

Supplementary Tables belonging to the manuscript:

Microbial community and enzymatic activities on natural forest, forest plantations and cropping soils.

Table S1 Results of a three-way ANOVA about the effect of land-use-change, soil horizon, season, and their interactions on enzyme activities: a) Cellulase, b) FDA and c) Urease activity.

a) Cellulase activity				
Source of variation	Sum of squares	Degrees of freedom	F ratio	P value
Ecosystem (a)	56.530	3	32.826	1.09×10^{-14} ***
Soil Horizon(b)	25.979	1	45.256	1.25×10^{-9} ***
Season(c)	87.059	5	30.332	$< 2.00 \times 10^{-16}$ ***
a x b	41.152	3	23.896	1.23×10^{-11} ***
a x c	44.537	15	5.172	2.00×10^{-7} ***
b x c	6.006	5	2.093	0.01629
a x b x c	18.516	15	2.150	0.0334 *
Error	55.108	96		
b) FDA				
Source of variation	Sum of squares	Degrees of freedom	F ratio	P value
Ecosystem (a)	499.495	3	51.30	$< 2 \times 10^{-16}$ ***
Soil Horizon(b)	130.506	1	40.21	7.43×10^{-9} ***
Season(c)	361.890	5	22.30	8.97×10^{-15} ***
a x b	67.882	3	6.97	0.000271 ***
a x c	284.433	15	5.84	2.10×10^{-8} ***
b x c	17.772	5	1.09	0.368145
a x b x c	53.820	15	1.00	0.362069
Error	31.155.7	96		
c) Urease activity				
Source of variation	Sum of squares	Degrees of freedom	F ratio	P value
Ecosystem (a)	1.988.080	3	101.888	$< 2 \times 10^{-16}$ ***
Soil Horizon(b)	36.099	1	5.550	0.0205 *
Season(c)	2.032.733	5	30.332	$< 2 \times 10^{-16}$ ***
a x b	75.742	3	3.882	0.0115 *
a x c	669.840	15	6.866	7.39×10^{-10} ***
b x c	61.214	5	1.882	0.1045
a x b x c	97.576	15	1.000	0.4616
Error	62.4397	96		

Table S2. Pearson correlation coefficients between biological and physicochemical variables from soils under different land uses.

Parameter	Richness	Shannon	Richness	Shannon	Celulase	FDA	Urease
	Fungal		Bacterium		Activity		
pH	-0.50	-0.46	n.s	n.s	n.s	n.s	n.s
SOM	n.s	n.s	-0.41	-0.48	0.54	0.60	0.57
N	n.s	n.s	-0.41	-0.49	0.50	0.51	0.50
P	n.s	n.s	-0.50	-0.57	0.51	0.47	0.47
Al	-0.53	n.s	n.s	n.s	n.s	n.s	n.s
K	-0.45	n.s	n.s	n.s	n.s	n.s	n.s

Ca	-0.43	n.s	-0.57	-0.60	0.41	n.s	n.s
Mg	-0.48	n.s	-0.48	-0.50	n.s	n.s	n.s
Na	-0.45	-0.46	n.s	n.s	n.s	n.s	n.s
SB	n.s	-0.50	-0.53	0.44	n.s	n.s	n.s
CICE	n.s	n.s	-0.54	-0.57	0.45	n.s	n.s
AlS	n.s	0.50	0.43	n.s	n.s	n.s	n.s
Ks	n.s	n.s	n.s	n.s	n.s	-0.59	n.s
Cas	-0.62	-0.49	n.s	n.s	n.s	n.s	n.s
Sd	n.s	n.s	-0.48	-0.55	0.63	0.65	0.55
Mn	n.s	n.s	n.s	-0.46	0.47	0.60	0.63
Zn	n.s	n.s	-0.46	-0.53	0.61	0.57	0.53
Cu	n.s	n.s	-0.44	-0.49	0.45	0.50	0.53
B	n.s	n.s	n.s	n.s	n.s	0.56	0.49
Clay	n.s	n.s	n.s	n.s	0.51	0.65	0.52
Silt	-0.46	-0.55	n.s	n.s	n.s	-0.66	-0.58
Sand	-0.46	-0.54	n.s	n.s	n.s	-0.66	-0.60
Q _b	0.42	0.48	n.s	n.s	n.s	n.s	n.s

n.s = No significant at $p < 0.05$.

Table S3. Phylogenetic assignment bacteria of major DGGE bands Bacteria A-h horizon.

