## ORIGINAL ARTICLE

# Morphological characters and molecular data reveal two new species of *Postia* (Basidiomycota) from China

Lu-Lu Shen · Hong-Xia Liu · Bao-Kai Cui

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**Abstract** Two new species of *Postia* are described from China based on morphological characters and molecular data. *Postia gloeopora* sp. nov. is characterized by pileate and white flabelliform basidiomata, glue pores when dry, gelatinous hyphae at the dissepimental edge, abundant oily substances in context and trama, and ellipsoid basidiospores ( $4-4.5 \times 2-$ 2.5 µm). *Postia ochraceoalba* sp. nov. is characterized by imbricate basidiomata, ochraceous pileal surface with concentric zones, white pore surface, small angular pores (6-7 per mm) with dentate dissepiments, and allantoid basidiospores ( $4-4.5 \times 1-1.5$  µm). Phylogenetic analysis based on the internal transcribed spacer and nuclear large subunit ribosomal RNA gene regions confirmed the affinity of the new species in *Postia* and indicated their relationships with other species in the genus.

**Keywords** Brown-rot fungi · Fomitopsidaceae · Polypore · Taxonomy

#### Introduction

*Postia* Fr. was established by Fries (1874); it belongs to Fomitopsidaceae of Polyporales and contains about 60 species (Jülich 1982; Larsen and Lombard 1986; Renvall 1992; Buchanan and Ryvarden 2000; Wei and Dai 2006; Hattori

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et al. 2011; Dai 2012). Species in the genus have an annual growth habit, a monomitic or dimitic hyphal system with clamped generative hyphae, allantoid to cylindrical or ellipsoid basidiospores, which are usually thin-walled, negative in Melzer's reagent and acyanophilous in Cotton Blue, and cause a brown-rot decay (Hattori et al. 2011; Cui and Li 2012).

Previously, most species in Postia were placed in Tvromvces P. Karst.; however, Tvromvces is restricted to species causing a white rot (Gilbertson and Ryvarden 1987; Ryvarden 1991; Ryvarden and Gilbertson 1994), which has been supported by phylogenetic studies (Yao et al. 1999; Binder et al. 2005), while species in Postia cause a brown rot (Jülich 1982; Niemelä 2005). Species in Postia were addressed in Oligoporus Bref. by Gilbertson and Ryvarden (1987), Ryvarden and Gilbertson (1994), and Núñez and Ryvarden (2001), but other mycologists prefer to use *Postia* instead (Renvall 1992; Niemelä 2005; Wei and Dai 2006; Hattori et al. 2011; Cui and Li 2012; Pildain and Rajchenberg 2013; Shen and Cui 2014). For more detailed discussion on the nomenclature of Postia and Oligoporus, see Donk (1960), Larsen and Lombard (1986), Walker (1996), and Pildain and Rajchenberg (2013), who support the use of *Postia*, and Ryvarden (1991), who supports the use of Oligoporus. Recent phylogenetic studies supported the independent use of Oligoporus and Postia (Binder et al. 2013; Ortiz-Santana et al. 2013; Cui et al. 2014). Therefore, in the current paper, we prefer to use *Postia* according to Wei and Dai (2006) and Ortiz-Santana et al. (2013).

In recent years, taxonomy and phylogeny of *Postia* have been carried out in China; nine new species were described, and a total of 32 species were found (Wei and Dai 2006; Dai et al. 2009; Wei and Qin 2010; Yuan et al. 2010; Cui and Li 2012; Dai 2012; Shen and Cui 2014; Shen et al. 2014). As a continuation of these studies, two additional species of *Postia* were newly described based on morphological characters and phylogenetic analysis of internal transcribed spacer (ITS)

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combined the nuclear large subunit (nLSU) rRNA gene regions, both were discovered on gymnosperm wood in subalpine forests at high altitude of southwest China.

