Twelve Undescribed Species of Macrofungi from Korea

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ABSTRACT: A survey of the indigenous fungal resources of Korea was undertaken during 2014-2015. All specimens collected in this study were identified at the species level, based on their morphological characteristics and rDNA sequence data. Among them, 12 macrofungal species, viz. Agaricus guizhouensis, Amanita orientifulva, Armillaria cepistipes, Crepidotus inhonestus, Daldinia chilidae, Elmerina cladophora, Lycoperdon scabrum, Marasmius brunneoaurantiacus, Otidea butonia, Pluteus hongoi, Pluteus variabilicolor, and Russula grisea have not been previously reported in Korea.

KEYWORDS: Diversity, Macrofungi, Undescribed species

Introduction

Macrofungi usually called mushrooms are known to be one of the most important constituents of the forest ecosystem with forest trees. Most of them are in temperate regions and constitute a significant part of terrestrial ecosystems. Their edibility, poisonous nature, and medicinal value, have made them economically, biotechnologically, and medically important [1]. The study of fungal biodiversity has been carried out the world over and so far only 6.7% of 1.5 million species of fungi estimated in the world have been described [2], while 4,686 species of fungi are recorded in Korea by 2015 (National Institute of Biological Resources, https://species.nibr.go.kr). To secure, preserve, and manage the genetic biological resources in Korea, a research project entitled survey and discovery of Korean indigenous fungal species has been performed by aid of National Institute of Biological Resources (NIBR) under the Ministry of Environment, Republic of Korea since 2006.

Materials and Methods

In this study, the distribution of macrofungi at Chungnam, Chungbuk and Jeonnam Provinces, Korea was investigated by analyzing fungal specimens collected during from August 2014 to October 2015. Each specimen was photographed, and details regarding the collection site, habitat, host, substrates, and fruiting bodies of each specimen were recorded prior to collection. Specimens were then brought to the laboratory and dried over mild heat for several days. Dried specimens were deposited in the NIBR. Taxonomic classification of species and the associated nomenclature were assigned using the Index Fungorum database (http://www.index-fungorum.org). Measurements and drawings were made from slide preparations mounted in 3% KOH [3] using a BAM-102i light microscope (MRC Lab, Holon, Israel). Twenty randomly selected mature basidiospores and basidia from each specimen were measured. For molecular identification, total DNA was extracted from dried specimens using an AccuPrep Genomic DNA Extraction Kit (Bioneer, Daejeon, Korea). The internal transcribed spacer (ITS) and partial LSU rDNA regions were amplified using primers ITS5 [4] and LR3 [5], as described by Lee and Jung [6]. DNA sequencing was performed at the DNA Synthesis and Sequencing...
Facility, Macrogen (Seoul, Korea), using the aforementioned primers and an ABI 3730XL DNA Analyzer. The resulting nucleotide sequences were edited using jPHYDIT [7] and deposited in GenBank (accession nos. KX963782 ~KX963793). Specimens were initially identified on the basis of their macro- and microscopic features according to published descriptions (Fig. 1) [8-16].

**Results and Discussion**

Species identities were confirmed by comparison with GenBank reference sequences using BLASTn (Table 1) [17]. A Neighbor-joining (NJ) phylogenetic analysis was implemented in PAUP 4.0b10 [18] with a Jukes-Cantor correction. The robustness of inferred NJ topologies was