

Distance-Based Analysis of Soil Mycofloral Communities of Hot Arid Region of India

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ABSTRACT

Ecological dynamics of soil fungal communities have been explored from different hot arid regions of the world with different scientific approaches along with bi or multi-directional cause and effect relationships. In general, such studies documented large heterogeneity in soil fungal population which were linked with various bottom-up (vegetation, climatic features, land use and anthropogenic) and top down factors (soil physical-chemical properties) and hence at large geographical level, generalization about their population dynamics cannot be figure out. Thus, a method is required which not only can provide a cumulative ecological grouping of fungal species cultivated from different zones and land use but can also reduce the non-normality of original data set. With such approach, a researcher can provide a confident threshold population list and grouping for a large geographic region. Population dynamics of 69 soil fungal species (4 zone) were evaluated pertain to three land-use types with their abundance and modified functional dispersion (FD_M) values. Our modified algorithmic based approach is a pioneer one for fungal population and provides an integrated weighted ecological grouping. Such grouping inherently accommodates spatial and land-use attributes. Our FD_M also significantly relate with species specific spatial pattern.

Key Words: Fungal Population; Heterogeneity; Relative Abundance; Functional Dispersion; Spatial Pattern; Principal Component Analysis.

INTRODUCTION

Environmental heterogeneity is omnipresent in natural systems and persuades population dynamics and community structure (Yang et al. 2015). Soil microbial communities fluctuate in accordance with plant community and soil components. Such relationships have been explored and modeled with individual and or with response to interactions of various factors. Fungal community compositions and diversity were studied by many workers across soil pH gradient (Rousk et al. 2010), salinity gradient (Mohamed and Martiny 2011, Muthukrishnan et al. 2012), seasonal variations (Voriskova et al. 2014) and with response to aridity (Maestre et al. 2015). Diversity and variability in soil fungi were studied in detailed with respect to specific

land-uses like forests (Chandini and Rajeshwari 2017), grazing lands (Guleri et al. 2013), croplands (Liu et al. 2004), wastelands (Pratt 2008). Further, Pasternak et al. (2013) concluded the deterministic importance of environmental factors over microbial biogeography in arid and semi arid soil and suggested the meager impacts of geographic distances and spatial distribution pattern. All such studies reported large variability in fungal abundances and diversity brought by various factors (Allison et al. 2007, Allison and Treseder 2008, Kivlin et al. 2014). No study has attempted to develop a method through which noise in the abundance data in fungal population could be minimized while considering all the potential factors that control their abundance.

Our aim was to assess the abundance behavior of different soil fungal species at four hot arid zones of

India, to develop a method through which a cumulative ecological grouping can be developed and to reduce magnitude of non-normality of such abundance data set. A priori we believed that variations in fungal population dynamics were brought by both bottom up (vegetation) and top-down (soil) factors at three types of land uses viz. grazing lands, scrubland and wasteland. These lands also represent the impacts of grazing, protection and anthropogenic factors (mining, dumping sand quarry etc), respectively.

MATERIALS AND METHODS

Sampling Sites and Methodology

Study was conducted in four hot arid districts of Rajasthan (India) : Jodhpur (Zone-1), Jaisalmer (Zone-2) Barmer (Zone-3) and Bikaner (Zone-4). From these zones, during the rainy season (July to September) soil samples were collected from three main land-uses viz. grazing lands, scrub land and wastelands. Zone wise soil samples (up to 30 cm) were collected separately with the help of auger and kept in sterilized polythene bags for fungal assessment in laboratory. Soil fungi were isolated by dilution plate method as described by Johnson et al. (1959) using Czapek's Agar medium and potato dextrose medium. Petri plates were incubated at $25^{\circ}\text{C} \pm 3^{\circ}\text{C}$ and colonies were examined daily up to 10 days. For identification. Temporary and semi-permanent mounts of fungi were made in cotton blue and lactophenol. They were observed under microscope and identified by the help of fungal identification keys described by Gilman (1945), Barnett (1960), Ellis (1971, 1976) and Barron (1972). Isolates were finally identified and authenticated by Prof. D.K. Purohit (Senior Mycologist), Department of Botany JNV University, Jodhpur.

For further ecological analysis frequency, density and abundance were calculated using the following formulae:

$$\text{Frequency (\%)} = \frac{\text{No. of soil samples in which species occurred} \times 100}{\text{No. of total samples}}$$

$$\text{Density} = \frac{\text{No. of colonies in all soil samples}}{\text{No. of total samples}}$$

$$\text{Abundance} = \frac{\text{No. of individuals in all soil samples}}{\text{No. of soil samples in which species occurred}}$$

Relative Abundance Curve (RAC)

RAC was prepared to evaluate the abundance trends of different species from different zones. Basically, this is a component of biodiversity and summarize about how common or rare a species is relative to other species in a defined zone. In present study abundance of different species was converted into log transformation, arranged in descending order and graphically presented with the help of the Microsoft Excel software.

Species Spatial Distribution

Index of dispersion (I_D) i.e. variance to mean ratio was utilized to quantify the species spatial distribution behavior. An I_D values 1.0, zero and >1 indicates the random, uniform and aggregated spatial pattern, respectively. The significant departure from 1 on either side was declared based on their chi-square value (Mathur 2014).

Diversity Indices (λ , β and Υ)

Fungal species diversity was assessed at three levels (a) alpha diversity (diversity within a zone) was calculated with indices like - Fisher's α , Shannon's diversity index (H'), Simpson's diversity index (λ), Margalef's richness index (R1), Menhinick's richness index (R2), Brillouin index, and Evenness (E5). These alpha diversity indices are mathematically independent to each other (Heip et al. 1998). (b) beta (β diversity in between zones) was calculated with the Wilson Shimda index and this will provide the comparative similarity among zones and (c) gamma diversity (Υ diversity at long geographical region) was estimated with multiplication of average values of alpha and beta diversities and total number of zones (Schluter and Ricklefs 1993). All these diversity indices were calculated by using the software of Paleontological Statistics (PAST) Version 1.92. We utilized various forms of alpha diversity indices as recommended by study of Morris et al. (2014) suggested that diversity analysis with using multiple indices can provide greater insight into the interactions in a system.

