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Fungal Biodiversity Profiles 31-40

Kanad DAS[a], *Aniket GHOSH*[b], *Dyutiparna CHAKRABORTY*[a],
Jingwei LI[c], *Lihong QIU*[c], *Abhishek BAGHELA*[d], *Marek HALAMA*[e],
Manoj E. HEMBROM[f], *Tahir MEHMOOD*[b], *Arvind PARIHAR*[a],
Bartosz PENCAKOWSKI[g], *Monika BIELECKA*[g], *Kamila RECZYŃSKA*[h],
Dorota SASIELA[e], *Upendra SINGH*[b], *Yu SONG*[c],
Krzysztof ŚWIERKOSZ[e], *Katarzyna SZCZĘŚNIAK*[e], *Priyanka UNIYAL*[b],
Jianbin ZHANG[c] & *Bart BUYCK*[i]*

[a]*Cryptogamic Unit, Botanical Survey of India, P.O. Botanic Garden,*
Howrah 711103, India, email:daskanadbsi@gmail.com, arvind_peace@rediffmail.com, dyuti.parna.mail@gmail.com

[b]*Department of Botany & Microbiology, H.N.B. Garhwal University*
(A Central University), Srinagar, Garhwal, 246174, Uttarakhand, India,
email: ghosh.aniket87@gmail.com, uniyalsppriyanka@gmail.com,
mehmoodt898@gmail.com, upenrana04@gmail.com

[c]*State Key Lab of Biocontrol, School of Life Science, Sun Yat-sen University,*
Guangzhou 510275, China, email: qiulh@mail.sysu.edu.cn

[d]*MACS' Agharkar Research Institute, Biodiversity and Palaeobiology Group,*
National Fungal Culture Collection of India (NFCCI), G.G. Agarkar Road,
Pune – 411004, India, email: abhishekbaghela@aripune.org

[e]*Museum of Natural History, University of Wrocław, ul. Sienkiewicza 21,*
50-335 Wrocław, Poland; e-mail: marek.halama@uwr.edu.pl

[f]*Central National Herbarium, Botanical Survey of India, P.O. Botanic Garden,*
Howrah 711103, India, email: manojhembrom@yahoo.co.in

[g]*Department of Pharmaceutical Biotechnology, Wrocław Medical University,*
ul. Borowska 211a, 50-556 Wrocław, Poland

[h]*Department of Botany, University of Wrocław, ul. Kanonia 6/8,*
50-328 Wrocław, Poland

[i]*Museum National d'Histoire Naturelle, Institut de Systematique, Evolution,*
Biodiversité – UMR 7205 CNRS MNHN UPMC EPHE, CP 39,
12 rue Buffon, F-75005 Paris, France

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* Corresponding author: buyck@mnhn.fr

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Abstract – In this new series of Fungal Biodiversity Profiles, the authors describe ten Basidiomycetes, one recombination and nine taxa new to science, using both morphological and molecular data. Descriptions are provided for *Craterellus parvogriseus* sp. nov. (Cantharellales); for *Lactifluus maenanensis* sp. nov., *Russula albidogrisea* sp. nov., *R. aureorubra* sp. nov., *R. aureoviridis* sp. nov., *R. obscuricolor* sp. nov. and *R. pauriensis* sp. nov. (Russulales), for *Xerocomus reticulostipitatus* sp. nov. (Boletales) and for *Leucocybe houghtonii* comb. nov. and *Amanita rajendrae* sp. nov. (Agaricales).

Agaricales / Amanita / Boletales / Cantharellales / Craterellus / Lactifluus / Leucocybe / phylogeny / Russula / Russulales / systematics / Xerocomus

31. *Amanita rajendrae* Mehmood, K. Das, Uniyal *sp. nov*. **Figs 1-3**

MycoBank: MB 821683

GenBank: MF170174 (nrLSU).

Systematic position: Basidiomycota, Agaricomycetes, Agaricales, Amanitaceae.

Etymology: named in honour of Prof. Rajendra P. Bhatt for his contribution to the wild mushrooms of Uttarakhand in India.

Diagnosis: *Amanita rajendrae* is distinct from other known species of *Amanita* sect. *Vaginatae* by a combination of medium to large-sized basidiomata, pale yellow to light yellow pileus, subdistant lamellae, stipe which is covered by fibrils arranged in zigzag pattern, globose basidiospores (8.7-10.5 × 8.0-10 µm) and occurrence under *Cedrus deodara*.

Holotype: INDIA, Uttarakhand, Nainital district, Mukteshwar town, Shahar Phatak forest, N29°27.374' E79°44.588, alt. 2247 m a.s.l., on the ground under *Cedrus deodara* (Roxb.) G. Don in temperate coniferous forest. 15 Aug. 2016, *T. Mehmood* TM 16-1298, 16 Aug. 2016, *T. Mehmood*, TM 16-1317. (CAL 1530, **holotype**!).

Basidiocarps medium-sized. *Pileus* 50-96 mm wide, initially convex then plano-convex and finally plane-umbonate, slightly depressed at center; surface smooth, dry, shiny, pale yellow or light yellow (4A3-4) to ivory or platinum blond (4B3-4) over centre, yellowish white (4A2) to cream (4A3) toward margin; margin shortly striate up to 9-17 mm, non-appendiculate, slightly uplifted with age. *Pileus context* 5-8 mm thick, thinning evenly toward margin, white (1A1), unchanging when exposed or bruised. *Universal veil on pileus* absent. *Universal veil at stipe base* saccate, 45-60 × 17-28 mm, white (1A1-2A1) thick, membranous, persistent. *Lamellae* free, subdistant (5-6/cm at margin), 5 mm broad, white (1A1); lamellulae common, truncate, of various lengths, unevenly distributed. *Stipe* 110-177 × 12-20 mm, slightly tapering upward, white (1A1) densely covered by white (1A1) fibrils arranged in zigzag pattern. *Stipe context* white (1A1), hollow, unchanging when bruised or exposed. *Partial veil* absent. *Odor* indistinct. *Taste* not recorded. *Spore print* white.

Basidiospores [40/2/2] (8.0-)8.7-10.5(-12.3) × (7.7-)8.0-10(-11.7) µm, Q = (1.0-)1.02-*1.03*-1.05(-1.10), hyaline, colourless, thin-walled, inamyloid, globose, rarely subglobose, with multiguttulate contents, apiculus lateral to sublateral 1.0-1.5 µm long. *Basidia* (46-)52-68(-70) × (13-)14-15(-15.5) µm, 2- to 4-spored, thin-walled, colourless; sterigmata up to 6 × 2 µm. *Clamp connections* not observed at the base of basidia. *Subhymenium* w_{st}-*near* = 60-80 µm thick, w_{st}-*far* = 85-108 µm, basidia arising from small inflated cells (up to 12 × 20 µm wide). *Lamellae edge* sterile; inflated cells clavate or pyriform, 18-30 × 14-20 µm, colourless, thin-

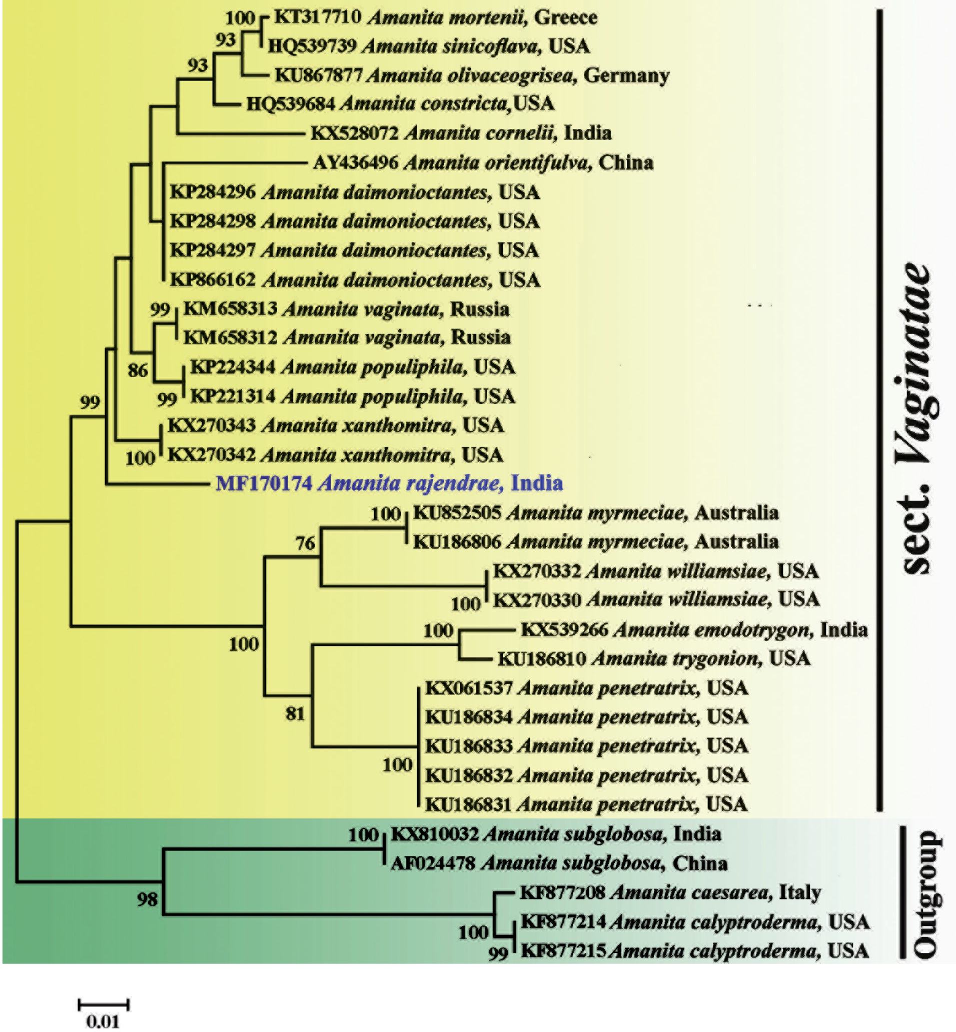


Fig. 1. Maximum Likelihood (ML) phylogeny of *Amanita* showing the position of *A. rajendrae.* In the present phylogenetic analysis, 33 nrLSU sequences of *Amanita* were considered including our new species; *A. subglobosa*, *A. caesarea* and *A. calyptroderma* are considered as outgroups. The sequence from TM 16-1298 (*Amanita rajendrae,* marked with bold and blue font) clusters with GenBank sequences of other available sequences for species of *Amanita* sec. *Vaginatae*. The nrLSU dataset was aligned with online version of MAFFT v. 7 (Katoh & Standley, 2013). No manual editing was done within the alignment. Phylogenetic analysis was conducted with Maximum Likelihood (ML) method implemented in MEGA 6.0 (Tamura *et al.*, 2013). One-thousand bootstrap replicates were analysed to obtain nodal support values. Bootstrap support values (> 50%) obtained from maximum likelihood (ML) analysis are shown above or below the branches at nodes. GenBank accession numbers are provided before each species name and followed by country of origin.

walled. *Hymenophoral trama* bilateral, divergent; w_{cs} = 40-60 µm; well rehydrated, filamentous undifferentiated hyphae (4-8) µm wide; vascular hyphae not observed. *Pileipellis* 250-450 µm thick, in two layers; suprapellis 90-150 µm thick, gelatinized, colorless, composed of filamentous undifferentiated hyphae (3-8 µm wide); subpellis

150-300 µm thick, not gelatinized, composed of filamentous undifferentiated, subradially and densely arranged hyphae (3-7 µm wide), containing brown intracellular pigmentation; vascular hyphae not observed. *Pileus trama* filamentous; hyphae 4-12 µm wide, undifferentiated, branched, septate, thin-walled, hyaline;

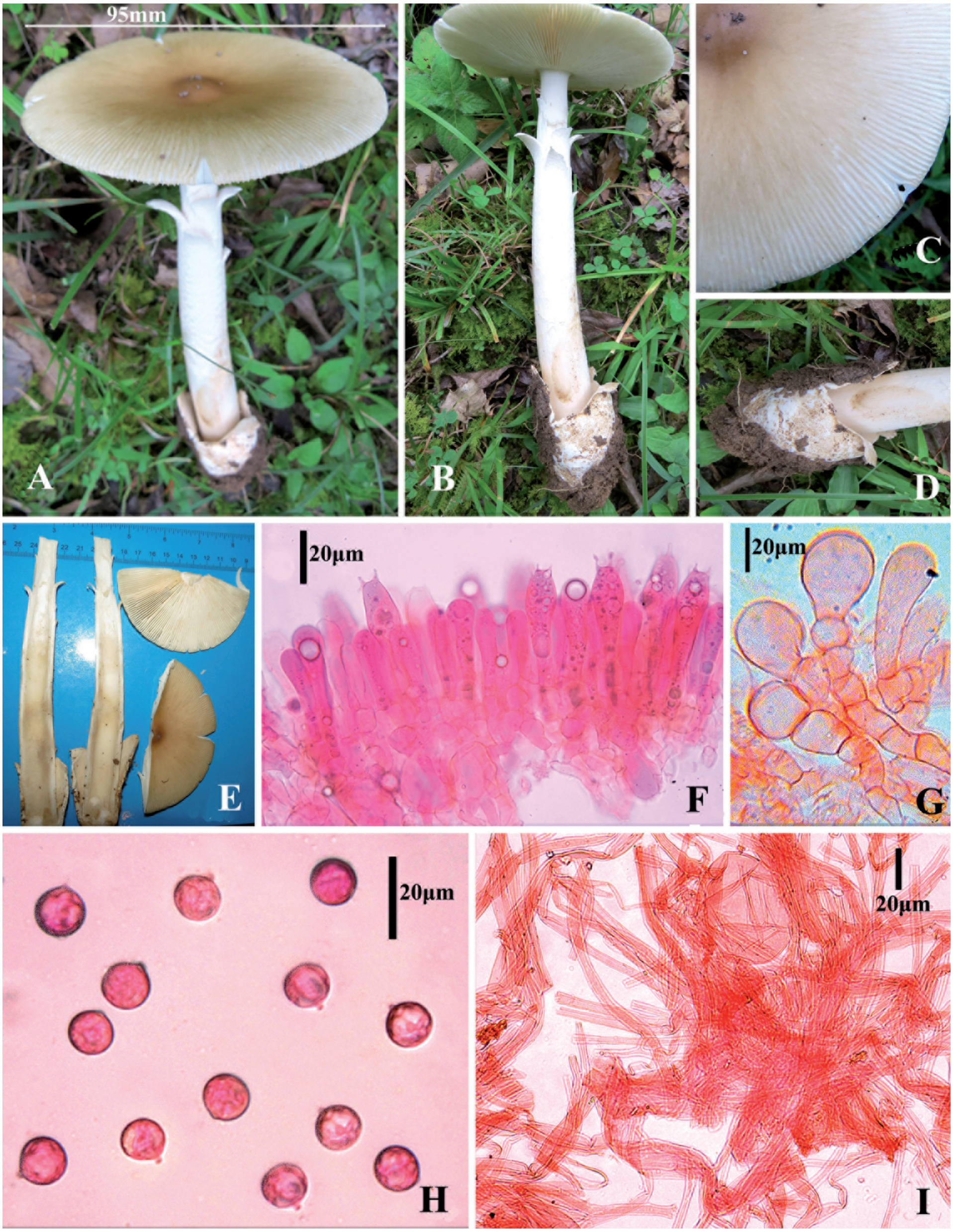


Fig. 2. *Amanita rajendrae* (holotype). **A-E.** Fresh basidiomata. **F.** Basidia and element of subhymenium. **G.** Lamellae edges cells. **H.** Basidiospores. **I.** Elements of universal veil from stipe base. Scale bars: **A** = 95 mm, **K-I** = 20 µm.

acrophysalides common up to 131 × 64 μm, thin-walled, hyaline; oleiferous hyphae up to 10-16 μm wide; vascular hyphae not observed. *Exterior surface of universal veil* (on stipe base) filamentous, mainly composed of undifferentiated hyphae, 4-14 μm wide, slightly thick-walled; inflated cells globose (up to 70 × 65 μm), narrowly ellipsoid to elongate (e.g. 78 × 25 μm), colourless. *Interior surface of universal veil* (on stipe base) filamentous, mainly composed of undifferentiated hyphae, 3-9 μm wide; inflated cells subglobose to ovoid (up to 76 × 58 μm), infrequent. *Stipe context* longitudinally acrophysalidic; composed of filamentous, undifferentiated hyphae, 3-8 μm wide; acrophysalides dominating, 130-200 × 35-55 μm. *Clamp connections* absent in all tissues.

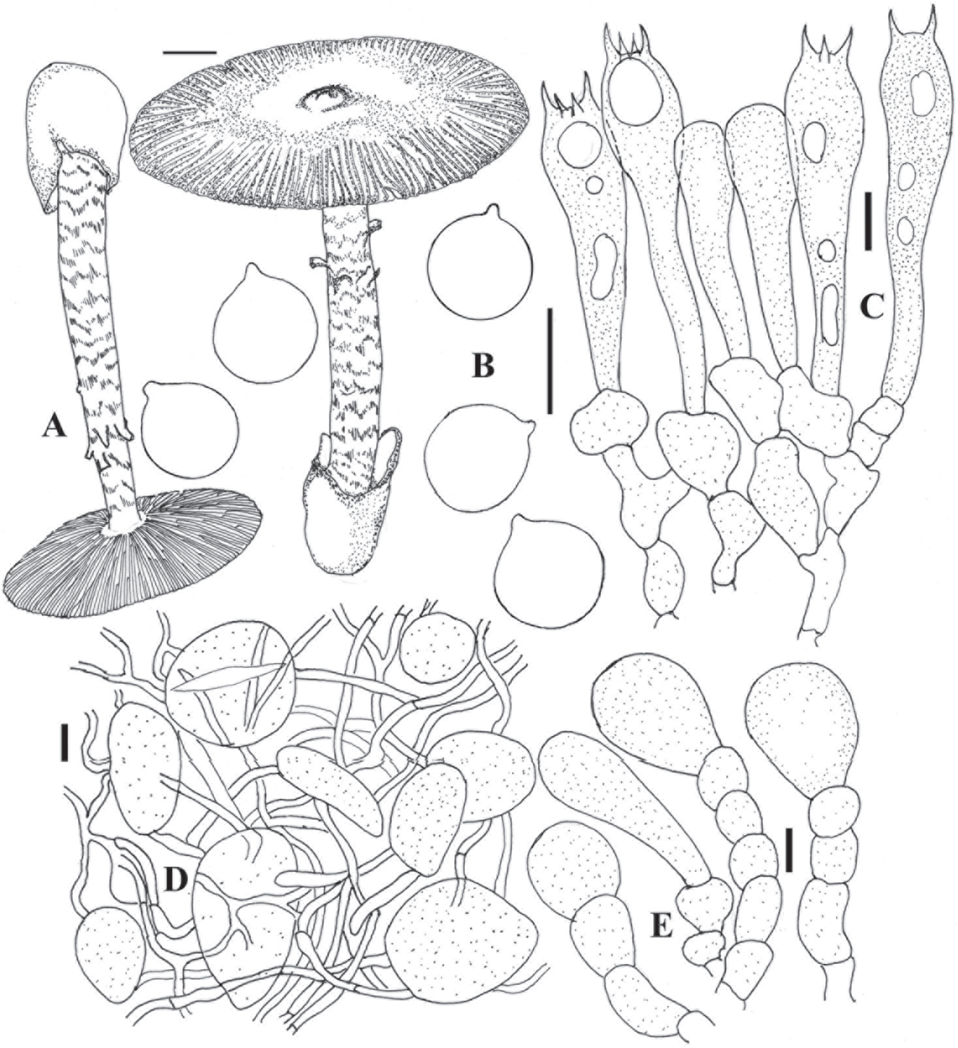


Fig. 3. *Amanita rajendrae* (holotype). **A.** Basidiomata **B.** Basidiospores **C.** Basidia and element of hymenium and subhymenium. **D.** Elements of universal veil at stipe base. **E.** Lamellae edges cells. Scale bars: **B**-**E** = 10 μm, **D** = 20 μm.

Notes: The combination of macro- and micromorphological features like inamyloid basidiospores, saccate volva, absence of a bulb and basidial clamps place *A. rajendrae* in *Amanita* subg. *Amanita* sect. *Vaginatae* sensu Yang (1997).

In eastern Asia, *A. rajendrae* might be confused with *A. brunneofuliginea* Zhu L. Yang, originally described from China (Yang 1997), however, the latter has a blackish brown to brownish black disc (at pileus), bearing a white to dirty white patch of universal veil on the pileus, having a saccate volva which is dirty white with plentiful pale-leather to orange spots on its outer surface and has subglobose to broadly ellipsoid basidiospores [Q = (1.04-)1.06-*1.13*-1.24(-1.26), see Yang (1997)]. *Amanita orientifulva* Zhu L. Yang, M. Weiss & Oberw., also reported from China, is morphologically somewhat similar to the present taxon, but differs by its brown to dark brown pileus, a darker ring-like zone at the inner end of its marginal striations on the pileus and has globose to subglobose basidiospores with Q values slightly higher than those of the present species [Q = 1.01-*1.06*-1.12(-1.23), see Yang (1997)].

Two species of sect. *Vaginatae* reported recently from India, i.e. *A. cornelii* Mehmood, K. Das, Iqbal Hosen, Tulloss & R.P. Bhatt and *A. emodotrygon* Mehmood, Tulloss, K. Das, Iqbal Hosen & R.P. Bhatt (GenBank numbers KX528072 and KX539266 respectively in Fig. 1), can easily be segregated from the present taxon. *Amanita cornelii* is a small-sized species which has crude and irregular pattern of brown subradial stripes on its pileus, a stipe with a pallid background color largely covered by gray to brown fibrils that become nearly black with bruising and globose to subglobose basidiospores with slightly higher Q value than the present taxon [Q = (1.00-)1.02-*1.06*-1.10(-1.25), see Tibpromma *et al.* (2017)]. *Amanita emodotrygon* has a greyish brown to olive, campanulate pileus which is deeply grooved toward margin, crowded white lamellae that become pale yellowish with age, basidiospores that are globose to subglobose with slightly lower Q values than those of our species; Q = (1.0-)1.05-*1.08*-1.12(-1.17), furthermore, it occurrs in coniferous forest under *Pinus roxburghii* (Tibpromma *et al.*, 2017).

Macro- and micromorphology (Figs 2-3) coupled with the LSU-based genetic differences, segregate *Amanita rajendrae* from previously known species of *Amanita* sect. *Vaginatae*. Both BLAST searches and our nrLSU-tree clearly indicate the genetic disimilarities (96% identity with 95% query coverage) of *A. rajendrae* from four taxa: *Amanita xanthomitra* Tulloss nom. prov. (originally reported from USA, see www.amanitaceae.org?Amanita%20xanthomitra) differs from the present taxa by its deep olive to yellowish olive pileus; pale gray to black crumb-like warts of universal veil on pileus and globose to subglobose basidiospores with slightly higher Q values than that of the present taxon, viz. Q = 1.0-*1.05*-1.09(-1.19). *Amanita rajendrae* is somewhat similar to *A.* aff. *vaginata* (Bull.: Fr.) Lam., however, the latter possesses a small basidiomata ca. 5 cm, brownish grey pileus, becoming grey toward margin (Yang *et al.*, 2001). *Amanita daimonioctantes* Tulloss nom. prov. (originally reported from Canada) possesses a pale orange pileus that becomes fulvous to red brown in the center, and has a white external volval surface that becomes orange-brown to rusty in numerous spots and has globose to subglobose basidiospores with slightly higher Q value compared to the present taxon, viz. Q = (1.02-)1.05-*1.07*-1.10(-1.18) [see www.amanitaceae.org?Amanita%20 daimonioctantes]. *Amanita populiphila* Tulloss & Moses described from North America differs from the present taxon by a unstriped, white to pale yellowish pileus that takes on rusty stains with time; cream-colored lamellae having pale orange or pinkish tint; occurrence of plentiful lamellulae and a weakly structured, white volva that tends to change color as the pileus does. *Amanita populiphila* has only been recorded with species of *Populus* (cottonwood and aspen) and has subglobose spores with slightly higher Q values than that of the present taxon, viz. Q = (1.0-)1.04-*1.11*-1.20(-1.61) (see Tulloss & Moses 1995).

32. ***Craterellus parvogriseus*** U. Singh, K. Das & Buyck ***sp. nov.*** **Figs 4-7**

MycoBank: MB 821920

GenBank: MF421099 (ITS), MF421098 (LSU)

Systematic position: Basidiomycota, Agaricomycetes, Cantharellales, Hydnaceae.

Etymology: Referring to small sized, grey colored basidiomata of type specimen.

Diagnosis: Distinct from all the known species of *Craterellus* by the combination of the following characters: basidiomata up to 40 mm high, 4-21 mm diam., small sized with non-perforate, grey to brownish grey pileus, upturned margin, white to greyish white hymenophore with irregular folds which clearly demarcate from the stipe apex, narrowly hollow stipe, basidiospores 7-*9.6*-12 × 6.5-*7.6*-9 µm, colourless in KOH, subcylindrical to subclavate basidia with 2-6 sterigmata, irregular subhymenium cells arranged in chain like pattern and lack of clamp connections.

Holotype: INDIA, Uttarakhand, Pauri Garhwal district, Adwani-Teka forest, N 30° 06.858’ E 078° 45.466’, alt. 1843 m, on the soil adjacent to the root outlets of *Quercus leucotrichophora* A. Camus in temperate mixed forest of Western Himalaya, 03 Oct. 2016, *Upendra Singh,* US 1422 (AL 1533, **holotype**!).

Basidiomata small-sized, 11-39 × 4-21 mm, caespitose to gregarious on the forest floor. *Pileus* 4-21 mm in diam., applanate when young, becoming uplifted with broadly upturned margin at maturity and shallow central depression, non-perforate, grey to brownish grey (5C1-5C2), sometimes fading to yellowish grey (4B2), yellowish white (4A2) toward margin; surface dry, glabrous, finely appressed fibrillose with tiny erect fibrils; margin wavy to irregularly undulate, plane when young, becoming broadly uplifted with age; context yellowish white (3A2), soft, thin, unchanging on exposure. *Hymenophore* irregularly folded, decurrent, covering entire underside of pileus, sharply demarcated from the stipe apex, white to greyish white (1B1), becoming greyish yellow (1B3) or sometimes brownish orange to brownish yellow (5C5-5C7) with age, unchanging at handling or bruising. *Stipe* 8-27 × 1-3 mm, central, glabrous, narrowly hollow, expanding toward base (up to 7 mm), irregularly grooved; surface greyish beige to greyish yellow (4C2-4C3), lighter toward base; context yellowish white (3A2), soft, thin, unchanging with KOH, $FeSO_4$ and Guaiacol. *Taste* indistinct. *Odour* chanterelle-like. *Spore print* not obtained.

Basidiospores 7-*9.6*-12 × 6.5-*7.6*-9 µm (n = 30, Q = 1.05-*1.25*-1.87), broadly ellipsoid to ellipsoid, rarely subglobose or narrow, smooth, inamyloid, hyaline in KOH, uniguttulate; wall up to 1 µm thick; hilar appendage up to 1 µm long. *Basidia* 47-78 × 8-9 µm, 2- to 6- spored, subcylindrical to subclavate, thin-walled, hyaline in KOH, granular contents with large vacuole; sterigmata 4-9 × 1-2 µm. Basidioles numerous, cylindrical to subclavate, hyaline in KOH, with granular contents. *Hymenial cystidia* absent. *Subhymenium* up to 112 µm; composed of thin-walled, elongated or irregular cells (up to 11 µm wide) arranged in chain like pattern. *Pileipellis* up to 209 µm thick, composed of mostly periclinal, cylindrical, 3-5 µm wide, thin-walled hyphae; terminal elements undifferentiated, thin-walled, cylindrical with rounded apex, hyaline in KOH. Pileus tramal hyphae with cells 11-58 × 4-13 µm, hyaline in KOH, with small guttules of different size, frequently branched. *Stipitipellis* composed of subparallel hyphae arranged anticlinally; terminal elements undifferentiated, cylindrical or subcylindrical with rounded apex, hyaline in KOH. Stipe trama hyphae 19-52 × 6-14 µm, hyaline in KOH, occasionally branched. *Clamp connections* absent on hyphae of all tissues.

