

# *Trogia venenata* (*Agaricales*), a novel poisonous species which has caused hundreds of deaths in southwestern China

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**Abstract** About 400 unexplained sudden deaths have occurred in Yunnan Province in southwestern China during summers over the last 35 years. Extensive field investigations revealed that a fungus called “little white mushroom” or “nail-like mushroom” by the local people could be one of the chief causes. Fieldwork showed that this fungus is a common saprophytic species growing on rotten wood in southwestern, central, and northwestern Yunnan in subtropical mountainous areas between 1,700 and 3,000 m altitude. Morphological and molecular phylogenetic analyses revealed that it is a new species of the genus *Trogia*, closely related to the palaeotropical *T. infundibuliformis* and its allies. Accordingly, *T. venenata* is described and illustrated.

**Keywords** Poisonous mushroom · Wood-rotting fungi · Taxonomy · Phylogeny · Distribution

## Introduction

Since 1978, more than 400 deaths and several dozen non-fatal cardiac cases in Yunnan Province of southwestern China have been attributed to a condition known as unexplained sudden death syndrome (Shi et al. 2006; Lu et al. 2010; Stone 2010). Field investigations revealed that a

fungus called the “little white mushroom” or “nail-like mushroom” might be the cause of a proportion of these deaths. This fungus is a common saprophytic species that grows on rotten wood in southwestern, central, and northwestern Yunnan between 1,700 and 3,000 m altitude. Two new non-protein amino acids, both of which are fatal to mice, were detected in basidiomata of this species. Furthermore, one of the non-protein amino acids was also detected from the blood of the heart of a man who died from the sudden death syndrome (Zhou et al. 2012). Morphological and molecular phylogenetic analyses showed that this mushroom is a new taxon of the genus *Trogia* Fr. (*Agaricales*, *Basidiomycota*) and closely related to *T. infundibuliformis* Berk. & Broome and its allies. It is described and illustrated here.

## Materials and methods

### Materials studied

Specimens of the “little white mushroom” or “nail-like mushroom” were intensively collected during the last several years in various parts of Yunnan Province, and deposited at the Herbarium of Cryptogams of Kunming Institute of Botany, Chinese Academy of Sciences, China (HKAS). Characteristics, sizes and colors of basidiomata were observed in fresh specimens. Color codes of the form “7A2” are from Kernerup and Wanscher (1981). Color names with first letters capitalized, e.g. “Pale Flesh Color”, are from Ridgway (1912). For microscopic studies, free-hand sections of dried basidioma were prepared. As mounting medium, 5% KOH was used. Basidiospores were examined in Melzer's reagent or in 5% KOH. Dimensions for basidiospores are given using notation of the form (a) b–c (d). The

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range b–c contains a minimum of 90% of the measured values. Extreme values, e.g., a or d are given in parentheses. Q is used to mean ‘length/width ratio’ of a spore in side view;  $\bar{Q}$  means average Q of all specimens  $\pm$  sample standard deviation.

#### DNA extraction, PCR amplification, and DNA sequencing

Total DNA was extracted from silica-gel-dried or herbarium materials using a modified CTAB procedure of Doyle and Doyle (1987). The 5' terminal domain of the nuclear gene coding for the ribosomal large subunit (nLSU-rDNA) was amplified using the primer combination LROR $\times$ LR5 (Vilgalys and Hester 1990). Primer combinations of ITS5 $\times$ ITS4, ITS1F $\times$ ITS4 (Gardes and Bruns 1993) were used to amplify the rDNA internal transcribed spacer (ITS) region. The PCR products were purified using the Biotek's Purification Kit (Biotek, Beijing, China). nLSU-rDNA and ITS were sequenced with an ABI 3730 DNA analyzer and an ABI BigDye 3.1 terminator cycle sequencing kit (Sangon, Shanghai, China). The nLSU-rDNA and ITS sequences obtained in this study have been deposited in GenBank. The accession numbers are presented in Table 1. Sequences of representative taxa of *Agaricales*, with an emphasis on samplings of members in the “*Xerulaceae*” (Redhead 1987) and marasmioid and gymnopoid fungi (Wilson and Desjardin 2005), were retrieved from GenBank and included in our analysis with GenBank accession numbers given in Table 1. DNA sequences were edited and aligned with BioEdit and Clustal X, and manually checked and adjusted where necessary (alignment deposited in TreeBASE with accession no. 12341).

#### Phylogenetic analysis

Three datasets were analyzed: the ITS dataset, the nLSU-rDNA dataset, and the combined ITS and nLSU-rDNA dataset. All datasets were analyzed using Maximum Parsimony (MP), Randomized Accelerated Maximum Likelihood (RAxML) and Bayesian Analysis (BA), respectively. Species in the genus *Gymnopus* (Pers.) Roussel, i.e. *G. contrarius* (Peck) Halling, was chosen as outgroup following the results of Wilson and Desjardin (2005).

