Diversity And Molecular Identification Of Selected Wood Degrading Fungi From Chitteri Hills, Eastern Ghats Of Tamilnadu, India

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ABSTRACT: Wood degrading fungi were seen abundant in the forest area of Chitteri hills, Eastern Ghats of Tamilnadu. Periodical field assessment was carried out from the year of 2015-2017. This research paper deals with the documentation of macrofungi of the Chitteri hills. On the basis of seasonal diversity 40 species of macrofungi belonging to 18 families were documented. Three wood degrading fungi were showed richest diversity among other species. Hence molecular technique was done by ITS-rDNA amplified by PCR and ITS region sequenced for the accurate identification. This confirms the notion that Eastern Ghats of Tamilnadu especially Chitteri hills host a rich biodiversity of macrofungi which were threatened in the study area due to anthropogenic activities.

KEYWORDS: Biodiversity, Macrofungi, Eastern Ghats, Chitteri hills, Molecular identification

1 INTRODUCTION

Fungi are key functional components of forest flora and fauna (Brown et al., 2006). Macrofungal diversity is an imperative module of the global biodiversity (Li Shujiang et al., 2012). Macrofungi also used extensively in the daily life of agriculture and medicine (Cowan, 2001; Chang and Miles, 2004). The macrofungi were also playing a vital role in food industry, textiles, bioremediation, natural cycling and decomposing the dead organic matter (Pilz and Monila, 2001). Medicinal mushrooms were used in traditional oriental therapies (Hobbs, 2000; Wasser, 2002). The wild mushrooms are richer sources of protein and have a lower amount of fat than commercial mushrooms (Barros et al., 2008). Macrofungi are decomposers, mutualists, pathogens and producers of pharmaceuticals and other industrial products (Schimit and Mueller, 2006). Some of the macrofungi have antitumour, anticancer, anticholesterol and anti-hemorrhage effects (Bushwell and Chang, 1993). Several molecular techniques were employed for the identification of wood degrading fungi. SDS-PAGE was used widely to identify the wood decaying fungi (Vigrow et al ., 1991). DNA based molecular techniques and AFLP were adopted for the identification of wood decaying fungi (Glaeser and Lindner, 2010; Terashima et al ., 2002). Molecular sequencing data of rDNA-ITS region was used to identify the wood rot fungi (Schmidt and Moreth, 2002). Standard Primers were used in Polymerase chain reaction (PCR) to detect wood decaying fungi (Moreth and Schmidt, 2005). In Eastern Ghats of Tamilnadu there were no previous reports explored about the documentation of mycoflora from the study area.

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The present work has been undertaken to study the diversity of macrofungi in Chitteri hills of Dharmapuri district, Eastern Ghats. The climatic condition due to sufficient rainfall results the prosperous diversity of macrofungi from the study area. The forest range is quite disturbed by the anthropogenic activities. Hence mycological survey of the macrofungi from the study area was carried out

2.MATERIALS AND METHODS

2.1. Study area

Chitteri Hills (654.52 km²) are one of the fragment of Eastern Ghats of Tamil Nadu and the geographical limit of 78°15'−78°45' E longitude and 11°44'−12°08' N latitude. The withhold various vegetation types such as the evergreen, semi-evergreen, riparian, dry mixed deciduous, dry deciduous scrub and the southern thorn scrub forests. The least and highest temperature of the area is 19 °C (in winter) and 40 °C (in summer) correspondingly. The yearly rainfall differs from 620 to 900 mm and it received northeast and southwest monsoons mutually. The hills contain twisted ridges and narrow valleys running in the northeast and southwest directions, enclosing numerous constricted valleys (rivers), viz. Kallar, Varattar, Kambalai and Anaimaduvu. The study area is surging with an altitude varying from 240 to 1266 m. The study area covers Kambalai Beat, Arasanattham Beat, Tholthukki, Pallipatti North Beat, Irulappatti, Pallipatti Central Beat, Pallipatti Extension Beat, Nochikuttai Beat, Kalasapadi Beat, Sandhumalai East Beat, Sandhumalai West Beat, Kundal maduvu Beat, Chitteri Beat, Erumakadai, Kalnadu, Kalnadu Extension Beat, Suriyakadai Beat.

