

Article

First Report of the Genus *Lanmaoa* (Boletaceae) from Indian Himalaya Uncovers a Novel Species with Morpho-Taxonomy and Molecular Phylogeny

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Abstract

Our exploration of Indian boletoid mushrooms (Boletaceae and related fleshy poroid fungi) led to the discovery of a species belonging to the genus *Lanmaoa*, marking the first record of this genus from the country. During macrofungal explorations in different parts of subtropical to temperate Uttarakhand (a Himalayan state in India), a new species of *Lanmaoa* was collected. After thorough studies of Indian collections this species is proposed herein as *Lanmaoa atropurpurea* sp. nov. and presented with conventional morpho-taxonomy and multigene molecular phylogeny. A provisional key to Asian species of *Lanmaoa* is also given.

Keywords: Boletales; macrofungi; new species; phylogeny; taxonomy

1. Introduction

The genus *Lanmaoa* G. Wu & Zhu L. Yang was erected by Wu et al. (2016) [1], with *Lanmaoa asiatica* G. Wu & Zhu L. Yang from southwestern China designated as the type species. Species of *Lanmaoa* are characterized by stipitate-pileate basidiomata with a cream-yellow to lemon-yellow hymenophore that typically stains dull blue upon bruising. The tubes are concolorous with the hymenophoral surface or occasionally light red. The stipe is centrally positioned, yellow to lemon-yellow at the apex and gradually transitions to light or dark purplish red toward the base. Basidiospores are smooth, narrowly suboblong, subellipsoid to subfusiform, while the pileipellis is organized as an (ixo) trichoderm or (ixo) subcutis [1–4].

Lanmaoa is morphologically similar to another boletoid genus, *Baorangia* G. Wu & Zhu L. Yang; however, multilocus phylogenetic analyses have consistently resolved the two genera as distinct evolutionary lineages within the Boletaceae [5,6]. The circumscription of *Lanmaoa* remains a subject of taxonomic debate, with some authors proposing its inclusion within a third boletoid genus, *Cyanoboletus* Gelardi, Vizzini & Simonini based on their close phylogenetic relationship and partially overlapping morphological characteristics [1,4,6–9]. *Cyanoboletus* is generally distinguished by predominantly dull brown basidiomata, whereas species of *Lanmaoa* typically exhibit conspicuous yellow and



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red pigmentation [1,6,8–10]; however, this distinction is not always a reliable generic delimitation. Wu et al. [1,6] proposed the relatively thin hymenophore (approximately one-third to one-fifth the thickness of the pileus context) as a diagnostic character for *Lanmaoa*. However, this character has proven to be inconsistent, as it has also been observed in *Cyanoboletus instabilis* (W.F. Chiu) G. Wu & Zhu L. Yang and in some *Baorangia* species [e.g., *B. emileorum* (Barbier) Vizzini, Simonini & Gelardi] and varies within *Lanmaoa*, including in *L. rubriceps* N.K. Zeng & Hui Chai [8] or *Lanmaoa macrocarpa* N.K. Zeng, H. Chai & S. Jiang [9]. These observations indicate that no single morphological character can separate *Lanmaoa* from *Cyanoboletus*. Consequently, the delimitation of these genera should rely on an integrative approach combining morphology with multilocus phylogenetic evidence, as done by Wu et al. (2023) [11].

Currently, *Lanmaoa* comprises 12 accepted species (<https://www.speciesfungorum.org/>) (accessed on 30 August 2026). The genus exhibits a broad geographic distribution, with confirmed records from Asia, Europe, North Africa, North America, and Australia [1,3,12]. Species of *Lanmaoa* are ectomycorrhizal, forming symbiotic associations primarily with members of the Pinaceae and Fagaceae, indicating an important ecological role in temperate and subtropical forest ecosystems [1,3,4]. Despite its occurrence in China [1,8,9], no species of *Lanmaoa* has previously been confirmed from India, to the best of our knowledge.

Field surveys and integrative taxonomic approaches that combine morphological observations with molecular phylogenetic analyses are likely to uncover additional undescribed taxa from underexplored habitats. During a recent field survey in forested areas of Chamoli district, Uttarakhand (India), specimens of *Lanmaoa* were collected that closely resembled *L. angustispora* G. Wu & Zhu L. Yang; however, detailed morphological and molecular analyses confirm that they represent a new species forming a distinct lineage within the genus *Lanmaoa*.