For MP analyses, the phylogenetic relationships among the taxa were estimated in PAUP\* v.4.01 (Swofford 2004) under the Maximum Parsimony criterion. MP analysis in PAUP\* used a heuristic search strategy with the following settings: the heuristic search option using the tree bisection–reconstruction algorithm. All sites were treated as unordered and unweighted, with gaps treated as missing data. The strength of the internal branches of the resulting trees was tested with bootstrap analyses using 200 replications with the step-wise addition option set as simple. Tree scores, including tree length, consistency index (CI), retention index (RI), rescaled consistency index (RC), were also calculated.

For ML analyses, we used the RAxML web-server program available at the CIPRES portal in San Diego (<http://8ball.sdsc.edu:8889/cipres-web/Home.do>). This online version implements a very efficient and rapid bootstrap heuristic in RAxML (Stamatakis et al. 2008). For each analysis, a maximum likelihood search using the GTR plus Gamma model plus estimation of invariable sites was selected and a total of 1000 bootstrap replicates were performed.

For BA estimation, all datasets were analyzed further with a Bayesian approach (Metropolis-coupled MCMC or MC3) using MrBayes (Huelsenbeck and Ronquist 2005). Posterior probabilities (PP) were determined twice by running one cold and three heated chains in parallel mode, saving trees every 1,000th generation. Runs were terminated once the average standard deviation of split frequencies went below 0.01. The trees in a burn-in period were excluded, and the 50% majority-rule consensus tree of the remaining trees was calculated by PAUP\* to determine Bayesian Posterior Probability (PP) of each clade.

#### Results

Seventeen specimens with pinkish, dirty white to brownish basidiomata were examined. They all represented the same species within the genus *Trogia*, which we have named *T. venenata* (see below). Morphological characteristics of this species are shown in Figs. 1 and 2. The morphological characteristics of the closely related *T. infundibuliformis* are shown for comparison in Fig. 3. The nLSU-rDNA and ITS sequences from four *T. venenata* collections and two *T. infundibuliformis* collections were analyzed together with sequences of selected taxa in *Agaricales*. The whole length of the nLSU generated for this study ranged from 953 base pairs (*T. infundibuliformis*) to 1,289 bp (*T. venenata*). Each sequence of the latter species has an intron with >412 bp which is 16 bp upstream of the LR5 primer site. Such inserted sequences are identical in length and insertion site to the intron in *T. infundibuliformis* (AY639442) in our nLSU dataset analysis. However, both nLSU sequences of *T. infundibuliformis* from our collections have no intron located 16 bp upstream of the LR5 primer site. Thus, the inserted introns were excluded. The final alignment for ITS, nLSU, combined ITS and nLSU were 908 bp, 918 bp, and 1,826 bp, respectively. Data for the former two separate datasets are not shown here. The combined dataset was analyzed using MP, RAxML and Bayesian method. In the MP analysis, 927 characters were constant, 121 variable characters were parsimony-uninformative, and 778 characters were parsimony-informative. The MP analysis resulted in two equally parsimonious trees of 4,163 steps with CI=0.421, RI=0.673, and RC=0.284. The bootstrap values

