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ORIGINAL ARTICLE

Diversity of Fungi in Different Age Series of Iron Ore Mine Overburden Waste Dumps in Chhattisgarh, Central India

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ABSTRACT
We investigated the diversity of fungi in Dalli-Rajhara (Chhattisgarh, India) mine overburden (OB) dump and compares with natural forest soils of adjoining areas. 119 Soil samples were collected from rhizosphere region of planted and naturally growing tree species in mine OB dump. The fungi were isolated by pour plate count method and density was calculated. Total 4112 fungal colonies were observed. Isolated fungi was belongs to 2 phylum Zygomycota and Ascomycota. Isolated 29 genera were mainly belonging to 11 families. All the 99 different fungal species were isolated from the NS. However from the fresh dump (D_0), no fungal colonies could be detected. From the subsequent age series dumps (D_3, D_7, D_8 and D_9) the numbers of species encountered were 68, 76, 55 and 72 respectively. All the 99 detected species of fungi belong to 29 genera and the genus Aspergillus sp. was noted to be the taxonomically most diverse with 16 to 22 species. Dominance of Aspergillus sp. was followed by Penicillium sp.
Key word: *Dominance, Evenness Index, Species Richness, SHE analysis, Similarity Index,*

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INTRODUCTION

The dependence of primitive societies upon mined product is illustrated by the nomenclature of those epochs: Stone age, Bronze age and Iron age, a succession which also show the increasing complexity of society's relationship with mining [11]. India is a developing country and produces as many as 84 minerals comprising 4 fuels, 11 metallic, 49 non-metallic industrial and 20 minor minerals [14]. Chhattisgarh is the richest state in terms of mineral wealth with 28 varieties. Rich deposits of bauxite, limestone, dolomite, coal, iron ore and limestone. Deposits of diamonds, gold, base metal, alexandrite, gemstones, beryl, garnet and rock crystal and corundum are found in the state (CMDC). The main environmental effects due to mining are changes in soil stratification, reduced biotic diversity, modification of structure and functioning of ecosystems; these changes ultimately influence water, nutrient dynamics and tropic interactions [20; 43]. Some worker [47; 58] concluded that establishing the vegetation on these areas is generally complex because of altered pH, variable texture, lack of organic matter, deficiency of minerals and essential elements, fragmented rocks and many other adverse biological factors including microbes and toxic chemicals.

The role of soil microbes in successful rehabilitation of mine waste is significant with addition to other technique in most inhospitable sites where some tree species need symbiotic association of microorganisms for their establishment, growth and development. For such soil a fully structured and functional soil microbial community is required (63; 62).

Fungi are nature's original recyclers (56; 57), converting toxic organic compounds to harmless products, often carbon dioxide and water (60). The use of fungi accelerates the establishment of higher species in overburden (61; 64). Inoculating with suitable, improved microflora including mycorrhiza (59), bacteria and fungi may be helpful in breaking down the available organic matter and establishing the green pioneers.

In these habitats, fungi may occur either as resting propagules or as active mycelia depending on the availability of nutrients and favorable environmental conditions. So the spores can be easily found in the soil samples. It has now become necessary to measure the status of existence of fungi in disturbed sites. Against this background, in the present investigations, an attempt was made to determine the status of fungi in Dalli Rajhara mine overburden soil.

MATERIAL AND METHODS

Study Area: The study site, Dalli is located on a hill range bounded by 20°33'0" and 20°34'30" N latitude and 81°1'0" and 81°4'30" E longitude and Rajhara mines falls in between 20°33'0" and 20°35'0" N latitude and 81°0'45" and 81°07'0" E longitude under Balod district, in the state of Chhattisgarh, India.

Sample collection: Soil samples were collected from different age series dump by random sampling method. Samples were collected from the rhizosphere of plants and from bulk soil and finally mixed to get a homogenous mixture. These sub-samples were brought to the laboratory in sterilized polythene bags and mixed thoroughly to form a composite sample. After sorting out larger pieces of materials and root fragments, the samples were subjected to sieving in 2mm mesh. Each of the samples was divided into three replicates for analysis. Soil sample from adjoining area (natural soil) of the waste dump was taken as control.

Isolation of fungi: The fungi were isolated from soil samples by serial dilution method on potato dextrose agar (PDA) medium by pour plate count method [67] with 3 replicates. The Petri dishes were placed in the BOD incubator at 27±2ºC for 3 to 4 days [1].

