

branched and MUFAs are used as useful markers for the proportion of gram-positive and gram-negative bacteria [33, 57].

Table 2. Distribution of different PLFAs groups (%) in the different age series iron mine overburden spoil as well as nearby NF soil.

Sample	Straight	Branched	Hydroxy	MUFA	PUFA	DMA	18:1 w9c	18:2w6	10- methyl
IB ₀	40.21	10.91	0.15	12.03	31.01	2.99	1.34	0.41	0.73
IB ₂	31.65	11.72	0.31	15.53	33.12	3.16	1.62	0.65	1.12
IB ₄	33.69	14.53	0.77	10.67	33.61	3.31	2.67	0.63	0
IB ₆	38.94	10.15	nd	10.54	32.48	3.52	3.14	0.78	0.24
IB ₈	43.53	9.31	nd	10.12	28.42	3.87	3.42	0.91	0.19
IB ₁₀	43.67	11.52	nd	10.61	24.94	3.47	3.96	1.13	0.31
IB ₂₅	44.91	11.83	nd	12.73	21.55	3.23	3.99	1.25	0.15
NF	45.12	11.95	nd	12.85	20.32	2.75	4.19	1.98	0.32

nd: beyond detectable limit.

Gram-negative bacteria contain unique hydroxyl fatty acids in lipopolysaccharides as cell wall composition, which act as an indicator of gram-negative bacteria in environmental samples [29, 64]. It is evident from the study that soil microbes with hydroxyl fatty acids were confined to IB₀ (0.15%), IB₂ (0.31%) and IB₄ (0.77%). Higher relative abundance of methyl branching PLFAs was observed in IB₂ (1.12%) compared to different age series iron mine spoil (Table 2). The distribution of MUFAs and PUFAs in NF soil accounted to 12.85% and 20.32% respectively (Table 2). Relatively higher level of PLFAs 18:1w9c (4.19%) and 18:2w6c (1.98%) representing fungi were observed in NF soil compared to different iron mine spoil. The study indicated that the differences in PLFA profiles could be attributed to the variation in lipid contributing microbial communities; environmental conditions and microbial amelioration during spontaneous succession in iron mine overburden spoil over time [65-66].

C. Microbial community composition

The short-term responses of microbial mediated processes and community structure to perturbation constitute important aspects of soil quality assessment and productivity. Thus, it is necessary to analyze their relative distribution or composition and microbial diversity, which provide better understanding of soil quality. Such analysis of microbial community composition has relied on the relative distribution of microbial PLFAs. Besides, PLFAs have several features that reinforce their use as indicator of environmental stress. They respond to environmental disturbances either by phenotypic plasticity or altering PLFAs composition in microbial membrane and thereby shifting microbial community structure [50]. Marked differences in microbial community composition were observed across the different age series iron mine overburden spoil over time (Table 3).

Table 3. Relative distribution of microbial communities (%) in different age series iron mine overburden spoil as well as nearby NF soil.

Soil sample	Gram positive	Gram negative	Anaerobes	Actinomycetes	A.M. Fungi	Fungi	Methanobacter	Eukaryote
IB ₀	17.89	26.14	5.06	0.91	0	0.54	0.65	48.81
IB ₂	15.32	23.52	5.31	1.37	0.62	0.72	0.98	52.16
IB ₄	14.35	21.91	4.83	0	0	1.07	0	57.84
IB ₆	14.08	19.75	5.24	0.41	0	1.24	0	59.28
IB ₈	12.36	17.64	6.92	0.37	0	1.52	0	61.19
IB ₁₀	11.18	14.48	6.77	1.02	0.85	2.13	0	63.57
IB ₂₅	10.71	13.78	6.09	0.33	1.33	1.83	0	65.93
NF	10.12	13.25	5.06	0.45	2.13	2.74	0	66.25

nd: beyond detectable limit.

The fresh iron mine spoil represents disequibrated geomorphic system with altered physicochemical properties, which disrupts soil quality/stability and pedogenic processes [67]. Relatively higher level of MUFAs [65, 68] with lower level of PUFAs were reported as biomarkers for gram-negative bacteria [63], which explained relative abundance of gram-positive bacteria in IB₀ (17.89%) (Table 3). The existence of hydroxyl PLFAs substantiated the higher occurrence of gram-negative bacteria in IB₀ (26.14%) compared to different age series iron mine spoils and NF soil [29, 64]. Further, higher level of gram-positive bacteria (17.89%) was estimated in IB₀, which may be due to higher relative occurrence of branched chain fatty acids [68-69]. The study revealed higher relative dominance of gram-negative bacterial PLFAs in heavy metal contaminated mine spoil (IB₀) with concomitant decrease in gram-positive bacterial PLFAs in chronosequence iron mine spoil over time [9, 13, 70]. Higher level of DMA PLFAs indicates relatively higher distribution of anaerobes in IB₈ (6.92%) compared to different age series iron mine spoil [13, 38, 42]. The methyl-branched PLFAs represent the dominance of actinomycetes in IB₂ (1.37%) [13, 36, 37], which may be due to their potentiality to withstand

