Coprinellus* from PAKISTAN; and *Ramiphialis* from BRAZIL. Authors also offer three new combinations in *Cercospora*, *Ellismarsporium*, and *Microthecium*.

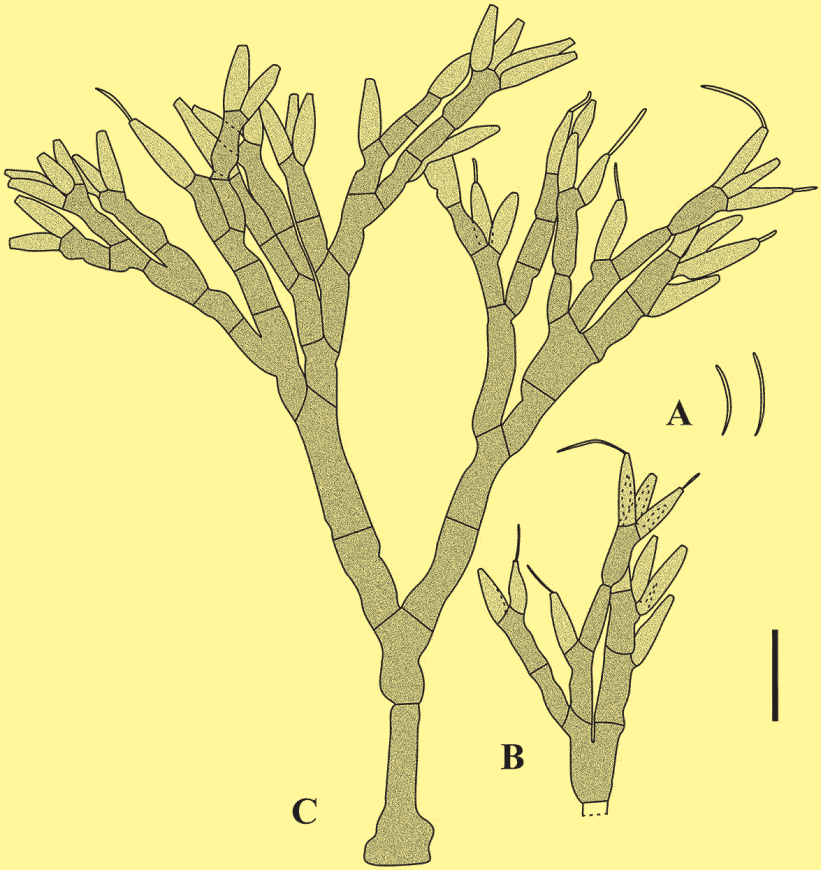
Range extensions are reported for [ascomycetes] the powdery mildew *Golovinomyces* (CHINA) and truffle *Elaphomyces* (TURKEY); [basidiomycetes] the agarics *Pluteus* (EUROPE) & *Xerula* (ARGENTINA), secotioid *Entoloma* (SLOVAKIA), and rust *Aecidium* (PAKISTAN); [lichens] the leprose *Lepraria* (IRAN), assorted graphidoid & thelotremoid taxa (INDIA), and crustose *Carbonea* & *Rinodina* (POLAND); and [myxomycetes] the slime molds *Badhamia* & *Trichia* (BELARUS).

We also offer phylogenetic explorations of *Acrospeira*, *Armillaria*, *Coprinellus*, *Ellismarsporium*, *Golovinomyces*, *Pluteus*, *Vanderbylia*, and *Westerdykella*; a key to the *Lepraria* species of Iran; reevaluation of three *Calicium* taxa proposed in 1909; and a comprehensive index of fungal names derived from te reo Māori. Finally, we announce three new www.mycotaxon.com mycobiota covering Australian marine fungi, Brazilian corticioids, and a global list of aquatic glomeromycotans.

Best wishes for excellent health and with warm regards,

Lorelei L. Norvell (*Editor-in-Chief*)

8 July 2020



Ramiphialis ronuroensis sp. nov.