Notes: *Craterellus parvogriseus* is easy to recognize in the field on account of its small-sized basidiomata, the non-perforate, grey to brownish grey pileus with upturned margin, the much paler, white to greyish white hymenophore having irregular folds and clearly demarcated from the sterile stipe apex, the narrowly

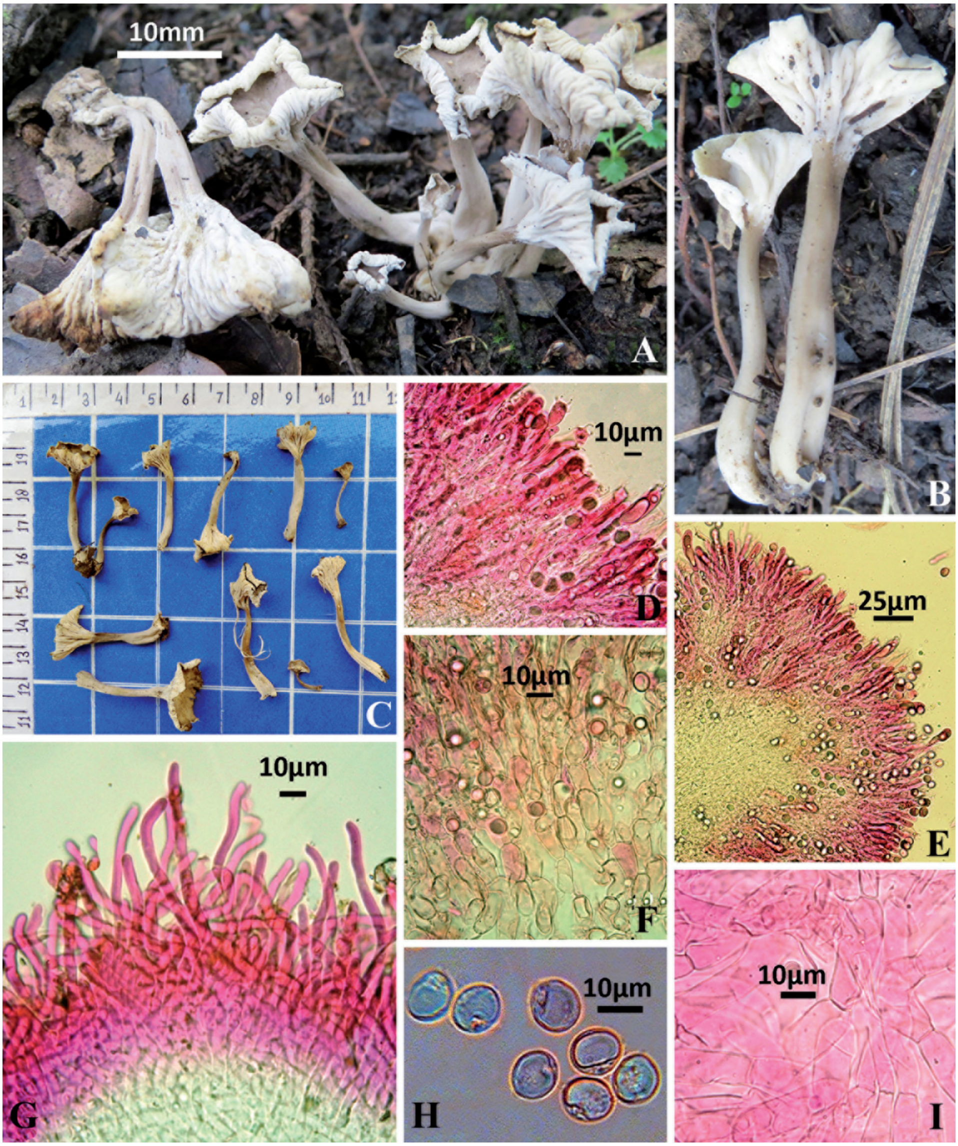


Fig. 4. *Craterellus parvogriseus* (holotype). **A, B & C.** Fresh basidiomata in the field. **D & E.** Transverse section through hymenophore showing basidia and basidioles. **F.** elements of subhymenium. **G.** pileipellis. **H.** Basidiospores. **I.** Pileus tramal hyphae. Scale bars: A = 10 mm, D & F-I = 10 µm, e = 25 µm.

hollow stipe is laterally compressed or even longitudinally folded-grooved and slightly expands toward the base. Microscopically, this species is characterized by combination of smooth, colourless basidiospores, basidia with 2-6 sterigmata, irregular cells of subhymenium arranged in chain like pattern, guttules of different sizes in hyphae of pilear trama, thin-walled hyphal extremities in the pileipellis and lack of clamp connections.

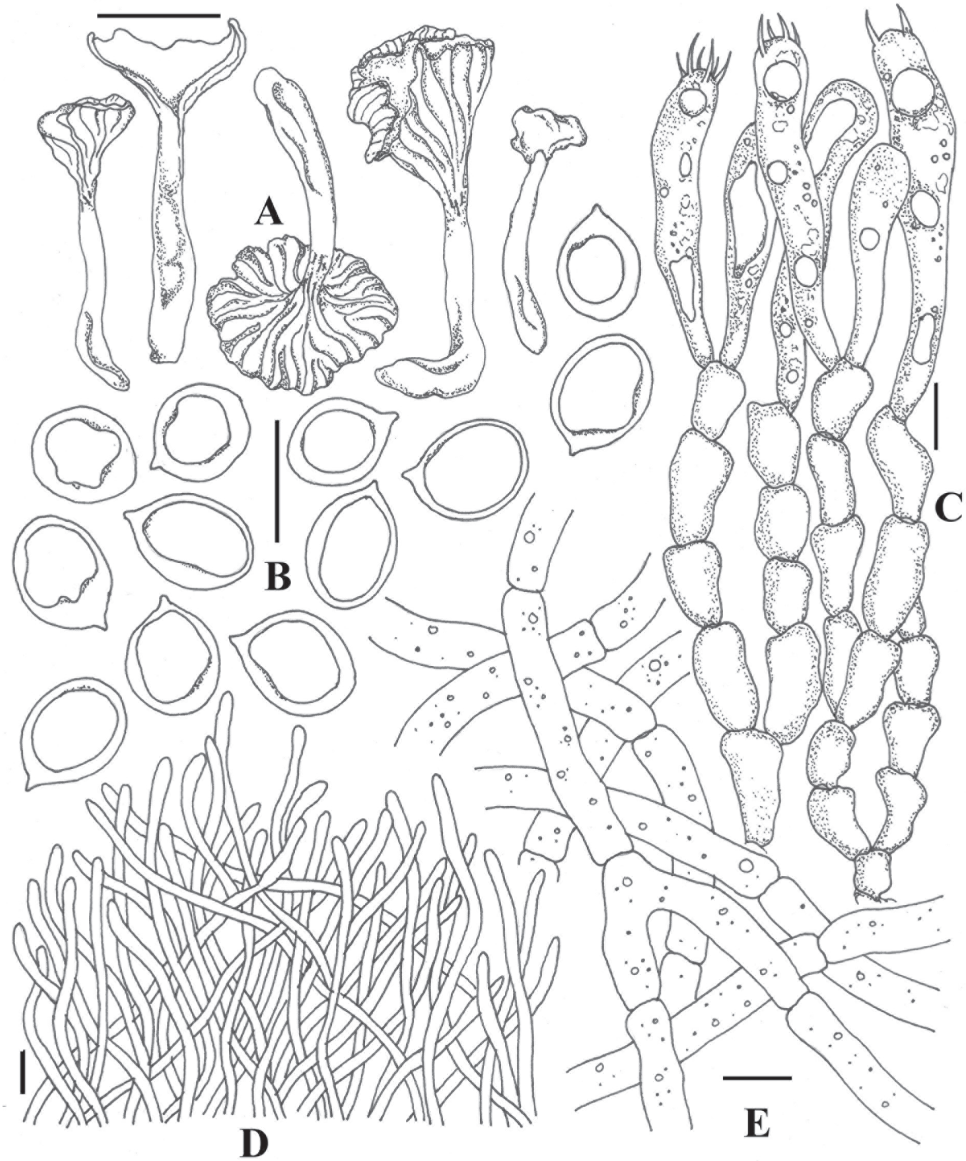


Fig. 5. *Craterellus parvogriseus* (holotype). **A.** Fresh and dissected basidiomata. Microscopic features: **B.** Basidiospores; **C.** Basidia and basidioles with elements of subhymenium; **D.** pileipellis; **E.** Pileus tramal hyphae. Scale bars: A = 10 mm, B-E = 10 µm.

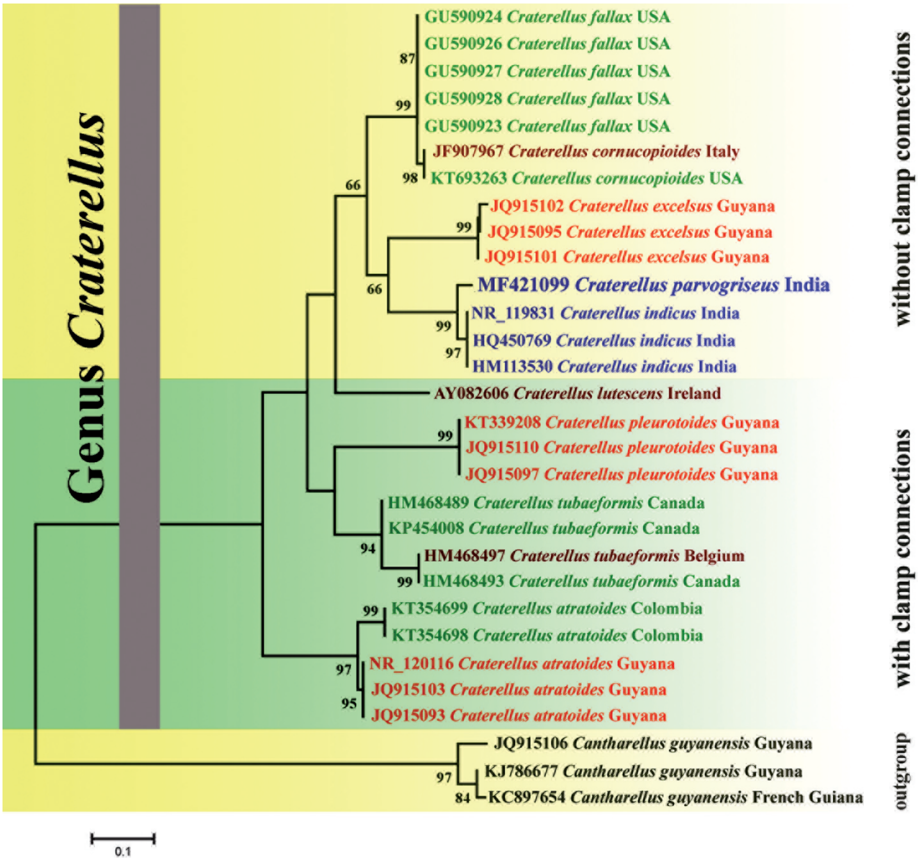


Fig. 6. Maximum Likelihood phylogeny of *Craterellus* showing the position of *Craterellus parvogriseus*. The nrITS dataset comprised 30 sequences and *Cantharellus guyanensis* was used as outgroup. Alignment was performed with online version of MAFFT v. 7 (Katoh & Standley, 2013) and no manual editing was done within the alignment. One-thousand bootstrap replicates were analyzed to obtain nodal support values. Maximum Likelihood (ML) analyses were conducted with MEGA 6.0 (Tamura *et al.*, 2013).

In our phylogenetic analyses (Figs 6-7), our new species appears most closely related to some other Indian *Craterellus* that lack clamp connections, viz. *C. indicus* Deepika, Upadhyay & Reddy and the recently described *C. shoreae* Hembrom, K. Das, Parihar & Buyck. The latter species differs significantly from our new taxon because of its overall bright yellow color and very different general habit as well in its association with dipterocarps in tropical habitats (see Hembrom *et al.* 2017). *Craterellus indicus*, on the other hand, is much more similar to *C. parvogriseus,* but is clearly genetically different (forming a well-supported clade from our taxon in both analyses) and differs also in its slightly smaller basidiospores (7.5-10.5 × 6-7 µm versus 7-*9.6*-12 × 6.5-*7.6*-9 µm in our species) and a pileipellis embedded in a partially gelatinized matrix (Kumari *et al.*, 2012).

Two other *Craterellus* of more or less similar coloration have been described from India (Reid *et al.* 1958) but are still without sequence data: *C. cymatodermoides*

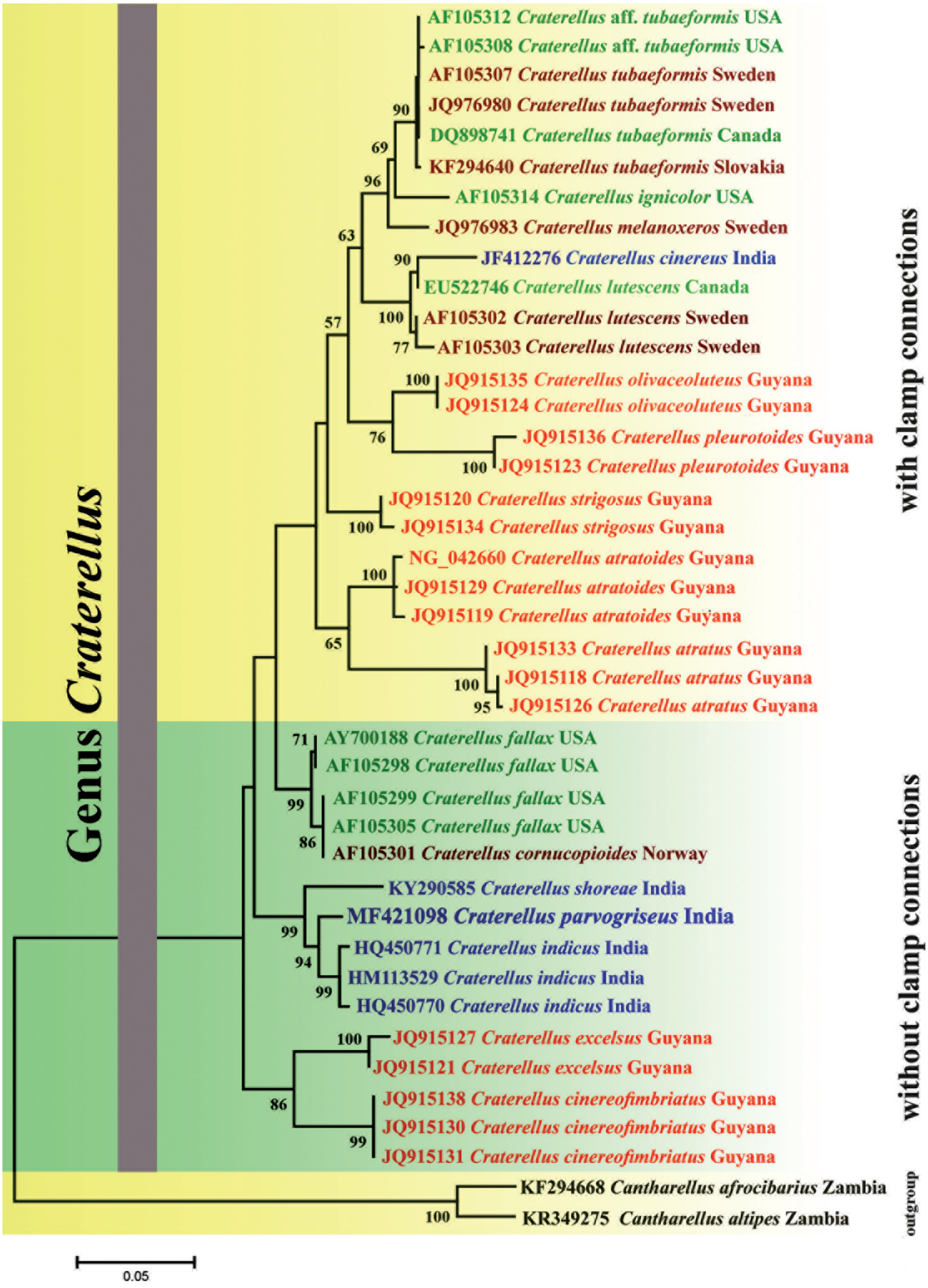


Fig. 7. Maximum Likelihood nrLSU phylogeny of *Craterellus* showing the position of *C. parvogriseus,* using *Cantharellus afrocibarius* and *C. altipes* as outgroup. The nrLSU dataset was aligned with online version of MAFFT v. 7 (Katoh & Standley, 2013) and no manual editing was done within the alignment. One-thousand bootstrap replicates were analyzed to obtain nodal support values. Maximum Likelihood (ML) analyses were conducted with MEGA 6.0 (Tamura *et al.*, 2013).

Reid *et al.* and *C. mussooriensis* Reid *et al.* The former differs in the dark violaceous tinges on the pileus and the strongly radially veined-crested hymenophore (as reported for some *Pterygellus* species, see Corner 1966) and has distinctly smaller spores [(6-)7-8 × 5-5.5 µm], whereas *C. mussooriensis* is very similar in the field but the crestate sulcations of the hymenophore do not reach the pileus margin and the upper stipe is mostly enclosed in a pouch-like sac (as in *C. indicus*). Moreover, *Cr. mussooriensis* produces similar spores, but has four-spored basidia and conspicuous, brown incrustations on the hyphal extremities in the pileipellis.

C. verrucosus Massee, reported from Malaysia, is also notably similar to *C. parvogriseus* because of its caespitose habit, grey hymenium, thin context and size of basidiospores, but can be distinguished from *C. parvogriseus* by its fuscous fuliginous to black basal stem, larger basidiomata (30-70 mm), larger, subclavate basidia (55-95 µm), and inflated tramal hyphae up to 25 µm wide (see Corner, 1966).

33. ***Lactifluus maenamensis*** K. Das, D. Chakr. & Buyck ***sp. nov.*** **Figs 8-10**

MycoBank: MB 822707

GenBank: MF928074 (ITS), MF928075 (ITS)

Systematic position: Basidiomycota, Agaricomycetes, Russulales, Russulaceae.

Etymology: Referring to Maenam wild life sanctuary, the type locality.

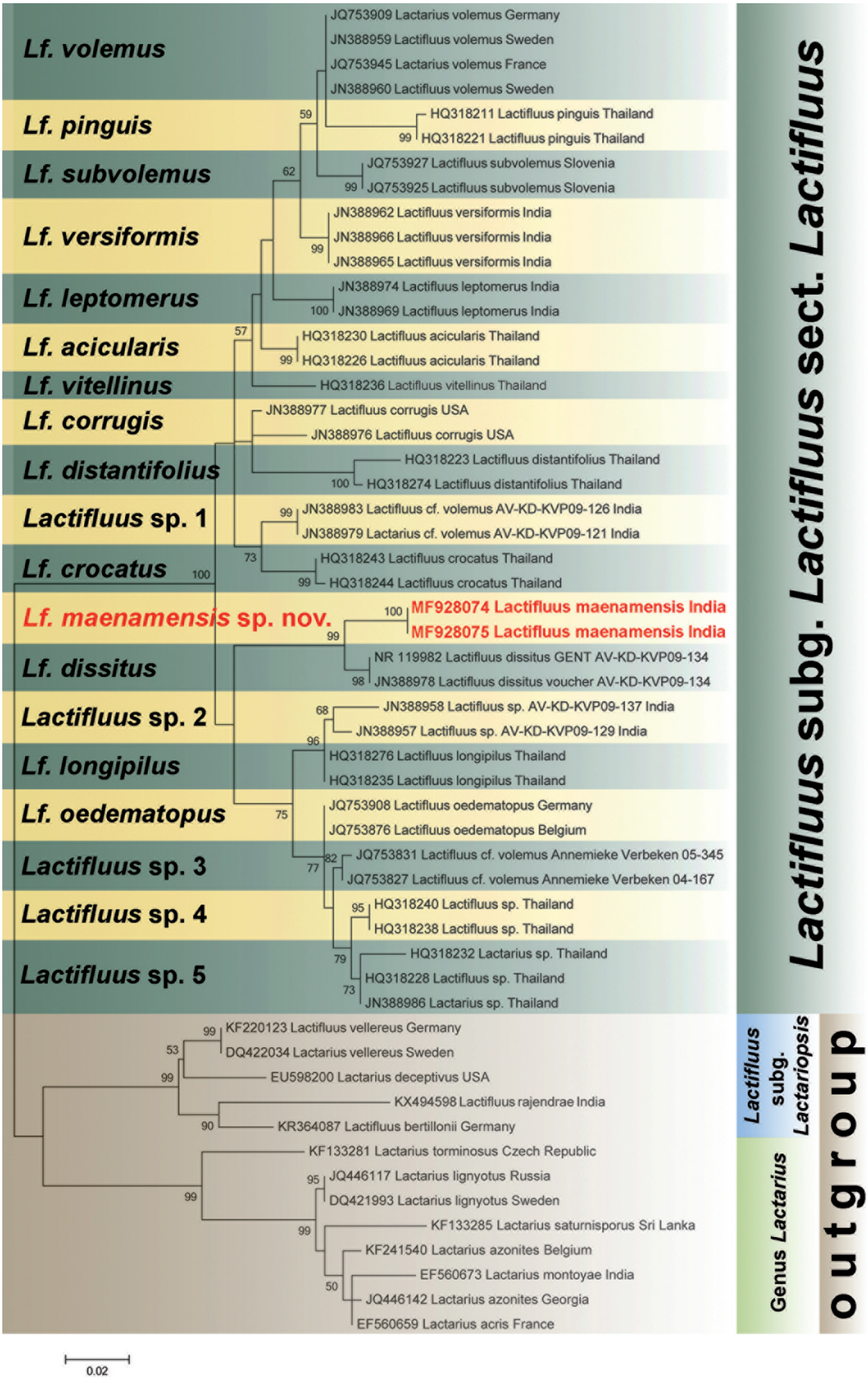
Diagnosis: Distinct from closest ally *Lactifluus dissitus* by possessing distinctively robust basidiomata, larger basidiospores and nrITS sequence data.

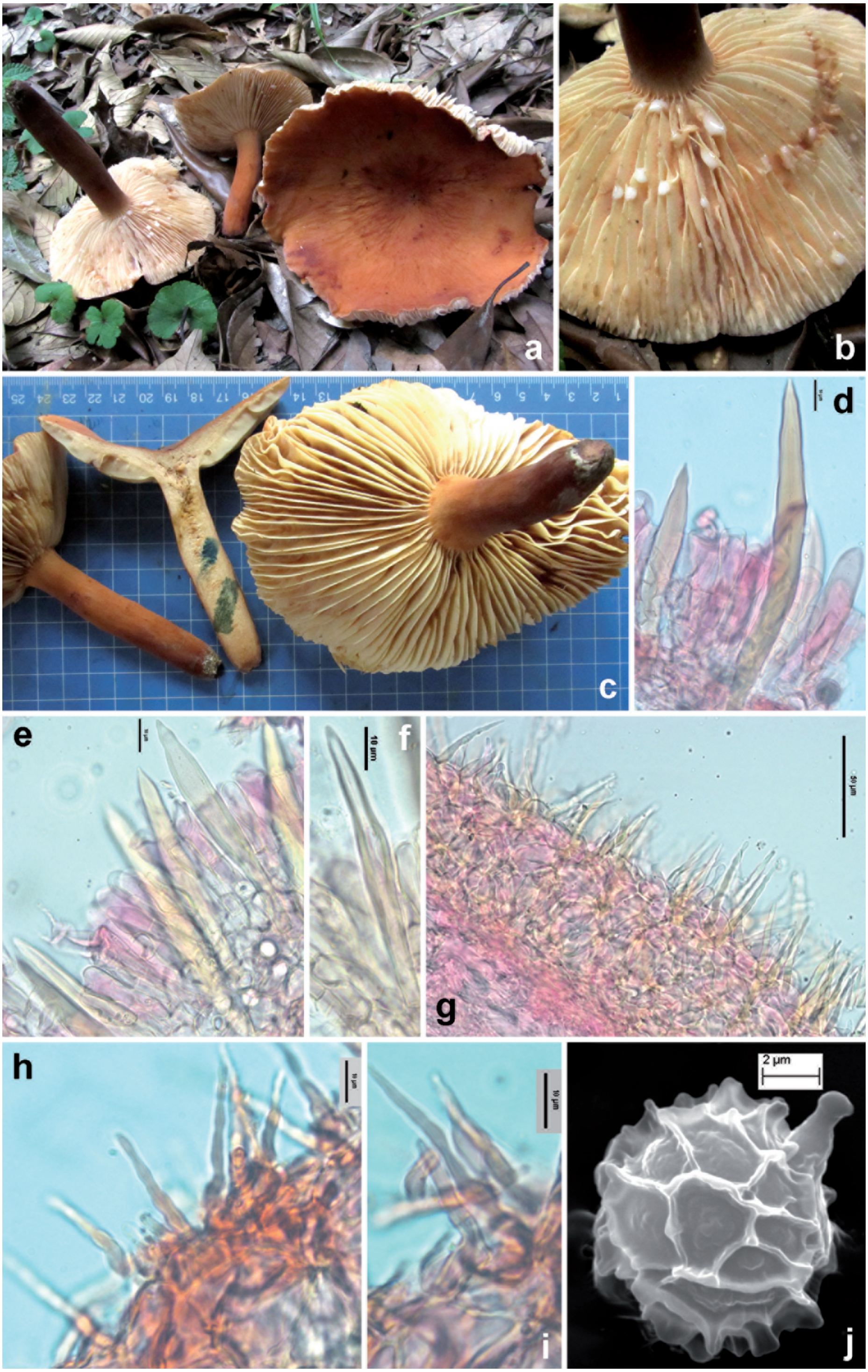
Holotype: INDIA, Sikkim, South district, Maenam wild life sanctuary, N 27° 19’21.5” E 088°22’7.9”, 1843 m asl., under *Lithocarpus* in temperate broadleaf forest, 18 August, 2016, *Kanad Das,* KD 16-13 (CAL 1606, **holotype**!).

Pileus 75-170 mm diam.; plane to planoconcave when young, planoconcave with depressed center or infundibuliform when mature; margin uplifted, irregularly wavy or undulated when mature; surface dry, rugose, velutinose, radially wrinkled, greyish orange (6B4), getting paler towards the margin, light orange (5A5) at margin, young specimens mostly reddish brown (7D7-7E7). *Lamellae* adnexed with or without small tooth, beige yellow (4C3), becoming brown (6D6-4 or 5C5) when bruised, rather close (10-12L + l/cm), rather narrow (1-3 mm), with lamellulae in 5 series of different lengths; edge smooth and concolourous. *Stipe* 70-90 × 11-18 mm, subcylindrical to tapering downwards, centrally attached; surface dry, smooth, light orange (5A4) near apex, gradually brown to orange red (7D8-8D8) towards base and reddish brown (8E8) at base. *Latex* very copious, white, watery, unchanging when isolated, slowly turning reddish grey to brownish grey (8B-C2-3) on exposed lamellae, turning cut lamellae (8C3-8D3); taste mild. *Context* moderately thick in pileus, solid in stipe, pale yellow (4A3), gradually turning brownish when exposed; taste mild; smell fragrant to seafood-like. Macrochemical reactions: stipe context almost immediately turning pastel yellow (3A5) with 10% KOH; dull green (27E4) with $FeSO_4$ and immediately becoming dark turquoise (24F5) with guaiacol.

