Chapter V. Summary
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SUMMARY

The marasmioid group morphologically refers to all of those fungi that possess a marasmioid stature like the genus *Marasmius*, possess the ability of reviving in situ, contain conic to convex pilei with striate to sulcate margin, adnexed to adnate attachment of lamellae and filiform, tough stipes. In comparison, the gymnopoid fungi represent a group of morphologically look-a-like, small, and dull mushroom-forming fungi possessing basidiomes with nonstriate pileus margin, variously attached lamellae and nonfiliform stipes. However, taxa categorizing under these heads due to presence of such morphological features has begun to clarify with the frame of modern taxonomic protocols. To date, marasmioid fungi includes the genera like *Marasmius* (sects. Sicci, Marasmius, and Globulares), *Chaetocalathus*, *Cryptomarasmius*, *Crinipellis* and are categorized under the family *Marasmiaceae* (with exception to *Cryptomarasmius* that currently belongs to *Physalacriaceae*), whereas the gymnopoid fungi falls in the family *Omphalotaceae* and predominantly refer to members of the genus *Gymnopus*, as well as species of related genera like *Marasmiellus*, *Rhodocollybia*, *Lentinula*, and *Mycetinis*.

Throughout the world, among marasmioid genera, there are reports on the occurrence of ca. 600 species of *Marasmius*, 75 well recognized species of *Crinipellis*, and around 28 species of *Cryptomarasmius*. Among gymnopoid genera, ca. 400 epithets had been published on the genus *Marasmiellus*. Compared to the other regions of the world, little attention has been paid for exploring diversity of marasmioid and gymnopoid fungi from India as evident from the previous reports. At present, India is represented by only 69 species of *Marasmius*, three species of *Crinipellis*, four species of *Marasmiellus*, seven species of *Gymnopus*, and there are no reports on the occurrence of the genus *Cryptomarasmius*. Among these reported species from India, most of the attention had been paid from the southern part of India as compared to the Eastern India and the exploration of the diversity of marasmioid and gymnopoid fungi from West Bengal is scarce in the literatures. From West Bengal, the genus *Marasmius* was known only by seven species, *Gymnopus* by two species, and there was no report on the occurrence of *Crinipellis*, *Cryptomarasmius*, *Marasmiellus* till the present study was undertaken.
The study area, West Bengal, shares its topographical extension starting from Himalayas in the north to the Bay of Bengal in the south with regions such as plateau and Ganges delta prevailing in between. The soil characteristics of the region also varies from nutrient poor lateritic sandy loam to clay loam or silty clay loam, sandy to sandy loam, alluvial and partially saline, deltaic alluvial etc. Keeping in view of these enourmous area, favourable ecological conditions, presence of amiable microclimax, the previously reported number of taxa seemed to be an underestimate that soughts for a systematic and thorough exploration of the group. Further many of the previously reported taxa were not systematically worked out in the light of modern taxonomic protocols and their circumscriptions remained incompletely known. To feel all these gaps, the study of marasmioid and gymnopoid fungi of West Bengal was undertaken.

The present work had the following objectives: 1) Identification and documentation of marasmioid and gymnopoid fungi from West Bengal; 2) Assessment of phylogenetic relationship among the collected marasmioid and gymnopoid species based on their molecular (ITS sequences) data; and 3) To provide suitable keys to aid in the identification of marasmioid and gymnopoid species found in West Bengal.

To fulfill the objectives, fresh basidiocarps of the studied groups were collected following standard protocols during subsequent field trips from 2010 to 2016. Microscopic features were observed from dried specimens by making thin handmade sections with the help of Carl Zeiss AX10 Imager A1 phase contrast microscope. For conducting phylogenetic analyses, nrITS region of all the collected taxa were amplified. For PCR amplification, primer pair ITS1 and ITS4 were used. The amplified products were then viewed by performing Agarose gel electrophoresis. The generated sequences were edited manually using BioEdit sequence alignment editor version 7.0.9.0 and used for BLAST searches in the GenBank database to find similar sequences. ClustalX or MUSCLE softwares were used for aligning the newly generated sequences plus sequences acquired from GenBank. The appropriate model of sequence evolution for phylogenetic analyses were determined using jModeltest 2.1.6 v20140903. Maximum likelihood analysis of each data set was performed with RAxML v.8.2.9 and Bayesian inferences were carried out using MrBayes v. 3.2.2.