(Barbosa & al.— FIG. 2, p. 296)

PATRICIA OLIVEIRA FIUZA, *artist*

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Armillaria xiaocaobaensis sp. nov. from China

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ABSTRACT—A new wood-inhabiting fungal species from Yunnan Province, China, is proposed based on morphological and molecular characters. *Armillaria xiaocaobaensis* is characterized by a central stipe, striate to furrowed orange yellow to pinkish brown pileus surface, membranous annulus, and ellipsoid, a monomitic hyphal system with generative hyphae bearing simple septa, and slightly thick-walled basidiospores averaging $7.7 \times 4.9 \mu\text{m}$. TEF1 sequence analyses support *A. xiaocaobaensis* as a distinct taxon in *Armillaria*.

KEY WORDS—*Agaricales*, phylogenetic, *Physalacriaceae*, pathogenic fungi, taxonomy

Introduction

Species in *Armillaria* (Fr.) Staude (*Physalacriaceae*, *Basidiomycota*) are well known as important plant pathogens that can cause serious root diseases on diverse trees and woody plants, resulting in huge economic losses (Wargo & Shaw 1985, Baumgartner 2004, Lalande & al. 2018).

Armillaria includes approximately 40 species (Volk & Burdsall 1995, Kirk & al. 2008, Brazeel & al. 2012, Hood & Ramsfield 2016, Elías-Román & al. 2018) worldwide, and ten *Armillaria* species are currently recognized in China (Qin & al. 2000, 2007; Sun & al. 2003; Zhao & al. 2008; Coetzee & al. 2015; Guo & al. 2016).

Recent phylogenetic studies of *Armillaria* based on sequences of the internal transcribed spacer (ITS) region, the large subunit of nuclear

ribosomal RNA gene (nLSU), translation elongation factor 1- α (TEF1), and β -tubulin have greatly increased the number of identified fungal species and revealed the relationships among species in this genus (e.g., Maphosa & al. 2006, Hasegawa & al. 2010, Ross-Davis & al. 2012, Tsykun & al. 2013, Coetzee & al. 2015, Park & al. 2018). Lima & al. (2008) described one new South American species, *Armillaria paulensis* Capelari, based on morphology and ITS sequences that showed its closeness to *A. luteobubalina* Watling & Kile, while Brazee & al. (2012) introduced *A. altimontana* Brazee & al. in North America based on morphological and molecular phylogenetic evidence. In New Zealand, Hood & Ramsfield (2016) revealed *A. aotearoa* I.A. Hood & Ramsfield using morphology, interfertility cultures, and DNA sequence data. Guo & al. (2016) analyzed Chinese *Armillaria* samples using the sequences of ITS, TEF1 and β -tubulin gene, which revealed 15 phylogenetic lineages of *Armillaria* from China and showed that TEF1 was the most parsimony informative. Koch & al. (2017) resolved phylogeny and biogeography of *Armillaria*, *Desarmillaria* (Herink) R.A. Koch & Aime, and *Guyanagaster* T.W. Henkel & al. Elías-Román & al. (2018) described *A. mexicana* Elías-Román & al. based on morphology, DNA-sequence data (ITS, nLSU and TEF1), and phylogenetic analyses.

Our research on macrofungi in southern China revealed specimens that could not be assigned to any described species within *Armillaria*. The authors sampled previous research using the translation elongation factor-1 alpha gene (TEF1) sequences to explore the taxonomy and phylogeny of this undescribed species, proposed below as *Armillaria xiaocaobaensis*.

Materials & methods

Macroscopical descriptions were based on field notes. Color terms follow Petersen (1996). Dried material was examined microscopically using a compound microscope following Dai (2012). The following abbreviations were used: KOH = 5% potassium hydroxide, CB = cotton blue, CB- = acyanophilous, IKI = Melzer's reagent, IKI- = both inamyloid and nondextrinoid, L = mean spore length (arithmetic average of all spores), W = mean spore width (arithmetic average of all spores), Q = variation in the L/W ratios between the specimens studied, n (a/b) = number of spores (a) measured from given number (b) of specimens. The specimens studied are deposited at the herbarium of Southwest Forestry University, Kunming, China (SWFC).

