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Species Diversity of Macrofungi from Aravalli Mountain Range Forest of Rajasthan

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ABSTRACT

The present study revealed exploration and documentation of macrofungal diversity of the Aravalli Mountain Range of Rajasthan state of wild life sanctuaries viz., Mount Abu wildlife sanctuary, Kumbhalgarh wildlife sanctuary and The Sitamata wildlife sanctuary. Combination of molecular characteristics (ITS-5.8S gene sequences) and morphological traits (macroscopic and microscopic features), basidiocarp specimens designated 77 species comprised 58 genera belonging to 32 family. Presence of climatic factors with vegetation types are the potential reasons of distribution of macrofungi throughout the Aravalli range forest. Authenticity of different macrofungi species with their habitat, occurrences, ecological significances, etheno-mycological importance were highlighted ecosystem stability and human welfare purposes.

Key words: Fungal diversity, Macrofungi, Diagnostics, ITS-5.8S gene sequences.

INTRODUCTION

Aravalli mountain range is the most dynamic and ecologically sensitive zones lying between (Himalayan mountain range (North India) and Western ghat range (South India). It is an eroded stub mountain range originated in the Precambrian period (Roy, 1990). The Aravalli mountain forest exhibits versatile ecological habitats due to juxtaposition of Palaeoartic, Oriental and Saharan elements. It is characterized by high erratic rainfall, extremes of diurnal and annual temperature, high humidity and low wind velocity. Soil profiles are characterized by normal contents of silt, clay and humus. Vegetation types are dry deciduous forest, thorn forest and mixed xerophytes woodland (Bhalla, 2016).

Macrofungi from Aravalli Mountain forests have been under estimated wealth of fungal diversity, which needs to be documented. DNA based methods have been employed for truthful identification of fungi. The nuclear ribosomal DNA (rDNA) gene sequence i.e. Internal Transcribed Spacer (ITS) encompassing the 5.8S gene is universally accepted molecular marker approach for the authentication of species specially macrofungi (White *et al.*, 1990) since ITS polymorphism can occur at the genus, species, inter-species and intra-species level that distinguish organisms (Singh *et al.,* 2005a; 2005b, 2013; Kakani *et al.,* 2011).

The objective of the present study is to use ITS rDNA sequences supported by basidiocarp morphology to characterize and document macrofungi from Aravalli Mountain range forest for revealing biodiversity, community structure and their possible future assessment in neutraceutical, pharmaceutical and industrial purposes.

MATERIALS AND METHODS

Study areas and collection of macrofungi basidiocarps

Three sanctuaries viz., Mount Abu wildlife sanctuary (coordinate 24º36’ N and 72º42’ E, average temperature 15°C to 30°C and average rainfall 1615 mm), Kumbhalgarh wildlife sanctuary (coordinate 25º08' N and 73º35' E, average temperature 25°C to 40°C and average rain fall 725 mm) and The Sitamata wildlife sanctuary (coordinate 24.04' N and 74.25' E, average temperature 25°C to 42°C, average annual rainfall of about 756 mm) located at Aravalli mountain range were surveys for collection of naturally occurring macrofungi during rainy season (July to

October Month, Year 2021-2023). Standard methods of collection, preservation, macroscopic and microscopic observation were used as described by Natarajan and Manjula (1981). Collection of ground-dwelling macrofungi specimen comprises careful removal of whole fruit body from the ground ensuring that the basal surface remains intact. The tree dwelling macrofungi were sampled by cutting off the basidiomata from the trees and collected into the paper bags that were further stored in small card board box and brought to the laboratory. The specimen was preserved under -20 °C until used. Photographs were taken for macroscopic characteristics. Inquiries were also made about the utility of specimen from foresters and local persons. The utilization of different macrofungi for food and as medicine has been documented from the available literature.

Morphological characterization of macrofungi

The collected macrofungi basidiocarps specimens were characterized for morphological (macroscopic and microscopic) characteristics. Observations on morphological and other phenotypic parameters (different part of fruiting bodies like shape, size, colour, texture, cap, stalk, attachment of stipe gills, volva, annulus, basidia, basidiospores etc.) were recorded. Microscopic studied of the hyphae, mycelia, gills, basidia, cystidia and basidiospore were studied by preparing semi-permanent slide. Photomicrographs were done with a Light Microscope Olympus CH 20I attached with a digital Camera Canon DS126491. Basidiocarps were matched with the macrofungi taxonomic literature reviewed by Singer (1986), Pegler (1997), Jordan (2004) Phillips (2006) Cannon and Krick (2007) and Mohanan (2011).

