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Fungal Biodiversity Profiles 1-10

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Abstract – The authors describe ten new taxa for science using mostly both morphological and molecular data. In Ascomycota, descriptions are provided for *Bambusistroma didymosporum gen. et spec. nov.* (Pleosporales), *Neodeightonia licuriensis* sp. nov. (Botryosphaeriales) and *Camposporium himalayanum* sp. nov. (Fungi imperfecti). In Zygomycota, *Gongronella guangdongensis* sp. nov. (Mucorales) is described. Finally, in Basidiomycota descriptions are provided for *Boidinia parva* sp. nov. and *Russula katarinae* sp. nov. (Russsulales), *Gloiocephala parvinelumbonifolia* sp. nov. (Agaricales), *Hypochnicium austrosinensis* sp. nov. (Polyporales), *Phallus ultraduplicatus* sp. nov. (Phallales) and *Suillus lariciphilus* sp. nov. (Boletales).

Agaricales / Boletales / Botryosphaeriales / Fungi imperfecti / Mucorales / Phallales / phylogeny / Pleosporales / Polyporales / Russulales / systematics

1a. *Bambusistroma* D.Q. Dai & K.D. Hyde, ***gen. nov.***

Index Fungorum number: IF***, *Facesoffungi number*: FoF: 00582.
Systematic placement: Ascomycota, Pezizomycotina, Dothideomycetes, Pleosporomycetidae, Pleosporales, Massarinaceae.
Etymology: In reference to the species forming stroma on bamboo.
Type species: *Bambusistroma didymosporum* D.Q. Dai & K.D. Hyde.

Saprobic on decaying bamboo culms. **Sexual morph:** *Ascomata* stromatic, uniloculate, solitary to clustered, immersed under host issue, becoming erumpent when mature, subglobose to slightly conical, with centrally located ostiole lined with periphyses. *Peridium* comprising host and fungal tissues, composed of brown and thick-walled cells of *textura angularis*, with the basal part composed of thinner, hyaline, smaller cells. *Hamathecium* of dense, long, anastomosing and branching pseudoparaphyses above the asci. *Asci* 8-spored, bitunicate, cylindrical, with a short furcate pedicel, with a shallow apical chamber. *Ascospores* 2-3-seriate, slightly broad fusiform, 1-septate, hyaline, guttulate, straight to curved, smooth-walled, constricted at septum, surrounded by a mucilaginous sheath. **Asexual morph:** undetermined.

Note: *Bambusistroma* is characterized by solitary to clustered, immersed to erumpent, subglobose to slightly conical and uniloculate ascomata, cylindrical, and bitunicate asci which produce hyaline, broad fusiform ascospores surrounding by mucilaginous sheath.

1b. *Bambusistroma didymosporum* D.Q. Dai & K.D. Hyde, ***sp. nov.*** **Figs 1-2**

Index Fungorum number: IF***, *Facesoffungi number*: FoF: 00583.
Etymology: In reference to two celled ascospores.
Systematic placement: Ascomycota, Pezizomycotina, Dothideomycetes, Pleosporomycetidae, Pleosporales, Massarinaceae.
Holotype: MFLU 15-**.

Saprobic on decaying bamboo culms. **Sexual morph:** *Ascomata* stromatic, uniloculate, 180-350 µm high, 300-450 µm diam., solitary to clustered, immersed under host tissue, becoming erumpent, still covered by dark mycelium mixed with host tissue, subglobose to slightly conical, with centrally located ostiole lined with periphyses. *Peridium* comprising host and fungal tissues, laterally 25-40 µm thick in the upper side, composed of brown and thick-walled cells of *textura angularis*, with the basal part composed of thinner, hyaline, smaller cells, with side wall composed of 5-8 µm large cells of *textura prismatica*. *Hamathecium* of dense, long and 1.5-3 µm wide, anastomosing pseudoparaphyses branching above the asci. *Asci* 110-160 × 8-13 µm ($\bar{x}$ = 130.1 × 12.8 µm, n = 20), 8-spored, bitunicate, cylindrical, with a short furcate pedicel, with a shallow apical chamber. *Ascospores* 20-22.5 × 6.5-7.5 µm ($\bar{x}$ = 21.5 × 7.2 µm, n = 20), 2-3-seriate, slightly broad fusiform, 1-septate, constricted at the septum, narrowly rounded at both ends, hyaline, guttulate, straight to curved, smooth-walled, constricted at septum, surrounded by a mucilaginous sheath. **Asexual morph:** undetermined.

Culture on PDA: *Germination* of ascospores on PDA within 24 h and germ tubes produced from both ends. *Colonies* circular, with even margin, dark brown at the centre, light-colored at the periphery, floccose, slow growing, 20 mm diam. in 45 days at 25-32°C.

Material examined: THAILAND, Chiang Rai Province, Doi Mae Salong, temple side, on decaying culm of bamboo, 15 August 2013, Dong-Qin Dai DDQ00276 (MFLU XX, holotype), (isotype in KUN, under the code of HKAS), ex-type living culture, MFLUCC 13-0862, CBS; *ibid.,* DDQ00276-2, MFLU 15-XX, living culture, MFLUCC 15-XX.

Note: *Bambusistroma didymosporum* is morphologically similar to *Didymella aptrootii* K.D. Hyde & S.W. Wong in having fusiform spores with each

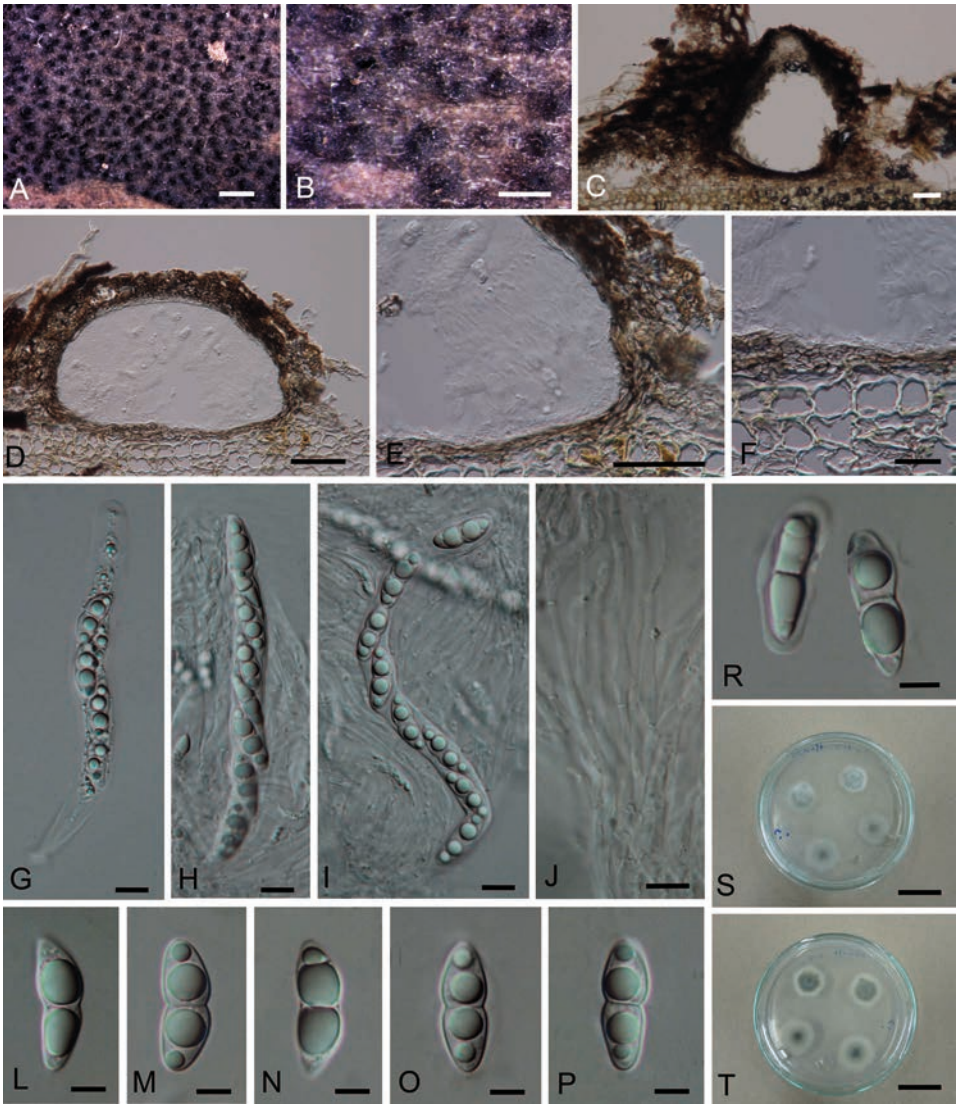


Fig. 1 *Bambusistroma didymosporum* (holotype). **A, B.** Ascomata developing on bamboo culm. **C, D.** Section of ascoma. **E, F.** Peridium of ascoma. **G-I.** Asci. **J.** Pseudoparaphyses. **L-P.** Ascospores. **R.** Ascospores with gelatinous sheath. **S, T.** Culture on PDA. Scale bars: A, B = 500 μm, C-E = 50 μm, F-R = 5 μm, S, T = 25 mm.

cell having one larger and many smaller guttules. However, our species has narrower (cylindrical and 8-13 µm wide versus clavate to subglobose and 18-25 µm wide) asci (Hyde & Wong 1999). *Bambusistroma didymosporum* can also be compared with *Massarina igniaria* (C. Booth) Aptroot (Basionym: *Didymosphaeria igniaria* C. Booth) as both species have cylindrical asci and broad fusiform, ascospores. However, *B. didymosporum* differs in having ascomata covered by host tissue mixed with black mycelium. In addition, *B. didymosporum* has hyaline and smooth-walled ascospores versus *M. igniaria* which has brown, verruculose ascospores (Booth 1968).

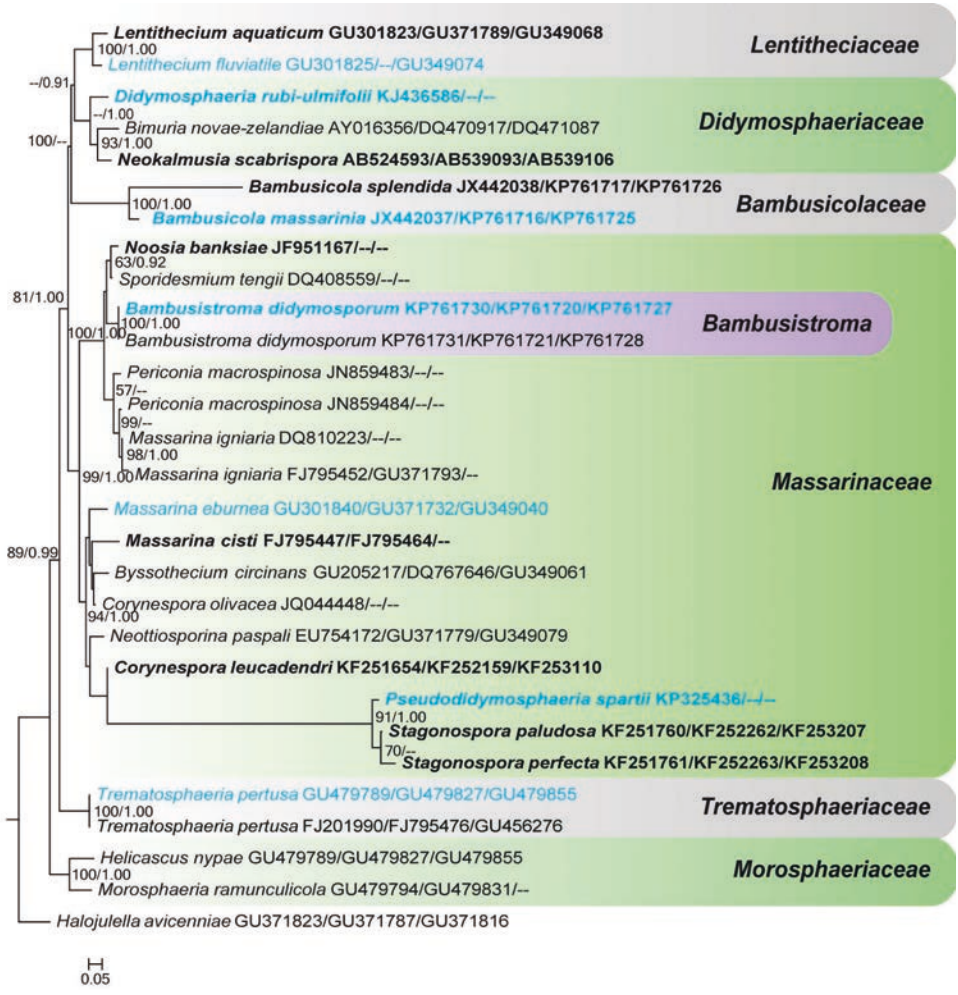


Fig. 2. Phylogenetic tree generated from RAxML and Bayesian analysis of combined LSU, RPB2 and TEF sequence data. Bootstrap support (BS) values above 50% are shown at nodes. Hyphen ("--") indicates a value lower than 70% (BS) or 0.95 (BPP). The original isolate numbers or GenBank codes are noted after the species names. Ex-type strains are in bold and the type species are indicated in blue. The tree is rooted with *Halojulella avicenniae* (BCC 18422).

Bambusistroma is phylogenetically placed in family *Massarinaceae* based on combined data set of LSU, RPB2 and TEF sequence, with high bootstrap support (99%/1.00 MLBS/BPP, see Fig. 2), but in a strongly supported clade (100%/1.00 MLBS/BPP), which is both morphologically and phylogenetically distinct from other genera of *Massarinaceae*.

2. *Boidinia parva* Ghobad-Nejhad, S.L. Liu, Y.C. Dai & E. Langer, **sp. nov.**
Figs 3-4

MycoBank: MB 810635.
GenBank: KP017261 (ITS).
Systematic position: Basidiomycota, Agaricomycotina, Russulales.
Etymology: parva (Lat.), referring to the short basidiospores.
Diagnosis: *Boidinia parva* sp. nov. is characterized by its closely adnate, cream-colored, smooth hymenophore, urniform basidia, obclavate gloeocystidia, and strongly amyloid, verrucose basidiospores.

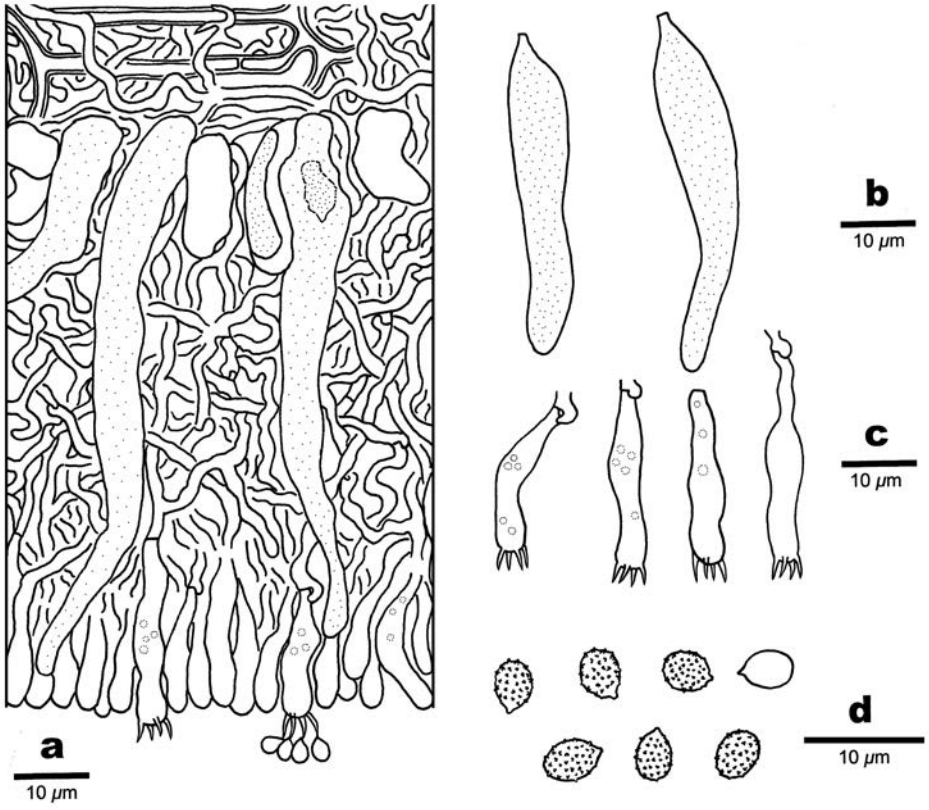


Fig. 3. Line drawings from a cross section of the basidiocarp of *Boidinia parva* sp. nov. (holotype). **a.** Basidiocarp section, **b.** Gloeocystidia, **c.** Basidia, **d.** Basidiospores.

Holotype: **China**, Jilin Province, Antu County, Erdaobaihe, Changbaishan Nature Reserve, Huangsongpu, mixed secondary forest with *Populus davidiana, Acer, Abies, Larix, Picea, Sorbus,* also some very old stands of natural *Populus ussuriensis*, and *Pinus koraiensis*; 42.248 Lat., 128.150 Long., elev. ca. 1010-1020 m; on fallen decorticated indet. log, 6 Sept. 2011, leg. Ghobad-Nejhad, Dai, Wu & Sohrabi (holotype Ghobad-Nejhad 2236, in hBJFC, no. BJFC012115; isotype in Ghobad-Nejhad ref. coll.).