Genomic DNA was extracted from dried specimens using the EZNA HP Fungal DNA Kit according to the manufacturer's instructions with some modifications. A small piece (about 30 mg) of dried fungal specimen was ground to powder with liquid nitrogen. The powder was transferred to a 1.5 mL centrifuge tube, suspended

in 0.4 mL of lysis buffer, and incubated in a 65 °C water bath for 60 min. After 0.4 mL phenol-chloroform (24:1) was added to the tube, the suspension was shaken vigorously. After centrifugation at 13,000 rpm for 5 min, 0.3 mL supernatant was transferred to a new tube and mixed with 0.45 ml binding buffer. The mixture was then transferred to an adsorbing column (AC) for centrifugation at 13,000 rpm for 0.5 min. Then, 0.5 mL inhibitor removal fluid was added in AC for a centrifugation at 12,000 rpm for 0.5 min. After washing twice with 0.5 mL washing buffer, the AC was transferred to a clean centrifuge tube, and 100 ml elution buffer was added to the middle of adsorbed film to elute the genomic DNA. TEF1 was amplified with primer pairs EF1-983F and EF1-2218R (Rehner 2001). The PCR procedure for TEF1 was as follows: initial denaturation at 94 °C for 1 min, followed by 35 cycles at 94 °C for 30 s, 59 °C for 1 min and 72 °C for 1.5 min, and a final extension of 72 °C for 10 min. The PCR products were purified and directly sequenced at Kunming Tsingke Biological Technology Limited Company. All newly generated sequences were deposited in GenBank (TABLE 1).

GeneCodes Sequencher 4.6 was used to edit the DNA sequence. Sequences were aligned in MAFFT 7 (<https://mafft.cbrc.jp/alignment/server/index.html>) using the “G-INS-I” strategy and manually adjusted in BioEdit (Hall 1999). The sequence alignment was deposited in TreeBase (submission ID 24610). *Oudemansiella cubensis* (Berk. & M.A. Curtis) R.H. Petersen and *Strobilurus esculentus* (Wulfen) Singer were used as outgroup to root trees following Koch & al. (2017) in the TEF1 analyses.

Phylogenetic analyses of the TEF1 sequences were performed using maximum parsimony, maximum likelihood, and Bayesian inference methods. Maximum parsimony (MP) analyses followed Zhao & Wu (2017), and tree construction was performed in PAUP* version 4.0b10 (Swofford 2002). All characters were equally weighted and gaps were treated as missing data. Trees were inferred using the heuristic search option with TBR branch swapping and 1000 random sequence additions. Max-trees were set to 5000, branches of zero length were collapsed, and all parsimonious trees were saved. Clade robustness was assessed using bootstrap (BT) analysis with 1000 replicates (Felsenstein 1985). Tree length (TL), consistency index (CI), retention index (RI), rescaled consistency index (RC), and homoplasy index (HI) were calculated for each Maximum Parsimonious Tree (MPT) generated. Sequences were analyzed using Maximum Likelihood (ML) with RAXML-HPC2 through the Cipres Science Gateway (www.phylo.org; Miller & al. 2009). Branch support (BS) for ML analysis was determined by 1000 bootstrap replicates.

MrModeltest 2.3 (Nylander 2004) was used to determine the best-fit evolution model for each data set for Bayesian inference (BI). Bayesian inference was calculated with MrBayes_3.1.2 using a general time reversible (GTR) model of DNA substitution and a gamma distribution rate variation across sites (Ronquist & Huelsenbeck 2003). Four Markov chains were run for 2 runs from random starting trees for 5 million generations (TEF1) and trees were sampled every 100 generations. The first 25% of the generations were discarded as burn-in. A majority

TABLE 1. Sequences used in the phylogenetic analyses; new sequences in **bold**.