#### Materials and methods

#### Morphological studies

The studied specimens were deposited at the herbaria of the Institute of Microbiology, Beijing Forestry University (BJFC) and the Institute of Applied Ecology, Chinese Academy of Sciences (IFP). The microscopic routines followed Li et al. (2014). Sections were studied at magnification up to  $\times 1000$ using a Nikon Eclipse 80i microscope and phase contrast illumination (Nikon, Tokyo, Japan). Drawings were made with the aid of a drawing tube. Microscopic features, measurements, and drawings were made from slide preparations stained with Cotton Blue and Melzer's reagent. Spores were measured from sections cut from the tubes. In presenting the variation in the size of the spores, 5 % of measurements were excluded from each end of the range, and were given in parentheses. In the text, the following abbreviations were used: IKI = Melzer's reagent, IKI- = both inamyloid and indextrinoid, KOH = 5 % potassium hydroxide, CB = Cotton Blue, CB- = acyanophilous, L = mean spore length (arithmetic average of all spores), W = mean spore width (arithmetic average of all spores), O = variation in the L/W ratios between the specimens studied, n(a/b) = number ofspores (a) measured from given number (b) of specimens. Special color terms followed Petersen (1996).

#### Molecular study and phylogenetic analysis

A CTAB rapid plant genome extraction kit (Aidlab, Beijing, China) was used to extract total genomic DNA from dried specimens and performed the polymerase chain reaction (PCR), according to the manufacturer's instructions. The ITS regions were amplified with the primers ITS5 and ITS4 (White et al. 1990), and the nLSU regions with the primers LR0R and LR7 (http://www.biology.duke.edu/fungi/ mycolab/primers.htm). The PCR procedure for ITS was as follows: initial denaturation at 95 °C for 3 min, followed by 34 cycles at 94 °C for 40 s, 54 °C for 45 s, and 72 °C for 1 min, and a final extension of 72 °C for 10 min. The PCR procedure for nLSU was as follows: initial denaturation at 94 °C for 1 min, followed by 34 cycles at 94 °C for 30 s, 50 °C for 1 min, and 72 °C for 1.5 min, and a final extension of 72 °C for 10 min. The PCR products were purified and directly sequenced in Beijing Genomics Institute, China, with the same primers. All newly generated sequences were submitted to GenBank and are listed in Table 1.

 Table 1
 A list of species, specimens, and GenBank accession numbers of sequences used in this study

