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What is the radicate *Oudemansiella* cultivated in China?

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Abstract

A radicate *Oudemansiella* species, called “Heipijizong” or “Black Termite Mushroom”, has been widely cultivated in China in the past few years. It was regarded as either the European *O. radicata* or the North American *O. furfuracea* or even species of *Termitomyces*. This study aims to clarify the taxonomic position of this economically important mushroom. Phylogenetic analyses of “Heipijizong” and other related *Oudemansiella* species were carried out using ITS and nrLSU ribosomal RNA gene regions. Based on both morphological and molecular data, “Heipijizong” was identified as *Oudemansiella raphanipes*. Our study indicated that *O. raphanipes* possesses both 2-spored and 4-spored basidiomata. Detailed morphological descriptions and illustrations are provided for it.

Key words: Agaricales, edible mushroom, Physalacriaceae, taxonomy

Introduction

In the last few years, a new edible mushroom, commercially called “Heipijizong” or “Black Termite Mushroom”, has been widely cultivated in many parts of China (Li *et al.* 2012, Sun *et al.* 2016). “Heipijizong” was identified as *O. furfuracea* (Peck 1893: 91) Zhu L. Yang *et al.* (2009: 7) (Yu *et al.* 2002), *O. radicata* (Relhan 1786: 28) Singer (1936: 333) (Ji *et al.* 1982, Shim *et al.* 2006, Wu *et al.* 2013), *Termitomyces fuliginosus* R. Heim 1942: 147 (Li *et al.* 2012) or *T. badius* Otieno 1969: 161 (Sun *et al.* 2016). Although the radicate stipe of this species is somewhat similar to those of Termite Mushrooms, it belongs in fact to the genus *Oudemansiella* Spegazzini (1881: 24) rather than *Termitomyces* R. Heim (1942: 147).

The species *O. furfuracea* [as *Collybia radicata* var. *furfuracea* Peck (1893: 91)] and *O. radicata* [as *Agaricus radicatus* Relhan (1786: 28)] were originally described from North America and Europe respectively (Relhan 1786, Peck 1893, Petersen & Hughes 2010). Recent data indicated that many North American or European species of agarics, no matter saprophytic or mycorrhizal, do not occur in East Asia (Zeng *et al.* 2013, Zhao *et al.* 2013, Cai *et al.* 2014, Qin *et al.* 2014a, Cui *et al.* 2016). Petersen & Hughes (2010) also pointed out that *O. furfuracea* is restricted to eastern North America while *O. radicata* could only be found in Europe. The species of *Termitomyces* differ from the fungus “Heipijizong” significantly (Heim 1977).

In this study, cultures and specimens (including wild and cultivated basidiomata) of “Heipijizong” and its allied species are phylogenetically and morphologically studied in order to clarify the phylogenetic position and taxonomy of “Heipijizong”.

Materials and methods

Specimens and morphological descriptions

The macro-morphological descriptions are based on the field notes, and documented by photographs. Color codes of

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the form "5F6", indicating the plate, row, and color block respectively (Kornerup & Wanscher 1981). Specimens were deposited in the Herbarium of Cryptogams, Kunming Institute of Botany, Chinese Academy of Sciences (HKAS). The micro-morphological data were obtained from the dried specimens after sectioning and mounting in 5% KOH solution. All microscopic features were drawn by free hand. In the descriptions of basidiospores, the abbreviation [n/m/p] indicates that the measurements were made on 'n' basidiospores from 'm' basidiomata of 'p' collections; Dimensions of basidiospores were presented in the following form (a) b–c (d); in which 'b–c' contains a minimum value of 90% and extreme values 'a' and 'd' are kept in parentheses; Q is used to mean "length/width ratio" of a spore in side view; **Q** means average Q of all basidiospores ± sample standard deviation.

DNA extraction, PCR and sequencing

Genomic DNA was extracted from materials dried with silica gel or living cultures, using the modified CTAB method (Doyle & Doyle 1987). The nucleotide rDNA regions encompassing the internal transcribed spacers 1 and 2, along with the 5.8S rDNA (ITS) and the D1–D3 domains of nuclear 28S rDNA (nrLSU), were selected for phylogenetic analyses. Universal primers pairs ITS5/ITS4 (White *et al.* 1990) and LROR/LR5 (Vilgalys & Hester 1990) were applied for the amplification of ITS and nrLSU, respectively. The PCR reactions were performed in an ABI 2720 thermal cycler (Applied Biosystems, Foster City, CA, USA), and the PCR program was as follows: pre-denaturation at 94°C for 5 min; then followed by 35 cycles of denaturation at 94°C for 50 s, annealing at 50°C (ITS and nrLSU) for 50 s, elongation at 72°C for 60 s; afterwards, a final elongation at 72°C for 8 min was included. The PCR products were depurated with the Gel Extraction & PCR Purification Combo Kit (Spin-column, Bioteke, Beijing, China), and then sequenced on an ABI-3730-XL sequence analyzer (Applied Biosystems, Foster City, CA, USA) using the same primers as those used in amplifications.