Molecular characterization of specimens

Extraction of Genomic DNA

Genomic DNA was extracted from preserved freeze dried basidiocarps. Approximately 100 mg of mycelia mass from each specimen was ground with a micro-pestle in a 1.5 ml Eppendorf tube with liquid nitrogen. DNA was extracted in a Hi Pura® plant minikit (Hi Media Laboratories, India) following the protocols suggested by and Sambrook *et al.,* (1989).

PCR amplification of ITS region and sequence analysis

The polymerase chain reaction (PCR) was carried out using universal primers ITS-1 and ITS-4 (White *et al.,* 1990) to amplify the 5.8S rRNA region. Each amplification was performed in a total volume of 50 µl containing 0.2 µl Taq DNA polymerase (5 U/µl of Promega), 5 µl 10× PCR buffer (10 mM Tris HCl, pH 8.3, 500 mM KCl, 15 mM MgCl2: Sigma Chem.) 0.4 µl dNTP mix (MBI Fermentas), 1 µl each of ITS-1 and ITS-4 primers, 2 µl 5 % (v/v) glycerol, 4 µl genomic DNA and 36.4 µl dH_2O. The reactions were performed in a thermal cycler (Applied Biosystems, USA). with following conditions: 1 min denaturation at 95 °C, 30 s annealing at 50 °C, 1 min 20 s elongation at 72 °C, repeated for 34 cycles with a final elongation step of 10 min at 72 °C. Amplicons were separated on 1.6 % agarose gel, detected using ethidium bromide and photographed under UV light using the gel documentation system (BIO-RAD XR+ 170 – 8170). Sequence analysis Amplicons were sequenced using ITS-1 (forward primer) and ITS-4 (reverse primer) by the big dye terminator method in an ABI prism DNA sequencer (Model 3100 Avant). The sequence data obtained employing the ITS-4 reverse primer was inverted and complemented using Genedoc software, and joined with sequence data of ITS-1 after deleting the common portions to obtain the complete sequence of the ITS product.

Nucleotide Blast (NCBI) and GenBank accession number

Nucleotide sequence comparisons were performed using the Basic Local Alignment Search Tool (BLAST) network services of the National Centre for Biotechnology Information (NCBI) database. Fungal species were designated based on maximum similarity with the best aligned reference sequence of NCBI database. The complete rDNA sequences of ITS1 and ITS2, encompassing the 5.8S gene region of each of the macrofungi, were submitted to the NCBI database (GenBank) and accession numbers obtained.

RESULTS

The present study established with the collection of 881 macrofungal basidiocarp from the Aravalli mountain range. Out of these collections, 393 macrofungi specimens were collected from Mount Abu wildlife sanctuary, 264 basidiocarps were collected from Kumbhalgarh wildlife sanctuary and 224 basidiocarps were collected from the Sitamata wildlife sanctuary. On the basis of morphological resemblances, 77 basidiocarp specimens were scrutinized for species designation at molecular level (ITS-5.8S gene sequences). It is allowed to

annotate 62 specimens at the species level and 15 specimens at genus level **(Table 1).** Scrutinized 77 basidiocarps were also complimented by their morphological and microscopic characteristics.

The synchronized molecular and morphological data confirmed 77 macrofungal species **(Figure 1 to 77)** belonging to 58 genera and 32 families. The highest number of basidioma macrofungal species (74) found in Mount Abu wildlife sanctuary followed by 59 species from Kumbhalgarh wildlife sanctuary and 54 species from The Sitamata wildlife sanctuary. Present study computed family Agaricaceae (40.62%; 13 species of 8 genus), harboring the maximum number of species followed by Polyporaceae (28.12%; 9 species of 7 genus), Entolomataceae (15.62%; 5 species of 4 genus) and Hymenochaetaceae (12.5%; 4 species of 3 genus). Genus Agaricus was the dominant genus exhibited the maximum number of species (4 species) followed by *Cepidotus* (3 species) *Marasmius* (3 species) *Scleroderma* (3 species) and *Trametes* (3 species). It is observed that twenty-eight species were growing as saprophytic in nature that grow on dead twigs and wood log. Fourteen species were reported as wood decaying in nature (parasite on living wood). Nineteen species were found to be grown on leaf litters. Eighteen species were observed to grow on humus soil or grasslands. Three species were observed coprophilous in nature that grow on animal dung. One *Termitomyces sp***.** was observed to be associated with termite nest. Seven species viz., *G. multipileum, A. nigricans, A. srilankensis, S. albidum, S. citrinum, S. bovista* and *P. albus* were found persistly grown habitat after rainy season.

