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**SOIL MYCOBIOME OF A TEAK INHABITED LAND IN CHENGALPET, INDIA:
A METAGENOMIC STUDY**

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Abstract: Soil mycobiome plays a major role in soil health along with biotic and abiotic factors. They are found to increase or maintain soil health in nutritional as well as biotic components. Thus, it is interesting to note the members present in one such soil where the litter of Teak (*Tectona grandis*) was found dominated. The soil fungi were studied using metabarcoding. The study unveiled a rich and diverse microbial landscape crucial for the functioning of ecosystem. The eDNA extracted from the soil samples were analysed for the ITS region using Illumina sequencing which resulted in identifying 121 distinct fungal species, predominantly belonging to the Ascomycota phylum. Key fungal genera involved in critical ecological processes such as wood decay (*Asterostroma*, *Tylospora*) and general organic matter decomposition (*Penicillium*, *Talaromyces*) were highly represented. Notably, this study yielded the first records for India of five fungal taxa: *Tylospora asterophora*, a soil-dwelling basidiomycete; *Micarea myriocarpa*, a cosmopolitan lichenized fungus; *Talaromyces purgamentorum*, previously isolated from the Amazon; *Ramicandelaber taiwanensis*, originally described from Taiwanese soil; and *Dentiscutata savannicola*, primarily known from South America. The presence of lichenized genera like *Micarea* and *Verrucaria* suggested specific microenvironmental conditions within the woodland. This comprehensive molecular survey underscores the significant fungal biodiversity harbored within Indian teak ecosystems and highlights the efficacy of metabarcoding in revealing previously undocumented species and their potential ecological roles. The generated sequence data has been deposited in the NCBI

database under accession numbers PQ561267 to PQ561383, providing a valuable resource for future mycological research and conservation strategies in similar ecosystems across the globe.

Keywords: Teak woodland soil, Soil fungi, Metabarcoding, ITS, QIIME2, *Tylospora asterophora*.

Introduction

The intricate web of life within *Tectona grandis* (teak) woodlands represents an ecologically vital biome, playing a crucial role in regional biodiversity and ecosystem function¹. However, these ecosystems face increasing pressures from anthropogenic activities, including deforestation, habitat fragmentation, and land-use change, leading to significant habitat degradation^{2,3}. In many regions, teak plantations have been established for economic purposes. While these plantations provide valuable timber resources, the shift towards monoculture can alter the natural ecosystem dynamics, impacting nutrient cycling, soil health, and the community structure of decomposers⁴⁻⁶.

A critical, yet often overlooked, aspect of these altered ecosystems is the role of soil microorganisms, particularly fungi. Fungi are indispensable drivers of decomposition processes, especially in the breakdown of plant litter, which forms the foundation of soil organic matter and nutrient availability^{7,8}. The unique biochemical composition of teak leaves, characterized by relatively high concentrations of tannins and recalcitrant lignocellulosic compounds compared to other plant species, presents a particular challenge for decomposition^{9,10}. These compounds can inhibit or slow down the breakdown of organic matter, potentially influencing the composition and activity of the fungal communities responsible for litter decomposition and nutrient cycling.

Understanding the composition and functional roles of soil fungal communities in teak-dominated ecosystems is crucial for assessing the long-term sustainability and ecological health of these environments^{11,12}. Molecular techniques, such as Internal Transcribed Spacer (ITS) metabarcoding, offer powerful tools for characterizing fungal diversity with unprecedented resolution¹³. These methods enable the identification of a wide range of fungal taxa, including those that are difficult or impossible to culture using traditional methods^{14,15}. Despite the importance of soil fungi in ecosystem processes, there is a relative paucity of information regarding the specific fungal communities present in teak woodland soils, especially in regions where teak plantations are prevalent. Characterizing these communities is essential to understand their functional roles in the ecosystem.