OUT no.	Lineage (Taxonomic group) ^a	The closest species (accession no.)	Pairwise Similarity (%)
<i>Natural Forest Ah (0-18 cm)</i>			
1	<i>Acidobacteriaceae; Acidobacterium</i>	Uncultured <i>Acidobacterium</i> (JX114382.1.)	97%
2	<i>Bacterium; Proteobacteria; Alphaproteobacteria; Rhizobiales; anthobacteraceae; Pseudolabrys.</i>	Uncultured <i>Pseudolabrys</i> sp. (JX505115.1)	99%
3	<i>Bacterium</i>	<i>Bacillus cereus</i> strain (KP120954.1)	77%
4	<i>Bacterium; Proteobacteria; Alphaproteobacteria; Rhizobiales. Bradyrhizobiaceae; Bradyrhizobium</i>	<i>Bradyrhizobium</i> sp. (FN600560.2)	98%
10	<i>Bacterium; Proteobacteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae.</i>	Uncultured <i>Radyrhizobium</i> Sp. (KJ410572.1)	92%
12	<i>Bacterium</i>	Uncultured bacterium (jq695958.1)	90%
14	<i>Bacterium; Acidobacteria.</i>	Uncultured <i>Bacterium Acidobacteria</i> (Gu374361.1)	84%
18	<i>Bacterium; Gemmatimonadetes; Gemmatimonadales; Gemmatimonadaceae; Gemmatimonas.</i>	Uncultured <i>Gemmatimonas</i> Sp. (Jq087111.1)	97%
<i>Young plantation A-h (0-18 cm)</i>			
2	<i>Bacterium; Proteobacteria; Alphaproteobacteria; Rhizobiales; anthobacteraceae; Pseudolabrys.</i>	Uncultured <i>Pseudolabrys</i> sp. (JX505115.1)	99%
3	<i>Bacterium</i>	<i>Bacillus cereus</i> strain (KP120954.1)	77%
10	<i>Bacterium; Proteobacteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae.</i>	Uncultured <i>Bradyrhizobium</i> sp. (kj410572.1)	92%
12	<i>Bacterium</i>	Uncultured bacterium (jq695958.1)	90%
14	<i>Bacterium; Acidobacteria.</i>	Uncultured <i>Bacterium Acidobacteria</i> (Gu374361.1)	84%

16	Bacterium; Actinobacteria	Uncultured Actinobacterium. (Ef378837.1)	98%
18	Bacterium; Gemmatimonadetes; Gemmatimonadales; Gemmatimonadaceae; Gemmatimonas.	Uncultured Gemmatimonas Sp. (Jq087111.1)	97%
Adult plantation A-h (0-18 cm)			
2	Bacterium; Proteobacteria; Alphaproteobacteria; Rhizobiales; anthobacteraceae; Pseudolabrys.	Uncultured Pseudolabrys sp. (JX505115.1)	99%
10	Bacterium; Proteobacteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae; Bradyrhizobium.	Uncultured Bradyrhizobium Sp. (Kj410572.1)	92%
12	Bacterium	Uncultured Bacterium. (Jq695958.1)	90%
14	Bacterium; Acidobacteria.	Uncultured Bacterium Acidobacteria (Gu374361.1)	84%
16	Bacterium; Actinobacteria	Uncultured Actinobacterium. (Ef378837.1)	98%
18	Bacterium; Gemmatimonadetes; Gemmatimonadales; Gemmatimonadaceae; Gemmatimonas.	Uncultured Gemmatimonas Sp. (Jq087111.1)	97%
Agricultural Crops A-h (0-18 cm)			
2	Bacterium; Proteobacteria; Alphaproteobacteria; Rhizobiales; anthobacteraceae; Pseudolabrys.	Uncultured Pseudolabrys sp. (JX505115.1)	99%
10	Bacterium; Proteobacteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae; Bradyrhizobium.	Uncultured Bradyrhizobium Sp. (Kj410572.1)	92%
12	Bacterium	Uncultured bacterium (jq695958.1)	90%
18	Bacterium; Gemmatimonadetes; Gemmatimonadales; Gemmatimonadaceae; Gemmatimonas.	Uncultured Gemmatimonas Sp. (Jq087111.1)	97%

^athe phylogenetic assignment is based on sequences analysis by megablast of GenBank database from NCBI (<http://www.ncbi.nlm.nih.gov>). It is given the phylum as well as the lowest predictable phylogenetic rank.

Table S4. Phylogenetic assignment bacteria of major DGGE bands Bacteria B-h.