Basidiocarp annual, resupinate, effused, closely adnate, ca. 200 µm thick, patches about 10 cm long and 6 cm wide, ceraceous when wet, crustaceous in dry state. **Hymenial surface** cream to creamish buff, smooth, with cracks in dry material,

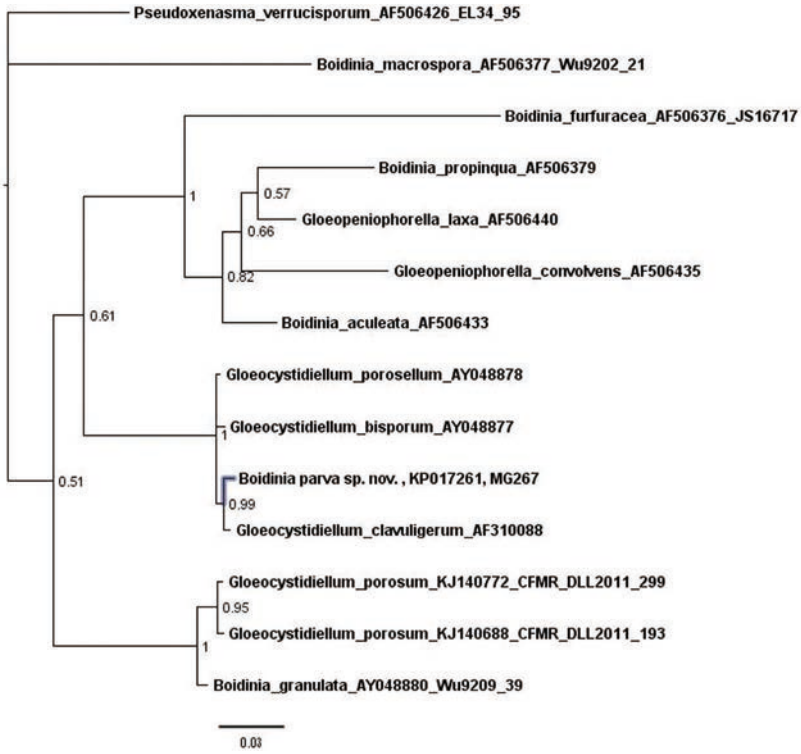


Fig. 4. Bayesian phylogram showing the position of *Boidinia parva* sp. nov. Posterior probabilities are shown inside nodes. Species names are followed by GenBank accession numbers and isolate numbers, respectively. *Pseudoxenasma verrucisporum* K.H. Larss. & Hjortstam was used as an outgroup after Smith *et al.* (2013). The alignment was obtained in MUSCLE (Edgar, 2004), adjusted in PhyDE v. 0.995 (Müller *et al.*, 2005), and optimized using Gblocks v. 0.91b (Castresana, 2000) which saved 67% of the original 2143 positions. The best-fit model for nucleotide evolution was determined using MrModeltest 2.3 (Nylander, 2004). Bayesian analysis was conducted with MrBayes v. 3.2.2 (Ronquist & Huelsenbeck 2003). The ITS dataset was analyzed using two independent runs, each with four MC^3 chains running for two million generations with tree and parameter sampling every 1000 generations. Burn-in was set to discard 50% of samples and majority-rule consensus tree was assembled from post burn-in tree samples. The final ITS dataset covered 14 taxa and 1438 nucleotides, including 1156 constant and 184 informative characters. The best fit model selected by MrModeltest was GTR + I + G. Average standard deviation of split frequencies reached 0.008032, with average PSRF equal to 1.000. The overlay plot for both runs was homogenous. The estimated marginal likelihood (Arithmetic mean) was -4608.10.

darkening in bruised parts; **margin** more or less distinct to finely thinning out, concolorous, without rhizomorphs. **Hyphal system** monomitic, hyphae hyaline, with clamps at all septa, frequently branched and strongly interwoven; hyphae in subhymenium very thin-walled, 1.5-3.0 µm wide. **Subiculum** very thin, with some crystals on hyphae, hyphae thin- to slightly thick-walled, 1.5-3.0 µm wide. **Gloeocystidia** numerous, enclosed or slightly emergent from hymenial surface, subcylindrical to obclavate, widened at base, narrowing towards apex, obtuse, thin-walled, 20-80 × 5-10 µm, contents granular, light refracting in 5% potassium hydroxide (KOH). **Basidia** subclavate to urniform, 19-30 × 4-5 µm, with 4 sterigmata. **Basidiospores** subglobose to broadly ellipsoid, verrucose-aculeate, ornamentations disappearing in KOH, thin-walled, strongly amyloid, cyanophilous, (3.2-)3.8-4.8(-5.0) × (2.8-)3.0-3.4(-3.6) µm, mean length = 4.19 µm, mean width = 3.10 µm, mean variation in length/width ratios = 1.35.

Commentary: The genus *Boidinia* Stalpers & Hjortstam (Russulales) is one of the segregates of *Gloeocystidiellum* Donk and was established for corticioid species with urniform basidia, gloeocystidia and ornamented amyloid spores (Hjortstam & Stalpers, 1982). According to MycoBank (www.mycobank.org) the genus currently comprises 16 described species. The generic type, *B. furfuracea* (Bres.) Stalpers & Hjortstam is placed within Russulaceae (Larsson, 2007).

In the present study, *Boidinia* appeared as highly polyphyletic (Fig. 4), as shown by previous studies (Miller *et al.*, 2006, Larsson, 2007), and its species were intermixed with *Gloeocystidiellum* spp. [type: *G. porosum* (Berk. & M.A. Curtis) Donk] and *Gloeopeniophorella* Rick spp. [type: *G. rubroflava* Rick, not sequenced yet]. *Gloeopeniophorella* is closely related to *Boidinia* (Larsson, 2007), sharing gloeocystidia and ornamented amyloid basidiospores, but has metuloid cystidia and lacks urniform basidia.

The sample belonging to the new species reported here was nested in a clade with three *Gloeocystidiellum* species (Fig. 4). Obviously, a rich taxon and gene sampling is needed to delimit the boundaries of *Gloeocystidiellum* s.s. and its segregates. For now, we believe that our new species best fits *Boidinia*, as its morphological characters matches well the concept of the genus, especially with regard to the generic type, *B. furfuracea*.

Morphologically, *Boidinia parva* most resembles *B. permixta* Boidin, Lanq. & Gilles which is, however, thin membranaceous with greyish-cream hymenophore turning whither towards margin, has some gloeocystidia with moniliform apex and larger spores. *Boidinia luteola* Sheng H. Wu is also similar, but it has a loose subiculum and its spores are more than 3.5 µm wide.

According to the megablast search of sequences of NCBIs GenBank nucleotide database, the closest hit (98% identity) to *B. parva* was *Gloeocystidiellum* sp. DLL2011-2 (GenBank KJ140720.1). This sample might be congeneric with our new species, but we were unable to access the voucher of this insufficiently identified material. It must also be noted that currently, the available sequences of *Boidinia* in GenBank are from 5.8S-ITS2-LSU region, and therefore our alignment was much cut, covering basically 5.8S-ITS2 region. It can be the reason why there are only few informative characters in our alignment. Attempts to get LSU from our sample failed, unfortunately. Both *Gloeocystidiellum* and *Boidinia* are polyphyletic genera (Larsson 2007), which is also confirmed here (Fig. 4). The next five best GenBank hits were *Gloeocystidiellum* spp. with only 53% query coverage: *G. clavuligerum* (Hoehn. et Litsch.) Nakas. superficially resembles *B. parva*, but the former has a warty hymenium, gloeocystidia with moniliform apex, clavate basidia and larger spores measuring 4.5-5.5(-6) × 3.5-4(-4.5) µm; *G. porosellum* Hjortstam lacks clamp, has gloeocystidia with schizopapilla and longer

spores measuring 5-5.5(-6) × 3-3.5 µm; *G. bisporum* Boidin, Lanq. & Gilles has no clamps and bears basidia with only two sterigmata (Boidin *et al.*, 1997).

KEY TO KNOWN *BOIDINIA* SPECIES [UPDATED FROM WU (1996) AND WU & BUCHANAN (1998)]

1. Hyphae simple-septate 2
1. Hyphae with clamps 10
2. Dendrophses present ..... *B. dendrophysata* Boidin & Gilles
2. Dendrophyses absent 3
3. Hymenial surface odontoid *B. aculeata* (Sheng H. Wu) E. Larss. & K.H. Larss.
3. Hymenial surface smooth 4
4. Basidiospores longer than 5.5 µm 5
4. Basidiospores shorter than 5.5 µm 7
5. Basidiospores wider than 5.5 µm ..... *B. borbonica* Boidin, Lanq. & Gilles
5. Basidiospores narrower than 5.5 µm 6
6. Subiculum with dense texture; hyphae thin-walled; basidiospores (5.5-)6-7(-8) × 3.5-5 µm ..... *B. crystallitecta* (G. Cunn.) Sheng H. Wu & P.K. Buchanan
6. Subiculum with loose texture; hyphae thick-walled; basidiospores 3.8-4.8 × 2.9-3.3 µm ..... *B. peroxydata* (Rick) Hjortstam & Ryvarden
7. Subiculum with loose texture ..... *B. lacticolor* (Bres.) Hjortstam & Ryvarden
7. Subiculum with dense texture 8
8. Hymenial surface grey; basidiocarp thinner than 100 µm ..... *B. cana* Sheng H. Wu
8. Hymenial surface cream; basidiocarp thicker than 100 µm 9
9. Basidiospores mostly longer than 4 µm ..... *B. peroxydata* (Rick) Hjortstam & Ryvarden
9. Basidiospores mostly shorter than 4 µm ..... *B. propinqua* (H.S. Jacks. & Dearden) Hjortstam & Ryvarden
10. Basidiospores longer than 10 µm ..... *B. macrospora* Sheng H. Wu
10. Basidiospores shorter than 10 µm 11
11. Encrusted (metuloid) cystidia present ..... *B. inconstans* (G. Cunn.) Sheng H. Wu
11. Encrusted (metuloid) cystidia absent 12
12. Hymenial surface grandiniod ..... *B. granulata* Sheng H. Wu
12. Hymenial surface smooth 13
13. Basidiospores reniform ..... *B. subasperispora* (Litsch.) Jülich
13. Basidiospores globose, subglobose, to broadly ellipsoid 14
14. Basidiocarp arachnoid-pellicular; basidiospores globose 5-6.5 µm wide ..... *B. furfuracea* (Bres.) Stalpers & Hjortstam
14. Basidiocarp ceraceous to membranaceous; basidiospores 3-5 µm wide 15
15. Gloeocystidia cylindrical; basidiospores 4.2-5.2 × 3.3-3.8 µm ..... *B. luteola* Sheng H. Wu
15. Gloeocystidia obclavate 16
16. Basidiocarp membranaceous; gloeocystidia with moniliform apex; basidiospores 4.5-6(-7) × 3.8-5 µm ..... *B. permixta* Boidin, Lanq. & Gilles
16. Basidiocarp ceraceous; gloeocystidia obtuse, without moniliform apex; basidiospores (3.2-) 3.8-4.8(-5.0) × (2.8-)3.0-3.4(-3.6) µm ..... ***B. parva*** Ghobad-Nejhad, S.L. Liu, Y.C. Dai & E. Langer, **sp. nov.**

3. *Camposporium himalayanum* I. B. Prasher & R. K. Verma **sp. nov. Figs 5-6**

Mycobank: MB 811213.

Etymology: The epithet refers to the Himalayas where the specimen was collected.

Systematic position: Ascomycota, asexual morph.

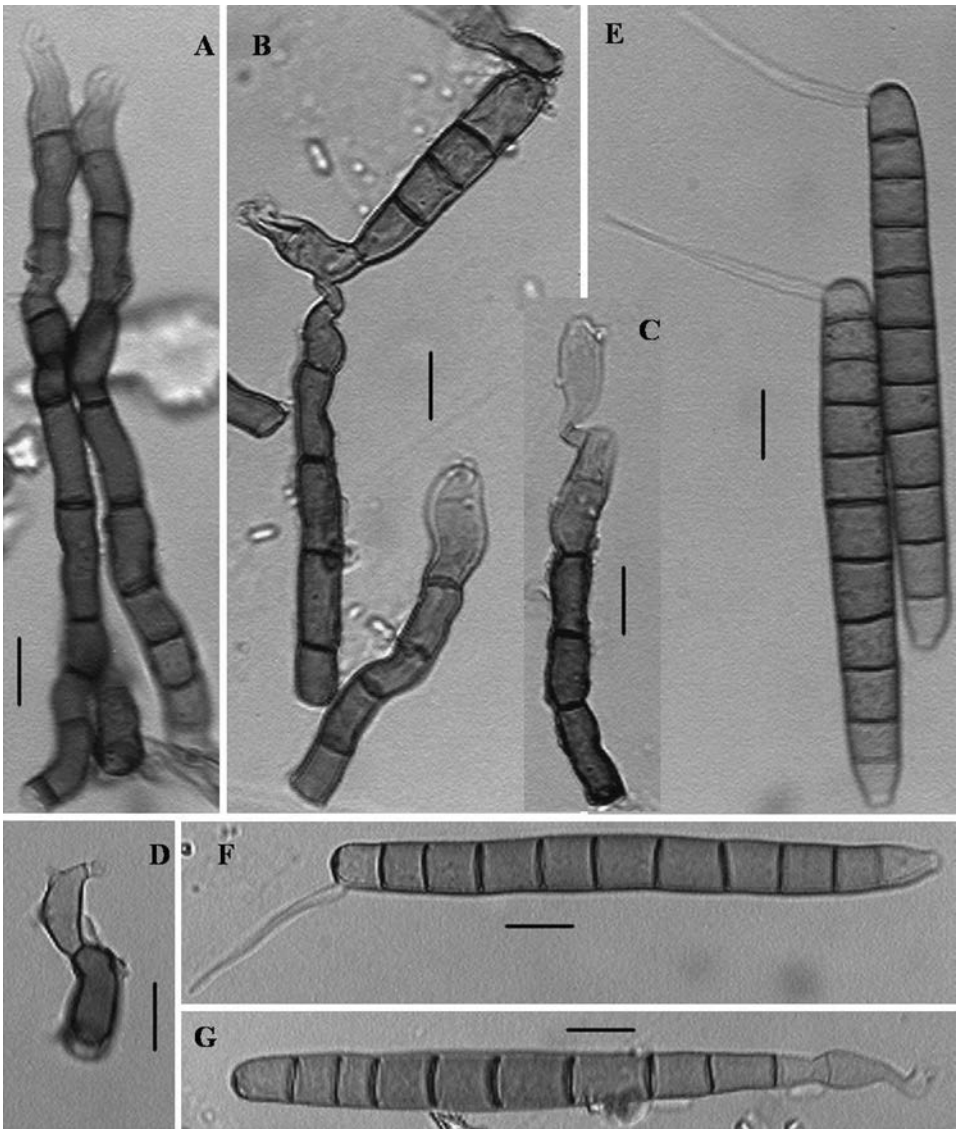


Fig. 5. *Camposporium himalayanum*. **A-C.** Conidiophores, Conidiogenous cell and Conidia. **D.** Conidiogenous cell. **E-F.** Conidia with single appendage. **G.** Conidium without appendage. Scale bars = 10 µm. Specimens mounted in 4% KOH, lactophenol and cotton blue 0.01% in lactophenol (Kirk *et al.*, 2008), observed under Matrix stereo trinocular microscope (VL-Z60) and transmission microscope (VRS- 2*f*) with measurements taken using Pro MED software.

Diagnosis: *Camposporium himalayanum* sp. nov. is characterized by terminal, polyblastic conidiogenous cells with dry, cylindrical, elongate, brown or pale brown conidia bearing often a single apical, non-septate appendage.

Holotype: India**,** Himachal Pradesh, Sundernagar, collected on dead petiole base of *Phoenix* sp. 19 Nov. 2013 I. B. Prasher and Rajnish Kumar Verma, PAN 30502 (herbarium of Botany Department, Panjab University, Chandigarh, India).

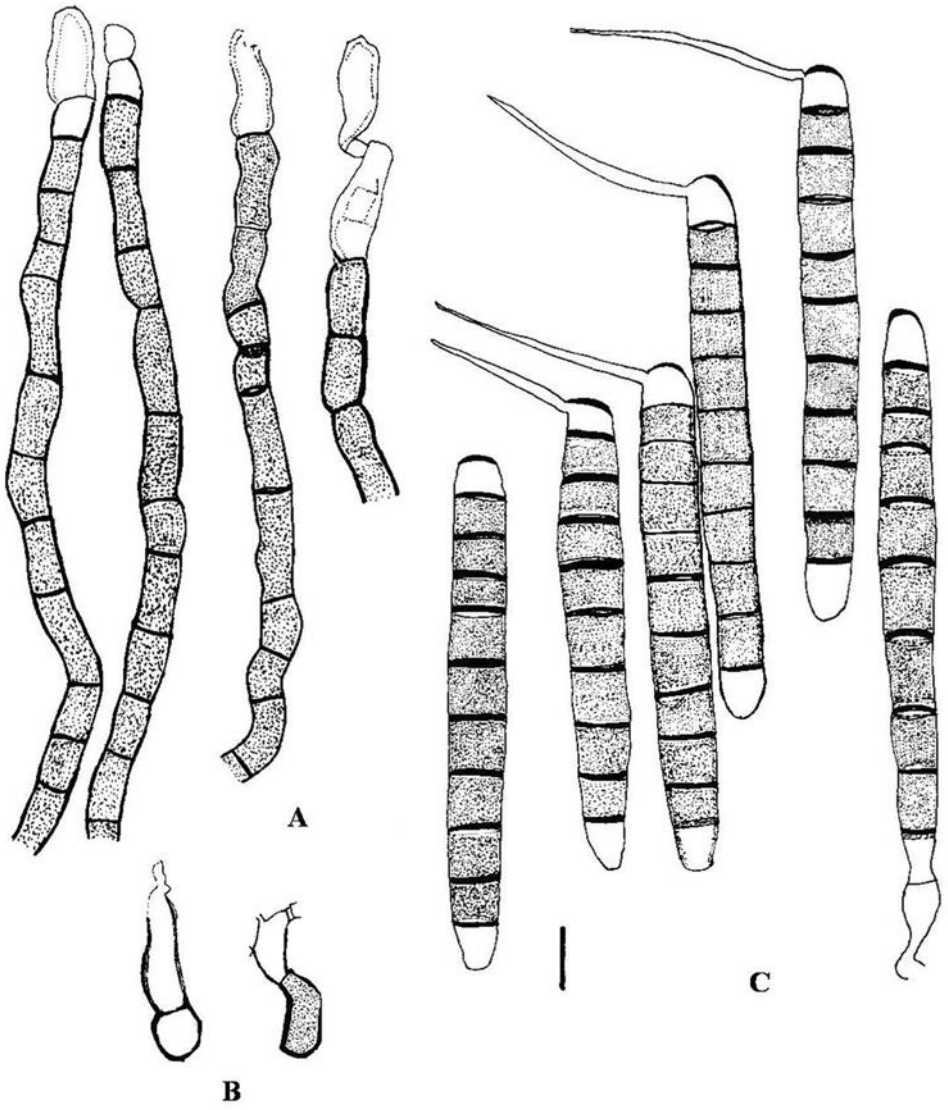


Fig. 6. *Camposporium himalayanum*. **A.** Conidiophore and attached Conidiogenous cell. **B.** Conidiogenous cell. **C.** Conidia with or without appendage. Scale bars = 10 μm.

