

Aureoboletus pseudorussellii sp. nov., A Newly Discovered Species in Genus *Aureoboletus* of Zhejiang Province, China

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ABSTRACT

A morphological and phylogenetic analysis has been conducted on a new species, *Aureoboletus pseudorussellii*, belonging to the genus *Aureoboletus* Pouzar (nrLSU + *TEF1-a*) and provided a detailed description. It grows on the ground under the mixed forest of Fagaceae and Pinaceae in Zhejiang Province, and is named after its similarity to *A. russellii*. The distinctive features of this species include a pileus uncracked in maturity, with a subtomentose surface, which darkens to reddish brown to blackish brown when injured. It is also marked by a yellowish white to white short veil at the margin. The stipe is adorned with prominent white to pale reddish brown carinate stripes, and its context ranges from yellowish white to orange, showing no discoloration when bruised. Basidiospores $(14\text{--}14.5\text{--}20.5\text{--}21) \times (7.5\text{--}8\text{--}9\text{--}9.5) \mu\text{m}$. A detailed description of the novel species and its differences from similar species is provided below.

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1. Introduction

Aureoboletus Pouzar, typified by *A. gentilis* (Quél.) Pouzar, was established in 1957 [1]. The genus is distinguished by its viscid and downy pileus, featuring a hymenophore adorned with yellow tubes and pores, and a surface that is slightly sunken at the top of the stipe [2,3]. The stipe is neither reticulate nor glandulose, with a cylindrical and a slightly swollen lower portion, and it often forms symbiotic mycorrhiza with plants from the Fagaceae and Pinaceae families [4].

The recognition of *Aureoboletus* as a distinct genus was a lengthy process. Initially, in 1942, it was categorized as a mere section within *Xerocomus* [5]. Subsequently, numerous species previously belonging to this genus were reassigned to *Boletellus*, *Boletus*, and *Pulveroboletus* [5–11]. In 1957, however, Pouzar [1] reestablished it as an independent genus, with *A. gentilis* designated as the type species. Yet, this reclassification was not promptly embraced by the mycological community for a considerable time [8–13]. *Aureoboletus* was subsequently equated with *Sinoboletus* by Zang [14] in 1992, before eventually being acknowledged as a synonym of *Aureoboletus* by Wu et al. [15]. It was only after molecular analysis

was performed on *Aureoboletus* that the taxonomy of this genus was firmly established [16,17]. Klofac classified 13 species within *Aureoboletus* and presented an identification key for the genus in 2010 [4]. As of now, the Index Fungorum acknowledges 58 species belonging to *Aureoboletus* [1,4,18–25], among which 35 species have been identified in China [26–41].

Recently, our team has acquired several boletus specimens from Zhejiang Province. Following morphological and phylogenetic evaluations, some of these specimens are indeed part of *Aureoboletus*, and classified as a novel species. Detailed description is presented in this study.

2. Materials and methods

2.1. Specimen information

The specimens were contributed by Bin Chen (August 19 2024) and Xiaomin Yan (August 24 2024), were collected on the ground under the mixed forest of Fagaceae and Pinaceae in Meishu Village, Zuoxi Town, Qingyuan County, Lishui City, Zhejiang Province, and were dried at a temperature range of 41–56 °C under the guidance of Zhou [42]. Specimens

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were deposited in the Specimen Museum of Kunming Edible Fungi Research Institute (KEF).

2.2. Morphological studies

The macroscopic morphological characteristics were meticulously observed and recorded from field studies of basidiomata. Color references were selected from “Taschenlexikon der Farben, 3rd edn” [43]. For the micromorphology observation and description, we adopted established methodologies from previous studies [44–47]. The microstructures were examined from dry specimens using a LEICA DM5000 B microscope (Leica GmbH, Wetzlar, Germany) and were illustrated by hand.

The notation for measured basidiospores follows the format “n/m/p”, denoting that “n” basidiospores were assiduously measured from “m” specimens collected from “p” sampling sites. The size of the basidiospores is expressed as “(a) b–c (d)”, with “b–c” representing at least 90% of the observed values, while “a” and “d” denote the extreme values. Q signifies the length-to-width ratio of the spores. Q_m denotes the average Q value $\pm$ the sample standard deviation of the basidiospores [48].

2.3. DNA extraction, amplification, and sequencing

The desiccated samples (KEF12827, KEF12828) were employed to extract whole genome DNA, adhering to the methodology outlined by Feng et al. [49]. The large subunit ribosomal region (nrLSU) genes and the translation elongation factor 1- α region (*TEF1- α*) genes were amplified using the primer pairs LR0R/LR5 [50,51] and *TEF1*-983F/*TEF1*-1567R [52], respectively.

The PCR amplification procedure is pre-denaturation at 94°C for 4min, followed by 35 cycles of denaturation at 94°C for 60s, annealing at 53°C (for nrLSU and *TEF1- α*) for 40s, and extension at 72°C for 80s, culminating in a final extension at 72°C for 8min [15].

The quality of DNA was detected in NanoDrop 2000 (Thermo Scientific, Waltham, MA) before being sequenced by TSINGKE Biological Technology (Kunming, China).

2.4. Phylogenetic analyses

The sequencing results were processed in MEGA X [53], and submitted to NCBI for sequence homology searches (<https://blast.ncbi.nlm.nih.gov/Blast.cgi>, accessed on August 30 2024) to ascertain the taxonomic placement of the specimens. All accessible sequences were

retrieved from NCBI and integrated into phylogenetic analyses to elucidate the genetic relationship between our samples and other species within the genus. The robustness of the *TEF1- α* intron region was assessed by comparing the outcomes of single-gene and multi-gene analyses [15,42,54]. Based on the studies of Zhang [30,34,39], Fang [35], and others [19,38], *Phylloporus imbricatus* and *Xerocomus* aff. *subtomentosus* were chosen as outgroups. All the data used are listed in Table 1.

Single gene dataset was sequentially submitted to MAFFT (<http://mafft.cbrc.jp/alignment/server/>, an online website, login on September 15 2024) for precise alignment, adhering to the methodology outlined by Katoh and Standley [68]. Subsequently, the aligned sequences of the two genes were merged within PhyloSuite [69]. Unavailable gene sequences were considered as missing data. In congruence with the findings from both single-gene and multi-gene phylogenetic assessments, the intron genes were found to be conserved [70]. ML and BI analyses were conducted on the integrated datasets using RAXML version 8 [71] and MrBayes v3.2 [72], respectively. For the ML analysis, the GTRGAMMAI model [73], was employed, with statistical robustness verified through 1000 iterations of rapid non-parametric bootstrapping [74]. In the BI analysis, the partition replacement model for the combined datasets was evaluated according to the Akaike information criterion (AIC) in PartitionFinder 2 [75], which was then applied to the phylogenetic analysis. The results of phylogenetic analysis are visualized and beautified by FigTree v1.4.4 [76], with only bootstrap frequencies of 50% or higher and posterior probabilities of 0.95 or above displayed on the branches.