water stress by resisting plasmolysis and maintain cell turgor by accumulating compatible solutes (proline and glycerol). In addition, they are filamentous enabling them to bridge air gaps between thin water films that occur in pore spaces during soil desiccation [71]. The occurrence of relatively lower fungal PLFAs (18:1 ω 9c, 18:2 ω 6, 18:2 ω 9c) indicated minimal fungal abundance in IB₀ (0.54%). The methanobacter population was confined to IB₀ (0.65%) and IB₂ (0.98%). Minimal existence of longer chain fatty acids in IB₀ (48.81%) indicated comparatively lower input from microeukaryotes, which may be due to the interaction of heavy metals with microbial membrane proteins resulting disturbances in protein conformations and activities [9, 70, 72].

The ability to maintain microbial community composition, nutrient turnover and functioning after disturbance defines the resistance capacity of a soil subsystem. Resilience expresses the degree of response of the system impacted by disturbances and the rate of recovery in the original versus restored state of system. In addition to abiotic factors, soil microbial community composition is considered as major components of soil resilience due to their key role in nutrient cycling. Therefore, the microbial community composition in different age series iron mine overburden spoil in chronosequence over time should be compared with IB₀. Comparatively higher level of MUFAs and PUFAs were detected in IB₂ compared to IB₀, which explained higher occurrence of gram-negative bacteria in IB₂ (23.52%) [65, 68]. Besides, the relative dominance of hydroxyl PLFAs in IB₄ revealed the occurrence of gram-negative bacteria in IB₄ compared to different iron mine spoils (Table 3) [29, 64]. Besides, higher level of gram-positive bacteria in IB₂ (15.32%) may be due to higher occurrence of branched chain fatty acids. Relatively lower level of anaerobes in IB₂ (5.31%) was attributed to lower occurrence of DMA PLFAs (Table 3). Higher level of fungal PLFAs (18:1 ω 9c) revealed higher fungal dominance in IB₂ (0.72%) compared to IB₀ due to gradual establishment of vegetation and inputs of allochthonous material [73-74]. Methyl-branched PLFAs representing actinomycetes was found to be relatively higher in IB₂ (1.37%) compared to IB₀ (0.91%) [13, 36-37]. Distribution of methanobacter was confined to IB₂ (0.98%) and IB₀ (0.65%) due to the presence of 10-methyl branched fatty acids. Further, higher occurrence of long chain fatty acids and PUFAs supported higher relative distribution of microeukaryotes in IB₂ (52.16%) compared to IB₀. Thus, the recovery of resource heterogeneity and pool size following restoration progress would indicate resilience of the system leading to variation in soil microbial community composition.

PLFA profiles suggested higher level of gram-negative bacteria in IB₄ (21.91%) and IB₆ (19.75%) compared to IB₈ (17.64%), which may be due to the higher level of MUFAs in IB₄ and IB₆ [63, 65, 68]. Higher relative distribution of gram-negative bacteria was observed in IB₁₅ (14.48%) compared to IB₂₅ (13.78%). Higher distribution of gram-positive bacteria was observed in IB₄ (14.35%) compared to IB₆, IB₈, IB₁₅ and IB₂₅, which may be due to higher occurrence of branched chain fatty acids in IB₄ (43.53%). Lower level of anaerobes was estimated in IB₄ (4.83%) compared to IB₆ (5.24%), which may be due to lower occurrence of DMA PLFAs. The distribution of actinomycetes was not observed in IB₄ due to absence of methyl-branched PLFAs. Methyl-branched PLFAs was found to be higher in IB₁₅ (1.02%) compared to IB₂₅ (0.33%). Higher level of fungal PLFAs (18:1 ω 9c) revealed higher fungal dominance in IB₁₅ (2.15%) compared to different age series mine spoils. Higher relative distribution of PLFA 16:1 ω 5c reflects the dominance of arbuscular mycorrhizal fungi in IB₂₅ (1.33%) compared to IB₁₅ (0.85%) and IB₂ (0.62%). However, the distribution of arbuscular mycorrhizal fungi was not observed in IB₀, IB₄, IB₆ and IB₈. Higher longer chain fatty acids indicate relatively higher inputs from microeukaryotes in IB₂₅ (65.93%) compared to different iron mine spoils.