This study aims to address this gap by investigating the diversity and composition of soil fungal communities in a teak plantation in Villiambakkam, Tamil Nadu, India. By employing ITS metabarcoding, this research provides a comprehensive analysis of the fungal taxa present, offering insights into their potential contributions to key ecological processes such as litter decomposition, nutrient cycling, and soil formation within these unique ecosystems.

Materials and Methods

Soil sampling and eDNA extraction

Nine Soil samples were collected from different zones of teak woodland plantation (Coordinates: 12.746281° N79.944866° E) by following standard guidelines (approximately 7 cm depth and 250 g each). Identical quantities of stone-free and dust-free soil were thoroughly mixed in a sterile, airtight plastic bag for immediate laboratory processing. From the homogenized soil, triplicate one-gram subsamples were transferred to sterile 2 ml tubes, resuspended in 500 µl of TE buffer (pH 8.0, Sigma-Aldrich), and vortexed at 2400 rpm for 2 minutes. Environmental DNA (eDNA) was then extracted using the CTAB method^{42,46}. To eliminate potential PCR inhibitors, the extracted DNA was purified with a 1.5X Agencourt AMPure XP System, following the manufacturer's instructions (Beckman Coulter). The quality and quantity of the purified eDNA were assessed via 1.5% agarose gel electrophoresis and a Qubit DNA BR Assay (Invitrogen), respectively.

ITS region amplification and Next Generation Sequencing

The purified eDNA served as the template for amplification of the ITS region using the forward primer ITS3 (5' GCATCGATGAAGAACGCAGC 3') and the reverse primer ITS4 (5' TCCTCCGCTTATTGATATGC 3')^{30,48}. The resulting amplicons underwent quality control (QC) and were then used for NGS library preparation with unique dual indexing adapters, employing the KAPA HyperPrep kit (Hoffmann-La Roche Ltd) according to the manufacturer's protocol. Sequencing was performed on an Illumina NextSeq 550 (San Diego, CA).

In Silico analysis and taxonomic arrangement

The sequenced data were demultiplexed and imported into the QIIME 2 Amplicon tool (<https://qiime2.org/>). Chimeric sequences were removed, and reads were truncated to a specific length using the qiime2-dada2 plugin. Taxonomic assignment of amplicon sequence variants (ASVs) or operational taxonomic units (OTUs) was performed using the qiime2-feature-classifier classify-sklearn tool against the UNITE fungal ITS database (version 10.15156,

<https://unite.ut.ee/>). A Naive Bayes classifier, trained with a confidence threshold of 99%, was employed for this classification.

Fungal diversity

Shannon alpha diversity and Pielou's evenness index were calculated using QIIME2^{16,17}. to assess species diversity. Fungal taxa abundance was determined based on OTU read counts: >1000 reads (dominant), 100-1000 reads (moderate), <100 reads (minor), and <10 reads (rare).

New Fungal Records

For the identified genera and species, further analysis was conducted to ascertain existing studies or records within India. This involved querying specialized mycological databases, including FUNGuild (<https://www.funguild.org/>), MycoBank (<https://www.mycobank.org/>), and Index Fungorum (<https://www.indexfungorum.org/>), alongside the academic literature search engine Google Scholar (<https://scholar.google.com/>).

Results and Discussion

This study provides a preliminary insight into the soil fungal community structure within a teak (*Tectona grandis*) woodland in Villiambakkam, Tamil Nadu, India, utilizing ITS metabarcoding. Our analysis of 192,541 reads, encompassing 2,858 features, identified 238 Operational Taxonomic Units (OTUs) (Table 1).