Basidiospores 8.3-*9.7*-*10.4*-12.8(-12.9) × 7.8-*9.2*-*9.9*-11.9 µm, globose to subglobose (Q = 1-*1.04*-*1.05*-1.16); ornamentation amyloid; ridges 1-1.6 µm high,

Fig. 8. Phylogram generated from Maximum Likelihood (ML) analysis based on ITS-rDNA sequences in MEGA6 (Tamura *et al.*, 2013) under Tamura 3-parameter model (Tamura, 1992). One thousand bootstrap replicates were analyzed to obtain the nodal support values. Bootstrap support values (> 50%) obtained from Maximum Likelihood (ML) analysis are shown above or below the branches at nodes. The novel Indian species *Lactifluus maenamensis* having GenBank Accession nrs. MF928074 and MF928075 (nrITS-rDNA) is shown in red and bold in the tree. ▶


Lf. volemus
JQ753909 Lactarius volemus Germany
JN388959 Lactifluus volemus Sweden
JQ753945 Lactarius volemus France
JN388960 Lactifluus volemus Sweden
Lf. pinguis
59
HQ318211 Lactifluus pinguis Thailand
99
HQ318221 Lactifluus pinguis Thailand
Lf. subvolemus
62
JQ753927 Lactifluus subvolemus Slovenia
99
JQ753925 Lactifluus subvolemus Slovenia
Lf. versiformis
JN388962 Lactifluus versiformis India
JN388966 Lactifluus versiformis India
99
JN388965 Lactifluus versiformis India
Lf. leptomerus
JN388974 Lactifluus leptomerus India
100
JN388969 Lactifluus leptomerus India
Lf. acicularis
57
HQ318230 Lactifluus acicularis Thailand
99
HQ318226 Lactifluus acicularis Thailand
Lf. vitellinus
HQ318236 Lactifluus vitellinus Thailand
Lf. corrugis
JN388977 Lactifluus corrugis USA
JN388976 Lactifluus corrugis USA
Lf. distantifolius
HQ318223 Lactifluus distantifolius Thailand
100
HQ318274 Lactifluus distantifolius Thailand
Lactifluus sp. 1
99
JN388983 Lactifluus cf. volemus AV-KD-KVP09-126 India
JN388979 Lactarius cf. volemus AV-KD-KVP09-121 India
73
Lf. crocatus
100
HQ318243 Lactifluus crocatus Thailand
99
HQ318244 Lactifluus crocatus Thailand
Lf. maenamensis sp. nov.
100
MF928074 Lactifluus maenamensis India
99
MF928075 Lactifluus maenamensis India
Lf. dissitus
NR 119982 Lactifluus dissitus GENT AV-KD-KVP09-134
98
JN388978 Lactifluus dissitus voucher AV-KD-KVP09-134
Lactifluus sp. 2
68
JN388958 Lactifluus sp. AV-KD-KVP09-137 India
JN388957 Lactifluus sp. AV-KD-KVP09-129 India
96
Lf. longipilus
HQ318276 Lactifluus longipilus Thailand
HQ318235 Lactifluus longipilus Thailand
Lf. oedematopus
75
JQ753908 Lactifluus oedematopus Germany
JQ753876 Lactifluus oedematopus Belgium
Lactifluus sp. 3
82
JQ753831 Lactifluus cf. volemus Annemieke Verbeken 05-345
77
JQ753827 Lactifluus cf. volemus Annemieke Verbeken 04-167
Lactifluus sp. 4
95
HQ318240 Lactifluus sp. Thailand
HQ318238 Lactifluus sp. Thailand
Lactifluus sp. 5
79
HQ318232 Lactarius sp. Thailand
HQ318228 Lactifluus sp. Thailand
73
JN388986 Lactarius sp. Thailand
99
KF220123 Lactifluus vellereus Germany
53
DQ422034 Lactarius vellereus Sweden
99
EU598200 Lactarius deceptivus USA
KX494598 Lactifluus rajendrae India
90
KR364087 Lactifluus bertillonii Germany
KF133281 Lactarius torminosus Czech Republic
95
JQ446117 Lactarius lignyotus Russia
99
DQ421993 Lactarius lignyotus Sweden
KF133285 Lactarius saturnisporus Sri Lanka
99
KF241540 Lactarius azonites Belgium
EF560673 Lactarius montoyae India
50
JQ446142 Lactarius azonites Georgia
EF560659 Lactarius acris France
0.02
Lactifluus subg. Lactifluus sect. Lactifluus
Lactifluus subg. Lactariopsis
Genus Lactarius
outgroup


a
b
c
d
e
f
10 µm
50 µm
g
h
10 µm
i
2 µm
j

forming a rather regular to slightly irregular complete reticulum, sometimes isolated warts present; plage distally to almost completely amyloid. *Basidia* 36-60 × 10-15 µm, clavate to subclavate, 4-spored, sterigma 5-11 × 1-3 µm. *Pleurolamprocystidia* 65-140 × 5-16 µm, very abundant, thick-walled [2-5.5 µm], fusiform to subfusiform with acute to pointed apex, rarely bifurcate, emergent up to 55 µm; arising from the subhymenium or the trama. *Pleuropseudocystidia* abundant, emergent or not, 4-6 µm diam., mostly cylindrical, lobed to tortuous or irregular in shape; apex obtuse, acute, often capitates or irregular. *Lamella-edge* fertile, composed of basidia and cheilocystidia. *Cheilolamprocystidia* 50-65 × 6-10 µm, similar to pleurolamprocystidia. *Hymenophoral trama* cellular, with abundant lactifers and nest of sphaerocytes. *Pileipellis* a lampropalisade; subpellis 60-80 µm thick, composed of rounded to elongated or irregularly shaped, thick-walled (1.5-2.2 µm) cells of 10-28 × 9-15 µm; suprapellis hairy, elements 12-56(-75) × 3-5.5 µm, slightly thick-walled (0.5-1 µm), subcylindrical with rounded, acuminate or obtuse apex, margin rarely undulating, often septate. *Clamp connections* absent from all tissues.

Other specimens examined: INDIA, Sikkim, South district, Maenam wild life sanctuary, N 27°19’6.9” E 88°21’59.7”, 2159 m asl., under *Lithocarpus* in temperate broadleaf forest, 16 August, 2016, *Kanad Das,* KD 16-008 (CAL 1607).

Notes: *Lactifluus volemus* (Fr.: Fr.) Kuntze is the type species of *Lactifluus* (Pers.) Roussel. Originally described from Europe, this name has later many times been misapplied to several of its look-alikes reported from different other continents or countries including India (Hesler & Smith, 1979; Saini & Atri, 1984; Le, 2007; Montoya *et al.*, 1996; Das & Sharma, 2005; Shimono *et al.*, 2007; Wang, 2007). All these look-alikes are considered as “*Lf. volemus* sensu lato”, including the present species, which is edible but not much appreciated by the local communities. In the field, *Lf. maenamensis* is easily confused with some other species of the “*Lf. volemus* sensu lato” complex. Still, the combination of robust basidiomata with rather close lamellae, radially wrinkled pilear surface, watery white and copious, mild latex, very large basidiospores with complete reticulum, long pleurolamprocystidia allow to distinguish the present species.

The closely allied (morphologically and phylogenetically) Indian (also from Sikkim) species *Lf. dissitus* Van de Putte, K. Das & Verbeken (Van de Putte *et al.* 2012) differs from *Lf. maenamensis* by distinctively smaller basidiomata (pileus 55-90 mm diam; stipe 50-62 × 13-17 mm), smaller basidiospores [(8.3-)8.5-9.6-9.9-10.9(-11.3) × (7.5-)7.7-8.6-9.0-9.6(-9.7) µm] and sequence data of nrITS region (showing only 96% identity under 99% query coverage).

Some other similar species include *Lf. longipilus* Van de Putte, Le & Verbeken, *Lf. distantifolius* Van de Putte, Stubbe & Verbeken, *Lf. crocatus* Van de Putte & Verbeken, *Lf. vitellinus* Van de Putte & Verbeken, *Lf. acicularis* Van de Putte & Verbeken (all reported originally from Thailand) and *Lf. oedematopus* (Scop.) Kuntze (originally reported from Europe). The other Asian species (*Lf. longipilus*, *Lf. distantifolius*, *Lf. crocatus*, *Lf. vitellinus* and *Lf. acicularis*) have distinctively smaller basidiomata. In addition, *Lf. distantifolius* has clearly distant lamellae (4-5/cm, including lamellulae), *Lf. longipilus* and *Lf. acicularis*

◀ Fig. 9. *Lactifluus maenamensis* (KD 16-13, holotype). **a & c.** Fresh basidiomata in the field and basecamp. **b.** Latex on cut lamellae. **d, e & f.** Pleurolamprocystidia. **g, h & i.** Radial section through pileipellis showing hair-like terminal elements. **j.** Basidiospores under SEM. Scale bars: d, e, f, h & i = 10 µm, g = 50 µm, j = 2 µm.

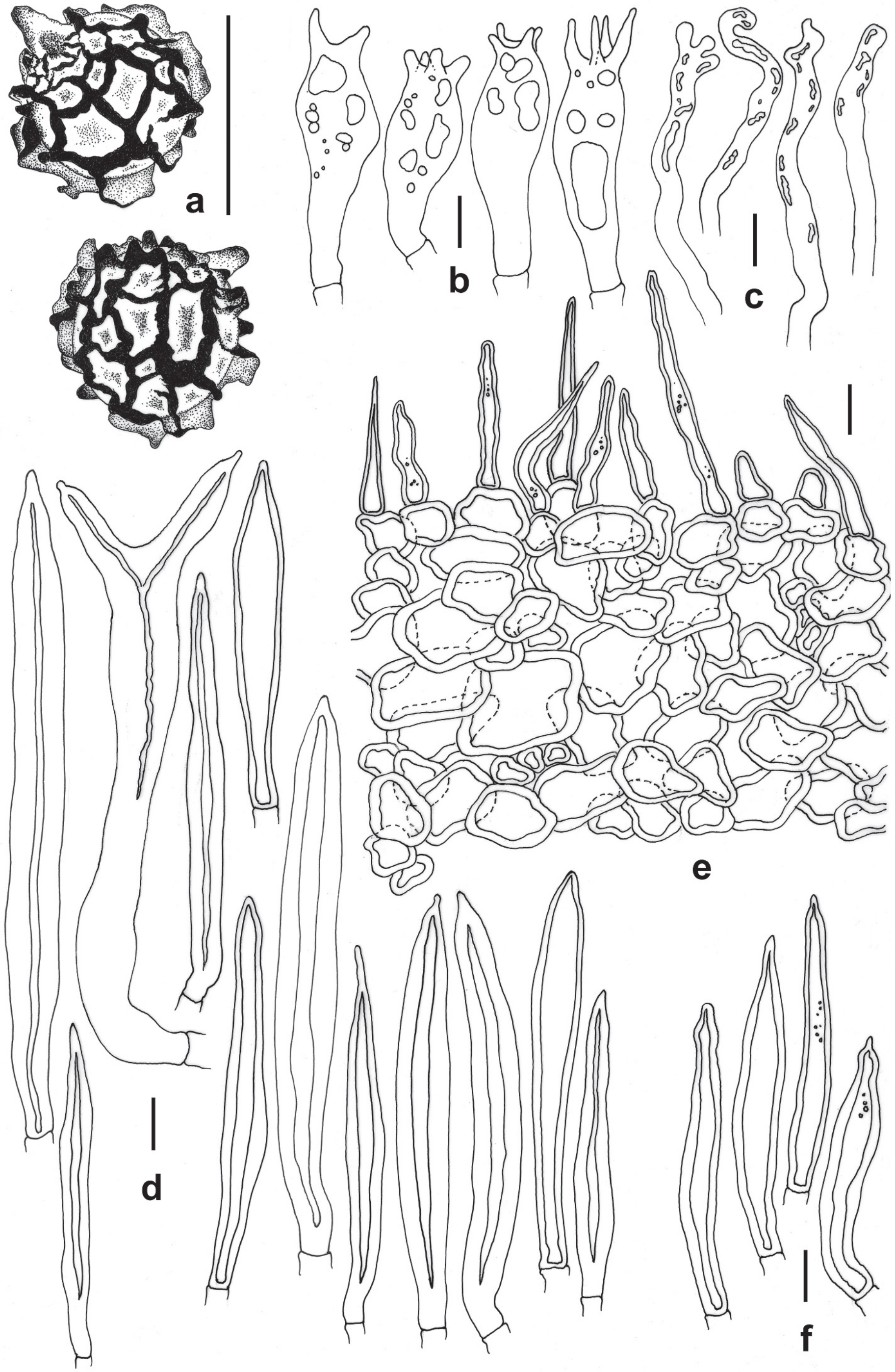


Fig. 10. The Line drawings of *Lactifluus maenamensis* (from KD 16-13, holotype). **a.** Basidiospores. **b.** Basidia. **c.** Pleuropseudocystidia. **d.** Pleurolamprocystidia. **e.** Pileipellis. **f.** Cheilolamprocystidia. Scale bars: a-f = 10 µm.

have exceptionally longer (up to 130 μm long) pileus hairs, *Lf. crocatus* has wider (10-75 × 4-11 μm) pileus hairs, whereas *Lf. vitellinus* has smaller basidiospores [(6.6-)7.1-7.9-8.0-8.9(-9.2) × (6.2-)6.6-7.3-7.4-8.3 μm] and shorter lamprocystidia (55-105 × 6-13 μm) (see Van de Putte *et al.* 2010). The European *Lf. oedematopus* also differs from the present novel species by possessing distinctively smaller basidiomata (pileus 30-70 mm diam., stipe 25-70 × 10-20 mm) and a pileus surface that is often cracked (never cracked in *Lf. maenamensis*); it also has smaller basidiospores [(6.9-)7.5-10.1(-10.3) × (6.3-)6.7-9.2 μm] and shorter pleurolamprocystidia (50-120 × 7-11 μm) (Van de Putte *et al.* 2015)

34. *Leucocybe houghtonii* (W. Phillips) Halama & Pencakowski, ***comb. nov.***

Figs 11-13

MycoBank: MB822677

Systematic position: Basidiomycota, Agaricomycetes, Agaricales, Tricholomataceae.

Synonyms:

≡ *Cantharellus houghtonii* W. Phillips [as '*Haughtoni*'], in Berkeley & Broome, *Ann. Mag. nat. Hist., Ser.* 4, 17 (no. 98): 135.1876, basionym.

≡ *Clitocybe houghtonii* (W. Phillips) Dennis [as '*houghtoni*'], *Kew Bull.* 9(2): 425. 1954.

= *Omphalia roseotincta* A. Pearson, *Trans. Br. mycol. Soc.* 35(2): 105. 1952.

Basidiomata solitary, gregarious (mostly) to subfasciculate. *Pileus* 7-45 mm broad, when young plano-convex, soon shallowly to deeply infundibuliform, with involute or slightly inflexed, later straight margin, usually undulate (rarely not undulate), hygrophanous, mostly shortly translucently striate at margin when moist, smooth, glabrous, white to pale pinkish (Sea Shell Pink, Light Buff), pallescent on drying to whitish and more isabella (Cartridge Buff) with age. *Lamellae* moderately crowded to distant, L = 20-35, l = 2-3, shortly decurrent, sometimes intervenose, up to 3 mm broad, pinkish (Pale Pinkish Buff), edge concolorous, smooth. *Stipe* 20-55 × 1.7-7 mm, cylindrical, tapering downwards or tapering upwards, often curved at base, when young solid, finally fistulose, concolorous with pileus or slightly less pinkish (Pale Pinkish Buff), nearly smooth to white-fibrillose (especially in upper part), with more or less distinct white tomentum at base. *Context* concolorous with pileus and stipe, with a faint – slightly fruity to unpleasant smell and indistinct to subraphanoid taste.

Basidiospores (6.5) 7-9 (10) × (3.5) 4-5.5 (6.5) μm, Q = (1.3) 1.5-2 (2.2) (n = 106), smooth, ellipsoid, with obtuse base, thin-walled, not congophilous, not cyanophilous, in exsiccates predominantly single. *Basidia* (20.5) 24.5-35 (39) × (5.5) 6-8 (8.5) μm (n = 46), 4-spored, clavate, clamped. *Cheilocystidia* not found. Hyphae of hymenophoral trama thin-walled, clamped, colourless, non-dextrinoid, cylindrical, 5-15 μm wide. *Pileipellis* a cutis, made up of parallel to slightly interwoven, cylindrical, smooth, thin-walled, clamped, up to 2-5.5 μm wide hyphae with intracellular pigment. *Stipitipellis* a cutis, of parallel, cylindrical, slightly thick-walled, clamped, up to 7 μm wide hyphae. Caulocystidia not found.

Examined material. POLAND, Wrocław Glacial Valley, Wrocław: "Las Lesicki" forest, *Ficario-Ulmetum minoris*, on wood of trunks, on wood of fallen branches, in the vicinity of *Acer* sp., *Carpinus betulus*, 51°11'44"N, 16°55'39"E, 122 m a.s.l., 18 Sept. 2013, *leg. K. Szczęśniak* (WRSL SK-2013-0296, as *Clitocybe houghtonii*); ibid., *Ficario-Ulmetum minoris*, on fallen bark, in the vicinity of *Acer* sp., *Carpinus betulus*, *Quercus* sp., *Tilia* sp., 51°11'42"N, 16°55'39"E, 124 m a.s.l.,

Fig. 11. Basidiomata of *Leucocybe houghtonii* (**A** – WRSL HM-2014-0371, **B** – WRSL HM-2014-0384). Photo M. Halama.

18 Sept. 2013, *leg. K. Szczęśniak* (WRSL SK-2013-0267, as *C. houghtonii,* GenBank KY474106); Wrocław: "Las Rędziński" forest, *Ficario-Ulmetum minoris*, on leaf litter, on rests of undetermined wood (mobile and strongly decayed), on wood of fallen twigs, on bark, in the vicinity of *Acer campestre*, *Carpinus betulus*, *Quercus* sp., and *Tilia Cordata*, 51°10'3"N, 16°56'46"E, 112 m a.s.l., 9 Oct. 2014, *leg. M. Halama* (WRSL HM-2014-0371, as *C. houghtonii*); ibid.: *Ficario-Ulmetum minoris*, on leaf litter, on rests of undetermined wood (mobile and strongly decayed), on wood of fallen twigs, in the vicinity of *Carpinus betulus, Quercus robur,* and *Tilia cordata*, 51°10'44"N, 16°56'10"E, 130 m a.s.l., 15 Oct. 2014, *leg. M. Halama* (WRSL HM-2014-0384, as *C. houghtonii*); ibid.: *Ficario-Ulmetum minoris*, on leaf litter and humus covered by litter, on rests of undetermined wood (mobile and strongly decayed), in the vicinity of *Carpinus betulus* and *Quercus robur*, 51°10'46"N, 16°56'9"E, 135 m a.s.l., 15 Oct. 2014, *leg. M. Halama* (WRSL HM-2014-0385, as *C. houghtonii,* GenBank: KY474105).

Additional examined material. ENGLAND, Surrey: Mickleham, Norbury Park, on the leaf litter, 8 Oct. 1950, *leg. P.D. Orton* (K 95885, syntype of *Omphalia roseotincta*); ibid., amongst litter of *Fagus*, on the scrubs, 14 Dec. 1993, *leg. N.W. Legon* (K 25204, as *Clitocybe houghtonii*); Surrey: West Molesey, New Road/ Churchfields corner, on soil in grass under *Cedrus deodara*, 26 Nov. 2014, *leg. B.M. Spooner* (K 195701, as *C. houghtonii*; GenBank: KY474107); Surrey: Norbury Park (Mickleham): Blackberry Wood, on soil (amongst grass) under *Fraxinus exscelsior*, 30 Oct. 2006, *leg. N.W. Legon* (K 141642, as *C. houghtonii*); Surrey: Dorking (nears), Holmwood Common, on soil under *Quercus robur*, 27 Oct. 2013, *leg. V.C. Hodge* (K 190012, as *C. houghtonii*); Co. Durham: Kepier Woods, in moss near *Acer pseudoplatanus*, 14 Oct. 2000, *leg. H. Ellis* (K 82540, as *C. houghtonii*); Middlesex: Hanwell Cemetery, on bare soil near *Taxus*, 14 Nov. 1998, *leg. E.W. Brown* (K 59569, as *C. houghtonii*); the same locality, under yew, 29 Oct. 1992, *leg. E.W. Brown* (K 20930, as *C. houghtonii*); ITALY, Sardinia: Sassari, Calangianus, Catala, *Alnus sp.*, 19 Oct. 2003, *leg. M. Contu* (K 163182, as *Clitocybe houghtonii*); GERMANY, Saxony, West Lusatian Hill Country and Uplands. Pulsnitz: cemetery, in the vicinity of *Picea*, 29 Nov. 2004, *leg. E. Herschel* (GLM 73034, as *Clitocybe houghtonii*; GenBank: KY474108); Forests over Lusatian Neisse "Drausendorfer Eichen", Drausendorf: on the twigs of deciduous trees, 14 Oct. 1994, leg. *D. Peukert* (GLM 33119, as *C. houghtonii*); East Upper Lusatia. Krobnitz: castle park, in deciduous shrubs, high humidity, 10 Oct. 2007, *leg. G. Zschienschang* (GLM 89310, as *C. houghtonii*); Görlitz-Weinhübel SE, small round shrubbery on the left from bike track towards Hagenwerder: on rotten stumps, 16 Dec. 2006, *leg. S. Hoeflich* (GLM 78902, as *C. houghtonii*); Königsbrück-Ruhland Heats. Königsbrück NW. Königshöhe, Pulsnitzaue: alder forest, 19 Sep. 1993, *leg. G. Zschienschang* (GLM 30974, as *C. houghtonii*).

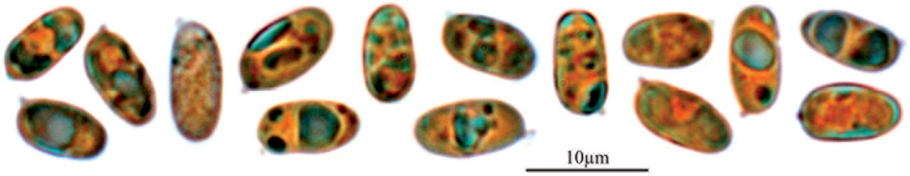


Fig. 12. Basidiospores of *Leucocybe houghtonii* (photographed from collection WRSL SK-2013-0267). Photo M. Halama.

Notes: *Clitocybe houghtonii* (W. Phillips) Dennis is macroscopically a relatively distinctive species (Fig. 11). In the field it is distinguished by its small to medium-sized basidiomata with pale to bright pink or pinkish orange tinges (which however may become paler during dehydration and change to nearly white), initially plano-convex, but soon shallowly to deeply infundibuliform and hygrophanous pileus without aeriferous covering, and usually a faint herbaceous smell – reminiscent of leaves of tomato. Microscopically, the presence of ellipsoid-oblong basidiospores (7-9 × 4-5 µm, see Fig. 12), not agglutinating in exsiccate, is also a good taxonomic character (Kuyper, 1995; Ludwig, 2012; Vesterholt, 2012a).

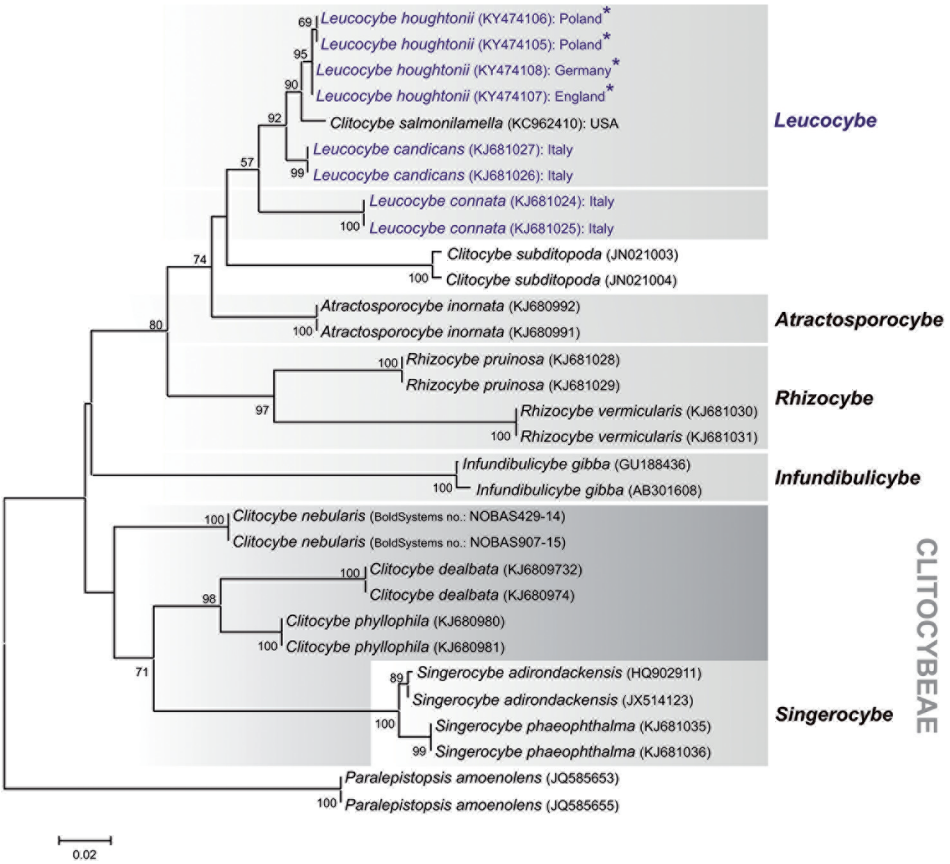
Clitocybe houghtonii generally occurs on decayed leaf litter and rotting hardwood remnants (mainly *Alnus, Fagus*) covered with soil (e.g., buried branches, twigs, acorns), but also on mossy stumps in deciduous forests, and only rarely is found in coniferous forests and juniper scrubs (Clémençon, 1984; Kuyper, 1995; Antonín & Vágner, 1997; Ludwig, 2012). In Britain, it is most often associated with *Fagus* in beech forests on calcareous soils (Legon *et al.*, 2005), however, according to Gminder & Krieglsteiner (2001), *C. houghtonii* avoids alkaline subsoil and prefers weakly acidic to neutral ground. The species fruits from August to December (January) (Kuyper, 1995; Ludwig, 2012). It seems to be a cold-tolerant fungus which exhibits a very high frequency of late fruiting (Krieglsteiner, 1983; Ludwig, 2012). In Britain, many noteworthy records of the species have been made in November and December (Legon *et al.*, 2005). *Clitocybe houghtonii* is known in Europe and

Fig. 13. Phylogenetic placement of *Leucocybe houghtonii* inferred from ITS rDNA data. Edited ITS rDNA region sequences of *Clitocybe houghtonii* were aligned with 27 ITS1-5.8S-ITS2 sequences of closely related taxa retrieved from GenBank and BoldSystems database using ClustalW application in MEGA 6.06 (Tamura *et al.*, 2013). The alignment was manually adjusted and employed for Maximum Likelihood phylogenetic tree reconstruction (Tamura 3-parameter model with gamma distribution, 1000 bootstrap (BP) replications) in MEGA 6.06. The initial tree used for the heuristic search was obtained by applying the Neighbour-Joining method to a matrix of pairwise distances estimated using the Maximum Composite Likelihood (MCL) approach. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 0.4655)). There were a total of 515 positions in the final dataset. Phylogenetic tree was drawn to scale, with branch lengths measured in the number of substitutions per site. All positions with less than 95% site coverage were eliminated. That is, fewer than 5% of alignment gaps, missing data, and ambiguous bases were allowed at any position.The best tree resulting from Maximum Likelihood Analysis is presented. Nodes were annotated with maximum likelihood bootstrap proportion (ML-BP). Only support values greater than 50% are shown. Names marked with asterisk belong to samples sequenced in the present study. Sequencing of the ITS rDNA region of *Clitocybe houghtonii* yielded 699 bp (KY474106), 669 bp (KY474105), 698 bp (KY474107) and 699 bp (KY474108) long fragments. According to BLAST analysis, combined ITS1&ITS2 sequence of Polish samples (KY474105, KY474105) revealed 99% identity with sequences obtained from reference material of *C. houghtonii* received from Britain (KY474107) and Germany (KY474108). At the same time all samples of *C. houghtonii* sequenced in the present study showed 97% identity with the sequence of *Clitocybe salmonilamella* H.E. Bigelow (KC962410; type specimen). The manually adjusted alignment of ITS rDNA region comprised 31 nucleotide sequences and was characterised by 289/675 variable sites. The tree with the highest log likelihood (-2675,9802) is shown (Fig. 13). The percentage of trees in which the associated taxa clustered together is shown next to the branches. *Paralepistopsis* Vizzini (Vizzini & Ercole, 2012) was chosen as the outgroup taxon. The collections sequenced in this study occupy an independent position in the phylogram and form a group with a high support together with *Leucocybe candicans* (Pers.) Vizzini, P. Alvarado, G. Moreno & Consiglio and *Clitocybe salmonilamella*. The presence of *Leucocybe connata* (Schumach.) Vizzini, P. Alvarado, G. Moreno & Consiglio as a closely related taxon is also suggested, but with significantly weaker support.

▶

south-western Asia (e.g., Kuyper, 1995; Sesli & Denchev, 2008). Gminder & Krieglsteiner (2001) characterized this species as distributed from sub-meridional to boreal regions, with sub-Mediterranean and sub-Atlantic centres of its geographic distribution. In Europe *C. houghtonii* is generally considered to be a quite widely distributed species, nevertheless it is considered everywhere a rare or very rare mushroom (Gminder & Krieglsteiner, 2001; Ludwig, 2012). Furthermore, it is classified as threatened at national levels and red-listed in Denmark (Vesterholt, 2012b), Germany (Benkert *et al.*, 1992), and the Czech Republic (Holec & Beran, 2006).