Bands	Taxonomic groups	Closest relatives or cloned sequences (accession no.) ^c	Similarity
Natural Forest A-h (18-50 cm)			
1	Bacterium; Actinobacteria; Streptomycetales; Streptomycetaceae; Streptomyces.	Streptomyces sp. (genbank: kt591698.1)	98%
2	Bacterium;	Uncultured bacterium (Genbank: jn642995.1)	86%
3	Bacterium;	Uncultured bacterium (Genbank: gq264391.1)	99%

4	Bacterium;	Uncultured bacterium (Genbank: kj014532.1)	96%
5	Bacterium;	Uncultured bacterium (Genbank: hq462560.1)	99%
6	Bacterium;	Uncultured bacterium (GenBank: JN839677.1)	96%
7	Bacterium;	Uncultured bacterium (GenBank: HQ598188.1)	98%
8	Bacterium;	Uncultured <i>Proteobacterium</i> (genbank: fr832343.1)	95%
9	Bacterium	Uncultured Bacterium (GenBank: AF524860.1)	97%
10	Bacterium; <i>Actinobacteria</i> ; <i>Micrococcales</i> ; <i>Micrococcaceae</i> ;	<i>Arthrobacter</i> sp. (Genbank: kx036596.1)	90%
11	Bacterium;	Uncultured bacterium (GenBank: GU598641.1)	84%
12	Bacterium; <i>Proteobacterium</i> ; <i>Alphaproteobacteria</i> ;	Uncultured <i>Alpha proteobacterium</i> (Genbank: ef220681.1)	90%
13	Bacterium;	Uncultured bacterium (Genbank: fj433095.1)	84%
17	<i>Proteobacterium</i> , <i>Proteobacterium</i> ; <i>Betaproteobacterium</i> ;	Uncultured <i>beta proteobacterium</i> (Genbank: kj750911.1)	99%
18	<i>Bacterium</i> ; <i>Gemmatimonadetes</i> ; <i>Gemmatimonadales</i> ; <i>Gemmatimonadaceae</i> ; <i>Gemmatimonas</i> .	Uncultured <i>Gemmatimonas</i> Sp. (Genbank: Jq087111.1)	97%
Young plantation A-h (18 -50cm)			
4	Bacterium;	Uncultured bacterium (Genbank: kj014532.1)	96%
5	Bacterium;	Uncultured bacterium (Genbank: hq462560.1)	99%
9	Bacterium	Uncultured Bacterium (GenBank: AF524860.1)	97%
10	Bacterium; <i>Actinobacteria</i> ; <i>Micrococcales</i> ; <i>Micrococcaceae</i> .	<i>Arthrobacter</i> sp. (Genbank: kx036596.1)	90%
11	Bacterium;	Uncultured bacterium (GenBank: GU598641.1)	84%
12	Bacterium; <i>Proteobacterium</i> ; <i>Alphaproteobacteria</i> .	Uncultured <i>Alpha proteobacterium</i> (Genbank: ef220681.1)	90%
13	Bacterium;	Uncultured bacterium (Genbank: fj433095.1)	84%
17	<i>Proteobacterium</i> , <i>Proteobacterium</i> ; <i>Betaproteobacterium</i> .	Uncultured <i>Beta proteobacterium</i> (Genbank: kj750911.1)	99%
19	<i>Bacterium</i> ; <i>Gemmatimonadetes</i> ; <i>Gemmatimonadales</i> .	Uncultured bacterium <i>Gemmatimonadaceae</i> (GenBank: KJ750948.1)	89%