Taxonomic arrangement

The fungal community analysis in the teak woodland soil reveals that within the fungal kingdom, the phylum Ascomycota is the most abundant at 36.7%, followed by Basidiomycota at 6.7%. Less abundant fungal phyla, including Rozellomycota and Kickxellomycota, each contribute 0.6% to the community composition, while Mortierellomycota and Glomeromycota each account for 0.3%, and Chytridiomycota is present at 0.2% (Figure-1). This initial assessment highlights a fungal community structure with a clear dominance of Ascomycota within the broader fungal population of the teak woodland soil. This finding aligns with previous studies that have consistently shown Ascomycota to be a major component of soil fungal communities across various ecosystems¹⁸⁻²⁰. Notably, a substantial portion of reads were

classified only at the kingdom level, suggesting the presence of potentially novel or poorly characterized fungal taxa.

At the family level the fungal community, Acarosporaceae overwhelmingly dominates, accounting for 76.49% of the identified sequences (Figure 2). Following this, Chaetomiaceae represents a notable proportion at 7.96%, with Nectriaceae (4.77%) and Aspergillaceae (3.84%) also contributing significantly to the community structure. Several other families are present at lower abundances, including Mortierellaceae (1.83%), Didymosphaeriaceae (1.06%), and Serendipitaceae (0.75%). The other families each contributing less than 0.25%, includes Xylariaceae, Agaricaceae, Glomeraceae, Polyporaceae, and many others, highlighting a diverse but less abundant component of the soil fungal community in this teak woodland (Figure 2 and Table 1). The pronounced dominance of Acarosporaceae, a lichen-forming fungal family prevalent in rocky and soil-based environments, particularly in mountainous regions, was the most abundant group. These organisms play a crucial role in ecosystem processes such as soil formation and nutrient cycling²¹, suggesting a potentially significant ecological role for this family within this specific environment.

Data revealed a diverse fungal assemblage dominated by Ascomycetes, with *Asterostroma*, *Penicillium*, *Tylospora*, *Micarea*, *Verrucaria*, *Talaromyces*, *Ramicandelaber*, *Humicola*, *Aspergillus*, and *Fusarium* as key identified genera. The identification of 121 fungal species, with corresponding sequences deposited in the NCBI database (Accession ID - PQ561267 to PQ589740) (Table 1), underscores the rich mycological diversity harbored within this specific teak woodland ecosystem. Teak, being a hardwood, relies on efficient breakdown of its litter and woody debris for nutrient turnover, and these genera are known to include saprophytic fungi capable of degrading complex plant polymers^{22,23}. This finding highlights the crucial contribution of Basidiomycetes to the overall health and resilience of the teak ecosystem.

The prevalence of Ascomycete genera such as *Penicillium* and *Talaromyces* aligns with findings from other soil fungal diversity studies^{24,25}. These genera are well-known for their diverse metabolic capabilities, including the decomposition of various organic substrates and their involvement in nutrient mobilization²⁶. Their abundance likely reflects their active participation in the broader soil organic matter processing within the teak woodland. The presence of lichenized fungi, *Micarea* and *Verrucaria*, indicates the existence of suitable substrates such as tree bark or rocks within the woodland microhabitats. While their direct contribution to soil processes might be less substantial compared to saprophytic fungi, their

presence adds to the overall biodiversity and can influence microenvironmental conditions at their attachment sites^{27,28}.

The detection of potential plant pathogens like *Fusarium* and *Colletotrichum* warrants further attention. While their presence does not necessarily indicate active disease outbreaks, their identification suggests a potential reservoir of these organisms within the soil. Future studies should investigate the specific species identified and their potential pathogenicity towards teak trees under various environmental conditions^{29,30}.

Fungal diversity

The teak woodland soil displays evidence of relatively high alpha diversity, supported by an alpha diversity index of 7.34 and a Pielou's evenness index of 0.69. Analysis of the 238 identified operational taxonomic units (OTUs) reveals a distribution where 15 OTUs are dominant (>1000 reads), 31 are moderately abundant (>100 reads), 90 are minor contributors (>10 reads), and a substantial portion, 102 OTUs, are considered rare (<10 reads) (Table 1). This distribution suggests a community with a notable number of highly abundant taxa alongside a considerable pool of less frequent organisms, contributing to the overall diversity observed.