Identification of fungi and maintenance of cultures: After incubation distinct colonies were identified. The cultures were identified on the basis of macroscopic (colonial morphology, colour, texture, shape, diameter and appearance of colony) and microscopic characteristics (spore bearing fruiting body, spore size, growth rate hyphae, septation in mycelium, presence of specific reproductive structures, shape and structure of conidia and presence of sterile mycelium). Pure cultures of fungi isolates were identified with the help of literature (41; 21; 40; 9; 16; 17; 53; 8; 10; 2; 33; 66 and Expert in Forest Pathology Division, T.F.R.I., Jabalpur were referred for identification of fungi. After the identification pure culture was stored in refrigerator for further use and preservation. The following indices of species structure were assessed (58):

1) Species Richness (SR)

SR= number of species present in particular site

2) Relative Spore Density (RSD)

$$RSD = \frac{\text{Spore density of a particular species}}{\text{Spore density of all species}} \times 100$$

3) Shannon Diversity Index (H) (48)

$$H = -\sum(ni / N \ln ni / N)$$

Where, ni = Relative spore density of each species;
N = Total Relative spore density of all species

4) Simpson Diversity Index (SDI) (49)

$$D = \sum (ni / N)2;$$

Where, D = Simpson Dominance Index; ni = Relative spore density of each species; N = Total Relative density of all species

5) Evenness Index (J) (37)

$$J = H/\ln S$$

Where, H= Shannon Diversity Index; S = Total no. of species

6) Similarity Index (Sorensen coefficient) (29;30)

$$Ss = 2a/(2a + b + c)$$

Where, Ss = Sorensen similarity coefficient; a = number of species common to both ecosystem; b = number of species common in first ecosystem; c = number of species common to second ecosystem; Ss usually is multiplied by 100%.

RESULTS AND DISCUSSION

Total 119 soil samples were collected from dump site at iron ore mined OB dumps and from NS (un-disturbed soil). Total 4112 fungal colonies were observed. Isolated fungi was belongs to 2 phylum Zygomycota and Ascomycota. Isolated 29 genera were mainly belonging to 11 family such as Mucoraceae (*Absidia* sp.*, Rhizopus* sp. and *Mucor* sp.), Trichocomaceae (*Aspergillus* sp.*, Penicillium* sp.*, Emericella* sp.*, Eupenicillium* sp.*, Tritirachium* sp. and *Paecilomyces* sp.), Hypocreaceae (*Trichoderma* sp.*, Gliocladium* sp. and *Nigrospora* sp.), Nectriaceae (*Acremonium* sp.*, Fusarium* sp.), Mycosphaerelleaceae (*Cladosporium*

sp.), Chaetomiaceae (*Botryotrichum* sp.), Pleosporaceae (*Alternaria* sp.*, Curvularia* sp. and *Bipolaris* sp.), Incertae sedis (*Phoma* sp.*, Memnoniella* sp.*, Scytalidium* sp.*, Cephalosporium* sp.*, Clamydomyces* sp. and *Periconia* sp.), Myxotrichaceae (*Oidiodendron* sp.), Plectorsphaerellaceae (*Verticillum* sp.) (Table 1).

3.1 Species richness, Diversity and Evenness of fungi

As evident from the table 2, all the 99 different fungal species were isolated from the NS. However from the fresh dump (D_0), no fungal colonies could be detected. From the subsequent age series dumps (D_3, D_7, D_8 and D_9) the numbers of species encountered were 68, 76, 55 and 72 respectively. All the 99 detected species of fungi belong to 29 genera and the genus *Aspergillus* sp. was noted to be the taxonomically most diverse with 16 to 22 species. Dominance of *Aspergillus* sp. was followed by *Penicillium* sp.