Sequence alignments and phylogenetic analyses

To understand the relationships of "Heipijizong" with its allied species in *Oudemansiella*, both ITS and nrLSU sequences of those species were retrieved from GenBank, and then combined with our newly generated sequences. *Paraxerula americana* (Dörfelt 1981: 278) R.H. Petersen (2010: 299), *Rhodotus palmatus* (Bulliard 1785: t. 216) Maire (1926: 308), *Strobilurus conigenoides* (Ellis 1876: 76) Singer (1962: 409), and *Xerula pudens* (Pers. 1801: 313) Singer (1951: 289) were selected as outgroups according to the previous phylogenetic studies (Hao *et al.* 2014, Qin *et al.* 2014b, Qin & Yang 2016) (Table 1). 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). The two datasets were then concatenated using Phyutility v2.2 for further analyses (Smith & Dunn 2008).

TABLE 1. Fungal taxa information and GenBank accession numbers of sequences used in this study.

Taxon	Voucher	GenBank Accession	
		ITS	LSU
"Cribbea gloriosa"	MEL 2313432	FJ178108	—
"C. lamellata"	MEL 21710	FJ178110	FJ178111
"Dactylosporina glutinosa"	MCA 1775	HM005074	HM005138
"D. steffenii"	TENN 58785	HM005071	HM005132
"Hymenopellis colensoi"	PDD 93362	HM005139	HM005119
"H. gigaspora"	REH 8676	GQ913357	HM005121
"H. incognita"	TENN 58768	GQ913424	HM005105
"H. limonispora"	TENN 59438	GQ913406	HM005133
"H. limonispora"	TENN 61379	GQ913403	HM005134
"H. radicata var. *bispora"*	TENN 57277	GQ913379	HM005122
"H. radicata"	TENN 62837	GQ913375	HM005125
"H. rubrobrunnescens"	TENN 52479	GQ913371	—

...Continued on next page

TABLE 1. (Continued)

Taxon	Voucher	GenBank Accession	
		ITS	LSU
"H. rubrobrunnescens"	TENN 52654	GQ913372	HM005112
"H. rugosoceps"	TENN 57307	GQ913395	HM005116
"H. rugosoceps"	TENN 60604	GQ913394	HM005117
"H. vinocontusa"	TMI 7669	GQ913370	—
"Mucidula brunneomarginata"	TENN 53020	GQ844243	HM005123
"M. mucida var. *asiatica"*	TENN 49897	GQ844238	HM005100
"M. mucida"	TENN 59324	GQ844235	HM005127
"Ponticulomyces kedrovayae"	TENN 60767	HM005146	HM005110
"P. orientalis"	HKAS 59611	KJ024102	KJ024107
"Protoxerula flavo-olivacea"	REH 8931	HM005149	HM005111
Oudemansiella apalosarca	DUKE 2875	AF321473	—
O. canarii	DUKE 4057	AF321479	AF261351
O. cubensis	TENN 51190	GQ892794	HM005114
"O. chiangmaiae" (holotype)	TENN 59791	KX964658	—
O. furfuracea	HKAS 93109	**KX688223**	**KX688250**
O. furfuracea	HKAS 59927	**KX688224**	**KX688251**
"H. furfuracea"	TENN 61671	GQ913362	HM005101
"H. furfuracea"	TENN 59876	GQ913367	HM005126
O. japonica	HKAS 61674	**KX688225**	**KX688252**
O. japonica	HKAS 83175	**KX688226**	**KX688253**
O. orientiradicata	HKAS 67938	**KX688227**	**KX688254**
O. orientiradicata	HKAS 70323	**KX688228**	**KX688255**
O. raphanipes	JBZ 2122002	**KX688229**	**KX688256**
O. raphanipes	JBZ 2122001	**KX688230**	**KX688257**
O. raphanipes	HKAS 93073	**KX688231**	**KX688258**
O. raphanipes	HKAS 95781	**KX688232**	**KX688259**
O. raphanipes	HKAS 93144	**KX688233**	**KX688260**
O. raphanipes	HKAS 75607	**KX688234**	**KX688261**
O. raphanipes	HKAS 80141	**KX688235**	**KX688262**
O. raphanipes	HKAS 95782	**KX688236**	**KX688263**
O. raphanipes	HKAS 93083	**KX688237**	**KX688264**
O. raphanipes	HKAS 95783	**KX688238**	**KX688265**
O. raphanipes	HKAS 93099	**KX688239**	**KX688266**
O. raphanipes	HKAS 95784	**KX688240**	**KX688267**
O. raphanipes	HKAS 69220	**KX688241**	**KX688268**
O. raphanipes	HKAS 71518	**KX688242**	**KX688269**
O. raphanipes	HKAS 38682	**KX688243**	**KX688270**

...Continued on next page

TABLE 1. (Continued)