2.2 Survey

Macrofungi were identified by the presence and absence they were visible to the naked eye. The seasonal survey was carried out just after the rainfall. The recurrent surveys were performed in all sampling areas during January 2015 to December 2017. Seventeen random transects were selected each measures 100m length and 100m width were laid in the study area (Mohanan, 2011). The subplots were also laid in each permanent plot for detailed investigation. The phenology of wood rot fungi differs throughout the year.

The study sites were randomly selected and latitude/ longitude were noted using GPS (Gramin ETrex 20).

2.3. Macrofungal collection and Preservation
Macrofungi were collected carefully not disturbing any sporomas. Some sporomas were collected with the substratum. The different morphological data and ecological data were noted in the fungal data book. They were photographed during the collection by using digital camera (Nikon D60 SLR Camera). The fungi were collected in newspaper and were labeled with unique collection number. The dehydrated fungi were sealed in covers and preserved by appropriate techniques. Delicate specimens were also preserved. The collected specimens were deposited in Department of Botany, School of Life Sciences, Periyar University, Salem.

2.4. Morphological identification of fungi
The specimens were identified based on their macro and micro morphological features (Yamashita et al., 2010). Wood rot fungi were examined for the presence and absence of varying morphological features, mainly colour, shape, size, volva, annulus, gills, pileus, stipe, pores, peridium and veils. Spore prints were also taken to know the spore colour (Magurran, 2004).

2.5. Data analysis
The qualitative analysis of Density, Frequency and Abundance were done to know the number of wood rot fungi per unit area it measures the numerical individuals. Frequency measures that how many samples contains sporomas of a given species. The dominance and abundance resembles the species dominance on the study area (Smith et al., 2002).

2.6 Frequency
The Frequency is nothing but degree of dispersion in individual species in the study area is mentioned in terms of percentage occurrence. Random sampling was done in the study area in various transects and the sporomas were recorded from the sampling units. Frequency calculated by the formula.
Frequency (F) = Number of transects of species occurrence/ Total number of transects studied.

2.7 Density
The numerical strength of the species was calculated by the formula.
Density (D) = Total number of sporomas in all quardrats/ Total number of transect studied.

2.8 Abundance
Abundance was determined by the number of sporomas of different species in the community per unit area.
Abundance (A) = Total number of sporomas in all transects/ Number of transects of occurrence.

2.9 Molecular identification
DNA isolation, PCR amplification and sequencing was done for accurate identification of wood degrading fungi. The ITS rDNA regions were amplified with ITS1 (5' TCCGTAGG-TGAACCTGCGG-3') and ITS4 (5'TCCTCCGCTTATTG-ATATGC-3') pair. The genomic DNA isolated from the mycelia culture, an approximately 300 base pair fragments of the rDNA – ITS region. The nucleotide sequences of three samples were obtained and analyzed for Basic Local Alignment Search Tool. According to the BLAST summary the samples were identified with their closely resembled species (White et al ., 1990). The following PCR protocol was taken for the study. An initial denaturization of 5 min at 95°C, 35 cycles of 45s at 95°C for denaturization, 45s at 55°C for annealing, 1 min at 72°C for extension and a final extension of 10min at 72°C. All sequences were studied bidirectionally.