New Fungal Records for India

Species with a sequencing depth exceeding 100x were ranked to identify potential novel records for India. A search of national and international databases based on taxon data revealed six species with no prior records in India, representing a significant contribution to soil geographical studies. Those newly recorded fungi from teak woodland soil are follows.

***Tylospora asterophora* (PQ561300):** Previously documented in Montenegro associated with pine forests, this finding in the teak woodland marks its first record in India^{31,32}.

***Micarea myriocarpa* (PQ589737):** While the lichen genus *Micarea* is cosmopolitan and found in other parts of Asia^{33,34}.

***Talaromyces purgamentorum* (PQ561302):** Originally described from leaf litter in the Colombian Amazon³⁵, despite the genus *Talaromyces* being known in the region³⁶.

***Ramicandelaber taiwanensis* (PQ561321)**: This species, initially isolated from soil in Taiwan and characterized by its small spores and branched sporangiophores³⁷, is now recorded for the first time in India.

***Aspergillus piperis* (PQ561285)**: While its direct impact on Indian plants or humans is not yet fully understood, this first record in India warrants further investigation due to its known antagonistic properties and the pathogenic potential of related species within the *Aspergillus* genus^{38,39}.

***Dentiscutata savannicola* (PQ561322)**: Primarily known from South America⁴⁰, this study marks the first documented occurrence of *Dentiscutata savannicola* in Indian soils.

The six newly recorded species contribute significantly to our knowledge of the soil fungal biogeography of India highlighting the efficacy of metabarcoding in detecting species often missed by traditional methods.

Conclusion

This metabarcoding study of a teak woodland in Tamil Nadu, India, revealed a diverse soil fungal community dominated by Ascomycota and the family Acarosporaceae. We identified 121 species, including key genera involved in decomposition and nutrient cycling. Notably, we discovered six fungal species (*Tylospora asterophora*, *Micarea myriocarpa*, *Talaromyces purgamentorum*, *Ramicandelaber taiwanensis*, *Aspergillus piperis*, and *Dentiscutata savannicola*) as new records for India, significantly expanding our understanding of regional fungal biogeography. The presence of potential plant pathogens warrants further investigation. Additionally, a significant portion of unclassified reads suggests the potential for novel fungal discoveries within this ecosystem. This study underscores the utility of metabarcoding for biodiversity assessment and provides a foundation for future ecological research in teak woodlands. Further research focusing on the temporal dynamics of these fungal communities and their response to management interventions is crucial for the long-term conservation of these economically and ecologically valuable ecosystems.

Declaration of competing interest

The authors declare that they have no known competing interests.

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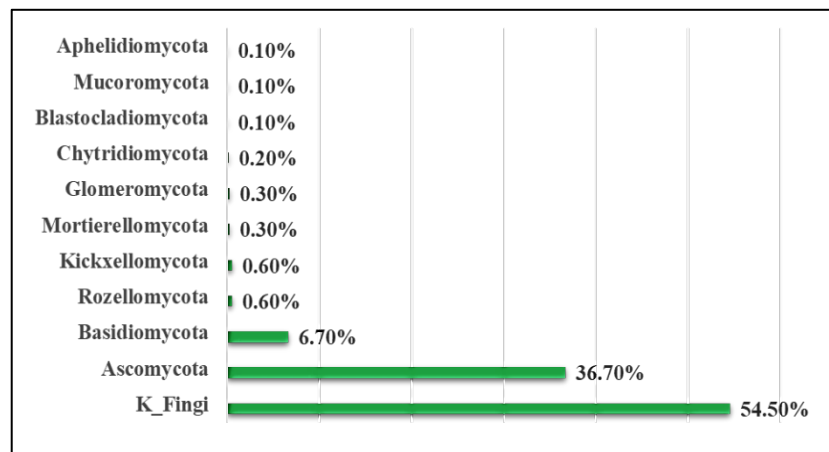