Taxon	Voucher	GenBank Accession	
		ITS	LSU
O. raphanipes	HKAS 39593	**KX688244**	**KX688271**
O. raphanipes	HKAS 42391	**KX688245**	**KX688272**
O. raphanipes	HKAS 95785	**KX688246**	**KX688273**
O. raphanipes	HKAS 95786	**KX688247**	**KX688274**
O. raphanipes	HKAS 93070	**KX688248**	**KX688275**
O. yunnanensis	HKAS 93106	**KX688249**	**KX688276**
Paraxerula americana	CLO 4746	HM005142	HM005094
Rhodotus palmatus	HMJAU 6872	KC179742	KC179752
Strobilurus conigenoides	TENN 61318	GQ892821	HM005091
Xerula pudens	TENN 59208	HM005154	HM005097

. *GenBank accession numbers of sequences generated in this study are in boldface.

Maximum likelihood algorithm (ML) and Bayesian Inference (BI) analyses were performed on RAxML (Stamatakis *et al.* 2008) and MrBayes (Ronquist & Huelsenbeck 2003), based on the combined dataset (ITS-nrLSU). GTR+I+G was chosen as the best fit models for both ITS and nrLSU partitions by using Mrmodeltest2.3 (Nylander 2004). For ML analysis, all parameters were kept at their default values except for the model choice as GTRGAMMAI, and the statistical support values were calculated using 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. Subsequently, trees were summarized and statistical supports were obtained by using the sump and sumt command implemented in MrBayes after discarding the first 25% of trees as burn-in.

Results

Molecular phylogeny

In the alignment of the combined dataset, 1109 characters were conserved, while 601 characters were variable, of which 405 were parsimony informative. The topologies of phylogenetic trees based on the combined dataset generated from ML and BI analyses were almost identical, while statistical supports showed slight differences. Our results showed that all samples of "Heipijizong", including 2-spored and 4-spored basidiomata, represented the same species, namely *O. raphanipes*, and nested within the genus *Oudemansiella.* A sequence generated from the holotype of *Xerula chiangmaiae* also nested in this clade. It was sister to *O. japonica* (Dörfelt 1984: 190) Pegler & T.W.K. Young (1987: 596) with relatively high statistical supports and was distinct from *O. radicata* and *O. furfuracea* (Fig. 1).

The genera *Cribbea* A.H. Smith & D.A. Reid (1962: 98), *Dactylosporina* (Clémençon 1979: 77) Dörfelt (1985: 236), *Hymenopellis* R.H. Petersen (2010: 80), *Mucidula* Patouillard (1887: 95), *Ponticulomyces* R.H. Petersen (2010: 311), and *Protoxerula* R.H. Petersen (2010: 318) were treated in *Oudemansiella* s.l. (Hao *et al.* 2014, Qin *et al.* 2014a) and thus, quotation marks were placed around the names in the cladogram and the table for those sequences download form GenBank.

