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Morphological and molecular characterization of some mushrooms in Kashmir Himalayan Forests

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ABSTRACT

Mushrooms comprise an important, yet less explored, part of the Himalayan biodiversity. Hence, intensive field surveys—were carried out in the coniferous forests of Yusmarg, Gulmarg, Mammer, Kellar and Pahalgam during the growing seasons of 2016-17 for collection of wild mushrooms. Overall 25 species of mushrooms were collected including the species namely Morchella esculenta, Coprinus comatus, Fomes fomentiarus, Ganoderma lucidum, Neolentinus sp.,Suillus sibiricus, Suillus granulates, Lactarius deliciosus, Russula atropurpurea, Russula aurea, Calvatia sp., Lycoperdon sp., Agaricus bisporus, Cantharellus cibarius, belonging to order Pezizales, Agaricales, Polyporales, Gloephyllales, Boletales, Russulales, Cantharellales and families Coprinaceae, Ganodermataceae, Gloeophyllaceae, Cantharellaceae, Agaricaceae. These were found growing mostly on leaf-litter except Coprinus comatus, Ganoderma and Fomes found on lignicolous habitat. The detailed morphometric measurements were undertaken. All these species are being molecularly characterized and their therapeutic potential is being worked out.

Keywords: Biodiversity, Himalayan, Mushrooms, Species

I. INTRODUCTION

Nature has bestowed Kashmir with special geographical settings, climatic conditions and forest cover, apt for sustaining bewildering diversity of mushrooms. Inadequate exploration and lack of proper identification is a major bottleneck in the way of fair assessment of their extent of diversity[1], calling for an urgent exploration for documentation and characterization. The present work is a part of our broad approach on assessment of the mushroom diversity of the Kashmir valley using molecular approaches. It was a gap –filling attempt to generate passport data to also identify different species on the basis of morphometric analysis.

II. MATERIALS AND METHODS

2.1 MORPHOLOGICAL CHARACTERIZATION:

Extensive field surveys were conducted in the coniferous forests of district Anantnag , Baramullah ,Budgam, Ganderbal, and Pulwama of Kashmir valley during 2016-2017 growing seasons. For the collection of sporocarps standard methods were followed [2]. Different mushroom species were collected in suitable collection bags. Photographs were taken by Nikon D5300 DSLR Camera with a zoom lens of 18 – 140 VR. Passport data and the micro-habitat characteristics of collected species were recorded in the field book (TABLE 1). Sample specimens of each type were properly labelled, given a voucher number and carried to laboratory for

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detailed morphometric examination[3]. Collected specimens were identified by keen observation of structures like pileus, stipe , their shape , structure , gill attachment etc using standard keys (eg . Mycokey, Index fungoram etc) and field guides. Varoius parameters like cap diameter , cap shape, cap color, cap margin, stipe length, stipe diameter, stipe color, thickness of gills, gill attachment, gill spacing, presence /absence of scales, presence /absence of annulus etc. were recorded .

2.2 MOLECULAR CHARACTERIZATION:

The molecular characterization of sporocarps involved the sequencing of internal spacer (ITS) region of the nuclear ribosomal genes (rDNA). [4]

2.2.1 DNA EXTRACTION

Genomic DNA was extracted from fresh sporocarps by manual CTAB method (cetyl trimethyl ammonium bromide). For each species DNA was isolated from five sporocarps and the samples were processed separately. [5] 200–250 mg of material was weighed and grand into fine powder with the aid of liquid nitrogen. 5 ml pre-warmed CTAB buffer (1 M TrisHCl pH 8.0, 5 M NaCl, 0.5 M EDTA pH 8.0, CTAB, 2 % b-Mercaptoethanol) was added to this powder. This mixture was subjected to various steps like addition of chloroform, iso-propyl alcohol, phenol, isoamyl alcohol ribonuclease and finally the DNA pellet was kept in 50 µl TE buffer at -20 C⁰. The purified DNA was separated in a 1 % agarose gel stained with ethidium bromide and the concentration was estimated by comparison with known length standards. [6]