During survey, Basidiocarps of *A. subrufescens, A. parviniveus, X. epipastus, C. sterquilinus, Coprinus sp., Microspalliota sp., T. operculatum, P. pistillaris, Bolbitius sp., Conocy beaurea, C. utricystidiata, C. applanatus, P. rogueiana, C. aureogranulatus, L. pretense, M. brunneoaurantiacus, M. leveilleanus, Porotheleum* sp., *G. keralense, Mycena* sp., *P. djamor, R. brunneoaurantiaca, Tricholosporum sp., Termitomyces sp,. S.commune, P. albus, S. albidum, Scleroderma citrinum, T. ellipsospora, T. pavonia, M. xanthopus, G. multipileum, H. tenuis, P. lacerate, P. fulvum, E. tuberculata, A. nigricans, F. senex, Fuscoporia gilva ,Phylloporia* sp. and *Ramaria* sp. were noticed frequently occurring.

P. albus was observed as large number of individuals. Five species viz., *P. albus, S. albidum, S. citrinum, S. bovista, A. nana* were found to associated with tree roots as ecto-mycorrhizal association.

Ethenomycological survey and study revealed, 19 species are edible viz., *A. subrufescens, A. glabriusculus, A. parviniveus, T. operculatum, P. pistillaris, L. pretense, C. holothurioides, C. Menehune, H. furfuracea, P. djamor, C. prunulus, Termitomyces sp., G. sacchari, T. pavonia, G. multipileum, A. nigricans, A. srilankensis, Geastrum, triplex* and *G. xerophilum.* Five species viz., *A. manicata, A. nana, Ramaria* sp*., O. olivascens* and *L. birnbaumii* are poisonous. Six species viz. *Lentinus sp., G. multipileum, M. xanthopus, T. elegans, S. commune* and *A. nigricans* are medicinally important. Nine species viz., *T. ellipspora, G. multipileum, Entoloma sp., P. albus, A. nigricans, P. pistilaris, Termitomyces sp., S. commune,* and *Lentinus sp.* found economically significance for ethenomycophilic society. They collected every year and have formed an integral part of their diet, medicine and other use during the onset of the monsoon.

DISCUSSION

The Aravalli Mountain range are ancient mountains since Precambrian period of mountains in India approximately 692 km in a South-West direction, from Delhi through Rajasthan to Gujarat. The Aravalli mountain range mainly representing tropical dry deciduous vegetation that is one of the extremely most threatened ecosystems in the world. The oldest mountain range exhibits a wide variety of habitats and a considerable biodiversity due to juxtaposition of Palaeoartic, Oriental and Saharan elements.

Table 1 revealed 77 basidiocarp specimens identified by using of ITS-5.8S gene sequences with the best match. Although some specimen have less than 99.1% similarity to their best match, but by using morphology characteristics features (macroscopic, microscopic features) correct species were identified. Borg Dahl *et al.,* (2017) advocated that Genbank reference sequences having 99.1% similarity threshold for name of species validation but Irina *et al.,* (2005) contempt that identification of fungi through single marker i.e. ITS-5.8S gene sequences has certain limitations.

Table 1. Nucleotide length, similarity percent identity and Genbank accession number of Macrofungi along with their reference sequences.

S. No.	Basidiocarps specimen collection code	Nucleotide conting length (bp)	Closest GenBank match	Similarity (%)	Putative Identified species	Family	Genbank accession number
1	JP3	669	*Crepidotus applanatus* MZ648447	98.51	*Crepidotus applanatus*	Crepidotaceae	OR827556
2	JP5	631	*Tramete ellipsospora* isolate DQS23F MZ735409	99.68	*Trametes ellipsospora*	polyporaceae	OR827557
3	JP12	632	*Trametes pavonia* isolate DQS3F MZ735400	99.68	*Trametes pavonia*	Polyporaceae	OR827558
4	JP15	701	*Porotheleum* sp. Voucher MO302934	85.47	*Porotheleum sp.*	Porotheleaceae	OR827560
5	JP16	670	*Marasmius brunneoaurantiacus* Voucher JES 218 (SFSU) KX149014	99.54	*Marasmius brunneoaurantiacus*	Marasmiineae	OR827561
6	JP17	657	*Microporus xanthopus* strain N.L. Bougher NLB 1312 ON715789	99.09	*Microporus xanthopus*	Polyporaceae	OR827562
7	JP21	624	*Trametes elegans* isolate B1 MF377404	99.84	*Trametes elegans*	Polyporaceae	OR827563
8	JP22	641	*Ganoderma multipileum* isolate GANO_LM OR052683	99.84	*Ganoderma multipileum*	Polyporaceae	OR827564
9	JP23	644	*Pluteus sp*. JR-2021a voucher JAD 342 (SFSU) OM060384	99.22	*Pluteus sp.*	Pluteaceae	OR827565
10	JP24	748	*Agaricus subrufescens* Strain JSR3 MT525362	99.33	*Agaricus subrufescens*	Agaricaceae	OR827566
11	JP25	660	*Entoloma sp*. 'TN07' PP526104	97.88	*Entoloma sp.*	Entolomataceae	OR827567

