



## *Veluticeps fasciculata* sp. nov. (Gloeophyllaceae, Basidiomycota), a close relative to *V. berkeleyi*

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### Abstract

A new brown-rot fungal species, *Veluticeps fasciculata*, is described from southern China. It is characterized by perennial effused basidiocarps with smooth or tuberculose hymenophore, nodose-septate generative hyphae, fasciculate cystidia (as hyphal pegs in hymenophore) and relatively small basidiospores. It occurs on wood of *Cunninghamia* and *Cryptomeria*. Although similar to *Veluticeps berkeleyi*, morphological and molecular (ITS rDNA sequences) data show that *V. fasciculata* is a distinct species. Complete description and illustrations are provided for the *V. fasciculata*. In addition, *V. fimbriata* is reported from China for the first time.

**Key words:** brown rot, Gloeophyllales, taxonomy, wood-inhabiting fungi

### Introduction

*Veluticeps* (Cooke 1879: 20) Pat. (1894: 78) is a distinctive genus characterized by single or fascicled cystidia, relatively long basidia, fusiform basidiospores and causes a brown rot on gymnosperm or angiosperm wood (Nakasone 1990). Currently, nine species are accepted in the genus (Nakasone 2004, He & Li 2013). Phylogenetically it belongs in the Gloeophyllales and is closely related to *Chaetodermella* Rauschert (1988: 52, Garcia-Sandoval *et al.* 2011).

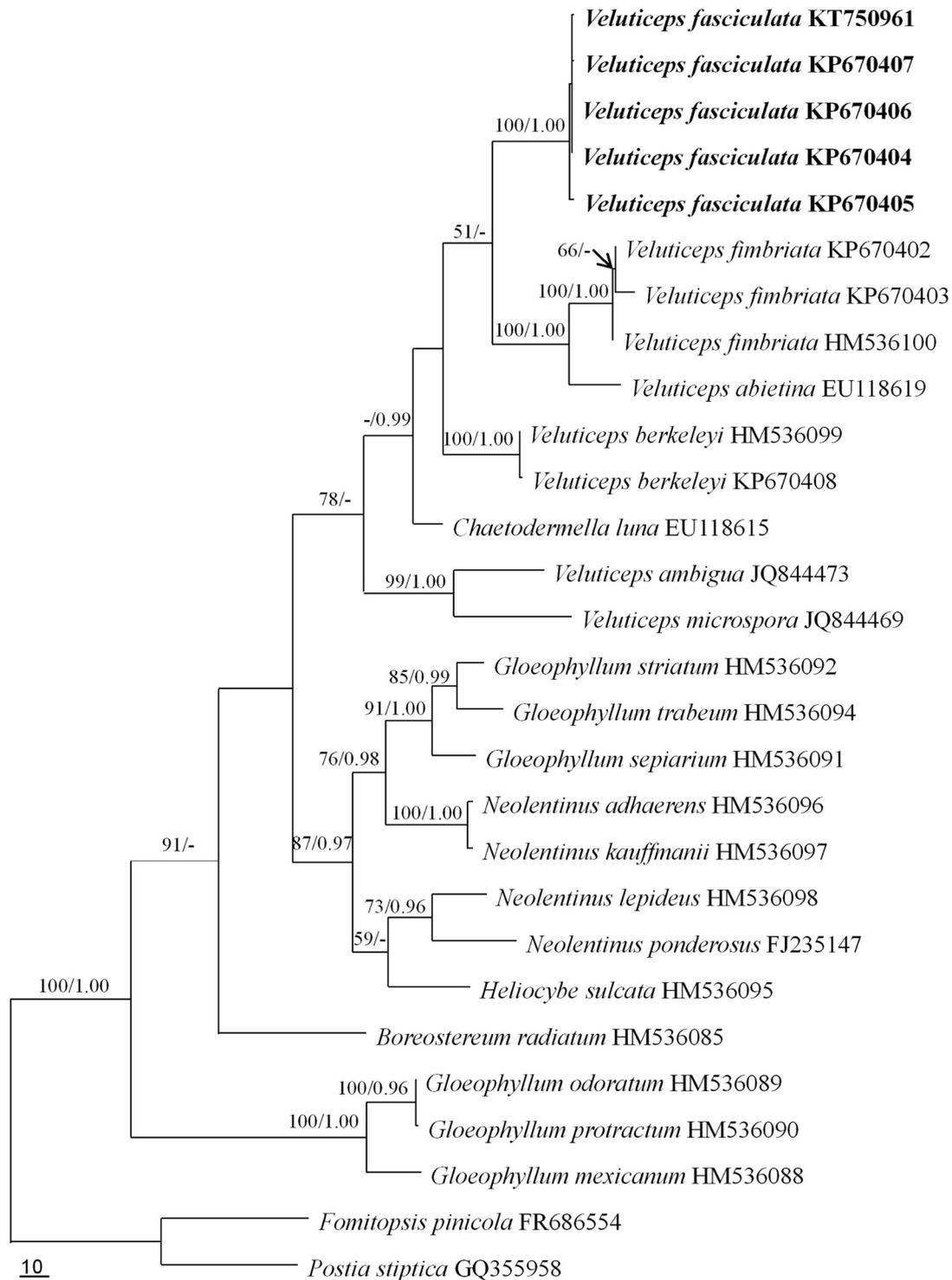
Three species, *Veluticeps abietina* (Pers. 1801: 573) Hjortstam & Tellería (1990: 54), *V. ambigua* (Peck 1894: 145) Hjortstam & Tellería (1990: 54), and *V. microspora* S.H. He & Hai J. Li (2013: 368) are known from mainland China (Dai 2011, He & Li 2013). *Veluticeps berkeleyi* Cooke in Patouillard (1894: 78) is reported from Taiwan (Chen 1973, Davidson & Chen 1976, Nakasone 1990). Recently, several *Veluticeps* specimens on *Cunninghamia* and *Cryptomeria* were collected from southern China, and superficially they were similar to the generic type *V. berkeleyi* that was described from North America on *Pinus*. Upon further study, we were able to readily distinguish the Chinese taxon from *V. berkeleyi* by morphological details and molecular sequences. In this paper, we describe the new species *Veluticeps fasciculata* and report the occurrence of *V. fimbriata* (Ellis & Everh. 1885: 149) Nakasone (1990: 634) in China for the first time.