Ordination Analysis

Principal Component Analysis (PCA) was utilized to calculate the distance of each species from the centroid for the quantification of functional dispersion. This ordination technique not only provides ecological

distance of a species from centroid but also give a calculated distance from other species. PCA bi-plot was interpreted according to Mathur (2014).

Functional Dispersion Trait (Modified)

This is a distance-based tool for homogeneity of dispersion and rely on mean distance in multi-dimensional character space of an individual species to the centroid of all species. Mathematically it is similar to Rao's Quadratic entropy Q but this not affected with species richness. This was calculated by following modified formula originally proposed by Laliberté and Legendre (2010).

Modified Functional Dispersion (FD_M)

$$FD_M = \left(\frac{\sum a_j z_j}{\sum a_j} \right) * R_N$$

FD_M is the functional dispersions, a_j is the abundance of species and z_j is the distance of that species from centroid. In Laliberte and Legendre (2010) method, we added a multiplication factor pertain to number of zone (R_N) from where a species was recorded. With our new index we would reduce the noise of abundance data set brought by various bottom up (vegetation) and top-down factors (soil) associated with three types of land uses and four arid zones. At the species level the percent departure from relative abundance was quantified with following formula

$$\left(\left[\frac{RA_S - FD_{MS}}{RA_S} \right] * 100 \right)$$

RA_S and FD_{MS} are the relative abundance and modified functional dispersal values of a species, respectively. Further, departure from a specific spatial pattern (regression) was assessed both with relative abundance and functional dispersion (modified) along with the autocorrelations (Durbin Watson statistic method) in data sets. This analysis was carried out with XLSTAT software (2007).

Neighbor Joining Cluster Analysis

Neighbor joining is a base-up (agglomerative) clustering strategy for the formation of phylogenetic trees and this multi-variant technique was utilized to relate the species

with their functional dispersion trait. This was also calculated with PAST software.

Non-Parametric Test

Frequency distribution analysis was performed to examined the noise level of species data set pertains to different zones and this analysis was carried out with the help of STATICA software. This test would provide the level of heterogeneity of species data set related to FD_M data set compared to relative abundance of species from different zone. Results of frequency distribution interpreted with Skewness, Kurtosis and Kolmogorov-Smirnov tests.

RESULTS AND DISCUSSION

Altogether 69 fungal species were reported from four districts of Indian Thar Desert with the composition of 5.79% Zygomycetes, 5.79% Ascomycetes, 84.05% Anamorph Hyphomycetes and 4.34%, Anamorph Coelomycetes. Maximum fungal species were reported from Zone-1 (69 species) and subsequently from Zone-4 (61 species), Zone-3 (54 species), and Zone-2 district (48 species). *Aspergillus niger* was recorded as most abundant species at zone I (11.76) and zone 4 (12.37) followed by *Fusarium chlamydosporum* (10.82 and 11.92) at both zones, respectively. *F. chlamydosporum* and *Aspergillus wentii* (13.6) were the most abundant species at zones 2 and 3, respectively. *Alternaria alternate*, *Thielavia terricola* and species of *Alternaria*, *Fusarium* and *Phoma* were identified as rare at zone 1 while *Alternaria porri*, *Cephalophora irregularis*, *Fusarium oxysporum* and *Aspergillus* sp. were rare at both zone 1 and zone 4.

Relative Abundance Curve

Within a community three basic types of distribution can be found viz. geometric, broken-stick and lognormal. Geometric distribution type prevails at relative species poor community where a single environmental resource (like moisture) is extremely important to species survival and is utilized in a strongly hierarchical fashion. Under such condition a single dominant species preempts a large fraction of the resource; the next most successful species preempts a smaller fraction of the remaining resources and so forth. Broken-stick model assumes that the species in a community partition or utilize some

critical resources with no overlapping between the species while large species assembly with sub-equal abundance is the characteristic feature of log normal model (Clarke 1990). Lognormal expect that the significance of species is governed by the connections between a substantial numbers of factors deciding success in the niche hyperspace (Clarke 1990).

The relative abundance curve for various zones is depicted in Figure 1. We found log-normal distribution types at all the studied zones. In such type of model, occupation of niche space is basically governed by various interfacing factors that influence the result of inter-specific competition, abundances governed by many independent factors and in such situation resource utilization characterized as multidimensional. Such results are with the conformity of Lussenshop (1981 in Zak and Willing 2005) in Wisconsin rhizosphere fungal forest study. He disagreed the approach that accentuate that if fungi are collected from many micro-habitats and mixed during sampling, the resultant distribution is a relic and such outcome indicated a number of independent environmental factors controlling species abundance. Lognormals could arise simply as the result of the multiplicative interaction of many normal random processes affecting the growth of population or could arise by combining unrelated samples (Mathur 2015). This tool was utilized by many workers for the study of fungal communities specifically for arbuscular-mycorrhizal fungus in tropical forest and pasture (Picone 2000), tropical timber tree (Gamboa and Bayman 2001), and dry deciduous forest of southwestern India (Banakar et al. 2012).

In this study *Aspergillus niger*, *A. fumigatus*, *A. ochraceus* and *Fusarium chlamydosporum* were the most abundant species at four zones while *Oedocephalum glomerulosum*, *Arthrotrrys superba*, *Ulocladium sp.*, *Gliomastrix aterrima* and *Fusarium lateritium* were the least abundant species and were located at tail of the curves of the different zones. Log-normal curves of different zones are basically intermingled with each other (Figure 1) that revealed the similar patterns of distribution however, we also found that a log abundance value of 0.4 works as threshold level and below which the curves of different zone separated to each other and showed sudden drops in abundances.

Spatial Patterns

Information on species specific horizontal pattern is important to management of soil fungi. Within the community a species may exhibit regular (in which individuals within population consistently separated), random (pattern in which all individuals have an equivalent shot of living anywhere within zone) or a aggregated pattern (in which individuals have a higher likelihood of being found in some area than in others (Mathur 2014).