S. No.	Basidiocarps specimen collection code	Nucleotide conting length (bp)	Closest GenBank match	Similarity (%)	Putative Identified species	Family	Genbank accession number
12	JP26	657	*Omphalotus olivascens* voucher GKVK-14 MF403068	99.85	*Omphalotus olivascens*	Omphalotaceae	OR827568
13	JP27	743	*Agaricus sp.* AA-2016b KU848188	94.93	*Agaricus sp.*	Agaricaceae	OR827569
14	JP29	752	*Leucocoprinus birnbaumii* voucher SL1291 OR434569	99.47	*Leucocoprinus birnbaumii*	Agaricaceae	OR827570
15	JP30	632	*Pisolithus albus* strain CMU52-8 JQ365190	99.84	*Pisolithus albus*	Pisolithaceae	OR827571
16	JP-31	659	*Leucocoprinus cepistipes* Voucher HAW: JKS91 MK412593	99.23	*Leucocoprinus cepistipes*	Agaricaceae	OR827572
17	JP-32	556	*Auricularia nigricans* isolate TFB11410 JX065176	100	*Auricularia nigricans*	Auriculariaceae	OR827573
18	JP33	696	*Clitopilus prunulus* voucher KWGM 37 KY630515	99.84	*Clitopilus prunulus*	Entolomataceae	OR827574
19	JP34	736	*Phylloporia sp*. 'CA01' OR800061	88.20	*Phylloporia sp.*	Hymenochaetaceae	OR827575
20	JP37	678	*Scleroderma bovista* strain 5-1 HM237175	99.85	*Scleroderma bovista*	Sclerodermataceae	OR827576
21	JP40	628	*Rhodocybe brunneoaurantiaca* Voucher CUH AM720 MW023201	99.84	*Rhodocybe brunneoaurantiaca*	Entolomataceae	OR827577
22	JP41	811	*Gymnopus menehune* SFSU DED5866 NR-185505	99.38	*Collybiopsis menehune*	Omphalotaceae	OR827578

S. No.	Basidiocarps specimen collection code	Nucleotide conting length (bp)	Closest GenBank match	Similarity (%)	Putative Identified species	Family	Genbank accession number
23	JP42	693	*Xanthagaricus epipastus* voucher HMJAU:45197 MH166763	99.25	*Xanthagaricus epipastus*	Agaricaceae	OR827579
24	JP43	438	*Stereopsis radicans* isolate MT02 Ok446718	97.72	*Stereopsis radicans*	Agaricomycetes	OR827580
25	JP44	649	*Gyrodontium sacchari* voucher MEL:2382749 KP012932	99.85	*Gyrodontium sacchari*	Coniophoraceae	OR827581
26	JP45	673	*Tulostoma operculatum* Strain B2102 MK278642	100	*Tulostoma operculatum*	Agaricaceae	OR827582
27	JP47	561	*Phlebiopsis lacerate* Voucher SWFC00003747 MT180949	99.82	*Phlebiopsis lacerata*	Phanerochaetaceae	OR827583
28	JP48	693	*Tricholosporum sp*. BAB-5013 KR002902	100	*Tricholosporum sp.*	Asproinocybaceae	OR827584
29	JP49	683	*Stropharia sp.* 'OH01' isolate OMDL PP156305	94.42	*Stropharia sp.*	Strophariaceae	OR827585
30	JP51	754	*Marasmius hypochroides* voucher L 0783588AKD OR242230	99.46	*Marasmius hypochroides*	Marasmiaceae	OR827586
31	JP52	711	*Gerronema keralense* CAL 1666 NR_159832	98.55	*Gerronema keralense*	Porotheleaceae	OR827587
32	JP54	693	*Lycoperdon pratense* isolate iNAT 37437365 OM203514	96.30	*Lycoperdon pratense*	Lycoperdaceae	OR827588
33	JP56	686	*Mycena* sp. voucher CT20160222_Mycena_luguensis MG324366	99.53	*Mycena sp.*	Mycenaceae	OR827589