3.RESULTS AND DISCUSSION
A total of 40 species belonging to 18 families were collected from the study site represented in Plate 1. Eleven Genera were belongs to the family Polyporaceae, seven assigned to Hymenochaetaceae, three each from Meruliaceae and Ganodermataceae, two each reported in Dacrymycetaceae and Agaricaceae. The Cyphellaceae, Pleurotaceae, Mycenaceae, Omphalotaceae, Geastraceae, Xylariaceae, Amylostereaceae, Stereaceae, Gloeophyllaceae, Fomitopsidaceae, Phanerochaetaceae and Fomitopsidaceae consist only one species from each family. Phylum Basidiomycota, Sub-division Agaricomycotina, Class agaricomycetes, Sub-class Agaricomyceidae, Order Agaricales consists of five families and represents six species namely Chondrostereum purpureum (Pers.) Pouzar, Pleurotus pulmonarius (Fr.) Quel. Mycena haematopus (Pers.) P. Kumm. Leucocoprinus cepaestipes (Sowerby) Pat. Leucocoprinus cretaceous (Bull.) Locq. Omphalotus olearius (DC.) Singer, Sub-class Phallomycetidae has order Geastrales, family Geastraceae and species Geastrum saccatum Fr. was presented in Table 1. The Phyllum Basidiomycota, Sub-Division Basidiomycotina, Class Dacrymycetes confirms the presence two species namely Dacrymyces stillatus Nees and Dacryopinax elegans (Berk.&M.A.Curtis) G.W. Martin presented in Table 2. Table 3 shows only one species Xylaria symploci was identified from Phyllum Ascomycota, Sub-division Pezizimycotina, Class Sordariomycetes, Sub-class Xylariomycetidae, Order Xylariales was reported from the family Xylariaceae. The Class Agaricomycetes comprises four Orders and Ten Families. The maximum numbers of Thirty fungal species were identified and was represented in Table 4. The investigations concerning the understanding on habitat, environmental interaction were considered fundamental to understand the sustainability of woodland bionetwork. The samples were collected and given with the collection number during the field study. The edibility were also reported in this study was enumerated in Table 5. Nearly twenty nine species were Saprophytic, Eleven were Parasitic in ecological relationship. Totally 40 macrofungal species were found from different Habitats likely Hard Wood, Living trees, Dead Hard Wood, Dead wood, Dead broad leaved trees and Living Hard wood trees. The diversity analysis indicated by the detailed analysis of number of individual species and their occurrence, density, frequency and abundance shows the species richness of the study area are shown in Table 6. Maximum numbers of individual species were reported from Inonotus dryadeus (Pers.) Murrill, Ganoderma applanatum (Pers.) Pat. and Trametes hirsuta (Wulfen) Pilat. were showed highest occurrence and Omphalotus olearius (DC.) Singer shows lowest occurrence among the species. The

rDNA – ITS (Ribosomal DNA Internal Transcribed Spacers) fragments of genomic DNA were amplified using ITS1 (Internal Transcribed Spacers 1) and ITS4 primers. The PCR amplification products showed that Sample 1 gave around 228 bp amplified band and Sample 4 showed bands at 220 bp. Band around 111 bp was observed in Sample 3. The macrofungi were identified as follows Sample 1- Ganoderma applanatum (99% JN167598); Sample 4 - Trametes hirsuta (99% AY972129); Sample 3 - Inonotus dryadeus (100% AF311011) (Table 7). These PCR products were gel purified, run in 1% agarose gel and processed for nucleotide sequencing. Phylogenetic analyses of closed related species were inferred from the sequence data. A survey of the fruit bodies of mushrooms is an important aspect of documenting fungal diversity of any biogeographic region (Bakshi, 1971). A total of 22 mushrooms representing 16 genera, 14 families and 6 orders were documented from Meghalaya, Northeast India (Kalitha et al., 2016). The survey and identification of 250 macrofungi were collected from Gorakhpur District, Uttar Pradesh, India (Vishwakarma et al., 2017). Rapid depletion of the reserved forest area and resulted with increasing reduction of the plant species as well as the number of fungal species. Hence several works were done in different parts of India and all over the world. A total of 39 species of macrofungi were reported from 25 genera and 17 families from Coromandel coast of Tamil Nadu, Southern India (Mani and Kumaresan, 2009). Several macrofungal survey were reported from the state of Karnataka (Swapna et al., 2008) collected 778 species of macrofungi belonging to 101 genera of 43 families. (Abolfazl and Janardhana 2011) identified Sinotermitomyces taiwanensis, (Pushpa and Purushothama, 2012) isolated 90 species of macrofungi. Several researchers were described the diversity, taxonomy and distribution of Western Ghats (Farook et al., 2013). Some macroscopic mushrooms were collected from Karur, Namakkal, Nagapattinam, Tiruchirappalli and Thiruvarur and given with their edibility status (Soosairaj et al., 2012). Fifty six samples were collected from Western Ghats area of Tamil Nadu and Karnataka, South India and they were screened for their ligninolytic activity based on their ability to oxidize dyes, poly R – 478 and remazol brilliant blue to degrade native lignin (Selvam et al., 2012). Macrofungi were reported for their therapeutic values for preventing from various diseases (Mau et al., 2002). (Venkatachalapathi and Paulsamy, 2016) reported 30 medicinal mushroom species belonging to 23 genera in 13 families from Tamilnadu. The Armillaria species shows very closely related four isolates and A.mellea differs hence species specific primer is used (Potyralska et al ., 2002). Few of Ganoderma species were differentiated from the similar fruit bodies of other Ganoderma species by ITS sequencing (Guglie et al., 2010; Terho et al., 2007). There were no such attempts have been made from Chitteri Hills especially Southern Eastern Ghats of Tamilnadu. The study area was disturbed by speedy anthropogenic activities. Such behavior reduces the forest area further hastily. Therefore documentation of innate resources chiefly macrofungi from this area was considered greatest importance before they wiped out from our planet.