3. Results

3.1. Molecular phylogenetic results

Four novel sequences, comprising two nrLSU and two *TEF1- α* , were derived from two distinct samples.

The nuclear large subunit dataset was composed of 94 taxonomic units and spanned 961 characters, while the *TEF1- α* dataset has 70 entries and 721 bases. The integrated dataset, which merged the nrLSU and *TEF1- α* , included 100 taxa and featured 1682 nucleotide positions. TrN + I + G and TIMeF + I + G have been identified as the best alternative models for the nrLSU and *TEF1- α* partitions, respectively. BI analyses were performed with two MCMC runs, each with four chains, and the number of generations was set to 2,500,000. After completion, the average deviation of the splitting

Table 1. Data on *Aureoboletus* species used in phylogenetic analyses.

Species	Voucher	Locality	LSU	TEF1- α	Reference
<i>Aureoboletus abruptibulbus</i>	4588	USA	KF030302	KF030401	[21]
<i>A. albipes</i>	FHMU2228*	China	OP630876	OP676221	[38]
<i>A. albipes</i>	FHMU2237	China	OP630877	OP676222	[38]
<i>A. auriflammeus</i>	CFMR BOS-699	USA	MK601706	MK721060	[18]
<i>A. auriporus</i>	BDCR0431	UK	HQ161871	–	[55]
<i>A. auriporus</i>	MAN020	Brazil	JQ003659	–	[56]
<i>A. ayuukii</i>	30448*	Mexico	OR421569	–	[19]
<i>A. betula</i>	MICH: KUO-10030904	USA	MK601736	–	[18]
<i>A. betula</i>	134/96	Germany	AF050642	–	[57]
<i>A. catenarius</i>	HKAS 54467*	China	NG_057093	KT990711	[31]
<i>A. catenarius</i>	HKAS54463	China	KT990509	KT990710	[31]
<i>A. citriniporus</i>	REH8719	USA	KF030298	–	[21]
<i>A. citriniporus</i>	JLF6091	USA	MH271618	–	[58]
<i>A. clavatus</i>	HKAS59802*	China	KR052044	KR052053	[28]
<i>A. clavatus</i>	GDGM42963	China	KR052046	KR052054	[28]
<i>A. conicus</i>	FHMU4730*	China	OP630878	–	[38]
<i>A. duplicatoporus</i>	HKAS:50498	China	KF112361	KF112230	[15]
<i>A. duplicatoporus</i>	GDGM52898	China	MN410708	–	[34]
<i>A. elvirae</i>	MEXU HO_29006*	Mexico	NG_243306	–	[19]
<i>A. erythraeus</i>	FHMU 3144*	China	NG_075380	MT650114	[36]
<i>A. erythraeus</i>	FHMU1053	China	MT650074	MT650112	[36]
<i>A. formosus</i>	GDGM44444	China	KT291750	MK165833	[30]
<i>A. formosus</i>	GDGM44441*	China	KT291749	KT291744	[30]
<i>A. garciae</i>	MEXU 29006*	Mexico	NG_075245	–	[20]
<i>A. gentilis</i>	ADK4865	Thailand	–	KT824027	[59]
<i>A. gentilis</i>	MG372a	China	KF112344	KF134014	[15]
<i>A. gentilis</i>	Pug1	USA	DQ534635	KF030399	[17]
<i>A. glutinosus</i>	GDGM 44477*	China	NG_068273	MH700205	[34]
<i>A. glutinosus</i>	GDGM44479	China	MH670256	MH700204	[34]
<i>A. griseorufescens</i>	ZM131	China	MH670279	–	[34]
<i>A. griseorufescens</i>	GDGM28490*	China	MH670278	–	[34]
<i>A. guangdongensis</i>	FHMU3797*	China	–	OM321040	[37]
<i>A. innixus</i>	MB03-104	USA	KF030239	KF030400	[21]
<i>A. innixus</i>	CFMR: BOS-544	USA	MK601707	MK721061	[18]
<i>A. liquidus</i>	TNS F-39710*	Japan	NG_056938	–	[22]
<i>A. longicollis</i>	HKAS:53398	China	KF112376	KF112238	[15]
<i>A. longicollis</i>	HKAS80127	China	KT990515	KT990719	[31]
<i>A. marroninus</i>	GDGM43288*	China	NG_057040	KT291746	[29]
<i>A. miniatoaurantiacus</i>	KD 22-004*	India	OR349659	–	[60]
<i>A. miniatoaurantiacus</i>	GDGM42855	China	MH670259	MH700202	[34]
<i>A. miniatoaurantiacus</i>	N.K. Zeng3077	China	MT829114	OP680540	[61]
<i>A. minimus</i>	GDGM 44400*	China	NG_243178	–	[62]
<i>A. minimus</i>	GDGM44401	China	OP901641	–	[63]
<i>A. mirabilis</i>	HKAS:57776	China	KF112360	KF112229	[15]
<i>A. mirabilis</i>	REH9765	USA	KP327661	KP327709	[23]
<i>A. moravicus</i>	MG374a	China	KF112421	KF112232	[15]
<i>A. moravicus</i>	PARMA 1544/11	Italy	KJ676958	KJ676959	[64]
<i>A. nanlingensis</i>	GDGM44759*	China	MH670276	MH700206	[34]
<i>A. nephrosporus</i>	HKAS 74929*	China	NG_057094	KT990721	[31]
<i>A. nephrosporus</i>	HKAS67931	China	KT990516	KT990720	[31]
<i>A. ornatipes</i>	FHMU1981*	China	OP630879	OP676223	[38]
<i>A. projectellus</i>	MICH: KUO-09111014	USA	MK601708	MK721062	[18]
<i>A. projectellus</i>	NYBG13392	USA	KP327622	KP327675	[23]
<i>A. projectellus</i>	AFTOL-ID 713	USA	AY684158	AY879116	[17]
<i>A. pseudorussellii</i>	KEF12827*	China	PQ346298	PQ352347	This study
<i>A. pseudorussellii</i>	KEF12828	China	PQ346299	PQ352348	This study
<i>A. pseudoauriporus</i>	JAB_80	USA	MW662588	MW737490	[24]
<i>A. pseudoauriporus</i>	JAB_320	USA	MW662585	MW737489	[24]
<i>A. quercus-spinosae</i>	GDGM 43755*	China	NG_057121	MK165836	[33]
<i>A. quercus-spinosae</i>	GDGM43758	China	KY039968	MK165837	[33]
<i>A. raphanaceus</i>	GDGM 45911*	China	NG_068304	–	[34]
<i>A. raphanaceus</i>	GDGM44832	China	MH670268	MH700194	[34]
<i>A. raphanaceus</i>	GDGM52590	China	MH670272	MH700193	[34]
<i>A. readii</i>	MEXU 30443*	Mexico	OR421566	–	[19]
<i>A. readii</i>	MEXU 30440	Mexico	OR421567	–	[19]
<i>A. roxanae</i>	CFMR: BOS-698	USA	MK601709	MK721063	[18]
<i>A. roxanae</i>	DS626-07	USA	KF030311	KF030402	[21]
<i>A. rubellus</i>	HKAS105265*	China	MN304782	–	[35]
<i>A. rubellus</i>	FHMU4453	China	–	OP676227	[38]
<i>A. rubellus</i>	FHMU4877	China	–	OP676226	[38]
<i>A. russellii</i>	BD391	UK	HQ161874	–	[55]
<i>A. russellii</i>	CFMR: BOS-716	USA	MK601710	MK721064	[18]
<i>A. shichianus</i>	HKAS:76852	China	KF112419	KF112237	[15]
<i>A. shichianus</i>	HKAS43373	China	AY647211	DQ408145	[65]
<i>A. singeri</i>	CFMR BZ-2395	USA	MK601711	MK721065	[18]
<i>A. sinobadius</i>	GDGM 71932*	China	NG_068305	–	[34]
<i>A. sinobadius</i>	GDGM70666	China	MN204547	–	[34]
<i>A. solus</i>	FHMU4377	China	–	OP680547	[38]
<i>A. solus</i>	GDGM49600	China	MN410707	–	[34]