S. No.	Basidiocarps specimen collection code	Nucleotide conting length (bp)	Closest GenBank match	Similarity (%)	Putative Identified species	Family	Genbank accession number
34	JP57	637	*Podoscypha petalodes* strain 1HB F 1616 KF475892	100	*Podoscypha petalodes*	Podoscyphaceae	OR827590
35	JP58	732	*Calvatia holothurioides* isolate KSRF0025 OR936849	99.86	*Calvatia holothurioides*	Lycoperdaceae	OR827591
36	JP61	806	Hymenopellis furfuracea isolate TWS (19)-YJM MN062770	99.12	*Hymenopellis furfuracea*	Physalacriaceae	OR827592
37	JP62	754	*Fomitiporia bannaensis* strain MUCL 46950 GU461943 383	99.87	*Fomitiporia bannaensis*	Hymenochaetaceae	OR827593
38	JP65	647	*Coriolopsis trogii* strain S-13 OP001426	99.84	*Coriolopsis trogii*	Polyporaceae	OR827594
39	JP66	710	*Crepidotus dentatus* Voucher HFJAU-TD375 MN622715	99.25	*Crepidotus dentatus*	Crepidotaceae	OR827595
40	JP69	639	*Punctularia atropurpurascens* isolate CA FUNDIS iNaturalist# 53879558 OR713804	99.68	*Punctularia atropurpurascens*	Punctulariaceae	OR827596
41	JP70	652	*Ramaria sp.* TENN055095 KY352639	81.71	*Ramaria sp.*	Gomphaceae	OR827597
42	JP73	713	*Podaxis pistilaris* Voucher LINN1287.7 MW430044	99.86	*Podaxis pistillaris*	Agaricaceae	OR827598
43	JP74	697	*Coprinellus aureogranulatus* voucherHMJAU 46304 MH379152	99.71	*Coprinellus aureogranulatus*	Psathyrellaceae	OR827599
44	JP76	679	*Scleroderma citrinum* Voucher 195 MH930125	99.85	*Scleroderma citrinum*	Sclerodermataceae	OR827600

S. No.	Basidiocarps specimen collection code	Nucleotide conting length (bp)	Closest GenBank match	Similarity (%)	Putative Identified species	Family	Genbank accession number
45	JP77	666	*Fuscoporia senex* Voucher ZD 16081601 MN523248	99.84	*Fuscoporia senex*	Hymenochaetaceae	OR827601
46	JP80	652	*Hexagonia tenuis* Voucher CLZhao 3629 MK268959	99.68	*Hexagonia tenuis*	Polyporaceae	OR827602
47	JP81	696	*Crepidotus indicus* voucher TBGT15950 MK370662	99.43	*Crepidotus indicus*	Crepidotaceae	OR827603
48	JP82	615	*Pleurotus djamor* voucher MIL329 KT273366	99.67	*Pleurotus djamor*	Pleurotaceae	OR827604
49	JP84	672	*Scleroderma albidum* voucher SMDB:14512 KJ676526	100	*Scleroderma albidum*	Sclerodermataceae	OR827605
50	JP88	688	*Conocybe aurea* strain AMO16 MG663237	99.56	*Conocybe aurea*	Bolbitiaceae	OR827606
51	JP90	641	*Earliella scabrosa* voucher biocode08-59 MZ996933	99.53	*Earliella scabrosa*	Polyporaceae	OR827607
52	JP91	611	*Efibula tuberculata* isolate MT34 OK446737	99.81	*Efibula tuberculata*	Irpicaceae	OR827608
53	JP96	596	*Geastrum triplex* voucher TNS:KH-JPN08-189 JN845135	90.36	*Geastrum triplex*	Geastraceae	OR827609
54	JP97	601	*Termitomyces sp.* BAB-4750 KR154979	97.17	*Termitomyces sp.*	Lyophyllaceae	OR827610
55	JP98	691	*Candolleomyces asiaticus* Voucher LAH36975 OK392606	99.42	*Candolleomyces asiaticus*	Psathyrellaceae	OR827611
56	JP99	633	*Porostereum fulvum* OQ784282	98.72	*Porostereum fulvum*	Phanerochaetaceae	OR827612