Species name	Sample no.	Location	GenBank No.	
			ITS	nLSU
Antrodia albida	FP 105979	UK	EU232189	EU232272
Postia alni	Cui 10094	China	KF699116	KJ684972
Postia alni	Dai 10854	China	KF699117	KJ684973
Postia balsamea	JV 8609-9	unknown	JF950570	_
Postia balsamea	Cui 8207	China	KF699118	KJ684974
Postia carbophila	MR 10758	Argentina	JX090114	JX090132
Postia carbophila	MR 12281	Argentina	JX090115	_
Postia caesia	MR12276	UK	JX090109	JX090129
Postia caesia	MR12421	UK	JX090110	JX090130
Postia dissecta	CIEFAP 328	Argentina	JX090106	JX090134
Postia dissecta	MR 12423	Argentina	JX090107	JX090135
Postia duplicata	Cui 10366	China	KF699124	KJ684975
Postia duplicata	Dai 13411	China	KF699125	KJ684976
Postia floriformis	X1295	Finland	KC595936	KC595936
Postia floriformis	Cui 10292	China	KM107899 <sup>a</sup>	KM107904 <sup>a</sup>
Postia fragilis	JV 0610-8	unknown	JF950573	_
Postia fragilis	Cui 10088	China	KF699120	KJ684977
Postia gloeopora	Cui 9517	China	KM107900 <sup>a</sup>	KM107905 <sup>a</sup>
Postia gloeopora	Cui 9507	China	KM107901 <sup>a</sup>	KM107906 <sup>a</sup>
Postia guttulata	Cui 10018	China	KF727432	KJ684978
Postia guttulata	Cui 10028	China	KF727433	KJ684979
Postia hibernica	K(M) 17352	Austria	AJ006665	_
Postia hibernica	Cui 8248	China	KF699126	KJ684980
Postia hirsuta	Cui 11237	China	KJ684970	KJ684984
Postia hirsuta	Cui 11180	China	KJ684971	KJ684985
Postia lactea	K(M) 31289	UK	AJ006664	_
Postia lactea	Dai 12643	Finland	KF699121	KJ684981
Postia lateritia	KUO 020197	unknown	JF950566	_
Postia lateritia	KUO 021153-1	unknown	JF950567	_
Postia leucomallella	Cui 9599	China	KF699122	KJ684982
Postia leucomallella	Cui 9577	China	KF699123	KJ684983
Postia lowei	X1373	Finland	KC595941	_
Postia lowei	X1417	Finland	KC595942	_
Postia ochraceoalba	Cui 10825	China	KM107902 <sup>a</sup>	KM107907 <sup>a</sup>
Postia ochraceoalba	Cui 10802	China	KM107903 <sup>a</sup>	KM107908 <sup>a</sup>
Postia pelliculosa	MR 10671	Argentina	JX090101	JX090123
Postia pelliculosa	MR 10592	Argentina	JX090102	JX090124
Postia pileata	Cui 5721	China	KF699127	_
Postia pileata	Cui 5715	China	KF699128	_
Postia placenta	JV 0108/98	Slovakia	JN592501	_
Postia placenta	Wei 1406	China	KF699129	_
Postia punctata	MR 11100	Argentina	JX090112	JX090128
Postia punctata	MR 12398	Chile	JX090111	JX090127
Postia rennyi	MR 10497	Argentina	JX090117	_
Postia rennyi	KEW 57	unknown	AY218416	AF287876
Postia sericeomollis	MJL-3788-Sp	USA	KC585366	KC585195
Postia sericeomollis	L-15571-Sp	China	KC585363	KC585192
Postia stiptica	BRFM 1151	France	JX082382	_
Postia stiptica	Cui 9268	China	KF727431	_
Postia venata	MR 12368	Argentina	JX090113	JX090133
Postia zebra	Dai 7131	China	KF727430	KM190902 <sup>a</sup>

<sup>a</sup> Sequences newly generated in this study

The combined ITS and nLSU sequences were aligned with other related sequences downloaded from GenBank (Table 1) using BioEdit (Hall 1999) and ClustalX (Thompson et al. 1997). *Antrodia albida* (Fr.) Donk was used as outgroup. Prior to phylogenetic analysis, ambiguous sequences at the start and the end were deleted and gaps were manually adjusted to optimize the alignment. Sequence alignment was deposited at TreeBase (http://purl.org/phylo/treebase/; submission ID 16159).

Maximum likelihood (ML) and Bayesian inference (BI) methods were used to analyze the alignment. Substitution models suitable for each partition in the dataset were determined using Akaike Information Criterion implemented in MrMODELTEST2.3 (Nylander 2004). RAxML v7.2.6 (Stamatakis 2006) was used for ML analysis. All parameters in the ML analysis used the default setting, and statistical support values were obtained using nonparametric bootstrapping with 1,000 replicates. BI was calculated with MrBayes3.1.2 (Ronquist and Huelsenbeck 2003), with a general timereversible model of DNA substitution and an invgamma distribution rate variation across sites. Eight Markov chains were run from the random starting tree for 8 million generations of the combined ITS and nLSU dataset. Trees were sampled every 100 generations. The burn-in was set to discard the first 25 % of the trees. A majority rule consensus tree of all remaining trees was calculated. Branches that received bootstrap values for ML  $\geq$ 75 % and Bayesian posterior probabilities  $\geq 0.95$  (BPP) were considered significantly supported.

#### Results

Taxonomy

# *Postia gloeopora* L.L. Shen, B.K. Cui & Y.C. Dai, sp. nov. (Figs. 1a–b, 2)

MycoBank no.: MB 811121

*Postia gloeopora* is characterized by pileate and white flabelliform basidiomata, glue pores when dry, gelatinous hyphae at the dissepimental edge, abundant oily substances in context and trama, and ellipsoid basidiospores  $(4-4.5 \times 2-2.5 \ \mu\text{m})$ .