A total of 45 taxa distributed over five genera like Marasmius (34), Crinipellis (1), Cryptomarasmius (1), Gymnopus (6), and Marasmiellus (3) are fully described with details
illustration in the present work. Artificial keys are provided for all of the encountered taxa, wherever applicable, to the section, subsection, series and species. Description of each species are supplemented with author citations, detailed collection data and information on their distribution. Colour photographs for all of the collected species in their natural habitat and stature is provided. Hand drawing of the microscopic features are also provided.

The most important outcome of the present study includes the discovery of 19 species new to science. Among these, the genus Marasmius consists 16 new species, two new varieties and one new form (including Marasmius midnapurensis, Marasmius vladimirii, and Marasmius luculentus that have been validly published as new to science during the tenure of the present study), Gymnopus includes one new species, and the genus Marasmiellus includes two new species among which Marasmiellus foliophilus has already been validly published during the tenure of the present work. Besides, three species of Marasmius (viz. Marasmius trichotus, M. imitarius, and M. tenuissimus) including one form (Marasmius haematocephalus f. violaceus), two species of Gymnopus (G. menehune, and G. melanopus), one species of Crinipellis (C. cupreostipes), and one species of Cryptomarasmius (Cryptomarasmius exustoides) represent their first distributional record from India. Among other collected taxa, a total of seven species viz. Marasmius beniensis, Marasmius hypochroides, Marasmius leveilleanus, Marasmius leucorotalis, Marasmius pellucidus, and Marasmiellus purpureoalbus are reported for the first time from West Bengal.

The genera with most encountered species were Marasmius with 34 species, followed by Gymnopus with six species, and Marasmiellus with three species. A single representative of each of the genus Crinipellis (C. cupreostipes) and Cryptomarasmius (C. exustoides) was encountered. Of the total number of collected species of Marasmius, 23 belongs to the section Sicci, sect. Neosessiles is represented by a single species, and the sects. Marasmius and Globulares includes four species each. Among 23 species categorized under the sect. Sicci, series Spinulosi includes one species (Marasmius trichotus), ser. Atrorubentes includes five species, ser. Haematocephali consists of five species and series Leonini includes 12 species. All of the six collected species of Gymnopus belong to the section Vestipedes. Three encountered species of the genus Marasmiellus belong to three sections: Rameales (Marasmiellus foliophilus), Candidi (Marasmiellus species 1), and Marasmiellus (Marasmiellus purpureoalbus). The genus Crinipellis and Cryptomarasmius is represented by
a single species each and the occurrence of the genus *Cryptomarasmius* constitutes the first report of the genus from India.

The molecular analysis of taxa belonging to the marasmioid and gymnopoid group based on the nrITS sequence data resulted phylogenetic trees that showed the relative placement of the collected species of *Marasmius, Crinipellis, Cryptomarasmius, Gymnopus* and *Marasmiellus*. For each of the phylogenetic analyses, the ML and BA resulted in trees those were identical in topology. The phylogenetic analyses served well to distinguish between morphologically related species for all the taxa. For the genus *Marasmius*, the presently available morphological features for circumscribing the collected specimens to their corresponding section and subsections were not proved to be much satisfactory based on the nrITS region data alone that reveals the necessity for the incorporation of additional gene regions sequences.

Beside the discovery of ca 42% new species among all of the collected taxa, another major outcome of the present work includes the amplification and newly sequenced 61 nrITS region. This includes 50 sequences for the genus *Marasmius*, six for *Gymnopus*, three for *Marasmiellus*, and one for *Crinipellis* and *Cryptomarasmius* each. All of the newly generated nrITS sequences has been deposited in the GenBank nucleotide database.

The present work constitutes the first thorough and systematic approach towards unveiling the diversity of marasmioid and gymnopoid fungi from India and especially from the state West Bengal with the light of modern taxonomic concept and using molecular sequence data. The voucher specimens deposited in the recognized repository along with the deposited nrITS sequences in the GenBank would create a proper background representation to the future workers with regard to the diversity of marasmioid and gymnopoid fungi from the state West Bengal as well as to the country.