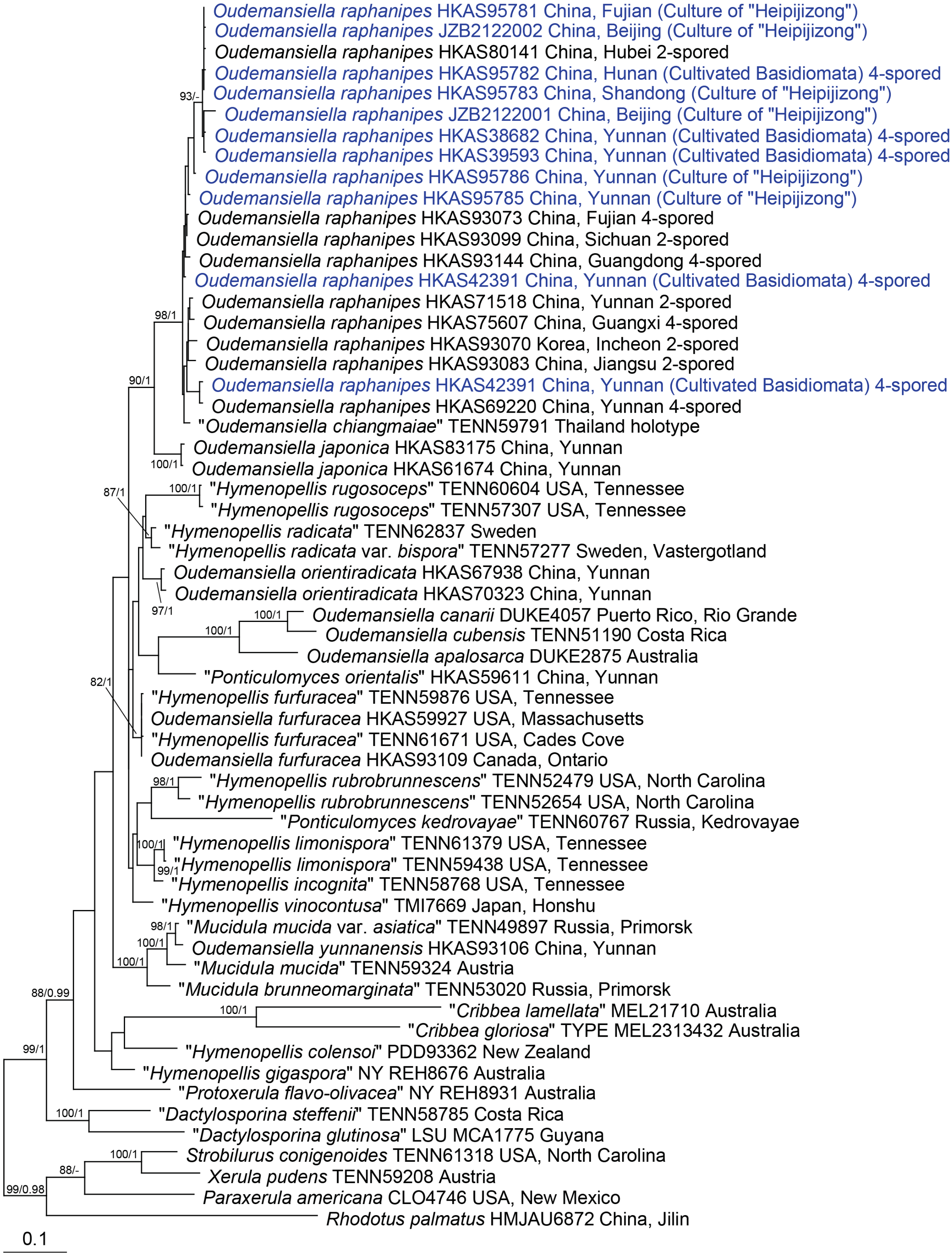

FIGURE 1. Phylogenetic tree generated from the combined ITS and nrLSU dataset using ML method. Bootstrap values (≥ 50%) derived from ML analysis and posterior probabilities from Bayesian inference (≥ 0.95) are shown above or beneath the branches. Sequences of cultures and cultivated basidiomata of "Heipijizong" are highlighted in blue. "2-spored" or "4-spored" indicates that the basidia of the collection are with 2 or 4 sterigmata.

Taxonomy

Oudemansiella raphanipes (Berk.) Pegler & T.W.K. Young, Trans. Br. mycol. Soc. 87(4): 596, 1987 (1986)

Basionym: *Agaricus raphanipes* Berk., Hooker's J. Bot. Kew Gard. Misc. 2: 48, 1850
≡ *Collybia raphanipes* (Berk.) Sacc., Syll. fung. (Abellini) 5: 202, 1887
≡ *Xerula raphanipes* (Berk.) Dörfelt, Feddes Repert. 94(7–8): 557, 1983
≡ *Xerula chiangmaiae* var. *raphanipes* (Berk.) R.H. Petersen, Rep. Tottori Mycol. Inst. 43: 20, 2006
≡ *Hymenopellis raphanipes* (Berk.) R.H. Petersen, Nova Hedwigia Beih. 137: 213, 2010
Synonym: *Xerula chiangmaiae* R.H. Petersen & Nagas., Rep. Tottori Mycol. Inst. 43: 17, figs. 15–20, 2006
≡ *Oudemansiella chiangmaiae* (R.H. Petersen & Nagas.) Zhu L. Yang, G.M. Muell., G. Kost & Rexer, Mycosystema 28: 7, 2009
≡ *Hymenopellis chiangmaiae* (R.H. Petersen & Nagas.) R.H. Petersen, in Petersen & Hughes, Nova Hedwigia, Beih. 137: 119, 2010
Figs. 2–4

FIGURE 2. Basidiomata of *Oudemansiella raphanipes* a. HKAS 95782 (cultivated). b. HKAS 71518 (in nature). c. HKAS 39593 (cultivated). d. HKAS 93144 (in nature).

Basidiomata (Fig. 2a–d) very small to large. **Pileus** 1–12 cm, convex to applanate with low umbo to slightly concave, glutinous when wet, grayish brown, yellowish brown, light brown, brown to blackish brown (5F6–5F8, 6E5–6E7, 6F3–6F8) over disc or when immature, smooth with nearly black "veins" radiating from the disc onto or over the limb, sometimes with reticulate "veins" near the margin; Context white to dirty white, unchanging in color when cut.

Lamellae adnate to sinuate or slightly decurrent, subdistant, with lamellulae, thick, white to cream; lamellar edge white. **Stipe** 2–30 × 0.2–2.1 cm, subcylindrical, enlarged at ground line, surface dirty white to grayish, densely covered with brownish felted squamules but nearly white at apex; pseudorhiza dirty white. **Taste** mild to somewhat sour; odor indistinct. **Spore print** white to cream.