4. CONCLUSION

The new effort was taken for documentation from the Eastern Ghats of Tamilnadu discovered the inevitability of comprehensive studies to discover more macrofungal species. The checklist of macrofungi from the Eastern Ghats was done to exhibit the importance of macrofungi from various aspects. The molecular identification method was considered in contrast to traditional. These molecular identification methods were done fast and more accurate. The molecular identification of selected wood degrading fungi and Phylogenetic analysis of closely related species provide much accurate identification of specified species identification. Hence proper conservation and documentation was more essential. Additional investigations were mandatory to uncover the mycodiversity of the study area. The documentation and systematic collection of macrofungi was considered vital not only to reveal their ecosystem dynamics it may bring abundant infrequently known fungi which may fade from our mother earth.

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TABLE – 1 : *THE MACROFUNGAL SPECIES OF PHYLUM OR DIVISION BASIDIOMYCOTA, SUB – DIVISION AGARICOMYCOTINA*

Class	Sub-Class	Order	Family	Species
Agaricomycetes	Agaricomycetidae	Agaricales	Cyphellaceae	Chondrostereum purpureum (Pers.) Pouzar
			Pleurotaceae	Pleurotus pulmonarius (Fr.) Quel.
			Mycenaceae	Mycena haematopus (Pers.) P. Kumm.
			Agaricaceae	Leucocoprinus cepaestipes (Sowerby) Pat.
				Leucocoprinus cretaceous (Bull.) Locq.
			Omphalotaceae	Omphalotus olearius (DC.) Singer
	Phallomycetidae	Geastrales	Geastraceae	Geastrum saccatum Fr.
	Total Number of Species			07

TABLE – 2: *THE MACRO FUNGAL SPECIES OF PHYLUM OR DIVISION BASIDIOMYCOTA, SUB – DIVISION BASIDIOMYCOTINA*

Class	Order	Family	Species
Dacrymycetes	Dacrymycetales	Dacrymycetaceae	Dacrymyces stillatus Nees
			Dacryopinax elegans (Berk.&M.A.Curtis) G.W. Martin
	Total Number of Species		02

TABLE - 3: *THE MACRO FUNGAL SPECIES OF PHYLUM OR DIVISION ASCOMYCOTA, SUB – DIVISION PEZIZOMYCOTINA*

Class	Sub-Class	Order	Family	Species
Sordariomycetess	Xylariomycetidae	Xylariales	Xylariaceae	Xylaria symploci Pande, Waingankar, Punekar & Ran[a]dive
	Total Number of Species			01