(Continued)

Table 1. Continued.

Species	Voucher	Locality	LSU	TEF1- α	Reference
<i>A. tenuis</i>	FHMU2225	China	OP615201	–	[38]
<i>A. tenuis</i>	GDGM42601*	China	KF534789	KT291745	[30]
<i>A. thibetanus</i>	HKAS76655	China	KF112420	KF112236	[15]
<i>A. thibetanus</i>	HKAS89494	China	KT990525	KT990729	[31]
<i>A. thibetanus</i>	AFTOL-ID 450	USA	AY700189	DQ029199	[17]
<i>A. tomentosus</i>	HKAS59694	China	KT990513	KT990714	[31]
<i>A. velutipes</i>	GDGM 44713*	China	NG_068272	MH700191	[34]
<i>A. velutipes</i>	GDGM42608	China	MH670251	MH700190	[34]
<i>A. venustus</i>	FHMU4776	China	OP615204	OP680548	[38]
<i>A. venustus</i>	HKAS 77700*	China	NG_057099	–	[32]
<i>A. viscidipes</i>	HKAS77103	China	KT990519	KT990723	[31]
<i>A. viscidipes</i>	FHMU5526	China	OP615206	–	[38]
<i>A. viscosus</i>	OR0361	Thailand	–	MH614703	[66]
<i>A. yunnanensis</i>	HKAS75050	China	KT990520	KT990724	[31]
<i>A. yunnanensis</i>	GDGM26359	China	MN204560	MN549670	[34]
<i>A. yunnanensis</i>	HKAS 57581*	China	KF112422	KF112233	[15]
<i>A. zangii</i>	HKAS74766	China	KT990522	KT990726	[31]
<i>A. zangii</i>	HKAS63217*	China	KT990526	–	[31]
<i>A. zangii</i>	HKAS74751	China	KT990521	KT990725	[31]
<i>Phylloporus imbricatus</i>	HKAS 54859	China	JQ967203	JQ967160	[67]
<i>Xerocomus aff. subtomentosus</i>	HKAS 58865	China	KF112389	KF112294	[15]

The newly generated sequences are marked in bold. (–) means the data is missing.

*Holotype.

frequency is 0.007020. The ML tree and BI tree exhibited congruent topologies, with only the ML trees that possessed both BS and PP values being presented (Figure 1).

In phylogenetic tree, *Aureoboletus pseudorussellii* (KEF12827, KEF12828) formed an independent branch and clustered into a clade with *A. mirabilis*, *A. projectellus*, and *A. russellii*, and has the closest phylogenetic relationship with *A. russellii*.

3.2. Taxonomy

Aureoboletus pseudorussellii D.F. Sun, R. Hua, F. Zhou & J.B. Zhang, sp. nov. (Figures 2 and 3).

Mycobank number: MB857541, *Fungal Names No.*: FN 571200.

Etymology: The epithet “*pseudorussellii*” signifies the new species resemblance to *A. russellii*.

Holotype: China. Zhejiang Province: Lishui City, Qingyuan County, Zuoxi Town, Meishu Village, elev. 913 m, August 19 2024, ZF032 (KEF12827).

Description: Basidiomata are small to medium-sized. Pileus 3–8 cm in diameter, hemispherical to flattened, occasionally with a central depression, featuring a dry surface that remains uncracked with age, white (4A1) to yellow-brown (6A5) subtomentose turning reddish brown (7C7) to blackish brown (7D3) after bruised when young, with an ochre (6A3) to brown (6B4) center, and fringed with a yellow-white (4A2) to white (4A1) short veil at the margin. Context 0.3–0.9 cm thick at the pileus center, whitish (1A1) to pale yellow white (1A2), remains unchanged when injured. Hymenophore is adnate and depressed around the top of stipe; pores are circular, 1–3 per mm, exhibiting a pale-yellow (2A2) in their youth, transitioning to a deeper yellow (2A4) or a yellow

brown (4B2) as they mature; tubes extending up to 10 mm in length, yellow (2A2) to pale brown (2B2), no color change even when damaged. Stipes 8.4–15 × 0.6–2.1 cm, central and solid, clavate, curved in the lower part, the upper part 0.6–1.1 cm diameter, the lower part up to 2.1 cm, reddish brown (7C5), surface viscid when wet, uneven, with obvious white (7A1) to pale reddish brown (7B2) carinate stripes; context is yellowish-white (5A2) to orange (5A5), no reaction when bruised; the base of the stipe is covered by dense yellowish-white mycelium. Odor indistinct.