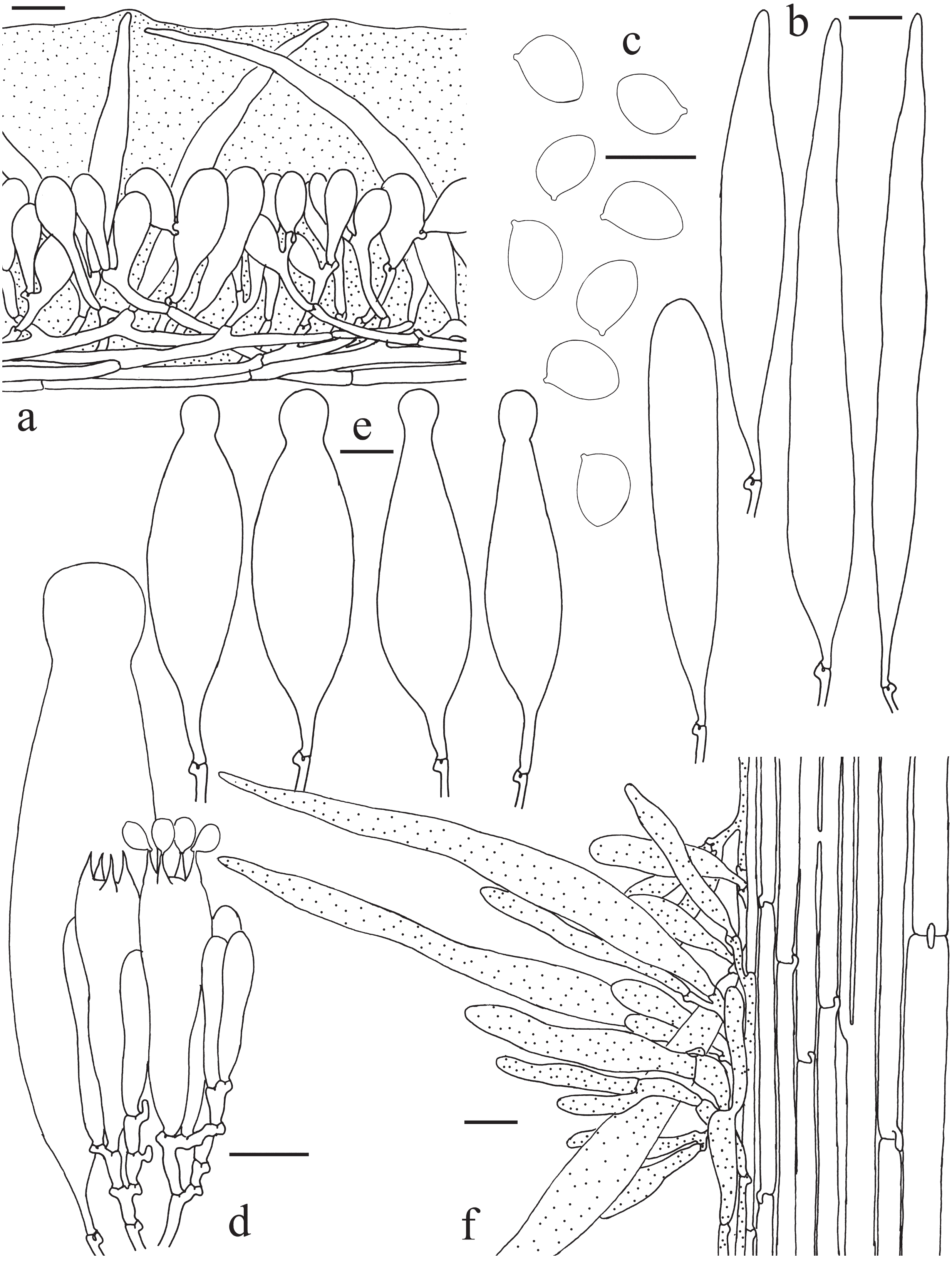

FIGURE 3. Microscopic features of 4-spored *Oudemansiella raphanipes* (HKAS 93144) a. Radial-vertical section of pileipellis. b. Cheilocystidia. c. Basidiospores. d. Basidia, basidioles and pleurocystidium e. Pleurocystidia. f. Surface of stipe in longitudinal section showing caulocystidia. Bars = 20 µm.