Some fungi *Aspergillus parasiticus*, *Aspergillus versicolor, Penicillium commune* and *Penicillium rugulosum* was only absent in 3 year old OB dump. In 7 year old dumps *Absidia fusca* and *Alternaria tenuissima* wasabsent.*Aspergillus clavatus, Aspergillus flavus var. oryzae*, *Aspergillus fumigates, Aspergillus* sp. 4, *Aspergillus sydowii, Cladosporium variabile, Clamydomyces palmarum, Curvularia indica, Fusarium poae, Fusarium* sp. and *Penicillium nigricans, Penicillium novae-zeelandiae* wasabsent in 8 year old OB dump. In 9 year old OB dump *Botryotrichum piluliferum, Cephalosporium indicum, Cladosporium oxysporum*, *Fusarium chlamydosporum* was absent. *Fusarium udum,* Non sporolating hypomyctes*Penicillium restrictum, Phoma glomerata, Rhizopus stolonifer, Trichoderma* sp. 1and *Alternaria humicola* was only absentin 3 and 8 year old dumps. *Aspergillus restrictus* was absent in 8 and 9 year old dumps. *Memmoniella echinata* was absent in 3 and 9 year old dumps*. Oidiodendron maius*, sterile fungi 1, 3, 4, 10, *Trichoderma* sp. 1 and *Verticillum* sp. was only present in 7 year old dumps. *Paecilomyces lilacinus* was only present in 3 year old dumps. *Penicillium adametzi* was absent only in 7 and 9 year old OB dumps. *Phoma* sp. was absent only in 8 and 9 year old OB dumps. *Rhizopus* sp. was present in only 9 year old dumps (Table 1).

Some fungi was isolated from all age dumps and natural soil *Acremonium strictum, Alternaria alternata, Aspergillus awamori, Aspergillus candidus, Aspergillus flavus, Aspergillus flavus var. columnaris, Aspergillus humicola, Aspergillus janus, Aspergillus nidulars var. echinulatus, Aspergillus niger, Aspergillus repens, Aspergillus* sp. 1, *Aspergillus* sp. 2, *Aspergillus terreus, Aspergillus unguis, Bipolaris halodus, Emericella nidulans, Eupenicillium* sp., *Fusarium oxysporum,Fusarium javanicum, Fusarium moniliforme, Fusarium roseum, Fusarium solani, Gliocladium deliquescens, Mucor hiemalis, Nigrospora oryzae, Nigrospora padwicki, Nigrospora panici, Penicillium asperum, Penicillium aurantiogriseum, Penicillium citreonigrum, Penicillium citrinum, Penicillium funiculosum, Penicillium oxalicum*, *Penicillium roseopurpureum, Penicillium* sp. 1, *Penicillium* sp. 2, *Penicillium* sp. 3, *Periconia hispidula, Phoma* sp. 1*, Scytalidium thermophilum, Trichoderma strctipilis, Tritirachium dependens, Aspergillus* sp. 3 (Table 1).

Value of species richness, species diversity and evenness of fungi are tabulated in table 2. In dump soil species richness was highest in 7 year old plantation (76) followed by 9 year old plantation (72), 3 year old plantation (68), while lowest number of species was present in 8 year old plantation (55). 99 species was recorded in natural soil. The value of Shannon wiener diversity index ranged between 1.75614-1.91483. These were highest in 7 year old plantation followed by 3 year old plantation, 9 year old plantation and lowest diversity index was observed in 8 year old plantation. Simpson diversity index of all age dumps and natural soil was all most similar, expect 8 year old plantation. The species evenness ranges from zero to one with zero signifying no evenness and one a complete evenness. The value of evenness ranged between 0.876177-0.955351. Maximum evenness in dump soil was observed in 7 year old plantation followed by 3 year old plantation. Natural soil have maximum evenness index. 8 year old plantation show lowest evenness index.

Similarity index (Sorensen coefficient) of soil fungi

Maximum species similarity was observed in between 7 year old plantation and NS (90.61%) followed by between 9 year old plantation and NS (88.14%), 7 and 9 year old plantation (87.5%). Minimum species similarity was observed in between 7 and 8 year old plantation (74.13%) followed by between 8 and 9 year old plantation (78.62%). Similarity index between 3 and 9 year old plantation and between 3 year old plantation and NS have similar value (Table 3).

SHE analysis of soil fungi

In the studied community it was observed that Shannon-wiener's information index for fungal species is more infused by species richness, with the increase in richness the diversity increase there was negligible effect of evenness on Shannon-wiener's information index (fig 1).