SPECIES	SAMPLE NO.	GENBANK NO. TEF1	REFERENCE
<i>Armillaria altimontana</i>	D 82	JN944611	Brazee & al. 2012
	POR 100	JN944606	Brazee & al. 2012
<i>A. aotearoa</i>	NZFRIM 5283	KU295542	Hood & Ramsfield 2016
<i>A. borealis</i>	HKAS 56108	KT822293	Guo & al. 2016
	HKAS 76263	KT822294	Guo & al. 2016
<i>A. calvescens</i>	ST 17	JF895836	Brazee & al. 2011
	ST 18	JF895837	Brazee & al. 2011
	ST 3	JF895835	Brazee & al. 2011
<i>A. cepistipes</i>	F 011081	KT822416	Guo & al. 2016
	S 20	JF313116	Brazee & al. 2011
<i>A. fumosa</i>	CMW 4955	DQ435646	Maphosa & al. 2006
<i>A. fuscipes</i>	CMW 3164	DQ435621	Maphosa & al. 2006
	CMW 4953	DQ435622	Maphosa & al. 2006
<i>A. gallica</i>	M 70	HQ432899	Direct Submission
	ST 22	HQ432897	Elías-Román & al. 2018
<i>A. gemina</i>	ST 8	JF313136	Brazee & al. 2011
	ST11A	JF313133	Brazee & al. 2011
<i>A. heimii</i>	K 59	FJ618644	Elías-Román & al. 2018
	PH 8724	FJ618651	Elías-Román & al. 2018
<i>A. himmulea</i>	CMW 4980	DQ435648	Maphosa & al. 2006
<i>A. limonea</i>	CMW 4680	DQ435655	Maphosa & al. 2006
	CMW 4991	DQ435656	Maphosa & al. 2006
	Plim 8466	FJ618654	Elías-Román & al. 2018
<i>A. luteobubalina</i>	CMW 4977	DQ435657	Maphosa & al. 2006
	CMW 8876	DQ435658	Maphosa & al. 2006
<i>A. mellea</i>	CMW 4613	DQ435637	Maphosa & al. 2006
	G 0405414	KT822345	Guo & al. 2016
	MEX 74	KC111011	Elías-Román & al. 2018
<i>A. mexicana</i>	MEX 85	KR061313	Elías-Román & al. 2018
	MEX 87	KR061314	Elías-Román & al. 2018
	MEX 88	KR061315	Elías-Román & al. 2018
<i>A. nabsnona</i>	C 21	JF313119	Elías-Román & al. 2018
	HKAS 85523	KT822411	Guo & al. 2016
<i>A. novae-zelandiae</i>	CMW 4722	DQ435652	Maphosa & al. 2006
	CMW 5448	DQ435653	Maphosa & al. 2006
<i>A. ostoyae</i>	EC4	JF746925	Brazee & al. 2011
	EC 5	JF746926	Brazee & al. 2011
<i>A. pallidula</i>	3626	FJ618665	Elías-Román & al. 2018
	CMW 4971	DQ435647	Maphosa & al. 2006
<i>A. puiggarii</i>	MCA 3111	KU289104	Koch & al. 2017
	TH 9751	KU289113	Koch & al. 2017

SPECIES	SAMPLE NO.	GENBANK NO. TEF1	REFERENCE
<i>A. sinapina</i>	A 9601539	KT822422	Guo & al. 2016
	M 50	JF313114	Brazee & al. 2011
	ST 12	JF313132	Brazee & al. 2011
	ST 13	JF313131	Brazee & al. 2011
<i>A. solidipes</i>	P 1404	JF313140	Brazee & al. 2011
	ST 2	JF313139	Brazee & al. 2011
<i>A. xiaocaobaensis</i>	SWFC 12637	MN298777	This study
	SWFC 12638[T]	MN298778	This study
	SWFC 12639	MN298779	This study
<i>Desarmillaria ectypa</i>	7001113	KT822438	Guo & al. 2016
	CMW 15693	FJ875698	Koch & al. 2017
	MY 84941	FJ618643	Koch & al. 2017
<i>D. tabescens</i>	90158	KT822439	Koch & al. 2017
	I 9912213	KT822441	Guo & al. 2016
	PT 8412	FJ618658	Koch & al. 2017
<i>Guyanagaster necrorhizus</i>	G 314	KU289110	Koch & al. 2017
	G 352	KU289109	Koch & al. 2017
	MCA 3950	KU289107	Koch & al. 2017
	RAK 31	KU289108	Koch & al. 2017
<i>Oudemansiella cubensis</i>	MCA 5434	KU289105	Koch & al. 2017
<i>Strobilurus esculentus</i>	Yang 5027	KF530581	Koch & al. 2017