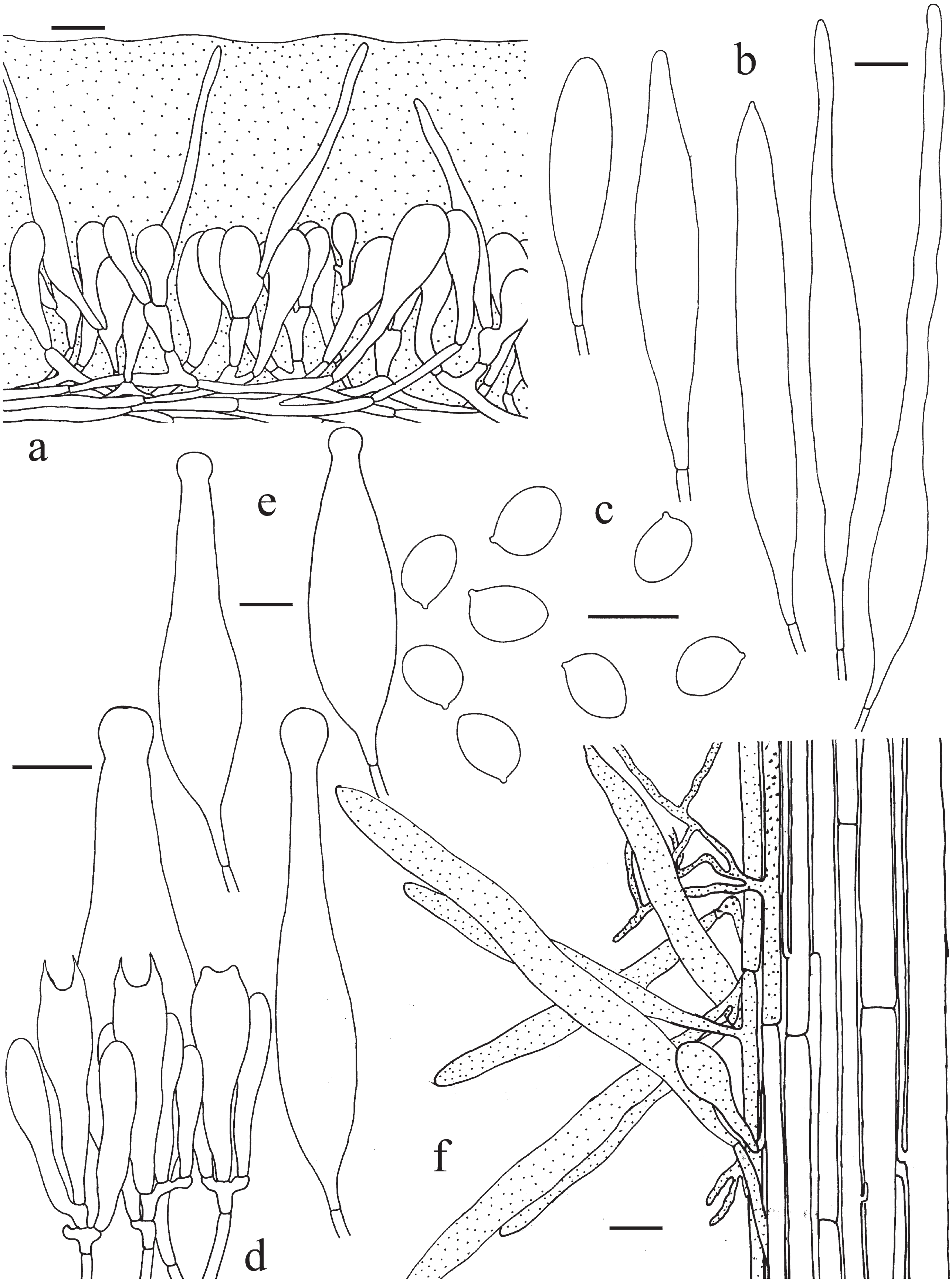

FIGURE 4. Microscopic features of 2-spored *Oudemansiella raphanipes* (HKAS 71518) a. Radial-vertical section of pileipellis. b. Cheilocystidia. c. Basidiospores. d. Basidia, basidioles and pleurocystidium. e. Pleurocystidia. f. Surface of stipe in longitudinal section showing caulocystidia. Bars = 20 µm.

Lamellar trama ± regular, composed of branching, nearly colorless and hyaline, slightly thick-walled (≤ 1 µm thick), filamentous to inflated hyphae 3–25 µm wide. **Basidia** (Fig. 3d; Fig. 4d) 34–80 × 9–20 µm, 2-spored or 4-spored, thin-walled, colorless hyaline, without any siderophilous granulation; sterigmata up to 12 µm in length. **Spores** (Fig. 3c; Fig. 4c) [240/12/11] (13) 14–18 (21) × (9) 10–13 (16) µm, Q = (1.06) 1.20–1.50 (1.64), **Q** = 1.30 ± 0.09, ellipsoid, ovoid to sublimoniform, thin-walled, colorless and hyaline, non-amyloid, non-dextrinoid. **Pleurocystidia** (Figs. 3e, 4e) 70–200 × 17–52 µm, pedicellate, fusiforms with prominent capitate apex, sometimes incrusted brownish to golden substances, thin-walled to slightly thick-walled, colorless and hyaline. **Cheilocystidia** (Figs. 3b, 4b) 25–240 × 5–41 µm, crowded and numerous, pedicellate, fusiform, narrowly clavate, subcylindrical to cylindrical, thin-walled, colorless and hyaline. **Pileipellis** (Figs. 3a, 4a) an ixohymeniderm of 120–190 µm thick, composed of clavate, broadly clavate to sphaeropedunculate, brownish to brown intracellularly pigmented cells (18–80 × 10–47 µm) embedded in a gelatinized matrix. **Pileocystidia** (Figs. 3a, 4a) abundant, subcylindrical to narrowly fusiform, 70–190 × 3–12 µm, thin-walled, nearly colorless or with brownish to brown intracellular pigment; apex acute or narrowly rounded. **Stipitipellis** composed of vertically arranged, branching, slightly yellow to slight brown, hyaline, slightly thick-walled (ca. 0.5 µm thick), filamentous hyphae 3–25 µm broad. **Caulocystidia** (Figs. 3f, 4f) 45–250 × 8–22 µm, numerous and crowded, caespitose, narrowly clavate to subcylindrical, thin- to slightly thick-walled (ca. 0.5 µm thick), with grayish brown to yellowish brown intracellular pigment, occasionally nearly colorless and hyaline. Clamp connections abundant in every part of 4-spored basidioma, but absent in 2-spored basidioma.