In literature the species was introduced twice, for the first time as *Cantharellus houghtonii* W. Phillips (Berkeley & Broome, 1876) and the second time as *Omphalia roseotincta* A. Pearson (Pearson, 1952; nom. illegit., Art. 53.1). According to Dennis (1954), a formal description of *Cantharellus houghtonii* was made using the material presumably collected in Preston (Lancashire) in the West Midlands region of England, while the type locality of *Omphalia roseotincta* is the Norbury Park near Mickleham (Surrey), in the south east of England. A careful review of the descriptions, figures and authentic material of *Cantharellus houghtonii*



and *Omphalia roseotincta* by Dennis (1954) showed that these two taxa are conspecific. Consequently, the name *O. roseotincta* is to be considered a synonym of *C. houghtonii*. At the same time, Dennis (1954) questioned the generic position of *Cantharellus houghtonii* and transferred this taxon into *Clitocybe* (Fr.) Staude, where it is traditionally classified within the section *Fragrantes* (Clémençon, 1984), *Candicantes* (Bon, 1997) or it is presented without a formal infrageneric classification (Kuyper, 1995).

Molecular data are still lacking for *Clitocybe houghtonii* as the species was not included in any DNA study of broadly defined genus *Clitocybe* (Fr.) Staude and allies (Redhead *et al.*, 2002; Walther *et al.*, 2005; Ammirati *et al.*, 2007; Garnica *et al.*, 2007; Vizzini *et al.*, 2010; Vizzini *et al.*, 2011a; Vizzini & Ercole, 2012; Alvarado *et al.*, 2015; Sesli *et al.*, 2016). As part of an investigation into phylogenetic relationships in the polyphyletic genus *Clitocybe*, we used phylogenetic analysis of nuclear ribosomal DNA (ITS) sequences to determine the phylogenetic position of *Clitocybe houghtonii*. Based on molecular data in particular, we present evidence that the species is nested within the recently created genus *Leucocybe* Vizzini, P. Alvarado, G. Moreno & Consiglio (Alvarado *et al.*, 2015) and not within *Clitocybe* (Redhead *et al.*, 2002), nor other clitocyboid taxa or allies. We also aimed to present the first Polish records of *C. houghtonii* with comments on the morphological variability of the species and its ecological requirements.

Our collections of *Leucocybe houghtonii* represent the first record of the species in Poland. All these collections originate from man-influenced forest habitats with more or less natural tree species composition. Although both investigated stands within Lesicki and Rędziński Forests are generally not older than 120 years, they include relics of the former riparian forests such as 250-300 years old specimens of *Quercus robur* (the circuit of the oldest specimen is 734 cm). This indicates the natural character of studied forest communities, which can be treated as ancient forests. Nevertheless, these forests have changed remarkably during recent years. Due to the Oder engineering (Jankowski & Świerkosz, 1995) they have been deprived of frequent floods and changed their species composition. Currently, they are colonized by species typical of oak-hornbeam forests (such as: *Carpinus betulus*, *Tilia cordata*, *Dactylis polygama*), occurrence of which reflects the gradual drainage of these habitats (Stefańska-Krzaczek, 2013). Additionally, as a result of a pathogen impact/invasion, causing a dieback of mature trees in Europe, the tree layer of Lesicki and Rędziński forests lack species such as: *Fraxinus excelsior* and *Ulmus minor* (cf. Boyd *et al.*, 2013; Pautasso *et al.*, 2013). It also should be noted that there is a large number of nitrophilous species (*Geum urbanum*, *Urtica dioica*, *Galium aparine*, *Glechoma hederacea*, *Alliaria petiolata*) within discussed communities and, in some patches, a mass participation of an alien, invasive plant *Impatiens parviflora*. These processes indicate a strong eutrophication of studied habitats.

Generally, the data on ecological requirements of *Leucocybe houghtonii* from various parts of Europe are heterogeneous. The current data suggest, however, that this fungus usually occurs in localities fulfilling at least the following conditions: a relatively humid microclimate and the presence of a substantial amounts of litter and fine woody debris (of deciduous trees). In this context, and with a view to the fact that mycologists have been active in this region since late 1800s (e.g. Schröter, 1885-1889), the question then arises: why the species was found here only recently? It is possible that *L. houghtonii* was relatively recently introduced to the Lesicki and Rędziński forests and may be considered alien to investigated forest communities. However, this hypothesis has to be confirmed.

In general, all Polish collections of *Clitocybe houghtonii* fit well, both macro- and microscopically, with published descriptions, and clearly correspond to the species concept proposed by Phillips (Berkeley & Broome, 1876) and elaborated by other researches (e.g. Dennis, 1954; Kuyper, 1995; Vesterholt, 2012a). The Polish material also fits well within the range of morphological (and genetic; see below) variability displayed by British, German and Italian species collections. The only discrepancy relates to the nature of the flesh odour. Namely, the perception of smell performed by M.H. on fresh-cut basidiomata resulted in a faint sensation of fruity to rather unpleasant smell rather than a pungent scent of fresh tomato leaves. It is, however, an open question whether or not the odours represent population differences or they are highly subjectively perceived properties. Moreover, it should be emphasised at this point that the type material of *Cantharellus houghtonii* was not available for loan and re-examination (including biometric and molecular genetic studies) due to the age and poor condition.

The derived phenogram illustrated divergence between the studied fungi (Fig. 13). Several main clusters could be identified deviating from the main lineage of the genus *Clitocybe*, typified by *C. nebularis* (Batsch) P. Kumm. They are represented by recently proposed or resurrected genera, i.e.: *Singerocybe* Harmaja (Harmaja, 1988; Qin *et al.*, 2014), *Infundibulicybe* Harmaja (Harmaja, 2003; Matheny *et al.*, 2006; Vizzini *et al.*, 2011b), *Rhizocybe* (Alvarado *et al.*, 2015), *Atractosporocybe* (Alvarado *et al.*, 2015), *Leucocybe* (Alvarado *et al.*, 2015), and additionally by the sequences of North American *Clitocybe subditopoda* Peck. Employed sequence data analysis of the ITS regions of rDNA confirms the affiliation of Polish collections for *Clitocybe houghtonii* (WRSL HM-2014-0371, WRSL HM-2014-0385) with selected material originated from England (K 195107) and Germany (GLM 73034) and clearly supports the inclusion of *Clitocybe houghtonii* into the genus *Leucocybe* as suggested by Moreau *et al.* (2015). While the relatively poor resolution at the top of the phylogeny presented here restricts thorough phylogenetic inferring, *Leucocybe houghtonii* is most closely related to *Clitocybe salmonilamella* H.E. Bigelow (KC962410) – a wood-inhabiting species known from North America with very similar appearance and growth habit (Bigelow, 1976). Morphologically, both species are distinguished from the other whitish clitocyboid fungi formerly classified in *Clitocybe* section *Candicantes* (Bigelow, 1982; Bon, 1997) by the pinkish coloured lamellae in combination with the relatively large basidiospores ((6.5) 7-8 × 4-5.0 μm vs. (6.5) 7.0-9.0 (10.0) × (3.5) 4.0-5.0 (5.5) μm), which are white in deposit (Bigelow, 1976; Kuyper, 1995; cf. Table 1). Our results indicate that *C. salmonilamella* (KC962410; Svetasheva and Malysheva, unpubl.) should also become a member of the genus *Leucocybe*, which is consistent with the conclusions made by Alvarado *et al.* (2015). To support this idea, more investigation should be made by implementing other criteria (e.g. morphological characters), it exceeds the scope of our current work though.

In summary, our study proved that *L. houghtonii* deviates from the type of the genus *Clitocybe*, *C. nebularis* and that the genetic relationship among *Leucocybe* species can be determined based on comparisons of ITS sequences. Moreover, the genus *Leucocybe* now contains three whitish clitocyboid species, i.e.: *L. candicans*, *L. connata* and *L. houghtonii* with adnate or slightly decurrent lamellae, white or whitish when young, becoming greyish, brownish white or pinkish to salmon with age. Molecular data showed that these taxa should be subsumed under a single generic name, however, no common and consistent morphological features can be identified for this genetic lineage at the moment.

Table 1. Fungi species fitting the present genetic concept of *Leucocybe* lineage and their ecological and morphological characteristics

Feature	*Leucocybe candicans*	*Leucocybe connata*	*Leucocybe houghtonii*	*Clitocybe salmonilamella*
Source of information	Kuyper 1995; Gminder and Krieglsteiner 2001; Ludwig 2012; Vesterholt 2012a; Alvarado *et al.* 2015	Gminder and Krieglsteiner 2001; Kalamees 2004; Vesterholt 2012a; Alvarado *et al.* 2015	Kuyper 1995; Gminder and Krieglsteiner 2001; Ludwig 2012; Vesterholt 2012a	Bigelow 1982
Growth habit (predominant)	scattered, gregarious	gregarious, caespitose, rarely connate	scattered, gregarious, subcespitose	scattered, gregarious, or subcespitose
Microhabitat	leaves and needles in deciduous, sometimes also coniferous forests, rarely wood debris	soil in deciduous or coniferous forests, parks, ruderal areas, forest tundra; frequently adjacent to forest paths	soil, wood debris (twigs, small branches), mossy stumps or leaf litter (mainly *Alnus, Fagus*), in deciduous (rarely coniferous) forests and scrubs	wood debris (probably of *Umbellularia* or *Quercus*)
Phenology	August – December	August – November	August – December	December
Distribution	Europe, North Asia, North Africa?, North America, South America?	Europe, North Asia, North America	Europe, South-Western Asia	North America
Pileus: colour (at maturity)	whitish pruinose on a pale greyish, pale isabella to pale brown background	whitish pruinose on a cream b-ackground (dark-blue, violet with $FeSO_4$)	pale pinkish isabella, pink	pale butterscotch (pale ochraceous salmon)
Pileus: colour (on drying)	pallescent	white to pale greyish	pallescent to whitish	pallescent to whitish
Pileus: hygrophanity	hygrophanous	hygrophanous	hygrophanous	hygrophanous
Pileus: surface of margin	mostly not striate (exceptionally striate when old)		translucently striate or not striate	not striate

Lamellae: attachment	adnate to deeply decurrent	broadly adnate to short decurrent	decurrent	decurrent throughout development
Lamellae: colour (when young)	white or whitish	white or whitish	white or whitish	?
Lamellae: colour (at maturity)	white to cream	white to cream (violet, dark-blue with $FeSO_4$)	pink tinged	salmon tinged, fading to whitish
Stipe: colour (at maturity)	cream to isabella	white	concolorous with pileus or slightly less pinkish, whitish fibrillose	whitish fibrillose over a yellowish (cream buff) ground colour
Flesh: smell	almost absent or faint: spicy, grass-like, reminiscent of tomato leaves	sweetish-aromatic, cyanic to sickly sweetish	absent, faint or distinct: reminiscent of tomato leaves	faint, pleasant
Basidiospore deposit	white	white	white	white
Basidiospores: dimensions	(4.5) 5.0-6.5 (7.0) × 2.5-3.5 (4.0) µm	5.0-6.0 (7.5) × 3.0-4 (4.5) µm	(6.5) 7.0-9.0 (10) × (3.5) 4.0-5.0 (5.5) µm	(6.5) 7-8 × 4-5 µm
Basidiospores: general shape	ellipsoid to oblong; Q = 1.5-1.8 (1.9)	ellipsoid to obovoid; Q = 1.4-2	ellipsoid to ellipsoid oblong; Q = 1.5-2.1 (2.3)	ellipsoid to ellipsoid oblong; Q = ?
Basidiospores: in exsiccates	not agglutinating	not agglutinating	not agglutinating	?
Basidiospores: reactions	without iodine reactions; not cyanophilous; not congophilous	without iodine reactions; not cyanophilous	without iodine reactions; not cyanophilous; not congophilous	without iodine reactions (not amyloid)
Hymenophoral trama	regular; hyphae 3-10 (12) µm wide	hyphae (2) 3-6 (15) µm wide	subregular; hyphae 4-13 (16) µm wide	subregular to regular; hyphae 3-7 µm wide
Hyphae of pileipellis	repent to ascending, sometimes slightly coralloid, 2-6 µm wide; pigment intracellular, colourless	(2) 3-8 (12) µm wide	parallel to slightly interwoven, 2-5 µm wide; pigment intracellular	cylindrical, at times short celled and contorted near surface, 1.5-4 µm wide
Clamps	present	present	present	present

35. *Russula albidogrisea* J. W. Li and L. H. Qiu ***sp. nov.*** **Figs 14-16**

Mycobank: MB820195

Systematic position: Basidiomycota, Agaricomycetes, Russulales, Russulaceae.

Etymology: Referring to the character of whitish gray pileus.

Diagnosis: *Russula albidogrisea* sp. nov. is well characterized by its white to grayish pileus with acute, even to slightly undulate margin; white, equal and rarely forked lamellae; white spore print; subglobose to globose basidiospores, (5.1) 5.3-5.6-6.0 (6.4) × (4.6) 4.8-5.1-5.3 (5.6) µm, [Q = (1.04) 1.07-1.10-1.15 (1.22), Qm = 1.10 ± 0.03], with distinctive warts connected with lines which form an almost complete reticulum, and non-amyloid suprahilar spot; the orthochromatic pileipellis with ellipsoid cell ending of tapering to subcylindrical terminal hyphae and contain one-celled, SV negative pileocystidia with mucronate to capitate apex.

Holotype: CHINA. Guangdong Province, Dinghu Mountain, near Zhaoqing City, 12 Sept 2015, J. W. Li and J. B. Zhang K15091234 (GDGM48781, **holotype**!).

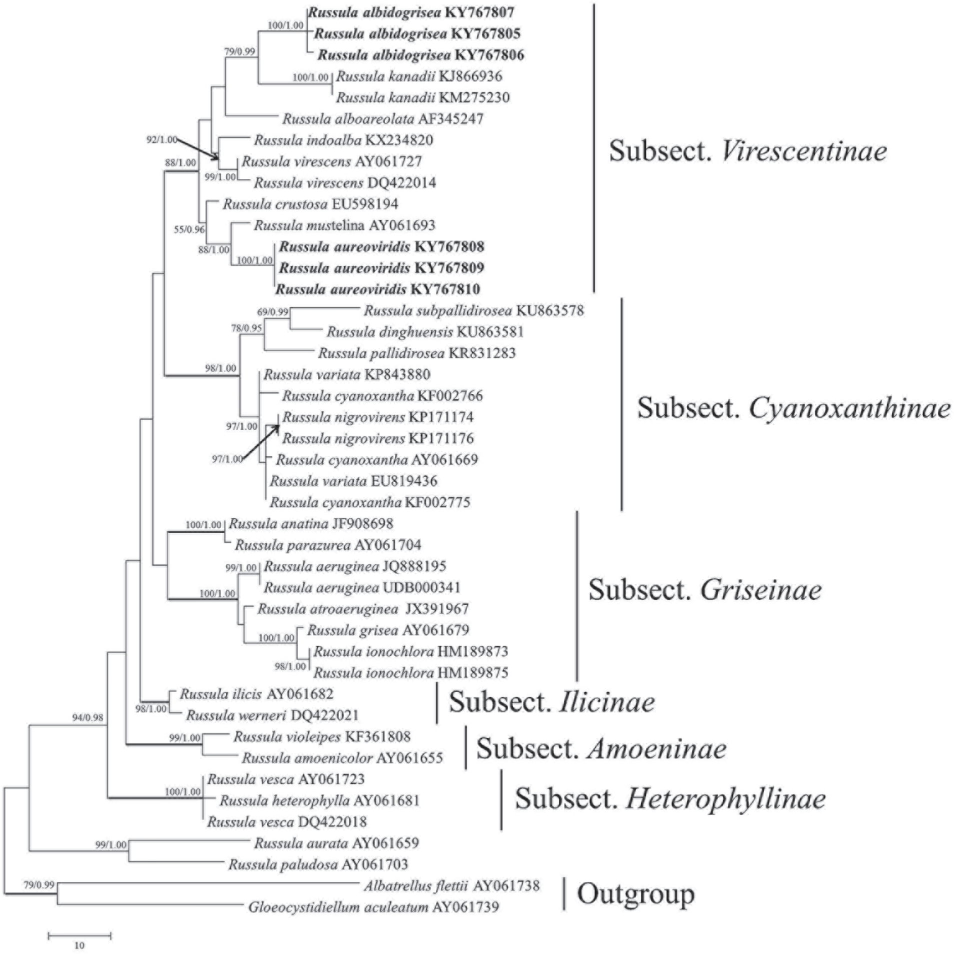
Basidiomata medium size. *Pileus* hemisphaerical when young and applanate to plano-concave when mature, 3.8-6 cm in diam., surface dry, smooth, whitish gray, not peeling readily; margin acute, even, sometimes slightly undulate, striate with age. *Lamellae* white, equal, rarely forked around stipe, 2.5-3 mm wide, medium distant, 14-.15/cm at mid-radius, adnate, venose-connected**,** cream when dried. *Stipe* 3-5 × 0.8-1.2 cm, cylindrical, smooth, dry, whitish, color unchanged when bruised. *Context* 2-3 mm thick, white, color unchanged after exposed in air, becoming cream when dry, salmon red in $FeSO_4$. *Smell* none. *Taste* mild. *Spore print* whitish.

Spores [40/3/3] globose to subglobose, rarely broadly ellipsoid, (5.1) 5.3-*5.6*-6.0 (6.4) × (4.6) 4.8-*5.1*-5.3 (5.6) µm, Q = (1.04) 1.07-*1.10*-1.15 (1.22),

Fig. 14. MP tree of *Russula* subg. *Heterophyllidia* based on ITS dataset showing the taxonomic position of *Russula albidogrisea* sp. nov. and *Russula aureoviridis* sp. nov.. A total of 42 ITS (Table 1) sequences (average 663bp) representing 29 taxa, including outgroups, were analyzed by MP and BI algorithm. *Albatrellus flettii* Morse ex Pouzar and *Gloeocystidiellum aculeatum* Sheng H. Wu were chosen as outgroups according to study of Miller & Buyck (2002). Sequences were aligned with Clustal X and manually modulated when necessary. Some ambiguously aligned terminal regions were excluded. The final aligned dataset was submitted to Tree BASE (20658). For phylogenetic analyses, both maximum pasimony (MP) and Bayesian inference (BI) algorithms were employed. MP analyses were performed using MEGA 7.0.18 and gaps in alignment were treated as missing data. Bootstrap analysis was conducted with 1000 replicates. Bootstrap value (BV) exceeding 50% was considered as significantly supported. Bayesian inference analyses were performed with MrBayes v3.2.5 using the Markov chain Monte Carlo method under the GTR + I + G model. Analyses were run with 4 chains of 1,000,000 generations, and trees were sampled every 100 generation. Bayesian posterior probabilities (PP) values were obtained from the 50% majority-rule consensus trees.Values to the left of "/" are Bootstrap values (BV), and those to the right are Bayesian posterior probabilities (PP) of that clade. BV ≥ 50% and PP values > 0.95 are shown. In the aligned ITS matrix, 257 characters were constant, 375 variable characters were parsimony-uninformative, and 293 characters were parsimony-informative. Both the MP and BI analyses produced similar tree topologies and only the tree inferred from MP analysis was shown (Fig. 14). The phylogram showed that *Russula* subg. *Heterophyllidia* was a monophyletic group with strong support (BV 85%, PP 1.00) and five subsections of this subgenus also formed well-supported clades. The overall structure of the tree was in line with the result of Dutta *et al.* (2015) and Zhao *et al.* (2015). The two new taxa, *R. aureoviridis* sp. nov. and R. albidogrisea sp. nov., were confirmed by each forming strongly supported clades (both with BV 100%, PP 1.00). BLAST query in GenBank with ITS sequences showed that *Russula aureoviridis* sp. nov. is close to *Russula mustelina* Fr., while *Russula albidogrisea* sp. nov. is close to *Russula virescens* (Schaeff.) Fr., both belong to *Russula* subg. *Heterophyllidia* subsection *Virescentinae*. Classification of *Russula* followed Sarnari (1998).

▶

ornamentation composed of conical to hemisphaerical warts up to 0.3-0.4 µm high, interconnected with lines measured 0.1-0.2 µm high, forming complete amyloid reticulum mesh, suprahilar area not amyloid. *Basidia* 41-48 × 9-11 µm, mostly with four sterigmata, rarely two or three, hyaline, clavate to subclavate-pedicellate, sterigmata 4-6 µm long. *Lamellar trama* mainly composed of large sphaerocytes. *Pleurocystidia* 35-50 × 5-11 µm, abundant, distinctly projecting 11-14 µm beyond the hymenium, clavate to subclavate, thin walled, with abundant refractive contents, rounded-obtuse at apex, unchanged in SV. *Cheilocystidia* is similar to pleurocystidia morphologically, 37-46 × 9-12 µm, clavate to subclavate, thin walled, with some refractive contents, also not obvious reacted in SV. *Pileipellis* orthochromatic in Cresyl blue, composed of suprapellis and subpellis; suprapellis a trichoderm 80-95 µm deep, dense, with hyphal terminations similar to those of *R. virescens*. The ascending subcylindrial or apex slightly narrowing terminal cells measured 14.8-*20.8*-29.0 × 2.7-*3.6*-5.5 µm, originating from inflated, subglobose, short-celled, about 5-8.5 µm wide elements. Subpellis 90-115 µm deep, composed of interwoven



to subparallel hyphae, measured 3-4 µm wide. Pileocystidia only observed in suprapellis, measuring 21.3-35.1-51.5 × 3.1-4.0-5.1 µm, fusiform to cylindrical, attenuated and usually with mucronate or capitate apex, with abundant refringent contents, negative to SV. *Stipitipellis* a cutis with some repent to interwoven hyphae, thin-walled, hyaline, cylindrical, hyphae 3-5.5 µm in diameter Caulocystidia absent. *Clamp connection* absent from all tissues.

Habitat and distribution: Solitary in monsoon evergreen broadleaf forest and pine-broadleaf mixed forest.

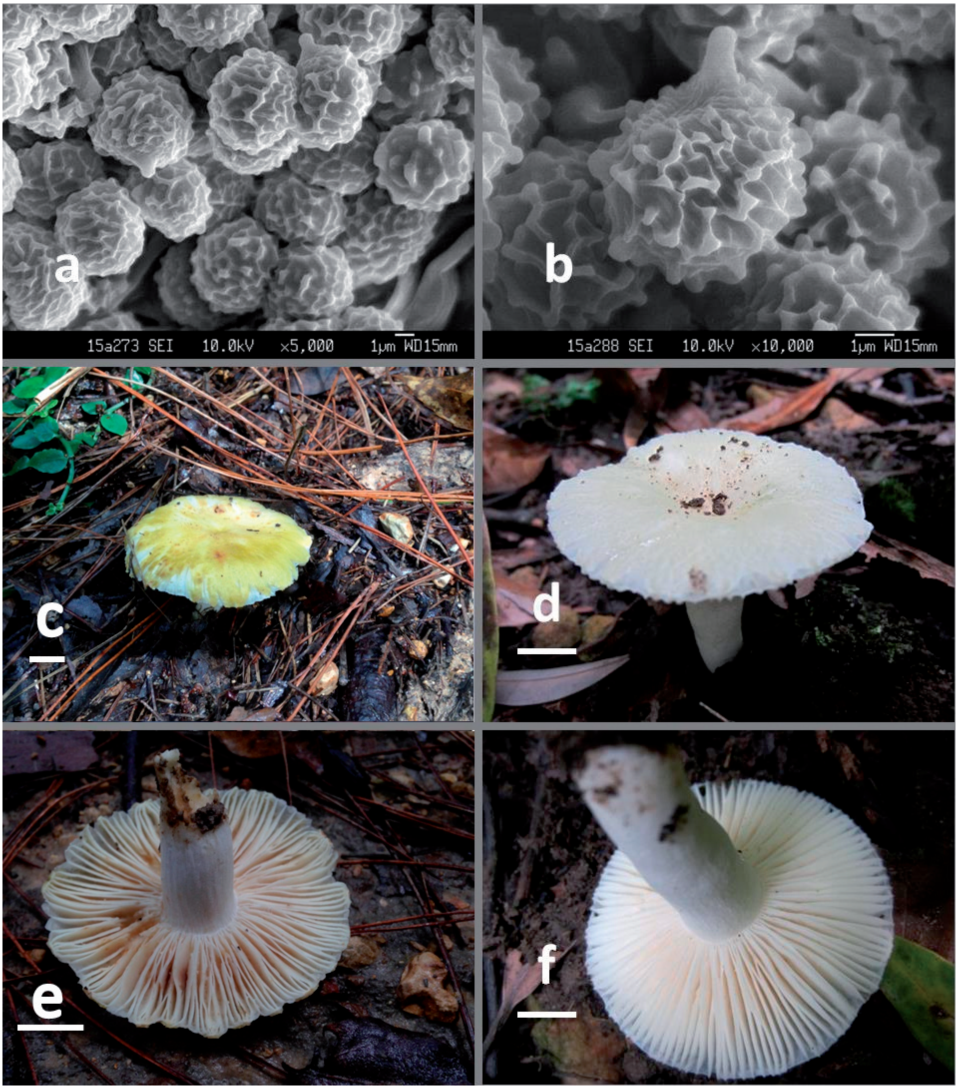


Fig. 15. *Russula aureoviridis* sp. nov. (a, c, e. Holotype GDGM 48785) and *Russula albidogrisea* sp. nov. (b, d, f. Holotype GDGM 48781). Scanning Electronic Micrographs (a and b. scale bars = 1 µm) and field photographs (c-f. scale bars = 1 cm).

Additional examined material: CHINA, Guangdong Province, Zhaoqing City, 20 June 2015, J. W. Li and J. B. Zhang GDGM 48782; 7 June 2015, J. W. Li and J. B. Zhang GDGM 48783.

Notes: Although China is considered a country rich in *Russula* species, there are only 24 new species and 3 varieties described from the region up to now (Singer 1935; Ying 1983; Bi & Li 1986; Zang & Yuan 1998; Wen & Ying 2000; Song *et al.* 2007; Wang *et al.* 2009; Li *et al.* 2011; Li *et al.* 2012; Li *et al.* 2013; Li *et al.* 2013; Li *et al.* 2015; Li *et al.* 2015; Zhao *et al.* 2015; Zhang *et al.* 2017). The Dinghushan Biosphere Reserve (DHSBR), located in southern subtropical China, is considered a region with highly diverse macrofungi for its excellent climate and abundant vegetations (Zheng *et al.* 1985; Bi *et al.* 1994).

Russula albidogrisea sp. nov. can be well characterized by its white to grayish pileus with acute, even to slightly undulate margin; white, equal and rarely forked lamellae; white spore print; subglobose to globose basidiospores with distinctive warts connected with lines which form an almost complete mesh, and non-amyloid suprahilar spot; the orthochromatic pileipellis with ellipsoid cell ending of tapering to subcylindrical terminal hyphae; one-celled and SV negative pileocystidia with mucronate to capitate apex. This combination of characters assigns it to *Russula* subg. *Heterophyllidia* subsection *Virescentinae* (Sarnari 1998), which is also supported by molecular analysis based on ITS sequences (Fig. 14).

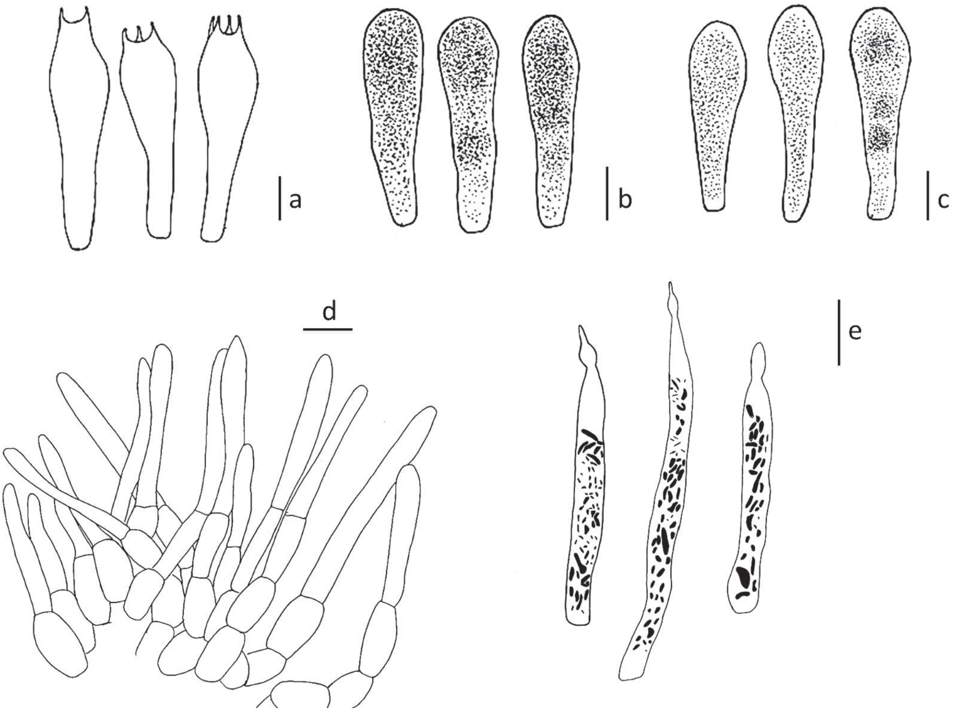


Fig. 16. *Russula albidogrisea* sp. nov. (Holotype GDGM 48781). **a.** Basidia; **b.** Cheilocystidia; **c.** Pleurocystidia; **d.** Pileipellis; **e.** Pileocystidia. Scale bars = 10 µm.