2. Materials and Methods

2.1. Sampling and Morphological Observations

Fresh specimens ranging from young to mature were collected from mixed temperate forests of northwestern Himalaya. The macro-morphological features and substrate details were recorded both in the field and at the respective basecamps. Images of basidiomata were captured using a Nikon D3500 DSLR camera, (Nikon Corp., Tokyo, Japan). The terminology for macro-morphological characters was adopted from [13], while ref. [14] was primarily consulted for color codes and their respective terms. After collection and macro-morphological characterization, samples were dried in an electric field dryer at the temperature ranging from 40–50 °C, for approximately 10 h under continuous warm-air circulation, with regular monitoring to prevent overheating. Micro-morphological characters were examined with free-hand sections prepared from dried specimens. The sections were mounted in a mixture of 5% KOH and 1% ammoniacal Congo red and observed under an Olympus CX 41 compound microscope (Olympus, Tokyo, Japan), equipped with an Olympus DP-22 camera (Olympus, Tokyo, Japan). Illustrations of the micro-morphological features were observed under 1000× magnification and drawn with the help of a dedicated drawing tube at same magnification. Basidiospore measurements and length/width ratios (Q) are represented as minimum–mean–maximum. Basidia length measurements exclude the length of sterigmata. Herbarium acronym follows Thiers (continuously updated) [15].

2.2. DNA Extraction, Polymerase Chain Reaction (PCR) and Sequencing

Genomic DNA was isolated from approximately 100 mg of dried basidioma tissue using the HiPurA® Fungal DNA Purification Kit (HIMEDIA, Mumbai, India), following the manufacturer's protocol. The amplification (PCR) of four nuclear loci, the internal transcribed spacer (ITS1-5.8S-ITS2 = ITS), partial 28S rDNA D1-D2 regions (28S), translation elongation factor 1- α (*TEF1*- α) and region between conserved domains 6 and 7 of second largest subunit of RNA polymerase II (*RPB2*), were done using the primer pairs ITS1 F and ITS4, LR0R and LR5, ef1-983F and ef1-1567R, brpb2-6F and frpb2-7cR [16–19] respectively in ProFlex PCR System (Applied Biosystems, Waltham, MA, USA). PCR reaction conditions were adapted from the protocols described by Zeng et al. (2013, 2015) [20,21] with certain modifications. The thermal cycling conditions included an initial denaturation at 95 °C for 3 min, followed by 35 cycles of denaturation at 94 °C for 30 s, annealing at 52–54 °C for 30 s, and extension at 72 °C for 1 min. A final extension step was performed at 72 °C for 10 min. The resulting PCR products were purified using the QIAquick PCR Purification Kit (QIAGEN, Hilden, Germany). Both strands of the amplicons were sequenced using the same primer set on an ABI 3500 automated DNA analyzer (Applied Biosystems, Waltham, MA, USA). Raw sequence data were assessed for quality using Sequence Scanner Software version 1 (Applied Biosystems). Sequence alignment assembly and editing were performed in Geneious version 5.1 [22]. All newly obtained sequences have been deposited in GenBank (<https://www.ncbi.nlm.nih.gov/genbank/>) (accessed on 26 September 2026). The GenBank accession numbers of all sequences used in the phylogenetic analysis are provided in corresponding Table 1 and Figure ??.

Table 1. GenBank accession numbers correspond to the sequences used in the phylogenetic analyses. The newly generated sequences are indicated in bold and missing sequences are indicated by -.

Species Name	GenBank Accessions					
	Voucher	Locality	ITS	28S (LSU)	<i>RPB2</i>	<i>TEF1</i> - α
<i>Baorangia pseudocalopus</i>	HKAS 63607	China	-	KF112355	KF112677	KF112167
<i>Baorangia pseudocalopus</i>	HKAS 75081	China	-	KF112356	-	KF112168
<i>Cyanoboletus brunneoruber</i>	HKAS80579-1	China	-	KT990568	KT990401	KT990763
<i>Cyanoboletus brunneoruber</i>	HKAS80579-2	China	-	KT990569	KT990402	KT990764
<i>Cyanoboletus hymenoglutinosus</i>	DC 14-010	India	KT907355	KT860060	-	-
<i>Cyanoboletus instabilis</i>	HKAS 59554	China	-	KF112412	KF112698	KF112186
<i>Cyanoboletus pulverulentus</i>	9606	USA	-	KF030313	-	KF030418
<i>Cyanoboletus sinopulverulentus</i>	HKAS 59609	China	-	KF112366	KF112700	KF112193
<i>Cyanoboletus</i> sp.	HKAS59418	China	-	KT990570	KT990403	KT990765
<i>Lanmaoa angustispora</i>	HKAS 74759	China	-	KM605140	KM605178	KM605155
<i>Lanmaoa angustispora</i>	HKAS 74752	China	PV694363	KM605139	KM605177	KM605154
<i>Lanmaoa angustispora</i>	HMJAU 60054	-	-	-	OP495818	OP495820
<i>Lanmaoa angustispora</i>	HMJAU 60055	-	-	-	OP495819	OP495822
<i>Lanmaoa angustispora</i>	HMJAU 60056	-	-	-	-	OP495821
<i>Lanmaoa asiatica</i>	N.K. Zeng 2795	China	-	MG030469	-	MG030480
<i>Lanmaoa asiatica</i>	N.K. Zeng2125	China	MG030477	MG030470		MG030481
<i>Lanmaoa asiatica</i>	HKAS 63592	China	-	KM605142	KM605175	KM605152
<i>Lanmaoa asiatica</i>	HKAS 63603	China	-	KM605143	KM605176	KM605153
<i>Lanmaoa asiatica</i>	HKAS63516	China	-	KT990584	KT990419	KT990780
<i>Lanmaoa asiatica</i>	HKAS 54095	-	-	KM605141	KM605174	KM605151
<i>Lanmaoa asiatica</i> (as <i>Boletus</i> aff. <i>carnipes</i>)	HKAS 54094	China	-	KF112353		KF112161
<i>Lanmaoa atropurpurea</i>	SC/PU/25/12, holotype	India	PZ747753	PZ747759	PZ770682	QB001907
<i>Lanmaoa atropurpurea</i>	SC/PU/25/15	India	PZ747754	PZ747760	PZ770683	QB001908