### Materials and methods

Voucher specimens are deposited in the herbaria of Beijing Forestry University (BJFC) and Center for Forest Mycology Research (CFMR). Microscopic procedures follow Dai (2010). In the text the following abbreviations are used: L = mean spore length, W = mean spore width, Q = variation in the L/W ratios between the specimens studied, n = the number of spores measured from given number of specimens, IKI- = inamyloid and nondextrinoid, CB- = acyanophilous. Color designations are from Kornerup & Wanscher (1978).

CTAB Plant genome rapid extraction kit-DN14 (Aidlab Biotechnologies Co., Ltd) was employed for DNA extraction and PCR amplification from dried specimens and cultures according to the manufacturer's instructions. Approximately 600 base pairs of the ITS rDNA were amplified with primers ITS5 and ITS4, using the following

procedure: initial denaturation at 95 °C for 3 min, followed by 34 cycles of 94 °C for 40 s, 58 °C for 45 s and 72 °C for 1 min, and a final extension of 72 °C for 10 min. DNA sequencing was performed at Beijing Genomics Institute, and the newly generated sequences were deposited in the GenBank database.



**FIGURE 1.** Strict consensus tree obtained from Maximum Parsimony analysis of ITS sequences of taxa in the Gloeophyllales. Parsimony bootstrap values (>50 %, before the slash markers) and Bayesian posterior probabilities ( $\geq 95$  %, after the slash markers) are shown.