Basidia 38–53 × 14–19 μ m, thin-walled, clavate, with four sterigmata, 3.5–8 μ m long. *Basidiospores* [40/2/2] (14–)14.5–20.5(–21) × (7.5–)8–9(–9.5) μ m, $Q = (1.57–)1.60–2.40(–2.44)$, $Q_m = 2.04 \pm 0.28$, amygdaloid to fusiform, with thin walls and a surface marked by distinct carinate stripes, light yellow to golden in KOH. *Hymenophoral trama* boletoid, composed of slender hyphae, 3–7 μ m wide, hyaline to pale grayish in KOH. *Cheilocystidia*, commonly found, are 57–68 × 11–13 μ m, fusiform to subclavate, thin walls and hyaline to pale gray in KOH. *Pleurocystidia* are 56–70 × 15–18 μ m, frequently occurring, stout clavate to cystidioid. *Pileipellis* is composed of interlaced hyphae, appearing colorless to light gray in KOH, with thin walls, a diameter of 5–11 μ m, subcylindrical to subclavate terminal cells (28–61 × 6–11.5 μ m). *Pileal trama* is composed of hyphae 4–8 μ m in diameter, thin walls, and hyaline in KOH. *Clamp connections* are absent across all tissues.

Habitat: Under the mixed forests of Fagaceae (*Quercus*) and Pinaceae (*Pinus*).

Distribution: Zhejiang Province, China.

Additional specimens examined: China. Zhejiang Province, Lishui City, Qingyuan County, Zuoxi Town,

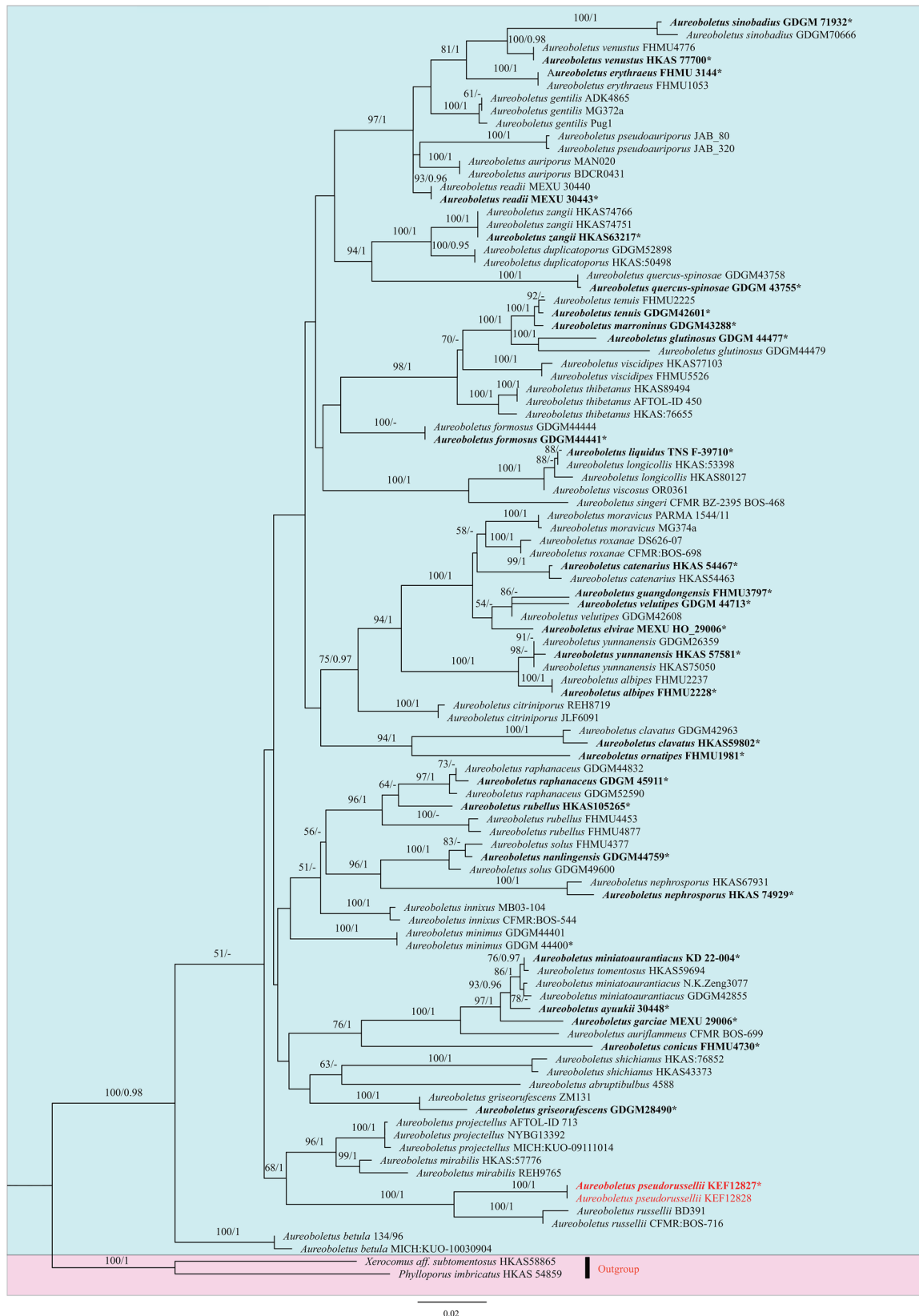


Figure 1. The ML phylogenetic tree of *Aureoboletus*, showcasing BS ≥ 50% and PP ≥ 0.95. The novel species is marked in red, with the type specimen denoted in bold.

Meishu Village, elev. 918 m, August 24 2024, ZF039 (KEF12828).