Figure 1. Phylum level disturbing of fungi at teak woodland soil

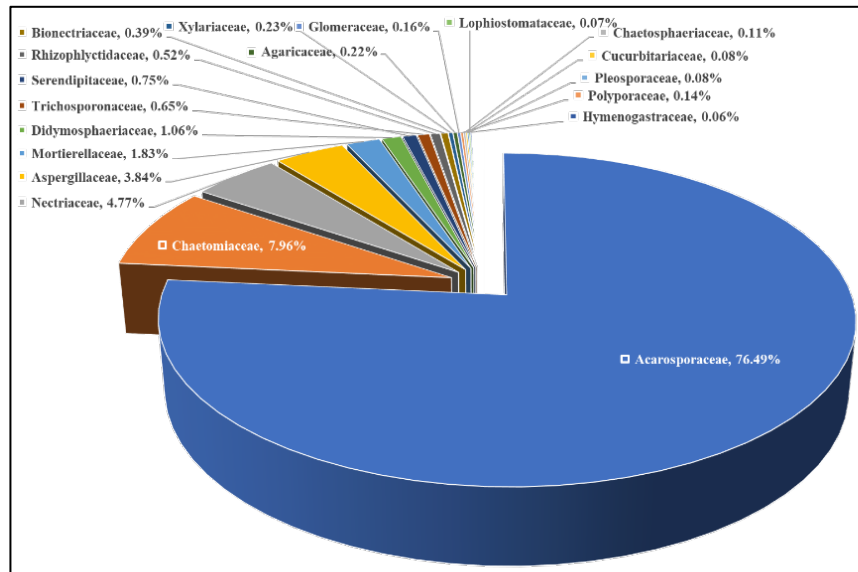


Figure 2. Fungal distribution at the level of family in teak woodland soil

Table 1. List of fungal species recorded in a Teak inhabited land, Chengalpet

Hierarchical level	Taxon	Sequence reads
Fungi	Species belonging to Fungi	104960
Aphelidiomycota	<i>Aphelidiomycetes</i>	103
Ascomycota	<i>Acarosporaceae</i>	24205
	<i>Ascomycota</i>	18544
	<i>Lecanoromycetes</i>	6407
	<i>Penicillium</i> sp. (PQ561292)	2821
	<i>Chaetomiaceae</i>	2518
	<i>Pleosporales</i>	2214
	<i>Nectriaceae</i>	1508
	<i>Micarea myriocarpa</i> * (PQ589737)	1633
	<i>Aspergillaceae</i>	1216
	<i>Eurotiales</i>	1168
	<i>Verrucaria</i> sp. (PQ589734)	976
	<i>Talaromyces purgamentorum</i> * (PQ561302)	967

<i>Sordariomycetes</i>	867
Hypocreales	826
<i>Humicola</i> sp. (PQ589735)	722
<i>Aspergillus piperis</i> * (PQ561285)	432
<i>Fusarium</i> sp. (PQ561279)	361
<i>Didymosphaeriaceae</i>	337
<i>Trichoderma</i> sp. (PQ561351)	291
<i>Trichoderma brevicompactum</i> (PQ561278)	164
<i>Helotiales</i>	147
<i>Bionectriaceae</i>	122
<i>Talaromyces</i>	118
<i>Talaromyces amyrossmaniae</i> (PQ561361)	115
<i>Sordariales</i>	110
<i>Tzeanania taiwanensis</i> (PQ561368)	98
<i>Preussia</i> sp. (PQ561288)	86
<i>Xylariales</i>	84
<i>Pichia mandshurica</i> (PQ561308)	80
<i>Dothideomycetes</i>	74
<i>Xylariaceae</i>	74
<i>Aspergillus</i> sp. (PQ561305)	71
<i>Keithomyces indicus</i> (PQ561315)	69
<i>Saccharomycetales</i>	61
<i>Leptoxyphium glochidion</i> (PQ561314)	55
<i>Acrocalymma</i> sp. (PQ561299)	55
<i>Chaetothyriales</i>	51
<i>Campylocarpon</i> sp. (PQ561270)	48
<i>Phaeopezia calongei</i> (PQ561360)	43
<i>Amphisphaeriales</i>	42
<i>Staphylotrichum coccosporum</i> (PQ561289)	42
<i>Sodiomyces alkalinus</i> (PQ561353)	40
<i>Chaetosphaeriaceae</i>	36
<i>Wardomyopsis litoralis</i> (PQ561272)	34