S. No.	Basidiocarps specimen collection code	Nucleotide conting length (bp)	Closest GenBank match	Similarity (%)	Putative Identified species	Family	Genbank accession number
57	JP101	700	*Marasmius leveilleanus* voucher NW1337 MW426416	99.71	*Marasmius leveilleanus*	Marasmiaceae	OR827613
58	JP102	658	*Entoloma luteodiscum* CAL 1312 NR_152918	99.85	*Entoloma luteodiscum*	Entolomataceae	OR827614
59	JP103	671	*Coprinus sterquilinus* culture CBS:114.21 MH854689	99.55	*Coprinus sterquilinus*	Agaricaceae	OR827615
60	JP106	611	*Geastrum xerophilum* MG987624	98.85	*Geastrum xerophilum*	Geastraceae	OR827616
61	JP107	690	*Hymenochaetaceae sp.* JCM 28405 LC133842	99.57	*Fuscoporia gilva*	Hymenochaetaceae	OR827617
62	JP109	545	*Bolbitius sp.* voucher biocode08-212 MZ996991	99.45	*Bolbitius sp.*	Bolbitiaceae	OR827618
63	JP112	612	*Schizophyllum commune* Isolate NSC MH221094	100	*Schizophyllum commune*	Schizophyllaceae	OR827619
64	JP113	692	*Psathyrella rogueiana* MICH 12031 NR-173216	98.56	*Psathyrella rogueiana*	Psathyrellaceae	OR827620
65	JP8	749	*Amanita manicata* voucher RET 387-4 HQ625014	99.87	*Amanita manicata*	Amanitaceae	PP059067
66	JP38	698	*Conocybe utricystidiata* MHO94243	99.05	*Conocybe utricystidiata*	Bolbitiaceae	PP059068
67	JP59	672	*Micropsalliota sp.* OVM-2.021a voucher LE312536O KJ257212	89.66	*Micropsalliota sp.*	Agaricaceae	PP059070
68	JP139	720	*Rhodophana sp.* FM-2024b voucher LAH38133 PP357038	86.94	*Rhodophana sp.*	Entolomataceae	PP059071

S. No.	Basidiocarps specimen collection code	Nucleotide conting length (bp)	Closest GenBank match	Similarity (%)	Putative Identified species	Family	Genbank accession number
69	JP140	593	*Itajahya rosea* voucher LAH108210 KF481955	99.83	*Itajahya rosea*	Phallaceae	PP059072
70	JP201	534	*Chlorophyllum palaeotropicum* voucher Z.W. Ge 2519 MG741977	99.44	*Chlorophyllum palaeotropicum*	Agaricaceae	PP059073
71	JP202	743	*Agaricus parviniveus* voucher PU318 MH997906	100	*Agaricus parviniveus*	Agaricaceae	PP059074
72	JP203	676	*Coprinus sp*. Voucher JLF6813 OR272259	95.17	*Coprinus sp.*	Agaricaceae	PP059075
73	JP204	518	*Auricularia srilankensis* Voucher Dai 19520 MZ647508	100	*Auricularia srilankensis*	Auriculariaceae	PP059076
74	JP205	672	*Lentinus sp.* GZMS-25 KX377592	94.31	*Lentinus sp.*	Polyporaceae	PP059077
75	JP206	653	*Agaricus glabriusculus* voucher CUH AM002 OL444817	99.54	*Agaricus glabriusculus*	Agaricaceae	PP059078
76	JP207	709	*Disciseda hyalothrix* voucher NSK1014099 MN151399	97.04	*Disciseda hyalothrix*	Lycoperdaceae	PP059079
77	JP208	630	*Amanita nana* voucher KS45 OR434193	99.84	*Amanita nana*	Amanitaceae	PP59080