Table 1: Relative density of soil fungi (D0= fresh dump, D3 =three years old dump, D7 = seven year, D8 eight year and D9 = nine year old dump)

S. No.	Name of Fungi	Relative spore density				
		D_3	D_7	D_8	D_9	NS
1	*Absidia fusca* Linnemann	0.53	0	1.27	1.58	1.12
2	*Acremonium strictum* W. Gams	0.66	0.08	1.63	1.67	1.54
3	*Alternaria alternata* (Fr.) Keissl	0.79	0.09	2.44	1.05	1
4	*A. humicola* Oudem	0	0.04	0	2.29	1.62
5	*A. tenuissima* (Kunze) Wiltshire	1.32	0	2.08	1.49	1.29
6	*Aspergillus awamori* Nakaz.	1.58	0.11	4.07	1.41	1.62
7	*A. candidus* Link.	2.37	0.14	1.08	1.32	1.7
8	*A. clavatus* Desm.	1.84	0.08	0	1.06	1.12
9	*A. flavus* Link.	1.97	0.16	0.81	1.32	1.16
10	*A. flavus var. columnaris* Raper & Fennel	1.58	0.09	1.36	1.41	1.21
11	*A. flavus var. oryzae* (Ahlb.) Kurtzman	1.45	0.14	0	0.18	0.5
12	*A. fumigates* Fresen.	2.37	0.15	0	0.79	0.75
13	*A. humicola* Chaudhuri & Sachar.	1.71	0.12	1.18	1.32	0.62
14	*A. janus* Raper & Thom	0.79	0.18	1.36	0.79	0.96
15	*A. nidulars var. echinulatus* Fennell & Raper	0.92	0.16	1.27	1.58	1.33
16	*A. niger* Tiegh	2.24	0.15	1.63	1.85	0.75
17	*A. parasiticus* Speare.	0	0.09	1.9	0.53	1.21
18	*A. repens* (Corda) Sacc.	1.18	0.11	2.17	0.18	1.62
19	*A. restrictus* Sm.	3.29	0.12	0	0	1
20	*Aspergillus* sp. 1	0.53	0.18	1.9	0.35	0.33
21	*Aspergillus* sp. 2	1.05	0.19	1.54	0.7	0.17
22	*Aspergillus* sp. 3	0.53	0.22	3.53	1.67	0.46
23	*Aspergillus* sp. 4	0.26	0.56	0	1.85	0.87
24	*A. sydowii* (Baineir & Sartory) Thom & Church	0.26	0.25	0	1.58	0.46
25	*A. terreus* Thom, in Thom & Church	2.11	0.22	0.63	1.05	0.91
26	*A. unguis* (Weil & L. Gaudin) Thom & Raper	1.18	0.16	1.72	1.14	0.62
27	*A. versicolor* (Vuill.) Tiraboschi	0	0.07	2.53	0.7	0.5
28	*Bipolaris halodus* (Drechsler) Shoemaker	0.4	0.08	1.63	1.41	0.75
29	*Botryotrichum piluliferum* Sacc. & March.	1.58	0.09	0.54	0	0.87
30	*Cephalosporium indicum* Petch	1.84	0.18	0.81	0	1.08
31	*Cladosporium oxysporum* Berk. & M.A. Curtis	2.11	0.12	0.72	0	2.33
32	*C. variabile* (Cooke) G.A. de Vries	2.37	0.14	0	0.26	1.16
33	*Clamydomyces palmarum* (Cooke) Mason	0.79	0.13	0	1.23	1
34	*Curvularia indica* Subram.	1.18	0.12	0	1.41	3.24
35	*Emericella nidulans* (Eidam) Vuill.	0.79	0.06	3.25	3.34	2.16
36	*Eupenicillium* sp.	0.92	0.07	2.62	1.93	1.33
37	*Fusarium oxysporum* Schlecht	1.58	0.07	1.54	3.25	0.79
38	*F. chlamydosporum* Wollenw. & Reinking	1.97	0.04	2.26	0	0.71
39	*F. javanicum* Koord.	0.79	0.15	2.62	0.09	1.37
40	*F. moniliforme* J. Sheldon	1.05	0.12	3.53	0.18	1.33
41	*F. poae* (Peck) Wollenw.	0.53	0.07	0	1.23	1.29
42	*F. roseum* Link. Ex Fries	0.79	0.08	1.08	0.18	1.46
43	*F. solani* (Maritus) Appel & Wollonweber	1.18	0.09	1.54	0.79	1.62
44	*Fusarium* sp.	1.05	0.06	0	1.41	1.29
45	*Fusarium udum* Butler	0	0.08	0	1.76	0.58
46	*Gliocladium deliquescens* Sopp.	0.39	0.11	0.18	0.35	0.67
47	*Memmoniella echinata* (Rivolta) Galloway	0	0.14	1.63	0	1.16
48	*Mucor hiemalis* F. sp. Silvaticus (Hagen) Schipper	0.53	0.01	1.08	0.7	0.46
49	*Nigrospora oryzae* (Berk. & Br.) Petch	0.79	0.02	0.81	1.05	0.71
50	*N. padwicki* Prasad, Agnihotri & Agarwal	1.05	0.05	1.36	0.53	1.21
51	*N. panici* Zimm	1.58	0.18	0.72	1.58	0.87
52	Non sporolating hypomyctes	0	0.09	0	1.05	1.04
53	*Oidiodendron maius* Barron.	0	0.12	0	0	0.37
54	*Paecilomyces lilacinus* (Thom) Samson.	1.58	0	0	0	0.08

