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A new species of *Phylloporus* (Agaricales, Boletaceae) from India

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Abstract

A new species of *Phylloporus* from Kerala State, India is described, illustrated and discussed based on morphological and molecular characters. The phylogenetic relationship with related species based on ITS sequences is also provided.

Key words: Agarics, Kerala, mycorrhizal host, taxonomy, tropical genus

Introduction

The lamellate genus *Phylloporus* Quél., of Boletaceae is a comparatively small genus with about 70 species known worldwide (Neves & Halling 2010; Neves *et al*. 2012). Members of this predominantly tropical genus are known to form mycorrhizal association with native trees of various families such as Dipterocarpaceae, Fabaceae, Fagaceae, Myrtaceae, Pinaceae and others. The genus was so far known from India by a single species, *P. rhodoxanthus* (Schwein.) Bres. from the pine forests of Kashmir (Abraham, 1993). During our study on the agarics of Kerala, we came across an interesting species of *Phylloporus*, which is described and discussed here.

Materials and methods

Morphological Studies:—Conventional morphology based taxonomic methods were employed for this study. Colour notations refer to Kornerup & Wanscher (1978). Descriptive terms used in the descriptions follow Vellinga (1988). The holotype is deposited at the Herbarium of the Royal Botanic Gardens, Kew (K), and all isotypes and additional materials examined are deposited at the Mycological Herbarium of Jawaharlal Nehru Tropical Botanic Garden and Research Institute, Trivandrum [TBGT (M)].

Molecular studies:—Standard procedures for DNA isolation, PCR and sequencing were applied (Justo *et al*. 2011). The ITS region was amplified using primer pairs ITS1-F and ITS4 (Gardes & Bruns 1993; White *et al*. 1990). ITS sequences generated and additional GenBank sequences were used for the phylogenetic analysis. The newly generated sequences were deposited in GenBank (ITS: KP789659). GenBank sequences of closely related taxa, based on a BLAST search, were used for preparing an ITS sequence data matrix for the phylogenetic analyses.

The ITS sequence data matrix included 26 taxa and *Xerocomus illudens* was used as the outgroup. Sequences were initially aligned in CLUSTALX 2.1 and then manually corrected using MacClade 4.0 (Maddison & Maddison 2000). Ambiguously aligned sequences were excluded, and gaps were treated as missing data. Alignments have been deposited in TreeBASE (TB2:S17133). A Maximum Parsimony analysis was run using PAUP* 4.0 (Swofford 2002), with 1000 heuristic bootstrap replicates, random step-wise addition, and by holding one tree at each step. Max trees was set to 1000. Tree bisection-reconnection (TBR) branch swapping algorithm was used for assessing branch support.

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