Other whitish russulas have been attributed to subg. *Heterophyllidia* subsect. *Virescentinae* and are therefore similar to *R. albidogrisea*: the Japanese *R. alboareolata* Hongo, the Indian species *R. kanadii* (A.K. Dutta & Acharya, Dutta *et al.* 2015) and *R. indoalba* A. Ghosh, Buyck, A. Baghela, K. Das & R.P. Bhatt (in Hyde *et al.* 2016), as well as the American *American species described by Murrill: R. albiduliformis*, *R. heterosporoides* and *R. maculosa* (see Buyck & Adamcík 2011). Both MP and BI analysis showed that *Russula albidogrisea* sp. nov. formed a highly supported sister group with *R. kanadii* (MPbs = 79%, BPP = 0.99) but their ITS sequence similarity is only 89.3%. These two taxa are somewhat similar to each other in terms of white sulcate pileus, absence of lamellulae, white stipe and the size of basidiospores, but they differ in the lamellae that are rarely forked around stipe for *R. albidogrisea* but heavily forked for *R. kanadii*; anastomosing veins are present between gills for the former but absent for the latter; basidiospores are almost completely reticulate for *R. albidogrisea* but reticulation is poor for the latter, and also pleurocystidia are shorter (35-50 × 5-11 vs. 65-70 × 8-10). *Russula indoalba* is here shown (Fig. 14) to be genetically closer to *R. virescens*. Sequence data are not yet available for the American taxa which, however, should be genetically different.

36. ***Russula aureorubra*** K. Das, A.Ghosh, A. Baghela & Buyck ***sp. nov***.

Figs 17-19

MycoBank: MB 822653

GenBank: MF667557 (ITS).

Systematic position: Basidiomycota, Agaricomycetes, Russulales, Russulaceae.

Etymology: Referring to the yellow color of stipe and gills and the yellow-red (“aureo” + “rubra”) pileus of basidiomata.

Diagnosis: Distinct from all the known species of *Russula* by the unique combination of characters: greenish yellow to pastel yellow or golden yellow longitudinally fibrillose stipe, yellow gills with many shorter lamellulae producing a white spore print. It shares with other members of subsect. *Emeticinae* the relatively large basidiospores (7-*7.5*-8 × 6-*6.98*-7.6 µm) with reticulate ornamentation and reddish tints on the pileus.

Holotype: INDIA, Sikkim, South district, Maenam wild life sanctuary, N 27° 19’21.5” E 088°22’7.9”, 1843 m asl., under *Lithocarpus* in temperate broadleaf forest, 19 August, 2016, *Kanad Das,* KD 16-58 (CAL 1605 **holotype**).

Pileus 28-40 mm. in diam., hemispheric with a depressed centre when young, becoming convex to planoconvex or applanate with a broad central depression at maturity; surface viscid when moist, easily peeled off 1/3rd to 1/2nd toward centre, orange red to yellowish red to brownish red (8B-C8) or rarely reddish orange (7A8) at centre, gradually paler toward margin but mostly in combination with pastel yellow to light yellow (2A4-5) and at margin always pastel yellow to light yellow (2A4-5) at maturity, unchanging when bruised. *Lamellae* subdecurrent, unequal by the presence of quite many lamellulae of different length, normally spaced (8-9/cm at pileus margin), often bifurcate near stipe, brittle, pale yellowish (3A2); edges concolorous, entire. *Stipe* 35-68 × 6-9 mm, central, cylindrical, slowly broadening toward base; surface longitudinally fibrillose, light greenish yellow to mainly pastel yellow (2A4) but paler toward apex, unchanging when bruised but turning greenish grey to grayish green (26B2-3) with $FeSO_4$, often with white basal mycelia. *Context* solid in stipe, translucent-yellow, gradually (1A4) toward base, but turning greenish grey (26B2) with $FeSO_4$, unchanging with Guaiac and KOH. *Taste* at first strongly bitter, then acrid. *Spore print* white (1A1).

Basidiospores subglobose to broadly ellipsoid, rarely globose, 7-*7.5*-8 × 6-*6.98*-7.6 µm, (n = 30, Q = 1-*1.07*-1.2), ornamentation amyloid, composed of warts and low ridges that are aligned or connected to give almost complete reticulum; warts 1-1.5 µm high, ridges 0.1-0.2 µm high. *Basidia* 26-44 × 7-12 µm, 4-spored, cylindrical to subclavate, sterigmata up to 8 µm long. *Pleurocystidia* 31-61 × 7-10 µm, abundant, cylindrical to subclavate with appendiculate, mucronate or rounded apex, emergent up to 35 µm, with dense fibrillose content. *Lamellae edge* fertile with basidia and cystidia. *Cheilocystidia* 31-47 × 6.5-11 µm, cylindrical to subclavate with mostly rounded apex, with dense fibrillose content. *Pileipellis* up to 130 µm thick, a trichoderm, composed of branched, septate irect to suberect hyphae (2-4.5 µm broad) with rounded or blunt apex and cystidia. *Pileocystidia* abundant, short to long, aseptate to septate (with 2-3 septation), cylindrical (5-11 µm broad) with clavate to subclavate apex, with dense fibrillose, SV+ contents. *Clamp connections* and *lactifers* absent from all tissues.

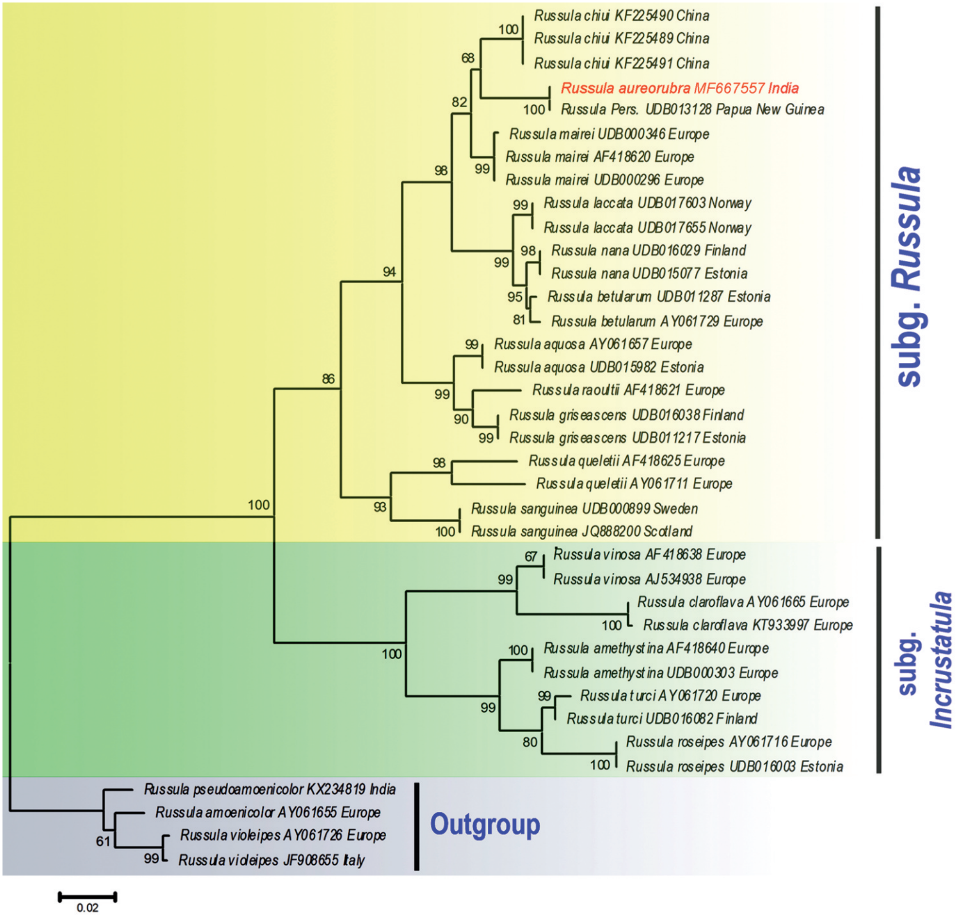
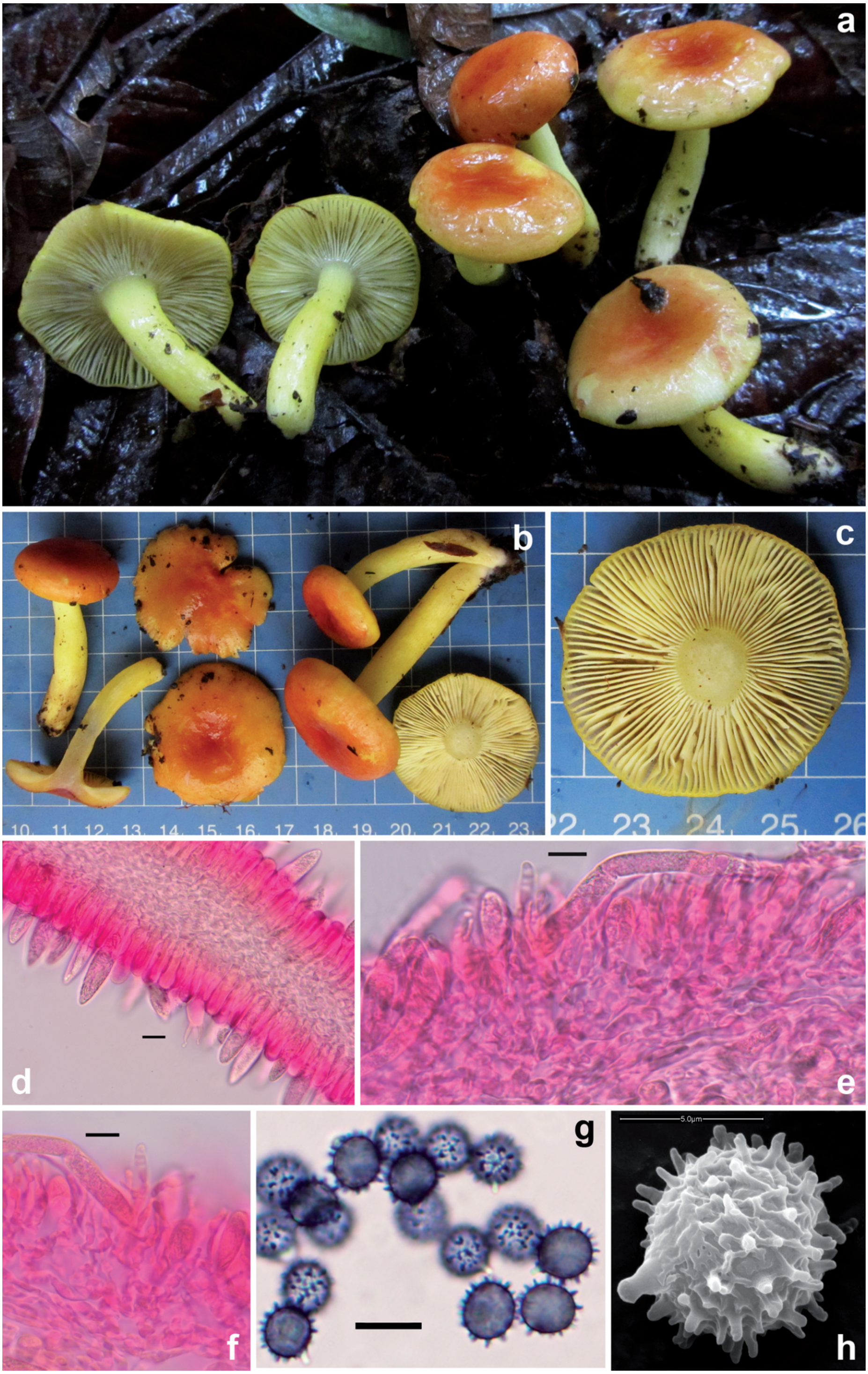


Fig. 17. Phylogram generated from Maximum Likelihood (ML) method based on ITS-rDNA sequences from MEGA6 (Tamura *et al.*, 2013) under Tamura 3-parameter model (Tamura, 1992). The tree with the highest log likelihood (-1003.5314) is shown. One thousand bootstrap replicates were analyzed to obtain the nodal support values. Bootstrap support values (> 50%) obtained from Maximum Likelihood (ML) analysis are shown above or below the branches at nodes. The novel Indian species *Russula aureorubra* having GenBank Accession Number MF667557 (ITS-rDNA) is shown in red and bold in the tree.


a
b
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10. 11. 12. 13. 14. 15. 16. 17. 18. 19. 20. 21. 22. 23.
22. 23. 24. 25. 26
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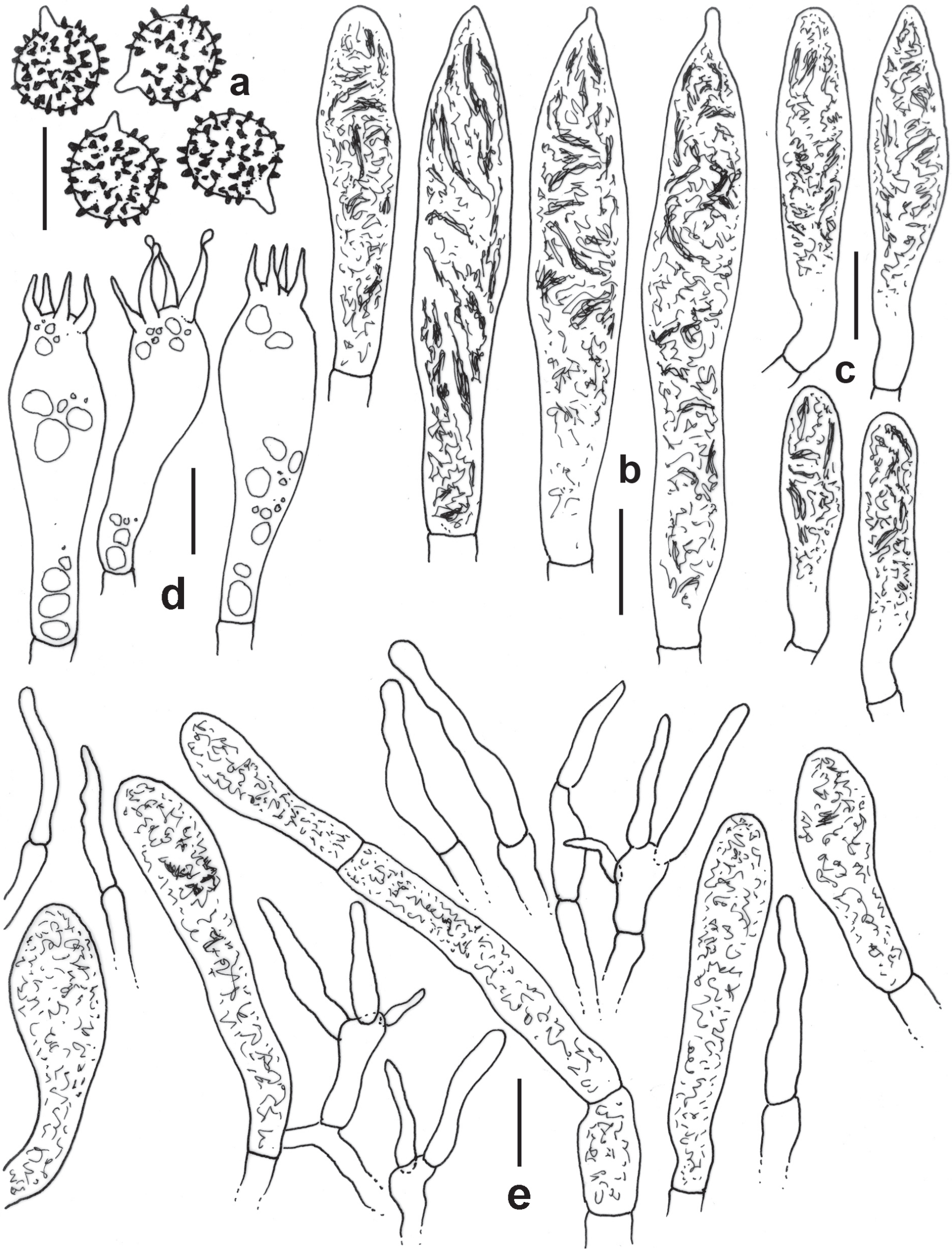


Fig. 19. *Russula aureorubra.* Microscopic features (from KD 16-58, holotype). **a.** Basidiospores. **b.** Pleurocystidia. **c.** Cheilocystidia. **d.** Basidia. **e.** Pileipellis. Scale bars: a-e = 10 µm.

◀ Fig. 18. *Russula aureorubra* (KD 16-58, holotype). **a & b.** Fresh basidiomata in the field and basecamp. **c.** Lamellae. **d.** Hymenium layer showing basidia and pleurocystidia. **e & f.** Radial section through pileipellis. **g.** Amyloid basidiospores. **h.** Basidiospores under SEM. Scale bars: d-g = 10 µm, h = 5 µm.

Notes: Our phylogeny places this new species firmly in subsect. *Emeticinae* (MLBS 98%) where it occupies a sister position to the Chinese *Russula chiui* G.J. Li & H.A.Wen, both of which form again a sisterclade to the European *R. mairei* Sing. (most probably because American members of *Emeticinae* are absent from the phylogeny). *Russula chiui* differs from our species in its white stipe and lamellae and more reddish pileus (as is the case in most other *Emeticinae*) and so do most of the other possibly closely related species described from China or neighbouring countries (see Li *et al.* 2015).

Russula aureorubra is unique among *Emeticinae* because of its entirely yellow color of the basidiomata although it shares with the other species a pileus that is tinged with red. This overall yellow color, extending also to the lamellae, make it not evident to recognize it immediately as a member of *Russula*. Another unique feature among *Emeticinae* – and indeed among all species of subg. Russula – is the remarkabe abundance of shorter lamellulae which can be nearly as abundant as normal lamellae. The latter feature, therefore, is reminiscent of species in *Russula* subg. *Archaea* (see Hongsanan *et al.* 2015; Buyck *et al.* 2017). Both of these characters make *R. aureorubra* an unmistakable and phylogenetically interesting species.

37. *Russula aureoviridis* J. W. Li and L. H. Qiu ***sp. nov.*** **Figs 14-15, 20**

Mycobank: MB 820197

Systematic position: Basidiomycota, Agaricomycetes, Russulales, Russulaceae.

Etymology: Referring to the golden-green pileus.

Diagnosis: *Russula aureoviridis* sp. nov. is recognized by the yellowish green to golden green pileus, white to cream, frequently forked lamellae producing a cream spore print; subglobose to ellipsoid, subreticulate basidiospores, (4.9) 5.3-*5.7*-6.1 (6.7) × (4.4) 4.8-*5.1*-5.5 (6.0) µm, [Q = (1.03) 1.07-*1.13*-1.20 (1.23)], that are weakly ornamented with lines and ridges, and have a non-amyloid suprahilar spot; an orthochromatic pileipellis of inflated, short-celled and sometimes furcate hyphal terminations with subulate to subcylindrial terminal cells, mixed with one-celled, SV negative, and often mucronate pileocystidia.

Holotype: CHINA. Dinghu Mountain, Zhaoqing City, **Guangdong Province**, 26 August 2016, J. W. Li and L. H. Qiu H16082612 (GDGM 48785, **holotype**!).

Basidiomata medium sized. *Pileus* hemisphaerical when young and plano to plano-concave when mature, 4.5-8.2 cm diameter; surface dry and smooth, yellowish green (#D8F781) to golden-green (#CCFF33), peeling readily near margin which is dull and smooth, becoming striate with age, uncracked when matured. *Lamellae* adnate, equal, venose-connected, compacted, forked near margin, 14-16 L/cm at mid-radius, pale cream when fresh, changing to brown when dry, unchanging when bruised. *Stipe* 3-5 × 0.8-1.2 cm, cylindrical, white to pale cream, unchanging when bruised, smooth, dry. *Context* white, turning brown after exposion to air or when dry, salmon red with $FeSO_4$. *Taste* mild. *Smell* none. *Spore print* cream.

Spores [40/3/3] subglobose to broadly ellipsoid, rarely globose, (4.9) 5.3-*5.7*-6.1 (6.7) × (4.4) 4.8-*5.1*-5.5 (6.0) µm, [Q = (1.03) 1.07-*1.13*-1.20 (1.23)], ornamentation amyloid but nearly smooth, warts not distinguishable and, lines and ridges not exceeding 0.2 µm in hight, forming an incomplete reticulum; suprahilar area non-amyloid. *Basidia* 33-48 × 8-12 um, mostly (2-3)4-spored, sterigmata 3-4 µm long, clavate to fusiform. *Lamellar trama* mainly consist of large sphaerocytes. *Pleurocystidia* 38-50 × 7-12 µm, abundant, projecting about 10 µm beyond hymenium, slender, subclavate to clavate, rarely fusiform, usually apex obtuse, mucronate-appendiculate also observed, refractive contents, not changing in SV.

Cheilocystidia 27-40 × 6-10 µm, narrowly clavate to clavate, mostly apex obtuse, some with long appendages or subterminally constricted, with some refractive contents, SV negative. *Marginal cells* 21-28 × 4-6 µm, similar to cheilocystidia morphologically, subclavate to clavate. *Pileipellis* orthochromatic in Cresyl blue, composed of suprapellis and subpellis; subpellis 70-105 µm thick, composed of interwoven to subparallel cylindrical hyphae, thin walled, hyaline, measuring 3-5 µm wide. Suprapellis a trichoderm 70-85 µm deep, with hyphal terminations similar to *R. virescens*. Hyphal terminations short-celled, inflated, hyphal ca. 5-12 µm, ending of subulate to subcylindrial terminal cells, measuring 10.3-14.2-21.6 × 2.8-3.3-4.3 µm. Pileocystidia one-celled, ca. 21.7-31.3-47.7 × 3.1-4.0-4.7 µm, attenuated, narrowly fusiform, often mucronate-appendiculate, moniliformous appendages also present. *Stipitipellis* a cutis with some repent and oblique hyphae, thin-walled, cylindrical, 2.5-4 µm in diameter. *Clamp connections* absent from all tissues.

Habitat and distribution: Solitary in monsoon evergreen broadleaf forest and pine-broadleaf mixed forest.

Additional specimens examined: CHINA, Guangdong Province, Zhaoqing City, 8th May 2016, J. W. Li and J. B. Zhang GDGM48786; 14th September 2015, J. W. Li and J. B. Zhang GDGM48787.

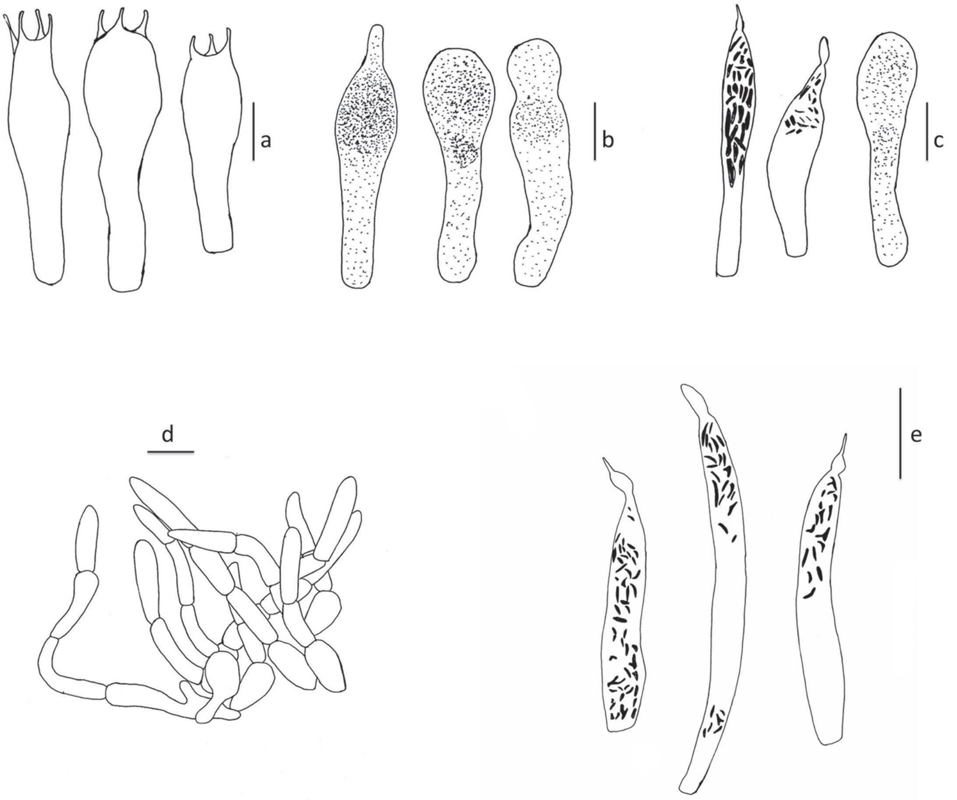


Fig. 20. *Russula aureoviridis* sp. nov. (Holotype GDGM 48785). **a.** Basidia; **b.** Cheilocystidia; **c.** Pleurocystidia; **d.** Pileipellis; **e.** Pileocystidia. Scale bars = 10 µm.

Notes: *Russula aureoviridis* sp. nov. is recognized by the yellowish green to golden green pileus, white to cream, forked lamellae producing a cream spore print; subglobose to ellipsoid, subreticulate basidiospores that are weakly ornamented with lines and ridges, and non-amyloid suprahilar spot; its orthochromatic pileipellis consists of inflated, short-celled and sometimes furcate hyphal terminations with subulate to subcylindrial terminal cells; and one-celled, SV negative, and often mucronate pileocystidia.

The forked lamellae and overall color of this species are reminiscent of subsect. *Cyanoxanthinae* but the cream spore print and orthochromatic pileipellis contradict this position.

BLAST results as well as phylogenetic analysis based on ITS sequence data showed that *R. aureoviridis* sp. nov. is monophyletic with *R. mustelina* Fr. with strong support, but *R. aureoviridis* differs in its general color and smaller spores (5.3-6.1 × 4.8-5.5 vs. 6.0-9.5 × 5.3-7.8 µm) without warts. In addition, the ITS sequence similarity is only 90.2%. Together with *R. crustosa* Peck (ITS sequence similarity of 87.8%) these three species differ from the other *Virescentinae* in our analysis by the presence of dermatocystidia in their subpellis.

38. ***Russula obscuricolor*** K. Das, A. Ghosh & Buyck ***sp. nov.*** **Figs 21-23**

MycoBank: MB822861

GenBank: MF804816 (ITS); MF804817 (ITS).

S*ystematic position*: Basidiomycota, Agaricomycetes, Russulales, Russulaceae.

Etymology: named for the dark coloration of the pileus center.