The distribution of gram-positive, gram-negative, anaerobes and actinomycetes in NF soil was found to be 10.12%, 13.25%, 5.06% and 0.45% respectively (Table 3). Relative abundance of gram-negative as compared to gram-positive bacteria in NF soil indicated profound effect of vegetation on mine spoil genesis and lipid profile. Higher relative distribution of arbuscular mycorrhizal fungi (2.13%), fungi (2.74%) and microeukaryotes (66.25%) were observed in NF soil, which may be due to allochthonous inputs, root turnover and symbiotic nitrogen fixation contributed to formation of highly localized soil resources characterized by higher level of organic C and N that are believed to support more diverse heterotrophic microbial population. Greater PLFA diversity also concurred with studies on vegetation succession [75-76]. Further, fungi are adapted to degrade lignin and formation of organic matter [61]. Comparative analysis based on the distribution of PLFAs suggested that the heavy metal contamination in mine spoil resulted decline in PLFAs (a15:0, 16:1 ω 5c, 18:1 ω 7c, 18:1 ω 9c, 18:2 ω 6c and 18:3 ω 6c) in IB₀ compared to NF soil [9, 13, 24, 69, 72].

Further, PLFA markers were used to quantify the relative abundance of gram-positive (i14:0, i15:0, a15:0, i16:0, 10Me16:0, i17:0, a17:0, 10Me17:0) to gram-negative bacteria (15:1 ω 4c, 16:1 ω 7c, 16:1 ω 9c, cy17:0, 17:1 ω 9c, 18:1 ω 7c, 18:1 ω 9c, cy19:0; cy19:0 ω 7c) ratio in different age series iron mine overburden spoil and NF soil [27, 42, 62, 77]. The ratio of gram-positive to gram-negative bacteria exhibited a decline trend from IB₀ (2.129) to IB₂₅ (1.137) and was found to be minimum in NF soil (1.104) compared to different iron mine overburden spoil (Figure 2). Such increase in gram-negative bacteria may be attributed to gradual improvement in organic C supported by vegetation development in chronosequence iron mine overburden spoil over time [67], which provides more stable and readily available substrate for supporting higher microbial activity of gram-negative bacteria [78]. Several investigations have suggested that the gram-negative bacteria were closely associated with MUFAs, which correspond to the gradual increase in organic matter and high substrate

availability [58, 79]. Thus, the combined effect contributed by the changes in aboveground and belowground inputs would influence the microbial community structure by altering C inputs from root exudates and litter in chronosequence iron mine overburden spoil influencing the pace and progress of mine spoil restoration over time [19, 35, 66].

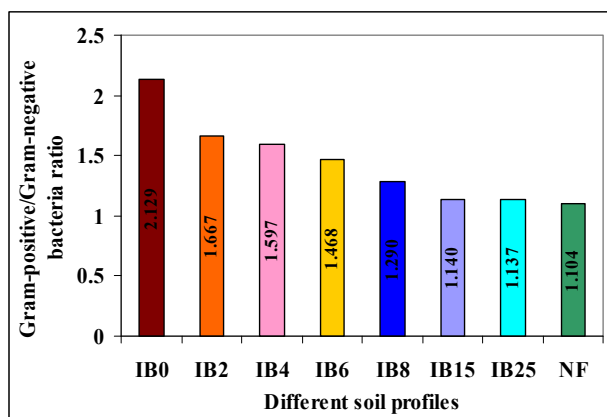


Figure 2. Gram-positive to gram-negative bacteria ratio in the different age series iron mine overburden spoil (IB₀ → IB₂₅) as well as nearby NF soil across the sites.

D. Shannon-weaver diversity index

The numerical strength and biomass of microorganisms affect ecosystem functioning. Microorganisms can change, modify and regulate microenvironment through their activities. Thus, the periodic assessment of microbial community structure with space and time is pre-requisite so as to understand their role in ecosystem stability and development. In addition, the ability of an ecosystem to withstand extremities may contribute to variation in microbial community structure and hence microbial diversity. The commonly used form of diversity index is Shannon Weaver index (H), which is frequently used in microbial ecology studies. Diversity index is a quantitative measure that not only accounts the existence of PLFAs richness (R) but also accounts how evenly they are distributed (evenness). Total diversity depends upon (a) the number of species or number of parts (variety component), (b) the evenness component or the distribution of relative abundance. Higher overall diversity occurs when the number of species and the evenness component are larger. The bacterial and fungal PLFAs are mostly used as the measure of relative distribution of different microbial groups based on their relative abundance of certain PLFAs [20], which differ considerably among different microbial groups [58]. The study revealed significant variation in PLFA richness, Shannon diversity index and evenness in different age series iron mine overburden spoil and nearby NF soil (Table 4).

Table 4. Shannon diversity index and Pielou's evenness index based on the distribution of 75 PLFAs in the seven different age series iron mine overburden spoil (IB₀→IB₂₅) as well as NF soil across the sites.