Note: *Aureoboletus pseudorussellii* features a hemispherical to applanate pileus, uncracked with age, exhibiting a pale yellow to yellow-brown subtomentose

surface that darkens to reddish brown to blackish brown upon bruising in youth, and adorned with a yellow-white to white, short veil at the margin; a surface is marked by distinct white to pale reddish brown carinate stripes stipes, a yellowish-white to

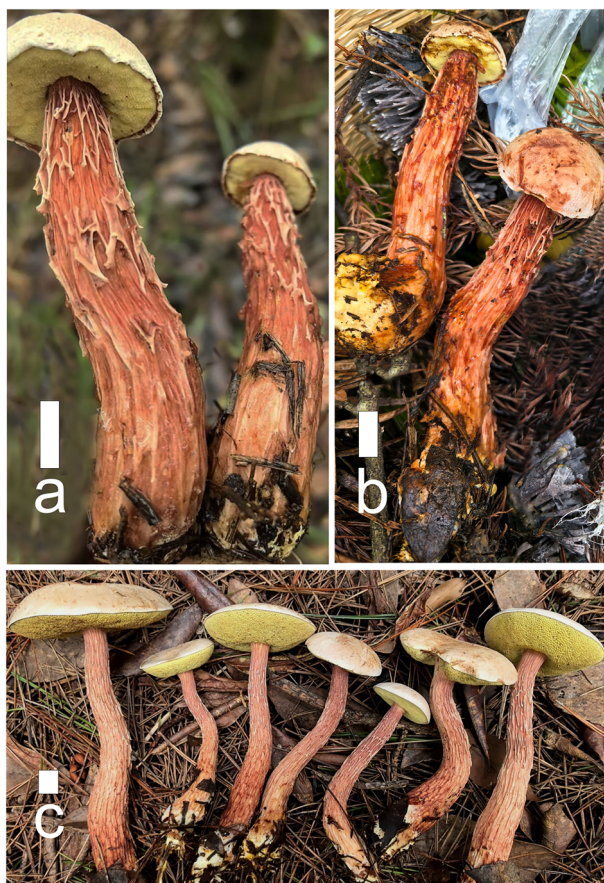


Figure 2. Habitat of *Aureoboletus pseudorussellii*. (a, b) KEF12827 (holotype), photos by Bin Chen; (c) KEF12828, photos by Xiaomin Yan. Scale bars = 10 mm.

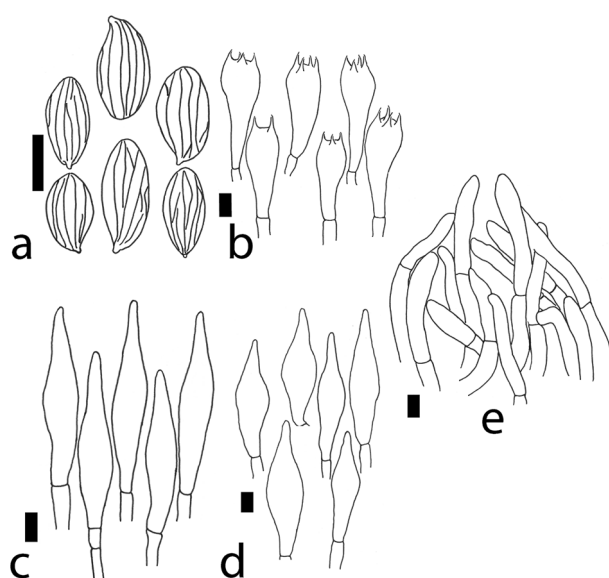


Figure 3. *Aureoboletus pseudorussellii* (KEF12827, Holotype). (a) Basidiospores; (b) Basidia; (c) Cheilocystidia; (d) Pleurocystidia; (e) Pileipellis. The scale is 10 µm. Drawn by F. Zhou.

orange context that does not react to bruising; basidiospores $(14\text{--})14.5\text{--}20.5(\text{--}21) \times (7.5\text{--})8\text{--}9(\text{--}9.5)$ µm, with pronounced carinate stripes. Morphologically and phylogenetically, *A. pseudorussellii* is closest to *A. russellii*. However, *A. russellii* differ from *A.*

pseudorussellii in its color of pileus and stipe, and the reaction in color of context when injured, and the size of basidia, pleurocystidia, and cheilocystidia.

4. Discussion

Aureoboletus pseudorussellii exhibits similar characteristics in its stipes to those of *A. mirabilis* (Murrill) Halling, *A. projectellus* (Murrill) Halling, and *A. russellii* (Frost) G. Wu & Zhu L. Yang. However, *A. mirabilis*, initially described from North America, can be distinguished by its longer and smooth basidiospores $((20) 22\text{--}27 (28) \times 9\text{--}13$ µm), larger pleurocystidia $(72\text{--}85 \times 14\text{--}21$ µm), and a pileus that transitions from grayish ruby to cherry to ruby with pale-colored spots, featuring distinctly coarse, pale yellow to dull yellow reticulations on the stipes [23]. *Aureoboletus projectellus* has larger and smooth basidiospores $((27.3) 30.1 \pm 2.3 (36.4) \times (7.8) 10.8 \pm 1.2 (13.3)$ µm), and smaller basidia $((36.4) 41 \pm 3.9 (44.2) \times (12.7) 14.9 \pm 1.1 (17.9)$ µm), and larger pleurocystidia $((82.9) 84.2 \pm 11.5 (85.8) \times (15.6) 18.8 \pm 2.5 (23.4))$, and the color of stipe is yellowish to brownish yellow to reddish [23]. *Aureoboletus russellii* also has pronounced carinate stripes basidiospores and stipes, but can be differentiated by its reddish brown with a yellowish background pileus, and its context turns pink to pale red when bruised, the context of the stipe turns reddish brown when injured, along with smaller basidia $(32\text{--}40 \times 10.4\text{--}15.2$ µm), larger pleurocystidia $(66.5\text{--}76.8 \times 15.2\text{--}24.7$ µm), and shorter cheilocystidia $(30\text{--}52 \times 11.2\text{--}13.6$ µm) [31].

In phylogenetic analyses, *Aureoboletus pseudorussellii* and *A. mirabilis*, *A. projectellus*, *A. russellii* are clustered into a clade, and have the closest phylogenetic relationship with *A. russellii*, and combined with morphological structure, we named the new species as *A. pseudorussellii*.

It is documented that *Aureoboletus mirabilis*, *A. projectellus* and *A. russellii* are fit for consumption [19,77]. Consequently, the newly discovered species we have acquired might also be edible; however, this hypothesis necessitates substantiation through subsequent research endeavors.

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Author contributions

Conceptualization was carried out by F.Z., J.-B.Z., R.H., and D.-F.S. Methodology was devised by F.Z., J.-B.Z.,

Q.-M.L., S.-X.L., X.L., X.-K.L., C.-L.L., and L.W. The experiment was conducted by F.Z. Formal analysis was performed by F.Z. and J.-B.Z. Resources were provided by F.Z. and J.-B.Z. The original draft was written by F.Z., with review and editing assistance from R.H. and D.-F.S. Supervision was provided by R.H. and D.-F.S., who also administered the project and acquired funding.

Disclosure statement

No potential conflict of interest was reported by the author(s).