In this study we found that only seven species namely, *Aspergillus porri*, *Aspergillus wentii*, *Aspergillus sp.*, *Alternaria alternate*, *Alternaria sp.*, *Thielavia terricola* and *Phoma sp.* exhibited aggregated pattern (Figure 2). These species having more than one variance: mean ratio along with their significant chi-square values. While other species showed random spatial distribution;

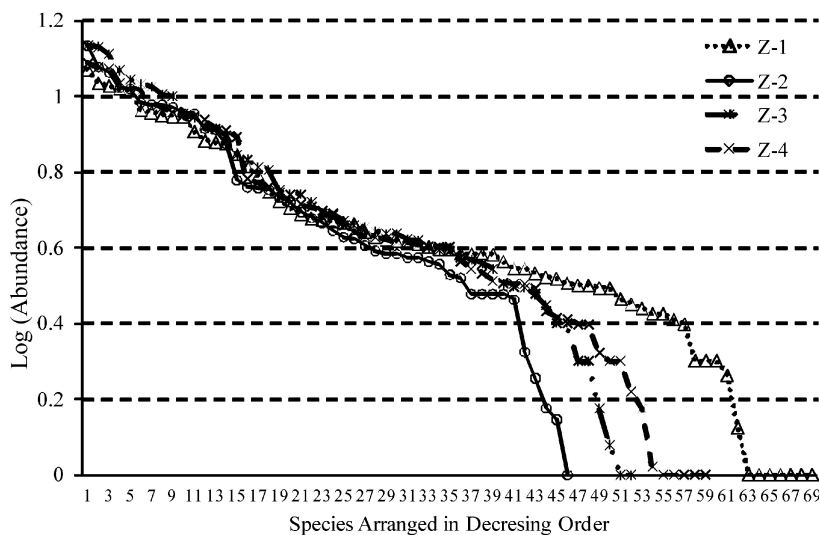


Figure 1. Relative Abundance Curve of fungal species at four arid zones

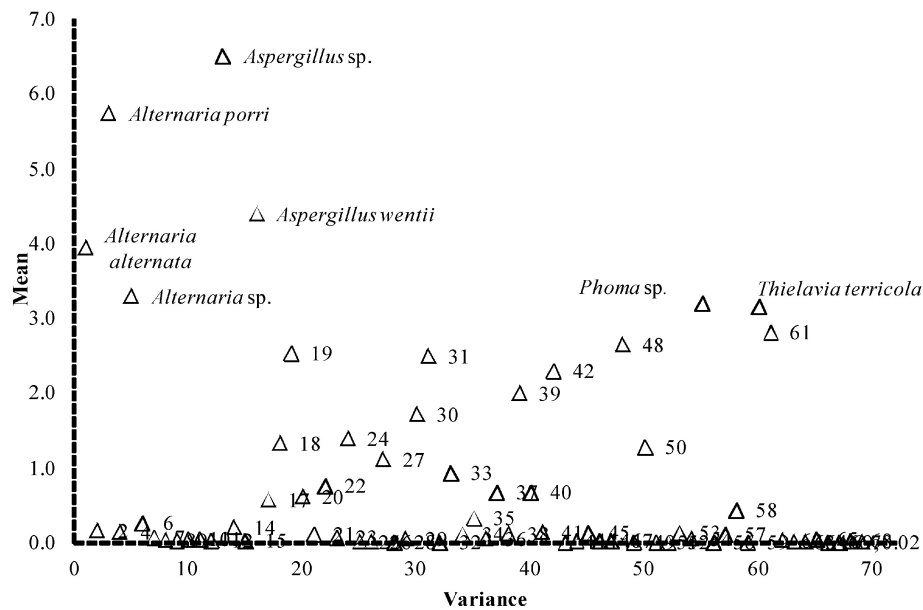


Figure 2. Spatial Patterns of 69 fungal species at four arid zones

species like *Chaetomium caprinum*, *Cladosporium macrocarpum*, *Cunninghamella sp.*, *Curvularia maculans*, *Curvularia pallescens*, *Fusarium sp.*, *Helminthosporium turcicum*, *Nigrospora sphaerica*, *Papulospora sepedonioides* and *Torula herbarum* also having more than one VM ratio but their chi-square tests were non-significant. Thus, their distributions were also declared as random.

In our analysis majority of random distribution suggested high level of competition among species while aggregated pattern reflected the synergism in resource consumption and niche requirement and this assumption is corroborated with the study of Wehner et al. (2014). Specifically for aggregation pattern, Pan and May (2009) suggested that interspecific interactions among microbial taxa are important governing factor and accordingly species will display non-random coexistence patterns. Aggregated spatial patterns of *Aspergillus flavus* and *Aspergillus niger* were reported by Griffin et al. (2001).

Variations in spatial paternity could be attributed with host phylogeny, soil type and seasonality (Wehner et al. 2014). Gomez-Aparicio et al. (2012) suggested that pathogen abundance in the Mediterranean forest soil was non-random and influenced by both abiotic and particularly, biotic factors (tree and shrub species) and such information is useful for restoration of Mediterranean forests. O'Brien et al. (2016) reviewed the microbial

biogeography explored at regional to continental gradients as well as at the centimeter scale and with these studies, we could narrow down the factors controlling community patterns and which can be relate to observed heterogeneity in biogeochemical processes. Such distribution patterns were worked out by many researcher from different arid and semi arid parts of the world like Spain (Barea et al. 2011), China (He et al. 2013), USA (Chaudhary et al. 2014). However, such types of patterns and their associated exploratory factors need to be work out from the Indian hot arid region.

Species Diversity

Species diversity can be expressed at three levels, alpha diversity, beta diversity and gamma diversity. Different diversity indexes gave the valuable informations about community status. The two basic components of species diversity are simply the total number of species actually present and the degree to which they are equally important. Species diversity in resource-limited, competitive communities is a simple function of three variables; (1) diversity of available resources or the overall size of the niche space, or hyper-volume, (2) diversity of utilization of these resources by an average species or mean niche breadth, and (3) the extent to which resources are shared or the amount of niche

overlap (Magurran 2004). Values of alpha diversity indices for different zones are presented in Table 1. Simpson index of dominance (λ) which basically measures the probability that two individuals selected at random from a sample will belong to same species and it ranges from 0 to 1 and in this study, it was recorded maximum (0.028) and minimum (0.019) at zone 2 and zone 1, respectively. Since Simpson index is actually an index of dominance, tend to be contrarily to evenness and richness, in our study this trend was also recorded with richness (being recorded maximum 69 at zone 1 and minimum 48 at zone 2). However, Shannon-weaver index is a diversity index and it ranges between 1.5 to 3.5 and its higher value demonstrated higher diversity while lower value suggests the complete dominance of one or few species.. Results of this index also follow the richness trend, recorded higher (4.07) and minimum (3.70) at zone 1 and 2, respectively. However, we found almost similar evenness trend across the different zones.