Agaricus subrufescens isolate JP24


Agaricus glabriusculus isolate JP206

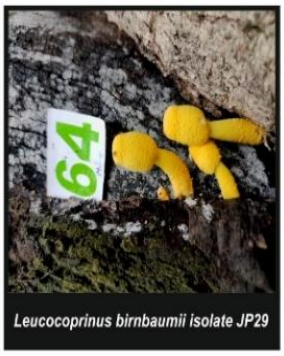

Agaricus parviniveus isolate JP202

Agaricus sp. isolate JP27


Xanthagaricus epipastus isolate JP42


Coprinus sterquilinus isolate JP103


Coprinus sp. isolate JP203



Leucocoprinus birnbaumii isolate JP29

Leucocoprinus cepistipes isolate JP-31

Chlorophyllum palaeotropicum isolate JP201

Microspalliota sp. isolate JP59


Tulostoma operculatum isolate JP45

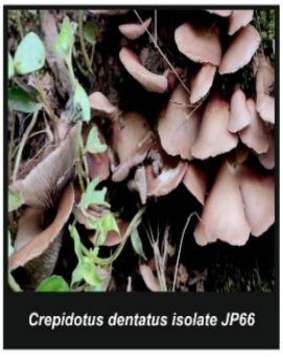

Podaxis pistillaris isolate JP73

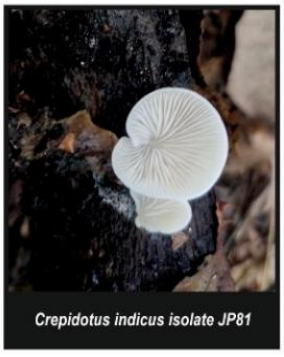

Bolbitius sp. isolate JP109

Conocybe aurea isolate JP88

Conocybe utricystidiata isolate JP38


Crepidotus applanatus isolate JP3

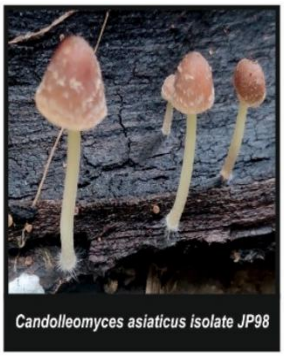

Crepidotus dentatus isolate JP66


Crepidotus indicus isolate JP81

Stropharia sp. isolate JP49

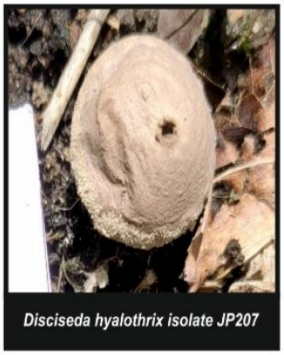

Psathyrella rogueiana isolate JP113

Coprinellus aureogranulatus isolate JP74


Candolleomyces asiaticus isolate JP98


Lycoperdon pretense isolate JP54

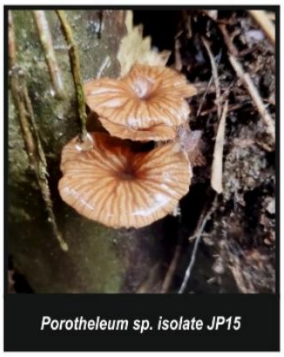
Calvatia holothurioides isolate JP58


Disciseda hyalothrix isolate JP207


Marasmius brunneoaurantiacus isolate JP16


Marasmius hypochroides isolate JP51


Marasmius leveilleanus isolate JP101

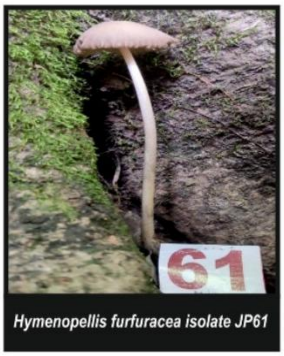

Porotheleum sp. isolate JP15

Gerronema keralense isolate JP52


Omphalotus olivascens isolate JP26


Collybiopsis menehune isolate JP41

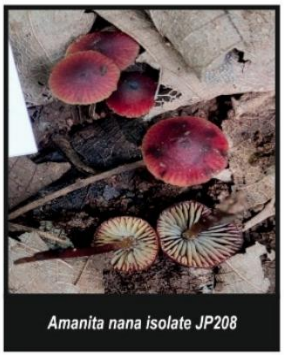

Mycena sp. isolate JP56



Hymenopellis furfuracea isolate JP61

Pluteus sp. isolate JP23

Amanita manicata isolate JP8


Amanita nana isolate JP208


Pleurotus djamor isolate JP82

Entoloma luteodiscum isolate JP102


Entoloma sp. isolate JP25

Clitopilus prunulus isolate JP33


Rhodocybebrun neoaurantiaca isolate JP40

Rhodophana sp. isolate JP139


Tricholosporum sp. isolate JP48

Termitomyces sp. isolate JP97


Schizophyllum commune isolate JP112

Pisolithus albus isolate JP30


Scleroderma albidum isolate JP84


Scleroderma citrinum isolate JP76


Scleroderma bovista isolate JP37


Gyrodontium sacchari isolate JP44


Trametes ellipsospora isolate JP5

Trametes pavonia isolate JP12


Trametes elegans isolate JP21


Ganoderma multipileum isolate JP22


Microporus xanthopus isolate JP17


Coriolopsis trogii isolate JP65

Hexgonia tenuis isolate JP80

Earliella scabrosa isolate JP90


Lentinus sp. isolate JP205


Phlebiopsis lacerate isolate JP47

Porostereum fulvum isolate JP99


Podoscypha petalodes isolate JP57


Efibula tuberculata isolate JP91

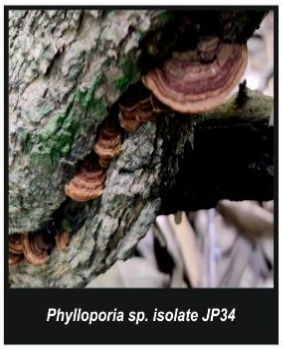

Auricularia nigricans isolate JP-32


Auricularia srilankensis isolate JP204


Fomitiporia bannaensis isolate JP62


Fuscoporia senex isolate JP77

Fuscoporia gilva isolate JP107


Phylloporia sp. isolate JP34


Punctularia atropurpurascens isolate JP69


ramaria sp. isolate JP70

Geastrum triplex isolate JP96


Geastrum xerophilum isolate JP106


Itajahya roseae isolate JP140


Stereopsis radicans isolate JP43

Therefore consideration of macro- and micro-morphology parameters must be incorporate for accurate identification of fungi specially macrofungi. Present study uncovered authentication of diverse 77 macrofungal species of 58 genera belonging to 32 family occurring in Aravalli mountain range forest, Rajasthan. Similarly, Bhatt *et al.,* (2014) studied macrofungal diversity in Adwani forest of Garhwal Himalaya, Uttarakhand and found 365 macrofungal specimens that assigned to 24 species, 12 genera of 6 families. Sharma *et al.,* (2022) identified 83 wild macrofungal species belonging to 35 genera, 24 families and 9 orders from Kishtwar High Altitude National Park (KHANP), Jammu and Kashmir, India.