55	*Penicillium adametzi* Zaleski	0.79	0	1.36	0	0.91
56	*P. asperum* (Shear) Raper & Thom	0.92	0.16	1.99	1.23	1.21
57	*P. aurantiogriseum* Dierckx	2.11	0.21	1.45	0.53	1.29
58	*P. citreonigrum* Dierckx	1.58	0.09	1.63	1.23	1.75
59	*P. citrinum* Thom	1.58	0.09	1.08	0.18	1.66
60	*P. commune* Thom	0	0.08	1.63	1.23	0.67
61	*P. funiculosum* Thom	1.58	0.09	1.54	1.14	0.08
62	*P. nigricans* Bain. Ex Thom	1.84	0.05	0	0.18	0.75
63	*P. novae-zeelandiae* Beyma, Antonie Van Leeuwnhoek	2.5	0.08	0	1.32	0.46
64	*P. oxalicum* Currie & Thom	1.97	0.06	0.63	0.79	0.42
65	*P. restrictum* Gilman & Abbott	0	0.09	0	0.18	1.29
66	*P. roseopurpureum* Dierckx	1.05	0.12	0.72	0.26	0.75
67	*P. rugulosum* Thom	0	0.09	1.08	0.7	0.91
68	*Penicillium* sp. 1	1.84	0.39	4.34	0.18	3.28
69	*Penicillium* sp. 2	1.18	0.07	1.72	3.95	2.83
70	*Penicillium* sp. 3	1.71	0.1	1.08	0.18	0.5
71	*Periconia hispidula* (Pers.) E.W. Mason & M.B. Ellis	1.71	0.09	1.08	0.18	0.75
72	*Phoma glomerata* (Corda) Wollenw. & Hocapfel	0	0.05	0	1.23	1.12
73	*Phoma* sp.	2.11	0.06	0	0	1.95
74	*Phoma* sp. 1	1.05	0.08	0.72	0.44	1.5
75	*Rhizopus* sp.	0	0	0	0.7	1.58
76	*Rhizopus stolonifer* Ehrenb.	0	0.08	0	4.13	1.75
77	*Scytalidium lignicola* Pesante	2.5	0.12	0	1.41	0.5
78	*S. thermophilum* (Cooney & R. Emers) Austwick	0.4	0.08	1.45	0.18	0.33
79	Sterile fungi 1	0	0.11	0	0	0.87
80	Sterile fungi 2	0	0	0	0	0.21
81	Sterile fungi 3	0	0.07	0	0	0.29
82	Sterile fungi 4	0	0.18	0	0	0.25
83	Sterile fungi 5	0	0	0	0	0.17
84	Sterile fungi 6	0	0	0	0	0.33
85	Sterile fungi 7	0	0	0	0	0.5
86	Sterile fungi 8	0	0	0	0	0.12
87	Sterile fungi 9	0	0	0	0	0.08
88	Sterile fungi 10	0	0.23	0	0	1.83
89	*Trichoderma aureoviride* Rifai	2.5	0	1.9	3.34	0.42
90	*T. polysporum* (Link) Rifai	2.37	0	1.08	0	0.5
91	*T. pseudokoningii* Rifai	1.45	0	2.44	1.41	0.75
92	*T. reesei* E.G. Simmons	1.18	0	1.36	1.58	1.04
93	*Trichoderma* sp.	0.79	0	1.54	3.6	1.25
94	*Trichoderma* sp. 1	0	0.06	0	2.55	0.5
95	*T. strctipilis* Bissett	0.39	0.11	1.72	2.64	0.37
96	*T. viride* Pers.	1.97	0.18	0	1.41	1.25
97	*Tritirachium dependens* Limber	1.58	0.17	2.44	1.32	0.5
98	*Verticillum* sp.	0	0.22	0	2.64	1.41
99	*Verticillum terrestre* (Pers.) Sacc.	0	0	0	3.43	1.75