**Table 1** Specimens used in molecular phylogenetic studies and their GenBank accession numbers

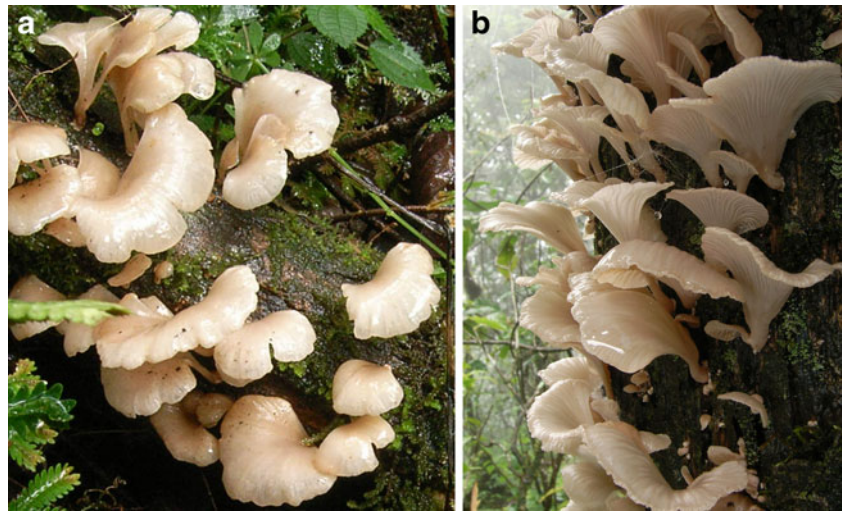
Taxon	Voucher	Locality	GenBank accession	
			nrLSU	ITS
<i>Anthracoephyllum archeri</i>	–	–	NG_027641	DQ444308
<i>Anthracoephyllum lateritium</i>	–	–	AF261324	DQ444309
<i>Baeospora myosura</i> <sup>a</sup>	–	–	AY207146	DQ868344
<i>Baeospora myosura</i> <sup>b</sup>	–	–	AF261363	DQ868345
<i>Baeospora myriadophylla</i>	–	–	AF042634	DQ868346
<i>Calypotella capula</i>	PB315	Norway	AY570995	AY571031
<i>Calypotella</i> sp.	7110217	Japan	AB512346	AB512316
<i>Clitocybula atroalba</i>	PBM1250	Washington	DQ457659	DQ192179
<i>Clitocybula oculus</i>	PBM1156	–	DQ151452	DQ192178
<i>Cylindrobasidium laeve</i>	HHB8633-T	–	DQ234541	DQ205682
<i>Dactylosporina steffanii</i>	TENN58785	–	HM005132	HM005071
<i>Flammulina velutipes</i>	–	–	AY207200	FJ810165
<i>Gerronema strombodes</i>	–	–	AF261364	FJ596789
<i>Gloiocephala aquatica</i>	–	–	DQ097343	DQ097356
<i>Gymnopus contrarius</i>	–	–	DQ457670	DQ486708
<i>Marasmius rotula</i>	PBM2563	–	DQ457686	DQ182506
<i>Megacollybia platyphylla</i> <sup>a</sup>	–	–	AY207239	EU623712
<i>Megacollybia platyphylla</i> <sup>b</sup>	–	–	AM946457	EU623713
<i>Meripilus giganteus</i> <sup>a</sup>	–	–	AJ406537	FR686567
<i>Meripilus giganteus</i> <sup>b</sup>	–	–	AF287874	GQ355959
<i>Mycena amicta</i>	PBM1582	Washington	DQ457692	DQ490645
<i>Neonothopanus nambi</i>	–	–	AF135175	DQ444306
<i>Nolanea sericeum</i>	CBS153.46	–	AF223171	AF357020
<i>Oudemansiella canarii</i>	TENN49023	Puerto Rico	HM005115	GQ892792
<i>Physalacria bambusae</i>	CBS712.83	Japan	DQ097349	DQ097367
<i>Physalacria maipoensis</i>	–	–	AF426959	DQ097368
<i>Porothelium fimbriatum</i>	CBS788.86	–	DQ457673	DQ490626
<i>Quadrispora oblongispora</i>	ID1725	–	AF388746	AF325566
<i>Resinomyccena rhododendri</i>	TENN50793	USA	EU532599	EU517509
<i>Resupinatus applicatus</i>	PB335	France	AY571022	AY571059
<i>Strobilurus conigenoides</i>	–	–	HM005091	GQ892819
<i>Strobilurus esculentus</i>	–	–	AM946468	GQ892801
<i>Strobilurus tenacellus</i>	–	–	AM946470	GQ892812
<i>Thaxterogaster porphyreum</i>	–	–	AF261551	AF325576
<i>Trogia infundibuliformis</i> <sup>a</sup>	KUN-HKAS56709	SW China	*JQ031781	*JQ031776
<i>Trogia infundibuliformis</i> <sup>b</sup>	KUN-HKAS63661	SW China	*JQ031780	*JQ031775
<i>Trogia venenata</i> <sup>a</sup>	KUN-HKAS54710	SW China	*JQ031778	*JQ031772
<i>Trogia venenata</i> <sup>b</sup>	KUN-HKAS48686	SW China	DQ268004	*JQ031774
<i>Trogia venenata</i> <sup>c</sup>	KUN-HKAS56421	SW China	*JQ031777	*JQ031771
<i>Trogia venenata</i> <sup>d</sup>	KUN-HKAS56679	SW China	*JQ031779	*JQ031773
<i>Xeromphalina campanella</i>	–	–	AY207312	GU320009
<i>Xeromphalina junipericola</i>	AH19695	–	GU320010	GU320007
<i>Xerula furfuracea</i>	–	–	EU522838	FJ596856

\*Sequences obtained in this study. Both nrLSU and ITS sequences for the same collection were from following works. Sequences for *Cylindrobasidium laeve*, *Marasmius rotula* and *Mycena amicta* were from Matheny et al. (2007a, b). Sequences for *Gloiocephala aquatica*, *Physalacria bambusae* and *Porothelium fimbriatum* were from Binder et al. (2006). Sequences for *Dactylosporina steffanii* and *Oudemansiella canarii* were from Petersen and Hughes (2010). Sequences for *Calypotella capula* and *Resupinatus applicatus* were from Bodensteiner et al. (2004). Sequences for *Resinomyccena rhododendri* were from Petersen et al. (2008). Sequences for *Nolanea sericeum* were from Moncalvo et al. (2002). The rest sequences of the table were from GenBank. *SW* southwestern. Superscripts (a, b, c and d) are used to relate individual collections of the same taxon to their corresponding sequence data shown in Fig. 4