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References

- [1] Pouzar Z. Nova genera macromycetum I. Česká Mykol. 1957;11:48–50.
- [2] Quélet L. Quelques espèces critiques ou nouvelles de la flore mycologique de France. Comp Rend l'Assoc Franç pour l'Avance Sci. 1884;12:498–512.
- [3] Saccardo PA. Sylloge Hymenomycetum, Vol. II. Polyporeae, Hydneae, Thelephoreae, Clavariaeae, Tremellinae. Sylloge Fungorum. 1888;6:1–928.
- [4] Klofac W. The genus *Aureoboletus*, a world-wide survey. A contribution to a monographic treatment. Österr Z Pilzk. 2010;19:133–174.
- [5] Singer R. Das System der Agaricales. II. Ann Mycol. 1942;40:132.
- [6] Singer R. The Boletoidae of Florida with notes on extralimital species III. Am Midl Nat. 1947;37(1):1. doi: [10.2307/2421647](https://doi.org/10.2307/2421647).
- [7] Pahlich E, Gerlitz C. A rapid DNA isolation procedure for small quantities of fresh leaf tissue. Phytochemistry. 1980;19(1):11–13. doi: [10.1016/0031-9422\(80\)85004-7](https://doi.org/10.1016/0031-9422(80)85004-7).
- [8] Smith AH, Thiers HD. The boletes of Michigan. Ann Arbor: University of Michigan Press; 1971.
- [9] Corner EJH. Boletus in Malaysia. Singapore: Government Printing Office; 1972.
- [10] Bessette A, Roody WC, Bessette AR. North American Boletes: a color guide to the fleshy pored Mushrooms. Field Mycol. 2000;1:141–142.
- [11] Šutara J. Central European genera of the Boletaceae and Suillaceae, with notes on their anatomical characters. Czech Mycol. 2005;57(1–2):1–50. doi: [10.33585/cmy.57101](https://doi.org/10.33585/cmy.57101).
- [12] Singer R. The Agaricales in modern taxonomy. 4th ed. Koenigstein: Koeltz Scientific Books; 1986. doi: [10.2307/1219523](https://doi.org/10.2307/1219523).
- [13] Both EE. The boletes of North America: a compendium. New York: Buffalo Society of Natl Sciences; 1993.
- [14] Zang M. *Sinoboletus*, a new genus of Boletaceae from China. Mycotaxon. 1992;45:223–227.
- [15] Wu G, Feng B, Xu J, et al. Molecular phylogenetic analyses redefine seven major clades and reveal 22 new generic clades in the fungal family Boletaceae. Fung Divers. 2014;69(1):93–115. doi: [10.1007/s13225-014-0283-8](https://doi.org/10.1007/s13225-014-0283-8).
- [16] Binder M. Zur molekularen Systematik der Boletales: Boletineae und Sclerodermatineae subordo nov. Regensburg [dissertation]. Universität Regensburg, Nat. Fak. III-Biol. u. Vorkl. Med.; 1999.
- [17] Binder M, Hibbett D. Molecular systematics and biological diversification of Boletales. Mycologia. 2006;98(6):971–981. doi: [10.1080/15572536.2006.11832626](https://doi.org/10.1080/15572536.2006.11832626).
- [18] Kuo M, Ortiz-Santana B. Revision of leccinoid fungi, with emphasis on North American taxa, based on molecular and morphological data. Mycologia. 2020;112(1):197–211. doi: [10.1080/00275514.2019.1685351](https://doi.org/10.1080/00275514.2019.1685351).
- [19] Ayala-Vásquez O, Martínez-Reyes M, Pérez-Moreno J, et al. Five new species of *Aureoboletus* and *Chalciporus* (Boletaceae, Boletales) and their ethnomycological aspects. J Fungi. 2023;9(10):1041. doi: [10.3390/jof9101041](https://doi.org/10.3390/jof9101041).
- [20] Haelewaters D, Dima B, Aii A-H, et al. Fungal systematics and evolution: FUSE 6. Sydowia. 2020;72:231–356.
- [21] Nuhn M, Binder M, Taylor A, et al. Phylogenetic overview of the Boletineae. Fungal Biol. 2013;117(7–8):479–511. doi: [10.1016/j.funbio.2013.04.008](https://doi.org/10.1016/j.funbio.2013.04.008).
- [22] Terashima Y, Takahashi H, Taneyama Y, et al. The fungal flora in southwestern Japan: agarics and boletes. Tokai: Tokai University Press; 2016.
- [23] Halling RE, Fechner N, Nuhn M, et al. Evolutionary relationships of *Heimioporus* and *Boletellus* (Boletales), with an emphasis on Australian taxa including new species and new combinations in *Aureoboletus*, *Hemileccinum* and *Xerocomus*. Aust Syst Bot. 2015;28(1):1–22. doi: [10.1071/SB14049](https://doi.org/10.1071/SB14049).
- [24] Farid A, Ae B, Ar B, et al. Investigations in the boletes (Boletaceae) of southeastern USA: four novel species and three novel combinations. Mycosphere. 2021;12(1):1038–1076. doi: [10.5943/mycosphere/12/1/12](https://doi.org/10.5943/mycosphere/12/1/12).
- [25] Hongo T, Nagasawa E. Notes on some bolete from Tottori V. Vol. 18. Report of the Tottori Mycological Institute; 1980. p. 133–141.
- [26] Shi X-F, Liu P-G. *Aureoboletus zangii* (Boletaceae), a new species from China. Mycotaxon. 2013;123(1):451–456. doi: [10.5248/123.451](https://doi.org/10.5248/123.451).
- [27] Zhang M, Li T-H, Song B. A new slender species of *Aureoboletus* from Southern China. Mycotaxon. 2014;128(1):195–202. doi: [10.5248/128.195](https://doi.org/10.5248/128.195).
- [28] Zeng N-K, Zhang M, Liang Z-Q. A new species and a new combination in the genus *Aureoboletus* (Boletales, Boletaceae) from southern China. Phytotaxa. 2015;222(2):129–137. doi: [10.11646/phytotaxa.222.2.5](https://doi.org/10.11646/phytotaxa.222.2.5).
- [29] Zhang M, Li T-H, Jiang X, et al. A new violet brown *Aureoboletus* (Boletaceae) from Guangdong of China. Mycoscience. 2015;56(5):481–485. doi: [10.1016/j.myc.2015.02.002](https://doi.org/10.1016/j.myc.2015.02.002).
- [30] Zhang M, Li T-H, Wang C, et al. *Aureoboletus formosus*, a new bolete species from Hunan Province of China. Mycol Progress. 2015;14(12):7. doi: [10.1007/s11557-015-1142-z](https://doi.org/10.1007/s11557-015-1142-z).