*Type*. CHINA. Xizang Autonomous Region (Tibet), Bomi County, on stump of *Pinus densata*, 19 September 2010, Cui 9507 (Holotype in BJFC).

*Etymology. gloeopora* (Lat.): refers to the glue pores when dry.

*Basidiomata.* Annual, sessile, solitary, soft corky, without odor or taste when fresh, hard corky and light in weight when dry. Pileus flabelliform, projecting up to 3 cm, 4 cm wide, and 0.8 cm thick at base. Pileal surface velutinate and white colored when fresh, becoming glabrous and cream to buff when dry, with shallow radial furrows; margin concolorous with pileal surface, thin and fimbriate when fresh, becoming acute upon drying. Pore surface white when fresh, becoming buff to olivaceous buff when dry; sterile margin narrow to almost lacking; pores angular, 3–4 per mm; dissepiments thin, lacerate. Context white to cream, corky, up to 6 mm thick. Tubes concolorous with pore surface, soft corky when fresh, brittle upon drying, up to 2 mm long.

**Fig. 1** Basidiomata of *Postia* gloeopora (**a**–**b**) and *P. ochraceoalba* (**c**–**d**). Bars **a**–**d**=1 cm

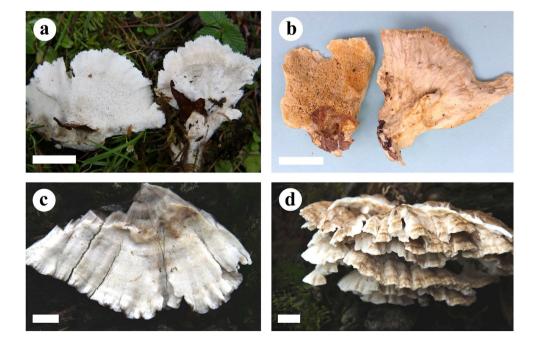
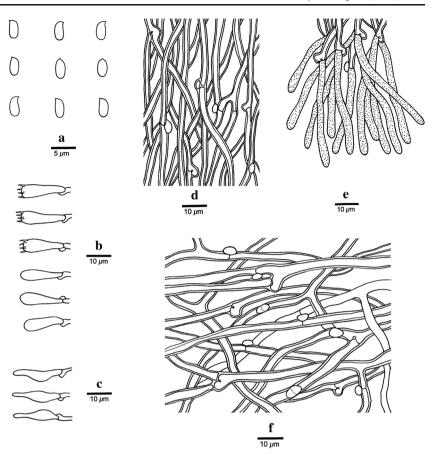


Fig. 2 Microscopic structures of *Postia gloeopora* (drawn from the holotype). **a** Basidiospores. **b** Basidia and basidioles. **c** Cystidioles. **d** Hyphae from trama. **e** gelatinous hyphae at the dissepimental edge. **f** Hyphae from context. *Bars*  $\mathbf{a}$ =5 µm,  $\mathbf{b}$ – $\mathbf{f}$ =10 µm



*Hyphal structure.* Hyphal system monomitic; generative hyphae with clamp connections, IKI–, CB–; hyphae unchanged in KOH.

*Context.* Generative hyphae hyaline, thin- to slightly thick-walled with a wide lumen, frequently branched, loosely interwoven,  $3-6 \mu m$  in diam. Abundant oily substance present among hyphae.

Tubes. Generative hyphae hyaline, thin- to slightly thick-walled with a wide lumen, occasionally branched, 2–4  $\mu$ m in diam. Hyphae at the dissepiment edge strongly gelatinous, thin-walled. Cystidia absent, some fusoid cystidioles occur in the hymenium, hyaline, thin-walled, 10–24.5×2–4  $\mu$ m. Basidia clavate, bearing four sterigmata and a basal clamp connection, 12–20×4–5  $\mu$ m; basidioles dominant, in shape similar to basidia, but smaller. Abundant oily substance present in trama.