<i>Colletotrichum tanacetii</i> (PQ561354)	29
<i>Acremonium</i> sp. (PQ561282)	28
<i>Helminthosporium</i> sp. (PQ561374)	26
<i>Cucurbitariaceae</i>	25
<i>Leptodiscella sexualis</i> (PQ561382)	24
<i>Pleosporaceae</i>	24
<i>Arthrographis kalrae</i> (PQ561383)	22
<i>Lophiostomataceae</i>	22
<i>Ciliophora</i> sp.	20
<i>Septoriella allojunci</i> (PQ561301)	19
<i>Orbiliales</i>	19
<i>Pichia membranifaciens</i> (PQ561358)	19
<i>Neocucurbitaria aetnensis</i> (PQ561379)	18
<i>Metarhizium robertsii</i> (PQ561297)	18
<i>Pestalotiopsis</i> sp. (PQ561275)	17
<i>Eurotiomycetes</i>	16
<i>Acrocalymma ampeli</i> (PQ561381)	15
<i>Cladophialophora</i> sp.	15
<i>Cyclothyriella rubronotata</i> (PQ561377)	14
<i>Diaporthales</i>	14
<i>Pseudolophiostoma vitigenum</i> (PQ561375)	13
<i>Rutola graminis</i> (PQ561369)	13
<i>Yamadazyma</i> sp.	13
<i>Botryosphaeriaceae</i>	11
<i>Pseudochaetosphaeronema</i> sp. (PQ561290)	11
<i>Herpotrichiellaceae</i>	11
<i>Lipomyces</i> sp. (PQ561359)	11
<i>Neocucurbitaria ribicola</i> (PQ561378)	11
<i>Codinaea</i> sp. (PQ580806)	11
<i>Hypocreaceae</i>	11
<i>Acrophialophora levis</i> (PQ561348)	11
<i>Cryptocoryneum japonicum</i> (PQ561380)	10

<i>Exserohilum</i> sp. (PQ561371)	10
<i>Pseudotetraploa curviappendiculata</i> (PQ561370)	10
<i>Leotiomyces</i>	10
<i>Saturnispora diversa</i> (PQ561313)	10
<i>Gymnoascus udagawae</i> (PQ561293)	9
<i>Dactylella ramosa</i> (PQ561311)	9
<i>Microascus chinensis</i> (PQ561350)	9
<i>Ophiostomataceae</i>	9
<i>Xenodidymella clematidis</i> (PQ561280)	8
<i>Sarimanas shirakamiense</i> (PQ561373)	8
<i>Plectosphaerellaceae</i>	8
<i>Mycosphaerellaceae</i>	7
<i>Lophiostoma</i> sp.	7
<i>Exserohilum rostratum</i> (PQ561267)	7
<i>Sporormiaceae</i>	7
<i>Candida parapsilosis</i> (PQ561357)	7
<i>Ceratocystiopsis synnemata</i> (PQ561349)	7
<i>Neostagonosporella sichuanensis</i> (PQ561372)	6
<i>Westerdykella reniformis</i> (PQ561291)	6
<i>Testudinaceae</i>	6
<i>Aspergillus croceus</i> (PQ561366)	6
<i>Lecanicillium cauligalbarum</i> (PQ561352)	6
<i>Occultibambusaceae</i>	5
<i>Sympoventuriaceae</i>	5
<i>Aspergillus citrisporus</i> (PQ561367)	5
<i>Penicillium tanzanicum</i> (PQ561362)	5
<i>Eremomyces bilateralis</i> (PQ561271)	4
<i>Westerdykella</i> sp.	4
<i>Trichomeriaceae</i>	4
<i>Hyaloscyphaceae</i>	4
<i>Apiosporapseudorasikravindrae</i> (PQ561356)	4