Adult plantation A-h (18-50 cm)			
4	Bacterium;	Uncultured bacterium (Genbank: kj014532.1)	96%
5	Bacterium;	Uncultured bacterium (Genbank: hq462560.1)	99%
7	Bacterium;	Uncultured bacterium (GenBank: HQ598188.1)	98%
8	Bacterium;	Uncultured <i>Proteobacterium</i> (Genbank: fr832343.1)	95%
9	Bacterium	Uncultured Bacterium (GenBank: AF524860.1)	97%
10	Bacterium; <i>Actinobacteria; Micrococcales; Micrococcaceae.</i>	<i>Arthrobacter sp.</i> (Genbank: kx036596.1)	90%
13	Bacterium;	Uncultured bacterium (Genbank: fj433095.1)	84%
17	<i>Proteobacterium, Proteobacterium; Betaproteobacterium.</i>	Uncultured <i>beta proteobacterium</i> (Genbank: kj750911.1)	99%
18	<i>Bacterium; Gemmatimonadetes; Gemmatimonadales; Gemmatimonadaceae; Gemmatimonas.</i>	Uncultured <i>Gemmatimonas Sp.</i> (Genbank: Jq087111)	97%
19	<i>Bacterium; Gemmatimonadetes; Gemmatimonadalel.</i>	Uncultured bacterium <i>Gemmatimonadaceae</i> (GenBank: KJ750948.1)	89%
Agricultural Crops B-h horizon (18 -50cm)			
4	Bacterium;	Uncultured bacterium (Genbank: kj014532.1)	96%
5	Bacterium;	Uncultured bacterium (Genbank: hq462560.1)	99%
9	Bacterium	Uncultured Bacterium (GenBank: AF524860.1)	97%
10	Bacterium; <i>Actinobacteria; Micrococcales; Micrococcaceae.</i>	<i>Arthrobacter sp.</i> (Genbank: kx036596.1)	90%
11	Bacterium;	Uncultured bacterium (GenBank: GU598641.1)	84%
12	<i>Bacterium; Proteobacterium; Alphaproteobacterium.</i>	Uncultured <i>Alpha proteobacterium</i> (Genbank: ef220681.1)	90%
13	Bacterium;	Uncultured bacterium (Genbank: fj433095.1)	84%
17	<i>Proteobacterium, Proteobacterium; Betaproteobacterium.</i>	Uncultured <i>Beta proteobacterium</i> (Genbank: kj750911.1)	99%
18	<i>Bacterium; Gemmatimonadetes; Gemmatimonadales; Gemmatimonadaceae; Gemmatimonas.</i>	Uncultured <i>Gemmatimonas Sp.</i> (Genbank: Jq087111)	97%
19	<i>Bacterium; Gemmatimonadetes; Gemmatimonadales.</i>	Uncultured bacterium <i>Gemmatimonadaceae</i>	89%

(GenBank: KJ750948.1)

^athe phylogenetic assignment is based on sequences analysis by megablast of GenBank database from NCBI (<http://www.ncbi.nlm.nih.gov>). It is given the phylum as well as the lowest predictable phylogenetic rank.

Table S5. Phylogenetic assignment fungi of major DGGE bands Fungal A-h horizon.