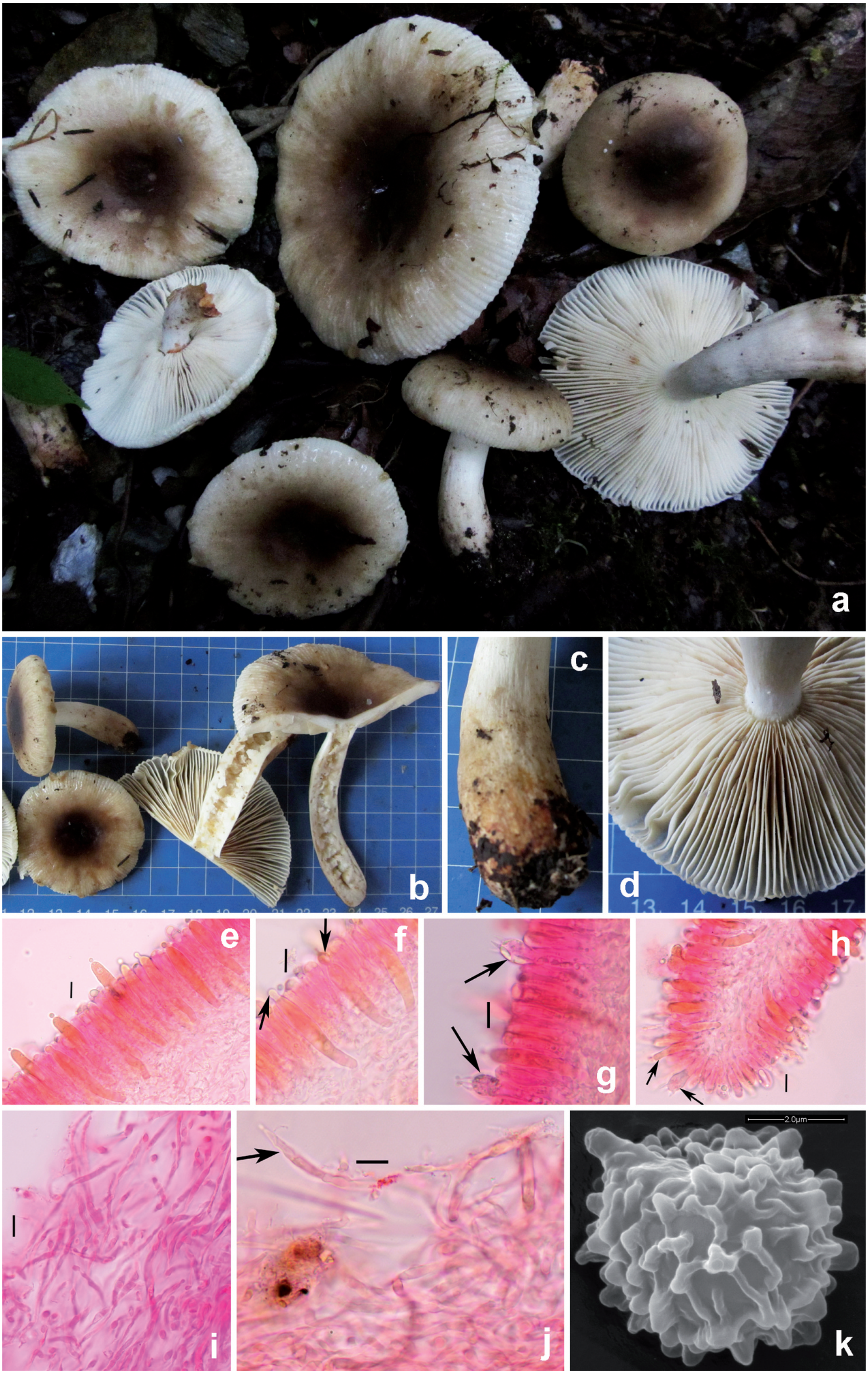
Diagnosis: differs from the closely allied Asian species of subg. *Ingratula* by the ITS sequences and combination of features: blood red coloration at stipe base, taste of bitterish pungent.

Holotype: INDIA, Sikkim, South district, Maenam Wild Life Sanctuary, on ground, under *Castanopsis* sp, mixed broadleaf forest, N 27°15’34.7” E 88°21’25.7”, alt. 2136 m a.s.l., 18 August 2016, *K. Das*, KD 16-30. (CAL1602, holotype!).

Pileus 30-75 mm. in diam., hemispheric, convex to planoconvex when young, then applanate at maturity; surface viscid when moist, heavily gluten; cuticle peeled 15 mm. from margin then broken into small pieces; brown to chocolate brown (6E4-6F4) at center and pale yellowish white (2A2) at margin; margin incurved when young then gradually decurved at maturity, strongly sulcate. *Lamellae* yellowish white (2A2), unchanging of faintly brownish on maturity, forked at stipe apex or at middle; lamellulae less, present in 2 series. *Stipe* 40-65 × 12-20 mm, central, clavate gradually broader at base, dry, smooth, yellowish white (1A2) becoming dingy after handling, blood red at base; salmon pink (6A3) with the application of $FeSO_4$ and, turning grayish green (25E5-25E6) and pale yellow (3A3) with guaiacol and KOH respectively. *Taste* pungent and bitterish like radish. *Spore print* yellowish white (2A2).

Basidiospores 6-$\underline{6.5}$-7.5 × 5-$\underline{5.45}$-6 µm (n = 20, Q = 1-$\underline{1.19}$-1.4), mostly subglobose to broadly ellipsoid rarely globose and ellipsoid; ornamentation amyloid, composed of somewhat conical warts and ridges connected to give partial to incomplete reticulum; warts 0.4-0.9 µm high; suprahilar region inamyloid. *Basidia*

Fig. 21. *Russula obscuricolor* (KD 16-30, holotype). **a & b.** Fresh or dissected basidiomata. **c.** Stipe base. **d.** Lamellae. **e & f.** Pleurocystidia. **g.** Basidia. **h.** Lamellae edge showing basidium and cheilocystidium. **i & j.** Pileipellis. **k.** Basidiospores under SEM. Scale bars: e-j = 10 µm; k = 2 µm. ▶


a
b
c
d
e
f
g
h
i
j
k
2.0μm

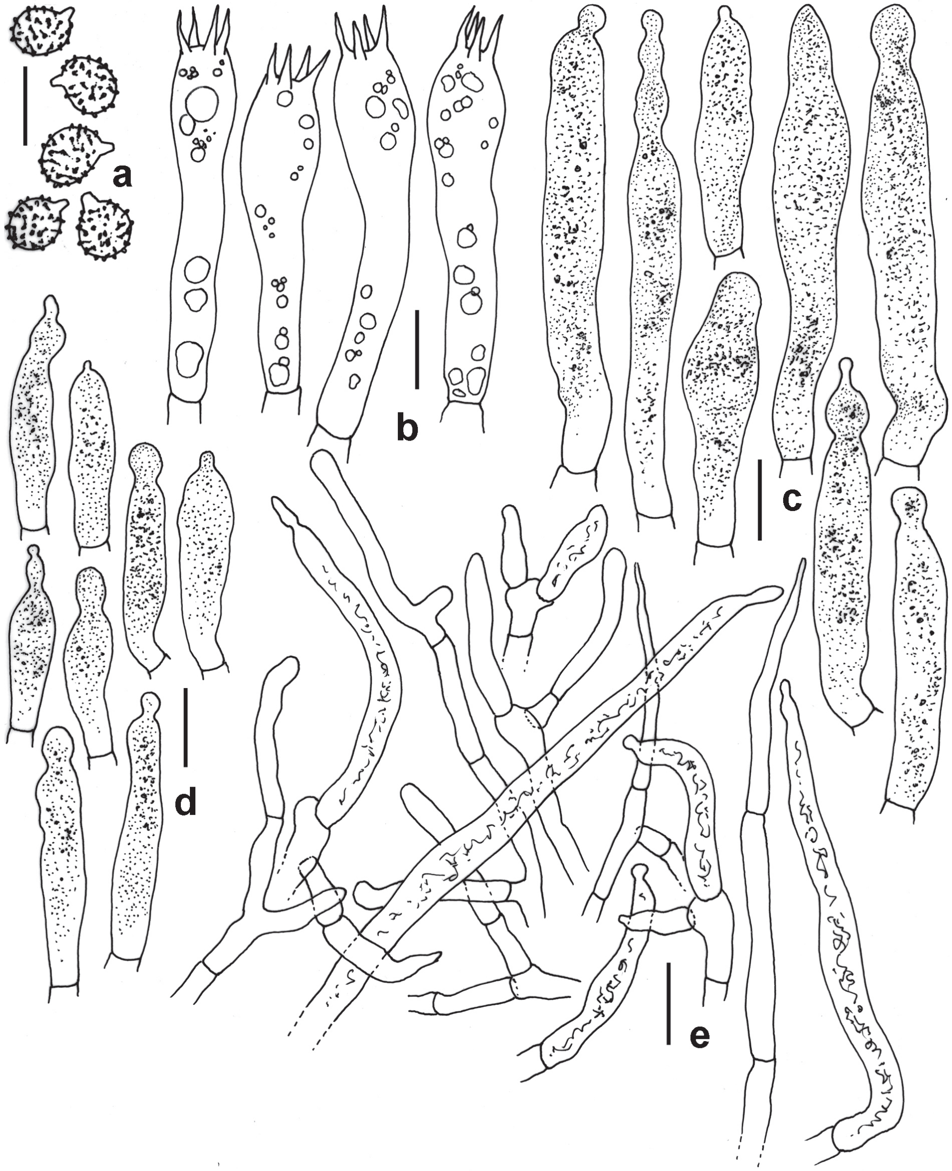
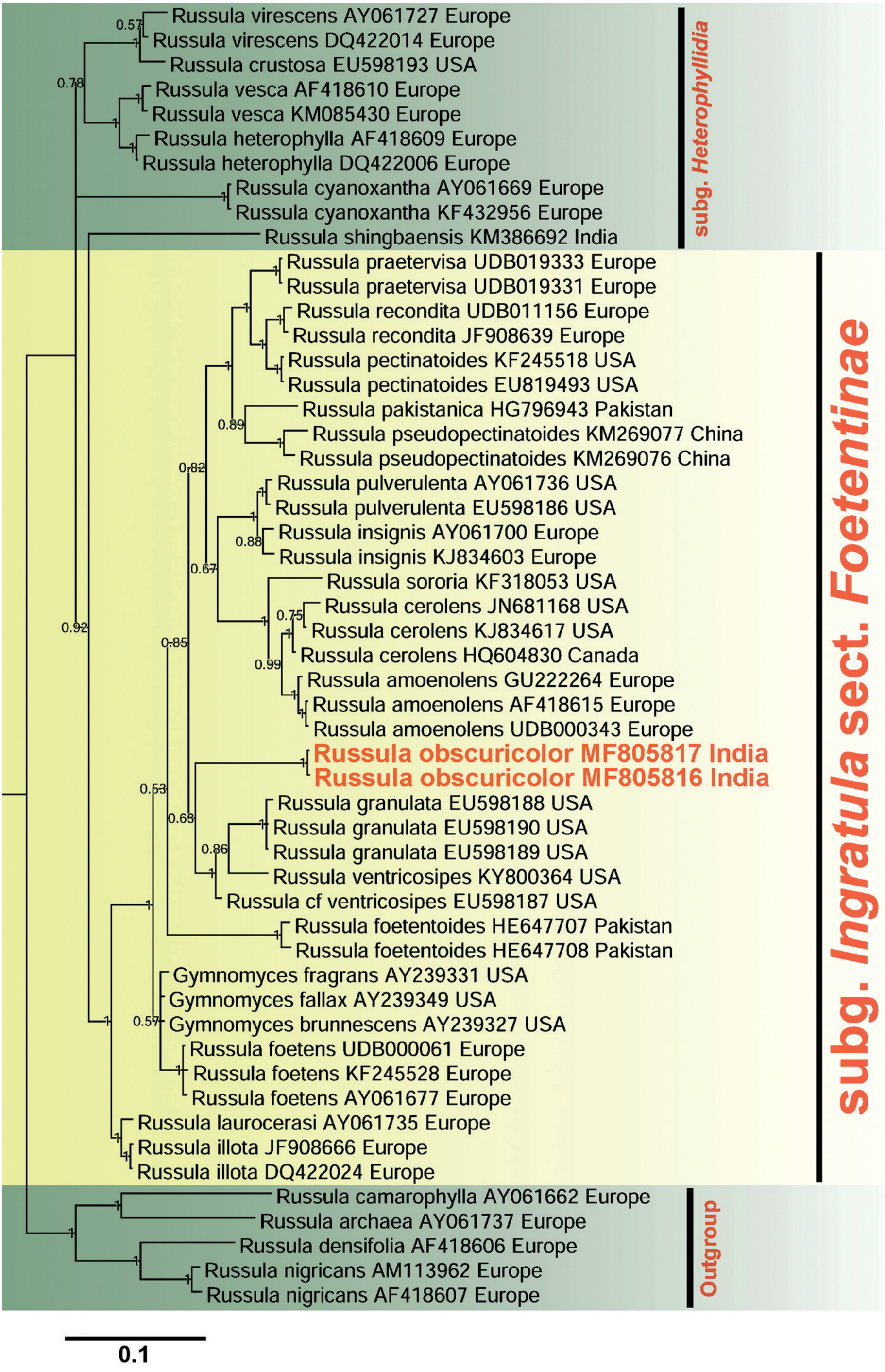


Fig. 22. *Russula obscuricolor* (from KD 16-30, holotype). Microscopic features: **a.** Basidiospores. **b.** Basidia. **c.** Pleurocystidia. **d.** Cheilocystidia. **e.** Pileipellis. Scale bars = 10 μm.

Fig. 23. Bayesian phylogram inferred from the ITS dataset based on MrBayes under TrNef + G model of nucleotide evolution. Support values (Bayesian posterior probability) are indicated above or below clade branches. The position of our new species, *Russula obscuricolor* (GenBank numbers MF805816 and MF805817), is shown in red and bold font. ▶


Russula virescens AY061727 Europe
Russula virescens DQ422014 Europe
Russula crustosa EU598193 USA
Russula vesca AF418610 Europe
Russula vesca KM085430 Europe
Russula heterophylla AF418609 Europe
Russula heterophylla DQ422006 Europe
Russula cyanoxantha AY061669 Europe
Russula cyanoxantha KF432956 Europe
Russula shingbaensis KM386692 India
Russula praetervisa UDB019333 Europe
Russula praetervisa UDB019331 Europe
Russula recondita UDB011156 Europe
Russula recondita JF908639 Europe
Russula pectinatoides KF245518 USA
Russula pectinatoides EU819493 USA
Russula pakistanica HG796943 Pakistan
Russula pseudopectinatoides KM269077 China
Russula pseudopectinatoides KM269076 China
Russula pulverulenta AY061736 USA
Russula pulverulenta EU598186 USA
Russula insignis AY061700 Europe
Russula insignis KJ834603 Europe
Russula sororia KF318053 USA
Russula cerolens JN681168 USA
Russula cerolens KJ834617 USA
Russula cerolens HQ604830 Canada
Russula amoenolens GU222264 Europe
Russula amoenolens AF418615 Europe
Russula amoenolens UDB000343 Europe
Russula obscuricolor MF805817 India
Russula obscuricolor MF805816 India
Russula granulata EU598188 USA
Russula granulata EU598190 USA
Russula granulata EU598189 USA
Russula ventricosipes KY800364 USA
Russula cf ventricosipes EU598187 USA
Russula foetentoides HE647707 Pakistan
Russula foetentoides HE647708 Pakistan
Gymnomyces fragrans AY239331 USA
Gymnomyces fallax AY239349 USA
Gymnomyces brunnescens AY239327 USA
Russula foetens UDB000061 Europe
Russula foetens KF245528 Europe
Russula foetens AY061677 Europe
Russula laurocerasi AY061735 Europe
Russula illota JF908666 Europe
Russula illota DQ422024 Europe
Russula camarophylla AY061662 Europe
Russula archaea AY061737 Europe
Russula densifolia AF418606 Europe
Russula nigricans AM113962 Europe
Russula nigricans AF418607 Europe
subg. Heterophyllidia
subg. Ingratula sect. Foetentinae
Outgroup
0.57
0.78
0.92
0.89
0.82
0.88
0.67
0.75
0.99
0.85
0.53
0.63
0.86
0.57
1
0.1

36-52 × 8-10 µm, cylindrical, 4-spored, sterigmata 3-5 µm high. *Subhymenium layer* up to 20 µm thick, pseudoparenchymatous. *Pleurocystidia* 30-65 × 6-9 µm, emergent up to 34 µm, abundant, cylindrical, with capitates, rounded, mucronate apex; content dense granular. *Gill edges* fertile, with basidia and cystidia. *Cheilocystidia* 23-33 × 5-7 µm, cylindrical with mucronate, capitate apex; content same as in pleurocystidia. *Pileipellis* up to 120 µm thick, an ixotrichoderm, composed of branched, septate hyphae (2-4 µm). Pileocystidia (3-6 µm broad), cylindrical with capitate, rounded to appendiculate apex. *Clamp connections* absent.

Specimens examined: INDIA, Sikkim, South district, Maenam Wild Life Sanctuary, on ground, under *Castanopsis* sp, mixed broadleaf forest, N 27°15'34.7" E 88°21'25.7", alt. 2136 m a.s.l., 18 August 2016, *K. Das*, KD 16-30 (CAL1602, holotype!); ibid., South district, Maenam Wild Life Sanctuary, on ground, under *Castanopsis* sp, mixed broadleaf forest, N 27°14'50.9" E 88°21'59.7", alt. 2159 m a.s.l., 18 August 2016, *K. Das*, KD 16-22 (CAL1603).

Notes: Our phylogenetic analyses (Fig. 23) place this new species sister to the American *R. granulata* Peck but without significant support. Both these species are then again placed sister without support to a well-supported clade (90% MLBS) of European and American *Ingratae* (= subg. *Ingratula*) comprising several other dark-coloured species such as *R. amoenolens* Romagn., *R. cerolens* Shaffer or *R. sororia* (Fr.) Romell. The only other species of *Ingratae* in our analyses that were equally described from this part of the world, i.e. the Chinese *R. pseudopectinatoides* G.-L. Li & H.A. Wen and the Pakistani *R. foetentoides* Razaq, Khalid & Niazi, and *R. pakistanica nom. prov.* are unrelated. *Russula pseudopectinatoides* is placed in a well-supported clade comprising the European *R. praetervisa* Sarnari, *R. recondita* Melera & Ostellari and the American *R. pectinatoides* Peck.

However, several more *Ingratae* have been described from Asia these past years and, although no sequence data are available for those, morphological features allow to distinguish them. The Indian *R. natarajani* K. Das, J.R. Sharma & Atri (in Das *et al.* 2006) has been attributed to *Ingratae* based on morphological features and is easily distinguished by the white pileus and subreticulate, cristate, low spore ornamentation. *Russula tsokae* K. Das, Van de Putte & Buyck (in Das *et al.* 2010) clearly belongs to a different species group in *Ingratae* because of the yellowish orange stipe surface and winged spore ornamentation up to 2 um high and is likely closer to *R. senecis* Imai, originally described from Japan but also more largely distributed in Asia (Khatua *et al.* 2015), while *R. dubdiana* K. Das, Atri & Buyck (in Das *et al.* 2013) differs in acrid taste, more yellowish to rusty brown pileus and spores measuring 5.2-*6.1*-7.0 × 4.2-*4.8*-5.5 µm (Q = 1.17-*1.27*-1.45).

39. ***Russula pauriensis*** A. Ghosh, K. Das & Buyck ***sp. nov.*** **Figs 24-26**

MycoBank: MB822859

GenBank: MF535185 (ITS).

Systematic position: Basidiomycota, Agaricomycetes, Russulales, Russulaceae.

Etymology: named after the type locality (Pauri district, Uttarakhand).

Diagnosis: This new species differs from the recently described *R. mukteshwarica,* another Indian member of *Amoeninae* that was collected under the same host tree in the same area (Pauri district in Uttarakhand, India), in its smaller spores being particularly more narrow (5.5-*6.3*-7 µm versus 7.3-8.2 µm in the latter species) and in the considerably higher spore ornamentation (up to 2 µm versus lower than 0.75 µm in *R. mukteshwarica*. The six known specimens for *R. mukteshwarica* seem to indicate that the constantly much darker pileus color of the latter is another character that distinguishes both species.

Holotype: INDIA, Uttarakhand, Pauri district, Phedkhal, on ground, under *Quercus* sp mixed broadleaf forest, N 30°09.700' E 79°51.186', alt. 1911 m a.s.l., 16 July 2016, *A. Ghosh*, AG 16-1088. (CAL1608, **holotype**!).

Basidiomata 53-63 mm in height. *Pileus* 37-60 mm in diam., hemispherical to convex when young, becoming planoconvex to plane with maturity, slightly depressed at center; margin decurved to plane, entire, slightly tuberculately striate;

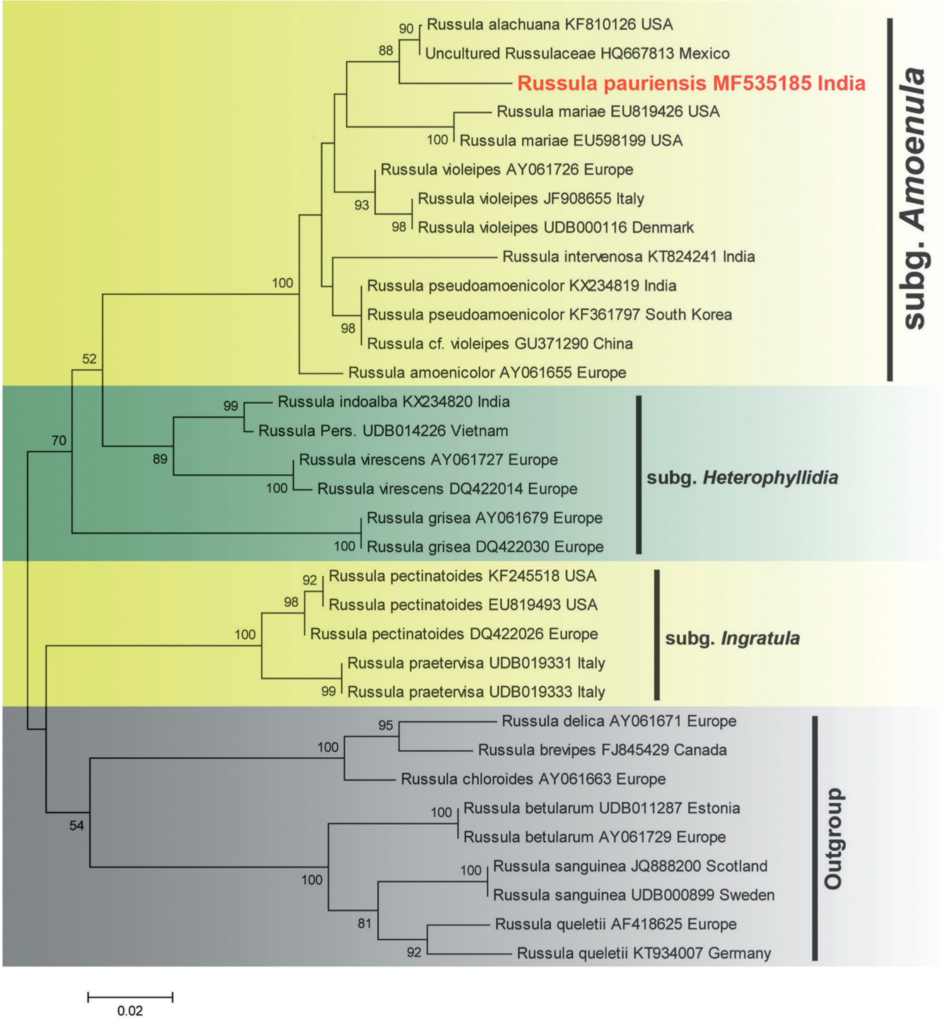


Fig. 24. Phylogram generated from Maximum Likelihood (ML) method based on ITS-rDNA sequences from MEGA6 (Tamura *et al.*, 2013) under Tamura 3-parameter model (Tamura, 1992). The tree with the highest log likelihood (-1003.5314) is shown. One thousand bootstrap replicates were analyzed to obtain the nodal support values. Bootstrap support values (> 50%) obtained from Maximum Likelihood (ML) analysis are shown above or below the branches at nodes. The novel species (*R. pauriensis*, Genbank MF535185) is shown in blue, bold font. The out-group consists of *R. delica*, *R. brevipes*, *R. chloroides*, *R. betularum*, *R. sanguinea* and *R. queletii*.

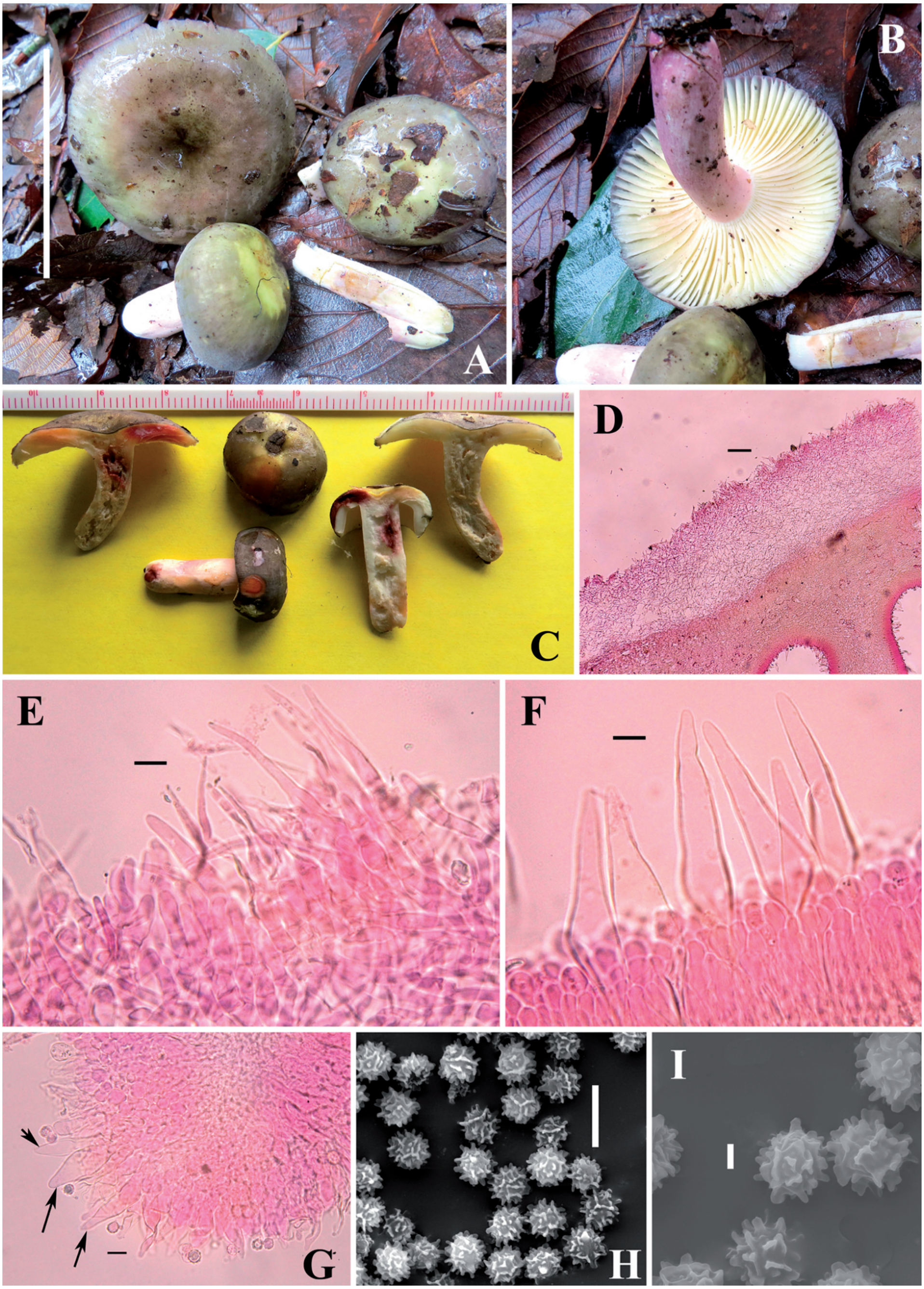


Fig. 25. *Russula pauriensis* (holotype). **A, B, C.** Fresh basidiomata in the field and basecamp. **D, E.** Radial section through pileipellis showing elements. **F.** Transverse section through lamellae showing pleurocystidia. **G.** Transverse section through lamellae edges showing cheilocystidia. **H, I.** SEM images of basidiospores. Scale bars: **A** = 60 mm, **D**, **E**, **F**, **G, H** = 10 µm, I = 2 µm.