Habitat and known distribution: Growing on decaying wood buried in soil; during Spring and Summer (April to August) at 300–2400 m elev., in East and South Asia. Originally described from Sikkim, India.

Specimens examined: CHINA. Guangdong Province: Zhaoqing, Fengkai County, Heishiding Natural Reserve, elev. 500 m, 13 April 2013, *Fang Li* 1214 (HKAS 93144!). Guangxi Autonomous Region: Guilin, Maoershan National Natural Reserve, elev. 1900 m, 24 July 2012, *Qing Cai* 873 (HKAS 75607!). Hubei Province: Huanggang, Macheng City, Wunaoshan National Forest Park, elev. 320 m, 26 June 2013, *Yan-Jia Hao* 861 (HKAS 80141!). Jiangsu Province: Lianyungang, Huaguoshan, elev. unknown, 27 August 2011, *Xiang-Huang Wang* 3030 (HKAS 93083!). Sichuan Province: Mianyang, elev. unknown, date unknown, *Xin-Sheng He* s.n. (HKAS 93099!). Yunnan Province: Tengchong County, Gaoligongshan National Natural Reserve, elev. 2090 m, 11 August 2010, *Yan-Jia Hao* 236 (HKAS 69220!); Baoshan, the border of Baoshan District and Tengchong County, elev. 2400 m, 8 August 2011, *Yan-Jia Hao* 409 (HKAS 71518!); Kunming, Kunming Institute of Botany, elev. 1980 m, 20 August 2001, *Fu-Qiang Yu* 531 (HKAS 38682!); same location, 10 May 2002, *Zhu-Liang Yang* 3223 (HKAS 39593!); same location, *Li-Fang Zhang* 163 (HKAS 42391!). REPUBLIC OF KOREA. Inchon, 16 August 2011, *Xiao-Fei Shi* 805 (HKAS 93070!).

Specimens of *Oudemansiella furfuracea* examined: CANADA. Ontario: Halmiton, McMaster University, 2 September 2015, elev. 70 m, *Bang Feng* 1935 (HKAS 93109!); same data and location, *Bang Feng* 1939 (HKAS 93110!).

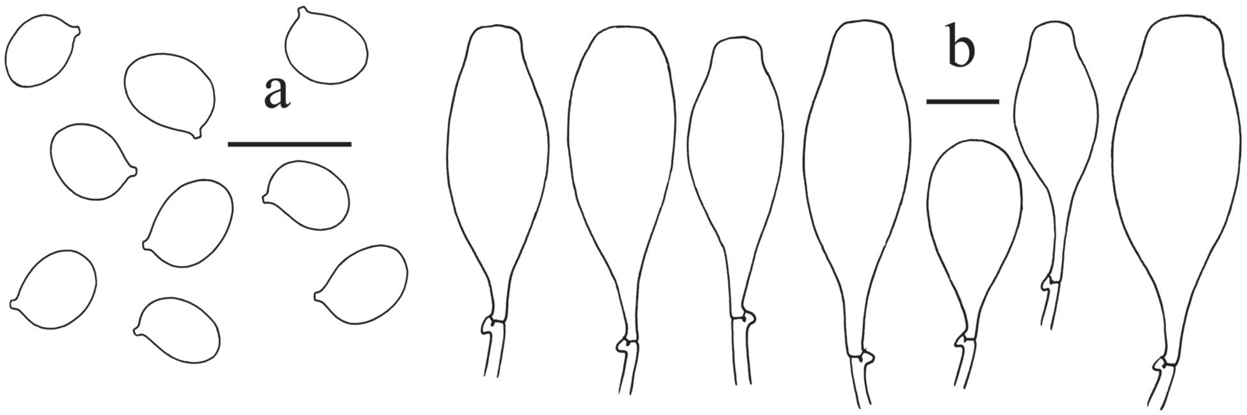

FIGURE 5. Microscopic features of *Oudemansiella furfuracea* (HKAS 93109) a. Basidiospores. b. Pleurocystidia. Bars = 20 µm.