- [31] Wu G, Li Y-C, Zhu X-T, et al. One hundred noteworthy boletes from China. *Fung Divers.* 2016;81(1):25–188. doi: [10.1007/s13225-016-0375-8](https://doi.org/10.1007/s13225-016-0375-8).
- [32] Li F, Zhao K, Deng Q-L, et al. Three new species of Boletaceae from the Heishiding Nature Reserve in Guangdong Province, China. *Mycol Progress.* 2016;15(12):1269–1283. doi: [10.1007/s11557-016-1233-5](https://doi.org/10.1007/s11557-016-1233-5).
- [33] Zhang M, Li T-h, Nuhn ME, et al. *Aureoboletus quercus-spinosae*, a new species from Tibet of China. *Mycoscience.* 2017;58(3):192–196. doi: [10.1016/j.myc.2017.01.007](https://doi.org/10.1016/j.myc.2017.01.007).
- [34] Zhang M, Li T-H, Wang C, et al. Phylogenetic overview of *Aureoboletus* (Boletaceae, Boletales), with descriptions of six new species from China. *MycKeys.* 2019;61:111–145. doi: [10.3897/mycokeys.61.47520](https://doi.org/10.3897/mycokeys.61.47520).
- [35] Fang J-Y, Wu G, Zhao K. *Aureoboletus rubellus*, a new species of bolete from Jiangxi Province, China. *Phytotaxa.* 2019;420:72–78.
- [36] Wang YI, Su M-S, Jiang S, et al. The genus *Hourangia* in China and a description of *Aureoboletus erythraeus* sp. nov. *Phytotaxa.* 2020;472:87–106.
- [37] Zhang XU, Tian RUN, Tang LI-P, et al. Morphological and phylogenetic evidence reveal three new species of *Aureoboletus* (Boletaceae, Boletales) from China. *Phytotaxa.* 2022;567(2):127–148. doi: [10.11646/phytotaxa.567.2.2](https://doi.org/10.11646/phytotaxa.567.2.2).
- [38] Xue R, Zhang X, Xu C, et al. The subfamily Xerocomoideae (Boletaceae, Boletales) in China. *Stud Mycol.* 2023;106(1):95–197. doi: [10.3114/sim.2023.106.03](https://doi.org/10.3114/sim.2023.106.03).
- [39] Liu S-L, Wang X-W, Li G-J, et al. Fungal diversity notes 1717–1817: taxonomic and phylogenetic contributions on genera and species of fungal taxa. *Fung Divers.* 2024;124(1):1–216. doi: [10.1007/s13225-023-00529-0](https://doi.org/10.1007/s13225-023-00529-0).
- [40] Yang Z-L, Wang X, Binder M. A study of the type and additional materials of *Boletus thibetanus*. *Mycotaxon.* 2003;86:283–290.
- [41] Patouillard NT. Enumeration des champignons recoltés par les RR. PP. Farges at Soulie, dans le Thibet oriental at le Su-tchuen. *Bull Soc Bot France.* 1895;11:196–199.
- [42] Zhou F, Gao Y, Song H-Y, et al. *Retiboletus atrofus-cus* (Boletaceae, Boletales), a new species from China. *Arch Microbiol.* 2022;204(7):381. doi: [10.1007/s00203-022-03006-5](https://doi.org/10.1007/s00203-022-03006-5).
- [43] Kornerup A, Wanscher JH. Taschenlexikon der Farben. 3rd ed. Germany: Muster-Schmidt Verlag Göttingen; 1981.
- [44] Li YC, Feng B, Yang ZL. *Zangia*, a new genus of Boletaceae supported by molecular and morphological evidence. *Fung Divers.* 2011;49(1):125–143. doi: [10.1007/s13225-011-0096-y](https://doi.org/10.1007/s13225-011-0096-y).
- [45] Zeng N-K, Cai Q, Yang ZL. *Corneroboletus*, a new genus to accommodate the southeast Asian *Boletus indecorus*. *Mycologia.* 2012;104(6):1420–1432. doi: [10.3852/11-326](https://doi.org/10.3852/11-326).
- [46] Zeng N-K, Liang Z-Q, Yang ZL. *Boletus orientalisbus*, a new species with white basidioma from subtropical China. *Mycoscience.* 2014;55(3):159–163. doi: [10.1016/j.myc.2013.07.004](https://doi.org/10.1016/j.myc.2013.07.004).
- [47] Hosen MI, Feng B, Wu G, et al. *Borofutius*, a new genus of Boletaceae from tropical Asia: phylogeny, morphology and taxonomy. *Fung Divers.* 2013;58(1):215–226. doi: [10.1007/s13225-012-0211-8](https://doi.org/10.1007/s13225-012-0211-8).
- [48] Zeng N-K, Chai HUI, Jiang S, et al. *Retiboletus nigrogriseus* and *Tengioboletus fujianensis*, two new boletes from the south of China. *Phytotaxa.* 2018;367(1):45. doi: [10.11646/phytotaxa.367.1.5](https://doi.org/10.11646/phytotaxa.367.1.5).
- [49] Feng Y-L, Sun D-F, Fang Y, et al. *Cystoderma yong-pingense* sp. nov. (Squamanitaceae, Agaricales) a new species from southwestern China. *Mycoscience.* 2024;65(3):151–155. doi: [10.47371/mycosci.2024.02.008](https://doi.org/10.47371/mycosci.2024.02.008).
- [50] Vilgalys D, Gonzalez D. Organization of ribosomal DNA in the basidiomycete *Thanatephorus praticola*. *Curr Genet.* 1990;18(3):277–280. doi: [10.1007/BF00318394](https://doi.org/10.1007/BF00318394).
- [51] James TY, Kauff F, Schoch CL, et al. Reconstructing the early evolution of Fungi using a six-gene phylogeny. *Nature.* 2006;443(7113):818–822. doi: [10.1038/nature05110](https://doi.org/10.1038/nature05110).
- [52] Rehner S, Buckley E. A *Beauveria* phylogeny inferred from nuclear ITS and EF1- α sequences: evidence for cryptic diversification and links to *Cordyceps teleomorphs*. *Mycologia.* 2005;97(1):84–98. doi: [10.3852/mycologia.97.1.84](https://doi.org/10.3852/mycologia.97.1.84).
- [53] Kumar S, Stecher G, Li M, et al. MEGA X: molecular evolutionary genetics analysis across computing platforms. *Mol Biol Evol.* 2018;35(6):1547–1549. doi: [10.1093/molbev/msy096](https://doi.org/10.1093/molbev/msy096).
- [54] Zhou F, Gao Y, Song H-Y, et al. Phylogenetic and morphological evidence reveal five new species of boletes from Southern China. *J Fungi.* 2023;9(8):814. doi: [10.3390/jof9080814](https://doi.org/10.3390/jof9080814).
- [55] Dentinger BTM, Ammirati JF, Both EE, et al. Molecular phylogenetics of porcini mushrooms (*Boletus* section *Boletus*). *Mol Phylogenet Evol.* 2010;57(3):1276–1292. doi: [10.1016/j.ympev.2010.10.004](https://doi.org/10.1016/j.ympev.2010.10.004).
- [56] Neves MA, Binder M, Halling RE, et al. The phylogeny of selected *Phylloporus* species, inferred from NUC-LSU and ITS sequences, and descriptions of new species from the Old World. *Fung Divers.* 2012;55(1):109–123. doi: [10.1007/s13225-012-0154-0](https://doi.org/10.1007/s13225-012-0154-0).
- [57] Binder M, Fischer M. Molekularbiologische charakterisierung der gattungen *Boletellus* und *Xerocomus*: *Xerocomus pruinatus* (Fr. & Hoek) Quel. und verwandte Arten. *Boll Gruppo Micol G Bresadola.* 1997;40:79–90.
- [58] Frank JL. GenBank: National Center for Biotechnology Information; c2018 [Internet] [cited 2024 Sep 15]. Available from: <https://www.ncbi.nlm.nih.gov/nuccore/MH271618.1>
- [59] Raspé O, Vadthanarat S, Kesel A, et al. *Pulveroboletus fragrans*, a new Boletaceae species from Northern Thailand, with a remarkable aromatic odor. *Mycol Progress.* 2016;15(4):15. doi: [10.1007/s11557-016-1179-7](https://doi.org/10.1007/s11557-016-1179-7).
- [60] Das K. GenBank: National Center for Biotechnology Information; c2023 [cited 2024 Sep 15]. Available from: <https://www.ncbi.nlm.nih.gov/nuccore/OR349659>
- [61] Zeng N-K, Jiang S. GenBank: National Center for Biotechnology Information; c2020 [cited Sep 15]. Available from: <https://www.ncbi.nlm.nih.gov/nuccore/?term=N.K.+Zeng3077>
- [62] Zhang M GenBank: National Center for Biotechnology Information; c2022 [cited Sep 15]. Available from: https://www.ncbi.nlm.nih.gov/nuccore/NG_243178.1
- [63] Zhang M. GenBank: National Center for Biotechnology Information; c2022 [cited Sep 15]. Available from: <https://www.ncbi.nlm.nih.gov/nuccore/OP901641.1>

