

ABSTRACT

The present study deals with the molecular characterization of some mushrooms collected from Miandam, Swat Valley, KPK, Pakistan. Collected mushrooms were characterized based on molecular and phylogenetic techniques using universal primers (ITS1 & ITS4) for amplification of 5.8S rRNA gene of LSU (larger subunit) after extracting DNA using most reliable methods. Eleven (11) taxa belonging to six different Genera viz. *Amanita*, *Crepidotus*, *Inocybe*, *Mycena*, *Russula* and *Turbinellus* were characterized through molecular and phylogenetic analyses of amplified target region. In this analyses their genetic variability and phylogenetic relatedness was studied. These include *Amanita franchetii* (Boud.) Fayod, *Crepidotus* sp. MD32, *Mycena pura* (Pers.) P. kumm., *Inocybe* sp. MD19, *Inocybe* sp. MD34, *Russula* sp. MD03, *Russula* sp. MD13, *Russula* sp. MD14, *Russula nigricans* (Bull.) Fr., *Turbinellus* sp. MD29, and *Turbinellus* sp. MD31. Out of these eleven taxa, *Crepidotus* sp. MD32, *Inocybe* sp. MD19, *Inocybe* sp. MD34, *Turbinellus* sp. MD29, and *Turbinellus* sp. MD31 may be new to science after complete morpho-anatomical characterization. *Russula* sp. MD03, *Russula* sp. MD13, both closely resemble to each other and with some unidentified specie sequences already present in GenBank. Thus these may also be new to science if their morpho-anatomic characterization is done. Whereas *Amanita franchetii* (Boud.) Fayod, *Mycena pura* (Pers.) P. Kumm., *Russula nigricans* (Bull.) Fr., and *Russula* sp. MD14, seem to be never described earlier from Swat Valley, KPK, Pakistan. After phylogenetic data analyses maximum intraspecific variations were observed within *Turbinellus* sp. MD29 (39.9%), and *Turbinellus* sp. MD31 (37.3%). Minimum intraspecific variations were found within the sequences of *Amanita franchetii* (Boud.) Fayod. (5.97%), and *Mycena pura* (Pers.) P. kumm. i.e (-5.17%). This study may serve as baseline for further research to explore the factors responsible for such variations and their effects on the natural adaptability of Mushrooms to our changing environment. Further research should also be taken up to find out how climatic conditions and genetic variability can influence fungal phenology and diversity.