The molecular phylogeny was inferred from the ITS sequences of 19 species of Gloeophyllales. Most of the sequences were retrieved from open databases and originated from Larsson (2007), Garcia-Sandoval *et al.* (2011), and He & Li (2013). *Fomitopsis pinicola* (Sw. 1810: 88) P. Karst. (1881: 9) and *Postia stiptica* (Pers. 1801: 525) Jülich

(1982: 424) from Polyporales were selected as outgroup taxa (He & Li 2013). The sequences were aligned using the ClustalX 1.83 (Chenna *et al.* 2003). Alignments were optimized manually in BioEdit 7.0.5.3 (Hall 1999).

Maximum parsimony (MP) analyses were performed using PAUP\* 4.0b10 (Swofford 2002). Gaps in the alignments were treated as missing data. Trees were generated using 100 replicates of random stepwise addition of sequence and tree-bisection reconnection (TBR) branch-swapping algorithm, with all characters given equal weight. Branch supports for all parsimony analysis were estimated by performing 1000 bootstrap (BT) replicates (Felsenstein 1985) with a heuristic search of 10 random-addition replicates for each bootstrap replicate. The tree length (TL), consistency indices (CI), retention indices (RI), rescaled consistency indices (RC) and homoplasy index (HI) were calculated for each tree generated.

For Bayesian inference (BI), best models of evolution were estimated by using MrModeltest 2.2 (Nylander 2004), and posterior probabilities (BPP) were determined by Markov Chain Monte Carlo sampling (BMCMC) in MrBayes 3.1.2 (Ronquist & Huelsenbeck 2003), using the estimated model of evolution. Four simultaneous Markov chains were run for 2,000,000 generations, and trees were sampled every 100th generation. The first one-fourth trees, which represented the burn-in phase of the analyses, were discarded, and the last three-fourth trees were used for calculating posterior probabilities (BPP) in the majority rule consensus tree.

### Phylogeny results

The ITS dataset included 28 sequences representing 21 taxa. The dataset had an aligned length of 631 characters, of which 283 were parsimony informative. MP analysis yielded four equally most-parsimonious trees (TL = 1014, CI = 0.580, RI = 0.724, RC = 0.420, HI = 0.420). The best-fit evolution model for BI was “GTR+I+G”. BI resulted in a similar topology with an average standard deviation of split frequencies = 0.004071. The strict consensus MP tree is shown in Fig. 1, and both BT values (>50%) and BPPs ( $\geq 0.95$ ) are shown at the nodes. The analyses show that taxa in the Gloeophyllales are well separated from the outgroups, and *V. fasciculata* is a distinct lineage in the *Veluticeps/Chaetodermella* group. It was closely related to *V. berkeleyi* and *V. abietina/V. fimbriata* (Fig. 1). The ITS sequences similarity between *V. fasciculata* and *V. berkeleyi* is 85.1% of 565 characters.



**FIGURE 2.** Basidiocarps of *Veluticeps* species (scale bars = 1 cm). a. *Veluticeps berkeleyi* (R.L. Gilbertson 10028). b. *V. fasciculata* (Y.C. Dai 14900). c. *V. fasciculata* (Y.C. Dai 6280). d. *V. fimbriata* (S.H. He 20120920-9).