- [64] Nonis U, Ponzi E. *Aureoboletus moravicus* (Vacek) W. Klofac f. *luteus* f. nov. Boll Cent Micol Friul. 2014;2014:27–30.
- [65] Horak E. Supplementary remarks to *Austroboletus* (Corner) Wolfe (Boletaceae). Sydowia. 1980;33:71–87.
- [66] Vadthanarat S, Lumyong S, Raspé O. *Cacaoporus*, a new Boletaceae genus, with two new species from Thailand. MycoKeys. 2019;54:1–29. doi: [10.3897/mycokeys.54.35018](https://doi.org/10.3897/mycokeys.54.35018).
- [67] Zeng N-K, Tang L-P, Li Y-C, et al. The genus *Phylloporus* (Boletaceae, Boletales) from China: morphological and multilocus DNA sequence analyses. Fung Divers. 2013;58(1):73–101. doi: [10.1007/s13225-012-0184-7](https://doi.org/10.1007/s13225-012-0184-7).
- [68] Katoh K, Standley DM. MAFFT Multiple sequence alignment software version 7: improvements in performance and usability. Mol Biol Evol. 2013;30(4):772–780. doi: [10.1093/molbev/mst010](https://doi.org/10.1093/molbev/mst010).
- [69] Zhang D, Gao F, Jakovlić I, et al. PhyloSuite: an integrated and scalable desktop platform for streamlined molecular sequence data management and evolutionary phylogenetics studies. Mol Ecol Resour. 2020;20(1):348–355. doi: [10.1111/1755-0998.13096](https://doi.org/10.1111/1755-0998.13096).
- [70] Cui Y-Y, Feng B, Wu G, et al. Porcini mushrooms (*Boletus* sect. *Boletus*) from China. Fung Divers. 2016;81(1):189–212. doi: [10.1007/s13225-015-0336-7](https://doi.org/10.1007/s13225-015-0336-7).
- [71] Stamatakis A. RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. Bioinformatics. 2014;30(9):1312–1313. doi: [10.1093/bioinformatics/btu033](https://doi.org/10.1093/bioinformatics/btu033).
- [72] Ronquist F, Teslenko M, van der Mark P, et al. MrBayes 3.2: efficient Bayesian phylogenetic inference and model choice across a large model space. Syst Biol. 2012;61(3):539–542. doi: [10.1093/sysbio/sys029](https://doi.org/10.1093/sysbio/sys029).
- [73] Stamatakis A. RAxML-VI-HPC: maximum likelihood-based phylogenetic analyses with thousands of taxa and mixed models. Bioinformatics. 2006;22(21):2688–2690. doi: [10.1093/bioinformatics/btl446](https://doi.org/10.1093/bioinformatics/btl446).
- [74] Felsenstein J. Confidence limits on phylogenies: an approach using the bootstrap. Evolution. 1985;39(4):783–791. doi: [10.1111/j.1558-5646.1985.tb00420.x](https://doi.org/10.1111/j.1558-5646.1985.tb00420.x).
- [75] Lanfear R, Frandsen PB, Wright AM, et al. PartitionFinder 2: new methods for selecting partitioned models of evolution for molecular and morphological phylogenetic analyses. Mol Biol Evol. 2017;34(3):772–773. doi: [10.1093/molbev/msw260](https://doi.org/10.1093/molbev/msw260).
- [76] Rambaut A. FigTree, a graphical viewer of phylogenetic trees. Edinburgh: Institute of Evolutionary Biology, University of Edinburgh; 2009.
- [77] Li H, Tian Y, Menolli N, et al. Reviewing the world's edible mushroom species: a new evidence-based classification system. Compr Rev Food Sci Food Saf. 2021;20(2):1982–2014. doi: [10.1111/1541-4337.12708](https://doi.org/10.1111/1541-4337.12708).