. 2.2.2 PCR ANALYSIS

The ITS region of rDNA was amplified by polymerase chain reaction (PCR) using ITS1 and ITS4 primers in Applied Biosystems 2720 Thermal Cycler. The 50 μ l reaction mixture for PCR amplification contained 2 μ l template DNA, 5 μ l PCR buffer, 5 μ l of 2 mM DNTps, 1 μ l of each primer, and 0.4 μ l of Taq polymerase,4 μ l MgCl₂ and 31.6 millique water. Amplification program started with an initial denaturation step of 94 0 C for 5 min followed by 35cycles of 94 0 C for 40 secs , with an annealing step of 54 0 C for 30 secs, and 72 0 C for 2 min, and a final extension of 72 0 C for 10 min. The purified PCR products of the ITS amplified region were directly sequenced in both directions using the ITS1 and ITS4 pair of amplification primers.[I]

2.2.3 DNA SEQUENCE ASSEMBLY AND ALIGNMENT

Finally the sequenced PCR amplicons were BLAST (Basic Local Alignment Search Tool) searched using the National Center for Biotechnology Information (NCBI),USA data-base for comparison of sequences .The initial alignment of all sequences were made directly using Clustal X multiple alignment program (Higgins et al 1992)(Fig 1 and Fig 2)

III. RESULTS:

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Extensive field surveys were conducted in coniferous forests of District Ganderbal, Anantnag, Pulwama, Baramullah and Budgam (TABLE 2) areas of Kashmir Region[7][8]. A total of 25 different types of mushrooms have been collected so far (TABLE 3). A few of them are unknown.

- In general mushrooms were found abundantly in moist and shady habitats of coniferous forests which are least disturbed.[9]
- Most of mushrooms form mycorrhizal associations with coniferous trees like Pinus wallchiana, Abies pindrow, Piceae smithiana. Few of them like Ganoderma applantum and Fomes have lignocolous growth habit.[10]
- In the present study 25 species of mushrooms belonging to 16 genera and 13 families were recorded. Conspectus of species distribution revealed that Agaricaceae, Coprinaceae and Russulaceae were the dominant families.
- The basidiomycetes constituted the major proportion i.e; 22 species while Ascomycetes constituted only 3 species.
- Majority of mushrooms collected belong to gilled fungi while as species of Boletaceae were porous fungi. Puffballs and cup fungi also lack gills.
- Species of Coprinus, Flammulina, Peziza were found in clusters while as other species occur in scattered patches.
- Mushrooms belonging to genus Suillus and Neolentinus have been characterized molecularly. The sequenced result of two specimens have been shown in the form of a chromatogram. (Fig 3 and 4)

IV. FIGURES AND TABLES:

TABLE1. PASSPORT DATA OF Cantharellus cibarius

S.NO	SCIENTIFI	LOCATION	HABITAT	SEASON	DESCRIPTION
	C NAME				
1.	Cantharellus	Gulmarg	Dense forest area	Summer	Length of stipe =5.5 cm
	cibarius		with mixed		Diameter of cap =5.3 cm
			plantation found		Stipe diameter =0.7 cm
			on moist soil		Gill spacing = 0.1 cm
			under shrubs		Cap shape : Infundibuliform
					Cap color: yellowish cream
					Cap margin :Wavy and inrolled
					Thickness of gills : Venticose
					Stipe base : Unswollen
					Attachment of gills :Decurrent
					Stipe attachment : Central
					Gill branching: Dichotomous
					Gill margin : Smooth and entire

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	Stipe shape :Cylindrical
	Stine interior · Solid

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TABLE 2. STUDY AREA FOR THE COLLECTION OF MUSHROOMS

Site Name	Altitude	Latitude	Longitude	Site Characteristics	District
	masl				
Kellar	1630	33 °46' N	74°46′ E	Open coniferous forests	Pulwama
Gulmarg	2703m	34°03' N	74°23' E	Dense forest area with mixed plantation	Baramulla
Yusmarg	2400m	33°50' N	74°38′ E	Open forests and some grassy forest fields	Budgam
Pahalgam	2740 m	34°01N	74°31' E	Open Coniferous forests	Anantnag
Mammer	2400 m	34°14N	75°01' E	Open forest areas with coniferous trees	Ganderbal