TABLE - 4: *THE MACRO FUNGAL SPECIES OF PHYLUM OR DIVISION BASIDIOMYCOTA, SUB – DIVISION AGARICOMYCOTINA*

Class	Order	Family	Species
Agaricomycetes	Russulales	Amylostereaceae	Artomyces pyxidatus (Pers.) Julich
		Stereaceae	Stereum rugosum Pers.
	Gloeophyllales	Gloeophyllaceae	Gloeophyllum abietnum (Bull.) P.Karst.
	Polyporales	Meruliaceae	Bjerkandera adusta (Willd.) P.Karst
			Phlebia tremellosa (Schrad. Nakasone & Burds)
			.Steccherinum ochraceum (Pers.ex J.F. Gmel.) Gray
		Fomitopsidaceae	Laetiporus sulphureus (Bull.) Murrill
		Polyporaceae	Cellulariella acuta (Berk.) Zmitr. & V. Malysheva
			Cryptoporus volvatus (Peck) Shear
			Daedalea flavida (Lev.) A.Roy & A.Mitra
			Daedaleopsis confragosa var confragosa (Bolton) J. Schrot
			Fomes excavates (L.) Fr.
			Fomes fasciatus (Sw.) Cooke
			Hexagonia hydnoides (Sw.)M.Fidalgo
			Microporus affinis (Blume & T. Nees) Kuntze
			Microporus xanthopus (Fr.) Kuntze
			Polyporus cinnabarinus (Jacq.) P. Karst.
			Trametes hirsuta (Wulfen) Pilat.
		Ganodermataceae	Ganoderma adspersum (Schulzer) Donk
			Ganoderma applanatum (Pers.) Pat.
			Ganoderma lipsiense (Batsch) G.F.Atk.
		Phanerochaetaceae	Byssomerulius corium (Pers.) Parmasto
		Fomitopsidaceae	Fomitopsis spraguei (Berk.& M.A.Curtis)
	Hymenochaetales	Hymenochaetaceae	Inonotus dryadeus (Pers.) Murrill
			Phellinus gilvus (Schwein.) Pat.
			Phellinus populicola Niemela
			Phellinus robiniae (Murrill) A. Ames
			Phellinus sarcites (Fr.) Ryvarden
			Phellinus tremullae (Bondartsev) Bondartsev & P.N. Borisov
			Tropicoporus linteus (Berk. & M.A. Curtis)
		Total Number of Species	30

