





http://dx.doi.org/10.11646/phytotaxa.186.1.1

Fungi of the Russian Far East 2. New species and new records of *Marasmius* and *Cryptomarasmius* (Basidiomycota)

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Abstract

During the study of mycobiota in the Russian Far East several interesting collections belonging to the genera *Marasmius* and *Cryptomarasmius* were made. Here we report the first records of *Marasmius* cf. *ochroleucus*, *M. occultatiformis* and *Cryptomarasmius aucubae* for the investigated territory. Two species (*Marasmius macrocystidiosus*, *M. insolitus*) and one variety (*M. cohaerens* var. *mandshuricus*) are described as new. Detailed morphological descriptions and illustrations are given. The relationships of the studied taxa with close species are discussed. Molecular phylogenetic reconstructions based on ITS and nrLSU data sets were conducted.

Key words: new species; new records; *Marasmiaceae*; *Physalacriaceae*; taxonomy; molecular phylogeny; Far East of Russian Federation

Introduction

This paper represents the second part of a series devoted to the Agaricomycetes of the Russian Far East (Malysheva *et al.* 2013). The genus *Marasmius* Fr. is distributed worldwide and composed of 500–600 species (Tan *et al.* 2009, Wannathes *et al.* 2009a, 2009b, Antonín & Noordeloos 2010). As a result of recent phylogenetic studies this genus has been restricted to a monophyletic lineage containing only members of morphological sections *Marasmius, Sicci, Globulares, Neosessiles* and *Leveilleani* which are accepted by the majority of modern mycologists (Wilson & Desjardin 2005, Tan *et al.* 2009, Antonín & Noordeloos 2010). The other sections recognized by Singer (1976, 1986) were segregated and classified into new genera: sect. *Androsacei* in the genus *Setulipes* (Antonín & Noordeloos 1993), currently belonging to the genus *Gymnopus* (e.g. Wilson & Desjardin 2005), sect. *Alliacei* in the genus *Mycetinis* (Wilson & Desjardin 2005). According to Tan and co-authors (Tan *et al.* 2009), sect. *Fusicystides* should be considered as a synonym of *Setulipes* and sect. *Epiphylli* should be segregated in a new genus allied with *Gloiocephala* in the *Physalacriaceae* (Tan *et al.* 2009). Sect. *Hygrometrici*, maintained in the genus *Marasmius* for a long time, has been transferred to *Physalacriaceae* as a new genus *Cryptomarasmius* T.S. Jenkinson & Desjardin only recently (Jenkinson *et al.* 2014). This paper deals with members of the genus *Marasmius* sect. *Sicci* and *Globulares* as well as those of the recent genus *Cryptomarasmius*.

Advanced studies have shown that the largest sections of *Marasmius* in the modern sense, sect. *Globulares* and sect. *Sicci*, form a well-supported single clade (Wannathes *et al.* 2009b, Antonín & Noordeloos 2010). Conventionally, sect. *Sicci* was divided into series *Atrorubentes*, *Haematocephali*, *Leonini* and *Spinulosi* based on micromorphological features (Singer 1976, Desjardin 1989). All these infrasectional ranks were also found to be non-monophyletic and may be considered artificial groups (Antonín & Noordeloos 2010, Wannathes *et al.* 2009b). However a molecular-based

distinctiveness of the new species and variety. However, their phylogenetic relationships with close taxa and their position inside the genus were not elucidated.

The result of ITS data set analyses suggests that none of the conventional morphological sections or series can be definitely accepted. This conclusion is consistent with data obtained previously (Tan *et al.* 2009, Wannathes *et al.* 2009b, Antonín *et al.* 2012a). In preceding papers, it was supposed that the involvement of nrLSU sequences could be useful for an infrageneric delimitation of *Marasmius* s.str. (Tan *et al.* 2009). Our data indicate that this gene has probably a limited ability to resolve infrageneric groups. The existence of species with morphological features intermediate between conventional series, viz. *Marasmius insolitus*, demonstrates the necessity of updating infrageneric ranks.

It is hoped that further molecular analyses of *Marasmius* s.str. collections in the world based not only on ITS but also on more informative markers working at a higher taxonomic level will help to reveal evolutionary relationships within the genus.

Acknowledgements

We would like to thank the curators of the TENN, NY, TNS and BRNM herbaria for the loan of specimens. We are grateful to Dr. A. Justo (Clark University, USA) for providing the sequence of *Marasmius nigrodiscus* (collection Halling, 9236). Dr. N. Psurtseva, Dr. V. Malysheva (Komarov Botanical Institute), Dr. E. Pimenova (Botanical Garden-Institute, Far East Branch of the Russian Academy of Sciences, Russia) and Dr. M. Gromyko (Sikhote-Alinsky State Nature Reserve, Russia) are thanked for help with the field work. This study was supported by the Russian Foundation for Basic Research (projects N 11-04-01704a, N 12-04-33018 and N 13-04-00838). Studies of the third author were realized through support provided to the Moravian Museum by the Ministry of Culture of the Czech Republic as part of its long-term conceptual development programme for research institutions (DKRVO, ref. MK000094862). We also thank Jan W. Jongepier (Veselí nad Moravou, Czech Republic) who helped to improve the overall language of the manuscript.

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