	<i>Colletotrichum hainanense</i> (PQ561355)	4
	<i>Microascales</i>	4
	<i>Microascaceae</i>	4
	<i>Phyllosticta</i> sp.	3
	<i>Capnodiales</i>	3
	<i>Didymellaceae</i>	3
	<i>Kiskunsagia ubrizsyi</i> (PQ561376)	3
	<i>Massarina</i> sp.	3
	<i>Wiesneriomycetaceae</i>	3
	<i>Venturiaceae</i>	3
	<i>Aspergillus penicillioides</i> (PQ561365)	3
	<i>Penicillium monsserratidens</i> (PQ561363)	3
	Trichocomaceae	3
	<i>Blastenia</i> sp.	3
	<i>Chaetomella</i> sp. (PQ561312)	3
	<i>Orbiliaceae</i>	3
	<i>Pezizaceae</i>	3
	<i>Conlarium</i> sp. (PQ561306)	3
	<i>Colletotrichum</i> sp. (PQ589740)	3
	<i>Glomerellales</i>	3
	<i>Neocosmospora falciformis</i>	3
	<i>Stachybotryaceae</i>	3
	<i>Allocanariomyces tritici</i> (PQ561347)	3
	<i>Xenospadicoidaceae</i>	3
	<i>Delitschiaceae</i>	2
	<i>Tubeufia sympodilaxispora</i> (PQ561283)	2
Basidiomycota	<i>Asterostroma</i> sp. (PQ561307)	5483
	<i>Agaricomycetes</i>	2209
	<i>Tylospora asterophora</i>* (PQ561300)	1987
	<i>Basidiomycota</i>	616
	<i>Sebacinales</i>	399
	<i>Geastrum</i> sp. (PQ561304)	351

<i>Agaricales</i>	257
<i>Serendipitaceae</i>	238
<i>Trichosporonaceae</i>	205
<i>Apiotrichum</i> sp.	119
<i>Inocybe</i> sp. (PQ580805)	116
<i>Tremellales</i>	97
<i>Crinipellis</i> sp. (PQ561340)	94
<i>Agaricaceae</i>	70
<i>Polyporaceae</i>	44
<i>Atractiella rhizophila</i> (PQ561317)	44
<i>Agaricus hingganensis</i> (PQ561346)	36
<i>Serendipita</i> sp. (PQ561268)	34
<i>Septobasidium</i> sp. (PQ561310)	31
<i>Tulostoma eckbladii</i> (PQ561345)	26
<i>Tremellomycetes</i>	25
<i>Malassezia</i> sp. (PQ561329)	21
<i>Hymenogastraceae</i>	20
<i>Micropsalliota</i>	19
<i>Clitocybula lignicola</i> (PQ561344)	18
<i>Ceratobasidium</i> sp. (PQ561284)	17
<i>Gymnopilus</i> sp. (PQ561296)	15
<i>Tomentella</i> sp. (PQ561331)	15
<i>Malassezia restricta</i> (PQ561303)	14
<i>Saitozyma</i>	14
<i>Ganoderma wiiroense</i> (PQ561273)	13
<i>Ustilaginaceae</i>	13
<i>Antella niemelaei</i> (PQ561334)	12
<i>Agaricus</i> sp. (PQ589739)	11
<i>Pseudolagarobasidium baiyunshanense</i> (PQ561335)	10
<i>Tausonia pullulans</i> (PQ561328)	10
<i>Notholepista fistulosa</i> (PQ561343)	9