The statistically interpretation of present study revealed Aravalli Mountain range forest area was dominated by the family Agaricaceae harboring the maximum number of species followed by Polyporaceae, Entolomataceae and Hymenochaetaceae while, Agaricus was the dominant genus exhibited maximum number of species followed by *Cepidotus, Marasmius, Scleroderma,* and *Trametes.* Congruently, Pande *et al.,* (2004) reported *Amanita* (15 sp.), *Russula* (13 sp.), *Boletus* (12 sp.) and *Lactarius* (9 sp.) as the dominant genus from Western Himalayas (India). *P. albus* was observed large number of individuals with high reproductive success. Similarly, Panda *et al.,* (2019) studied Russula *delica* was the highest number of individual occurring species from Northan Orissa, India.

Present result demonstrated that twenty-eight species were reported as saprophytic in nature that grow on dead twigs and wood log, fourteen species were reported as wood decaying in nature (parasite on living wood), nineteen species were found to be grown on leaf litters, eighteen species were observed to grow on humus soil or grasslands, three species were coprophilous in nature, one species was associated with termite nest, seven species were found after rainy season and frequent re-occurrence of maximum species revealed the presence of adequate moisture, promising temperature, relative humidity, light, sunshine, surrounding vegetation, soil nutrients and other climatic factors are the potential reasons of different habitat species occurrence. Hu *et al.,* (2022) studied that the occurrence of macrofungi in different occupancy (habitation) of single ecosystem is mainly are primarily impacted by vegetation (tree residue, wood log, dead wood, leaf litter), soil type, topography, and environmental factors, such as precipitation, humidity and temperature. Sridhar (2009) state that apart from vegetation, macrofungi (saprophytic, mycorrhizal and wood decaying fungi) are directly or indirectly responsible for the stability and perpetuation of ecosystem habitat.

Present result revealed *P. albus, S. albidum, S. citrinum, S. bovista, A. nana* were found ecto-mycorrhizal association might playing significant role in stabilization of forest ecosystem, community maintenance, decomposition of organic materials and mineral recycling functioning. Abdel-Aziz and Bakhit (2023) testified that ectomycorhizal fungi associated with large number of forest tree roots play signified role in increase the rate of decomposition, water holding capacity of soil, mineralization of micronutrients, establishment of seedling, rate of seedling survival, seedling resistance to infection by certain feeder root pathogens, growth and development of seedling.

Present ethnomycological survey result and sideways literature study revealed, 19 species were edible, five species were poisonous, six species were medicinally important, nine species were economically significance to ethenomycophilic society exposed significance of diverse macrofungi occurring in Aravalli mountain range not only for stability of ecosystem but also for human welfare. Weiqi *et al.,* (2023) evaluated significance of macrofungi species diversity with forest resources and ecosystem stability.

CONCLUSION

The present study revealed that the Aravalli Mountain range forest is good habitat of macrofungi encompassing a significant number, diverse types of species, their distribution and etheno-mycological significances. Study revealed macrofungi is directly or indirectly associated with decomposing of leaf litters, soil fertility, mineral recycling suggested a correlation with forest health. The study also provided baseline information of macrofungi species diversity that can be used to measure rate of decomposition, rate of mineralization, soil minerals profile, mycorrhizal association etc. that directly or indirectly effect on stability of ecosystem.

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