Table 1. Cont.

Species Name	GenBank Accessions					
	Voucher	Locality	ITS	28S (LSU)	RPB2	TEF1- α
<i>Lanmaoa borealis</i>	2858	USA	-	JQ326998	-	JQ327021
<i>Lanmaoa carminipes</i>	MB06-001	USA	-	JQ327001	-	JQ327022
<i>Lanmaoa flavoviridis</i>	NY775777	Costa Rica	PV694355	JQ924339	KF112681	KF112160
<i>Lanmaoa fragrans</i>	MG780	Italy	PX991779	-	-	-
<i>Lanmaoa macrocarpa</i>	N.K. Zeng 3021 (FHMU 1982)	-	-	MH879684	-	MH879713
<i>Lanmaoa macrocarpa</i>	N.K. Zeng 3251 (FHMU 2212)	-	MH885347	MH879685	-	MH879714
<i>Lanmaoa pseudosensibilis</i>	DS615-07	USA	-	KF030257	-	KF030407
<i>Lanmaoa pseudosensibilis</i>	Mushroom Observer#339050	USA	ON705305	OQ754987	-	-
<i>Lanmaoa roseocrispans</i>	FLAS RB92-10	USA	-	KP327615	-	KP327616
<i>Lanmaoa rubriceps</i>	N.K. Zeng 2766	China	MG030472	MG030465	-	-
<i>Lanmaoa rubriceps</i>	N.K. Zeng 2767	China	MG030474	MG030467	-	-
<i>Lanmaoa rubriceps</i>	N.K. Zeng 2773	China	MG030475	MG030468	-	MG030479
<i>Lanmaoa rubriceps</i>	N.K. Zeng 2774	China	MG030476	MG030471	-	-
<i>Lanmaoa rubriceps</i>	N.K. Zeng 3006 (FHMU 1967)	China	MH885346	MH879683	-	MH879712
<i>Lanmaoa sp.</i>	HKAS 52518	China	-	KF112354	-	KF112162
<i>Lanmaoa subulurida</i>	Farid 1023	USA	MW675736	MW662572	MW737460	MW737485
<i>Lanmaoa subulurida</i>	Farid 631	USA	MW675743	MW662578	MW737464	MW737487
<i>Rugiboletus brunneiporus</i>	HKAS 68586	China	-	KF112402	KF112719	KF112197
<i>Rugiboletus brunneiporus</i>	HKAS 83009	China	-	KM605133	KM605169	KM605146
<i>Rugiboletus extremiorientalis</i>	HKAS74754	China	-	KT990639	KT990469	KT990832