<i>Cortinarius rubrophyllus</i> (PQ561342)	9
<i>Bandoniozyma noutii</i> (PQ561325)	9
<i>Anthracocystis grodzinskae</i> (PQ561323)	9
<i>Psilocybe</i> sp. (PQ589738)	7
<i>Lycoperdon rupicola</i> (PQ561341)	7
<i>Ceratobasidiaceae</i>	6
<i>Polyporales</i>	6
<i>Fomes meliae</i> (PQ561298)	5
<i>Sebacina</i> sp. (PQ561332)	5
<i>Rhodosporeidiobolus</i> sp.	5
<i>Rhynchogastremaceae</i>	5
<i>Trichosporon</i> sp.	5
<i>Peniophoraceae</i>	4
<i>Vishniacozyma</i> sp. (PQ561326)	4
<i>Entolomataceae</i>	3
<i>Pleurotus cystidiosus</i> (PQ561339)	3
<i>Pluteus</i> sp.	3
<i>Psathyrella mycenoides</i> (PQ561338)	3
<i>Stropharia rugosoannulata</i> (PQ561337)	3
<i>Scleroderma</i> sp. (PQ561277)	3
<i>Cantharellales</i>	3
<i>Hydnaceae</i>	3
<i>Hymenochaetaceae</i>	3
<i>Irpicaceae</i>	3
<i>Albatrellus subrubescens</i> (PQ561333)	3
<i>Pseudobensingtonia fusiformis</i> (PQ561330)	3
<i>Cystobasidiomycetes</i>	3
<i>Cystobasidium</i> sp.	3
<i>Bulleribasidiaceae</i>	3
<i>Dioszegia</i> sp. (PQ561327)	3
<i>Apiotrichum gracile</i> (PQ561324)	3
<i>Melanotaenium</i> sp.	3

Blastocladiomycota	<i>Blastocladiomycota</i> sp.	136
Chytridiomycota	<i>Rhizophlyctidaceae</i>	165
	<i>Rhizophydiales</i>	36
	<i>Chytridiomycota</i>	32
	<i>Chytridiales</i>	30
	<i>Spizellomycetaceae</i>	10
	<i>Spizellomycetales</i>	6
	<i>Cladochytriales</i>	4
	<i>Lobulomyces</i>	4
	<i>Sonoraphlyctis</i>	4
	<i>Rhizophlyctidales</i>	3
	<i>Operculomyces</i> sp.	3
Glomeromycota	<i>Dentiscutata savannicola</i> * (PQ561322)	306
	<i>Gigaspora decipiens</i> (PQ561309)	73
	<i>Paraglomeromycetes</i>	68
	<i>Glomeraceae</i>	51
	<i>Septoglo mus</i> sp. (PQ561295)	23
	<i>Gigasporales</i>	20
	<i>Pervetustaceae</i>	10
	<i>Kamienskia</i> sp. (PQ561287)	7
	<i>Diversisporaceae</i>	6
	<i>Gigaspora</i> sp. (PQ589736)	6
	<i>Glomeromycota</i>	3
	<i>Archaeosporales</i>	3
	<i>Gigaspora polymorphira</i> (PQ561276)	2
Kickxellomycota	<i>Ramicandelaber taiwanensis</i> * (PQ561321)	848
	<i>Ramicandelaber</i> sp. (PQ561286)	243
Mortierellomycota	<i>Mortierellaceae</i>	578
	<i>Mortierella</i> sp.	12
	<i>Linnemannia hyalina</i> (PQ561320)	3
Mucoromycota	<i>Cunninghamella blakesleeana</i> (PQ561281)	116
	<i>Mucor indicus</i> (PQ561269)	7

	<i>Mucor ardhlaengiktus</i> (PQ561274)	6
	<i>Mucor orantomantidis</i> (PQ561318)	3
Rozellomycota	<i>Rozellomycota</i>	1135

PQ561267 to PQ561383 - NCBI Accession IDs for the Identified genus/Species,

*- New Record in India