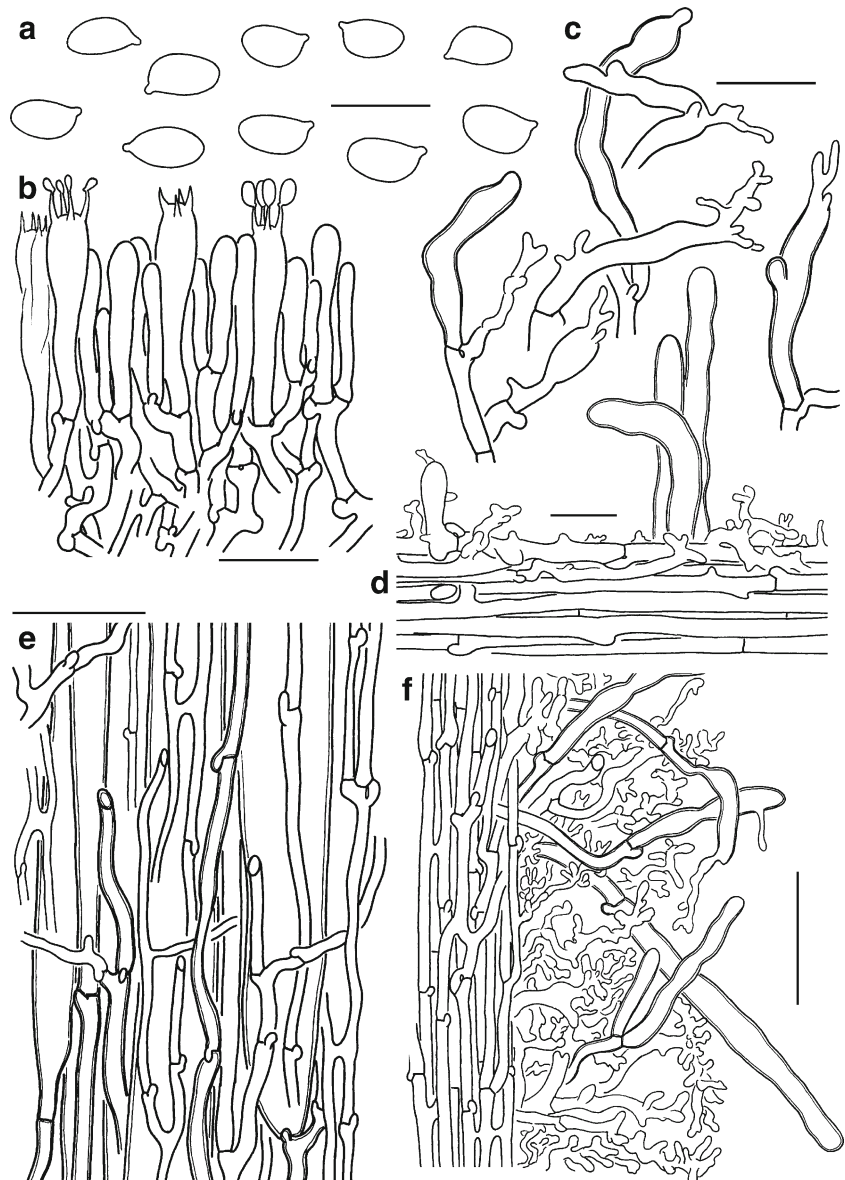
(≥50%) are shown in Fig. 4. Molecular phylogenetic analyses of combined ITS and nLSU-rDNA sequences using three different analysis suggested that *T. venenata* and *T.*

*infundibuliformis* are closely related but different species (Fig. 4). They are placed within *Agaricales* and clustered with *Megacollybia* with moderate support values (62/54).

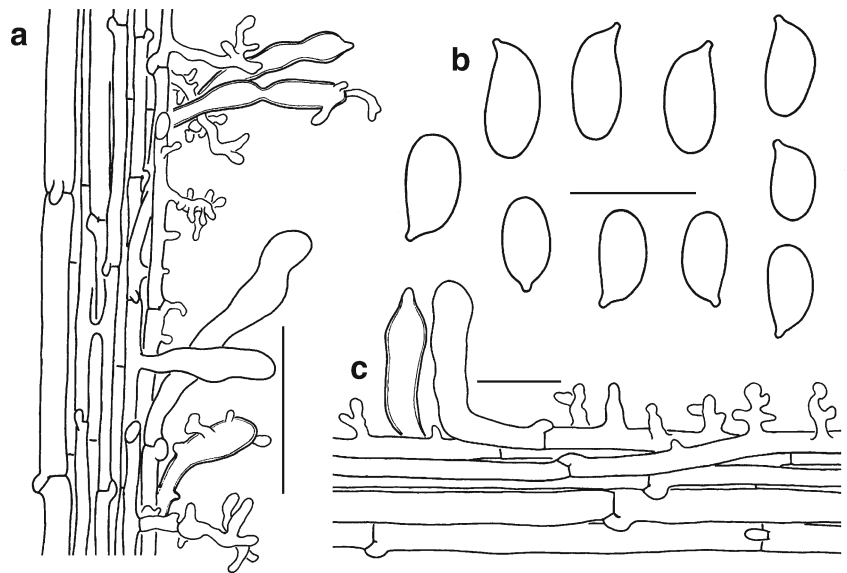
**Fig. 1** Basidiomata of *Trogia venenata*. **a** On a fallen trunk (holotype), **b** on a decaying stump (HKAS 56681)