rule consensus tree of all remaining trees was calculated. Branches that received bootstrap support for maximum likelihood (BS), maximum parsimony (BT), and Bayesian posterior probabilities (BPP) greater than or equal to 75% (BS, BT) and 0.95 (BPP) were considered significantly supported.

Molecular phylogeny

The TEF1 dataset included sequences from 62 fungal specimens representing 29 species (TABLE 1). The alignment comprised 544 characters of which 312 characters were constant, 29 variable and parsimony-uninformative, and 203 parsimony-informative. Maximum parsimony analysis yielded four equally parsimonious trees (TL = 728, CI = 0.496, HI = 0.504, RI = 0.781, RC = 0.387). Best model for the TEF1 dataset estimated and applied in the Bayesian analysis: GTR+I+G. Bayesian analysis and ML analysis resulted in a similar topology as MP analysis, with an average standard deviation of split frequencies = 0.003738 (BI).

The phylogeny inferred from TEF1 sequences placed *Armillaria xiaocaobaensis* in a monophyletic lineage with strong support (BS = 100%; BT = 100%; BPP = 1).

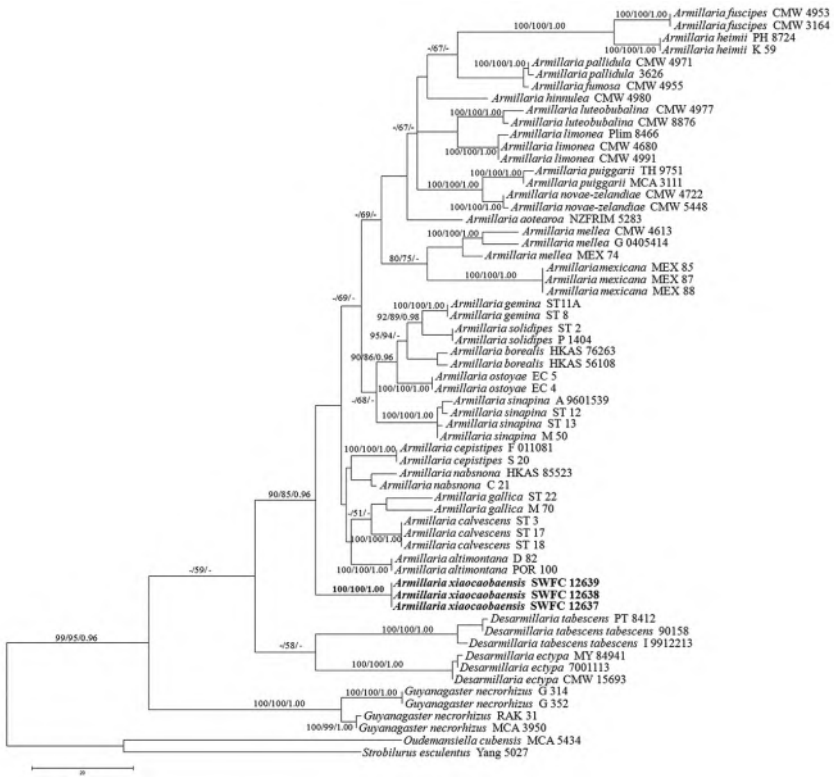


FIG. 1. Maximum parsimony strict consensus tree illustrating the phylogeny of *Armillaria xiaocaobaensis* and related species based on TEF1 sequences. Branches are labeled with maximum likelihood bootstrap >70%, parsimony bootstrap proportions >50%, and Bayesian posterior probabilities >0.95.