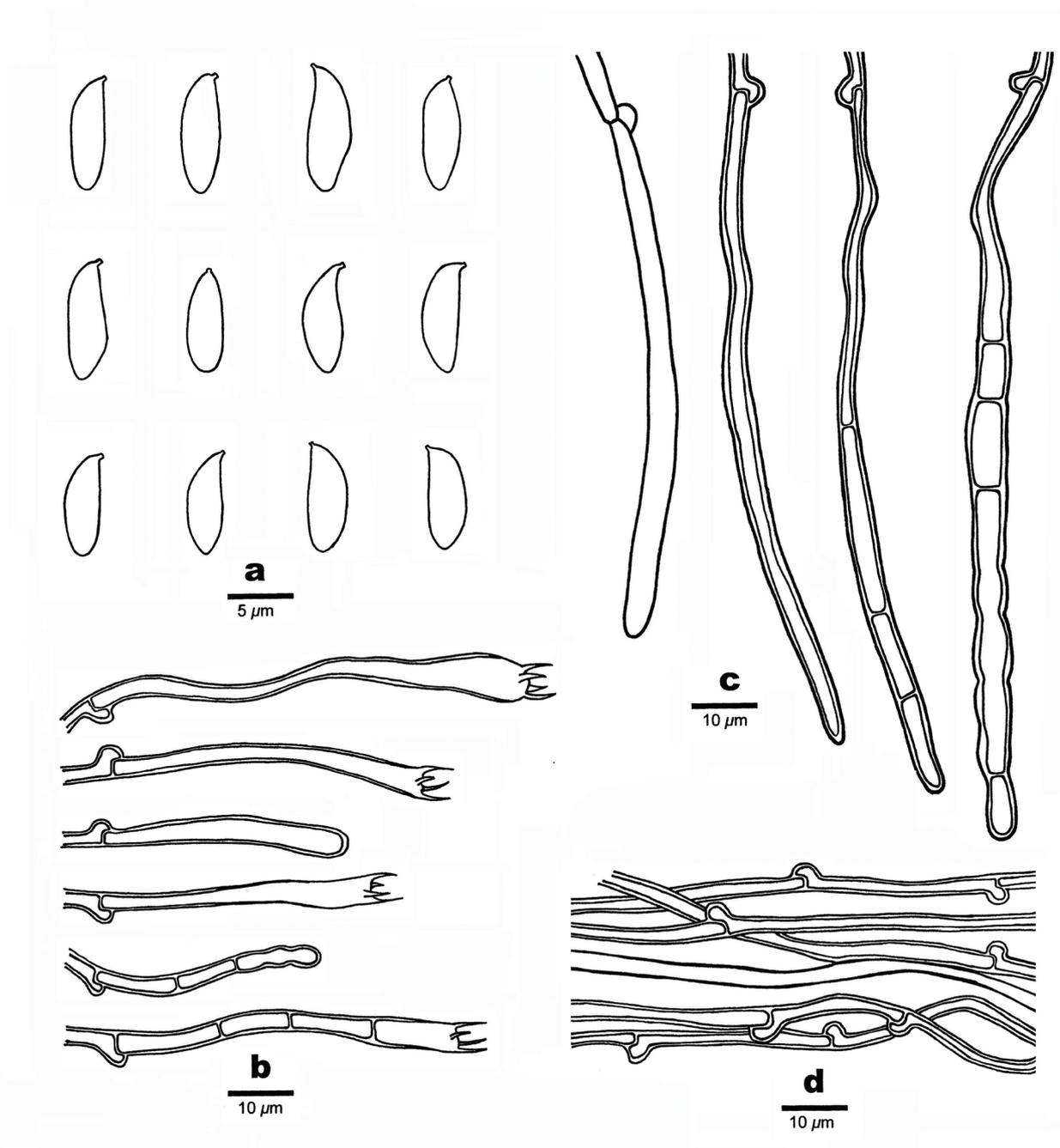
## Taxonomy

*Veluticeps fasciculata* Jiao Yang, Nakasone & S.H. He, *sp. nov.* (Figs. 2b–c, 3)

MycoBank: MB 807532

*Diagnosis.*—The species is distinct by effused basidiocarps, nodose-septate generative hyphae, fasciculate cystidia, and relatively small basidiospores. It is closely related to *V. berkeleyi* but differing in smaller basidia and basidiospores, distribution and host preferences.

*Type.*—CHINA. Jiangxi Prov., Xunwu County, Chejiangyuan, on stump of *Cunninghamia* sp., 17 December 2014, *Dai 15092* (holotype, BJFC!, ITS: KP670405).