Colonies on natural substratum effuse, minute, conidiophores scattered over the substratum. **Mycelium** immersed and superficial. Setae and hyphopodia absent. Stroma none. **Conidiophores** macronematous, mononematous, solitary, unbranched, erect, straight or flexuous, brown, paler toward the apex, 74-131 µm long, 6-8µm wide, smooth, 7-12 septate, thick walled slightly constricted at septa. **Conidiogenous cells** polyblastic, integrated into the apical region of the conidiophores, pale brown. **Conidia** 75.4-85.7 × 7-9 µm, solitary, dry cylindrical, elongate, brown or pale brown, concolorous or with 1 cell at each end paler in pigmentation than the rest of the conidium, 7-10 septate, slightly constricted at septa. Apical cell rounded with 0-1 simple, aseptate, hyaline, smooth, straight appendage, (9)14.5-26(27.5) µm long and 1.9-2.7 µm wide at the widest part, tapering toward the apex.

Table 1. Comparison of *Camposporium* species

Conidiophore			*Conidia*			*Reference*
Species	*Size [µm]*	*Septation*	*Size [µm]*	*Septation*	*Appendages*	
C. ontariense	45-200 × 5-7	6-8	20-53 × 6.5-12	3-9	0	*Fide* Whitton *et al.*, 2012
C. indicum	28.5-50.4 × 3.6-7.2	2-5	21.6-72 × 3.6-7.2	3-14	0	Rao and Rao, 1964
C. scolecosporum	10-20 × 2.5-4.5	0-3	48-108 × 3-4	6-12	0	Kobayasi, 1971
C. cambrense	22-95 × 5-7	9-15	62-115 × 8-10	9-15	1 (simple) Septate	Hughes, 1951
C. pellucidum	30-150 × 5-8	Up to 10	78-140 × 7.5-12	7-16	1 (simple) Septate	Hughes, 1951
C. hyalinum	10-40 × 4-6	0-1	20-75 × 3-5	2-6	1 (simple) Aseptate	Abdullah, 1980
C. marylandicum	41-127 × 2-3	0-5	24.7-44 × 4.5-6.5	5-10	1 (simple)	Shearer, 1974
C. ramosum	70-138 × 5.2-6	4-10	80-112 × 6.4-9.6	8-15	1 (1-3 branched) Septate	Whitton *et al.*, 2002
C. japonicum	37.5-77.5 × 5-6.5	5	42.5-70 × 5-7.5	7-10	1 (2-4 branched) Aseptate	Ichinoe, 1971
C. quercicola	15-60 × 3.5-4	1-3	28-45 × 3.5-4.5	5-9	0-3 (simple) Aseptate	Sierra *et al.*, 1995
C. laundonii	Up to 40 × 5-8	0-2	50-150 × 13-17	4-9	1-2 (simple) Septate	Ellis, 1976
C. antennatum	32-166 × 5-6	Up to 12	42.5-78 × 7.5-8.8	4-14	1-3 (simple) Aseptate	Harkness, 1884
C. microsporum	Up to 72 × 3.6-7	1-5	25.8-36 × 7.2-9	2-6	2 (simple) Aseptate	Rao and Rao, 1964
C. fusisporum	100-145 × 6.5-10	10-15	86-115 × 13.5-19	8-11	2-3 (simple) Aseptate	Whitton *et al.*, 2002
C. hyderabadense	25.2-39.6 × 3.6-5.4	1-3	32.4-54 × 3.6-7.2	5-9	1-4 (simple) Aseptate	Rao and Rao, 1964
C. himalayanum	74-131 × 6-8	7-12	75.4-85.7 × 7-9	7-10	0-1(simple) Aseptate	Present study

Commentary: *Camposporium* was introduced by Harkness (1884), as a monotypic genus with *C. antennatum* as type. The genus is characterized by dematiaceous, simple conidiophores with terminal, integrated and denticulate conidiogenous cells. The conidia are cylindrical, elongated, multiseptate, rounded at both or either end, the apex either simple or with one or more cylindrical appendages and the base typically has a persistent portion of the denticle attached to it. Conidia are usually smooth, and often the cells at each end are paler in pigmentation than the central cells (Hughes 1951, Ellis 1971, Ichinoe 1971). The criteria for species delimitation in *Camposporium* are mainly conidial characters *viz.* size, septation, pigmentation patterns, presence and type of apical appendage(s). Hughes (1951) accepted four species, Rao and Rao (1964) treated three new species from India whereas Ichinoe (1971) described six species from Japan, two being new to science. Whitton *et al.* (2002) described two new species of *Camposporium*, and provided a key to all fifteen species presently accepted in *Camposporium*.

Camposporium himalayanum differs from all other appendaged species of the genus in having 0-1 apical, non-septate conidial appendages (Table 1). It resembles *C. japonicum* in having 7-10 septate conidia but it differs markedly in size of the conidia and size and septation of the conidiophores. It also resembles *C. ramosum* in the size of conidiophores but differs from it in the size and septation of conidia.

4. *Gloiocephala parvinelumbonifolia* Chun Y. Deng, J. Qin & Zhu L. Yang, sp. nov. **Figs 7-9**

MycoBank: MB 809920.

GenBank: KM401968 (ITS), KM401969 (nucLSU).

Systematic position: Basidiomycota, Agaricomycetes, Agaricales, Physalacriaceae.

Etymology: "*parvinelumbonifolia*" is proposed because the basidiomata of the fungus look like tiny leaves of the well-known cultivated *Nelumbo nucifera.*

Diagnosis: Basidioma with smooth hymenophore; stipe densely covered with subcylindrical caulocystidia; basidiospores narrowly pip-shaped to subclavate; pileocystidia nearly ventricose to subfusiform, mixed with a few thick-walled long hairs; hymenial cystidia absent.

Holotypus: CHINA. Hainan Province: Ledong County, Jianfengling Nature Reserve, 18 April 2014, *Chun-Ying Deng* 65 (HKAS 82797, holotype!).

Basidiomata very small. **Pileus** 3-5 mm, concave, depressed at center or nearly infundibuliform, white to dirty white, dry, with brownish dots and conspicuous scattered white setose hairs under hand-lens. **Hymenophore** smooth, white to dirty white. **Context** very thin. **Stipe** 15-20 × 0.3-0.5 mm, central, subcylindrical, elastic, apex whitish, dark brown to blackish brown towards base, densely covered with grey to brownish grey, minute hairs, dry, solid, insititious. **Odour** absent.

Basidia 22-30 × 4-5 μm, narrowly clavate, 4-spored, thin-walled, clamped; sterigmata 3-4 μm in length; **basidioles** clavate to subfusiform with subacute apex. **Spores** [25/2/1] (7.5) 8-11 × 3-4 μm, Q = (2.14) 2.28-3.33 (3.67), Qm = 2.80 ± 0.39, subfusiform to narrowly pip-shaped to subclavate, inequilateral in profile, smooth, thin-walled, colorless and hyaline, non-amyloid, non-dextrinoid. Hymenial cystidia absent. **Pileipellis** a hymeniderm 30-40 μm thick, composed of non-gelatinous, thin- to slightly thick-walled (up to 1 μm thick), colorless and hyaline, clavate, broadly clavate to sphaeropedunculate cells (18-35 × 8-30 μm), intermixed with scattered,

Fig. 7. Basidomata of *Gloiocephala parvinelumbonifolia* in its natural habitat (from the holotype).

thick-walled (up to 3 μm thick), yellow-brown, clavate, broadly clavate to sphaeropedunculate cells (12-20 × 8-12 μm). **Pileocystidia** scattered, lanceolate to subcylindrical to subfusiform, 45-120 × 10-15 μm, thin-to slightly thick-walled, colorless and hyaline; hairs on each pileus scattered, 150-600 × 8-20 μm, at base subfusiform with very long cylindrical or gradually tapering neck and narrow and often pointed apex, usually thick-walled (up to 4 μm thick), nearly colorless and hyaline. **Pileal trama** ca. 50 μm thick, composed of gelatinous, thin-walled, colorless and hyaline, filamentous hyphae 2-3 μm wide. **Stipitipellis** composed of vertically arranged, yellow-brown, slightly thick-walled (ca. 0.5 μm thick), filamentous hyphae 2-7 μm broad. **Caulocystidia** numerous and crowded, subcylindrical, 20-70 × 2-3 μm, often flexuous, slightly thick-walled at lower part, often with a narrow-round apex, yellowish to brownish, but nearly colorless at apex. **Clamp connections** abundant in every part of basidioma.

Habitat: fruiting on mossy bark of rotten wood in a broad-leaved forest.

Commentary: To data, about 30 species have been described in the genus *Gloiocephala* Massee (Kirk *et al.*, 2008), which is typified by *G. epiphylla* Massee (Massee, 1892). However, recent molecular phylogenetic analyses indicated that *Gloiocephala* in its broad sense (Bas 1961; Singer 1976, 1986; Antonín 2007; Antonín & Noordeloos 2010) is probably polyphyletic (Moncalvo *et al.*, 2002; Binder *et al.*, 2006; Hao *et al.*, 2014). Our phylogenetic analysis (Fig. 9) based on ITS and nrLSU sequences indicated that the sample is indeed a species of Gloiocephala sensu stricto, and represents a new species, *viz.*, *Gloiocephala parvinelumbonifolia.*

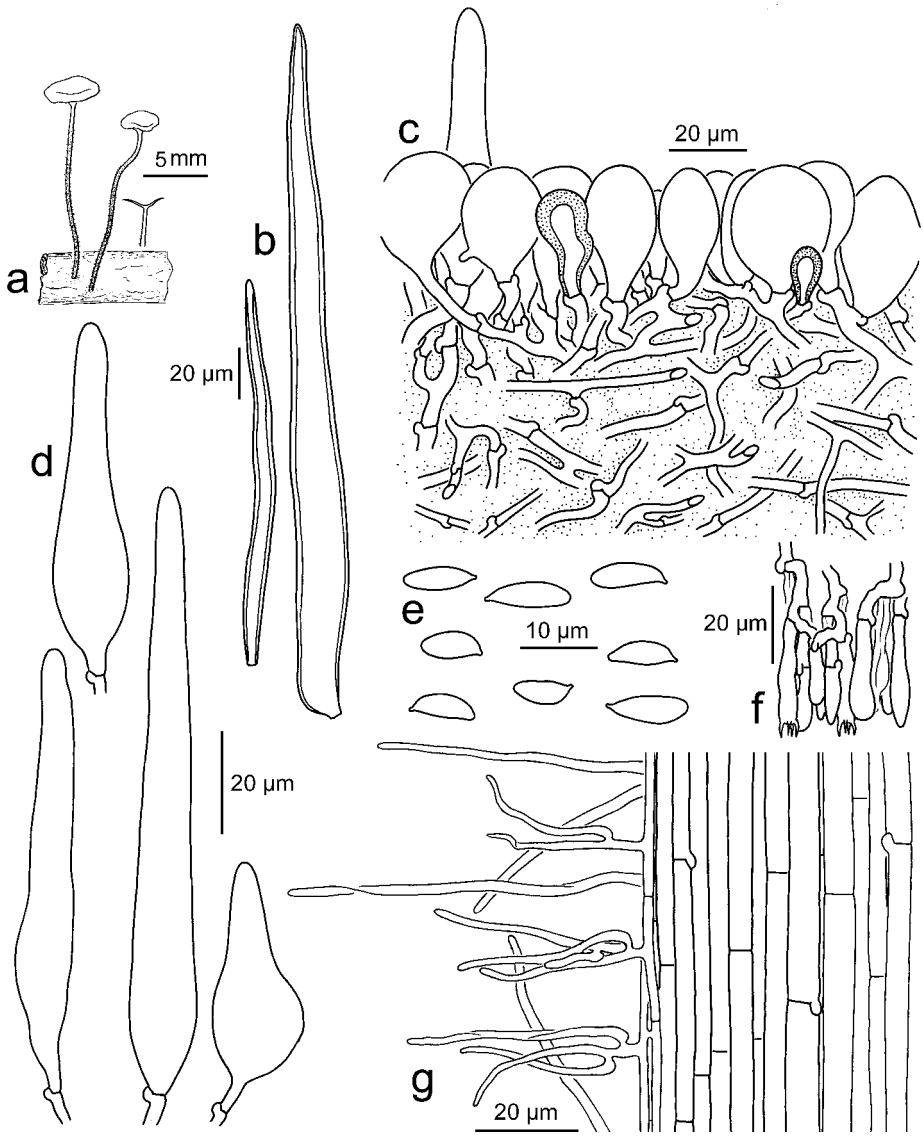
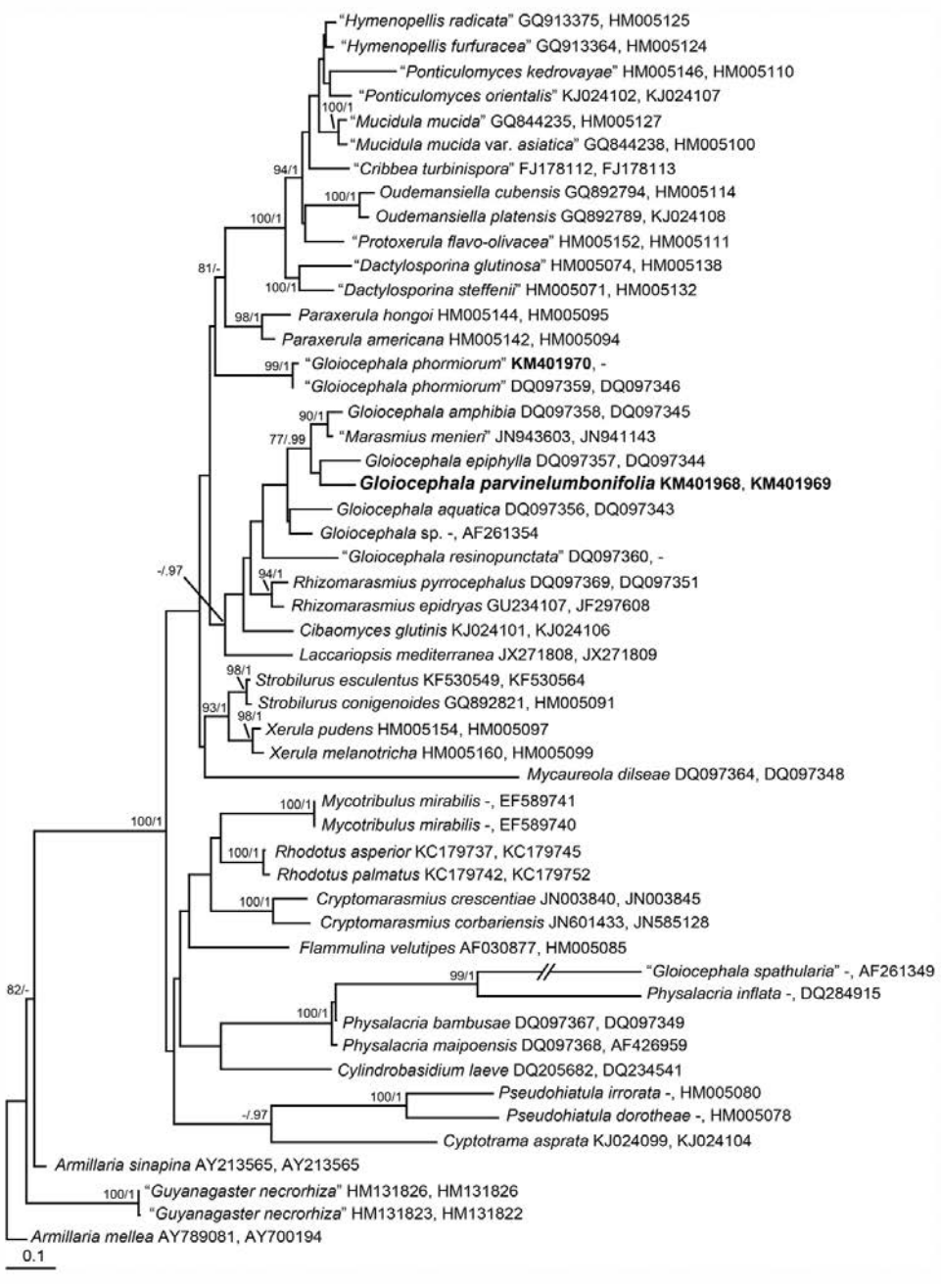


Fig. 8. Microscopic features of *Gloiocephala parvinelumbonifolia.* **a.** Habitus. **b.** Hairs on pileus. **c.** Radial-vertical section of pileipellis and pileal trama. **d.** Pileocystidia. **e.** Basidiospores. **f.** Basidia and subhymenium. **g.** Stipe in longitudinal section showing caulocystidia and trama of stipe (all from the holotype).

Gloiocephala parvinelumbonifolia is very similar to *G. tenuicrinita* Horak & Desjardin (1994) because of its infundibuliform, white pileus with a smooth hymenophore lacking hymenial cystidia, a pruinose stipe with thin-walled, hair-like caulocystidia, and subfusiform to pip-shaped basidiospores. However, *G. tenuicrinita* differs from our species by the abundant presence of thin-walled and hair-like pileocystidia and the absence of thick-walled long hairs.

Gloiocephala parvinelumbonifolia also resembles *G. epiphylla* in the depressed pileus with a smooth hymenophore, pruinose stipe and subfusiform to pip-shaped basidiospores. However, it differs from the latter in having ventricose pileocystidia without any capitate apex, the presence of thick-walled long hairs



on the pileus, and the subcylindrical often flexuous caulocystidia. Furthermore, *G. parvinelumbonifolia* grows on the bark of a rotten tree (Massee 1892; Singer 1960).

The thick-walled hairs on the pileus in *G. parvinelumbonifolia* are somewhat similar to those in *G. longifimbriata* Singer, originally described from Argentina, and *G. capillata* Singer, originally described from Mexico. The latter two species differ in the common presence of ventricose-capitate hymenial and pileal cystidia (Singer 1960, 1976). In addition, *G. capillata* has, among other features, longer basidiospores and much wider caulocystidia and hairs on the stipe surface.