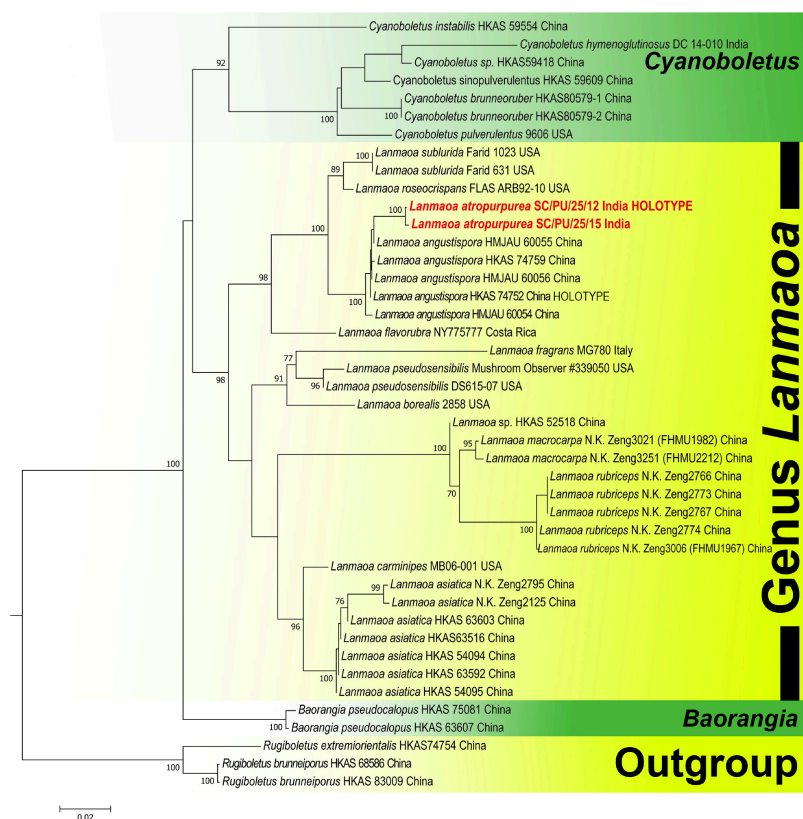


Figure 1. Phylogram generated by maximum likelihood analysis based on 4-locus (ITS, 28S, *TEF1- α* and *RPB2*) sequence data for *Lanmaoa atropurpurea* and allied species. Maximum likelihood bootstrap support values (MLBs) $\geq 70\%$ are shown above or below the branches at nodes. *Lanmaoa atropurpurea* is placed in bold red font to highlight its phylogenetic position in the tree.

2.3. Phylogenetic Analysis

Newly generated sequences of ITS, 28S, *RPB2* and *TEF1- α* , and their close relatives, were retrieved from BLASTN search against GenBank (<https://www.ncbi.nlm.nih.gov/genbank>) (accessed on 30 August 2026) and from relevant published phylogenies [6,8,9]. Taxa representing the closest relatives outside the ingroup were chosen to ensure appropriate tree rooting. Four raw datasets (ITS, 28S, *RPB2* and *TEF1- α*) were created separately. All the datasets were aligned separately using the online version of the multiple sequence alignment program MAFFT ver. 7 (<https://mafft.cbrc.jp/alignment/software/>) (accessed on 30 August 2026) with the L-INS-i [23] strategy, and normal alignment mode was used for alignment. The obtained alignment was checked and trimmed with the conserved motifs manually with MEGA ver. 7 [24]. The congruence of the datasets was tested using the incongruence length difference (ILD) test [25,26]. The analysis was performed in PAUP version 4.0b10 [27] using the partition-homogeneity test (PHT) option with 1000 heuristic search replicates. This test was used to assess the statistical congruence among datasets and to determine whether the individual data partitions could be combined for phylogenetic analysis. After testing congruence, the individual gene datasets were then concatenated into multi-locus dataset using BioEdit v. 7.0.9 [28] and processed for the phylogenetic analyses. Phylogenetic analysis was performed using the maximum likelihood (ML) method, the above-mentioned partitioned dataset with raxmlGUI 2.0 [29], and the GTRGAMMAI substitution model. This analysis was executed by applying the rapid bootstrap algorithm with 1000 replicates to obtain nodal support values. Maximum likelihood bootstrap (MLbs) values $\geq 70\%$ were shown with the novel species being represented in the phylogenetic tree in bold red font (Figure ??). Phylogenetic trees for the individual markers ITS, 28S, *RPB2*, and *TEF1- α* are provided as Supplementary Figures S1–S4. Estimations of evolutionary divergence between sequences were conducted using the maximum composite likelihood model [30]. The analyses involved 15 nucleotide sequences of ITS, 39 nucleotide sequences of LSU (28S), 20 nucleotide sequences of *RPB2* and 37 nucleotide sequences of *TEF1- α* . All positions containing gaps and missing data were eliminated. These evolutionary analyses were conducted in MEGA7 [24].

3. Results

3.1. Phylogenetic Inferences

A p -value ≥ 0.05 was considered to indicate no significant incongruence among the datasets. The ILD test resulted in a p -value of 0.539 indicating no significant incongruence among datasets. Therefore, the partitions were considered combinable for a combined phylogenetic analysis. The concatenated four-locus dataset (ITS + 28S + *RPB2* + *TEF1- α*) of *Lanmaoa* comprised 43 voucher specimens and 3015 nucleotide positions (including gaps and missing data). The aligned sequence lengths were 773 bp for ITS, 928 bp for 28S, 687 bp for *TEF1- α* and 627 for *RPB2*. The combined dataset contained 991 distinct patterns, 557 parsimony-informative sites, 228 singleton sites and 2230 constant sites. Phylogenetic analysis (Figure ??) of *Lanmaoa* with *Rugiboletus extremiorientalis* (Lj.N. Vassiljeva) G. Wu & Zhu L. Yang and *Rugiboletus brunneiporus* G. Wu & Zhu L. Yang as the outgroup [8,9] strongly supports the clustering of the Indian specimens as placing them in the same lineage of the Chinese *L. angustispora*; however, the analysis does not consistently resolve the two species as separate clades exclusively with the help of four-locus phylogeny (ITS + 28S + *RPB2* + *TEF1- α*). Even pairwise sequence-divergence analyses of the individual loci revealed varying levels of differentiation between the Indian species and *L. angustispora*. For ITS, *L. atropurpurea* (SC/PU/25/12 and SC/PU/25/15) were identical ($d = 0.000$) to *L. angustispora* HKAS 74752. The LSU (28S) locus also showed limited differentiation from *L. angustispora* HKAS 74759 and HKAS 74752 by only 0.002 substitutions per site. In contrast, *RPB2* provided substantially greater differentiation, where the proposed new Indian species