*Spores.* Basidiospores ellipsoid, slightly curved, hyaline, thin-walled, smooth, IKI–, CB–,  $(3.5–)4–4.5\times2–2.5 \ \mu\text{m}$ , L= 4.04  $\mu\text{m}$ , W=2.13  $\mu\text{m}$ , Q=1.86–2.16 (*n*=60/2).

#### Type of rot. Brown rot.

Additional specimen (paratype) examined. CHINA. Xizang Autonomous Region (Tibet), Bomi County, on fallen trunk of *Pinus densata*, 20 September 2010, Cui 9517 (BJFU).

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*Postia ochraceoalba* L.L. Shen, B.K. Cui & Y.C. Dai, sp. nov. (Figs. 1c-d, 3)

MycoBank no.: MB 811122

*Postia ochraceoalba* is characterized by imbricate basidiomata with ochraceous and concentrically zonate pileal surface and white pore surface, small angular pores (6–7 per mm) with dentate dissepiments, and allantoid basidiospores (4–4.5×1–1.5  $\mu$ m).

*Type.* CHINA. Sichuan Province, Luding County, Hailuogou Forest Park, on fallen trunk of *Picea* sp., 20 October 2012, Cui 10802 (Holotype in BJFC).

*Etymology. ochraceoalba* (Lat.): refers to ochraceous pileal surface and white pores.

*Basidiomata*. Annual, pileate, imbricate, soft to fibrous when fresh, without odor or taste, corky to slightly fragile when dry. Pileus semicircular, projecting up to 5.5 cm, 11 cm wide, and 1.2 cm thick at base. Pileal surface clay-buff, ochraceous to greyish brown when fresh, glabrous, concentrically zonate with fuscous zones, longitudinally grooved, becoming pale mouse-grey or deep-olive; margin acute, undulate, white when fresh, pale vinaceous grey and incurved when dry. Pore surface white when fresh, becoming cream to buff when dry; sterile margin narrow, greyish brown, up to 0.5 mm wide; pores angular, 6–7 per mm; dissepiments thin, dentate. Context white, hard corky to slightly fragile,

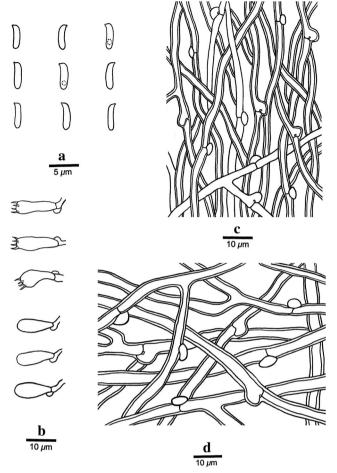


Fig. 3 Microscopic structures of *Postia ochraceoalba* (drawn from the holotype). **a** Basidiospores. **b** Basidia and basidioles. **c** Hyphae from trama. **d** Hyphae from context. *Bars*  $\mathbf{a}$ =5 µm,  $\mathbf{b}$ - $\mathbf{d}$ =10 µm

up to 1 cm thick. Tubes white to cream, corky, paler than pore surface, fragile, up to 2 cm long.

*Hyphal structure.* Hyphal system monomitic; generative hyphae with clamp connections, IKI–, CB–; hyphae unchanged in KOH.

Context. Generative hyphae hyaline, slightly thick-walled with a wide lumen, frequently branched, loosely interwoven,  $3-5.5 \ \mu m$  in diam.

*Tubes.* Generative hyphae hyaline, thin- to slightly thickwalled, occasionally branched, subparallel among the tubes, 2–3.5  $\mu$ m in diam. Cystidia and cystidioles absent. Basidia clavtae, bearing four sterigmata and a basal clamp connection, 12–18×4–6  $\mu$ m; basidioles dominant, in shape similar to basidia, but smaller.

Spores. Basidiospores allantoid, hyaline, thin-walled, smooth, occasionally bearing one guttule, IKI–, CB–, 4– $4.5(-5) \times 1-1.5 \mu$ m, L=4.46  $\mu$ m, W=1.37  $\mu$ m, Q=3.18–4.02 (n=90/3).

*Type of rot.* Brown rot.