Discussion

Four cultivated collections, seven cultivated cultures and nine wild collections of "Heipijizong" are phylogenetically analyzed (Figs. 1). These samples formed a distinct lineage with relatively high support value. Based on morphological characteristics and molecular phylogenetic evidence, "Heipijizong" was identified as *O. raphanipes*. It is not a species of the genus *Termitomyces*, which posess basidiomata with a pseudorhiza arising from a termite-comb, free pinkish to pink lamellae, a pinkish to pink spore print, siderophilous granule-filled basidia and a cutis pileipellis (Heim 1977, Singer 1986).

Oudemanisella raphanipes (*Agaricus raphanipes*) was originally described from Darjeeling, Sikkim, India (Berkeley 1850). The first report of *O. raphanipes* from China was in 1993, based on collections from southern part of Yunnan (Yang & Zang 1993). Thereafter, collections only from Yunnan were cited by Petersen and his co-authors as *Xerula chiangmaiae* var. *raphanipes* or *Hymenopellis raphanipes* (Petersen & Nagasawa 2006, Petersen & Hughes 2010). Our study showed that *O. raphanipes* is widely distributed in China, from east to west, including Fujian, Guangdong, Guangxi, Hubei, Jiangsu, Shandong, Sichuan and Yunnan, and also occurs in the Republic of Korea (HKAS 93070).

Oudemansiella raphanipes was reported from Australia, China, India, Japan and Thailand (Pegler & Young 1987, Yang & Zang 1993, Petersen & Nagasawa 2006, Petersen & Hughes 2010). In most cases, species from the Southern Hemisphere are different from those from the Northern Hemisphere. Therefore, further studies are needed to reveal whether those specimens from Australia belong to *O. raphanipes*.

Oudemansiella raphanipes was known as a species with 2-spored basidia (Petersen & Nagasawa 2006, Petersen & Hughes 2010). Our phylogenetic analyses indicated that sequences of 4-spored basidiomata were interspersed among the sequences of 2-spored basidiomata (Fig. 1) and all of these samples clustered in a highly supported clade, suggesting that they represent a single independent species. Petersen and Methven (1994) traced nuclear behavior in the 2-spored form of *Oudemansiella radicata* (as *Xerula radicata*), and concluded that it was an asexual state in which meiosis did not take place. Petersen & Hughes (2010) also found that sequences of 2-spored *O. raphanipes* (as *Hymenopellis raphanipes*) were interspersed among sequences of 4-spored *O. chiangmaiae* (Petersen & Nagasawa 2006: 17) Zhu L. Yang, G.M. Muell., G. Kost & Rexer (2009: 7) [as *Hymenopellis chiangmaiae* (Petersen & Nagasawa) Petersen (2010: 137)] as the same as what indicated in Fig. 1. In addition, there are no obvious differences in morphological characteristics between the 4-spored collections and 2-spored ones, except that the former ones have abundant clamp connections. As pointed out by Petersen & Hughes (2010), there was no reason to conclude that genetically, such 2-spored basidiomata different from 4-spored ones. In this study, we therefore expanded the concept of *O. raphanipes* to include both 2-spored and 4-spored basidiomata. Consequently, *O. chiangmaiae* is treated here as a later synonym of *O. raphanipes* in accordance with the principle “one fungus, one name” in the Melbourne code (McNeill *et al*. 2012). *Oudemansiella raphanipes* was regarded as *O. radicata* or *O. furfuracea* in China in the past (Ji *et al.* 1982, Yu *et al.* 2002, Shim *et al.* 2006, Wu *et al.* 2013). However, *O. radicata* differs from *O. raphanipes* by its glabrous stipe, utriform to tenpin-shaped pleurocystidia and the absence of pileocystidia and caulocystidia (Petersen & Hughes 2010, Petersen & Nagasawa 2006). *Oudemansiella furfuracea* differs from *O. raphanipes* by its broadly rounded apex of basidospores and subcapitate, cylindrical, utriform to tenpin-shaped pleurocystidia (Redhead *et al.* 1987, Petersen & Nagasawa 2006, Petersen & Hughes 2010, Fig. 5). Furthermore, our phylogenetic analyses indicated that they all three are distinct species (Fig. 1) and the occurrence of *O. radicata* or *O. furfuracea* in China is not confirmed.

Our phylogenetic analyses indicated that *O. raphanipes* is closely related to *O. japonica* (Fig. 1). Morphologically, they both have furfuraceous stipes, long, tapering pseudorhiza, capitated pleurocystidia and well-developed caulocystidia. However, *O. japonica* can be distinguished from *O. raphanipes* by the absence of pileocystidia, globose, subglobose to ovate basidiospores and fusiform, broadly clavate to utriform cheilocystidia (Petersen & Nagasawa 2006, Petersen & Hughes 2010).

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