**FIGURE 3.** Microscopic structures of *Veluticeps fasciculata* (drawn by Jiao Yang from the holotype). a. Basidiospores. b. Basidia and basidioles. c. Cystidia. d. Subicular hyphae.

*Etymology*.—*fasciculata* (Lat.) refers to the fasciculate cystidia.

*Fruitbody*.—Basidiocarps perennial, effused or with very slightly elevated margin, adnate, separable, coriaceous to soft corky, brittle when dry, first as small patches, later confluent, up to 10 × 4 cm and up to 6 mm thick. Hymenophore smooth, warted or tuberculose, covered with protruding hyphal pegs, not cracked or with few deep crevices, light brown (6D4), greyish brown (6D3) or brown (6E8), margin thinning out, fimbriate, up to 4 mm wide, lighter than hymenophore surface, sometimes concolorous, indistinct.

*Hyphal structure*.—Hyphal system monomitic; generative hyphae with clamp connections; tissue darkening but otherwise unchanged in potassium hydroxide.

*Anatomical structure*.—Cutis absent. Abhymenial tomentum, subiculum, subhymenium and hymenium present. Subiculum composed of more or less parallel and horizontally arranged generative and sclerified generative hyphae. Generative hyphae hyaline, thin- to slightly thick-walled, nodose-septate, moderately branched, 2–4 µm in diam. Sclerified generative hyphae brown, distinctly thick-walled, nodose-septate, not branched, 2–4.5 µm in diam.

*Stratified hymenium*.—Subhymenium thickening or distinctly thickened, composed of vertically arranged and somewhat agglutinated hyphae, collapsed hymenial elements, and fascicles of old cystidia. Hymenium composed of cystidial fascicles, basidia and basidioles. Cystidial fascicles scattered, composed of several to many, loosely clustered cystidia, vertically protruding hymenium into hyphal pegs on hymenophore. Cystidia hyaline to yellowish brown, narrowly cylindrical to slightly moniliform, usually with some slight constrictions in the upper part, with a clamp connection at base, walls thin- to slightly or distinctly thick-walled, up to 120 µm long, 3.8–5 µm in diam., protruding up to 100 µm above the hymenium. Hyphidia absent. Basidia narrowly clavate, stalked, walls thickening toward the base, hyaline, with four sterigmata and a basal clamp connection, 30–65 × 4.5–7 µm; basidioles numerous, similar to basidia but shorter.

*Spores*.—Basidiospores fusiform to cylindrical, mostly tapering at apiculus, hyaline, thin-walled, smooth, IKI-, CB-, 7.2–11.5 × 3–4 µm, L = 9.4 µm, W = 3.3 µm, Q = 2.6–3.1 (n = 60/2).

*Type of rot*.—Causing brown cubical rots on *Cunninghamia* and *Cryptomeria* stumps.

*Additional specimens examined (ITS GenBank number listed last)*.—*Veluticeps berkeleyi*: USA. Arizona, Pima County, Coronado National Forest, Santa Catalina Mts., Lemmon Mt., on fallen trunk of *Pinus ponderosa*, 16 August 1967, R.L. Gilbertson 7116 (KP670408); Cochise County, Coronado National Forest, Chiricahua Mts., Turkey Creek, on fallen trunk of *Pinus ponderosa*, 22 October 1970, R.L. Gilbertson 10028. *Veluticeps fasciculata*: China. Hunan Prov., Liuyang County, Daweishan Nat. Res., on stump of *Cryptomeria*, 10 July 2015, S.H. He 2321 (KT750961); Zhejiang Prov., Lin'an County, Tianmushan Nat. Res., on stump of *Cryptomeria*, 14 October 2004, Y.C. Dai 6236 & 6237 (KP670406), on stump of *Cunninghamia*, 14 October 2004, Y.C. Dai 6280 (KP670407); Guizhou Prov., Jiangkou County, Fanjingshan Nat. Res., on stump of *Cunninghamia*, 22 November 2014, Y.C. Dai 14900 (KP670404). *Veluticeps fimbriata*: China. Sichuan Prov., Luding County, Hailuoguo Forest Park, on gymnosperm wood, 20 September 2012, S.H. He 20120920-8 (KP670402) & 20120920-9 (KP670403).