In the alignment of the combined dataset, 992 characters were constant, while 956 characters were variable, of which 709 were parsimony informative. The genera *Cribbea*, *Dactylosporina*, *Hymenopellis*, *Mucidula*, *Ponticulomyces* and *Protoxerula* were treated in *Oudemansiella* s.l. as in Qin *et al.* (2014) and thus, quotation marks were placed around the names. Additionally, if the monophyly of the species with the same generic name is questionable, quotation marks were also put around the names. Due to the paraphyly of *Armillaria* with *Guyanagaster*, the names of *Guyanagaster* were cited with quotation marks.

5. *Gongronella guangdongensis* F. Liu, T.T. Liu & L. Cai, **sp. nov. Figs 10-11**

Mycobank: MB803147.
GenBank: KC462739.
Etymology: after the province where it was collected, *Guangdong*, China.
Systematic position: Zygomycota, Mucoromycotina, Mucorales, Mucoraceae.
Diagnosis: differs from *G. butleri* in the sporangiospores which are globose, hyaline or light yellow.

◀ Fig. 9. Phylogenetic tree generated from combined ITS and nrLSU dataset using ML method. Posterior probabilities from Bayesian inference (≥ 0.95) and bootstrap values (≥ 70%) derived from ML analyses are shown above or beneath the branches at nodes. GenBank accession numbers of sequences used in this study are shown after their fungal taxa. Newly generated sequences are highlighted in boldface. Protocols for DNA extraction, PCR, and sequencing followed those in Hao *et al.* (2014) and Qin *et al.* (2014). Two datasets, ITS sequences and nrLSU sequences, were aligned with MAFFT v6.8 (Katoh *et al.*, 2005) and manually optimized on BioEdit v7.0.9 (Hall 1999) or 4SALE v1.5 (Seibel *et al.*, 2006). To investigate the potential conflict between ITS and nrLSU, the partition homogeneity (PH) or incongruence length difference (ILD) test was performed with 1000 randomized replicates, using heuristic searches with simple addition of sequences in PAUP* 4.0b10 (Swofford 2002). Since the result showed that the two different gene fragments were not in conflict ($P < 0.5$), the two datasets were concatenated using Phyutility v2.2 for further analysis (Smith & Dunn 2008). Outgroups were selected according to recent phylogenetic studies (Wilson & Desjardin 2005; Ronikier & Ronikier 2011; Hao *et al.*, 2014). Bayesian Inference (BI) and Maximum Likelihood (ML) were employed by using MrBayes v3.1.2 (Ronquist & Huelsenbeck 2003) and RAxML v7.2.6 (Stamatakis 2006), respectively, based on the combined dataset (ITS-nrLSU). Substitution models suitable for each partition in the database were determined by using the Akaike Information Criterion (AIC) implemented in MrModeltest V2.3 (Nylander 2004). The models chosen as the best models for ITS and nrLSU were GTR + I + G and HKY + I + G, respectively. All parameters in the ML analysis used the default setting, and statistical support values were obtained using the nonparametric bootstrapping with 1000 replicates. BI analyses using selected models and 4 chains were conducted and stopped when the standard deviation of the split frequencies fell below 0.01 and ESS values > 200. Tracer v1.5 (http://tree.bio.ed.ac.uk/software/tracer/) was used to monitor the chain convergence. Trees were sampled every 100 generations. Subsequently, trees were summarized and statistic supports were obtained by using the sumt command complemented in MrBayes by discarding the first 25% generations as burn-ins.

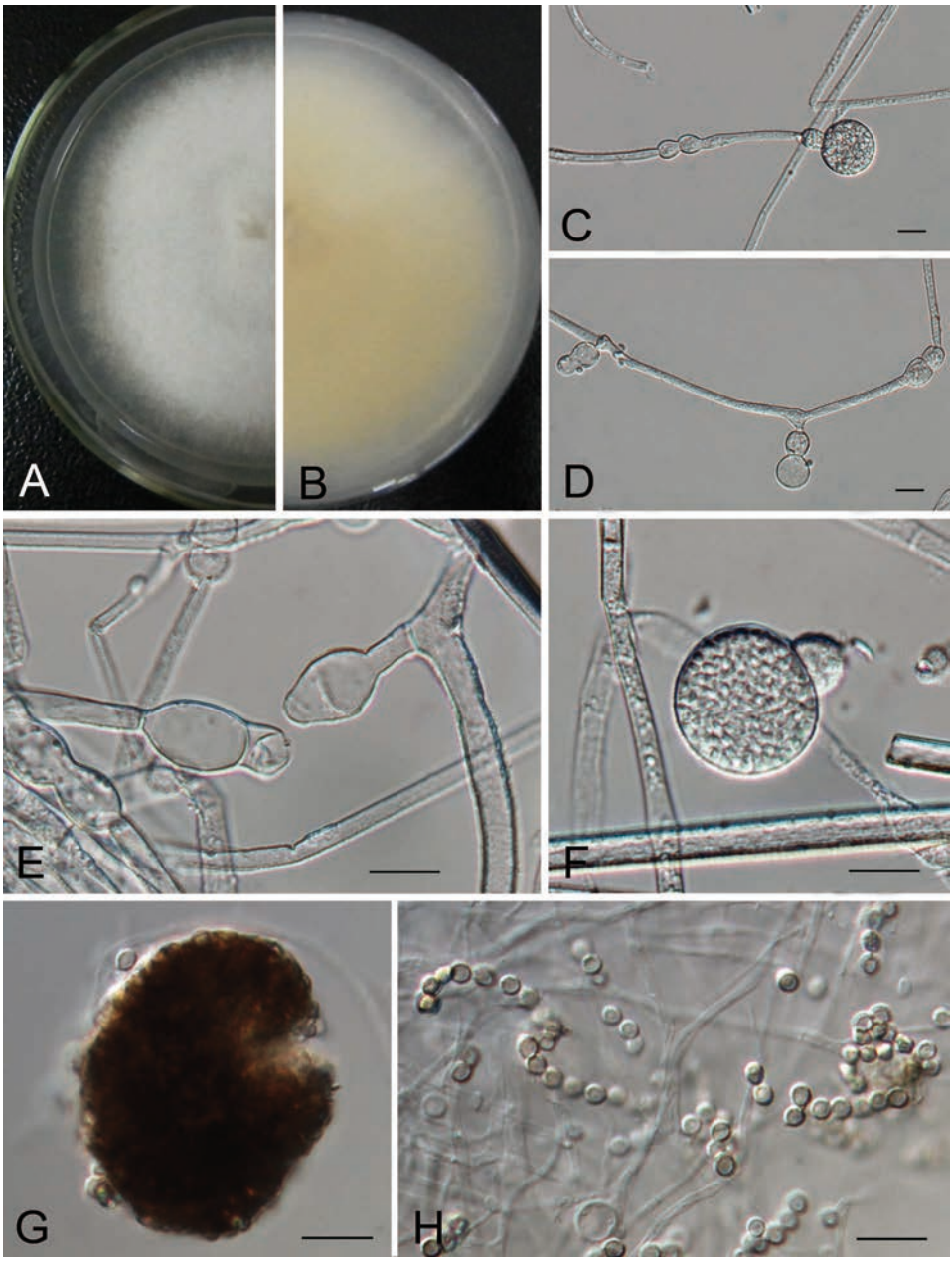


Fig. 10. *Gongronella guangdongensis* (ex-type CGMCC 3.15212). **A-B.** Colonies on PDA. **C.** Sporangium and chlamydospore. **D.** Columella and chlamydospore. **E.** Columella. **F-G.** Sporangia. **H.** Sporangiospores. *Bar* C-H 10 µm.

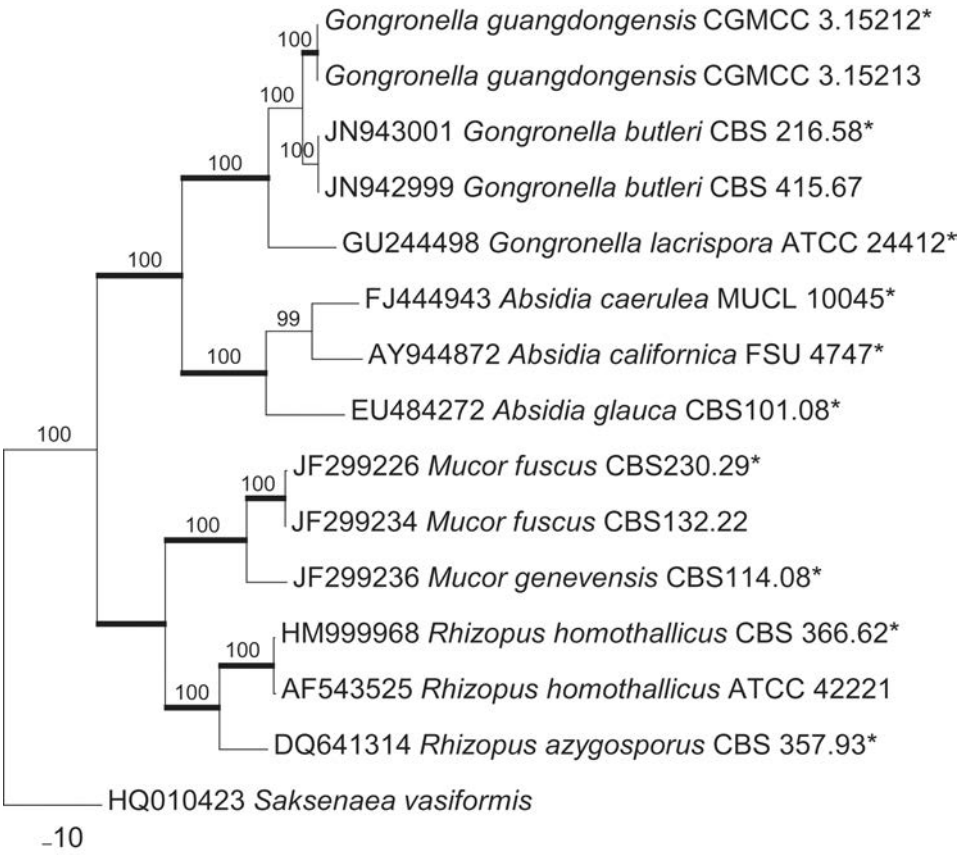


Fig. 11. Maximum parsimony phylogram inferred from ITS sequences showing phylogenetic relationships of *Gongronella guangdongensis* with closely related taxa. Bootstrap support values above 70% are shown above the branches. Thickened branches represent significant Bayesian posterior probabilities (equal or above 0.95). Ex-type isolates are indicated with asterisk.

Total genomic DNA was extracted using CTAB method (Porebski *et al.*, 1997). The internal transcribed spacers and 5.8S ribosomal RNA gene (ITS) were amplified using primers ITS1 & ITS4 (White *et al.*, 1990). Alignment with sequences of related species from GenBank were generated using MAFFT v.6 (Katoh and Toh 2010), and manually edited using MEGA5 (Tamura *et al.*, 2011). Phylogenetic analysis was performed using maximum parsimony as implemented in PAUP* 4.0b10 (Swofford 2002). Characters were equally weighted and gaps weretreated as missing data. Trees were inferred with the heuristic search option with TBR branch swapping and 1000 random sequence additions. Maxtrees were unlimited, branches of zero length were collapsed and all parsimonious trees were saved. Clade stability was assessed with a bootstrap (BS) analyses with 1000 replicates, each with 10 replicates of random stepwise of taxa. The dataset contains 749 characters including the alignment gaps, of which 469 characters were parsimony-informative; 93 were parsimony-uninformative and 187 were constant. Parsimony analysis yielded one parsimonious tree (TL = 1360, CI = 0.732, RI = 0.767, RC = 0.562, HI = 0.268). A second phylogenetic analysis using a Markov Chain Monte Carlo (MCMC) algorithm was conducted to generate trees with Bayesian posterior probabilities in MrBayes v.3.2.1 (Ronquist and Huelsenbeck 2003). Nucleotide substitution model was determined using MrModeltest 2.3 (Nylander 2004). Two analyses of four MCMC chains were run from random trees for one millions generations and sampled every 100 generations. The first 25% of trees were discarded as the burn-in phase of each analysis and posterior probabilities determined from the remaining trees.

Holotype: China, Guangdong Province, Ding-Hu Natural Reservation Park, isol. exsoil (S1105), 29 Sep. 2011, L. Cai (holotypus HMAS244381, culture ex-type CGMCC 3.15212 = LC1994).

Colonies on PDA white or pale, a height of 1-2 mm, 5 cm in diam. in 13 days at 25°C, margin irregular; colony reverse buff to honey; rhizoids and stolons absent. **Sporangiophores** erect, branched and septate, 28-100 × 2.0-2.5 μm, hyaline, smooth, always with a septum under the apophysis, branching irregularly or simply. **Sporangia** 14-21.5 μm in diam., at first pale to pale mouse grey, then olivaceous to brown vinaceous with age, always globose, many-spored, always with an apophysis, abortive sporangia sometimes present; sporangial wall thin and smooth; apophyses 5.5-9 μm in diam., hemispherical, hyaline to pale grey, smooth; columellae 2.5-12 × 2-12 μm, hemispherical, spherical or ovoid, smooth, often constricted at attachment to apophyses. **Sporangiospores** globose, 2-3μm in diam., hyaline or light yellow, smooth. **Chlamydospores** 13-20 × 5-11 μm, abundant, always two-celled, gourd-shaped, smooth. **Zygospores** not observed.

Other specimen examined: isolated from soil collected on Sep. 29, 2011 by L. Cainear the type locality: sample S1109 (living culture CGMCC 3.15213 = LC1995; ITS sequence GenBank KC462740).

Commentary: The genus *Gongronella* Ribaldi was proposed to accommodate *G. urceolifera* (Ribaldi 1952) for *Absidia*-like fungi having a globose apophysis with a constriction between the apophysis and the attachment of the sporangial wall. This species was later found to be synonymous (Peyronel and Dal Vesco 1955) with *Absidia butleri* Lendner, originally isolated from roots of *Cocos nucifera* from Malaya (Lendner 1926), while also Paine (1927) had already described the same species as *A. subpoculata* Paine from Iowa soil (United States). Both these *Absidia* had been recombined earlier in *Tieghemella* by Naumov (1935). The only other known species of *Gongronella*, *G. lacrispora* Hesselt & J.J. Ellis, has been described from soil from Maryland, USA (Hesseltine & Ellis, 1962). Both species are relatively slow growing and strictly soil inhabiting.

The new species *Gongronella guangdongensis* has morphological characters that fit the generic concepts very well and differ from both other accepted species: it is characterized by white colonies, slow growth rate, erect and branched sporangiophores, globose sporangium, columellae with a globose apophysis and one-celled sporangiospores. Phylogenetic analysis based on ITS sequences (Fig. 11) shows that the genus *Gongronella* is monophyletic and that our new species is phylogenetically distinct from both other *Gongronella* species and sister to *G. butleri.* Both species differ morphologically in the characters of their sporangiospores which are globose, hyaline or light yellow in *G. guangdongensis*, but hyaline, oval to flattened on one side or almost reniform in *G. butleri* (Hesseltine and Ellis 1964).

6. *Hypochnicium austrosinensis* W.M. Qin & L.W. Zhou, **sp. nov.** **Fig. 12**

MycoBank: MB 809858.

Etymology: *austrosinensis* (Lat.): referring to the type locality in eastern southern China.

Systematic position: Basidiomycota, Agaricomycetes, Polyporales, Meruliaceae.

Diagnosis: Differs from other *Hypochnicium* species by its combination of having both capitate and tubular cystidia and broadly ellipsoid to subglobose, non cyanophilous basidiospores.

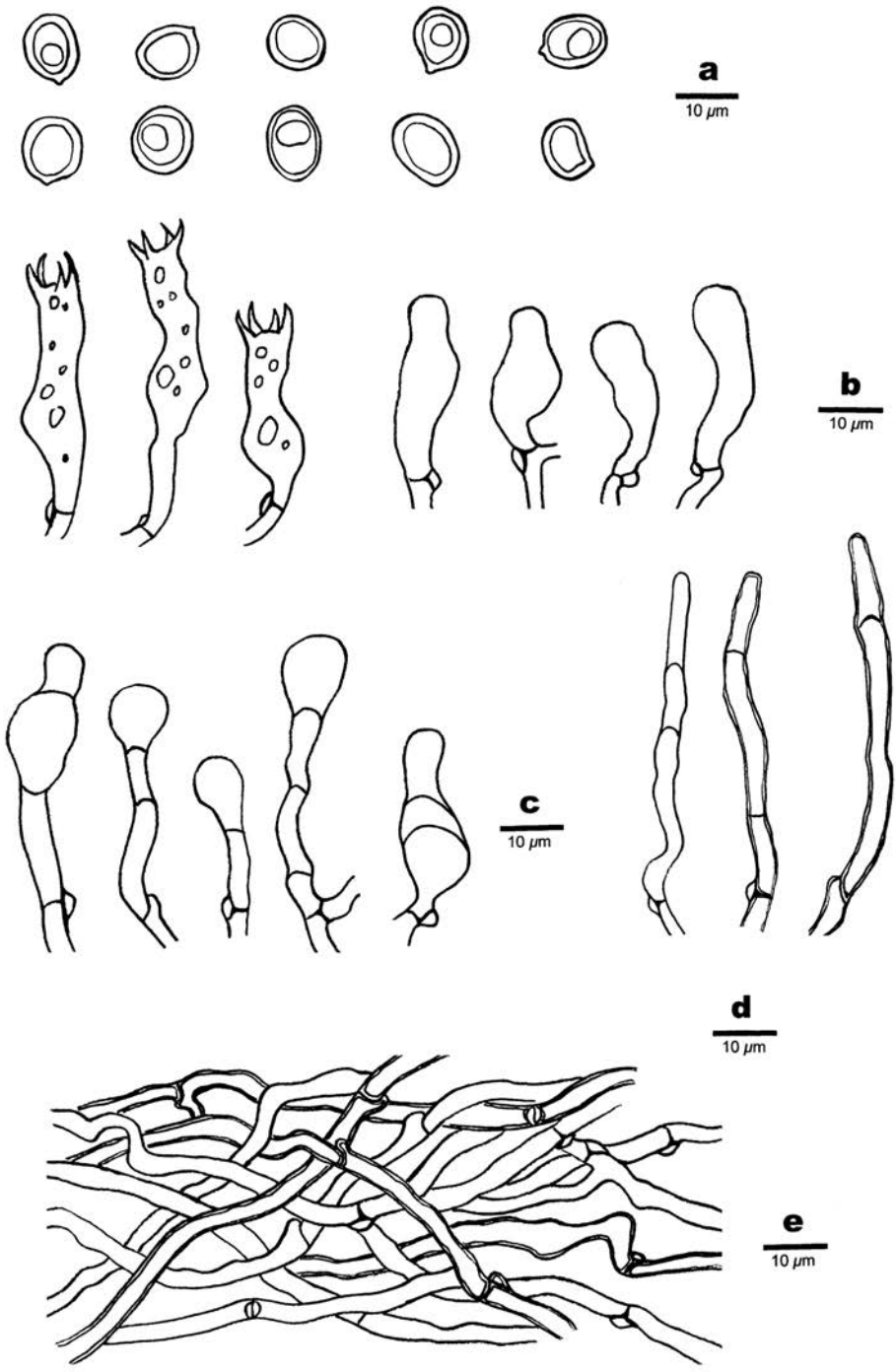


Fig. 12. Microscopic structures of *Hypochnicium austrosinensis* (drawn from the holotype). **a.** Basidiospores. **b.** Basidia and basidioles. **c.** Capitate cystidia. **d.** Tubular cystidia. **e.** Hyphae from subiculum.