**Fig. 2** Microscopic characters of *Trogia venenata* (holotype). **a** Basidiospores, **b** basidia and subhymenium, **c** cheilocystidia-like cells on lamellar edge, **d** radial section of pileipellis, **e** longitudinal section of trama of stipe, **f** surface of stipe in longitudinal section showing caulocystidia. Scale bars (**a**, **d**) 10  $\mu$ m, (**b**, **c**) 20  $\mu$ m, (**e**, **f**) 40  $\mu$ m



**Fig. 3** Microscopic characters of *Trogia infundibuliformis* (HKAS 56709). **a** Surface of stipe in longitudinal section showing caulocystidia, **b** basidiospores, **c** radial section of pileipellis. Scale bars (**a**) 40  $\mu\text{m}$ , (**b-c**) 10  $\mu\text{m}$



## Taxonomy

*Trogia venenata* Zhu L. Yang, Y.C. Li & L.P. Tang, sp. nov.  
Mycobank: MB 561711

Figs. 1 and 2

Etymology: “*venenatus*” means poisonous.

Pileus 1–6 cm latus, flabeliformis vel petaloideus, pallide incarnatus, albidus vel brunneolus, subtranslucentius, glabrus, margine undulato. Stipes 0.3–2 (3.5)  $\times$  0.2–0.4 cm, solidus, puberulus vel subglabrus, pallide incarnatus, albidus vel brunneolus. Lamellae angustae, 0.5–1 (3) mm altae, subdistantae vel distantae, pallide incarnatae vel albae, interdum dichotomis, decurrentibus. Caro in pileo tenuis, 0.5–1.5 mm crassa, albida vel pallide incarnata, inordora, ceraceo-mollis, in stipite ceraceo-mollis vel cartilaginea. Basidia 4-sporigera. Sporae 6–8 (9)  $\times$  (3.5) 4–5 (5.5)  $\mu\text{m}$ , non-amyloideae. Fibulae praesentes. Ad truncos delapsos in silva, gregaria.

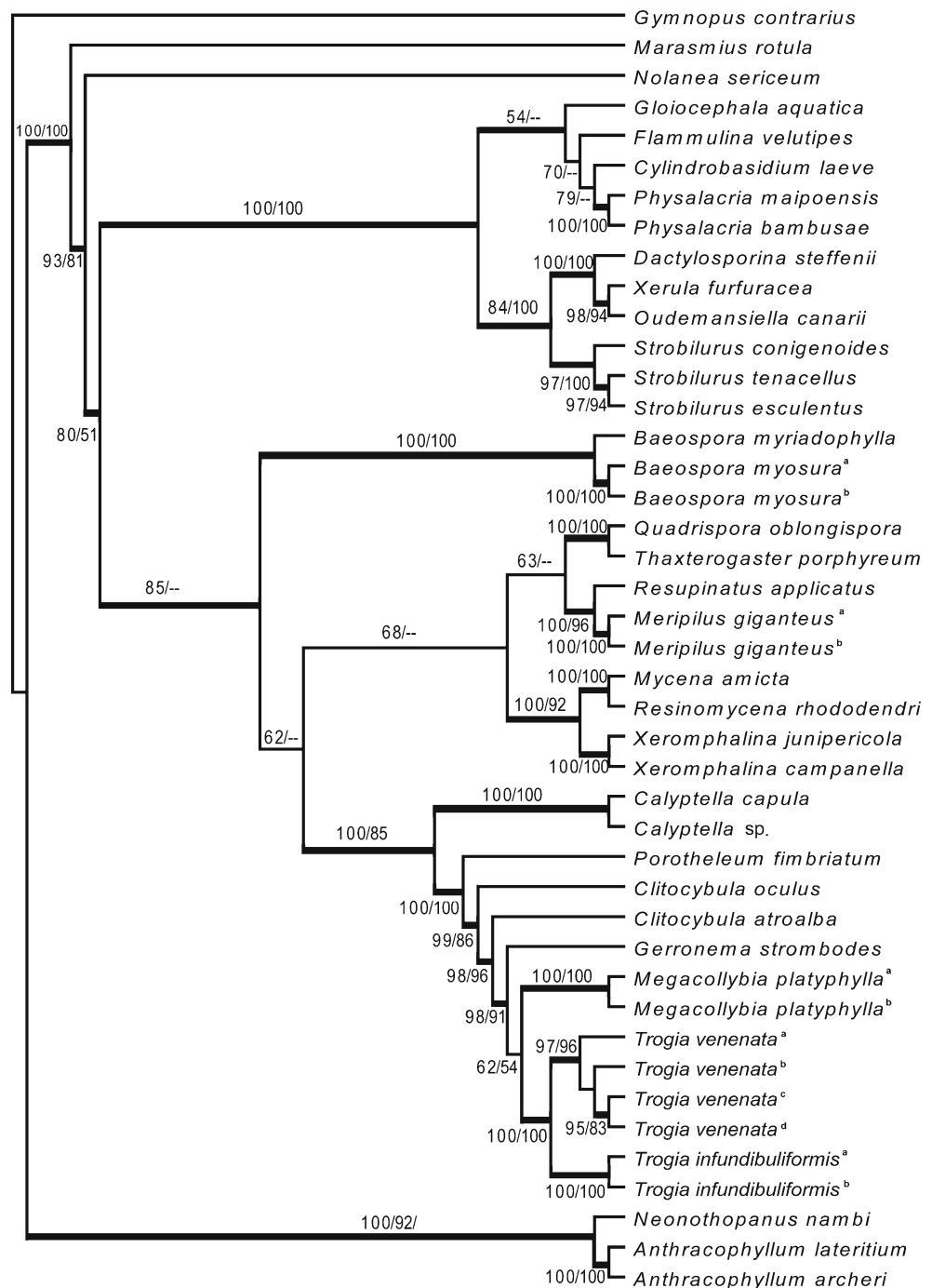
Holotype: Z.L. Yang 5256 (HKAS 56679), 3 July 2009, alt. 2100 m, Jietou, Tengchong, Yunnan, China.