Site	PLFA richness (R)	Shannon diversity index (H)	Pielou's evenness index (J)
IB ₀	49	2.726231353	0.700502887
IB ₂	47	2.849070813	0.739990023
IB ₄	27	2.490509005	0.755652997
IB ₆	43	2.717641045	0.722546252
IB ₈	49	2.794246578	0.717979342
IB ₁₅	49	2.783612478	0.715246919
IB ₂₅	48	2.74195037	0.708294496
NF	43	3.17054272	0.842960391

Greater PLFA richness (R) was attributed by IB₀, IB₈ and IB₈ (49) compared to other mine spoil profiles. Shannon diversity index (H) varies from 2.4905 (IB₄) to 2.8490 (IB₂) across the sites. The relative abundance of evenness is the apportionment of individuals among the species is an important component of diversity index, which quantifies how equal the community is numerically. It would be useful to assess the contribution of this component to the diverse index value. The evenness of PLFA reflects the broad-scale changes in terms of the relative dominance of certain microbial groups although an evenness index should be independent of the number of species [50]. The evenness of community otherwise called Pielous evenness index (J) is constrained between 0 and 1 represents the ratio of observed heterogeneity to maximum possible heterogeneity. The Pielous evenness index (J) based on the distribution of 75 PLFAs varies from 0.7005 (IB₀) to 0.7556 (IB₄) across the sites (Table 4). The more even the distribution of PLFAs or less variation in community between microbial groups, greater is

the microbial diversity. Thus, the value of diversity index increases when both the number of types of PLFAs and evenness increases.

Shannon diversity index based on the distribution of different microbial groups in different iron mine overburden spoil and NF soil was calculated. Higher Shannon Weaver index in IB₂ (1.2943) revealed higher population diversity compared to IB₀ (1.2633). Comparatively higher level of microbial diversity was exhibited by IB₆ (1.1378) than IB₄ (1.1228). Higher level of microbial diversity was exhibited by IB₁₅ (1.1643) compared to IB₈ (1.1341). However, IB₂₅ (1.1069) exhibited relatively lower microbial diversity compared to IB₈ and IB₁₅, which indicated that the microbial communities in less disturbed ecosystem like IB₂₅ may be dynamic in terms of functional responses to perturbation but more resistance to changes in microbial community composition [56]. The shift in microbial community structure and diversity among different iron mine overburden spoil may be attributed to the variation in microbial biomass nutrient to soil nutrients ratio (MB-C:OC), which represents the quantum of soil nutrients reflected in microbial biomass and used as functional index of the soil subsystem [80].

E. Fungal: bacterial biomass ratio

Fungal biomass was calculated based on the relative distribution of PLFA 18:2 ω 6c across the sites. Total bacterial biomass was obtained by summation of the distribution of PLFAs 14:0, 15:0, a15:0, i15:0, i16:0, 16:1 ω 7c, 16:1 ω 11c, 10Me 16:0, 17:0, a17:0, cy17:0, i17:0, 17:1 ω 8c, 10Me 17:0, 18:0 2OH, 18:1 ω 5c, 18:1 ω 7c, 10Me 18:0, 19:1 ω 6c and cy19:0 ω 8c. An index of fungal to bacterial (F/B) ratio of microbial biomass was used to study the state of microbial community in response to different environmental stresses [50]. The F:B ratio was suggested as the potential tool to discriminate the disturbed from undisturbed soil system [20, 71, 81]. The fundamental difference in bacterial/fungal physiology and ecology would suggest that the biogeography of each group would be influenced by different edaphic factors, which may vary among different soil profiles [82]. The bacteria and fungi are likely to have distinct functional roles in different mine spoil profiles and therefore more robust understanding of the site-specific effects of land use patterns and edaphic factors on these microbial population will improve the ability to predict changes in microbial community composition and function [50]. The F:B ratio exhibited an increasing trend from IB₀ (0.0233) to IB₂₅ (0.0640) over time. Comparatively higher F:B ratio was estimated in IB₂₅ (0.0640) compared to IB₂ (0.0263), IB₄ (0.0362), IB₆ (0.0405), IB₈ (0.0485) and IB₁₅ (0.0538). However, the difference in F:B ratio in chronosequence iron mine overburden spoil was less pronounced due to heavy metal contaminated extreme environmental conditions [13, 24, 70]. Highest F:B ratio was observed in NF soil (0.1116) compared to different age series iron mine overburden spoil, which may be due to higher prevalence of fungal PLFAs exhibiting higher C:N ratio and low bulk density [83]. The bacterial PLFAs increased considerably with the increase in pH and were found to be higher in NF soil [84]. However, fungal biomass is higher in acid soil with high C:N ratio indicating that pH appears to be the most important factor for microbial abundance, diversity and activities [55, 84-85]. In fact, soil pH affects microbial processes such as organic matter mineralization, which is slowed down or even stopped at higher acidic or alkaline pH [86-87]. Besides, the shift in microbial community may also be related to the capacity of fungi for translocation N to C availability or direct influence of N supply on plant belowground C allocation is thought to be important in NF soil with higher C:N ratio [81, 84]. Several investigations have suggested that the level of activity and size of microbial communities are C limited [88]. Further, higher F:B ratio in NF soil can be explained on the basis of the existence of higher relative distribution fungal PLFAs (2.74%) compared to different iron mine overburden spoil. In addition, NF soil was supported with distinct microbial communities that can be correlated with factors that define the land-use pattern and associated soil quality influencing microbial community composition [56]. It is evident that NF soil appeared to be set apart from other mine spoil profiles with higher abundance of arbuscular mycorrhizal fungi (2.13%), which may be better able to cope with available N and organic matter. These parameters show linear increase with increased abandonment duration consistent with fungal to bacterial ratio [81, 84, 89-90]. The study indicated that the disturbed ecosystems have lower F:B ratio whereas organically managed soil have increased F:B ratio than conventional system [91].