Taxonomy

Armillaria xiaocaobaensis Jia H. Peng & C.L. Zhao, sp. nov.

FIGS 2, 3

MB 832231

Differs from *Armillaria altimontana* by its centrally stipitate basidiomes with striate to furrowed, orange yellow to pinkish brown pileus surface, membranous annulus, and smaller, ellipsoid, thin-walled basidiospores.

TYPE: China. Yunnan Province: Zhaotong, Yiliang County, Xiaocaoba Town, on angiosperm trunk, 19 April 2019, Jia-Hua Peng (Holotype, SWFC 0012638; GenBank MN298777).

ETYMOLOGY: *xiaocaobaensis* (Lat.) refers to the locality (Xiaocaoba Town) of the type specimen.



FIG. 2. *Armillaria xiaocaobaensis* (holotype, SWFC 0012638).
Scale bars: A = 4 cm; B, C = 1 cm; D = 5 mm; E = 2 mm.

BASIDIOMATA pileate, centrally stipitate, caespitose. PILEUS 30–40 mm diam., umbonate, convex to plano-convex, orbicular in apical view, margin deflexed to lobed, pileus surface striate to furrowed, orange yellow to pinkish brown in the center, and pale yellow to pale brown at margin. LAMELLAE 5 mm deep, close,

decurrent, adnate, edges entire, buff to light yellow. LAMELLULAE attenuate, edges entire, multi-tiered. ANNULUS 4–5 mm wide, superior, persistent, membranous, appressed to stipe, buff to light yellow. STIPE 35–60 × 4–6 mm, central, cylindrical, solid, light yellow to pale pinkish brown to brown to black toward the base in fresh specimens, base bulbous. RHIZOMORPHS absent. TASTE AND ODOR not tested. SPORE PRINT white.

BASIDIOSPORES ellipsoid, hyaline, slightly thick-walled, smooth, IKI–, CB–, (6.5–)7–8.5(–9) × 4–5.5(–6) μm , L = 7.74 μm , W = 4.93 μm , Q = 1.53–1.64 (n = 90/3). BASIDIA barrel-shaped to clavate, with 2–4 sterigmata and a simple basal septum, 20–28 × 5.5–8.5 μm ; basidioles dominant, mostly clavate but slightly smaller than basidia. HYMENOPHORAL TRAMA generative hyphae bearing simple septa, hyaline, thin-walled, unbranched, 5–8 μm in diam. CYSTIDIA none observed. PILEIPELLIS hyphae hyaline, thin-walled, unbranched, 8–13 μm diam. CONTEXT 100–150 μm wide, hyphae hyaline, thin-walled, unbranched, 6–10 μm diam. STIPITPELLIS hyphae hyaline, thin-walled, unbranched, 3.5–5.5 μm diam. CLAMP CONNECTIONS absent.

ADDITIONAL SPECIMENS EXAMINED: CHINA. YUNNAN PROVINCE. Zhaotong: Yiliang County, Xiaocaoba Town, on angiosperm trunk, 19 June 2019, Jia-Hua Peng (SWFC 0012637; SWFC 0012639).

Discussion

Phylogenetic analyses and morphological characters support *Armillaria xiaocaobaensis* as a new species.

In the TEF1 analyses (FIG. 1), *A. xiaocaobaensis* formed a monophyletic lineage with strong support (BS = 100%; BT = 100%; BPP = 1) and grouped with *Armillaria altimontana*, *A. calvescens* Bérubé & Dessur., *A. cepistipes* Velen., *A. gallica* Marxm. & Romagn., and *A. nabsnona* T.J. Volk & Burds. However, morphologically *A. altimontana* differs from *A. xiaocaobaensis* by its tricholomatoid basidiomata with a reddish brown pileus bearing cream scales and short fibrils (Brazee & al. 2012) and from *A. calvescens* by the presence of pileus scales and fibrils, and larger basidiospores (8.5–10 × 5–7 μm ; Bérubé & Dessureault 1989). *Armillaria cepistipes* differs in its yellow ochraceous to ochraceous brown pileus, longer stipe (100 × 9–11 mm), and larger basidia (29–45 × 8.5–11 μm ; Antonín & al. 2009); and *A. gallica* by the presence of dark brown to pinkish brown pileus, long fibrillose pileus scales, and ellipsoid to amygdaloid, larger basidiospores (7.5–11 × 5–6.5 μm ; Antonín & al. 2009). *Armillaria nabsnona* has a hygrophanous pileus with a white context and larger basidiospores (8–10 × 5.5–6.5 μm ; Volk & al. 1996).