*Basidioma* (Fig. 1) pleurotoid. *Pileus* 1–6 cm in length and width, flabelliform to petal-like, glabrous or nearly so, pinkish to pale meat-colored (paler than 7A2, 8A2, 9A2, and 10A2; paler than Pale Flesh Color) to dirty white to whitish, becoming brownish when mature, subtranslucent; margin undulate, radially and translucently striate, sometimes radially fissile; context thin (0.5–1.5 mm in thickness), dirty white to pale pinkish, pliable and tough; order indistinct. *Lamellae* decurrent, narrow to very narrow, 0.5–1 (3) mm in height, pinkish to dirty white (paler than 7A2, 8A2, 9A2, and 10A2; paler than Pale Flesh Color), subdistant to distant, occasionally branched, edge sometimes

(but not always) canaliculate; lamellulae attenuate. *Stipe* 0.3–2(3.5)  $\times$  0.2–0.4 cm, subcylindrical, finely pubescent to subglabrous, pinkish to dirty white to brownish, tough, fibrous, solid; base discoid or not, but often with a white mycelium. *Basidiospores* white in mass. *Smell* indistinct.

*Basidiospores* (Fig. 2a) 6.0–8.0 (9.0)  $\times$  (3.5) 4.0–5.0 (5.5)  $\mu\text{m}$ ,  $Q=(1.33)$  1.40–1.75 (1.85) ( $Q=1.59\pm 0.12$ ), ellipsoid to pip-shaped, often with slightly attenuate base or apex, thin-walled, colorless, hyaline, smooth, non-amyloid; apiculus relatively large. *Basidia* (Fig. 2b) 38–50  $\times$  6.5–8  $\mu\text{m}$ , clavate, hyaline, 4-spored; sterigmata 3–4 (5)  $\mu\text{m}$  long. *Subhymenium* (Fig. 2b) tightly interwoven, composed of cylindrical cells 6–15  $\times$  3–5  $\mu\text{m}$ . *Lamellar trama* composed of irregularly arranged 2–8  $\mu\text{m}$  wide filamentous hyphae and 10–18  $\mu\text{m}$  wide inflated cells often with slightly thick wall ( $<1$   $\mu\text{m}$  thick). *Pleurocystidia* absent. *Lamellar edge* obtuse, sterile, composed of filamentous hyphae, and scattered arranged, clavate to narrowly clavate, thin- to slightly thick-walled (up to 1  $\mu\text{m}$  thick), colorless and hyaline, flexuose, cheilocystidia-like cells (20–60  $\times$  6–9  $\mu\text{m}$ ) often with terminal outgrowths (Fig. 2c). *Pileipellis* (Fig. 2d) 10–20  $\mu\text{m}$  thick, composed of radially arranged, thin-walled, colorless and subhyaline or with yellowish to brownish cell-walled filamentous hyphae 2–5  $\mu\text{m}$  diam with scattered, nodulose or diverticulate outgrowths 1–2.5  $\mu\text{m}$  in diam. *Pileocystidia* (Fig. 2d) 15–50  $\times$  4–7  $\mu\text{m}$ , cylindrical to narrowly clavate, slightly thick-walled ( $\leq 1$   $\mu\text{m}$  thick), colorless and hyaline, scattered, sometimes 2–5 in groups, smooth or occasionally with outgrowths 1–2  $\mu\text{m}$  in diam. *Pileal trama* composed of radially arranged, colorless, hyaline, branching, sometimes anastomosing, 2–10  $\mu\text{m}$  wide filamentous hyphae, and inflated, subfusiform to long ellipsoid cells (300–500  $\times$  10–20  $\mu\text{m}$ ) with slightly thick walls