Bands	Taxonomic group ^a	Closest relatives or cloned sequences (accession no.)	Similarity
Natural Forest A-h (0-18 cm)			
1	Fungi; Dikarya; Basidiomycota <i>Agaricomycotina</i> ; <i>Agaricomycetes</i> ; <i>Thelephorales</i> ; <i>Thelephoraceae</i>	Uncultured <i>Tomentella</i> (Genbank: EU625921.1)	94%
2	Fungi; Dikarya; Ascomycota; <i>Pezizomycotina</i> ; <i>Leoti-</i> <i>omycetes</i> ; <i>Helotiales</i> ; <i>Chaetomellaceae</i> ; <i>Chaetomella</i>	<i>Chaetomella Acutiseta</i> (Genbank: Ay544728.1)	99%
3	Fungi	Uncultured fungus (Genbank: EF628705.1)	97%
4	Fungi; Dikarya; Basidiomycota; <i>Agaricomy-</i> <i>cotina</i> ; <i>Agaricomycetes</i> ; <i>Russulales</i> ; <i>Russulaceae</i> ; <i>Lac-</i> <i>tarius</i>	<i>Lactarius southworthiae</i> (Genbank: kf386755.1)	98%
5	Fungi; Dikarya; Basidiomycota; <i>Agaricomy-</i> <i>cotina</i> ; <i>Agaricomycetes</i> ; <i>Cantharellales</i> ; <i>Cantharellaceae</i> ; <i>Craterellus</i> .	<i>Craterellus tubaeformis</i> (GenBank: DQ898683.1)	89%
8	<i>Alveolata</i> ; <i>Apicomplexa</i> ; <i>Conoidasida</i> ; <i>Coccidia</i> ; <i>Eucoc-</i> <i>cidiorida</i> ; <i>Eimeriorina</i> ; <i>Eimeriidae</i> .	<i>Eimeriidae</i> (Genbank: ef024843.1)	96%
9	Fungi; Dikarya; Ascomycota; <i>Pezizomycotina</i> ; <i>Leoti-</i> <i>omycetes</i> ; <i>Leotiomyces incertae sedis</i> ; <i>Myxotrichaceae</i> ; <i>Byssoascus</i> .	<i>Byssoascus striatosporus</i> (Genbank: af222535.1)	99%
12	Fungi; <i>Glomeromycota</i> ; <i>Glomeromycetes</i> ; <i>Archaeospo-</i> <i>rales</i> <i>Archaeosporaceae</i> .	Uncultured <i>archaeospora</i> (Genbank: am420394.1)	99%
15	Fungi; Dikarya; Basidiomycota; <i>Agaricomycotina</i> ; <i>Agaricomycetes</i> ; <i>Agaricomycetidae</i> ; <i>Agaricales</i> ; <i>Agari-</i> <i>caceae</i> .	<i>Agaricus bisporus</i> (Genbank: AY787216.1)	94%
16	Fungi; Dikarya; Ascomycota; <i>Pezizomycotina</i> ; <i>Leo-</i> <i>tiomyces</i> ; <i>Leotiomyces incertae sedis</i> ; <i>Collophora</i>	<i>Collophora rubra</i> (Genbank: GQ154627.1)	98%
17	Fungi; <i>Glomeromycota</i> ; <i>Glomeromycetes</i> ; <i>Archaeospo-</i> <i>rales</i> ; <i>Archaeosporaceae</i> .	Uncultured <i>Archaeospora</i> (GenBank: AM420394.1)	99%
18	Fungi incertae sedis; unclassified <i>zygomycetes</i>	<i>Zygomycete sp</i> (GenBank :EU428774.1)	95%
Young plantation A-h (0-18 cm)			
1	Fungi; Dikarya; Basidiomycota <i>Agaricomycotina</i> ; <i>Agaricomycetes</i> ; <i>Thelephorales</i> ; <i>Thelephoraceae</i>	Uncultured <i>Tomentella</i> (Genbank: EU625921.1)	94%
2	Fungi; Dikarya; Ascomycota; <i>Pezizomycotina</i> ; <i>Leoti-</i> <i>omycetes</i> ; <i>Helotiales</i> ; <i>Chaetomellaceae</i> ; <i>Chaetomella</i>	<i>Chaetomella Acutiseta</i> (Genbank: Ay544728.1)	99%
5	Fungi; Dikarya; Basidiomycota; <i>Agaricomy-</i> <i>cotina</i> ; <i>Agaricomycetes</i> ; <i>Cantharellales</i> ; <i>Cantharellaceae</i> ; <i>Craterellus</i> .	<i>Craterellus tubaeformis</i> (GenBank :DQ898683.1)	90%
6	Fungi; Dikarya; Basidiomycota; <i>Agaricomycotina</i> ; <i>Agaricomycetes</i> ; <i>Russulales</i> ; <i>Russulaceae</i> ; <i>Lactarius</i>	<i>Lactarius southworthiae</i> (GenBank :KF386755.1)	93%
7	Fungi; Dikarya; Basidiomycota; <i>Pucciniomy-</i> <i>cotina</i> ; <i>Microbotryomycetes</i> ; <i>Sporidiobolales</i> ; <i>mitosporic</i> <i>Sporidiobolales</i> ; <i>Rhodotorula</i> .	<i>Rhodotorula graminis</i> (GenBank :HM371376.1)	99%