differed from *L. angustispora* HMJAU 60055 by 0.043 substitutions per site, from HKAS 74759 and HKAS 74752 by 0.054, and from HMJAU 60054 by 0.055, while, *TEF1*- α showed poor differentiation, with the proposed novel species distinguished from *L. angustispora* HMJAU 60055 by 0.012 substitutions per site, from HKAS 74759 and HKAS 74752 by 0.012, and from HMJAU 60054 and HMJAU 60056 by 0.000 and 0.012, respectively.

3.2. Taxonomy

Lanmaoa atropurpurea Uniyal, Su. Datta, K. Das & Vizzini sp. nov. (Figures 2 and 3)

MycoBank: MB 865299

GenBank: ITS: PZ747753 (holotype), PZ747754; 28S: PZ747759 (holotype), PZ747760; RPB2: PZ770682 (holotype), PZ770683; *TEF1*- α : QB001907 (holotype), QB001908

Type: INDIA, UTTARAKHAND Chamoli District, Devasthali, in mixed temperate forest, 2213 m, N 30°03'44.86'' E 79°27'52.28'', June 26, 2025, Shikha Choudhary and Priyanka Uniyal SC/PU/25/12 (holotype! CAL 2425).

Etymology: Refers to the dark purple pileus surface of mature basidiomata.

Diagnosis: Characterized by a light brown to greyish red or dark purple viscid and cracked pileus, a chalky to greyish white pileus context, an ixotrichoderm pileipellis, a reticulate stipe with reddish brown context at base. It differs from *L. angustispora* by a yellowish orange with a reddish tinged hymenophore, a finely reticulate stipe near apex, and occurrence in mixed forests of *Quercus leucotrichophora* A. Camus and *Rhododendron arboreum* Sm.

Description: Basidiomata medium to large-sized. Pileus 70–110 mm diam., convex when young, later becoming plano-convex with uplifted margins, light brown (7D5) to greyish red (8D4) or turning dark brown (7E5) to dark purple upon handling or with maturity; surface smooth, velvety, viscid when wet, cracked irregularly at maturity; margin entire, incurved to uplifted. Hymenophore adnate, pore surface melon yellow to apricot yellow (3A6–B6) when young, changing to yellowish orange (4B5) with reddish tinge at maturity, turning immediately to light blue (21D5) when bruised; pores angular to radially elongated, 1–2/mm; tubes up to 3–6 mm long, pale yellow (1A3), turning blue (21D4) when cut. Stipe 60–70 × 8–13 mm, subclavate to cylindrical, eccentric, concolorous to pore surface up to middle, gradually greyish red to pastel red (9B5–10B4), at base turning brown (7F5); surface striate to finely reticulate near apex, covered with irregularly scattered greyish ruby (11C6) dots, bruising light blue when handled. Context in pileus chalky to greyish white (1A2), 5–12 mm thick; context in stipe white to pale yellow (2A5), reddish brown (6E5) at base, bruising immediately bluish (21D4) on cut. Basal mycelium whitish to greyish white (1A1), unchanging when bruised. Taste not recorded, odor indistinctive. Spore print not obtained.

Basidiospores 9.0–11.00–13.3 × 3.2–4.63–5.3 μ m, ($Q = 1.90$ –2.40–3.17) elliptical to oblong, olive-greenish brown in 5% KOH, smooth. Basidia 28.6–35 × 6.4–10 μ m, narrowly clavate, thin-walled, four-spored; sterigmata 2.7–4.3 μ m long. Pleurocystidia (24.5) 29.2–48.8 × 8.5–11.7 μ m, fusiform to subfusiform, ventricose to ventricose-rostrate, thin-walled, hyaline, sometimes yellowish pigmented in 5% KOH; emergent up to 22 μ m. Tube edge fertile. Cheilocystidia 24.4–33.9 (34.7) × 6.9–9.5 (10.3) μ m, ventricose to ventricose rostrate, subfusiform, thin-walled, hyaline, sometimes yellowish pigmented in 5% KOH, emergent up to 12.7 μ m. Subhymenium 4–4.5 μ m wide, composed of isodiametric cells. Hymenophoral trama divergent, composed of thin-walled, septate, gelatinous hyphae, 6–7.5 μ m wide. Pileipellis an ixotrichoderm 240–255 μ m thick, composed of erect to suberect, thin-walled, septate, rarely branched hyphae, compactly interwoven with a thin layer of gluten; terminal cells 23.9–51.4 × 4.2–8 μ m, subcylindrical to subfusiform. Stipitipellis a trichoderm, up to 150 μ m thick, composed of thin-walled, septate, branched, erect

to suberect hyphae, brown pigmented in 5% KOH; with infrequent tufts of cystidia and basidia; caulocystidia $28\text{--}35.5 \times 7.4\text{--}12.2 \mu\text{m}$, clavate, pyriform, fusiform to subcylindric; caulobasidia $29\text{--}31 \times 6.4\text{--}12 \mu\text{m}$, narrowly clavate, 4-spored. Clamp connections absent in all tissues.