Both the Shannon and Brillouin indexes give similar and frequently corresponded diversity assessment. However, when the two indices are utilize to quantify the diversity of a specific data set, the Brillouin index will always suggest the lower value (Table 1). This is because this index described a known assortment about which there is no uncertainty. While the Shannon index estimate the diversity of the un-sampled as well as the sampled portion of the community (Heip et al. 1998). Our Brillouin index results for different zones corroborate the above statement and follow the same trend; however, values are lower than H' index.

Further, species richness was studied by Margalef and Menhinick diversity indices. Margalef Richness Index (R1) is the proportion of number of species and log number of individual, while Menchinick (R2) is the

proportion of number of species and square root of number of individual (Magurran 2004). The Margalef index measures species richness and profoundly affected with sample size (Gamito 2010). This can also apply with the other indices that are conscious to evenness or changes in dominant species, such as the dominance Berger-Parker index (Berger and Parker 1970). Both Margalef and Menchinick are insensitive to changes in community structure and change to sample size, respectively (Mathur 2005). Results of both indices are presented in Table 1. Based on these indices, the richness trends are in the order of Z-1>Z-4>Z-3>Z-2. Fisher's Alpha (α) widely used as a diversity index and It's a parametric diversity test which assumes that species abundances follow log distribution. It is a scale independent indicator of diversity insensitive to tails of the distribution (very sparse community) (Ostertag et al. 2015). In our study we found its higher value (27.05) at zone-1 followed by zone 4 (23.24) and least (17.27) at zone 2.

Beta diversity represent inter-communities diversity or of species turnover rate (Mathur 2005) between different habitats in the same geographical area. High beta diversity is the results of low similarity between the species composition of different habitats or different sampling zone. The beta diversity is an important tool because it allows the comparison of habitat diversity of two different study systems, provides information about the degree of partitioning of site by species, and together with alpha diversity suggested overall diversity and biotic heterogeneity an area (Wilson and Shmida 1984). Zone 1 was more similar and dissimilar with zone 4 (0.062) and zone 2 (0.179), respectively. Similarly zone 2 was more similar with zone 3 (0.098) than zone 4 (0.138; Table 2).

Table 1. Alpha diversity indices at four arid zones

Diversity Indices	Zones			
	Z-1	Z-2	Z-3	Z-4
Simpson index (λ)	0.01945	0.02801	0.02537	0.02329
Shannon and Weaver Index	4.07	3.70	3.81	3.91
Evenness_e^H/S	0.85	0.84	0.84	0.81
Brillouin Index (HB)	3.73	3.41	3.52	3.59
Margalef Richness Index (R1)	11.79	8.45	9.30	10.54
Menhinick Richness Index (R2)	3.86	2.97	3.13	3.54
Fisher_alpha	27.05	17.27	19.26	23.24

Z-1 Jodhpur; Z-2 Jaisalmer; Z-3 Barmer and Z-4 Bikaner

Table 2. Beta Diversity through Wilson Shimda Index (among studied arid zones)

Zones	Z-1	Z-2	Z-3
Z-2	0.179	-	-
Z-3	0.122	0.098	-
Z-4	0.062	0.138	0.078
Gamma Diversity = 3.87*0.581*4 = 8.9			

The third type of diversity, gamma diversity, has been defined to even larger-scale phenomena, which reflect primarily evolutionary rather than ecological processes and it can be expressed by the number of species found in a landscape (Cody 1986). Like beta diversity, geographical diversity (Cody 1986) is based on the differences in the species composition between habitats. In this study we calculated 8.9 gamma diversity. This is the first report of fungal gamma diversity pertains to three types of land uses in four zones of the hot Indian arid region.

Principal Component Analysis

According to Mathur and Sundaramoorthy (2016) PCA was considered useful if their cumulative percentage of variance approached 80%. In present study, first three axes together accounted more than 80% variability (Supplementary table) with their individual contribution of 41.57, 34.55 and 23.55%, respectively. Plotting of correlation between variables and factors (Figure 3) on PCA bi-plot revealed that all the species are well distributed at all the axes and there is no arching problem found in present study. 25, 19 and 25 fungal species were located at three axes, with their eigenvalues of 28.69, 23.84, and 16.48 respectively. Axes length of each species and their correlations are presented in supplementary tables (available from the corresponding author). The lengths from centroid were further utilized for functional dispersion.

Functional Dispersion Trait (Modified)

Results of FD_M are presented in Table 3. With this approach the maximum FD_M (3.99) was recorded for