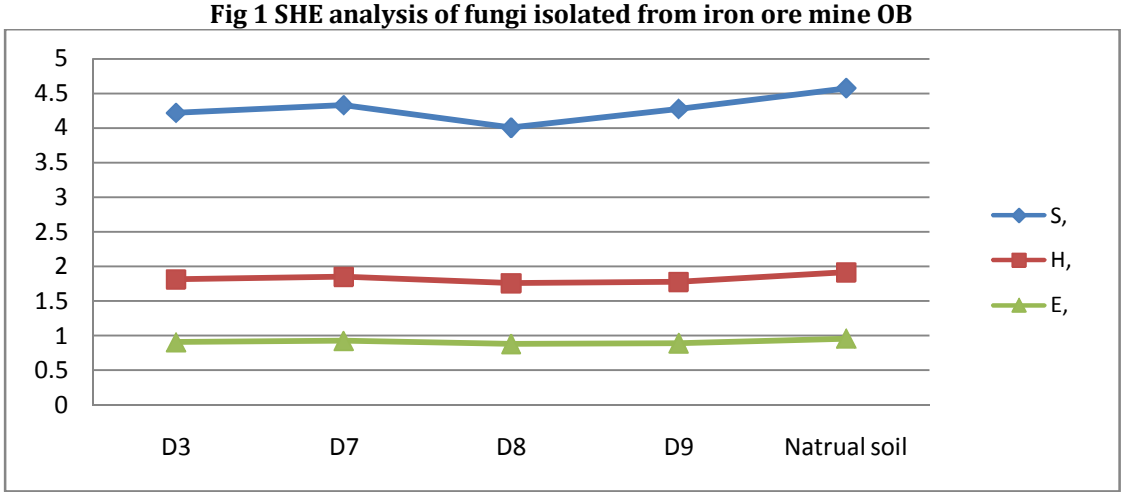
Table 2: Species richness and diversity of soil fungi in iron ore waste dump and natural soil ((D0= fresh dump, D3 =three years old dump, D7 = seven year, D8 eight year and D9 = nine year old dump)

S.No.	Waste dumps	Species richness	Diversity index		Evenness index
			Shannon	Simpson	
1	D_0	–	–	–	–
2	D_3	68	1.80987	0.983068	0.902984
3	D_7	76	1.84605	0.983015	0.921035
4	D_8	55	1.75614	0.978535	0.876177
5	D_9	72	1.77737	0.980166	0.886769
6	NS	99	1.91483	0.986019	0.955351

Table 3: Similarity index (Sorensen coefficient) of soil fungi isolated from iron ore mine OB land (D0= fresh dump, D3 =three years old dump, D7 = seven year, D8 eight year and D9 = nine year old dump)

	D3	D7	D8	D9	NS
D3	1				
D7	82.58	1			
D8	83.58	74.13	1		
D9	84.77	87.5	78.62	1	
NS	84.88	90.61	76.25	88.14	1

Fig 1 SHE analysis of fungi isolated from iron ore mine OB



Presence of soil fungi in mine OB land

The study of fungi present in the mine soils is an essential point to understand the biological rehabilitation possibilities, because these soil microorganisms which are important for improving the nutrient availability in soils [54; 25] for native plant growth [3] and are also beneficial for the nutrition and development of soil dependent animals [70; 25].