Additional specimens (paratypes) examined. CHINA. Sichuan Province, Luding County, Hailuogou Forest Park,

on fallen trunk of *Picea* sp., 20 October 2012, Cui 10825; Cui 10827 (BJFC).

Molecular phylogeny

The combined ITS and nLSU dataset included sequences from 51 fungal samples representing 27 taxa. ML and BI analyses yielded nearly congruent tree topologies, and thus only the BI tree was provided. Both bootstrap values ( $\geq$ 50 %) and BPPs ( $\geq$ 0.95) were showed at the nodes (Fig. 4).

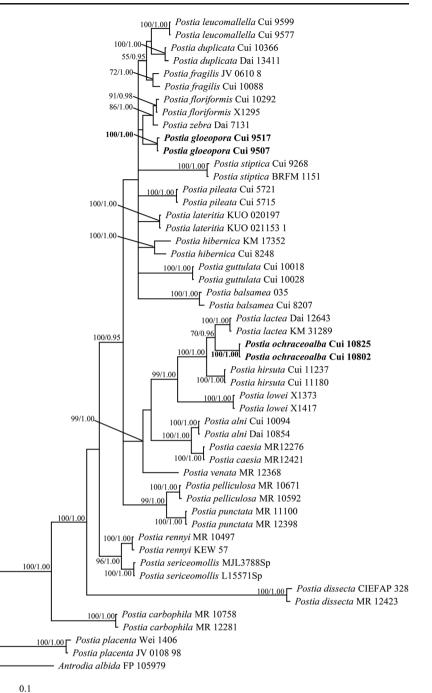
## Discussion

*Postia gloeopora* and *P. ochraceoalba* are herein described based on morphological characters and molecular data. The phylogenetic analysis (Fig. 4) showed that each of the two species formed a distinct lineage and is different from other taxa in the genus.

Phylogenetically, Postia gloeopora grouped with P. floriformis (Quél.) Jülich and P. zebra Y.L. Wei & W.M. Qin forming a weakly supported lineage (Fig. 4). In morphology, both P. gloeopora and P. floriformis produce pileate and white basidiomata when fresh and similarly sized ellipsoid basidiospores, but P. floriformis differs by its imbricate growth habit, smaller pores (6-8 per mm), and lack of gelatinous hyphae and cystidioles (Ryvarden and Melo 2014). Postia zebra and P. gloeopora share annual, pileate basidiomata with white pore surface and similarly sized ellipsoid basidiospores, but P. zebra has grey-brown zonate pileal surface, smaller pores (7-8 per mm), thin-walled tramal hyphae, and lacks gelatinous hyphae and cystidioles (Wei and Qin 2010). Geographically, P. floriformis is widely distributed in Europe, North America and northern China (Gilbertson and Ryvarden 1987; Dai 2012; Ryvarden and Melo 2014), while P. gloeopora and P. zebra are known only from China so far (Wei and Qin 2010).

*Postia dissecta* (Cooke) Rajchenb. may be confused with *P. gloeopora* in producing white applanate pileus with fimbriate margin and similar basidiospores, but it is different from *P. gloeopora* by its light brown pore surface, slightly smaller pores (4–5 per mm) with entire to incised dissepiments, a dense yellowish protoplasm in some hyphae and absence of gelatinous hyphae and cystidioles (Rajchenberg 1987). Moreover, the two species are different in the ITS combined nLSU rDNA-based phylogeny (Fig. 4).

*Postia ptychogaster* (F. Ludw.) Vesterh. and *P. wakefieldiae* (Kotl. & Pouzar) Pegler & E.M. Saunders also have pileate basidiomata with similar ellipsoid basidiospores. However, *P. ptychogaster* differs from *P. gloeopora* in the absence of gelatinous hyphae and cystidioles (Ryvarden and Melo 2014), and *P. wakefieldiae* is separated from *P. gloeopora* by having a zonate pileus with darker brownish Fig. 4 Phylogenetic positions of *Postia gloeopora* and *P. ochraceoalba* inferred by Bayesian inference based on ITS combined nLSU sequence data. Bootstrap proportions (*before the slash markers*) higher than 50 % and Bayesian posterior probabilities (*after the slash markers*) more than 0.95 are labeled in branches



concentric zones, slightly smaller pores (4–5 per mm), and absence of cystidioles (Pegler and Saunders 1994). Moreover, *P. ptychogaster* is widely distributed in North America and northern and central Europe, while *P. wakefieldiae* is known only from England and France (Ryvarden and Melo 2014; Gilbertson and Ryvarden 1987).