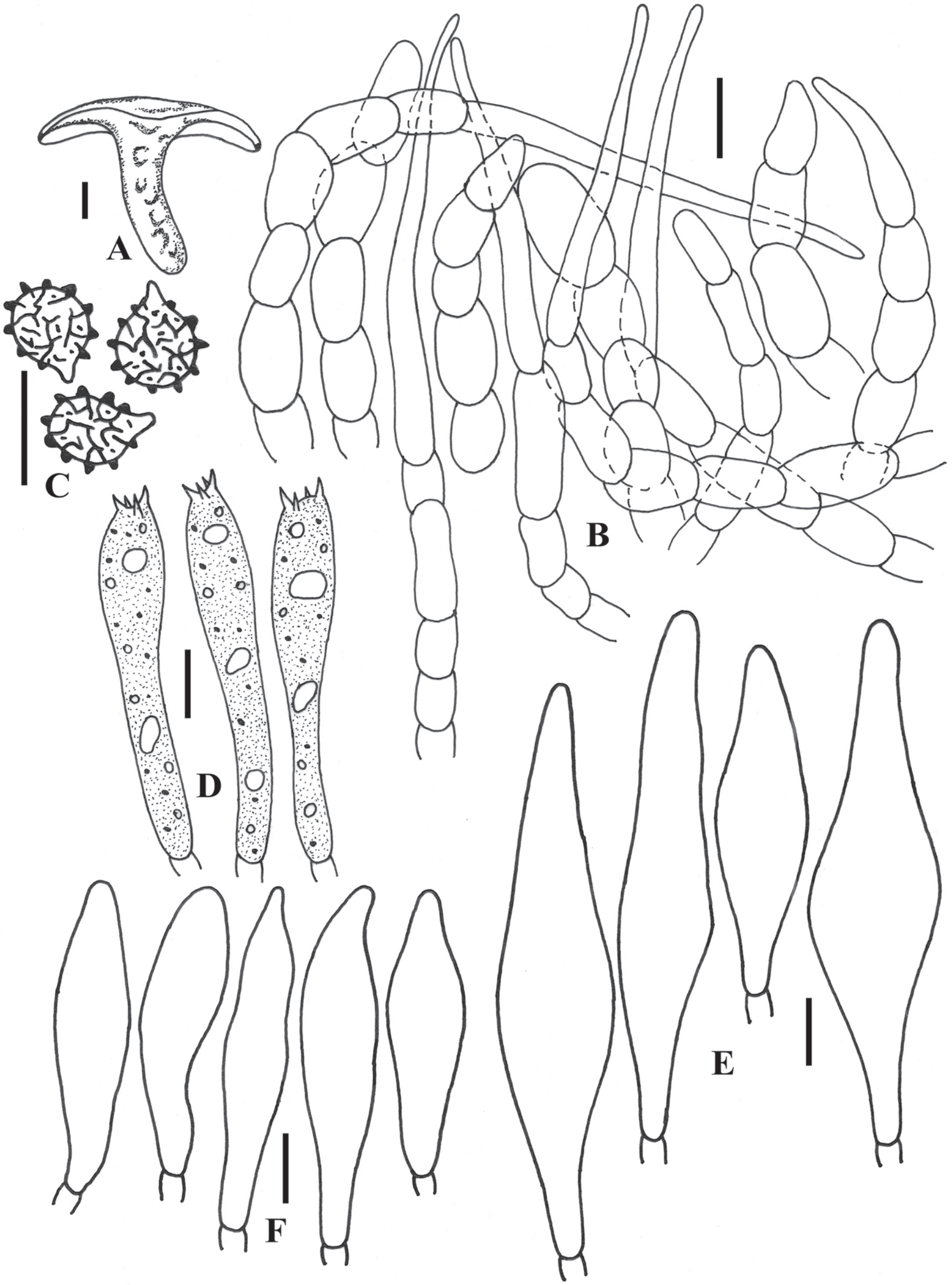


Fig. 26. *Russula pauriensis* (holotype). **A.** Dissected basidiomata. **B.** Radial section through pileipellis. **C.** Basidiospores. **D.** Basidia. **E.** Pleurocystidia. **F.** Cheilocystidia. Scale bars: **A** = 10 mm**, B**, **C**, **D**, **E, F** = 10 µm.

surface smooth, dry, viscid when moist, subvelvety, cuticle peeling 1/3th of the radius, variable in color, greyish green (1D4-1D7) to olive (2E4-2E6) cap with light yellow (1A5), greenish yellow (1A6-1A7), olive (2E8-2F6), violet white to pale violet (15A2-15A3) colored tinge found over the center and around the depression, turning orange to deep orange (6A7-6A8) with KOH; *pileus context* yellowish white (2A2), up to 5 mm thick, thining towards the margin, unchanging when bruished but turning reddish brown (8E6-8E8) with guaiacol, $FeSO_4$ (+). *Lamellae* adnexed, close to rather crowded (7-8/cm), forked near the stipe apex, moderately thick, pale yellow to pastel yellow (3A3-3A5), entire, with concolorous edges, unchanging when bruised; lamellulae absent. *Stipe* 41-47 × 12-13 mm, cylindrical to subclavate, slightly tapered at base, dry, smooth, brittle, central, purplish white (14A2), light lilac to purple (15A4-15A6); stipe context yellowish white (2A2), solid to stuffed, unchanging when bruised but turning reddish brown (8E6-8E8) with guaiacol, $FeSO_4$ (+). *Taste* mild. *Spore print* not obtained.

Basidiospores 6-6.99-8 × 5.5-6.3-7 µm (n = 30, Q 1-1.11-1.17), subglobose to broadly ellipsoid, rarely globose, ornamentation amyloid, up to 2 µm high, composed of obtuse warts & thick ridges forming incomplete cross linked, suprahilar plage inamyloid, apiculi up to 2 µm high. *Basidia* 43-66 × 8-12 µm, cylindrical to subclavate, 4-spored, sterigmata up to 4 µm high. *Subhymenium layer* up to 30 µm thick, pseudoparenchymatous. *Pleurocystidia* 55-135 × 12-22 µm, ventricose, subfusiform to fusiform with blunt apex or slightly acute apex, thick walled (1 µm thick), emergent up to 66 µm; content blank or insignificant, deeply embedded. *Gill edges* fertile, with basidia and cystidia. *Cheilocystidia* 36-68 × 8-15 µm, ventricose with blunt or appendiculate apex. *Pileipellis* up to 500 µm thick, composed of clustered erect to suberect elements composed of chains of 4-7 cells; terminal cells subulate, ellipsoid to subfusoid (9-64 × 4-10 µm wide); subterminal cells mostly cylindrical, rectangular, ellipsoid to occasionally rounded (inflated), measuring up to 12 µm wide. *Clamp connections* absent.

Notes: The combination of various microscopic characters such as absence of true macrocystidia, composition and shape of pileipellis elements and the inamyloid suprahilar spot undoubtedly place *R. pauriensis* in subsect. *Amoeninae* (= subg. *Amoenula* in Sarnari 1998).

This new species differs from *R. mukteshwarica* K. Das, S.L. Mill., J.R. Sharma & R.P. Bhatt in its smaller spores being particularly more narrow (5.5-6.3-7 µm versus 7.3-8.2 µm in the latter species) and in the considerably higher spore ornamentation (up to 2 µm versus lower than 0.75 µm in *R. mukteshwarica*). Such important microscopic differences seem to indicate clearly that both species are quite different, even if both were collected in the same state (Uttarakhand, India). Both species share with some other members in this subsection the subglobose spores, a tinted stipe surface and a near-identical pileipellis composition. Although we report here only one collection for our new species, the six known specimens for *R. mukteshwarica* seem to indicate that the constantly much darker pileus color of the latter also differentiates both species already in the field. Finally, *R. mukteshwarica* has been reported to produce a pure white spore print which is a quite unexpected feature for members of this subsection. Unfortunately we were unable to obtain a good spore print for our new species. At the time of publication of *R. mukteshwarica* the compliances for publication of new taxa were perhaps less strict and, although ITS sequence data had been produced (by S.L. Miller) and discussed in the paper (Das *et al.* 2006) on *R. mukteshwarica*, these have not been made publicly available on GenBank or similar depositories and are therefore unavailable for comparison with our new species.

Fortunately, sequence data are available for the two other, recently published members of the same subsection, both reported from the moist deciduous to mixed subtropical forests of India: *R. pseudoamoenicolor* A. Ghosh, Buyck, K. Das, A. Baghela & R.P. Bhatt (in Hyde *et al.*, 2016) and *R. intervenosa* S. Paloi, A.K. Dutta & K. Acharya (in Crous *et al.*, 2016).

The first, *Russula pseudoamoenicolor,* is yet another closely related species again described from the same area in the Indian Himalaya. Although more reddish in color it is very reminiscent in the field of *R. mukteshwarica* and the here newly described taxon but is genetically sufficiently different (Fig. 24). Recently deposited ITS sequence data on GenBank from South Korea (Park *et al.*, 2013, as *R. violeipes* – GenBank accession no. KF361797) and China (Xie *et al.*, 2010, as *R. cf violeipes* Quél. – GU371290) appear identical to the holotype of *R. pseudoamoenicolor* and therefore suggest that this species has a wide distribution in Asia where it seems at least also associated with *Pinus* (Xie *et al.*, 2010). However, LSU data obtained for these South Korean collections show that they are identical to Japanese *R. bella* Hongo (see Park *et al.*, 2013), another reddish species. Also the second Indian species, the equally more reddish colored *R. intervenosa,* might be more closely related to both *R. pseudoamoenicolor* and *R. bella* than to our new taxon as also suggested by our phylogenetic analysis (Fig. 24). The latter analysis offers only significant support for individual species within *Amoeninae*, as well as for this subsection as a whole, but does not allow to decide on affinities between the various species. Our new species is clearly suggested to be most closely related to some North American collections, but it is impossible to know to which species these correspond exactly as the taxonomic problems related to the interpretations of the ten or so different names attributed to this species complex in America are still in urgent need of attention.

40. ***Xerocomus reticulostipitatus*** Hembrom, D. Chakr., A. Parihar & K. Das, ***sp. nov.*** **Figs 27-29**

MycoBank: MB 821591

G*enBank*: MF167353 (ITS).

Systematic position: Basidiomycota, Agaricomycetes, Boletales, Boletaceae.

Etymology: Referring to the reticulation on the surface of the stipe apex.

Diagnosis: Distinct from closely allied *Xerocomus doodhcha*, another Indian temperate Himalayan species by presence of distinct brownish red to reddish brown reticulations on the surface of stipe apex and the sequence data.

Holotype: India, Uttarakhand, Bageshwar district, Dhakuri forest areas towards Khati village, 30°04’50.5”N 79°55’00.5”E, alt. 2750 m a.s.l., on the soil under *Quercus* sp., 03 Aug. 2016, *U. Rana*, *P. Uniyal* and *T. Mahmood*, *MEH* 16 B-7 (CAL 1540, **holotype**!).

Pileus 35-60 mm diam., initially convex, then planoconvex to applanate with maturity; surface moist, villose to subvelvety when fresh, punctate to glabrous towards maturity; cuticle not easily peeling off, pale orange to greyish orange (6A-B3) when young, light brown to raw Sienna (6D4-6D7) when mature, slightly deeper on bruising; margin entire, regular, concolorous with pileus. *Pore surface* lemmon yellow to greenish yellow, becoming turmeric yellow with maturity, slowly becoming greenish then brownish (after long exposure) on bruising; pores angular (mostly) to more or less round, 8-11 per 10 mm. *Tubes* 4-9 mm long, concolorous with the pore surface, becoming greenish on exposure. *Stipe* 50-70 × 5-8 mm, cylindrical, orange white to flesh or greyish orange (6A2-6B3) when young in most of the part, but covered with chalky white basal mycelium, gradually becoming camel (6D4) with age; surface with brownish red to reddish brown (9C7-9E8) reticulation on the paler background at apex, gradually disappearing towards base. *Context* 3-8 mm thick in pileus, orange white (6A2) to creamy white, unchanging on exposure; in stipe solid, cartilaginous, creamy white to pinkish white. Pileus surface turning greyish red to brownish red (8C5-8D6) with KOH; context turning light yellow with $FeSO_4$, orange with KOH and dull blue to dull violet (16C3-4) with Guiacol. *Taste* indistinct to slightly acrid. *Odor pleasant.*

Basidiospores 10.3-*12.2*-15.6 × 3.7-*4.4*-5.3 (n = 20, Q = 2.26-*2.79*-3.46), ellipsoide to elongate to fusiform, inequilateral; surface with bacillate ornamentation (almost smooth under light microscope). Basidia 36-42 × 9-11 µm, 4-spored, clavate.

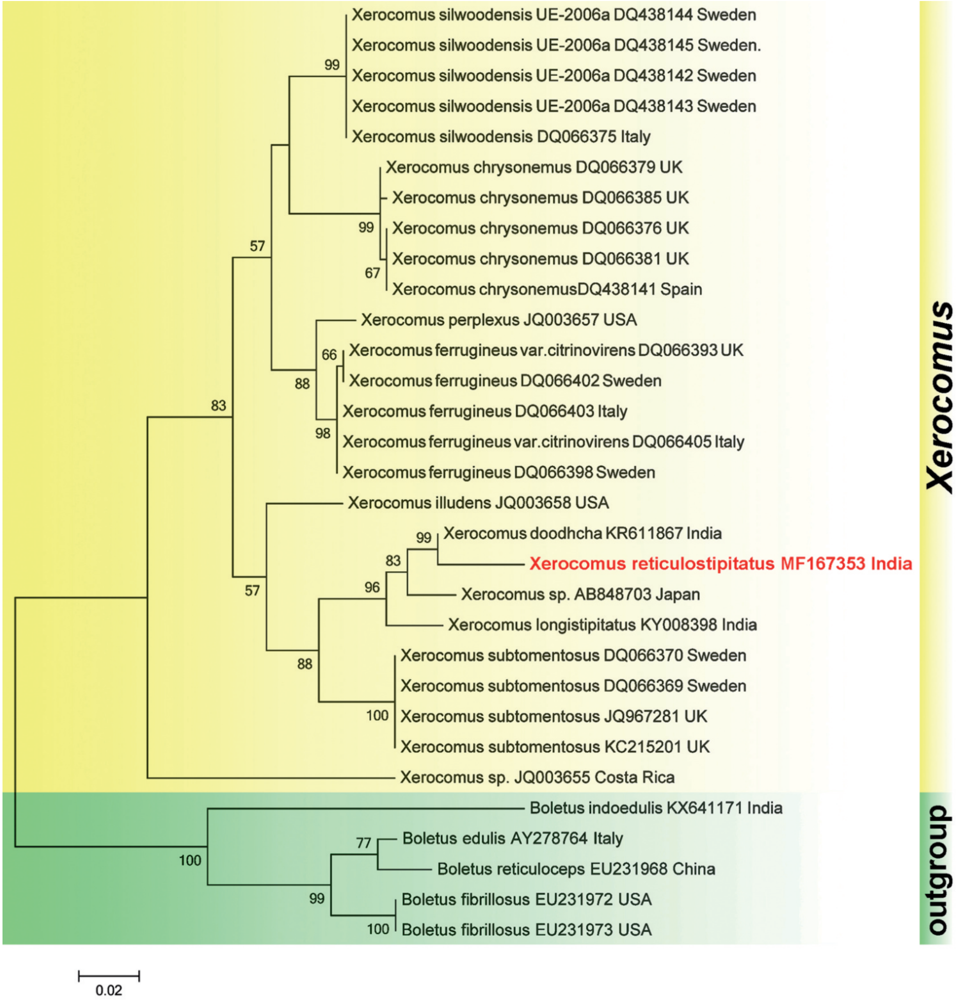


Fig. 27. Maximum Likelihood phylogenetic analysis of ITS sequence data for *Xerocomus* showing the position of *X. reticulostipitatus,* here in red and bold font. Bootstrap values (> 50) are indicated on the branches. Four species of the genus *Boletus* were used as outgroup. ITS sequences were aligned using the online version of MAFFT v. 7 (Katoh & Toh, 2008). Maximum Likelihood (ML) analyses were conducted with MEGA6 (Tamura *et al.* 2013).

Pleurocystidia 45-66 × 9.5-13 µm, emergent up to 42 µm, subfusoid to subventricose, or ventricose, thin-walled. *Subhymenial layer* up to 15 µm thick, pseudoparenchymatous. *Tube edge* fertile with basidia and cystidia; *cheilocystidia* similar to that of pleurocystidia, common, clavate. *Tube trama* phylloporoid; hyphae septate, gelatinous, up to 10 µm wide. *Pileipellis* an trichoderm, 200-350 µm thick, composed of erect hyphae of slightly inflated cells; terminal cells 18-40 × 7-15 µm, cylindrical to subcylindrical, sometimes subfusoid, with pale brown intracellular pigmentation.

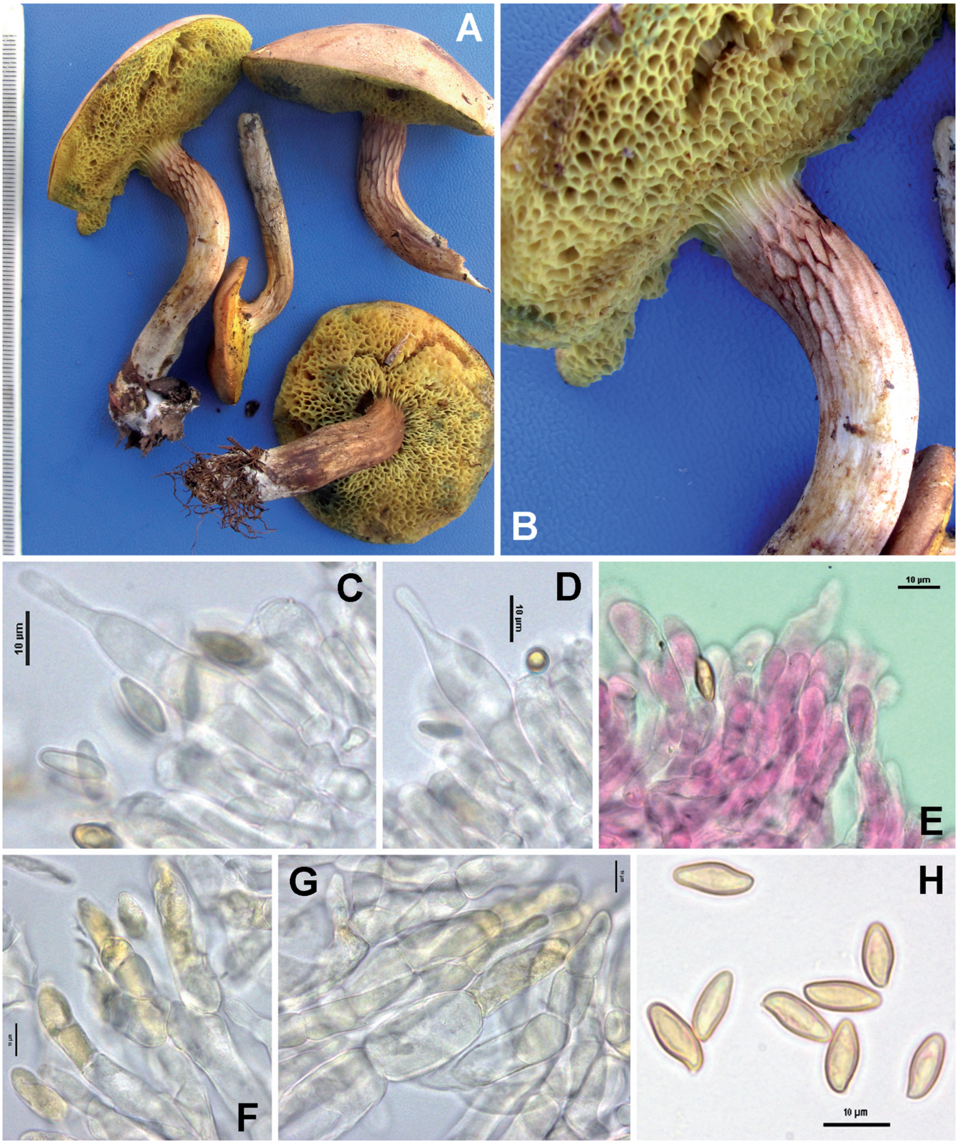


Fig. 28. *Xerocomus reticulostipitatus* (holotype). **A.** Fresh basidiomata. **B.** Stipe apex showing strong reticulation. **C & D.** Pleurocystidia. **E.** Caulocystidia. **F & G.** Transverse section through pileipellis. **F.** Basidiospores under Light microscope. Scale bars: C-H = 10 µm.

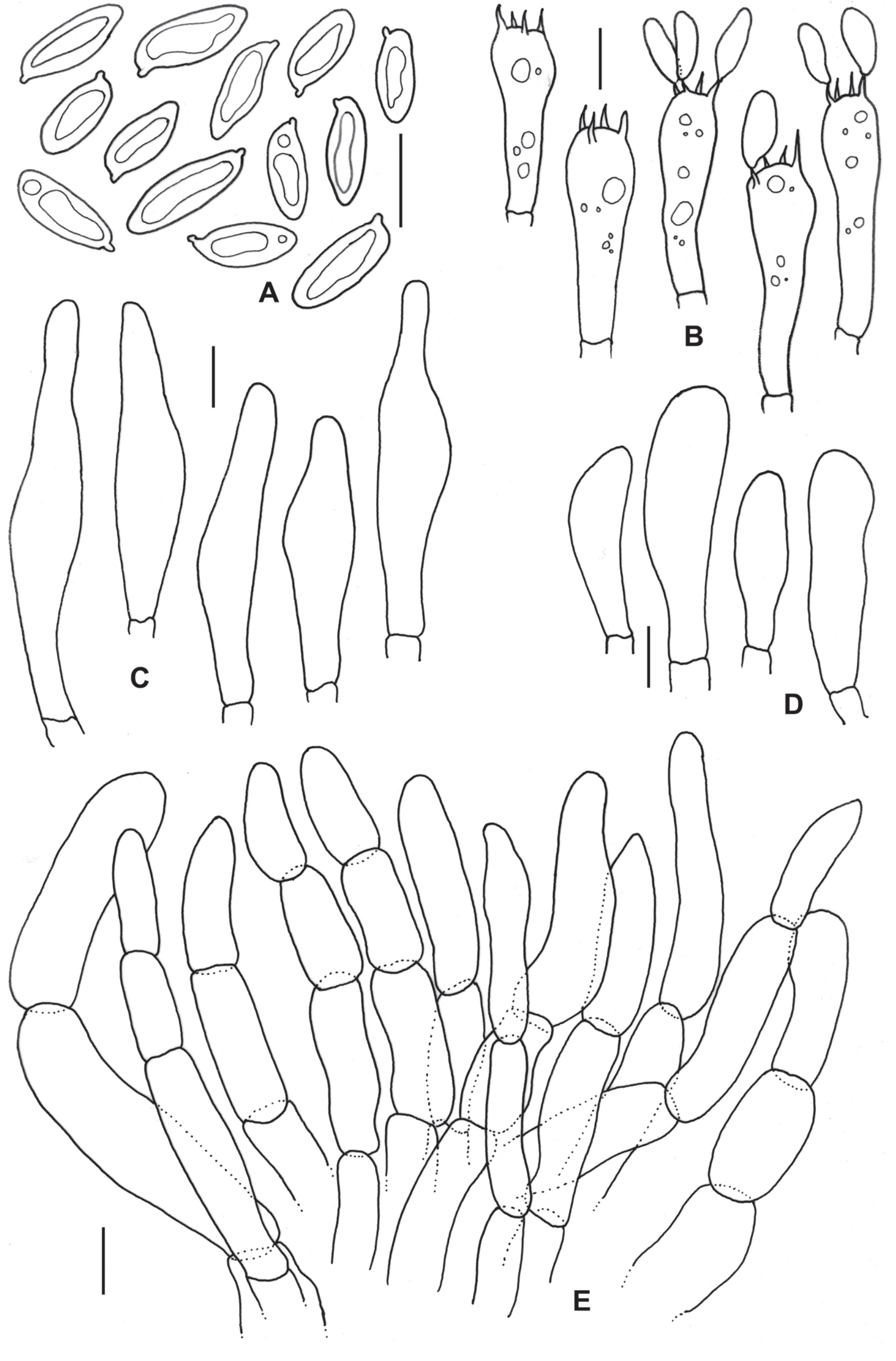


Fig. 29. *Xerocomus reticulostipitatus* (holotype). Microscopic features. **A.** Basidiospores. **B.** Basidia. **C.** Pleurocystidia. **D.** Caulocystidia. **E.** Transverse section through pileipellis. Scale bars = 10 µm.

Stipitipellis up to 120 µm thick, fertile near apex of stipe, composed of basidia and cystidia; caulobasidia 32-40 × 9-10 µm, 4-spored, clavate; *caulocystidia* 30-45 × 9-12 µm, broadly clavate to subclavate. Clamp connections absent.

Commentary: Our phylogenetic analysis resolves the genus *Xerocomus* (Boletaceae) with exception of an undetermined species from Costa Rica. *Xerocomus reticulostipitatus* is nested amongst three other Asian taxa of *Xerocomus* (*X. longistipitatus* K. Das, A. Parihar, D. Chakr. & A. Baghela, *X. doodhcha* K. Das, D. Chakr., A. Baghela, S.K. Singh & Dentinger and *Xerocomus* sp.), Although our single specimen can not receive bootstrap support it is genetically sufficiently different.

Two Indian species (see Fig. 27), *X. doodhcha* and *X. longistipitatus,* both also reported from Sikkim of Eastern Himalaya, are morphologically quite similar to *X. reticulostipitatus* but differ from our species in the field by their non-reticulate stipe apex. Moreover, *X. doodhcha* has smaller basidia (18-26 × 9-12 µm) and basidiospores [10.0-*11.03*-13.0 × 3.8-*4.4*-5.0 µm, see Das *et al.* (2016)]. *Xerocomus longistipitatus* differs from the present species in having a distinctively longer (70-185 mm), non-reticulate stipe, larger pileus (42-85 mm diam.) and ixotrichodermal pileipellis. *Xerocomus subtomentosus* (L.) Quél., reported from Europe and North America, can be confused in the field but is distinguished by its relatively robust nature of basidiomata (pileus 30-100 mm diam., stipe 40-100 × 8-25 mm), distinctly areolate pilear surface on maturity and blueing of pileus context. Furthermore, unlike *X. reticulostriatus,* the stipe apex of *X. subtomentosus* is without reddish brown reticulations (Breitenbach and Kränzlin 1991, Das *et al.* 2016). Another phylogenetically close taxon reported from Japan, *Xerocomus* sp. based on an ectomycorrhizal structure (Miyamoto *et al.* 2014, GenBank: AB848703 in Fig. 27) has yet to be described.

Xerocomus velutinus and *X. rugosellus*, both reported from China, also possess a yellow pore surface and tubes, large basidiospores (> 13 µm in length) and a bacillate surface ornamentation of basidiospores when viewed with a scanning electron microscope (Wu *et al.* 2016). However, unlike the present species, both *X. velutinus* and *X. rugosellus* lack the strong reticulation on their stipe surface. Moreover, *X. rugosellus* has more robust basidiomata (pileus 40-80 mm diam.; stipe 6-10 × 0.5-20 mm) and distinctively larger basidiospores [(12) 14-15.5 (18) × (4.5) 5-5.5 (7) µm] whereas, *X. velutinus* has smaller pileus (25-50 mm diam.) and larger hymenial cystidia (40-95 × 11-16 µm).

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REFERENCES

ALVARADO P., MORENO G., VIZZINI A., CONSIGLIO G., MANJÓN J.L. & SETTI L., 2015 — *Atractosporocybe, Leucocybe* and *Rhizocybe*: three new clitocyboid genera in the tricholomatoid clade (Agaricales) with notes on *Clitocybe* and *Lepista*. *Mycologia* 107(1): 123-136.

AMMIRATI J.F., PARKER A.D. & MATHENY P.B., 2007 — *Cleistocybe*, a new genus of Agaricales. *Mycoscience* 48(5): 282-289.

ANTONÍN V. & VÁGNER A., 1997 — New, rare and less-known macromycetes in Moravia (Czech Republic) – III. *Acta Musei Moraviae*, Sci. nat. 81: 147-156.

BENKERT D., DÖRFELT H., HARDTKE H.-J., HIRSCH G., KREISEL H., KRIEGLSTEINER G.J., LÜDERITZ M., RUNGE A., SCHMID H., SCHMITT J.A., WINTERHOFF W., WÖLDECKE K., ZEHFUß H.-D., EINHELLINGER A., GROß G., GROßE-BRAUCKMANN H., NUSS I. & WÖLFEL G., 1992 — Rote Liste der gefährdeten Großpilze in Deutschland. Eching, Deutsche Gesellschaft für Mykologie e.V. & Naturschutzbund Deutschland e.V. (NABU), IHW-Verlag, 144 p.

BERKELEY M.J. & BROOME C.E., 1876 — XVII. – Notices of British Fungi. Annals and Magazine of Natural History 17(4): 129-145.

BI Z.S. & LI T.H., 1986 — A preliminary note on *Russula* species from Guangdong, with a new species and a new variety. *Guihaia* 6(3): 193-199.

BI Z.S., ZHENG G.Y. & LI T.H., 1994 — Macrofungus flora of Guangdong Province. Guangdong Science and Technology Press, Guangzhou: 1-879.