8	Alveolata; Apicomplexa; Conoidasida; Coccidia; Eucoccidiorida; Eimeriorina; Eimeriidae.	Eimeriidae (GenBank:EF024843.1)	96%
16	Fungi; Dikarya; Ascomycota; Pezizomycotina; Leotiomycetes; Leotiomycetes incertae sedis; Collophora.	Collophora rubra (GenBank:Q154627.1)	16
Adult plantation A-h (0-18 cm)			
2	Fungi; Dikarya; Ascomycota; Pezizomycotina; Leotiomycetes; Helotiales; Chaetomellaceae; Chaetomella.	Chaetomella Acutiseta (Genbank: Ay544728.1)	99%
3	Eukaryota; Fungi	Uncultured fungus (GenBank:EF628705.1)	97%
6	Fungi; Dikarya; Basidiomycota; Agaricomycotina; Agaricomycetes; Russulales; Russulaceae; Lactarius.	Lactarius southworthiae (GenBank:KF386755.1)	93%
8	Fungi; Dikarya; Basidiomycota; Pucciniomycotina; Microbotryomycetes; Sporidiobolales; mitosporic Sporidiobolales; Rhodotorula.	Rhodotorula graminis (GenBank: HM371376.1)	99%
9	Fungi; Dikarya; Ascomycota; Pezizomycotina; Leotiomycetes; Leotiomycetes incertae sedis; Myxotrichaceae; Byssosascus.	Byssosascus triatosporus (GenBank: AF222535.1)	99%
11	Fungi; Dikarya; Basidiomycota; Agaricomycotina; Agaricomycetes	Uncultured Agaricomycetes (GenBank: FJ554148.1)	97%
12	Fungi; Glomeromycota; Glomeromycetes; Archaeosporales Archaeosporaceae.	Uncultured archaeospora (Genbank: am420394.1)	99%
16	Fungi; Dikarya; Ascomycota; Pezizomycotina; Leotiomycetes; Leotiomycetes incertae sedis; Collophora.	Collophora rubra (GenBank:Q154627.1)	16
Agricultural Crops A-h (0-18 cm)			
1	Fungi; Dikarya; Basidiomycota Agaricomycotina; Agaricomycetes; Thelephorales; Thelephoraceae.	Uncultured Tomentella (Genbank: EU625921.1)	94%
2	Fungi; Dikarya; Ascomycota; Pezizomycotina; Leotiomycetes; Helotiales; Chaetomellaceae; Chaetomella.	Chaetomella Acutiseta (Genbank: Ay544728.1)	99%
6	Fungi; Dikarya; Basidiomycota; Agaricomycotina; Agaricomycetes; Russulales; Russulaceae; Lactarius.	Lactarius southworthiae (GenBank:KF386755.1)	93%
8	Fungi; Dikarya; Basidiomycota; Pucciniomycotina; Microbotryomycetes; Sporidiobolales; mitosporic Sporidiobolales; Rhodotorula.	Rhodotorula graminis (GenBank: HM371376.1)	99%
13	Fungi; Glomeromycota; Glomeromycetes; Archaeosporales; Archaeosporaceae.	Uncultured Archaeospora (Genbank: AM420394.1)	93%
14	Fungi; Chytridiomycota; Chytridiomycetes; Polychytriales; Neokarlingia.	Neokarlingia chitinophila voucher (GenBank: HQ901766.1)	96%
15	Fungi; Dikarya; Basidiomycota; Agaricomycotina; Agaricomycetes; Agaricomycetidae; Agaricales; Agaricaceae; Agaricus.	Agaricus bisporus isolate (GenBank: AY787216.1)	94%

^athe phylogenetic assignment is based on sequences analysis by megablast of GenBank database from NCBI (<http://www.ncbi.nlm.nih.gov>). It is given the phylum as well as the lowest predictable phylogenetic rank.

Table S6. Phylogenetic assignment fungi of major DGGE bands Fungal B-h horizon.

Bands	Taxonomic group ^a	Closest relatives or cloned sequences (accession no.)	Similarity
Natural Forest B-h (18-50 cm)			
1	Fungi; Dikarya; Basidiomycota; Agaricomycotina;	Cuphophyllus Pratensis	98%

	<i>Agaricomycetes; Agaricomycetidae; Agaricales; Hygrophoraceae; Cuphophyllus.</i>	(Genbank: Kf291059.1)	
2	Fungi; Dikarya; Basidiomycota; Agaricomycotina; Agaricomycetes; Russulales; Russulaceae; Lactarius.	<i>Lactarius Southworthiae</i> (Genbank: Kf386755.1)	98%
3	Fungi; Dikarya; Basidiomycota; Agaricomycotina; Agaricomycetes; Cantharellales; Clavulinaceae; Clavulina.	Clavulina Sp. (Genbank: Ay757265.1)	99%
4	Fungi; Dikarya; Basidiomycota; Agaricomycotina; Agaricomycetes; Agaricomycetidae; Agaricales; Cortinariaceae; Cortinarius.	Cortinarius Violaceus (Genbank: Ay705950.1)	99%
5	Fungi;	Uncultured Fungi (Genbank: Ef628733.1)	98%
6	Fungi; Dikarya; Basidiomycota; Agaricomycotina; Agaricomycetes; Polyporales; Trametes	Trametes Versicolor (Genbank: Ay336751.1)	92%
7	Fungi; Dikarya; Basidiomycota; Agaricomycotina; Agaricomycetes; Agaricomycetidae; Agaricales; Hygrophoraceae; Neohygrocye	<i>Neohygrocye Ingrata</i> (Genbank: Kf381539.1)	94%
8	Fungi; Dikarya; Basidiomycota; Agaricomycotina; Agaricomycetes; Hymenochaetales; Hymenochaetaeae; Phellinus	<i>Phellinus Igniarius</i> (Genbank: Hm584803.1)	94%
10	Fungi; Dikarya; Basidiomycota; Agaricomycotina; Tremellomycetes; Tremellales; Trichosporonaceae; Trichosporon	<i>Trichosporon multisporum</i> (Genbank: Jn939428.1)	97%
11	Fungi; Dikarya; Basidiomycota; Agaricomycotina; Agaricomycetes; Russulales; Russulaceae; Lactarius	<i>Lactarius Southworthiae</i> (Genbank: Kf386755.1)	99%
13	Fungi; Dikarya; Ascomycota; Taphrinomycotina; Archaeorhizomycetales; Archaeorhizomycetaceae; Archaeorhizomyces	<i>Archaeorhizomyces Borealis</i> (GenBank: JF836023.1)	92%
16	Fungi; Dikarya; Basidiomycota; Agaricomycotina; Agaricomycetes; Agaricomycetidae; Agaricales; Tricholomataceae; Tricholoma	<i>Tricholoma sp.</i> (Genbank: Kj417173.1)	98%
Young plantation B-h (18 -50cm)			
1	Fungi; Dikarya; Basidiomycota; Agaricomycotina; Agaricomycetes; Agaricomycetidae; Agaricales; Hygrophoraceae; Cuphophyllus	<i>Cuphophyllus Pratensis</i> (Genbank: Kf291059.1)	98%
2	Eukaryota; Fungi; Dikarya; Basidiomycota; Agaricomycotina; Agaricomycetes; Russulales; Russulaceae; Lactarius	<i>Lactarius Southworthiae</i> (Genbank: Kf386755.1)	98%