Further, the changes in microbial community structure may be influenced by spatial variability in soil physicochemical properties (pH, moisture and nutrient availability), which influence microbial transformations altering nutrient cycling useful in providing insight how these microbes could affect the soil quality status. Differences in soil pH can arise due to the variation in vegetation pattern and management regimes. Thus, soil pH serves as one of the integrating variables and reasonably good predictor of microbial community composition [92-93]. The decline in soil pH from NF soil to IB₀ may be one of the major constraints/stresses that shift the microbial community structure [51, 67]. Comparative analysis of F:B ratio suggested that lower pH resulted decline in PLFAs (a15:0, 16:1 ω 5c, 18:1 ω 7c, 18:1 ω 9c, 18:2 ω 6c, 18:3 ω 6c) in IB₀ compared to undisturbed NF soil [55]. The decreased stress with gradual improvement in soil pH towards neutral in NF soil in chronosequence iron mine overburden spoil could be related to an increase in F:B ratio due to nutrient availability leading to the shift in microbial community structure [55, 67, 84, 94-95]. The study revealed positive correlation between F:B ratio and soil pH ($r = 0.966$, $p < 0.001$), which suggested that soil pH can

account 93.47% of the variability in F:B ratio (Figure 3a). Besides, the shift in microbial community as well as F:B ratio may be due to variation in moisture content from IB₀ to NF soil, which influence osmotic potential, transport of nutrients regulating microbial mediated processes and competitive interactions between microbial species [66, 96-97]. Soil moisture content exhibited positive correlation with F:B ratio ($r = 0.784$, $p < 0.001$), which can account 61.48% of the variability in F:B ratio across the sites (Figure 3b). The changes in moisture content can alter microbial community composition and function due to differences in drought tolerance among taxonomic and functional groups of soil microorganisms [98-99].

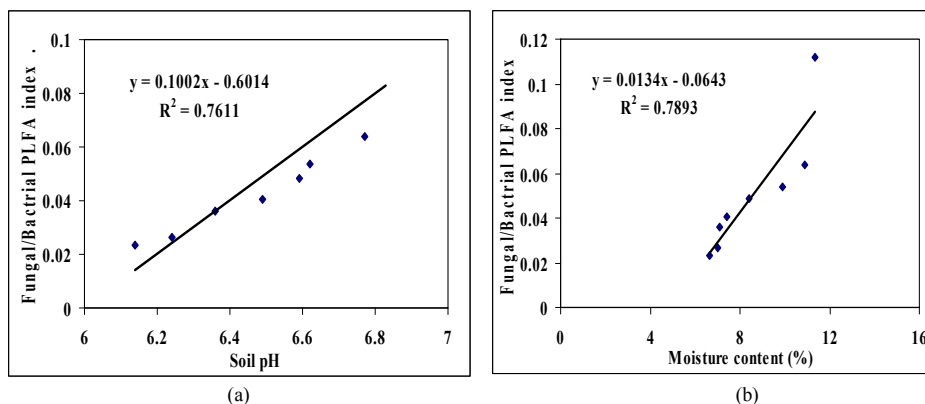


Figure 3. Correlation between fungal to bacterial ratio with (a) soil pH and (b) moisture content in the different age series iron mine overburden spoil and NF soil.