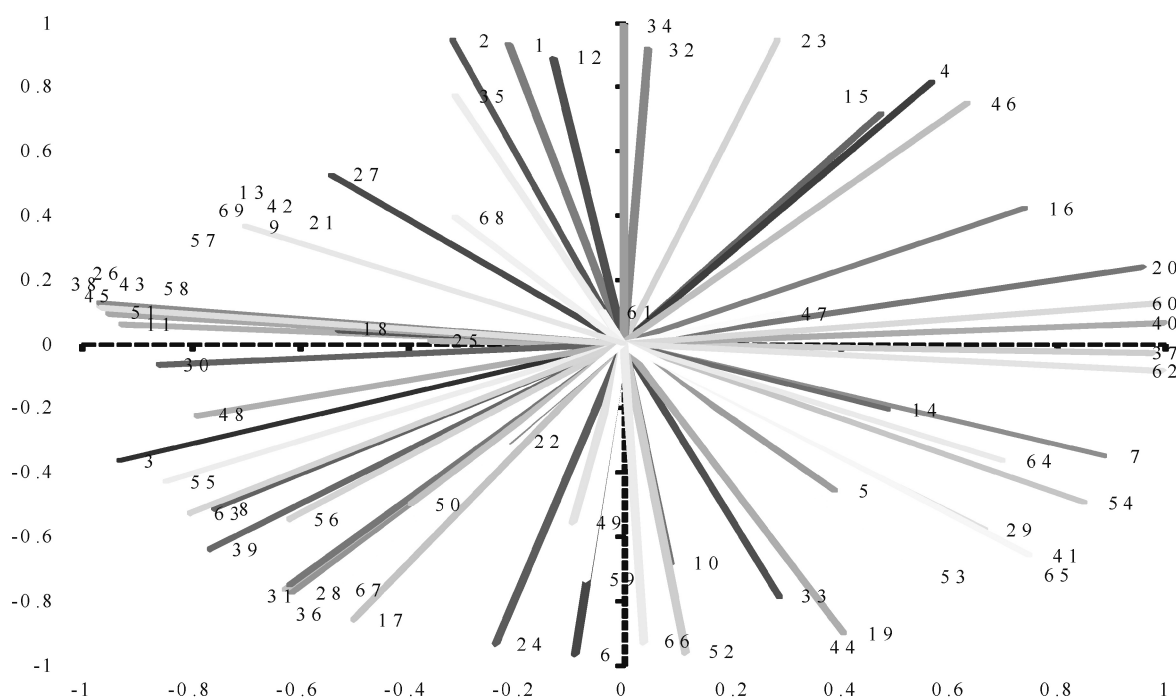


Figure 3. Principal Component Analysis conducted for distance from the centroid (Numbers refer to the species names in Table 3)

Table 3. Relative abundance and functional dispersion of 69 fungal species

S.N.	Species	Abundance				Relative abundance	Functional dispersion	Percent reduction
		Z-1	Z-2	Z-3	Z-4			
1	<i>Alternaria alternata</i>	3.95	0.00	0.00	0.00	3.95	0.37	90.63
2	<i>Alternaria brassicicola</i>	2.75	2.11	3.50	2.10	2.62	0.34	87.02
3	<i>Alternaria porri</i>	7.50	0.00	0.00	9.33	8.42	0.74	91.21
4	<i>Alternaria solani</i>	3.83	3.60	2.52	2.60	3.14	3.56	-13.38
5	<i>Alternaria sp.</i>	3.30	0.00	0.00	0.00	3.3	0.37	88.79
6	<i>Alternaria tenuis</i>	6.20	9.00	8.33	9.60	8.28	3.4	58.94
7	<i>Arthrobotrys superba</i>	1.00	1.40	0.85	0.80	1.01	3.26	-222.77
8	<i>Aspergillus flavipes</i>	8.83	9.50	9.00	8.13	8.87	2.96	66.63
9	<i>Aspergillus flavus</i>	10.36	9.62	10.78	10.83	10.4	0.52	95.00
10	<i>Aspergillus fumigatos</i>	10.63	10.52	10.12	11.85	10.78	3.39	68.55
11	<i>Aspergillus niger</i>	11.76	11.96	13.50	12.25	12.37	1.62	86.90
12	<i>Aspergillus ochraceus</i>	10.43	11.57	11.07	10.33	10.85	3.83	64.70
13	<i>Aspergillus sp.</i>	6.50	0.00	0.00	0.00	6.5	0.37	94.31
14	<i>Aspergillus tamarii</i>	7.55	8.16	8.21	10.60	8.63	3.72	56.89
15	<i>Aspergillus terreus</i>	5.30	5.72	4.91	5.19	5.28	3.77	28.60
16	<i>Aspergillus wentii</i>	7.00	0.00	13.66	7.80	9.49	0.72	92.41
17	<i>Botryotrichum piluliferum</i>	3.50	1.50	2.50	1.00	2.13	0.04	98.12
18	<i>Cephalophora irregularis</i>	2.00	0.00	0.00	2.00	2	0.46	77.00
19	<i>Chaetomium caprinum</i>	2.66	0.00	7.00	3.50	4.39	0.24	94.53
20	<i>Chaetomium flavum</i>	8.90	8.22	11.71	6.07	8.73	1.56	82.13
21	<i>Chaetomium globosum</i>	4.88	6.00	6.50	4.90	5.57	2.66	52.24
22	<i>Chaetomium indicum</i>	2.50	0.00	2.00	1.66	2.05	0.41	80.00
23	<i>Cladosporium cladosporioides</i>	7.62	7.50	6.40	8.20	7.43	2.62	64.74
24	<i>Cladosporium macrocarpum</i>	3.83	0.00	4.50	4.00	4.11	0.15	96.35
25	<i>Colletotrichum capsici</i>	4.11	4.25	4.57	4.05	4.25	2.66	37.41
26	<i>Corynespora cassiicola</i>	3.50	3.00	3.20	3.20	3.23	0.13	95.98
27	<i>Cunninghamella sp.</i>	3.12	3.66	0.00	2.71	3.16	2.79	11.71
28	<i>Curvularia falcata</i>	3.83	3.90	4.00	4.00	3.93	2.19	44.27
29	<i>Curvularia lunata</i>	9.06	9.50	7.85	8.66	8.77	3.96	54.85
30	<i>Curvularia maculans</i>	4.75	0.00	5.50	5.00	5.08	0.14	97.24
31	<i>Curvularia pallescens</i>	3.66	3.83	0.00	0.00	3.75	1.83	51.20
32	<i>Drechslera tetramera</i>	9.16	9.00	8.80	8.80	8.94	3.08	65.55
33	<i>Drechslera tritici</i>	2.66	0.00	3.00	2.50	2.72	0.23	91.54
34	<i>Fusarium chlamydosporum</i>	10.82	13.60	12.91	11.92	12.31	3.91	68.24
35	<i>Fusarium lateritium</i>	1.00	0.00	0.93	1.05	0.99	0.06	93.94
36	<i>Fusarium moniliforme</i>	8.85	10.45	10.00	9.07	9.59	3.99	58.39
37	<i>Fusarium oxysporum</i>	1.00	0.00	0.00	1.00	1	0.46	54.00
38	<i>Fusarium solani</i>	8.05	9.33	10.61	8.85	9.21	3	67.43
39	<i>Fusarium sp.</i>	2.00	0.00	0.00	0.00	2	0.37	81.50
40	<i>Gliomastrix aterrima</i>	1.00	0.00	0.00	1.00	2	0.46	77.00
41	<i>Helminthosporium sativum</i>	4.71	5.25	6.80	5.90	5.67	1.62	71.43
42	<i>Helminthosporium sp. turcicum</i>	3.50	0.00	0.00	3.40	3.45	0.43	87.54
43	<i>Macrophomina phaseolina</i>	5.57	5.40	5.66	5.76	5.6	1.42	74.64
44	<i>Memmoniella echinata</i>	2.57	3.00	2.52	2.58	2.67	3.39	-26.97
45	<i>Monilia fructigena</i>	2.00	1.80	2.00	1.00	1.7	1.14	32.94
46	<i>Mucor racemosus</i>	3.41	3.38	2.81	3.20	3.2	3.78	-18.13
47	<i>Myrothecium roridum</i>	3.33	3.00	3.12	3.66	3.28	2.29	30.18
48	<i>Nigrospora sphaerica</i>	3.11	0.00	4.40	0.00	3.76	0.56	85.11
49	<i>Oedocephalum glomerulosum</i>	1.00	0.80	1.00	0.85	0.91	1.57	-72.53
50	<i>Papulospora sepedonioides</i>	1.83	0.00	0.00	2.00	1.92	0.58	69.79