3	Eukaryota; Fungi; Dikarya; Basidiomycota; Agaricomycotina; Agaricomycetes; Cantharellales; Clavulinaceae; Clavulina.	Clavulina Sp. (Genbank: Ay757265.1)	99%
4	Fungi; Dikarya; Basidiomycota; Agaricomycotina; Agaricomycetes; Agaricomycetidae; Agaricales; Cortinariaceae; Cortinarius	Cortinarius Violaceus (Genbank: Ay705950.1)	99%
5	Fungi;	Uncultured Fungus (Genbank: Ef628733.1)	98%
6	Fungi; Dikarya; Basidiomycota; Agaricomycotina; Agaricomycetes; Russulales; Russulaceae; Lactarius	Lactarius southworthiae voucher. (GenBank: KF386755.1)	93%
7	Fungi; Dikarya; Basidiomycota; Pucciniomy- cotina; Microbotryomycetes; Sporidiobolales; mito- sporic Sporidiobolales; Rhodotorula.	Rhodotorula graminis strain (GenBank: HM371376.1)	99%
8	Fungi; Dikarya; Basidiomycota; Agaricomycotina; Agaricomycetes; Hymenochaetales; Hymenochaeta- ceae; Phellinus	Phellinus Igniarius (Genbank: Hm584803.1)	94%
10	Fungi; Dikarya; Basidiomycota; Agaricomycotina; Tremellomycetes; Tremellales; Trichosporonaceae; Trichosporon.	Trichosporon multisporum (Genbank: Jn939428.1)	97%
11	Fungi; Dikarya; Basidiomycota; Agaricomycotina; Agaricomycetes; Russulales; Russulaceae; Lactarius.	Lactarius Southworthiae (Genbank: Kf386755.1)	99%
13	Fungi; Dikarya; Ascomycota; Taphrinomycotina; Archaeorhizomycetales; Archaeorhizomycetaceae; Ar- chaeorhizomyces.	Archaeorhizomyces Borealis (GenBank: JF836023.1)	92%
15	Fungi; Dikarya; Basidiomycota; Agaricomycotina; Agaricomycetes; Cantharellales; Hydnaceae; Hyd- num.	Hydnum albomagnum (GenBank: AY665777.1)	99%
Adult Plantation B-h (18-50 cm)			
1	Fungi; Dikarya; Basidiomycota; Agaricomycotina; Agaricomycetes; Agaricomycetidae; Agaricales; Hy- grophoraceae; Cuphophyllus.	Cuphophyllus Pratensis (Genbank: Kf291059.1)	98%
2	Eukaryota; Fungi; Dikarya; Basidiomycota; Agaricomycotina; Agaricomycetes; Russulales; Russulaceae; Lactarius.	Lactarius Southworthiae (Genbank: Kf386755.1)	98%
3	Eukaryota; Fungi; Dikarya; Basidiomycota; Agaricomycotina; Agaricomycetes; Cantharellales; Clavulinaceae; Clavulina.	Clavulina Sp. (Genbank: Ay757265.1)	99%
6	Fungi; Dikarya; Basidiomycota; Agaricomycotina; Agaricomycetes; Russulales; Russulaceae; Lactarius.	Lactarius southworthiae voucher. (GenBank: KF386755.1)	93%
10	Fungi; Dikarya; Basidiomycota; Agaricomycotina; Tremellomycetes; Tremellales; Trichosporonaceae; Trichosporon.	Trichosporon Multisporum (Genbank: Jn939428.1)	97%