## Discussion

*Veluticeps fasciculata* is characterized by perennial, effused basidiocarps with a smooth or tuberculose hymenophore, nodose-septate generative hyphae, fasciculate cystidia, relatively small fusiform to cylindrical basidiospores and causing a brown cubical rot.

Two species, *Veluticeps berkeleyi* (Fig. 2a) and *V. australiensis* Nakasone (2004: 271) with fascicled cystidia (Nakasone 1990, 2004) and nodose-septate generative hyphae are most similar to *V. fasciculata*. However, they can be differentiated by basidiocarp habit, basidiospore size, host, and distribution (Table 1). *Veluticeps australiensis* has the largest basidiospores (17–21 × 5–6.5 µm), occurs on angiospermous trees, and is known only from Australia (Nakasone 2004). *Veluticeps berkeleyi* has longer hyphal pegs (protruding about 250 µm), larger basidia (65–100 × 7–8 µm), and larger basidiospores (12–14.5 × 4–5 µm, Nakasone 1990) than *V. fasciculata*. *Veluticeps fasciculata* and *V. microspora* have relatively small basidiospores (7–9 × 2.5–3 µm in *V. microspora*); however, the latter species develops firmer basidiocarps, single cystidia, and simple-septate generative hyphae (He & Li 2013).

Phylogenetically, *Veluticeps fasciculata* nests within the *Veluticeps/Chaetodermella* group, and forms a distinct clade (Fig. 1). The generic type, *V. berkeleyi* is a widely distributed species that is reported in the North and Central America, Europe and Eastern Asia on *Pinus*, *Abies*, *Juniperus*, *Chamaecyparis* and *Pasania* (Chen 1973, Davidson & Chen 1976, Nakasone 1990, 2004, Gorjón & Bernicchia 2010). However, our phylogenetic analyses show (data not

shown) that *V. berkeleyi* may be a species complex with strong host preferences. The ITS sequences of CFMR cultures (ZCC-1-R and RWD-1050-R) of *V. berkeleyi* from Taiwan on *Chamaecyparis* is only 83.6% and 95.3% similar to *V. berkeleyi* and *V. fasciculata*, respectively.

**TABEL 1.** Main characters useful for separating *Veluticeps* species with fasciculate cystidia.

	Basidiocarp habit	Basidiospores size	Substrate	Distribution
<i>V. australiensis</i>	effused	17–21 × 5–6.5 μm	Angiosperm	Australia
<i>V. berkeleyi</i>	effused, effused-reflexed or applanate	12–14.5 × 4–5 μm	<i>Pinus</i> , <i>Juniperus</i> , <i>Abies</i> , <i>Chamaecyparis</i> and <i>Pasania</i>	North America, Central America, South Europe and Eastern Asia
<i>V. fasciculata</i>	effused	7.2–11.5 × 3–4 μm	<i>Cryptomeria</i> and <i>Cunninghamia</i>	China

Two specimens collected from Sichuan Province, Southern China at a high altitude were identified as *Veluticeps fimbriata* by morphological characters and molecular sequences (Fig. 2d). This species is common in North America but is reported for the first time from China. Although brown rot fungi with poroid hymenophore have been intensively studied in temperate and boreal areas of China (Dai & Niemelä 2002, Wang *et al.* 2004, Dai & Penttilä 2006, Wei & Dai 2006, Cui *et al.* 2011, Cui & Dai 2013), the crust fungi in China, especially in subtropical and tropical forests, are still under-collected and poorly known. Future fungal surveys in China will undoubtedly uncover many more species new to science.

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