F. Cluster analysis

Relative distributions of 75 PLFAs among different age series iron mine spoil and NF soil profiles were subjected to cluster analysis based on distance matrix revealed the existence of seven clusters (I-VII) (Figure 4). The dendrogram revealed highest similarity (71.8998) between IB₀ and IB₆ (cluster VII). The relatedness between IB₀ and IB₈ (cluster-VI), IB₀ and IB₁₅ (cluster-V) and IB₀ and IB₂ (cluster-IV) exhibited similarity level 67.1458, 56.7162 and 52.6909 respectively. The similarity level between IB₄ and IB₂₅ was estimated to be 49.0519 (cluster-III). IB₀ and IB₄ exhibited similarity level (48.3590) representing cluster-II. Minimal similarity level (34.7702) was observed between IB₀ and NF (cluster-I). The study indicated that the seven clusters based on relative distribution of 75 PLFAs exhibited the tree likeness of original (unrandomized) tree was statistically well resolved (Figure 4).

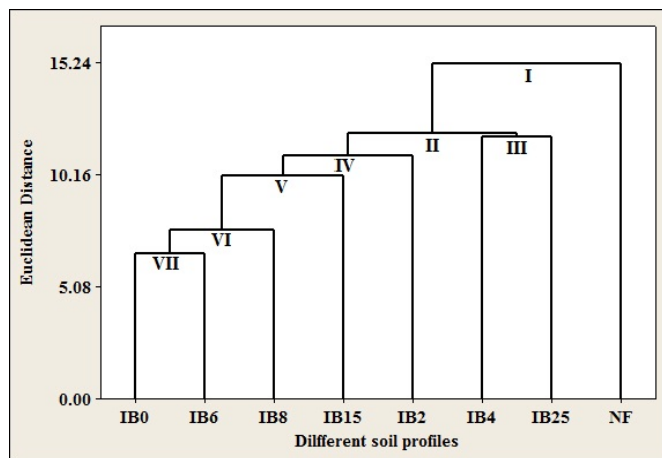


Figure 4. Cluster analyses illustrated the relatedness based on the relative distribution of 75 PLFAs among different age series iron mine overburden spoil as well as NF soil.

Further, principal component analysis was performed in order to discriminate seven different age series iron mine overburden spoil and nearby NF soil based on the relative distribution of 75 PLFAs across the sites (Figure 5) [100]. Eigen vectors determine the direction of maximum variability specifying the variances. Principal component analysis suggested that the Z1 and Z2 components explained maximum variance with their cumulative percentage of variance estimated to be 58.57%. The relative distribution of 75 PLFAs revealed differential microbial community structure among seven different age series iron mine overburden spoil in chronosequence and nearby NF soil were well segregated (Figure 5).

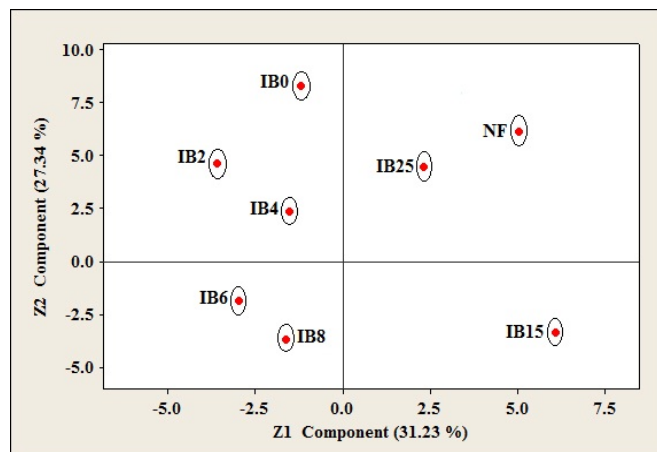


Figure 5. Principal component analysis based on the relative distribution of 75 PLFAs among the microbial communities in different mine overburden spoil as well as NF soil.

G. Multivariate analyses

Redundancy analysis was used to examine the patterns in PLFA data collected from different age series iron mine overburden spoil reflecting relationship between different mine spoil profiles, species and environmental gradients altogether. The changes in microbial community structure may occur in response to altered physico-chemical properties that affect the soil microenvironment with possible effects on the efficiency of readily mineralizable resource conservation by soil microbes. RDA analysis allowed examining the variation in PLFA patterns in terms of both iron mine overburden sites and the measured environmental gradients including enzyme activities, which was found to be significant ($p < 0.005$). A total of 61.62% of the variability could be explained based on the fitted PLFA data by the model from the canonical sum of eigen values. Seven different age series iron mine overburden sites and environmental gradient arrows for the RDA ordination of PLFA data were shown (Figure 6a). The slit and clay %, moisture content (MC), water holding capacity (WHC), pH, organic C (OC), total N (TN), extractable P (EP) and enzyme activity (amylase, invertase, protease, urease and dehydrogenase) increased in the general direction of IB₂₅, while sand % and bulk density (BD) increased towards IB₀. The increasing trend of these parameters correspond to enhance accumulation of organic C, available N and microbial community composition as vegetation succession proceeded over time reflecting the sign of mine spoil restoration [101-103].