TABLE 3: LIST OF COLLECTED MUSHROOMS

S no.	Family	Genus	Species
	Agaricaceae	Agaricus	
1.			1. Agaricus campestris
			2. Agaricus bisporus
		Lycoperdon	3.Lycoperdon pyriforme
			4.Lycoperdon perlatum
2.	Boletaceae	Suillus	5.Suillus granulatus
			6.Suillus sibiricus
3.	Cantharellaceae	Cantharellus	7 .Cantharellus cibarius
4.	Coprinaceae	Coprinus	8. Coprinus disseminatus
			9. Coprinus comatus
			10. Coprinus atramentaria
5	Fomitopsidaceae	Fomitopsis	11 .Fomitopsis rosea
6	Ganodermataceae	Ganoderma	12.Ganoderma applanatum
7.	Gloeophyllaceae	Neolentinus	13.Neolentinus lepideus

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3.	Morchellaceae	Morchella	14.Morchella esculenta
9.	Pezizomycetes	Peziza	15.Peziza vesiculosa
10.	Physalacriaceae	Flammunila	16 .Flammulina velutipes
11.	Polyporaceae	Fomes	17 .Fomes fomentarius
		Trametes	18.Trametes versicolor 19.Trameteshirsuta
12.	Russulaceae	Russula	20.Russula firmula
		Lactarius	21.Russula aurea 22 .Lactarius deliciosus 23 .Lactarius scrobiculatus
13.	Sclerodermataceae	Scleroderma	24 .Scleroderma citrinum

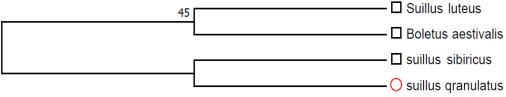


Figure 1. Phylogenetic tree of Suillus sp.

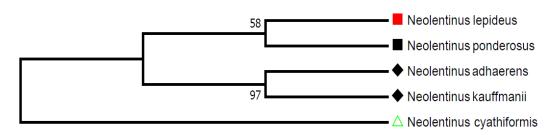
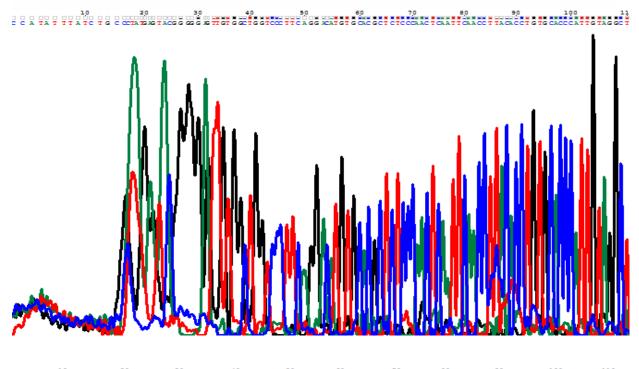


Figure. 1 Phylogenetic tree of *Neolentinus sp.*

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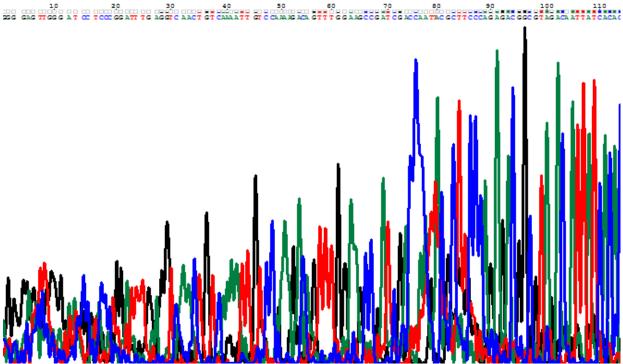


Figure 3 and 4 :Chromatograms showing sequenced results B17-ITS 1 and B17-ITS 4 (Neolentinus lepideus)

V.CONCLUSIONS

The present work enabled us to assess the diversity of mushrooms in the different regions of Kashmir Himalaya. By using different keys we have done the morphometric analysis of mushrooms that gives us an insight that

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even species belonging to same genus vary in certain traits. Furthermore, since there are many indiscrepancies in the accurate identification of mushrooms, therefore, applying the molecular approaches along with morphological approaches authenticated their taxonomic status and we able to identify them upto species level. This work will also lead us to discover new species as the fungal diversity is very huge.



Paxillus involutus

Lactarius deliciocus

Neolentinus lepideus







Suillus sibiricus

Coprinus comatus

Russula atropurpurea







Amanita pantherina

Ganoderma applanatum

Fometopsis pinicola

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