Holotype: **CHINA**, Hunan Province, Yizhang County, Mangshan National Forest Park, on dead angiosperm tree, 24 June 2007, H.X. Xiong, Xiong 2 (IFP 008949).

Basidiocarps annual, resupinate, effused, tightly adnate, farinaceous and soft, without odor or taste when fresh, crustaceous and tough upon drying, 50-150 μm thick in section (aculei excluded). **Hymenial surface** buff to cinnamon-buff, glabrous, smooth when young, becoming tuberculate with age; margin not especially differentiated, concolorous, usually thinning out to a pruinose zon; no rhizomorphs. **Hyphal system** monomitic; generative hyphae bearing clamp connections, IKI-, CB-; tissues unchanged in KOH. **Subiculum** with generative hyphae hyaline, slightly to distinctly thick-walled, flexuous, loosely interwoven, frequently branched and mostly at clamp connections, 3-4.5 μm in diameter. **Subhymenium** with hyphae hyaline, thin to slightly thick-walled, frequently branched, 2-4 μm in diameter. **Cystidia** numerous, of two kinds: capitate or rarely ventricose cystidia variably abundant, thin-walled, with a basal clamp and usually with few secondary simple septa, 20-42 × 6-10 μm; tubular to cylindrical cystidia, not encrusted, thin to slightly thick-walled, with one or a few secondary simple septa, 28-62 × 3-4.5 μm. **Basidia** suburniform or nearly utriform, flexuous, usually guttulate, with four sterigmata and a basal clamp connection, 36-45 × 8-10 μm; basidioles dominant, in shape similar to basidia, but slightly smaller. **Basidiospores** broadly ellipsoid or subglobose, hyaline, smooth, with 1-1.5 μm thick walls, usually bearing one guttule, IKI-, CB-, 9-10(-11) × (7.2-)7.5-8.8(-9) μm, L = 9.55 μm, W = 8.16 μm, Q = 1.17 (n = 30/1).

Type of rot. White rot.

Commentary: *Hypochnicium* J. Erikss. is a genus of corticioid, wood-inhabiting fungi recently classified (Larsson, 2007) in family Meruliaceae (Polyporales) with presently more than 30 species and a worldwide distribution. Until now eight species of *Hypochnicium* have been recorded in China (Dai, 2010; Dai, 2011; Gao & Qin, 2013; Xiong & Dai, 2009). The genus is recognized by its resupinate to adnate basidiomata, a monomitic hyphal system bearing clamp connections, by the more or less suburniform basidia and especially by the thick-walled, cyanophilous spores that are either smooth or ornamented (Erikson, 1958; Eriksson & Ryvarden, 1976; Nilsson & Hallenberg, 2003; Telleria *et al.*, 2010). *Hypochnicium* shares with *Hyphoderma* Wallr. the same kind of basidioma, hyphae and basidia, but it usually differs from the latter in having thick-walled, cyanophilous basidiospores. Wu (1990) more recently suggested that the spore wall cyanophily may be of minor importance for the delimitation of this genus, and described *H. globosum* Sheng H. Wu with non-cyanophilous basidiospores in the genus.

H. bicystidiatum Boidin & Gilles most closely resembles our species in having both capitate and tubular cystidia, but can be distinguished by its larger cystidia (capitate cystidia 95-110 × 9-12 μm, tubular cystidia 100-150 × 5-6 μm) and especially by its smaller basidiospores (4.8-5.3 × 3.5-4.3 μm) with thick cyanophilic walls (Boidin & Gilles, 2000).

7. *Neodeightonia licuriensis* A. R. Machado & O. L. Pereira, **sp. nov. Figs 13-15**

MycoBank: MB810662.

GenBank: KP165429; KP165430; KP165431.

Systematic position: Ascomyota, Pezizomycotina, Dothideomycetes, Botryosphaeriales, Botryosphaeriaceae.

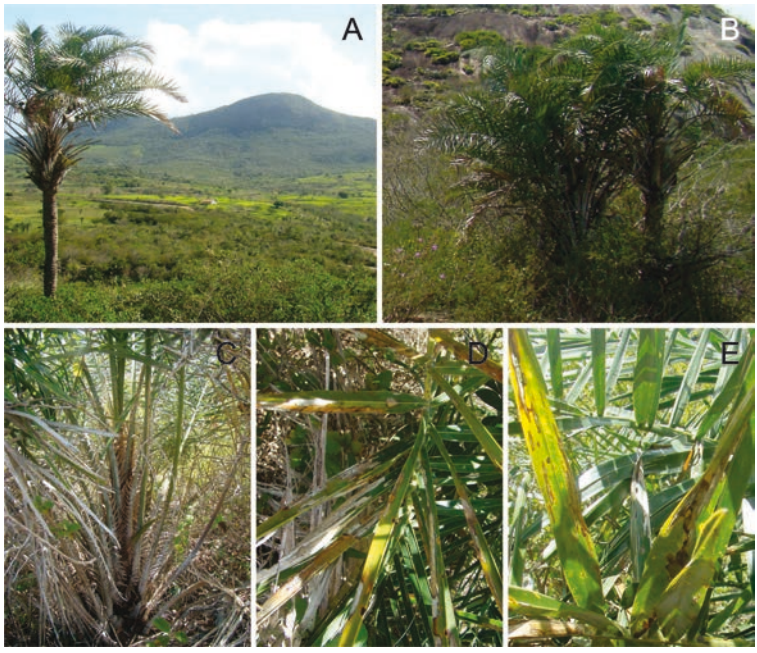


Fig. 13. Symptoms in palm tree *Syagrus coronata*. **A-B.** Caatinga biome and palm tree *Syagrus coronata*. **C.** Dead rachis. **D-E.** Leaves with necrotic lesions.

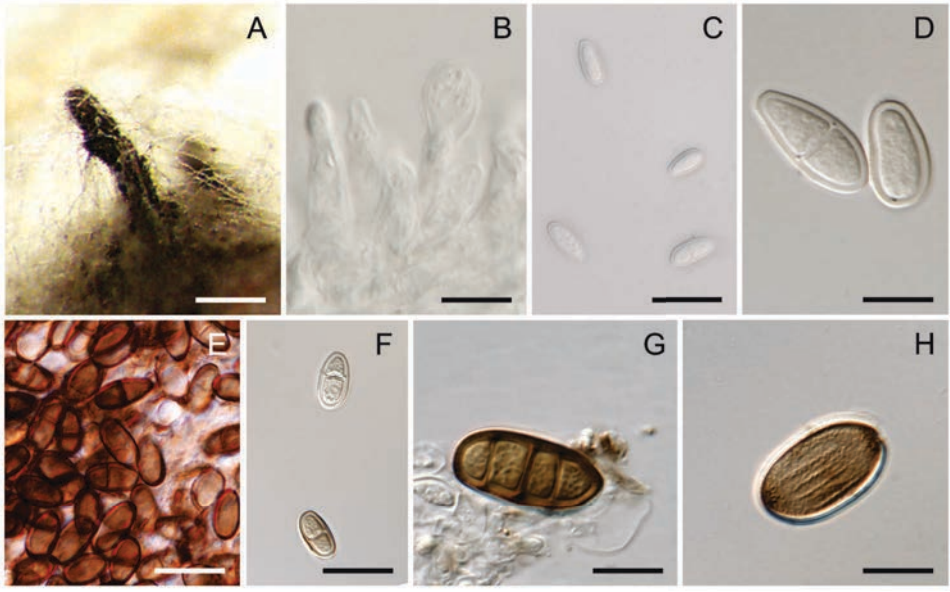


Fig. 14. *Neodeightonia licuriensis* strain COAD1780. **A.** Conidial mass released from the conidiomata of *Pinus* twigs in culture. **B.** Conidia developing on conidiogenous cells. **C-D.** Immature conidia. **E.** Mature conidia. **F.** Mature and immature septate conidia. **G.** Mature up to three-septate conidia. **H.** Conidial striation in mature conidia. Scale bars: A = 200 µm; B, D, G and H = 10 µm; C, E and F = 30 µm.

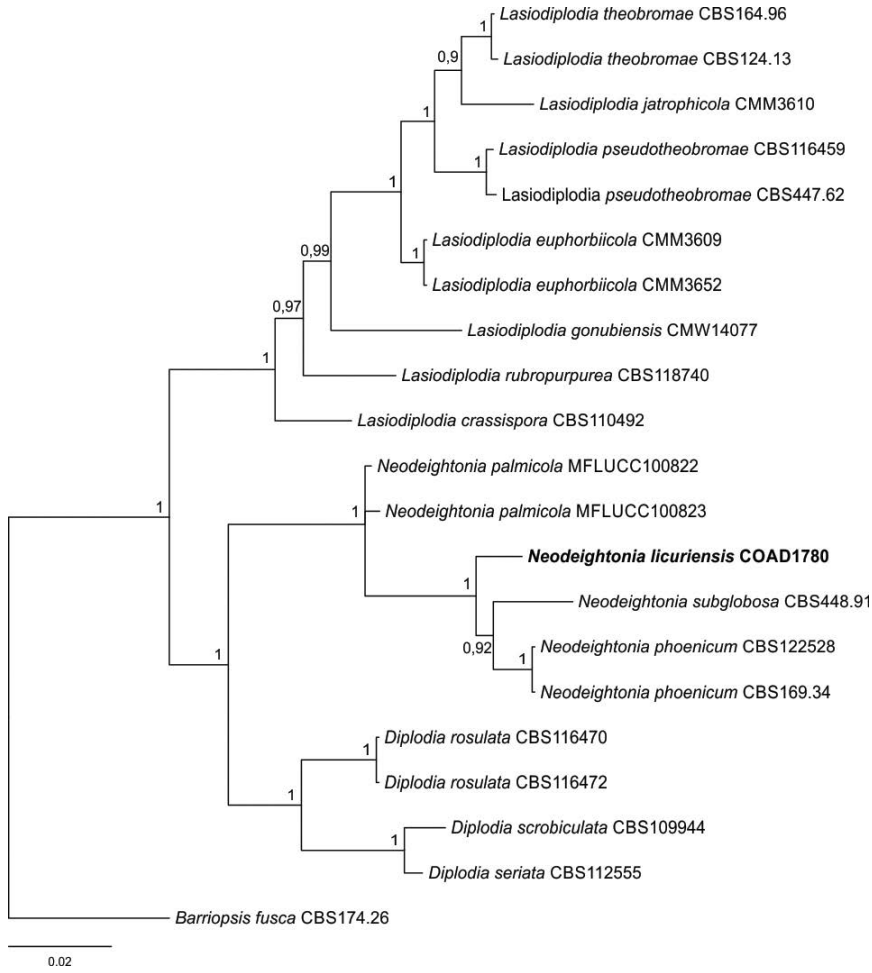


Fig. 15. A multilocus phylogenetic tree inferred from Bayesian analysis based on the combined sequences of the ITS, TEF-1α and βt (table 2). The Bayesian posterior probabilities are indicated above the nodes. The tree was rooted to *Barriopsis fusca* CBS174.26. The species from this study are highlighted in bold. The combined analyses of the ITS, TEF1-α and βt dataset included 21 taxa and contained 1172 characters, of which 207 were parsimony-informative, 297 were variable and 865 were conserved. The consensus tree generated with Bayesian analyses is shown. The nucleotide sequences were edited with the BioEdit software (Hall, 2014). All sequences were checked manually, and any nucleotides with ambiguous positions were clarified using sequences from both DNA strands. The resulting new sequences were deposited in GenBank (http://www.ncbi.nlm.nih.gov) and ITS sequences were also deposited in the UNITE database for molecular identification of fungi (http://unite.ut.ee) (Nilsson *et al*., 2014). Sequences of Internal Transcribed Spacer regions 1 and 2 including the 5.8S rRNA gene (ITS), Translation Elongation Factor 1-α (TEF1-α) and β-tubulin (βt) of additional species were retrieved from GenBank (Table 2). Consensus sequences were compared against GenBank's database using the Mega BLAST program. The closest hit sequences were aligned using the multiple sequence alignment program MUSCLE® (Edgar, 2004), built in MEGA v. 5 software (Tamura *et al*., 2011). Alignments were checked, and manual adjustments were made when necessary. The resulting alignment was deposited into TreeBASE (http://www.treebase.org/) under accession number S16546. Phylogenetic analyses were conducted as described by Machado *et al*. (2014); however, the models of evolution selected according to the Akaike Information Criterion (AIC) were GTR+G for TEF1-α and GTR+I for ITS and β-tubulin.

Diagnosis: Differs from other *Neodeightonia* species in its conidial dimensions and up to three-septate conidia. This species has larger conidia (14.6-20.5 × 8.3-11.4 µm) than *N. subglobosa* (9-12 × 6-9 µm) and smaller conidia than *N. phoenicum* (14.5-24 × 9-14 µm) and *N. palmicola* (17.5-24.5 × 9.5-12.5 µm).

Holotype: BRAZIL, along highway between the cities Castro Alves and Santa Terezinha, Bahia, on necrotic lesions on the rachis and leaves of *Syagrus coronata*, 2010, O. L. Pereira, (VIC42826 **holotype**; **culture ex-type** COAD1780).

Etymology: in reference to host name "licuri".

Conidiomata pycnidial, globose, unilocular, dark brown to black, formed superficially on twigs of *Pinus*. ***Conidiogenous cells*** holoblastic, cylindrical, hyaline, smooth and thin-walled, formed from cells lining the inner pycnidial walls, 8.7-16.2 × 2.3-4.4 µm. ***Paraphyses*** absent. ***Conidia*** acrogenous, thick-walled, ellipsoid to ovoid, hyaline when young, becoming dark brown when older, up to three-septate, frequently with rounded apices, sometimes truncate base, widest in the middle, 14.6-20.5 × 8.3-11.4 µm. Longitudinal striations were occasionally observed.

Colonies grew to 90 mm diam. in 10 days at 25°C on PDA, appearing white to slightly gray at maturity, producing sometimes a pink pigment.

Table 2. GenBank accession numbers of the DNA sequences used in the phylogenetic analyses. The species obtained in this study are shown in bold

Species	*Isolates*	*Host/Substrate*	*Genbank acession n°*		
			ITS	EF1-*α*	*βt*
Lasiodiplodia rubropurpurea	CBS118740	*Eucalyptus grandis*	DQ103553	EU673304	EU673136
Lasiodiplodia gonubiensis	CBS115812	*Syzygium cordatum*	DQ458892	DQ458877	DQ458860
Lasiodiplodia crassispora	CBS110492	*Unknown*	EF622086	EF622066	EU673134
Lasiodiplodia pseudotheobromae	CBS116459	*Gmelina arborea*	EF622077	EF622057	EU673111
Lasiodiplodia pseudotheobromae	CBS447.62	*Citrus aurantium*	EF622081	EF622060	EU673112
Lasiodiplodia euphorbicola	CMM3652	*Jatropha curcas*	KF234554	KF226715	KF254938
Lasiodiplodia euphorbicola	CMM3609	*Jatropha curcas*	KF234543	KF226689	KF254926
Lasiodiplodia jatrophicola	CMM3610	*Jatropha curcas*	KF234544	KF226690	KF254927
Lasiodiplodia theobromae	CBS164.96	*Unknown*	AY640255	AY640258	EU673110
Lasiodiplodia theobromae	CBS124.13	*Unknown*	DQ458890	DQ458875	DQ458858
Neodeightonia palmicola	MFLUCC100822	*Arenga westerhoutii*	HQ199221	–	–
Neodeightonia palmicola	MFLUCC100823	*Caryota urens*	HQ199224	–	–
Neodeightonia licuriensis	**COAD1780**	***Syagrus coronata***	**KP165429**	**KP165430**	**KP165431**
Neodeightonia subglobosa	CBS448.91	Keratomycosis in eye	EU673337	EU673306	EU673137
Neodeightonia phoenicum	CBS122528	*Phoenix dactylifera*	EU673340	EU673309	EU673116
Neodeightonia phoenicum	CBS169.34	*Phoenix dactylifera*	EU673338	EU673307	EU673138
Diplodia scrobiculata	CBS 109944	*Pinus greggii*	DQ458899	DQ458884	DQ458867
Diplodia seriata	CBS 112555	*Vitis vinifera*	AY259094	AY573220	DQ458856
Diplodia rosulata	CBS 116470	*Prunus africana*	EU430265	EU430267	EU673132
Diplodia rosulata	CBS 116472	*Prunus africana*	EU430266	EU430268	EU673131
Barriopsis fusca	CBS174.26	*Citrus* sp.	EU673330	EU673296	EU673109

Table 3. Main morphological characteristics of *Neodeightonia* spp.