12	Fungi; Dikarya; Ascomycota; Pezizomycotina; Leotiomyces; Helotiales; Helotiaceae; Chlorociboria.	Chlorociboria (Genbank: Ay544713.1)	98%
13	Fungi; Dikarya; Ascomycota; Taphrinomycotina; Archaeorhizomycetales; Archaeorhizomycetaceae.	Archaeorhizomyces Borealis (Genbank: Jf836023.1)	92%
14	Fungi; Dikarya; Basidiomycota; Agaricomycotina; Tremellomyces; Tremellales; Tremellaceae.	Uncultured Tremellaceae (GenBank: EF023247.1)	100%
15	Fungi; Dikarya; Basidiomycota; Agaricomycotina; Agaricomycetes; Cantharellales; Hydnaceae; Hydnum.	Hydnum albomagnum (GenBank: AY665777.1)	99%
Agricultural Crops B-h (18-50 Cm)			
1	Fungi; Dikarya; Basidiomycota; Agaricomycotina; Agaricomycetes; Agaricomycetidae; Agaricales; Hygrophoraceae; Cuphophyllus.	Cuphophyllus Pratensis (Genbank: Kf291059.1)	98%
2	Eukaryota; Fungi; Dikarya; Basidiomycota; Agaricomycotina; Agaricomycetes; Russulales; Russulaceae; Lactarius.	Lactarius Southworthiae (Genbank: Kf386755.1)	98%
3	Eukaryota; Fungi; Dikarya; Basidiomycota; Agaricomycotina; Agaricomycetes; Cantharellales; Clavulinaceae; Clavulina.	Clavulina Sp. (Genbank: Ay757265.1)	99%
4	Fungi; Dikarya; Basidiomycota; Agaricomycotina; Agaricomycetes; Agaricomycetidae; Agaricales; Cortinariaceae; Cortinarius.	Cortinarius Violaceus (Genbank: Ay705950.1)	99%
5	Fungi;	Uncultured Fungus (Genbank: Ef628733.1)	98%
6	Fungi; Dikarya; Basidiomycota; Agaricomycotina; Agaricomycetes; Russulales; Russulaceae; Lactarius.	Lactarius southworthiae voucher. (GenBank: KF386755.1)	93%
7	Fungi; Dikarya; Basidiomycota; Pucciniomycotina; Microbotryomycetes; Sporidiobolales; mitosporic Sporidiobolales; Rhodotorula	Rhodotorula graminis strain (GenBank: HM371376.1)	99%
8	Fungi; Dikarya; Basidiomycota; Agaricomycotina; Agaricomycetes; Hymenochaetales; Hymenochaetaceae; Phellinus	Phellinus Igniarius (Genbank: Hm584803.1)	94%
10	Fungi; Dikarya; Basidiomycota; Agaricomycotina; Tremellomyces; Tremellales; Trichosporonaceae; Trichosporon.	Trichosporon Multisporum (Genbank: Jn939428.1)	97%
11	Fungi; Dikarya; Basidiomycota; Agaricomycotina; Agaricomycetes; Russulales; Russulaceae; Lactarius.	Lactarius Southworthiae (Genbank: Kf386755.1)	99%
13	Fungi; Dikarya; Ascomycota; Taphrinomycotina; Archaeorhizomycetales; Archaeorhizomycetaceae.	Archaeorhizomyces Borealis (Genbank: Jf836023.1)	92%
15	Fungi; Dikarya; Basidiomycota; Agaricomycotina;	Hydnum albomagnum (GenBank: AY665777.1)	99%

<i>Agaricomycetes; Cantharellales; Hydnaceae; Hyd-</i>			
<i>num.</i>			
<i>Fungi; Dikarya; Basidiomycota; Agaricomycotina;</i>		<i>Tricholoma sp.</i>	
16	<i>Agaricomycetes; Agaricomycetidae; Agaricales; Tri-</i>	(Genbank: Kj417173.1)	98%
<i>cholomataceae; Tricholoma.</i>			

^athe phylogenetic assignment is based on sequences analysis by megablast of GenBank database from NCBI (<http://www.ncbi.nlm.nih.gov>). It is given the phylum as well as the lowest predictable phylogenetic rank.