S.N.	Species	Abundance				Relative abundance	Functional dispersion	Percent reduction
		Z-1	Z-2	Z-3	Z-4			
51	<i>Penicillium chrysogenum</i>	3.95	3.84	4.34	4.02	4.04	0.45	88.86
52	<i>penicillium citrinum</i>	3.82	4.03	4.20	4.12	4.04	2.17	46.29
53	<i>Penicillium sp.</i>	2.83	3.75	4.33	3.10	3.5	0.24	93.14
54	<i>Pestalotiopsis sp.</i>	4.37	4.62	3.90	5.10	4.5	3.46	23.11
55	<i>Phoma sp.</i>	3.20	0.00	0.00	0.00	3.2	0.37	88.44
56	<i>Rhizoctonia solani</i>	4.00	3.75	3.92	4.11	3.95	1.26	68.10
57	<i>Rhizopus nigricans</i>	4.25	2.90	3.69	4.23	3.77	0.08	97.88
58	<i>Rhizopus stolonifer</i>	4.63	5.66	3.75	2.50	4.14	2.86	30.92
59	<i>Stachybotrys atra</i>	4.60	4.20	4.56	4.41	4.44	1.09	75.45
60	<i>Thielavia terricola</i>	3.16	0.00	0.00	0.00	3.16	0.37	88.29
61	<i>Torula herbarum</i>	4.18	0.00	0.00	4.26	8.44	0.49	94.19
62	<i>Trichoderma harzianum</i>	4.66	4.77	5.26	5.57	5.07	2.7	46.75
63	<i>Trichoderma koningi</i>	5.08	5.75	5.50	5.25	5.4	3.94	27.04
64	<i>Trichoderma virence</i>	4.14	4.42	4.16	4.69	4.35	3.98	8.51
65	<i>Trichoderma viridi</i>	4.08	4.95	4.86	4.20	4.52	3.96	12.39
66	<i>Trichothecium roseum</i>	3.17	3.00	3.14	3.25	3.14	1.14	63.69
67	<i>Trichrus sp.</i>	1.33	1.50	1.50	1.50	1.46	2.8	-91.78
68	<i>Trichrus spiralis</i>	2.91	3.31	3.60	3.22	3.26	3.05	6.44
69	<i>Ulocladium sp.</i>	1.00	0.90	1.20	1.00	1.03	0.13	87.38

Fusarium moniliforme followed by *Trichoderma virence* (3.98), *Curvularia lunata* and *Trichoderma viridi* (3.96). The minimum (0.04) FD_M was recorded for *Botryotrichum piluliferum* and followed by *Fusarium lateritium* (0.06) and *Rhizopus nigricans* (0.08). We found 29 species with less than one functional dispersion, 10 species with more than one and less than two, 12 species with more than two and less than three and 18 species with more than 3 and less than four. We observed less (1.40) standard deviation in data set pertains to functional dispersion as compared to relative abundance (2.96). This indicated that our approach having the capability to reduce the high noise in fungal populations brought by many factors and their inter-relationships. Species specific per cent departure from relative abundance are presented in Table 3. More than 90 per cent departure were calculated for *Alternaria alternate*, *Alternaria porri*, *Aspergillus flavus*, *Aspergillus sp.*, *Botryotrichum piluliferum*, *Chaetomium caprinum*, *Cladosporium macrocarpum*, *Corynespora cassiicola*, *Curvularia maculans*, *Drechslera tritici*, *Fusarium lateritium*, *Penicillium sp.*, *Rhizopus nigricans* and *Torula herbarum*. However, less than 15 per cent were noticed for *Cunninghamella sp.*, *Trichoderma virence*, *Trichoderma viridi*, *Trichrus spiralis*. We also found higher functional dispersion values for the *Alternaria solani*, *Arthrotrichum superba*, *Memnoniella echinata*,

Mucor racemosus, *Oedocephalum glomerulosum* and *Trichrus sp.* as compared to the relative abundance value. And thus, we also noticed negative departure for these species which was maximum for *Arthrotrichum superba*. The reason behind this variation is associated with axes length of these species. For an example *Alternaria solani* and *Mucor racemosus* which are recorded in homogenous pattern at different zone (i.e. having more homogenous) and which also accounted by PCA matrix and thus having high axes length i.e. 0.89 and 0.94, respectively. These values are then utilized in FD_M and subsequently get higher value. Such similar (proximity with each other) behaviors for both these two species are also reflected in PCA biplot (Figure 3). Our results suggested that this approach works well both for rare (*Alternaria alternate*, *Alternaria porri*, *Cephalophora irregularis*, *Fusarium oxysporum*, *Thielavia terricola* and species of *Alternaria*, *Fusarium*, *Phoma* and *Aspergillus*) as well as for abundant (*Aspergillus niger*, *Aspergillus ochraceus*, *Fusarium moniliforme* and *Fusarium solani*) species. Such patterns have also been evaluated and visualized with Neighbor Joining Cluster Analysis.