Species	*Conidial dimensions (µm)*	*Conidiogenous Cells (µm)*	*Septa number*	*Reference*
N. subglobosa	9-12 × 6-9	–	1	Phillips *et al*., 2013
N. phoenicum	14.5-24 × 9-14	–	1	Phillips *et al*., 2008
N. palmicola	17.5-24.5 × 9.5-12.5	9-20 × 3-6	1	Liu *et al*., 2010
N. licuriensis	14.6-20.5 × 8.3-11.4	8.7-16.2 × 2.3-4.4	Up to 3	This study

Commentary: *Syagrus coronata* (Mart.) Becc. is a native palm tree from the Northeast of Brazil. It occurs mainly in regions of the semi-arid climate of the Brazilian Caatinga biome. In Brazil, this palm is popularly known as "licuri", and its fruits represent an important source of food for the local people. The endocarp can be consumed fresh and can be used in the manufacture of candies and culinary oils. The fruits are also consumed by cattle, birds and wild animals. The leaves are used in the manufacturing of handicrafts and as a food source for animals (Drumond, 2007; Rufino *et al*., 2008). During the study of mycobiota associated with native plants of the Caatinga biome in the Bahia State, necrotic lesions were observed in the rachis and leaves of this palm tree that gave rise to fungal structures resembling pycnidia. Through morphological analysis, a Botryosphaeriaceae genus similar to *Diplodia* or *Lasiodiplodia* was observed. Due to the absence of reliable morphological characteristics for distinguishing genera and species, the taxonomy of Botryosphaeriaceae has long been considered confusing. However, with the advances in molecular techniques in recent years and the use of multilocus DNA sequences in phylogenetic studies, progress has been made towards resolving the taxonomic difficulties associated with this group. In this way, several new species have been identified and defined (Crous *et al*., 2006; Slippers & Wingfield, 2007; Phillips *et al*., 2008; Slippers *et al*., 2013; Liu *et al*., 2010, 2012). *Neodeightonia* is a Botryosphaeriaceae that is morphologically similar to the *Diplodia* and *Lasiodiplodia*. It can be distinguished from *Lasiodiplodia* by the absence of conidiomatal paraphyses and from *Diplodia* by the presence of conidial striations (Phillips *et al*., 2008; 2013). In the past, this genus was synonymized with *Botryosphaeria* (von Arx & Müller, 1975); however, based on morphological and multilocus phylogenetic studies, Phillips *et al*., (2008) reinstated this genus. Until now, only three species have been recognized (see Table 3), *Neodeightonia phoenicum*, *N. subglobosa* and the more recent *N. palmicola* (Phillips *et al*., 2013).

8. *Phallus ultraduplicatus* X-D Yu, Wei Lv, Shu-Xia Lv, Xu-Hui Chen, Qin Wang, **sp. nov.** **Figs 16-18**

MycoBank: MB 808324.

Genbank: KJ591584, KJ591585 (ITS); KJ591586, KJ591587 (LSU).

Etymology: The name refers to the very short indusium in this species.

Systematic placement: Basidiomycota, Agaricomycetes, Phallales, Phallaceae.

Diagnosis: *Phallus ultraduplicatus* differs from similar *Phallus* species in the combination of its pileus with apical perforation, a whitish receptacle and a very short indusium.

Holotypus: CHINA, Liaoning Province, Benxi city, Village Majia, on the ground, 20 September 2013, leg. Xiao-Dan Yu, 2794 (HMAS 253050).

Fig. 16. *Phallus ultraduplicatus* (Holotype, HMAS 253050). **A-B.** Macroscopic habit. **C.** Basidiospores. **D.** Clamp connections on exoperidial hyphae. *Bars* **A, B.** 2 cm; **C, D.** 5 µm.

Immature basidiome ovoid to subglobose, 70-80 × 80-90 mm, covered with appressed, pubescent to felted scales, salmon when young, later flesh-ocher, with whitish, long, branched rhizomorphs up to 90 mm long, 2-3 mm diam. **Mature basidiome** 190-250 mm tall. **Receptacle** cylindrical, white, somewhat expanded at the base, dry, hollow, pliant, surface reticulate with deep or shallow lacunose. **Pileus** conical 40-50 mm high; apex perforate, 3-5 mm diam., strongly reticulate and white under the gleba. **Gleba** brownish olive to dark greenish olive, gelatinous. **Odor** strong, unpleasant. **Indusium** 20-40 mm long, fragile, white, with polygonal pores becoming gradually smaller from top to bottom, margin entire. **Volva** gelatinous, with outer surface flesh-ocher, the base whitish and with whitish, long, branched rhizomorphs.

Basidiospores 4.0-5.0 × 1.5-2.0 µm, Q = 2.4, oblong, smooth, thin-walled, hyaline, inamyloid. **Basidia** not observed. **Exoperidium** composed of interwoven hyphae 3-9 µm diam., cylindrical, hyaline, thin-walled, not gelatinous. **Indusium** composed of globose or subglobose cells, hyaline, thin-walled, 10-12 × 15-20 µm diam. **Stipitipellis** cells 22-25 × 25-28 µm diam., globose or subglobose, hyaline, thin-walled. **Clamp connections** observed only on exoperidial hyphae, absent elsewhere.

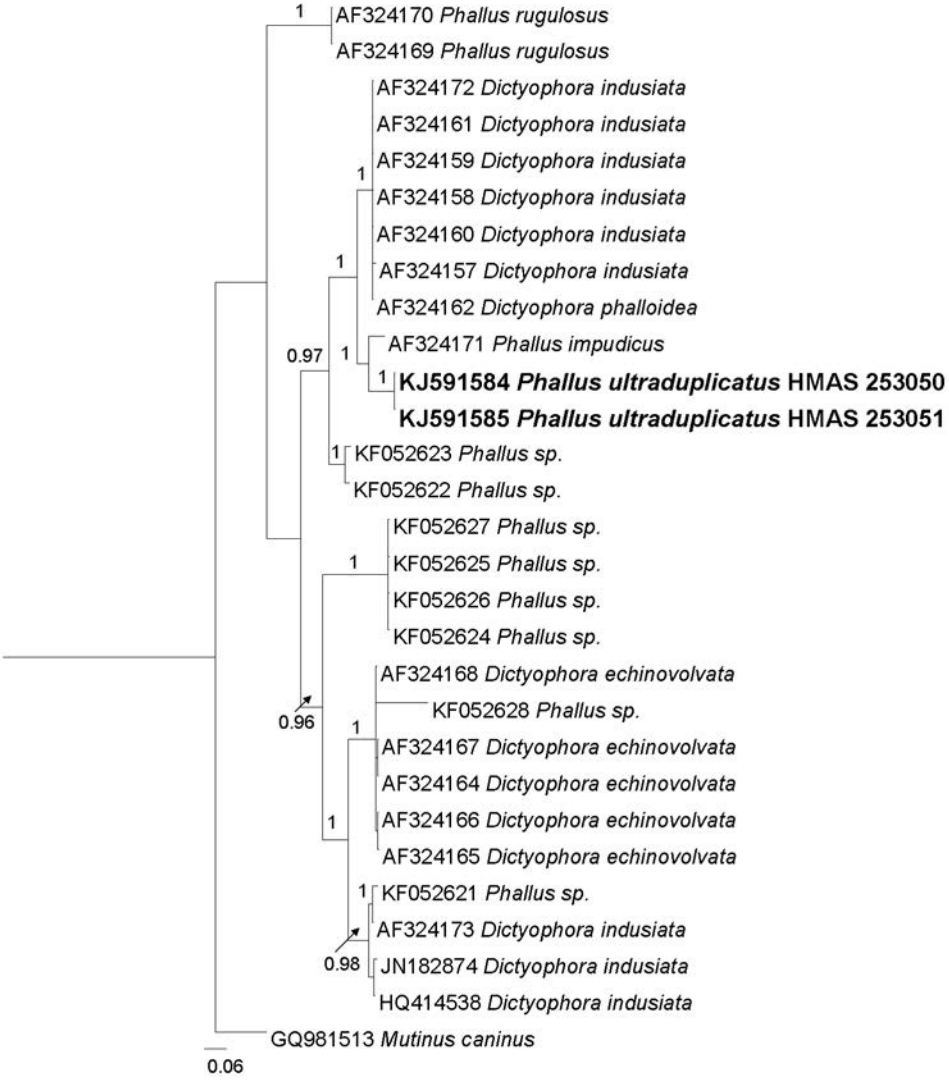


Fig. 17. Fifty-percent majority-rule Bayesian cladogram of *Phallus* produced from ITS sequence analysis with new sequences in bold. Bayesian posterior probabilities > 0.95 are indicated on the branches. Based on the results of Hosaka *et al*. (2006), the sequences of the genus *Mutinus* were used as outgroup. The GTR model was chosen as the best-fitting model of sequence evolution using MrModelTest v. 2.2 (Nylander, 2004). Bayesian analysis was run for 2,000,000 generations under a GTR model with four chains, and trees were sampled every 100 generations. The average split frequencies were checked to determine the optimal convergence of the chains below 0.01 after 2,000,000 generations. The first 500 trees were designated as burn-in, and the remaining samples were retained for further analyses. The topologies were used to generate a 50% majority rule consensus tree for Posterior Probabilities (PP). Alignments have been deposited in TreeBASE (http://purl.org/phylo/treebase/phylows/study/TB2:S15551). Primers ITS5/ITS4 (White *et al*., 1990) were used for amplification of the ITS region (including ITS1, 5.8S, and ITS2).

Specimens examined: CHINA, Liaoning Province, Benxi city, Village Majia, on the ground under broadleaf trees (*Juglans cathayensis*), 20 September 2013, leg. Xiao-Dan Yu 2794 (Holotype, HMAS 253050). *ibid.*, Village Shenjia, 7 September 2013, leg. Hong-Bo Guo 3858 (HMAS 253051).

Commentary: The infrageneric taxonomy of *Phallus* Junius ex L. is based on the shape and surface configuration of the pileus, and on the color of receptaculum, volva and mycelial strands (Kreisel, 1996). The presence or absence of the indusium was believed to be important for distinguishing between the genera *Dictyophora* Desv. and *Phallus* (Cunningham, 1944; Liu *et al*., 2005). However, Kreisel (1996) believed that species with or without indusium may be closely related and suggested that *Dictyophora* species should belong to the genus *Phallus sensu lato.* Kirk *et al*. (2008) accepted Kreisel's interpretation and listed *Dictyophora* as a synonym of *Phallus* including 18 species and a worldwide distribution (Kirk *et al*., 2008).

Kreisel (1996) divided the genus *Phallus* according to morphological criteria into five subgenera: *Aporophallus*, *Itajahya*, *Endophallus*, *Satyrus*, and, finally, subgenus *Phallus* which was again subdivided in five sections: *Granophallus*, *Clautriavia*, *Flavophallus*, *Dictyophora*, and *Phallus*. *Phallus ultraduplicatus* should be a member of the subgenus *Phallus* sect. *Phallus* based on its whitish receptaculum, volva, and presence of mycelial strands. The classification system of Kreisel (1996), however, was not supported by our molecular data and both the ITS and LSU sequence analyses (Figs 17-18) showed that the species of subgenus *Phallus* sect. *Dictyophora* and sect. *Phallus* did not form separate clusters, which was consistent

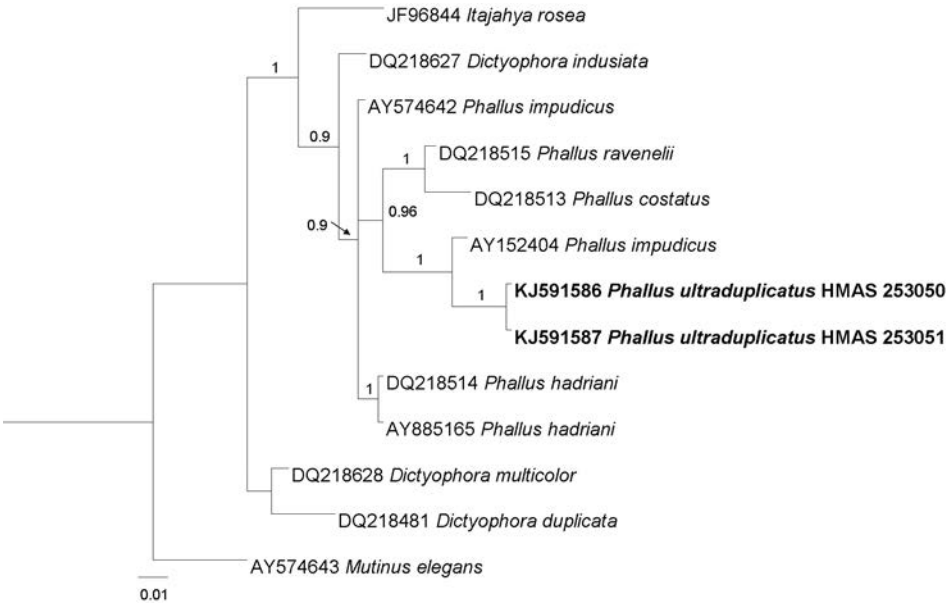


Fig. 18. Fifty-percent majority-rule Bayesian cladogram of *Phallus* produced from LSU sequence analysis with new sequences in bold. Bayesian posterior probabilities > 0.95 are indicated on the branches, and primers LROR/LR7 (Michot *et al*., 1984) were used for amplification of the 5' end of the 25S rRNA. Amplification reactions were performed in a PCR Amplifier (BIO-RAD S1000, Hercules, CA, USA) in 25-μL reaction mixtures. Both reaction mixtures and PCR conditions followed those in Yu *et al*. (2014).

with the results obtained by Hosaka *et al*. (2006). The indusium of *P. ultraduplicatus* is very short, vertical, and straight, resembling a "short and straight skirt", while the indusium of *Dictyophora* is long and extends outward, resembling a "princess's dress". Li *et al*. (2004) recombined and re-described *Dictyophora nanchangsis*, another species that has an incomplete veil and, therefore, seems intermediary between sect. *Dictyophora* and sect. *Phallus*. The reddish basidiome of *D. nanchangsis* is obviously distinct from the olive basidiome of our new species (Liu *et al*., 2005).

Phallus ultraduplicatus mainly differs from *Phallus impudicus* in having an obvious indusium. One of the morphological characters of *Phallus impudicus* var. *pseudoduplicatus* is the occurrence of wide polygonal meshes all over the indusium (Kreisel & Hausknecht, 2009), whereas, in the indusium of *P. ultraduplicatus*, the mesh openings become distally smaller. While *P. ultraduplicatus* is similar to *P. duplicatus* in having a short indusium, the indusium is substantially shorter in *P. ultraduplicatus* (20-40 mm) than in *P. duplicatus* (60-70 mm; Liu *et al*., 2005). The result of LSU sequence analyses (Fig. 3) also supported that *P. ultraduplicatus* and *P. duplicatus* (≡ *Dictyophora duplicata*) are two different species.

9. *Russula katarinae* Adamčík & Buyck, **sp. nov.** **Figs 19-20**

Mycobank: MB 811938.

Genbank: KP966377 holotype, KP966376 paratype (ITS).

Etymology: in honour of Katarína Adamčíková for her continuous support and understanding.

Diagnosis: differs from other north American fishy russulas by the combination of yellow-orange cap color, spores that are < 9 µm long and have mostly isolated, rather high warts, and rather poorly differentiated, more or less subcylindrical hyphal terminations near the cap margin with a terminal cell that is distinctly longer than the cell just below. The presence of yellow-pigmented hyphae in the pileipellis and a weak reaction of pileocystidia to sulfovanillin are other characters that distinguish our species.

Holotype: UNITED STATES. New York. Albany Co. South Bethlehem, close to the SUNY Cortland, Robert Brauer Memorial Field Research Station,, in northeastern mixed forest under *Pinus strobus*, 21 Sept. 2003, Buyck 03.159 (holotype, PC).

Cap 48-54 mm in diam., surface indistinctly striated on margin at maturity, not viscose not even when wet, shiny near the margin and pruinose in the centre, convex and nearly plane in the center, regular, cuticle separable to ¾ cap radius, orange to orange yellow or light yellow (3A4-3A6) to darker yellow (4A5-8), near margin also pale yellow (2A3-2A4). **Stipe** 43-53 × 10-16 mm, central to slightly eccentric, subcylindrical and somewhat wider near the base, white, becoming dirty brown with age or on handling, spongy within. **Gills** rather dense, equal, with some furcations near the stipe insertion, adnexed or adnate, 5-6 mm wide, ochraceous yellow (more brownish than 4A4). **Flesh** at first almost white, with age or when cut turning brown with some dirty greyish tinges, with $FeSO_4$ on stipe rapidly dirty greyish green. **Taste** mild. **Odor** becoming clearly fishy at maturity and even stronger so when cut or drying. **Spore print** insufficient, distinctly colored (cream to ochre?).

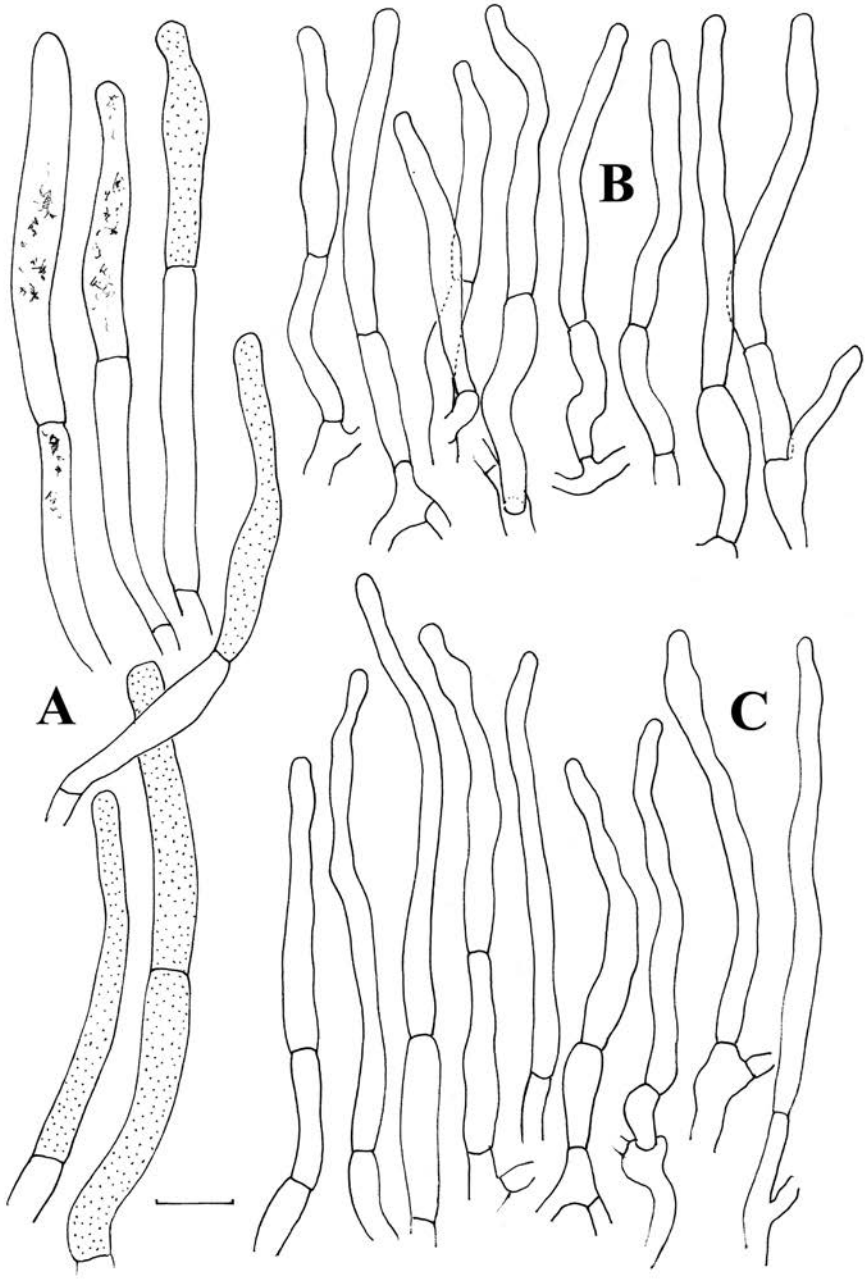


Fig. 19. *Russula katarinae* (holotype). **A.** Pileocystidia. **B.** Hyphal terminations near the pileus center. **C.** Hyphal terminations near the pileus margin. Cystidial contents as observed in Congo Red or indicated schematically. Scale bar = 10 µm.