**Fig. 4** Phylogenetic tree resulting from the combined ITS and nrLSU rDNA dataset using RAxML analysis. RAxML and MP BS support values (>50%) are indicated above or below the branches as RAxML BS/ MP BS. In Bayesian analysis, PP>0.94 are indicated with *thick branches*



( $\leq 1 \mu\text{m}$  thick); without pseudoparenchyma. *Stipitipellis* (Fig. 2f) composed of appressed, longitudinally arranged filamentous hyphae 2–7  $\mu\text{m}$  wide; surface covered with a layer composed of filamentous hyphae with nodulose or diverticulate outgrowths forming a Rameales-structure, which was often stretched and extensively distorted, and disrupted during the elongation of the stipe. *Stipe context* (Fig. 2e) composed of longitudinally arranged, inflated, fusiform cells (250–800  $\times$  15–25  $\mu\text{m}$ ) with thick walls (0.5–2  $\mu\text{m}$  thick), and branching, colorless and hyaline

hyphae 2–7  $\mu\text{m}$  wide. *Caulocystidia* (Fig. 2f) 30–100  $\times$  5–8  $\mu\text{m}$ , narrowly clavate to subcylindrical, usually thick-walled ( $\leq 1 \mu\text{m}$  thick), colorless and hyaline, moniliform to flexuose, occasionally with outgrowths. *Clamp connections* present in all tissues, abundant.

*Habitat* Scattered or in groups, on decaying stumps, trunks and branches in subtropical broad-leaved or mixed forests dominated by Fagaceae, Theaceae and Pinaceae. Common in rainy seasons in mountainous parts of southwestern, central and northwestern Yunnan at an altitude of 1,700–3,000 m.

*Collections of T. venenata examined CHINA*, Yunnan Province, Dayao County, Shiyang, Guzhen, 24.VIII.2010, Y. C. Li 2087 (HKAS 63662); Chuxiong County, Lucheng, Jiufangcun, 18.VII.2009, G. Q. Shi 2 (HKAS 56687); Jingdong County, Longjie, Shiyakou, 23.VII.2009, G. Q. Shi 3 (HKAS 56688); Kunming, Baoziqing, 28.IX.2008, Y.C. Li 1588 (HKAS 56421); Lufeng County, Gaofeng, Cangdi, 15.VII.2009, G.Q. Shi 1 (HKAS 56686); Nanjian County, Baohua, Mts. Wuliang, 28.VII.2009, G. Wu 29 (HKAS 57560); the same location, 28.VII.2009, Y.C. Li 1846 (HKAS 59594); the same location, alt. 2,230 m, 28.VII.2009, L.P. Tang 982 (HKAS 56939); Tengchong County, Jietou, Shuiqingcun, Zhoujiafen, alt. 2,100 m, in forest dominated by *Lithocarpus* and *Manglietia* sp., 3.VII.2009, Z.L. Yang 5256 (HKAS 56679, holotype); Tengchong County, Qushi, Linjiapu, alt. 2,100 m, in forest dominated by broad-leaved trees, sp. 4.VII.2009, Z.L. Yang 5258 (HKAS 56681); Yingjiang County, Xima, Huanglianhe, alt. 1700 m, 17.VII.2003, Z.L. Yang 3717 (HKAS 42902); Yingjiang County, Xima, Tongbiguan, alt. 2,170 m, 17.VII.2009, L.P. Tang 819 (HKAS 56776); Yulong County, Laojun Mountain, alt. 2,600 m, in forest of *Lithocarpus* sp. and *Pinus yunnanensis*, 2.VIII.2005, Z.L. Yang 4520 (HKAS 48686); Yulong County, Mts. Yulong, Sandaowan, 20.VII.2008, Y.C. Li 1321 (HKAS 56175); the same location, 24.VII.2008, Y.C. Li 1361 (HKAS 56215); the same location, 22.VII.2008, alt. 3,000 m, L.P. Tang 442 (HKAS 54673); Yulong County, Mts. Yulong, Heibaishui, 24.VII.2008, alt. 2,940 m, L.P. Tang 479 (HKAS 54710).

*Collections of T. infundibuliformis examined CHINA*, Yunnan Province, Pingbian County, Qingshuihe, Potoucun, 26.IX.2011, Z.W. Ge 3128 (HKAS 63661); Mengla County, Menglun, Cuipingfeng, alt. 600 m, in tropical limestone monsoon forest, 11.VIII.1995, Z.L. Yang 2158 (HKAS 29473); Mengla County, on the way from Mengla to Menglun, in tropical forest with *Ficus* and *Lithocarpus*, alt. 600 m, 10.VII.2009, L.P. Tang 752 (HKAS 56709).