Fungi are known to occur in almost all environments including soils [35]. The fungi isolated from the metal containing waste dump of iron ore mine soil. These fungi appear to be nutritionally diverse, as many fungi were able to grow in soil but only a few grew on in artificial medium in laboratory conditions. From these soils 99 fungi were successfully cultured belonging to 29 genera (Table 1). Almost all isolates of these fungi were also isolated from mining area of S. W. Sardinia in Italy [71]. Other workers also reported similar results [28; 52; 23]. Some worker was reported that Zygomycetes fungal species were more tolerant to cadmium than ascomycetes and conidial fungi [39]. [24] isolated sixty five species belonging to 16 genera of Hyphomycetes from the copper mines at Bahia in Brazil. *Rhizopus arrhizus, Mucor* sp, *S. apiospermum, Trichoderma* sp, *Alternaria alternata, Aspergillus niger, Fusarium* spand *Penicillium* sp were identified from magnesite soil. *Rhizopus arrhizus, Mucor* sp, *Rhodotorula* sp, *Aspergillus niger, Alternaria alternata, Microsporum* sp and *Penicillium* sp were found in bauxite soil [46]. A few other reports focused on the fungal diversity in mine soil includes, [22] who enumerated few fungal species (*Cladosporium* sp., *Penicillium* sp., *Trichosporon* sp., *Rhodotorula* sp. and *Aspergillus* sp.) from waste dump of copper mine in Bulgaria and microbial (fungus) diversity in coals mine tailings at Ingwe Mines in South Africa [13].

The most dominated genus was *Aspergillus* sp. in iron ore mine OB dumps. Similar result was observed by [18] other worker who isolated micromycetes from uranium mining in Czechoslovakia. *Penicillium* sp. was co-dominated in these soils; a similar result was also reported that *Penicillium* sp. such as *P. brevicompactum* and *P. miczynskii* were the dominant genus in copper polluted soils [68; 4]. 15 reported *P. waksmanii* among the cadmium resistant filamentous fungi. Another study, have enumerated soil saprotrophic microfungi from heavily metal polluted and limestone habitats [27; 31]. All these isolated fungi were also reported from iron ore mine OB dumps in the present study.

Aspergillus sp. and *Penicillium* sp. are ubiquitous fungi [38; 12; 26; 5; 19]. Both fungi were dominated in all environments due to their high sporulation capacity. *Penicillium* sp. was able to produced fungal and bacterial antibiotics, whereas *Aspergillus* sp. produced some kind of toxins such as aflotoxins, achrotoxins it may prevent the growth of other fungal species [45]. These results confirm variation in the sensitivity

between taxa of the same genus and the importance of the identification of microfungi to species level for a proper evaluation of changes in microbial community structure [55].

Melanized fungi (*Cladosporium* sp, *Alternaria alternata* and *Aureobasidium pullulans*), are often isolated from soil samples treated with toxic industrial wastes containing high concentrations of copper and mercury [69; 32]. These fungi were also inhabited in iron ore mined OB dumps.

In present finding *Trichoderma* sp was third most dominated species in iron ore mine OB land. *Trichoderma* sp. was also isolated from polluted and mine soil [46]. *Fusarium* sp. was also isolated from polluted and mine soil by 28; 52; 27; 31. In present finding *Aspergillus* sp, *Trichoderma* sp, *Fusarium* sp and *Penicillium* sp were commonly found in mine soils and indicate their efficiency to survive in any environment.

Species richness of soil fungi

Species richness of soil fungi was not following uniform pattern which means they did not show direct correlation between the age of dumps and species richness. Minimum species richness was observed in 3 year old dumps this may be due to lower amount of organic matter, humus and soil enzymatic activity in these dumps [6;7]. Number of species was increased in 7 year dumps this may be due to the fact that soil conditions favoring soil fungi was improved including increase in organic carbon, growth of planted and naturally growing species, improvement of rhizosphere near root zone of plants, etc. [51; 42; 50]. But fungal species richness was reduced in 8 year old dumps this may be because of increase in invasive plants like *Lantana* which inhibited growth of other planted and naturally growing species. These plants also secrete allelopathy chemical in rhizosphere region, which inhibited the growth of other microorganism [44; 36; 34].

SHE analysis of soil fungi

SHE Graph was plotted against the age of the dumps to study the change in phyto sociological characters and fungal species accumulation on the OB dumps with increasing age. The plot showed that the species diversity (H') was highest in the 3 year old dumps, it also increased in 7 year old dumps after that its slightly reduced in the 8 year old dump, it was constant in the 9 year old dump and maximum in Natural soil. There was no change in evenness of the species with increasing age of dump, while species richness increased through time. It can be concluded from SHE analysis that the diversity index in the OB areas is mostly regulated by evenness in the community (Fig 1).

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