Spores (7.1-)7.6-8.1-8.5(-9) × (6-)6.3-6.7-7.1(-7.3) µm, Q = (1.13-)1.15-1.21-1.26(-1.33), ornamentation formed of relatively distant, obtuse, amyloid warts [4-6 in a 3 µm circle on spore surface], 0.8-1.2 µm high, mostly isolated but occasionally connected by a few short and fine lines [0-1(-2) line connections in the circle] or fused in pairs or small groups [0-2 fusions in the circle]; suprahilar spot amyloid, large. **Basidia** (37-)45-50-55.5(-60) × 11-13-14(-15.5) µm, 4-spored, clavate-pedicellate; basidiola first cylindrical, utriform or ellipsoid, then clavate. **Subhymenium** pseudoparenchymatic. **Lamellar trama** mainly composed of large sphaerocytes. **Hymenial cystidia** (62-)68-77-85(-99) × 9-10.5-11(-12) µm, moderately numerous [ca 1000/mm^2] on gill sides, fusiform or clavate, pedicellate, with acute or rarely obtuse apices, occasionally mucronate, with thin- to slightly thickened walls (< 0.5 µm), contents granulous or banded and weakly graying in sulfovanillin. **Marginal cells** (15-)20-27-33(-37) × (2-)3.5-5-6 µm and mixed with numerous smaller cheilocystidia, very variable in shape, often flexuous and moniliform, sometimes mucronate, rarely nodulose. **Pileipellis** orthochromatic in Cresyl blue, well delimited from the underlying sphaerocytes of the context, ca. 150-170 µm deep, vaguely divided in 100-120 µm deep, strongly gelatinized suprapellis of ascending, near the surface aeriferous hyphae gradually passing into a more dense, ca. 50-60 µm deep subpellis of intricate, horizontally oriented, 2-4 µm wide hyphae. Incrustations absent. Hyphal terminations arising from an underlying dense tissue of intricate hyphae, bearing often yellow refringent contents and intermixed with pileocystidia; terminal cells of hyphae near the cap margin measuring (21-)26.5-35.5-44.5(-62)×(3-)3.5-4.2-5(-7.5) µm, mostly subcylindrical, occasionally clavate or attenuated, sometimes apically constricted to moniliform, towards the cap center narrower and more often apically constricted to slightly mucronate, measuring (20.5-)32-45-58(-69) × 2.5-3-3.5(-4) µm; subterminal cells usually distinctly shorter, equally wide, branching. Pileocystidia narrowly clavate or subcylindrical, occurring mostly in dispersed fascicules near the surface of the pileipellis, thin-walled, 1(-2)-celled, terminal cells measuring (34-)39.5-50-60(-72) × (4.5-)5-5.8-6.5(-7) µm, containing at the most a few scattered, granular to banded inclusions that hardly react in sulfovanillin. Cystidioid hyphae in subpellis and trama absent. **Clamp connections** absent.

Additional material examined: UNITED STATES. New York. Albany Co. South Bethlehem, close to the SUNY Cortland, Robert Brauer Memorial Field Research Station, in north eastern mixed forest under *Pinus strobus*, 20 Sept. 2003, Buyck 03.124 (paratype, PC0124383); West Virginia. Monroe Co., Moncove Lake State Park, 21 Aug. 2003, Donna Mitchell WV1047 (DEWV4801).

Commentary: *Russula* subsect. *Xerampelinae* Singer is well defined by its fishy smell (hence their name of "fishy russulas"), the typical grey-green discoloration of the flesh with iron sulphate and a context that is browning or sometimes also slightly greying, particularly in the stipe. In recent years, Buyck and Adamčík have been undertaking a revision of all types of native American *Russula* (Adamčík & Buyck, 2014; Buyck & Adamčík, 2013b), including over 20 species that were either suspected to belong in *Xerampelinae* or that had, at one time or another, been classified in this subsection (Adamčík & Buyck, 2010, 2011; Adamčík *et al.*, 2010; Buyck & Adamčík 2011, 2013a; Buyck *et al.*, 2008). As a result of these revisions, a key was finally published accepting a total of 10 North American species that they accepted as good species in *Xerampelinae* (Buyck & Adamčík, 2013b), thereby creating a sound and solid basis for the correct application of existing names and the future description of new taxa. Many species of this subsection have caps that come predominantly in (often dark) shades of wine red, violet, brown

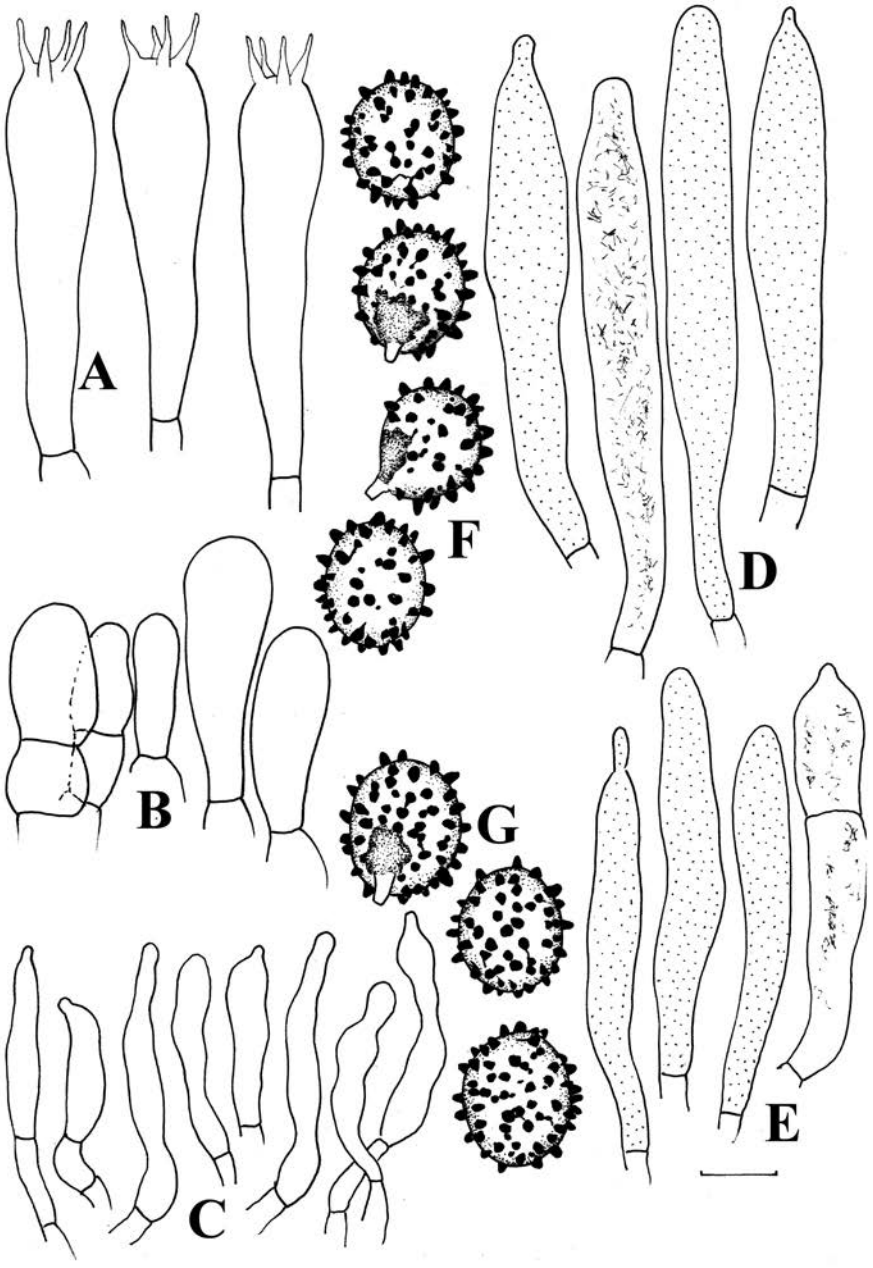


Fig. 20. *Russula katarinae* (holotype). **A.** Basidia. **B.** Basidiola. **C.** Marginal cells of the gill edge. **D.** Hymenial cystidia on gill sides. **E.** Hymenial cystidia near the gill edge. **F-G.** Spores as seen in Melzer's reagent (F. holotype; G. paratype). Cystidial contents as observed in Congo Red, but most elements with contents indicated schematically. Scale bar = 10 μm, but only 5 μm for spores.

to green tints, whereas another group of fishy russulas has predominantly bright red, orange to yellow colored caps. With its beautiful, yellow-orange cap, *R. katarinae* belongs clearly in the latter group, which comprises also the bright red *R. fucosa* Burl., the red to orange *R. levyana* Murrill and *R. pinophila* Murrill (Looney 2015) and the yellowish *R. ochrifloridana*. The latter three are clearly southern species, originally described from Florida (Adamčík & Buyck 2010; Adamčík *et al.*, 2010), whereas the former two have more northern distributions.

Fishy russulas are locally highly reputed as good edibles as their flesh is firm and the fishy odor disappears when cooking, yet they are infamous among taxonomists because of the apparently infinite variation and amplitude in color and their other features. As a result, many past mycologists have reduced the subsection to a single species: "*R. xerampelina sensu lato*". Beardslee (1918), who also adhered to this wide concept, was the first to discuss the existence of an orange form of *R. xerampelina* in the United States: "*A curious form of this species, which seems not to be common, is found in our pine woods. It varies from orange to yellow, and it is so distinct in appearance that it is hard to believe that it is the same as our red and purple forms*." Also Kibby & Fatto (1990) mentioned an orange fishy russula in their key to Northeastern Russulas and they called it *R. barlae* Quél. This European species remains, however, a dubious taxon as its protologue lacks any typical character for the subsection (see discussion in Adamčík 2004) and it would, therefore, be best to avoid the use of this name, even more so in case of an American taxon.

Besides the typical orange cap color of our species, additional features that define our species are microscopical, in particular the combination of these two: (1) spores are < 9 µm long and have mostly isolated warts, and (2): hyphal terminations near the cap margin are rather poorly differentiated and more or less subcylindrical with a terminal cell that is distinctly longer than the one just below. In addition, we can mention the presence of yellow-pigmented hyphae in the pileipellis, as well as the weak reaction of its pileocystidia to sulfovanillin. Nevertheless, compared to the other red to yellow fishy russulas described from the Eastern USA, the microscopical characters are quite similar and only the rare, southern and pale *R. ochrifloridana* is easily distingued because of its much lower spore ornamentation of denser and more interconnected warts and somewhat longer spores (average Q = 1.33). The red, often rapidly discoloring *R. levyana*, on the other hand, has a very similar spore ornamentation of equally high warts, although these are more interconnected, but the terminal cells in the cap are not considerably longer as is the case in our species. Furthermore, *R. levyana* seems to be a relatively common, southern species that is exclusively associated with three-needle pines (and not five-needle *Pinus strobus* as *R. katarinae*). Finally, the intensely red, velvety caps of *R. fucosa* may become very similar in color to our species when the cap discolors due to age or bad weather conditions and both species occur in the same area. Both species also share identical spores and even very similar hyphal terminations near the cap margin. However, in *R. fucosa* the terminal cells become shorter and more inflated toward the cap center, not narrower such as in our species.

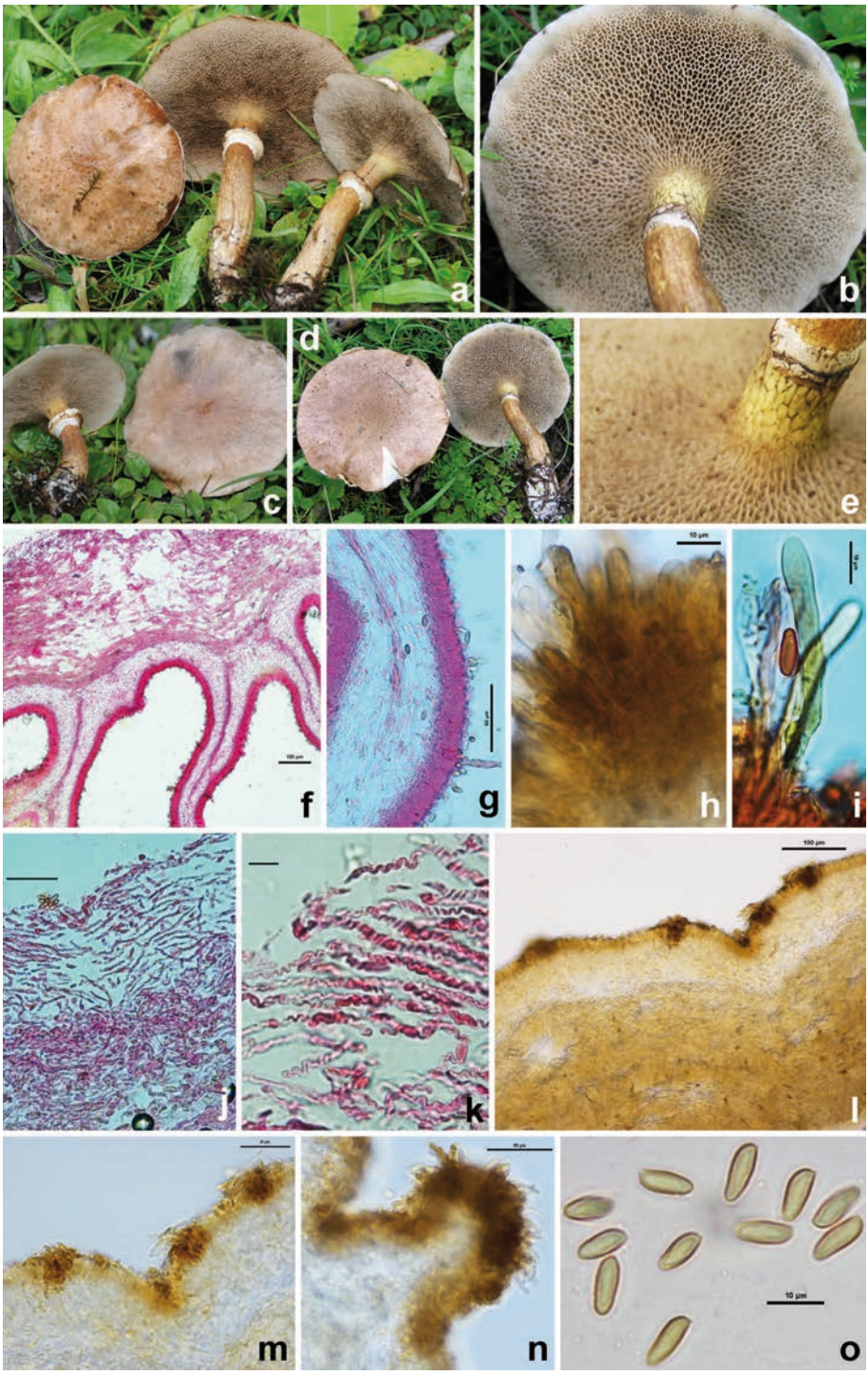
Finally, the *R. xerampelina* group is also quite difficult genetically speaking. Compared to russulas from other subsections, such as *Virescentinae* for example, where species are showing very high mutation rates in the ITS region that make it easy to distinguish between them, fishy russulas possess very similar ITS sequences. A 97% threshold for species delimitation, as used in many environmental papers for example, would probably not correspond to the reality. In the absence of sufficient, representative sequences for *Russula* subsection *Xerampelinae* in GenBank, a

phylogenetic analysis is presently impossible without a serious sequencing effort for the group as a whole. We therefore simply provided here ITS sequences for holo- and paratype.

10. *Suillus lariciphilus* K. Das, D. Chakr., K.P.D. Latha & Cotter, **sp. nov.**
Figs 21-23

MycoBank: MB 808779.
GenBank: KJ778009.
Systematic position: Basidiomycota, Agaricomycetes, Boletales, Suillaceae
Etymology: growing always in association with *Larix,* i.e. *Larix*-loving.
Diagnosis: distinct from allied taxa by the following combination of characters: persistent superior annulus on the stipe; white pileus context becoming yellowish white or pale orange to darker when young, but brownish at maturity and mostly with pale lavender tinges over the tubes that turn olive brown to olive gray brown with $FeSO_4$, light brown to pink orange with KOH, light brown without halo with NH_4OH; a yellowish white to light yellow stipe context but sometimes mustard yellow at base, mostly becoming brownish on exposure; pileus surface turning olive or bright green then brown with KOH; non-encrusted cystidia; ixocutis type of pileipellis.
Type: INDIA-SIKKIM, North District, Dombang, 2890 m, N27°44'07.0" E88°44'38.0", under *Larix griffithiana* Carrière, subalpine mixed (coniferous and broad leaf) forest, 23 July 2013, *K. Das*, KD 13-003 (holotype CAL).