***TABLE – 5** : LIST OF MACROFUNGI AND THEIR HABITAT, ECOLOGIGAL RELATIONSHIP AND EDIBILITY*

Collection No	Species Name	Habitat	Ecological relationship	Edibility
PU-BOT-WRF-37	Artomyces pyxidatus (Pers.) Julich	HW/DW	Saprophytic	Inedible
PU-BOT-WRF-41	Bjerkandera adusta (Willd.) P.Karst	HW/DW	Saprophytic	Inedible
PU-BOT-WRF-51	Byssomerulius corium (Pers.) Parmasto	LT/LHW	Saprophytic	Inedible
PU-BOT-WRF-40	Cellulariella acuta (Berk.) Zmitr. & V. Malysheva	DW	Saprophytic	Inedible
PU-BOT-WRF-50	Chondrostereum purpureum (Pers.) Pouzar	DHW	Saprophytic	Inedible
PU-BOT-WRF-56	Cryptoporus volvatus (Peck) Shear	HW/DW	Saprophytic	Inedible
PU-BOT-WRF-53	Dacrymyces stillatus Nees	DBT	Saprophytic	Edible
PU-BOT-WRF-39	Dacryopinax elegans (Berk.&M.A.Curtis) G.W. Martin	HW/DW	Saprophytic	Inedible
PU-BOT-WRF-52	Daedalea flavida (Lev.) A.Roy & A.Mitra	HW/DW	Saprophytic	Inedible
PU-BOT-WRF-57	Daedaleopsis confragosa var confragosa (Bolton) J. Schrot	DHW	Saprophytic	Inedible
PU-BOT-WRF-49	Fomes excavates (L.) Fr.	HW/DW	Saprophytic	Inedible
PU-BOT-WRF-73	Fomes fasciatus (Sw.) Cooke	HW/DW	Saprophytic	Inedible
PU-BOT-WRF-48	Fomitopsis spraguei (Berk.& M.A.Curtis)	LT/LHW	Saprophytic	Inedible
PU-BOT-WRF-55	Ganoderma adspersum (Schulzer) Donk	DW/DHW	Parasitic	Inedible
PU-BOT-WRF-54	Ganoderma applanatum (Pers.) Pat.	DW/DHW	Saprophytic	Inedible
PU-BOT-WRF-36	Ganoderma lipsiense (Batsch) G.F.Atk.	DW/DHW	Saprophytic	Inedible
PU-BOT-WRF-72	Geastrum saccatum Fr.	DBT	Saprophytic	Edible
PU-BOT-WRF-47	Gloeophyllum abietnum (Bull.) P.Karst.	DW/DHW	Parasitic	Inedible
PU-BOT-WRF-59	Hexagonia hydnoides (Sw.)M.Fidalgo	DW/DHW	Saprophytic	Inedible
PU-BOT-WRF-63	Laetiporus sulphureus (Bull.) Murrill	LT/LHW	Parasitic	Edible
PU-BOT-WRF-61	Leucocoprinus cepaestipes (Sowerby) Pat.	DW/DHW	Parasitic	Edible
PU-BOT-WRF-38	Leucocoprinus cretaceous (Bull.) Locq.	DW/DHW	Parasitic	Edible
PU-BOT-WRF-46	Microporus affinis (Blume & T. Nees) Kuntze	DW/DHW	Saprophytic	Inedible
PU-BOT-WRF-60	Microporus xanthopus (Fr.) Kuntze	DW/DHW	Saprophytic	Inedible
PU-BOT-WRF-58	Mycena haematopus (Pers.) P. Kumm	DW/DHW	Saprophytic	Inedible
PU-BOT-WRF-42	Omphalotus olearius (DC.) Singer	DBT/DW	Saprophytic	Inedible
PU-BOT-WRF-66	Inonotus dryadeus (Pers.) Murrill	LT/LHW	Parasitic	Inedible
PU-BOT-WRF-45	Phellinus gilvus (Schwein.) Pat.	DW/DHW	Parasitic	Inedible
PU-BOT-WRF-74	Phellinus populicola Niemela	DW/DHW	Parasitic	Inedible
PU-BOT-WRF-62	Phellinus robiniae (Murrill) A. Ames	LHW	Parasitic	Inedible
PU-BOT-WRF-67	Phellinus sarcites (Fr.) Ryvarden	DW/DHW	Parasitic	Inedible
PU-BOT-WRF-43	Phellinus tremullae (Bondartsev) Bondartsev & P.N. Borisov	DW/DHW	Parasitic	Inedible
PU-BOT-WRF-69	Phlebia tremellosa (Schrad. Nakasone & Burds)	DW/DHW	Saprophytic	Inedible
PU-BOT-WRF-71	Pleurotus pulmonarius (Fr.) Quel.	DHW/LHW	Saprophytic	Edible
PU-BOT-WRF-44	Polyporus cinnabarinus (Jacq.) P. Karst.	DHW/LHW	Saprophytic	Inedible
PU-BOT-WRF-65	Steccherinum ochraceum (Pers.ex J.F. Gmel.) Gray	DW/DHW	Saprophytic	Inedible
PU-BOT-WRF-70	Stereum rugosum Pers.	DW/DHW	Saprophytic	Inedible
PU-BOT-WRF-68	Tremetes hirsute (Wulfen) Pilat.	DW/DHW	Saprophytic	Inedible
PU-BOT-WRF-75	Tropicoporus linteus (Berk. & M.A. Curtis)	DW/DHW	Saprophytic	Inedible
PU-BOT-WRF-64	Xylaria symploci Pande, Waingankar, Punekar & Ran[a]dive	DW/DHW	Saprophytic	Inedible

HW-Hard Wood, DW-Dead Wood, LT-Living Trees, LHW-Living Hard Wood, DHW-Dead Hard Wood, DBT-Dead Broad Leaved Trees