Habitat: Scattered on the ground in forests dominated by *Quercus leucotrichophora* and *Rhododendron arboreum*.

Additional materials examined: INDIA, UTTARAKHAND: Chamoli District, Devasthali, in mixed temperate forest, 2244 m, N $30^{\circ}03'45.96''$ E $79^{\circ}28'52.25''$, 30 June 2025, Shikha Choudhary and Priyanka Uniyal SC/PU/25/15 (CAL 2426).

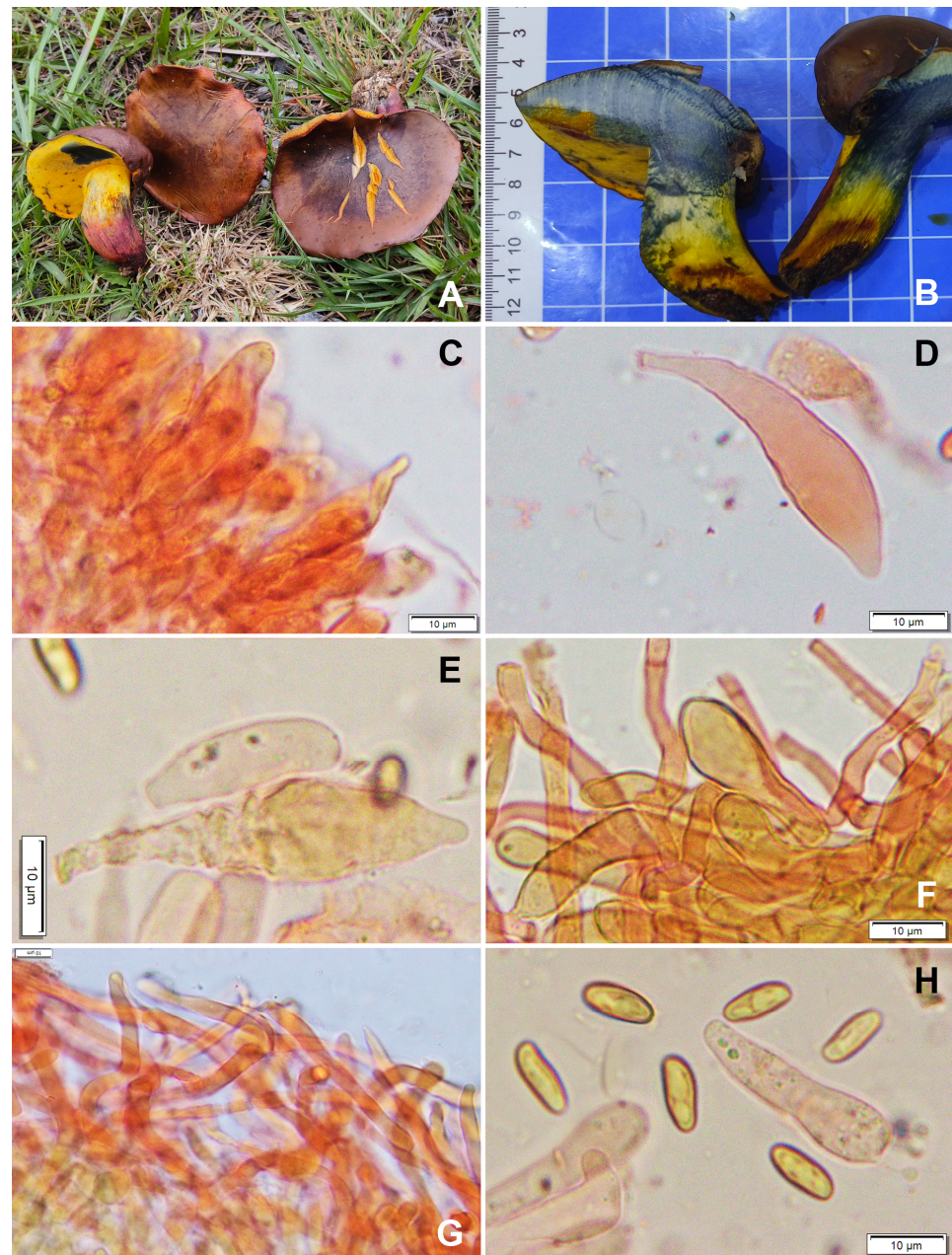


Figure 2. Photoplate of *Lanmaoa atropurpurea* (CAL 2425, holotype). (A,B)—Fresh and dissected basidiomata in the field and basecamp; (C)—Cheilocystidia; (D,E)—Pleurocystidia; (F)—Clusters of caulocystidia; (G)—Transverse section through the pileipellis showing its hyphal elements; (H)—Basidiospores and basidia. Scale bars—(C–H) = 10 μm .