The data related to physico-chemical properties and enzyme activities in chronosequence iron mine overburden spoil were taken for RDA analysis [67, 83]. The proportions of certain PLFAs were highly correlated with physico-chemical properties (Jackson *et al.*, 2003) in different iron mine overburden spoil over time (Figure 6b). The clay, pH, MC, WHC, OC, TN, EP and enzyme activities were highly correlated with PLFAs (a14:0, 14:1 ω 7c DMA, 14:1 ω 8c, 16:1 ω 5c, 16:1 ω 7c, 18:1 ω 7c, 18:1 ω 9c, 18:2 ω 6c, 18:3 ω 6c, 21:1 ω 8c and 24:0), while sand and BD with PLFAs (12:1 ω 8c, 14:1 ω 5c, a15:0, 16:0 aldehyde, 16:0 2OH, 16:2 DMA, 10Me 18:0, 18:1 ω 7c DMA, 19:0cy ω 7c and 10Me 19:1 ω 7c) across the sites. Further, the negative correlation coefficients indicated that the changes in microbial community structure in response to disturbances were associated with the decrease in respective soil properties in different mine spoil profiles. Although 75 PLFAs were included in RDA ordination, but the PLFAs with highest species scores in the first two ordination axes, which correlated well with environmental variables and important biological markers are displayed for clarity (Figure 6b). Some general patterns emerge from this analysis. The existence of higher level of methyl-branched PLFAs (10Me16:0; 10Me22:0) and saturated branched fatty acids (C₁₆ to C₁₉) in IB₀ suggested higher relative abundance of actinomycetes and anaerobic bacteria respectively. In addition, higher pyrite (FeS₂) contamination provides suitable condition for the existence of PLFA a17:0 reflecting higher distribution of sulfate reducing bacteria in IB₀. Further, the level of saturated branched fatty acids (C₁₄ to C₁₆) was found to be comparatively higher in IB₁₀ than different age series iron mine overburden spoil suggesting higher relative abundance of gram-positive bacteria in IB₁₀. Minimal longer chain PLFAs in IB₀ indicated comparatively lower input from microeukaryotes, which may be influenced by acidic pH and induced toxic metal contamination [57, 94, 105]. Higher relative abundance of arbuscular mycorrhizal fungi (16:1 ω 5c) and heterotrophic microeukaryotes were observed in IB₂₅. Higher level of fungal PLFAs 18:3 ω 6c and PLFAs 18:1 ω 9c, 18:1 ω 5c, 18:1 ω 7c suggested higher relative distribution of fungal population in IB₂₅ and IB₁₅ respectively. Besides, higher level of PLFAs 16:1 ω 5c and 16:1 ω 7c suggested higher relative distribution of aerobic bacteria in IB₂₅ and IB₁₅ respectively. The study suggested that the shift in microbial community structure from IB₀ to IB₂₅ may be attributed to the change in soil quality in the direction of IB₂₅ supplementing the mine spoil restoration over time.