***TABLE – 6** : LIST OF MACROFUNGI AND THEIR OCCURRENCE, FREQUENCY, DENSITY AND ABUNDANCE*

S.No	Species Name	NIS	O	F	F.P	D	A
1.	Artomyces pyxidatus (Pers.) Julich	05	2	0.11	11.7	0.29	2.50
2.	Bjerkandera adusta (Willd.) P.Karst	13	4	0.23	23.5	0.76	3.25
3.	Byssomerulius corium (Pers.) Parmasto	04	3	0.17	17.6	0.23	1.333
4.	Cellulariella acuta (Berk.) Zmitr. & V. Malysheva	33	11	0.64	64.7	1.94	3.00
5.	Chondrostereum purpureum (Pers.) Pouzar	14	08	0.47	47.0	0.82	1.75
6.	Cryptoporus volvatus (Peck) Shear	15	09	0.52	52.9	0.88	1.666
7.	Dacrymyces stillatus Nees	07	05	0.29	29.4	0.41	1.40
8.	Dacryopinax elegans (Berk.&M.A.Curtis) G.W. Martin	09	10	0.58	58.8	0.52	0.90
9.	Daedalea flavida (Lev.) A.Roy & A.Mitra	36	15	0.88	88.23	2.11	2.40
10.	Daedaleopsis confragosa var confragosa (Bolton) J. Schrot	31	13	0.76	76.4	1.82	2.38
11.	Fomes excavates (L.) Fr.	34	16	0.94	94.1	2	2.125
12.	Fomes fasciatus (Sw.) Cooke	23	14	0.82	82.3	1.35	1.64
13.	Fomitopsis spraguei (Berk.& M.A.Curtis)	11	08	0.47	47.0	0.64	1.375
14.	Ganoderma adspersum (Schulzer) Donk	16	13	0.76	76.4	0.94	1.230
15.	Ganoderma applanatum (Pers.) Pat.	38	17	1	100	2.23	2.235
16.	Ganoderma lipsiense (Batsch) G.F.Atk.	30	14	0.82	82.3	1.76	2.142
17.	Geastrum saccatum Fr.	03	02	0.11	11.7	0.17	1.50
18.	Gloeophyllum abietnum (Bull.) P.Karst.	04	03	0.17	17.6	0.23	1.333
19.	Hexagonia hydnoides (Sw.)M.Fidalgo	07	05	0.29	29.4	0.41	1.40
20.	Laetiporus sulphureus (Bull.) Murrill	12	07	0.41	41.1	0.70	1.714
21.	Leucocoprinus cepaestipes (Sowerby) Pat.	20	13	0.76	76.4	1.17	1.538
22.	Leucocoprinus cretaceous (Bull.) Locq.	33	04	0.23	23.5	1.94	8.250
23.	Microporus affinis (Blume & T. Nees) Kuntze	30	09	0.52	52.9	1.76	3.333
24.	Microporus xanthopus (Fr.) Kuntze	39	12	0.70	70.5	2.29	3.250
25.	Mycena haematopus (Pers.) P. Kumm	14	05	0.29	29.4	0.82	2.80
26.	Omphalotus olearius (DC.) Singer	08	01	0.05	5.88	0.47	8.00
27.	Inonotus dryadeus (Pers.) Murrill	40	10	0.58	58.8	2.35	4.00
28.	Phellinus gilvus (Schwein.) Pat.	19	07	0.41	41.1	1.11	2.714
29.	Phellinus populicola Niemela	16	14	0.82	82.3	0.94	1.142
30.	Phellinus robiniae (Murrill) A. Ames	09	03	0.17	17.6	0.52	3.00
31.	Phellinus sarcites (Fr.) Ryvarden	17	10	0.58	58.8	1	1.70
32.	Phellinus tremullae (Bondartsev) Bondartsev & P.N. Borisov	36	11	0.64	64.7	2.11	3.272
33.	Phlebia tremellosa (Schrad. Nakasone & Burds)	06	03	0.17	17.6	0.35	2.00
34.	Pleurotus pulmonarius (Fr.) Quel.	26	12	0.70	70.5	1.52	2.166
35.	Polyporus cinnabarinus (Jacq.) P. Karst.	22	03	0.17	17.6	1.29	7.333
36.	Steccherinum ochraceum (Pers.ex J.F. Gmel.) Gray	22	07	0.41	41.1	1.29	3.142
37.	Stereum rugosum Pers.	04	03	0.17	17.6	0.23	1.333
38.	Tremetes hirsuta (Wulfen) Pilat.	38	16	0.94	94.1	2.23	2.375
39.	Tropicoporus linteus (Berk. & M.A. Curtis)	06	04	0.23	23.5	0.35	1.50
40.	Xylaria symploci Pande, Waingankar, Punekar & Ran[a]dive	20	02	0.11	11.7	1.17	10.0

NIS – Number of individual species, O – Occurrence, F – Frequency, FP – Frequency Percentage, D – Density, A - Abundance