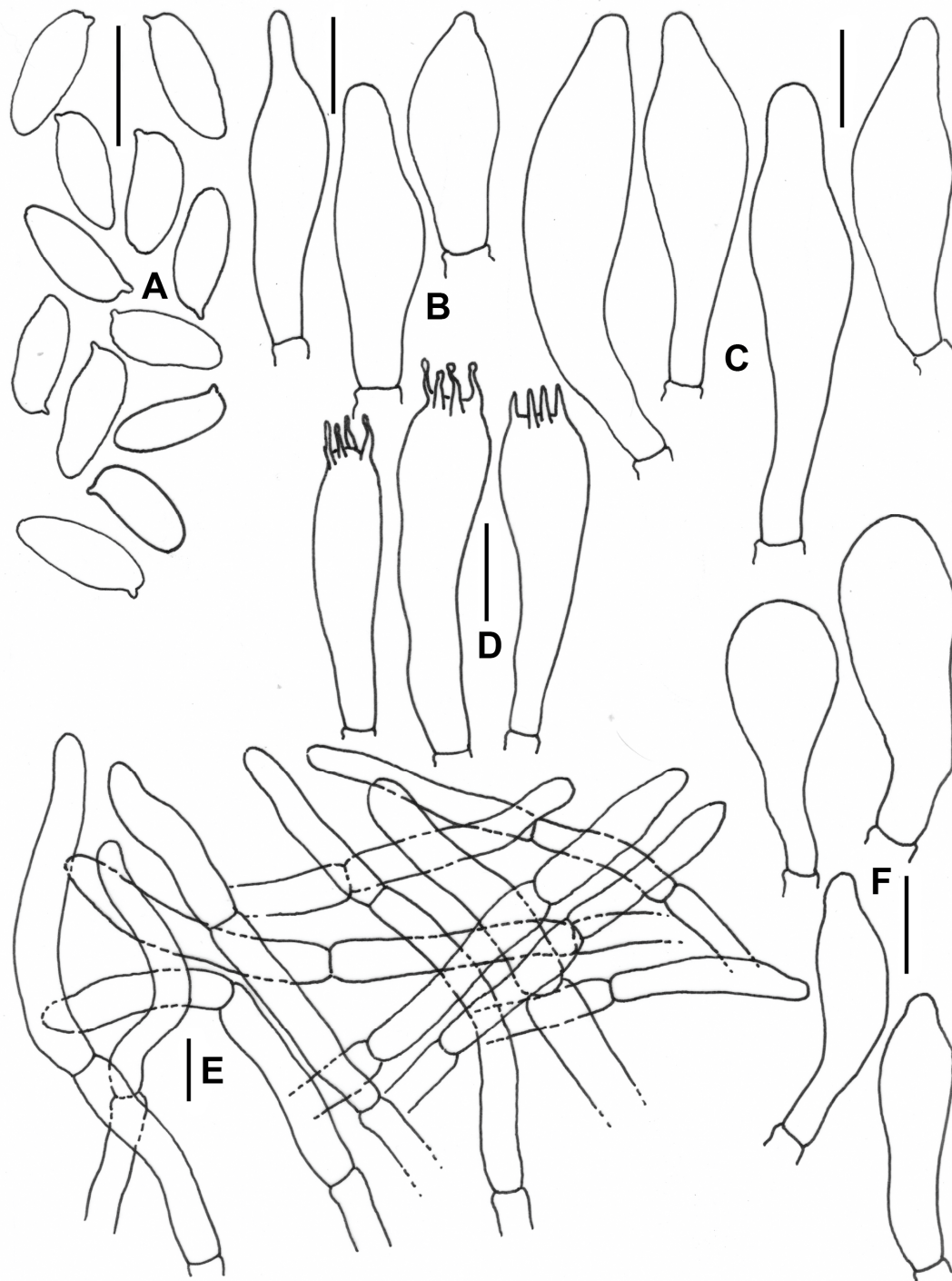


Figure 3. Micro-morphological drawings of *Lanmaoa atropurpurea* (CAL 2425, holotype). (A)—Basidiospores; (B)—Cheilocystidia; (C)—Pleurocystidia; (D)—Basidia; (E)—Elements of the pileipellis; (F)—Caulocystidia. Scale bars—(A–F) = 10 μ m.

