



## *Hymenoporus paradoxus* gen. et sp. nov., a striking fungus of the family Omphalotaceae (Agaricales, Basidiomycota) with tubular hymenophore

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### Abstract

*Hymenoporus paradoxus*, a new marasmioid fungal species belonging to the new genus is described from southern China. It differs from all other marasmioid species by a true tubular hymenophore, a character previously unknown in marasmioid fungi, and from all other tubular agarics by a hymenophore attached to a free collarium, and central, tough, dark and filiform stipe. The additional diagnostic characters are small basidiocarps, mostly convex pileus, smooth, hyaline, non-amyloid spores, densely packed dendriform cheilocystidia, and pileipellis composed of repent hyphae densely covered with simple to coralloid excrescences, intermixed with dendriform cells. As peculiar morphological characters had indicated, molecular phylogenetic analyses based on the 28S rDNA sequences confirm phylogenetic position of the new species in Omphalotaceae and a need to establish a new genus. Color photographs of macro- and micromorphological characters, SEM microphotographs, and a phylogenetic tree based on the partial 28S rDNA gene are provided.

**Key words:** biodiversity, mycobiota, phylogeny, taxonomy

### Introduction

During a mycological field research of Maoershan Nature Reserve in southern China (the Guangxi Zhuang Autonomous Region), the third author found a new species of marasmioid fungi with the true tubular hymenophore. Marasmioid fungi have been considered as agarics with rather small and often marcescent (reviving) basidiocarps, membranaceous and often striate or sulcate pileus, adnate to adnexed hymenophore (mostly lamellar, rarely alveolar, veined or smooth), tough and filiform stipe, and white or whitish spore print (Antonín & Noordeloos 1993, 2010; Wilson & Desjardin 2005). A true tubular hymenophore is a character previously unknown in marasmioid fungi. As peculiar morphological characters had suggested, molecular phylogenetic analyses based on the nLSU rDNA sequences confirmed that phylogenetic position of our new species requires establishment of a new genus in the family Omphalotaceae Bresinsky (Agaricales, Agaricomycetes, Basidiomycota).

Taxonomic concept of the family Omphalotaceae accepted here is based on molecular phylogenetic analyses (Owings & Desjardin 1997, Moncalvo *et al.* 2000, 2002; Wilson & Desjardin 2005, Matheny *et al.* 2007) which showed that marasmioid fungi are distributed in three phylogenetic clades/families: Marasmiaceae, Omphalotaceae and Physalacriaceae. Mata *et al.* (2007) conducted detailed phylogenetic and taxonomic study of the Omphalotaceae. The main morphological characters of the Omphalotaceae are tricholomatoid, collybioid, marasmioid or clitocybeoid basidiocarps, lamellate hymenophore (except in species described here), mostly normally developed, central or eccentric stipe, mostly absent veil, white, cream or pinkish spore print, and smooth, hyaline, non-amyloid spores. The family comprises ca. 10 already described genera (with ca. 600 known species), including *Gymnopus* (Pers. 1800: xii) Roussel (1806: 62), *Lentinula* Earle (1909: 416), *Marasmiellus* Murrill (1915: 243), *Mycetinis* Earle (1909: 414), *Omphalotus* Fayod (1889: 338) and *Rhodocollybia* Singer (1939: 71). However, aforementioned phylogenetic analyses reveal that two largest genera of Omphalotaceae, *Gymnopus* and *Marasmiellus*, are polyphyletic, so new taxonomic concepts on generic level should be established after more extensive phylogenetic research with more species and DNA sequences included. Some authors have a broader concept of Marasmiaceae which includes Omphalotaceae as well (e.g. Kirk *et al.* 2008, Knudsen & Vesterholt 2012).

## Discussion

According to all macromorphological characters except hymenophore, *H. paradoxus* is strongly reminiscent of the species of *Gymnopus*, section *Androsacei* (Kühner 1933: 91) Antonín & Noordel. in Noordeloos & Antonín (2008: 25) [e.g. *G. androsaceus* (Linnaeus 1753: 1175) Della Maggiora & Trassinelli 2014: 1]. The true tubular hymenophore (Fig. 1C) present in our species is a character previously unknown in marasmioid fungi, as well as in the family Omphalotaceae. In Marasmiaceae, some species of the genus *Campanella* Hennings (1895: 95) [e.g. *Campanella caerulescens* (Berkeley & Curtis 1868: 323) Singer (1945: 190), *C. gregaria* Bougher 2007: 328] and *Marasmius cladophyllus* Berkeley (1856: 138) have strongly anastomosing lamellae with an irregularly alveolate appearance at the most (Singer 1975, 1976). Among other agarics, species with a true tubular hymenophore and well-developed stipe are present in two genera of the family Mycenaceae, *Favolaschia* (Pat. 1887: 231) Pat. in Patouillard & Lagerheim (1892: 116) and *Mycena* (Persoon 1797: 69) Roussel (1806: 64) [including *Filoboletus* Hennings (1900: 146)] (Singer 1945, 1974; Maas Geesteranus 1992). Nevertheless, those species differ from *H. paradoxus* by the hymenophore that is attached to the non-filiform and  $\pm$  light colored stipe. Moreover, our species is distinctive by its specific dendriform cheilocystidia (Fig. 2M–P). Peculiar morphological characters of *H. paradoxus* indicated that this new species should be accommodated into the new genus, what is confirmed by phylogenetic analyses.

The results of our phylogenetic analyses based on 28S rDNA sequences demonstrate that *Hymenoporus paradoxus* belongs to the same clade with other Omphalotaceae species (Fig. 5). This finding is supported with high ML (95%) and PP (1.00) values. Somewhat isolated position of *H. paradoxus* in the Omphalotaceae clade supports a conclusion based on morphological characters that our new species belongs to a new, independent genus. Moreover, the pairwise distances between *H. paradoxus* and all other Omphalotaceae species in our study were much higher (0.1003–0.1263) than mutual distances between other representatives of the family (0.0013–0.0683). This confirms that our new species is considerably divergent from other species in genera within Omphalotaceae family and supports the recognition of *Hymenoporus* at generic level.

Mata *et al.* (2007), in their comprehensive phylogenetic study of the Omphalotaceae based on ITS sequence data, presented phylogenetic tree where *Omphalotus*, *Lentinula* and *Rhodocollybia* are resolved as monophyletic clades and separated from *Gymnopus* superclade (consists of 12 clades, A–N) which includes contemporary genera *Gymnopus*, *Marasmiellus* and *Mycetinis*. Our phylogenetic tree recovered *Rhodocollybia* and *Lentinula* clades which clustered together with clades containing *Marasmiellus* species and part of the genus *Gymnopus* (species nested in clade G–N in Mata *et al.* 2007). *Mycetinis* species (*Marasmius alliaceus* group, clade F) in Mata *et al.* (2007) are clustered together with *Marasmiellus* species and part of the genus *Gymnopus* (clades G–N). This is different from position of *Mycetinis* in our tree, where it is clustered together with another part of the genus *Gymnopus* (species nested in clades A, B and C in Mata *et al.* 2007).

## Acknowledgements

We are grateful to De-Bing Jiang, director of Maoershan Nature Reserve, for giving permission to Chun-Ying Deng to conduct a field research in the reserve. We are thankful to Mira Ristić and Marijan Marciuš for providing SEM photographs. This work was supported by grants from Croatian Ministry of Science, Education and Sports (No. 098-0982934-2719, 098-0982913-2478) and National Natural Science Foundation of China (No. 31260011).

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