TABLE : 7 *NUCLEOTIDE SEQUENCES OF THE SELECTED WOOD DECAYING SAMPLES*

Sample No.	Sequences
1/40	ATGTCCGAGACCGTGACCGCACTCACTTTCAGGCTCGCCTGGGAGGTCAAGAAGATCTCGTTCGACTACACCCCGAACTGGG GCCGCGGCAGCCCCAGCAGCTACATCGACAATCTCACCTTCCCGAAGGTCCTGACCGACAAGGCGTACACGTACCGCGTCGT CGTCTCCGGGCGCGACCTCGGCGTGCGCCCCTCGTACGAGGTCGCCAGCGATGGCTCGCAGAAGATCAACTTCCTCGAGTAC CACAATGGCTACGGCATTGCGGACACGAACACCATCCAGGTGTATGTCGTCGACCCCTCCACCGGCGACGACTTCATCATCGC CCAGTGGAACTAA
3/40	TAACAAGGATTCCCCTAGTAACTGCGAGTGAAGCGGGATGAGCTCAAATTTGAAATCTGGCGGTCTTGTTACCGTCCGAGTTGT AATCTGGAGAGGCGTTTTCCGCGTTGGACCGTGTACAAGTCTCCTGGAACGGAGCGTCATAGAGGGTGAGAATCCCGTCCATG ACACGGACCACCAATGCTATGTGATACGCCCTCGAAGAGTCGAGTTGTTTGGGAATGCAGCTCAAAATGGGTGGTAAATTCCAT CTAAAGCTAAATATTGGCGAGAGACCGATAGCGAACAAGTACCGTGAGGGAAAGATGAAAAGCACTTTGAAAAGAGAGTTAAAC AGTACGTGAAATTGTTGAAAGGGAAACGCTTGAAGTCAGTCGCGTTGCACGGAACTCAGCCTTGCTTCGGCTTGGTGTACTTTC TGTGTGACGGGTCAACGTCAATTTTGACCGGCGGAGAAAGGCGAGGGGAATGTAGCGCTGTTTCGGCGGCGTGTTATAGCCCT TTGTTGTATGCGTCGGTTGGGATTGAGGACCGCAGCACGCCTGTAAATTGGCCGGGGGTTCGCCCTACGTTACGTGCTTAGGA TGTTGGCATAATGGCTTTAAGCGACCCGTCTTGAAACACGGACCAAGGAGTCTAACATGCTTGCGAGTGTTCGGGTGGTAAACC CTTGCGCGAAATGAAAGTGAAAGTTGGGAACCTCCGCGAGGGGGTGCACCGACGCCCGGCCCTGACGTTCTCTGACGGTGCT GCGGTAGAGCAAGTATGTT GGGACCCGAAAGATGGTGAACTATGCCTGAATAGGGCGAAGCCAGAGGAAACTCTGGTGGAGGCTCGTAGCGATTCTGACGTG CAAATCGATCGTCAAATTTGGG
4/40	GCCTTCCGAGGCATGTGCACGCCCTGCTCATCCACTCTACACCTGTGCACTTACTGTAGGTTGGCGTGGGTTTCTAGCCTCCG GGCTGGGAGCATTCTGCCGGCCTATGTACACTACAAACTCTAAAGTATCAGAATGTAAACGCGTCTAACGCATCTTAATACAACTT TCAGCAACGGATCTCTTGGCTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATC ATCGAATCTTTGAACGCACCTTGCGCTCCTTGGTATTCCGAGGAGCATGCCTGTTTGAGTGTCATGAAATTCTCAACCCATAAGT CCTTGTGATCTATGGGCTTGGATTTGGAGGCTTGCTGGCCCTAGCGGTCGGCTCCTCTTGAATGCATTAGCTTGATTCCGTGCG GATCGGCTCTCAGTGTGATAATTGTCTACGCTGTGACCGTGAAGCGTTTTGGCAAAGCTTCTAACCGTCCATTAGGGACAATCTT T

PLATE – 1: *MACROFUNGI DOCUMENTED FROM CHITTERI HILLS, NAMES OF SPECIES ARE GIVEN IN (TABLE - 6) AS SERIAL NUMBERS 1-4*