## Discussion

### Generic concept of *Trogia*

The trama of the pileus and the stipe of *Trogia venenata* is composed of slightly thick-walled, fusiform inflated cells and slender filamentous hyphae, suggesting the so-called sarcodimitic tissue of Corner (1966). Corner (1966, 1991) included 90 species in *Trogia* based on the feature of the sarcodimitic trama and the lignicolous habitat of the species. In contrast, Singer (1986) accepted only three species in the genus based on the easily reviving basidioma, the narrow lamellae with interwoven hyphae in the lamellar trama, and other features. Corner's concept of *Trogia* seems to be

unwieldy (Reid 1967; Smith 1967; Redhead 1987; Mass Geesteranus 1990; Wilson and Desjardin 2005). Unfortunately, the type species of *Trogia*, *T. montagnei* Fr., originally described from southern India, is poorly known, and its type specimen remains untraceable. Accordingly, the taxonomic boundaries of *Trogia* remain unknown (Wilson and Desjardin 2005; Kumar and Manimohan 2009). In their molecular phylogenetic analysis, Wilson and Desjardin (2005) found that *T. infundibuliformis*, a species phenetically similar to the protologue of *T. montagnei*, forms a sister group to the marasmioid clade on a long branch. However, their analysis did not provide strong statistical support. In our DNA sequence analysis, the close relationship of *T. venenata* and *T. infundibuliformis* is strongly supported (Fig. 4). In comparison with the ITS region, the region of nLSU-rDNA, excluding indels, is quite conservative in *Trogia*. Only 6-bp differences were present between the two taxa in the nLSU-rDNA, while 26–27 bp differences were detected in the ITS.

### Morphological comparison with other similar species

*Trogia venenata* is characterized by pleurotooid, pale meat-colored to dirty white to brownish basidiomata; thin but tough and pliable, subtranslucent pilei with narrow to very narrow, distant lamellae; finely pubescent stipes; ellipsoid to pip-shaped basidiospores; a cutis pileipellis of filamentous hyphae with nodulose or diverticulate outgrowths and cylindrical to narrowly clavate pileocystidia; and a surface of the stipe covered with a layer composed of filamentous hyphae with nodulose or diverticulate outgrowths forming a Rameales-structure mixed with narrowly clavate to sub-cylindrical caulocystidia.

*Trogia venenata* is closely related to *T. infundibuliformis* (Fig. 3a–c), but differs from the latter by its flabelliform to petal-like basidioma and shorter basidiospores. Furthermore, *T. venenata* is widely distributed in subtropical areas and contains free amino acids, while *T. infundibuliformis* is restricted in tropical areas of Southeast Asia and South Asia (Corner 1966, 1991; Pegler 1986; Wilson and Desjardin 2005; Kumar and Manimohan 2009), tropical China (this report), and East Africa (Pegler 1977). The chemical constituents of the latter taxon are unknown.

Two additional poorly known taxa, *T. inaequalis* (Berk. & Broome) Corner and *T. grisea* (Berk.) Pat., originally described from Sri Lanka, are closely related to and may eventually be proved as identical to *T. infundibuliformis* according to Pegler (1986). *Trogia inaequalis* differs from *T. venenata* by its deeply infundibuliform orange pileus with ochraceous hymenophore and an orange central stipe (Corner 1966; Pegler 1986). *Trogia grisea* (Berk.) Pat., only known from the type collection, differs from *T. venenata* by its infundibuliform perforate pileus and central stipe, but it

may represent immature material of *T. infundibuliformis* (Pegler 1986).

*Trogia buccinalis* (Mont.) Pat., a species originally described from Guyana (Montagne 1854) is close to *T. infundibuliformis*. However, the neotropical species has a darker colored basidioma, a central stipe, and proportionally wider basidiospores (Montagne 1854; Corner 1966, 1991; Pegler 1983).

The caulocystidia of *T. venenata* are similar to those of *T. cervina* Corner, *T. marasmioides* Corner, *T. subtranslucens* Corner, and *T. venulosa* Corner. However, *T. cervina* has a stereoid basidioma with a smooth hymenophore, and much denser pileocystidia, and its young basidiomata are edible (Corner 1966, 1991). *Trogia marasmioides* has a basidioma with a central to lateral stipe, a pileus with an agglutinated layer composed of branched, gelatinized, 1–2 µm wide hyphae without any pileocystidia, and much higher lamellae (Corner 1991). *Trogia subtranslucens* has a stereoid basidioma with a smooth hymenophore or with faint, short gill-folds at the base, and a pileal surface with radially arranged filamentous hyphae with only nodulose or diverticulate outgrowths 1–3.5 µm in diameter (Corner 1991). *Trogia venulosa* has a basidioma with a central stipe, a lower lamella-like ridges of only 0.2 mm in height (which disappear on drying), and a pileus with much denser pileocystidia (Corner 1991).

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