Pileus 30-105 mm. diam.; convex when young, becoming broadly convex to plano-convex at maturity; surface wet, viscid to glutinous, shiny, glabrous, smooth, often with some minute scales at center, mostly darkest at center gradually becoming paler towards margin, when young brown to dark brown (6-7E-F8) over pale orange (5A3) base color which in button shows though only at margin or sometimes with yellowish white margin, when mature usually with light brown to brown (6D-E5-6)/(7D-E7) at centre, becoming paler to 4A2 or pale orange (5A3) margin with a base color of pale orange (5A3) to grayish orange (6B4) at centre becoming paler to yellow white at margin, ± indistinct pattern of radiating dark fine veins becoming bluish when bruised; margin mostly incurved often with a narrow to broad irregularly interrupted flap of sterile white to yellowish white tissue (veilar remnant). **Pore surface** white to yellowish white (1A2), gradually yellowish white to pale yellow (3-4A2-3) to grayish orange 5B3 with unchanging (1A2) margin, then becoming more darker to brownish orange (5C4) or grayish brown to dark blond (5D3-4) at maturity, changing in all stages when bruised, insignificant when young but gray-brown to gray or blue-gray when mature; pores 1-2/mm, compound, angular. **Tubes** 5-7 mm long, decurrent, concolorous to pore surface or paler. **Stipe** 55-100 × 7-14 mm, central, cylindric-clavate, becoming gradually broader towards the somewhat bulbous base, with a persistent superior annulus which is whitish to yellowish white when young often with a narrow brown strip at the apex and with a distinct brown reticulum over the yellow background above annulus. **Context** solid in pileus and stipe; pileus white, becoming yellowish white (3A2) or pale orange (5A3) to darker when young but brownish when mature and mostly with pale lavender tinges over the tubes, turning olive brown to olive gray brown with $FeSO_4$, light brown or pink orange with KOH, light brown with no halo with NH_4OH; stipe yellowish white to light yellow (3A2-5) and sometimes mustard yellow at base,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mostly becoming brownish on exposure. **Pileus surface** turning pale gray to light gray with $FeSO_4$, olive or bright green then brown with KOH, slowly greenish then olive without halo with NH_4OH. **Odor** indistinct or fungoid. **Taste** mild. **Spore print** light brown (6D4) to brown (6-7E6) or even darker reddish cinnamon.

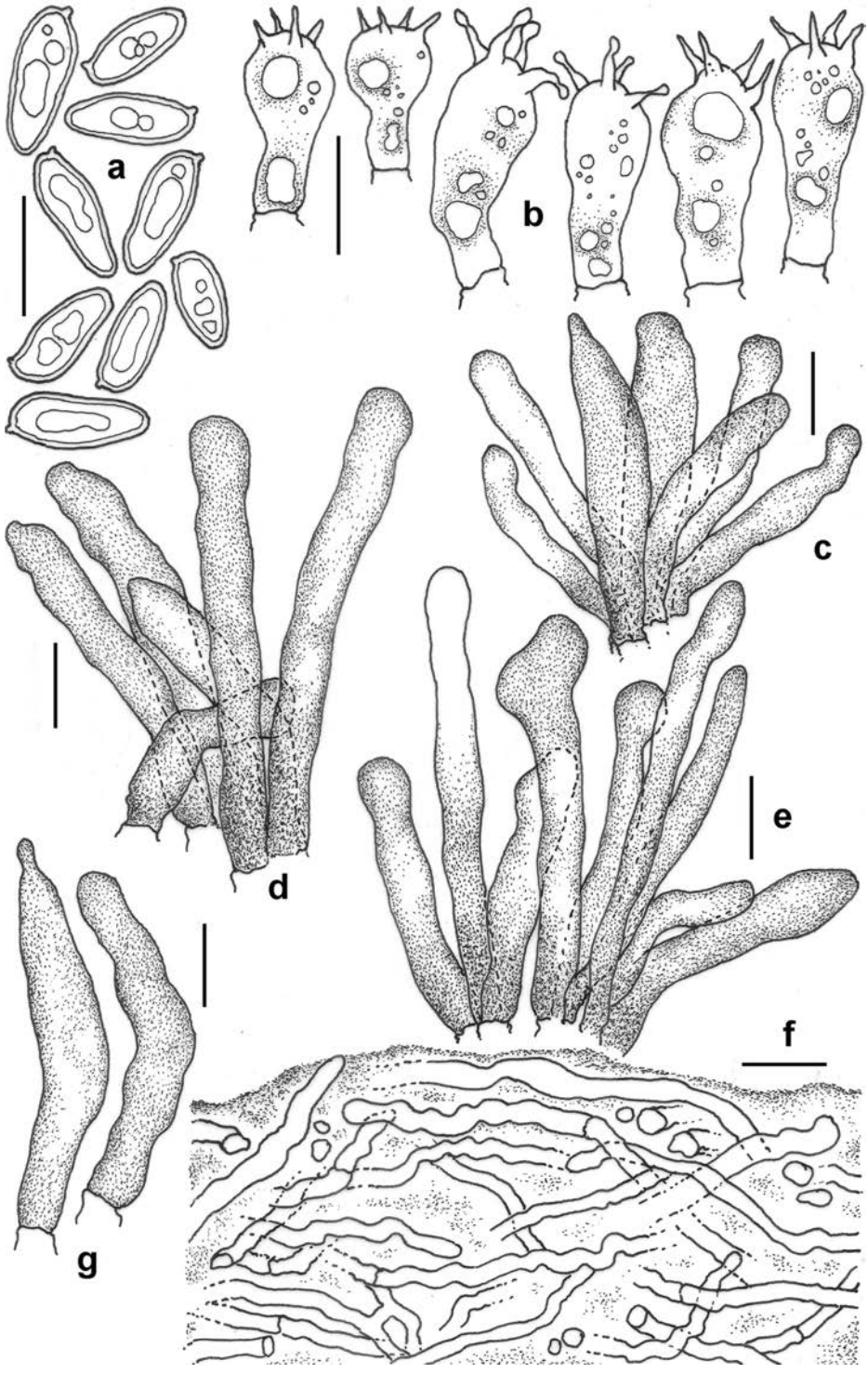
Basidiospores 7.8-*10.7*-12.5 × 3.5-*4.0*-5.0 µm (n = 20, Q = 2.0-*2.68*-3.0), ellipsoid to weakly subfusiform, smooth elliptic, dextrinoid, smooth, light yellow brown in KOH. **Basidia** 15-31 × 5-9.5 µm, clavate, 4-spored; sterigmata 3-5 × 1-2 µm, septa without basal clamp. **Tube edge** fertile. **Pleuro-** and **cheilocystidia** 28.5-71 × 5.5-9 µm, solitary, scattered or in clusters of 2-11, cylindrical to clavate with rounded to subcapitate or hammer-headed apex, content clear or dense, grainy, with brown pigmentation, without any incrustations. **Hymenophoral** trama divergent. **Pileipellis** 120-140 µm thick, an ixocutis composed of parallel to interwoven, 3.0-9.5 µm wide hyphae (often twisted) submerged in a thin, gelatinized layer. **Pileus trama** of hyaline, up to 14.5 µm broad, interwoven, septate hyphae. **Stipitipellis** 90-110 µm thick, two-layered. **Suprapellis** fertile, composed of numerous basidia, basidioles and cystidia growing single or in clusters; caulobasidia 11-21 × 7-10 µm, clavate to subclavate or oval, 4-spored; caulocystidia 21-69 × 5-8 µm, cylindric to narrowly clavate or ventricose with rounded, appendiculate or rarely hammer-headed apex, content mostly dense with brown pigmentation. **Subpellis** composed of loosely arranged branched septate hyphae, measuring 4-6 µm wide. **Clamp connections** absent in all parts.

Cultures obtained from pileus trama slowly growing, generally less than 30 mm in 4 weeks. Colony height variable, usually greater than 4 mm and cottony, with growth into agar less than 5 mm. Colony surface brilliant white ± light brown hues (5-6D-E5) or mottled white, gray yellow (4B-C3-4) and brown orange (5C-D3-4) ± overlaid with white with a white to brown white margin. Colony reverse center orange brown to brown to purple brown, sometimes dull yellow, middle brown mottled with orange and yellow or purple or orange white, margin of reverse white to yellow white ± brown hues. No pigment diffused into agar. Radial furrows and irregular wrinkling of colony surface well developed at week 4 and can be observed from the colony surface or reverse. Gum guaiac and syringaldazine spot tests both positive. No clamps observed. Hyphal strands present.

Specimens examined: INDIA-SIKKIM, North District, Dombang, 2890 m, N27°44'07.0" E88°44'38.0", under *Larix griffithiana*, subalpine mixed (coniferous and broad leaf) forest, 23 July 2013, *K. Das*, KD 13-003 (holotype CAL); NEPAL, Rasuwa District, Langtang National Park, 3070 m, under *Larix himalaica W.C.Cheng* & *L.K.Fu*, 6 Aug. 1985, H.V.T. Cotter, VC 1231 (KATH, NY); ibid., Langtang National Park, 3020 m, under *L. himalaica*, 9 Oct. 1985, H.V.T. Cotter, VC 1438 (KATH, NY); ibid., Langtang National Park, 3140 m, under *L. himalaica*, 11 Oct. 1985, H.V.T. Cotter, VC 1450 (NY).

Commentary: *Suillus lariciphilus* fruits in the subalpine Himalaya of Sikkim (India) and Nepal in association with *Larix griffithiana* and *L. himalaica* and is presumed to be ectomycorrhizal with these conifers. Apart from its association with

◀ Fig. 21. *Suillus lariciphilus* sp. nov. (KD 13-003, holotype). **a, c, d.** Fresh basidiomata in the forest floor. **b.** Pore surface. **e.** Reticulum on stipe surface. **f.** Divergent hymenophoraltrama. **g-i.** Cystidia (single or in clusters) in tube. **j-k.** Ixocutis pattern of pileipellis showing hyphae in twisted pattern. **l-m.** Stipitipellis showing basidia and several cystidial clusters. **n.** Caulocystidia in cluster on the elevated part of reticulum of stipitipellis. **o**. Basidiospores. Scale bars: f & l = 100 µm; g, j, m & n = 50 µm; h, i, k, o = 10 µm.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Larix, it is distinct by its unique combination of macro- and micromorphological characters (see diagnosis above).

In a megablast search of NCBI's GenBank nucleotide database using the ITS sequence from the holotype of *S. lariciphilus*, the closest hit was a collection labelled as *Suillus* cf. *laricinus* (GenBank L54120; Identities = 574/580 (99%), Gaps = 0/580 (0%)) followed by the other *Larix*-associated *Suillus* species at 97% similarity and lower. Subsequent molecular analysis yielded a phylogenetic tree (Fig. 21) that revealed a strongly supported monophyletic clade (95% bootstrap support) comprising the present species, *S. lariciphilus* together with seven other species of *Suillus*, all of them associated with *Larix*. Our species is sister to *Suillus* cf. *laricinus* with 97% bootstrap support. Based on the 99% similarity of the ITS and the geographical factor, the latter specimen identified as *S.cf. laricinus* and originally collected by Cotter (1987) in Nepal, is here considered as conspecific.

The other species of *Suillus* that have been reported in the literature as being associated with the same host genus are from Europe or America: *S. grevillei* (Klotzsch) Singer, *S. tridentinus* (Bres.) Singer, *S. viscidus* (L.) Roussel (= *S. laricinus* (Berk.) Kuntze fide Breitenbach & Kränzlin 1991, Kretzer *et al.*, 1996, www.speciesfungorum.org), *S. spectabilis* (Peck) Kuntze, *S. grisellus* (Peck) Kretzer & T.D. Bruns, *S. serotinus* (Frost) Kretzer & T.D. Bruns and *S. bresadolae* (Quél.) Gerhold.

Suillus laricinus and *S. serotinus* can be well distinguished from *S. lariciphilus* by the context turning greenish to bluish on exposure, at least initially. Moreover, *S. laricinus* has an ochraceous pileus dotted with gray-black squamules, a context turning bluish green on exposure, a faintly aromatic odor, encrusted cystidia and an ixotrichoderm type pileipellis (Breitenbach & Kränzlin, 1991; Phillips, 2006; Bessette *et al.*, 2010). *Suillus serotinus* has a chocolate-colored to reddish brown gluten on its pileus and a context that finally becomes reddish brown after long exposure (Smith & Thiers, 1971; Bessette *et al.*, 2010). The European *S. bresadolae* can be distinguished from *S. lariciphilus* by the vivid yellow color of its inner veil (Gerhold, 1985). *Suillus spectabilis* has a pinkish red to orange-red pileus and a yellow context that slowly turns pinkish then brown on exposure and it produces considerably larger basidiospores (9-15 × 4-6.5 µm, fide Bessette *et al.*, 2010). In *S. grevillei*, tubes and pore surface are yellow and the pileus yellow to orange-brown (Knudsen & Vesterholt, 2012), while in *S. tridentinus*, tubes and pore surface are orange and the pileipellis is of a trichoderma-type (Breitenbach & Kränzlin, 1991; Knudsen & Vesterholt, 2012). *Suillus grisellus* can be separated from the present species by whitish to pale olive or olive-grey pileus and a context that turns immediately bluish gray with $FeSO_4$ and pale pink with NH_4OH (Bessette *et al.*, 2010).

Other *Suillus* species reported from the Himalayan area are *S. luteus* (L.) Roussel, *S. sibiricus* (Singer) Singer, *S. bovinus* (L.) Roussel, *S. granulatus* (L.) Roussel and *S. placidus* (Bonord.) Singer (Adhikari, 2000), and none of them are found under *Larix* (Lakhanpal, 1996; Das, 2009). Both *S. luteus* and *S. sibiricus* have distinct glandular dots on the stipe surface, whereas *S. bovinus*, *S. granulatus* and *S. placidus* can easily be distinguished from *S. lariciphilus* as they lack the annulus on the stipe. Also the two recently described species, *S. indicus* B. Verma

◀ Fig. 22. *Suillus lariciphilus* sp. nov. (KD 13-003, holotype). **a.** Basidiospores. **b.** Basidia. **c.** Pleurocystidia in cluster. **d, e.** Cheilocystidia in clusters. **f.** Pileipellis of ixocutis pattern. **g.** Single pleurocystidia in tube. Scale bars: a-g = 10 µm.

& M.S. Reddy and *S. himalayensis* B. Verma & M.S. Reddy, differ in host association, growing with *Cedrus* or *Pinus*. Moreover, in *S. indicus* tubes and pore surface are yellow to brownish yellow and the stipe surface has glandular dots, whereas *S. himalayensis* has a yellowish white to pale yellow pileus with grayish green tinge, pale yellow context that turns grayish green after bruising (Verma & Reddy, 2014a & b).

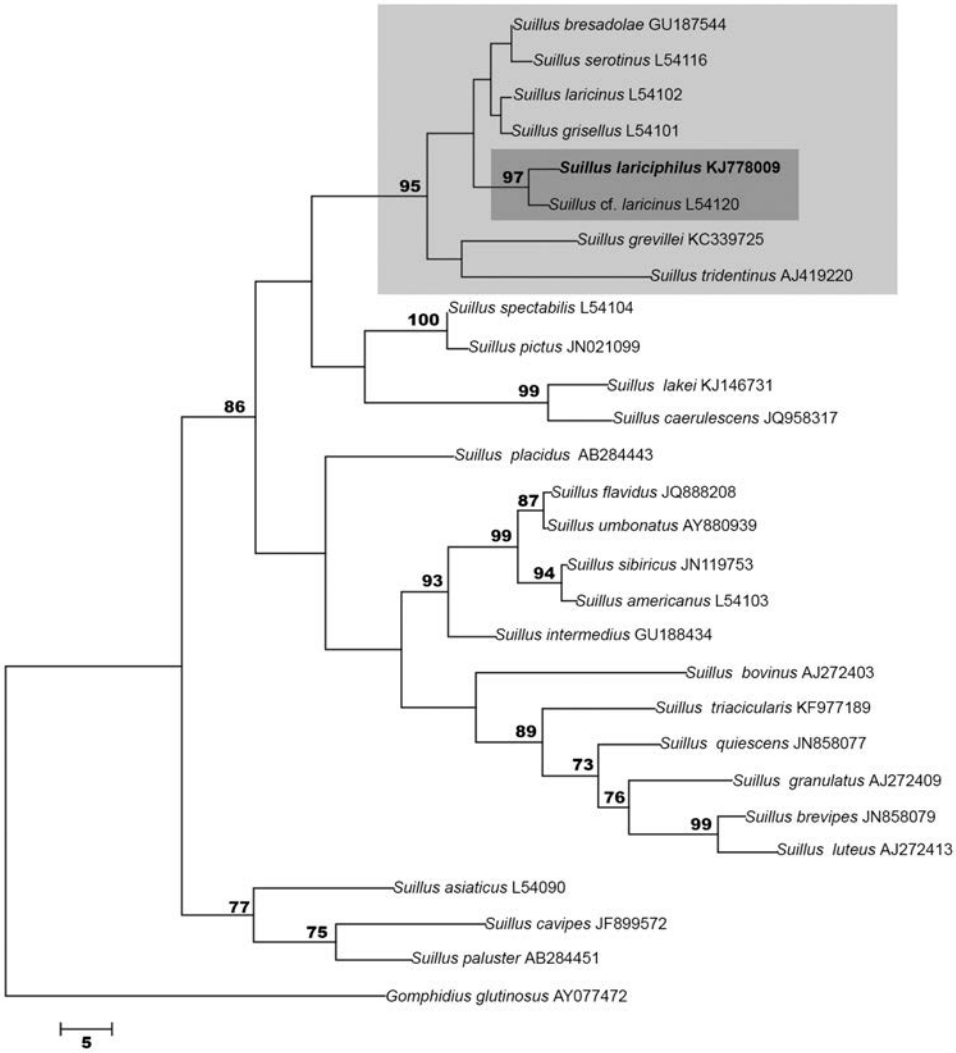

Fig. 23. The phylogenetic tree of *Suillus lariciphilus* constructed with a Maximum Parsimony (MP) analysis using ITS rDNA sequences by running *MEGA* v.5 (Tamura *et al*., 2011). *Gomphidius glutinosus* (Schaeff.) Fr. (AY077472) is the outgroup taxon (Kretzer *et al*., 1996). Bootstrap support values > 70% are given above branches. The phylogenetic position of *Suillus lariciphilus* (KD 13-003, holotype) is indicated in bold font. GenBank accession numbers are given after the name of each taxon. TreeBase no. (http://purl.org/phylo/treebase/phylows/study/TB2:S17056).

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