BIGELOW H.E., 1976 — Studies on some lignicolous *Clitocybes*. *Memoirs of the New York Botanical Garden* 28(1): 9-15.

BIGELOW H.E., 1982 — North American species of *Clitocybe*. Part I. *Beihefte zur Nova Hedwigia* 72: 1-280.

BON M., 1997 — Clitocybes, Omphales et ressemblants. *Documents Mycologiques*. Mémoire hors série No 4: 1-173.

BOYD I.L., FREER-SMITH P.H., GILLIGAN C.A. & GODFRAY H.C.J., 2013 — The consequence of tree pests and diseases for ecosystem services. *Science* 342(6160): 1235773.

BREITENBACH J. & KRÄNZLIN F., 1991 — *Fungi of Switzerland*. Vol. 3: Boletes and Agarics 1. Lucerne, Switzerland. 361 p.

BUYCK B. & S. ADAMČIK S., 2011 — Type studies in *Russula* subgenus *Heterophyllidia* from the Eastern United States. *Cryptogamie, Mycologie* 32(2): 151-169.

BUYCK B., 1989 — *Révision du genre Russula Persoon en Afrique Centrale*. Doctoral Thesis, Introductory part. Rijksuniversiteit Gent, Belgium.

BUYCK B., DUHEM B., DAS K., JAYAWARDENA R.S., NIVEIRO N., PEREIRA O.L., PRASHER I.B., ADHIKARI S., ALBERTÓ E.O., BULGAKOV T.S., CASTAÑEDA-RUIZ R.F., HEMBROM M.E., HYDE K.D., LEWIS D.P., MICHLIG A., NUYTINCK J., PARIHAR A., POPOFF O.F., RAMIREZ N.A., da SILVA M., VERMA R.K. & HOFSTETTER V., 2017 — Fungal Biodiversity Profiles 21-30. *Cryptogamie, Mycologie* 38(1): 101-146.

BUYCK B., THOEN D. & WATLING R., 1996 — Ectomycorrhizal fungi of the Guinea-Congo region. *Proceedings of the Royal Society of Edinburgh*. *Section B. Biological Sciences* 104: 313-333.

CHAKRABORTY D., PARIHAR A., MEHTA N., BAGHELA A. & DAS K., 2017 — A new species of *Xerocomus* (Boletaceae) from India. *Mycosphere* 8(1): 44-50.

CLÉMENÇON H., 1984 — Kompendium der Blätterpilze: *Clitocybe*. *Beihefte zur Zeitschrift für Mykologie* 5: 1-68.

CORNER E.J.H., 1966 — A monograph of cantharelloid fungi. *Annals of Botany, Mem* No. 2. Oxford, UK: Oxford Univ. Press. 255 p.

CROUS P.W., WINGFIELD M.J., RICHARDSON D.M., LE ROUX J.J., STRASBERG D., EDWARDS J., ROETS F., HUBKA V., TAYLOR P.W.J., HEYKOOP M., MARTÍN M.P., MORENO G., SUTTON D.A., WIEDERHOLD N.P., BARNES C.W., CARLAVILLA J.R., GENÉ J., GIRALDO A., GUARNACCIA V., GUARRO J., HERNÁNDEZ-RESTREPO M., KOLAŘÍK M., MANJÓN J.L., PASCOE I.G., POPOV E.S., SANDOVAL-DENIS M., WOUDENBERG J.H.C., ACHARYA K., ALEXANDROVA A.V., ALVARADO P., BARBOSA R.N., BASEIA I.G.,BLANCHETTE R.A., BOEKHOUT T., BURGESS T.I., CANO-LIRA J.F., ČMOKOVÁ A., DIMITROV R.A., DYAKOV M.YU., DUEÑAS M., DUTTA A.K., ESTEVE RAVENTÓS F., FEDOSOVA A.G., FOURNIER J., GAMBOA P., GOULIAMOVA D.E., GREBENC T., GROENEWALD M., HANSE B., HARDY G.E.ST.J., HELD B.W., JURJEVIĆ Ž., KAEWGRAJANG T., LATHA K.P.D., LOMBARD L.,

LUANGSA-ARD J.J., LYSKOVÁ P., MALLÁTOVÁ N., MANIMOHAN P., MILLER A.N., MIRABOLFATHY M., MOROZOVA O.V., OBODAI M., OLIVEIRA N.T., ORDÓÑEZ M.E., OTTO E.C., PALOI S., PETERSON S.W., PHOSRI C., ROUX J., SALAZAR W.A., SÁNCHEZ A., SARRIA G.A., SHIN H.D., SILVA B.D.B., SILVA G.A., SMITH M.TH., SOUZA-MOTTA C.M., STCHIGEL A.M., STOILOVA DISHEVA M.M., SULZBACHER M.A., TELLERIA M.T., TOAPANTA C., TRABA J.M., VALENZUELA-LOPEZ N., WATLING R. & GROENEWALD J.Z., 2016 — Fungal Planet description sheets: 400-468. *Persoonia* 36: 316-458.

DAS K., ATRI N.S. & BUYCK B., 2013 — Three new species of *Russula* (Russulales) from India. *Mycosphere* 4(4): 707-717.

DAS K., CHAKRABORTY D., BAGHELA A., SINGH S.K. & DENTINGER B.T.M., 2016 — New species of xerocomoid boletes (Boletaceae) from Himalayan India based on morphological and molecular evidence. *Mycologia* 108:753-764. http://dx.doi:10.3852/15-206.

DAS K., MILLER S.L., SHARMA J.R., SHARMA P. & BHATT R.P., 2005 —*Russula* in Himalaya 1: A new species of subgenus *Amoenula*. *Mycotaxon* 94: 85-88.

DAS K., PUTTE V.D.P., BUYCK B., 2010 — New or interesting *Russula* from Sikkim Himalaya (India). *Cryptogamie, Mycologie* 31: 373-387.

DAS K. & SHARMA J.R., 2005 — *Russulaceae of Kumaon Himalaya*. Botanical Survey of India, Ministry of Environment and Forests, Kolkata.

DAS K., SHARMA J.R., ATRI N.S., 2006 — *Russula* in Himalaya 3: a new species of subgenus *Ingratula*. *Mycotaxon* 95: 271-275.

DENNIS R.W.G., 1954 — A forgotten British fungus. *Kew Bulletin* 9(3): 423-425.

DUTTA A.K., PALOI S., PRADHAN P. & ACHARYA K., 2015 — A new species of *Russula* (Russulaceae) from India based on morphological and molecular (ITS sequence) data. *Turkish Journal of Botany* 39: 850-856.

GARNICA S., WEISS M., WALTHER G. & OBERWINKLER F., 2007 — Reconstructing the evolution of agarics from nuclear gene sequences and basidiospore ultrastructure. *Mycological Research* 111(9): 1019-1029.

GMINDER A. & KRIEGLSTEINER G.J., 2001 — Tricholomataceae Heim ex Pouzar 1983 (nom. cons.). In: Krieglsteiner G.J. (ed.) Die Großpilze Baden-Württembergs. 3. Ständerpilze: Blätterpilze. I. Stuttgart, Verlag Eugen Ulmer GmbH & Co., pp. 117-588.

HARMAJA H., 1988 — Studies on the agaric genera *Singerocybe* n.gen. and *Squamanita*. *Karstenia* 27: 71-75.

HARMAJA H., 2003 — Notes on *Clitocybe* s. lato (Agaricales). *Annales Botanici Fennici* 40: 213-218.

HEMBROM M.E., DAS K., ADHIKARI S., PARIHAR A. & BUYCK. B., 2017 — First report of *Pterygellus* from Rajmahal hills of Jharkhand (India) and its relation to *Craterellus* (Hydnaceae, Cantharellales). *Phytotaxa* 306(3): 201-210.

HESLER L.R. & SMITH A.H., 1979 — North American species of *Lactarius*. Univ. Michigan Press, Ann Arbor.

HESLER L.R., 1960 — A study of Russula types. *Memoirs of the Torrey Botanical Club* 21(2): 1-59.

HOLEC J. & BERAN M., 2006 — Červený seznam hub (makromycetů) České republiky. *Příroda* 24: 1-282.

HONGSANAN S., HYDE K.D., BAHKALI A.H., CAMPORESI E., CHOMNUNTI P., EKANAYAKA H., GOMES A.M., HOFSTETTER V., JONES E.B.G., PINHO D.B., PEREIRA O.L., TIAN Q., WANASINGHE D.N., XU J-C. & B. BUYCK, 2015 — Fungal Biodiversity Profiles 11-20. *Cryptogamie, Mycologie* 36(3): 355-380.

HYDE K.D., HONGSANAN S., JEEWON R., BHAT D.J., MCKENZIE E.H.C., JONES E.B.G., PHOOKAMSAK R., ARIYAWANSA H.A., BOONMEE S., ZHAO Q., ABDEL-AZIZ F.A., ABDEL-WAHAB M.A., BANMAI S., CHOMNUNTI P., CUI B.K., DARANAAGAMA D.A., DAS K., DAYARATHNE M.C., DE SILVA NL., DISSANAYAKE A.J., DOILOM M., EKANAYAKA A.H., GIBERTONI T.B., GÓES-NETO A., HUANG S.K., JAYASIRI S.C., JAYAWARDENA R.S., KONTA S., LEE H.B., LI W.J., LIN C.G., LIU J.K., LU Y.Z., LUO Z.L., MANAWASINGHE I.S., MANIMOHAN P., MAPOOK A., NISKANEN T., NORPHANPHOUN C., PAPIZADEH M., PERERA R.H., PHUKHAMSAKDA C., RICHTER C., DE SANTIAGO A.L.C.M.A., DRECHSLER-SANTOS E.R., SENANAYAKE I.C., TANAKA K., TENNAKOON T.M.D.S., THAMBUGALA K.M., TIAN Q., TIBPROMMA S., THONGBAI B., VIZZINI A., WANASINGHE D.N., WIJAYAWARDENE N.N., WU H., YANG J., ZENG X.Y., ZHANG H., ZHANG J.F., BULGAKOV T.S., CAMPORESI E., BAHKALI A.H., AMOOZEGAR A.M., ARAUJO-NETA L.S., AMMIRATI J.F., BAGHELA A., BHATT R.P., BOJANTCHEV S., BUYCK B., DA SILVA G.A., DE LIMA C.L.F., DE OLIVEIRA R.J.V., DE SOUZA C.A.F., DAI Y.C.,

DIMA B., DUONG T.T., ERCOLE E., MAFALDA-FREIRE F., GHOSH A., HASHIMOTO A., KAMOLHAN S., KANG J.C., KARUNARATHNA S.C., KIRK P.M., KYTŐVUORI I., LANTIERI A., LIIMATAINEN K., LIU Z.Y., LIU X.Z., LÜCKING R., MEDARDI G., MORTIMER P.E., NGUYEN T.T.T., PROPUTTHA I., RAJ K.N.A., RECK M.A., LUMYONG S., SHAHZADEH-FAZELI S.A., STADLER M., SOUDI M.R., SU H.Y., TAKAHASHI T., TANGTHIRASUNUN N., UNIYAL P., WANG Y., WEN T.C., XU J.C., ZHANG Z.K., ZHAO Y.C., ZHOU J.Z. & ZHU L., 2016 — Fungal diversity notes 367-490: taxonomic and phylogenetic contributions to fungal taxa. *Fungal Diversity* 80: 1-270.

JANKOWSKI W. & ŚWIERKOSZ K., 1995 — Oder as an ecological corridor. State-Functioning-Threats. Warszawa, Fundacja IUCN Poland, 220 p.

KATOH K.A. & STANDLEY D.M., 2013 — MAFFT multiple sequence alignment software version7: improvements in the performance and usability. *Molecular Biology and Evolution* 30: 269-285.

KHATUA S., DUTTA A.K. & ACHARYA K., 2015 — Prospecting *Russula senecis*: a delicacy among the tribes of West Bengal. *PeerJ.* 2015 Mar 10,3: e810.doi: 10.7717/peerj.810. eCollection 2015.

KRIEGLSTEINER G.J., 1983 — Über einige neue, seltene, kritische Makromyzeten in der Bundesrepublik Deutschland. IV. *Zeitschrift für Mykologie* 49(1): 73-106.

KUMARI D., UPADHYAY R.C. & REDDY M.S., 2012 — *Craterellus indicus* sp. nov., a new species associated with Cedrus deodara from the western Himalayas, India. *Mycological Progress* 11: 769-774 DOI 10.1007/s11557011-0788-4.

KUYPER T.W., 1995 — Genus *Clitocybe*. In: Bas C., Kuyper T.W., Noordeloos M.E. & Vellinga E.C. (eds.), *Flora Agaricina Neerlandica*. Critical monographs on families of agarics and boleti occurring in the Netherlands. Rotterdam, A.A. Balkema Publishers, pp. 42-62.

LE HT., 2007 — Biodiversity of the genus *Lactarius* (Basidiomycota) in northern Thailand. PhD dissertation. Chiang Mai University.

LEGON N.W., HENRICI A., ROBERTS P., SPOONER B.M. & WATLING R., 2005 — *Checklist of the British and Irish Basidiomycota*. Kew, Royal Botanic Gardens, 536 p.

LI G.J., LI S.F. & WEN H.A., 2011 — *Russula zhejiangensis* sp. nov. from East China. *Cryptogamie, Mycologie* 32(2): 127-133.

LI G.J., LI S.F., LIU X.Z. & WEN H.A., 2012 — *Russula jilinensis* sp. nov. (Russulaceae) from northeast China. *Mycotaxon* 120(1): 49-58.

LI G.J., ZHAO D., LI S.F. & WEN H.A., 2015 — *Russula chiui* and *R. pseudopectinatoides*, two new species from southwestern China supported by morphological and molecular evidence. *Mycological Progress* 14(6): 1-14. DOI 10.1007/s11557-015-1054-y

LI G.J., ZHAO D., LI S.F., YANG H.J., WEN H.A. & LIU X.Z., 2013 — *Russula changbaiensis* sp. nov. from northeast China. *Mycotaxon* 124(1): 269-278.

LI G.J., ZHAO Q., ZHAO D., YUE S.F., LI S.F., WEN H.A. & LIU X.Z., 2013 — *Russula atroaeruginea* and *R. sichuanensis* spp. nov. from southwest China. *Mycotaxon* 124(16): 173-188.

LI Y.K., ZHANG X., YUAN Y., CAO Z. & LIANG J.F., 2015 — Morphological and molecular evidence for a new species of *Russula* (Russulaceae) from southern China. *Phytotaxa* 202(2): 94-102.

LUDWIG E., 2012 — Pilzkompendium. Band 3. Beschreibungen. Die übrigen Gattungen der Agaricales mit weißem Sporenpulver. Berlin, Fungicon Verlag, 881 p.

MATHENY P.B., CURTIS J.M., HOFSTETTER V., AIME M.C., MONCALVO J.-M., GE Z.-W., YANG Z.-L., SLOT J.C., AMMIRATI J.F., BARONI T.J., BOUGHER N.L., HUGHES K.W., LODGE D.J., KERRIGAN R.W., SEIDL M.T., AANEN D.K., DENITIS M., DANIELE G.M., DESJARDIN D.E., KROPP B.R., NORVELL L.L., PARKER A., VELLINGA E.C., VILGALYS R. & HIBBETT D.S., 2006 — Major clades of Agaricales: a multilocus phylogenetic overview. *Mycologia* 98(6): 982-995.

MILLER S.L. & BUYCK B., 2002 — Molecular phylogeny of the genus *Russula* in Europe with a comparison of modern infrageneric classifications. *Mycological Research* 106(3): 259-276.

MIYAMOTO Y., NAKANO T., HATTORI M. & NARA K., 2014 — The mid-domain effect in ectomycorrhizal fungi: range overlap along an elevation gradient on Mount Fuji, Japan. *International Society for Microbial Ecology Journal* 8: 1739-1746. http://dx.doi: 10.1038/ismej.2014.34.

MONTOYA L., BANDALA V.M. & GUZMÁN G. 1996 — New and interesting species of *Lactarius* from Mexico including scanning electron microscope observations. *Mycotaxon* 57: 411-424.

MOREAU P.-A., COURTECUISSE R. & BELLANGER J.-M., 2015 — Les noms qui changent… (2): Agaricales, Boletales et Tricholomatales. *Documents Mycologiques* 36: 85-101.

PARK M.S., FONG J.J., LEE H., OH S.Y., JUNG P.E., MIN Y.J., SEOK S.J. & LIM Y.W., 2013 — Delimitation of *Russula* Subgenus *Amoenula* in Korea using three Molecular Markers. *Mycobiology* 41(4): 191-201.

PAUTASSO M., AAS G., QUELOZ V. & HOLDENRIEDER O., 2013 — European ash (*Fraxinus excelsior*) dieback – A conservation biology challenge. *Biological Conservation* 158: 37-49.

PEARSON A.A., 1952 — New records and observations. V. *Transactions of the British Mycological Society* 35(2): 97-122.

QIN J., FENG B., YANG Z.L., LI Y.-C., RATKOWSKY D., GATES G., TAKAHASHI H., REXER K.-H., KOST G.W. & KARUNARATHNA S.C., 2014 — The taxonomic foundation, species circumscription and continental endemisms of *Singerocybe*: evidence from morphological and molecular data. *Mycologia* 106(5): 1015-1026.

REDHEAD S.A., LUTZONI F., MONCALVO J.-M. & VILGALYS R., 2002 — Phylogeny of agarics: partial systematics solutions for core omphalinoid genera in the Agaricales (Euagarics). *Mycotaxon* 83: 19-57.

REID D.A., THIND K.S. & ADLAKHA K.L., 1958 — The Thelephoraceae of the Mussoorie Hills (India). *Transactions of the British Mycological Society* 41: 129-134, plate 6.

ROMAGNESI H., 1967 — *Les Russules d'Europe et d'Afrique du Nord*. Paris, Bordas, 998 p.

SAINI S.S. & ATRI N.S., 1984 — Studies on the North-West Himalayan Russulaceae. *Geobios New Reports* 3: 4-6.

SARNARI M., 1998 — Monografia Illustrata Del Genere *Russula* in Europa. Tomo Primo, Associazione Micologica Bresadola, Trento. Italy, 799 p.

SCHRÖTER J., 1885-1889 — *Die Pilze Schlesiens*. 3(1). Breslau, J.U. Kern's Verlag, 814 p.

SESLI E. & DENCHEV C.M., 2008 — Checklists of the myxomycetes, larger ascomycetes, and larger basidiomycetes in Turkey. *Mycotaxon* 106: 65-67 + online version (61-136, uploaded in February 2014).

SESLI E., VIZZINI A., ERCOLE E. & CONTU M., 2016 — *Clitolyophyllum akcaabatense* gen. nov., sp. nov. (Agaricales, Tricholomatineae); a new fan-shaped clitocyboid agaric from Turkey. *Botany* 94(2): 73-80.

SHIMONO Y., HIROI M., IWASE K. & TAKAMATSU S., 2007 — Molecular phylogeny of *Lactarius volemus* and its allies inferred from the nucleotide sequences of nuclear large subunit rDNA. *Mycoscience* 48: 152-159.

SINGER R., 1935 — Supplemente zu meiner monographie der guttung Russula. *Annales Mycologici* 33: 297-352.

SINGER R., 1957 — New and interesting species of Basidiomycetes. V. *Sydowia* 11: 141-272.

SINGER R., 1986 — *The Agaricales in modern taxonmy*. 4th ed. Koeltz Scientific Books, Koenigstein.

SONG B., LI T.H., WU X.L., LI J.J., SHEN Y.H. & LIN Q.Y., 2007 — Known species of *Russula* from China and their distribution. *Journal of Fungal Research* 5(1): 20-42.

STEFAŃSKA-KRZACZEK E., 2013 — Species richness of drained riparian forests in the urban area of Wrocław. Sylwan 157(5): 366-375.

TAMURA K., 1992 — Estimation of the number of nucleotide substitutions when there are strong transition-transversion and G + C-content biases. *Molecular Biology and Evolution* 9: 678-687.

TAMURA K., STECHER G., PETERSON D., FILIPSKI A & KUMAR S., 2013 — MEGA6: Molecular Evolutionary Genetics Analysis version 6.0. *Molecular Biology and Evolution* 30: 2725-2729.

TIBPROMMA S., HYDE K.D., JEEWON R., MAHARACHCHIKUMBURA, S.S.N. LIU, J.-K., BHAT D.J., JONES E.B.G., MCKENZIE E.H.C., CAMPORESI E., BULGAKOV T.S., DOILOM M., MONTEIRO DE AZEVEDO SANTIAGO A.L.C., DAS K., MANIMOHAN P., GIBERTONI T.B., LIM Y.W., EKANAYAKA A.H., THONGBAI B., LEE H.B., YANG J.-B., KIRK P.M., SYSOUPHANTHONG P., SINGH S.K., BOONMEE S., DONG W., RAJ K.N.A., LATHA K. P. D., PHOOKAMSAK R., PHUKHAMSAKDA S., KONTA S.C. JAYASIRI C. NORPHANPHOUN, TENNAKOON D.S., LI J., DAYARATHNE M.C., PERERA R.H., XIAO Y., WANASINGHE D.N., SENANAYAKE I.C., GOONASEKARA I.D., DE SILVA N. I., MAPOOK A., JAYAWARDENA R.S., DISSANAYAKE A.J., MANAWASINGHE I.S., CHETHANA K.W.T., LUO Z.-L., HAPUARACHCHI K.K., BAGHELA A., SOARES A.M., VIZZINI A., MEIRAS-OTTONI A. MEŠIĆ A., DUTTA A.K., FRAGOSO DE SOUZA C.A., RICHTER C., LIN C.-G., CHAKRABARTY D., DARANAGAMA D.A., LIMA D.X., CHAKRABORTY D., ERCOLE E., WU F., SIMONINI G., VASQUEZ G., DA SILVA G.A., PLAUTZ JR H.L., ARIYAWANSA H.A., LEE H., KUŠAN I., SONG J., SUN J., KARMAKAR J., HU K., SEMWAL K.C., THAMBUGALA K.M., VOIGT K., ACHARYA K., RAJESHKUMAR K.C., RYVARDEN L., JADAN M., HOSEN M.I., MIKŠIK M., SAMARAKOON M.C., WIJAYAWARDENE N.N., KIM N. K., MATOĆEC N., SINGH P. N., TIAN Q., BHATT R.P., VILELA DE OLIVEIRA R. J., TULLOSS R.E., AAMIR S., KAEWCHAI S., MARATHE S.D., KHAN S., HONGSANAN S., ADHIKARI S., MEHMOOD T., BANDYOPADHYAY T.K., SVETASHEVA T.Y., NGUYEN T.T.T., ANTOŃIN V., LI W.-J., WANG Y., INDOLIYA Y.,

TKALČEC Z., ELGORBAN A.M., BAHKALI A.H., TANG A. M. C., SU H.-Y., ZHANG H., PROMPUTTHA I., LUANGSA-ARD J., XU J., YAN J., JI-CHUAN K., STADLER M., MORTIMER P.E., CHOMNUNTI P., ZHAO Q., PHILLIPS A.J.L., NONTACHAIYAPOOM S., WEN T.-C. & KARUNARATHNA S.C., 2017 — Fungal diversity notes 491-602: taxonomic and phylogenetic contributions to fungal taxa. *Fungal Diversity* 83: 1-261.

VAN DE PUTTE K., NUYTINCK J., DAS K. & VERBEKEN A., 2012 — Exposing hidden diversity by concordant genealogies and morphology — a study of the *Lactifluus volemus* (Russulales) species complex in Sikkim Himalaya (India). *Fungal Diversity* 55: 171-194.

VAN DE PUTTE K., NUYTINCK J., DE CROP E., HUGHES K. & VERBEKEN A., 2015 — *Lactifluus volemus* in Europe: Three species in one – Revealed by a multilocus genealogical approach, Bayesian species delimitation and morphology. *Fungal Biology*. DOI: 10.1016/j.funbio.2015.08.015

VAN DE PUTTE K., NUYTINCK J., STUBBE D., LE H.T. & VERBEKEN A., 2010 — *Lactarius volemus* sensu lato (Russulales) from Northern Thailand: morphological and phylogenetic species concepts explored. *Fungal Diversity* 45: 99-130.

VESTERHOLT J., 2012a — *Clitocybe* (Fr.) Staude. In: Knudsen H. & Vesterholt J. (eds.), *Funga Nordica*. Agaricoid, boletoid, clavarioid, cyphelloid and gastroid genera. Copenhagen, Nordsvamp, pp. 451-462.

VESTERHOLT J., 2012b — The Danish Red Data Book. National Environmental Research Institute, Denmark: http://www2.dmu.dk/1_Om_DMU/2_Tvaer-funk/3_fdc_bio/projekter/redlist/artsgrupper_en.asp [Accessed: 10-2015].

VIZZINI A. & ERCOLE E., 2012 — *Paralepistopsis* gen. nov. and *Paralepista* (Basidiomycota, Agaricales). *Mycotaxon* 120(1): 253-267.

VIZZINI A., CONTU M. & ERCOLE E., 2011a — *Musumecia* gen. nov. in the Tricholomatoid clade (Basidiomycota, Agaricales) related to *Pseudoclitocybe*. *Nordic Journal of Botany* 29: 734-740.

VIZZINI A., CONTU M., MUSUMECI E. & ERCOLE E., 2011b — A new taxon in the *Infundibulicybe gibba* complex (Basidiomycota, Agaricales, Tricholomataceae) from Sardinia (Italy). *Mycologia* 103(1): 203-208.

VIZZINI A., MUSUMECI E. & MURAT C., 2010 — Trichocybe, a new genus for *Clitocybe puberula* (Agaricomycetes, Agaricales). *Fungal Diversity* 42(1): 97-105.

WALTHER G., GARNICA S. & WEIß M., 2005 — The systematic relevance of conidiogenesis modes in the gilled Agaricales. *Mycological Research* 109(5): 525-544.

WANG X.-H., 2007 — Type studies of *Lactarius* species published from China. *Mycologia* 99(2): 253-268.

WANG X.H., YANG Z.L., LI Y.C., KNUDSEN H. & LIU P.G., 2009 — *Russula griseocarnosa* sp. nov. (Russulaceae, Russulales), a commercially important edible mushroom in tropical China: mycorrhiza, phylogenetic position, and taxonomy. *Nova Hedwigia* 88(1-2): 269-282.

WEN H.A. & YING J.Z., 2000 — Studies on the genus *Russula* from China. II. Two new taxa from Yunnan and Guizhou. *Mycosystema* 20(2): 153-155.

WU G., LI Y-C., XHU X-T., XHAO, K., HAN, L-H., CUI, Y-Y., LI, F., XU, J-P. & YANG, Z.L., 2016 — One hundred noteworthy boletes from China. *Fungal Diversity*. DOI 10.1007/s13225-016-0375-8

XIE X.D., LIU P.G. & YU F.Q., 2010 — Species Diversity of Russuloid Mycorrhizae-forming Fungi *on Pinus yunnanensis* Seedlings and the Mycorrhizal Morphology. *Acta Botanica Yunnanica* 32(3): 211-220.

YANG Z.L., 1997 — Die *Amanita*-Arten von Südwestchina. *Bibliotheca Mycologica* 170: 1-240.

YANG Z.L., LI T.H. & WU X.L., 2001 — Revision of *Amanita* collections made from Hainan, southern China. *Fungal Diversity* 6: 146-165.

YING J., MAO X., MA Q. & WEN H. (1987). Icons of medicinal mushroom from China. Science, Beijing 151-155.

YING J.Z., 1983 — A study on *Russula viridi-rubrolimbata* sp. nov. and its related species of Subsection *Virescentinae*. *Mycosystema* 2(1): 34-37.

ZANG M. & YUAN M.S., 1999 — Contribution to the knowledge of new basidiomycetous taxa from China. *Acta Botanica Yunnanica* 21(1): 37-42.

ZHANG J.B., LI J.W., LI F. & QIU L.H., 2017 — *Russula dinghuensis* sp. nov. and *R. subpallidirosea* sp. nov., two new species from southern China supported by morphological and molecular evidence. *Cryptogamie, Mycologie* 38 (2): 1-13.

ZHAO Q., LI Y.K., ZHU X.T., ZHAO Y.C. & LIANG J.F., 2015 — *Russula nigrovirens* sp. nov. (Russulaceae) from southwestern China. *Phytotaxa* 236(3): 249-256.

ZHENG G.Y., LOH T.C., LI C. & LI T.H., 1985 — Some new species and varieties of Agaricales from Dinghu Mountain. *Microbiological Journal* (1): 24-30.