4. Discussion

Lanmaoa angustispora G. Wu & Zhu L. Yang from China shows overall morphological resemblance and a close phylogenetic affinity to the proposed novel species *L. atropurpurea*. However, *L. angustispora* can be distinguished by its thicker (12–20 mm) pileus context (5–12 mm in *L. atropurpurea*), geranium red to greyish red hymenophore with maturity (yellowish orange with a reddish tinge in *L. atropurpurea*), stipe with purplish red dotted elements (finely reticulate near apex with striations in *L. atropurpurea*), and ecologically by its occurrence in mixed forests dominated by *Castanea* and *Pinus* [1]. *Lanmaoa rubriceps* N.K.

Zeng & Hui Chai from China is readily distinguished by its red, crimson to orange-red pileus and a trichodermal pileipellis [8]. Similarly, *L. macrocarpa* N.K. Zeng, H. Chai & S. Jiang from Chian differs in possessing a dry, finely tomentose pileus, a yellow and thicker pileus context (up to 25 mm), longer tubes (up to 15 mm), a comparatively thinner pileipellis (120–160 µm thick) with a trichodermal structure, and a hymeniform stipitipellis [9]. *Lanmaoa asiatica* G. Wu & Zhu L. Yang from China can be distinguished by its dry, dull red to red or shell-pink pileus, thicker pileus context (10–30 mm), septate cheilocystidia, a trichodermal to subcutis pileipellis, and a hymeniform stipitipellis [1].

The combination of a light brown to greyish red or dark purple, viscid and cracked pileus, chalky white to greyish white pileus context, ixotrichodermal pileipellis, reddish-brown stipe context at the base, and a reticulate stipe, together with its distinct phylogenetic placement, supports recognition of the new taxon as a distinct species of *Lanmaoa*. The present study is based on two collections (CAL 2425 and CAL 2426) from the same locality, which may limit assessment of the full range of intraspecific variation. However, both collections comprised immature to mature basidiomata with consistent diagnostic macro- and micro-morphological characters, further supported by multilocus phylogenetic analysis. Additional later collections from the type locality and other localities will help characterize its morphological variability, ecological preferences, and geographical distribution.

It is worth noting that a four-locus molecular phylogeny alone does not clearly differentiate *L. angustispora* from the proposed new species, *L. atropurpurea*, as detailed in our ‘Results’ section (specifically under ‘Phylogenetic Inferences’). Instead, the robust delimitation of these species relies on combining morphological evidence with the concordance of multilocus data. This integration is crucial because pairwise sequence divergence is heavily influenced by sequence length. For instance, the ITS region included only one sequence for *L. angustispora* and exhibited greater variability compared to the 28S or *RPB2* regions. Therefore, pairwise distances do not provide a consistent criterion for species recognition, particularly given the lack of an established species-level threshold for *Lanmaoa*.

The genus *Lanmaoa* is currently represented in Asia by five species, with four previously known only from China and the present species representing the first generic record from India. An identification key to the Asian species is provided to facilitate field identification and further species delimitation.

A provisional key to the species of *Lanmaoa* from Asia

- 1a Pileus dry, pileipellis as a trichoderm. 2
- 1b Pileus viscid when wet, pileipellis as an ixotrichoderm. 4
- 2a Tubes long, up to 15 mm; pileus brownish red.*L. macrocarpa*
- 2b Tubes shorter, 3–7 mm; pileus crimson red or dull red to shell-pink, never brownish red. 3
- 3a Stipe comparatively smaller in length, 55–90 mm long, surface yellow, sometimes covered with brownish red minute squamules, reticulation absent; pore surface yellow, sometimes with reddish tinge at maturity, pores stuffed when young.*L. rubriceps*
- 3b Stipe comparatively longer, 80–110 mm long, yellow at the apex, greyish red to brownish red in the middle, greyish ruby towards the base, sometimes with reticulations at the upper part, squamules absent; pore surface yellow without red tinge, pores never stuffed.*L. asiatica*
- 4a Hymenophore surface geranium red to greyish red at maturity; stipe surface without any striation or reticulation, stipe context cream to pale yellow throughout the entire length.*L. angustispora*

- 4b Hymenophore surface orangish yellow with reddish tinge at maturity; stipe surface with striation or faint reticulation, stipe context white to pale yellow, reddish brown at base. *L. atropurpurea*

Supplementary Materials: The following supporting information can be downloaded at: <https://www.mdpi.com/article/10.3390/taxonomy6040064/s1>, Figure S1: Maximum likelihood phylogram of the ITS sequence data of *Lanmaoa atropurpurea* and allied species; Figure S2: Maximum likelihood phylogram of the 28S sequence data of *L. atropurpurea* and allied species; Figure S3: Maximum likelihood phylogram of the *RPB2* sequence data of *L. atropurpurea* and allied species; Figure S4: Maximum likelihood phylogram of the *TEF1- α* sequence data of *L. atropurpurea* and allied species.

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