In the ITS combined nLSU rDNA-based phylogeny (Fig. 4), *Postia lactea* (Fr.) P. Karst is closely related to *P. ochraceoalba*. Both species have annual, pileate basidiomata, slightly thick-walled generative hyphae with a wide lumen in context, and similarly sized basidiospores, but *P. lactea* has solitary basidiomata, convex to ungulate pileus with azonate pileus, and bigger pores (4–6 per mm; Lowe and Lombard 1973).

*Postia cana* H.S. Yuan & Y.C. Dai may be confused with *P. ochraceoalba*, and both species produce pileate, imbricate basidiomata, semicircular pilei with undulate, incurved margin when dry, zonate pilei surface, and similarly sized

basidiospores. However, *P. cana* can be readily distinguished from *P. ochraceoalba* by its clay pink to fawn pileal surface when fresh, pale brownish pore surface when bruised, bigger pores (4–6 per mm) and its swollen hyphae in KOH (Yuan et al. 2010).

*Postia ochraceoalba* is similar to *P. japonica* Y.C. Dai & T. Hatt., which has imbricate basidiomata, an indistinctly concentrically zonate pileus, and white pores when fresh, but *P. japonica* differs in droplets of amber liquid on pore surface, bigger pores (2–3 per mm), dextrinoid skeletal hyphae in trama, and ellipsoid basidiospores tapering toward apiculus ( $4.5-5.5 \times 3-3.5 \mu m$ , Dai and Hattori 2007).

*Postia* is a large and important genus in the brown-rot fungal group, and there are still many unknown species in the genus need to be discovered. Several phylogenetic studies were focused on *Postia*, it is clustered with other brown-rot genera, such as *Antrodia* P. Karst. and *Fomitopsis* P. Karst. in the antrodia clade (Binder et al. 2005; Ortiz-Santana et al. 2013; Pildain and Rajchenberg 2013; Cui et al. 2014), but only limited samples were included. In the current study, no distinct morphological features or geographic information could be assigned to the phylogenetic analysis. Evolutionary information from more samples and more gene markers is needed to make a comprehensive understanding of the phylogenetic relationships within species in *Postia* and related species in other genera.

Key to known species of Postia in China

1. Basidiocarps effused-reflexed, pileate, or stipitate2
1. Basidiocarps resupinate 28
2. Basidiocarps stipitate or substipitate
2. Basidiocarps effused-reflexed or pileate5
3. Pores 1–3 per mm······P. subundosa
3. Pores >3 per mm
4. Basidiocarps fragile when dry; pores 3-5 per
mm·····P. ceriflua
4. Basidiocarps tough to bone hard when dry; pores 6–8
per mm·····P. floriformis
5. Basidiocarps with distinct grey to bluish tints6
5. Basidiocarps white, cream, yellowish, or brown8
6. On angiosperm wood······P. alni
6. On gymnosperm wood······7
7. Basidiospores <1.8 µm wide·····P. caesia
7. Basidiospores >1.8 µm wideP. luteocaesia
8. Basidiocarps becoming brown when bruised or
dry9
8. Basidiocarps unchanged when bruised or dry
9. Gloeocystidia present
9. Gloeocystidia absent 11
10. Context duplexP. duplicata
10. Context homogeneous ······P. leucomallella
11. Basidiospores <1.6 µm wide
11. Basidiospores >1.7 μm wideP. fragilis

34. Pores 5–6 per mm; basidiospores mostly <1 μm wide------*P. simanii*34. Pores 3–4 per mm; basidiospores mostly >1 μm wide-----*P. hibernica*

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