In this study we found non-significant and significant departure from randomness with relative abundance (Departure from randomness = 0.156 x relative abundance of a species $R^2 = -0.011^{NS}$) and FD_M

(Departure from randomness = $0.178 \times FD_M R^2 = -0.287^*$ at 95 % probability level), respectively and results are depicted in Figures 4 and 5. This further proved that our FD_M approach is more informative and related with spatial pattern prediction compared to relative abundance data set and within the India arid zones fungal species showed more departure from randomness up to the value of 0 to 1 of FD_M . The Durbin Watson measurement is a test for autocorrelation in the residuals from a factual regression analysis. This range from 0-4 and lower and

higher values indicates positive and negative autocorrelation, respectively.

The Durbin-Watson statistic is always between 0 and 4. A value of 2 means that there is no autocorrelation in the sample. Values approaching 0 indicate positive autocorrelation and values toward 4 indicate negative autocorrelation. In this study we found 1.97 value with FD_M and 2.54 with relative abundance that indicated no autocorrelations within FD_M data set and thus, further proved our sampling and methodology efficiencies.

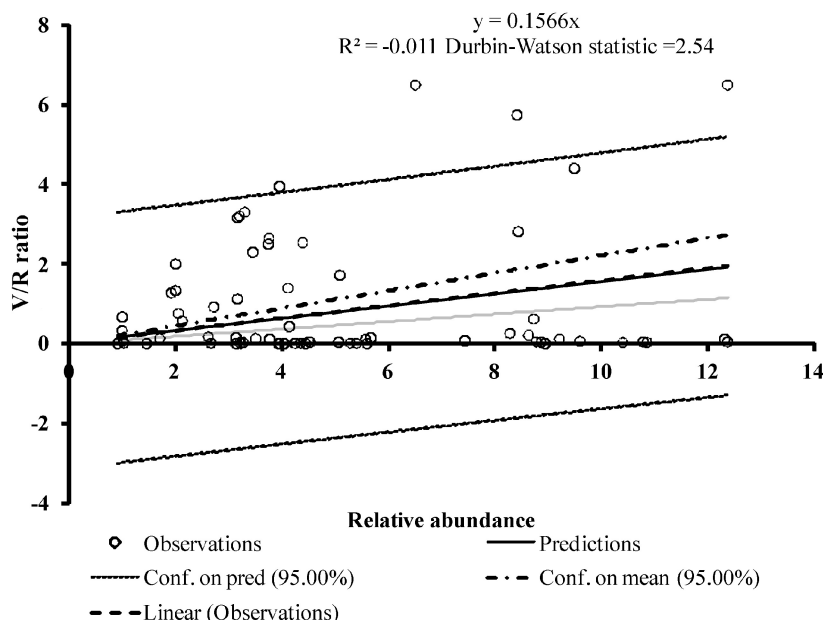


Figure 4. Departure from randomness with relative abundance data set

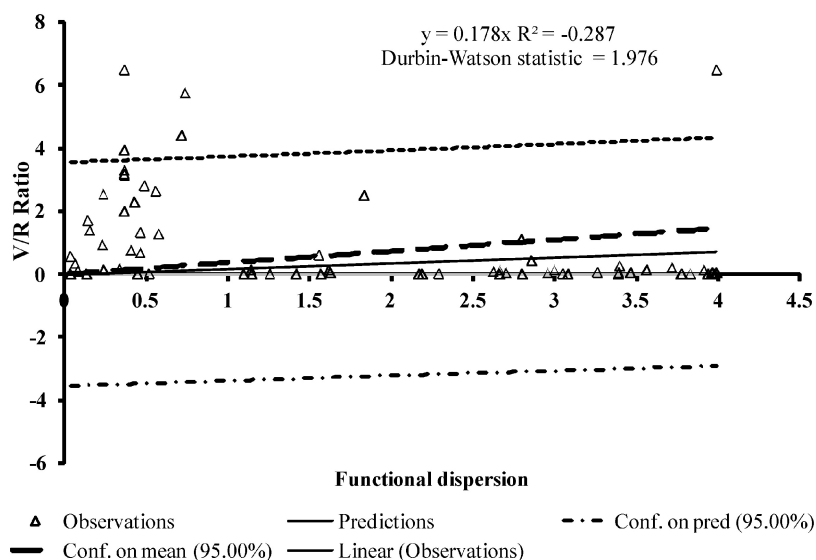


Figure 5. Departure from randomness with relative FD_M data set

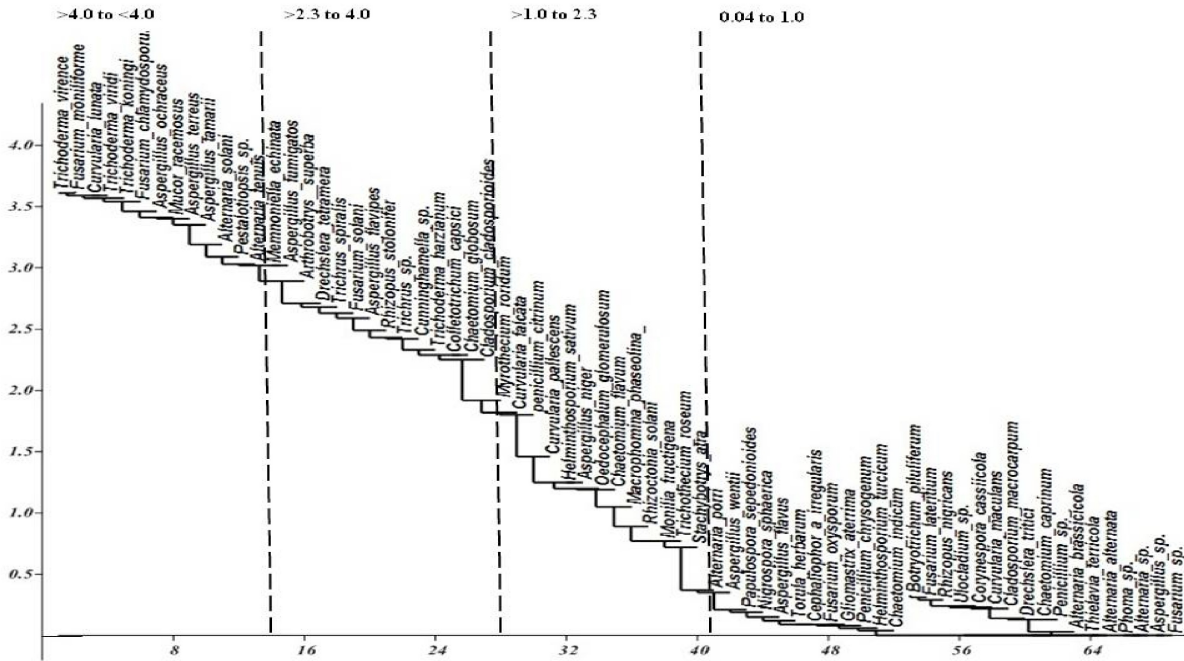


Figure 6. Neighbor-Joining Clustering (Euclidean Similarity) with Functional Dispersion