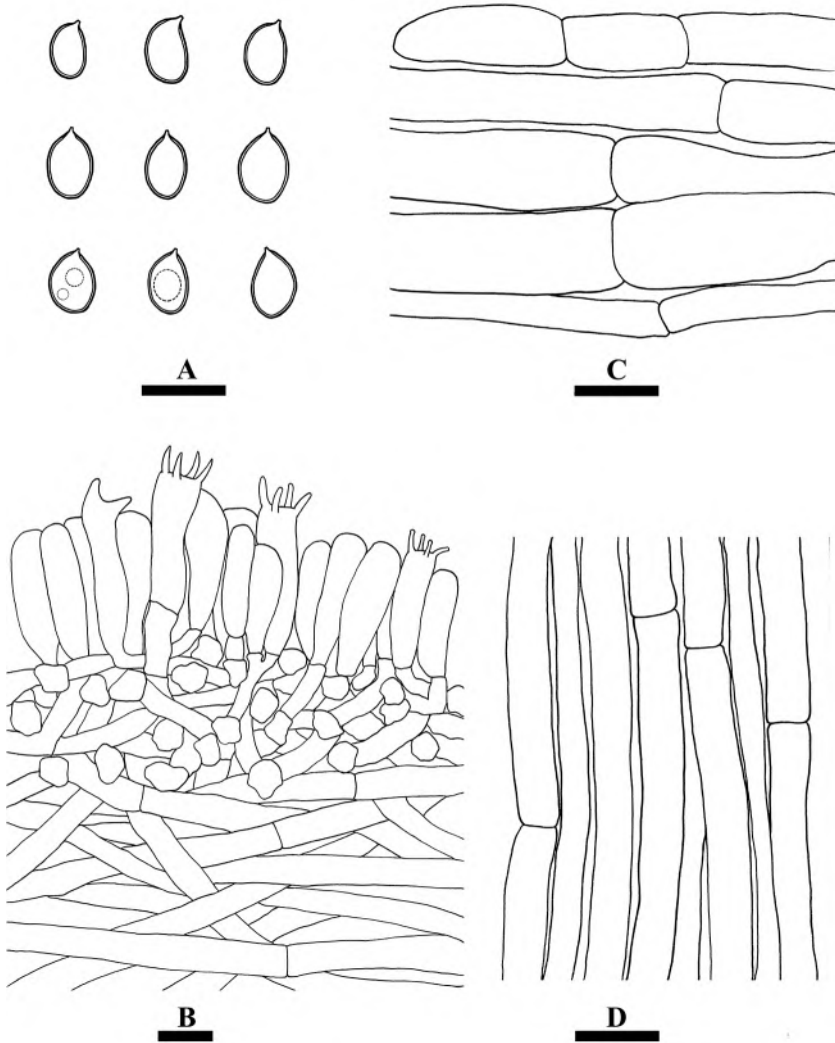


FIG. 3. Microscopic structures of *Armillaria xiaocaobaensis* (drawn from the holotype, SWFC 0012638). A. Basidiospores; B. Section of hymenium; C. Pileipellis; D. Stipitipellis. Scale bars: A–D = 10 μ m.

Armillaria xiaocaobaensis is close to *Desarmillaria*, a member in the sister genus based on the molecular data (FIG. 1). *Desarmillaria* is distinguished morphologically from *Armillaria* by the absence of an annulus (Koch & al. 2017).

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