Table 4. Parameters of frequency distribution analysis

Parameters	Relative Abundance		Functional Dispersion	
	Estimated	Theoretical	Estimated	Theoretical
Skewness	0.799	0.000	0.294	0.000
Kurtosis	-0.393	0.000	-1.552	0.000
Kolmogorov-Smirnov test (D Standardized)	1.54	0.017	1.54	0.013

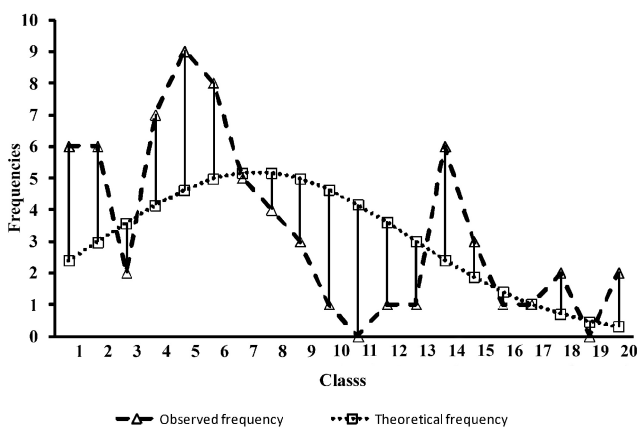


Figure 7. Frequency distribution of myco-flora relative abundance

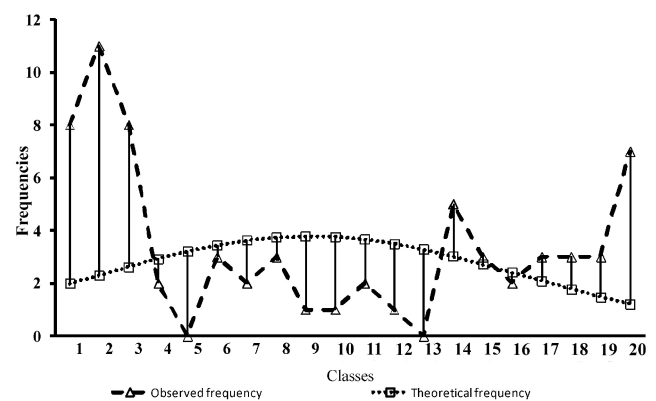


Figure 8. Frequency Distribution of mycoflora from Functional Dispersion

Neighbor Joining Cluster Analysis

Result of this multivariate analysis are presented in Figure 6. As described above, based on functional dispersal values this cluster analysis partitioned 69 different species into four groups. Such groupings are purely ecological which further open a new window to explore their taxonomical and molecular relationships. However, such grouping may be due to factors associated with physio-chemical properties of soil and community associates and diversity patterns. Such grouping can be visualized with relation to synergistic resource consumption (Wagg et al. 2011, Wagg et al. 2014). Tedersoo et al. (2016) based on DNA metabarcoding approach suggested that on a local scale, soil resources and tree species have stronger effect on the diversity and grouping of soil biota than their morphological and taxonomical relationships.

Frequency Distribution Analysis

In FD, Skewness is a measure of symmetry. A data set is symmetric in the vent that it appears to be identical at both the end. The skewness for a normal distribution is zero and a symmetric data ought to have skewness near zero. A symmetrical pattern with a long tail to the right (higher value) represent positive skew while an asymmetrical pattern with a long tail to the left (lower values) suggest negative skew. If the skewness is less than -1 or greater than +1, the distribution is profoundly skewed while, if the value ranges between -1 and $-1/2$ or between $+1/2$ and +1, the distribution will be declared as moderately skewed and if skewness is between $-1/2$ and $+1/2$, the distribution is approximately symmetric. Kurtosis measures whether the dispersion coordinates the Gaussian distribution, as a rule, a Gaussian distribution has a kurtosis of zero and a flatter distribution has a negative kurtosis. The reference standard is a normal distribution, which has a kurtosis of three. A normal distribution has kurtosis exactly 3 is called mesokurtic, <3 called platykurtic (its central peak is lower and broader) and >3 called leptokurtic (central peak is higher and sharper). In this study we observed more skewed (non-normal) patterns of species with relative abundance (0.799) compared to with functional dispersion (0.294). With functional dispersion data we observed higher platykurtic (-1.55) i.e. central peak is lower and broader compared with relative abundance (-0.39) and the results are depicted in Figures 7 and 8. As the computed p-values of Kolmogorov-Smirnov for both types of data

(0.017 and 0.013) were lower than the D standardized (1.543) with 0.05 alpha significance level, suggested to reject the null hypothesis (H_0 : the sample follows a normal distribution), and accept the alternate hypothesis (H_a : The sample does not follow a normal distribution; Table 4). However, the data with relative abundance was more non-normal compared with functional dispersion.

CONCLUSION

Through this study we quantify the weighted fungal functional dispersion grouping by using a modified approach that accommodate spatial and land-use pattern. Through this approach we were able to calculate more homogenous fungal population compared to their abundance. Further, we also addressed (a) how weighted ecological patterns are most common in arid region and (b) how weighted ecological pattern/grouping correlate with distribution patterns of species. Based on our approach, a researcher can quantify a weighted and normalized ecological grouping of soil fungi and this standardization automatically accommodate the different attributes of study areas that could affect fungal populations. This grouping type can further gauge through the types and extent of soil management, if requires as well as harvesting of beneficial fungal species like *Trichoderma* spp. (bio-control agents) and *Fusarium lateritium* (bioherbicide)

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