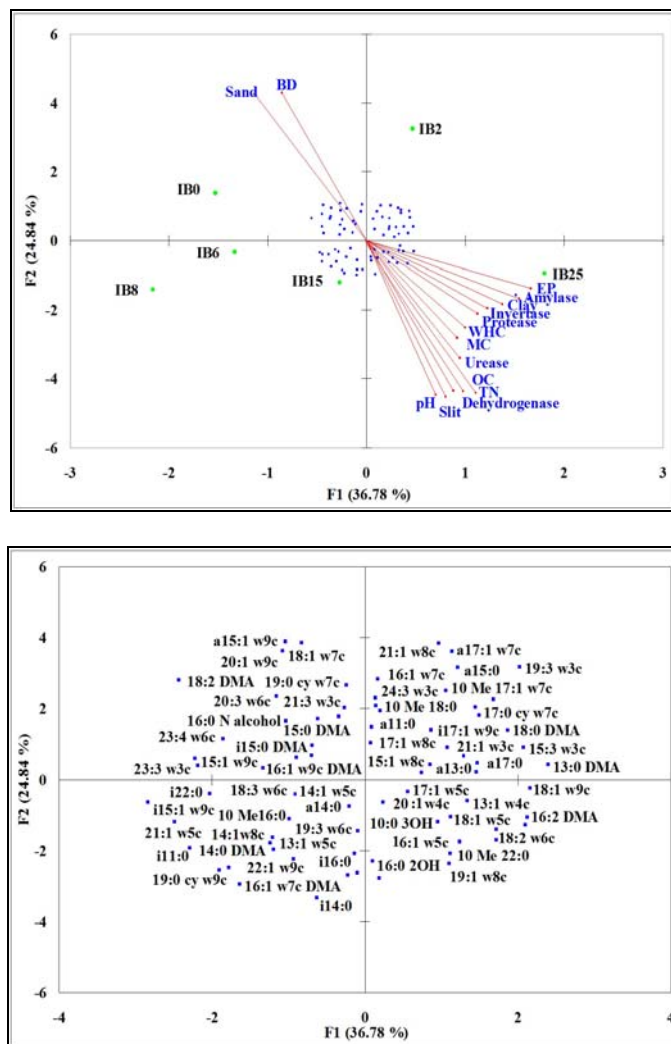


Figure 6. Redundancy analyses (RDA) of the PLFA data set for seven different age series iron mine overburden spoil, using 75 PLFAs and 11 environmental variables. (a) Site codes for each soil sample; (b) showed the PLFAs that had the highest absolute species scores on each of the two axes, along with additional PLFAs of biological interest.

IV. CONCLUSION

The changes in microbial community structure not only ascertain the microbial diversity, but also the function and nature of interactions among existing microbial species as well as the physiological state of ecosystem. A realistic ecological assessment of iron mine spoil restoration implies periodic monitoring. The presence and abundance of these signature fatty acids in mine spoil revealed the presence and abundance of a particular microbe or groups of microbes. PLFA analysis can be used for comparative assessment of physiological status of microbial communities in different mine spoil profiles. The multivariate analysis revealed that seven different age series iron mine overburden spoil had distinctly different PLFAs and microbial community composition. The spatial and statistical results of PLFA analysis revealed the pace or rapidity of alteration in microbial community structure. Further, the changes in microbial community composition may occur in response to altered physico-chemical properties with possible effects on the efficiency of C conservation mediated by soil microorganisms. Nevertheless, the readily mineralizable source of organic matter would enhance microbial processes including enzyme activities to change microenvironment. PCA revealed that the microbial communities were compositionally distinct. Thus, PLFA profiling provides a sensitive and meaningful measure of microbial community composition to monitor mine spoil restoration based on soil quality assessment in chronosequence iron mine overburden spoil over time compared to undisturbed NF soil.

V. ACKNOWLEDGEMENTS

The authors are thankful to Head, School of life Sciences, Sambalpur University for providing laboratory facilities. The investigation was made possible through the support rendered by the mining authority

by providing necessary facilities during sampling in the field. In particular, the authors are indebted to many, who helped in the laboratory as well as for computation of statistical analysis.

REFERENCES

- [1] K. L. Steenwerth, L. E. Jackson, F. J. Calderon, M. R. Stromberg and K. M. Scow. "Soil microbial community composition and land use history in cultivated and grassland ecosystems of coastal California", *Soil Biol Biochem*, vol. 34, pp. 1599-1611, 2002.
- [2] D. Edmeades. "The long-term effects of manures and fertilisers on soil productivity and quality: a review", *Nutr Cycl Agroecosyst*, vol. 66, pp. 165-180, 2003.
- [3] J. Harris. "Soil microbial communities and restoration ecology: facilitators or followers?" *Sci*, vol. 325, pp. 573-574, 2009.
- [4] M. Kujur, A. K. Patel. "PLFA Profiling of soil microbial community structure and diversity in different dry tropical ecosystems of Jharkhand", *Int J Curr Microbiol Appl Sci*, vol. 3(3), pp. 556-575, 2014.
- [5] E. Hackl, G. Bachmann and S. Zechmeister-Boltenstern. "Microbial nitrogen turnover in soils under different types of natural forest", *Forest Ecol Manage*, vol. 188, pp. 101-112, 2004.
- [6] P. Garbeva, J. A. van Veen, J. D. van Elsas. "Predominant Bacillus spp. in agricultural soil under different management regimes detected via PCR-DGGE", *Microb Ecol*, vol. 45, pp. 302-316, 2003.
- [7] A. Tunlid and C. White. "Biochemical analysis of biomass, community structure, nutritional status and metabolic activity of microbial communities in soil. In: Soil Biochemistry (eds) Bollag JM, Stotzky G, Dekker M, pp. 229-262, 1992.
- [8] L. Zelles, Q. Y. Bai, T. Beck and F. Beese. "Signature fatty acids in phospholipids and lipopolysaccharides as indicators of microbial biomass and community structure in agricultural soils", *Soil Biol Biochem*, vol. 24, pp. 317-323, 1992.
- [9] A. Frostegard, E. Baath and A. Tunlip. "Shifts in the structure of soil microbial communities in limed soils as revealed by phospholipid fatty acid analysis", *Soil Biol Biochem*, vol. 25, pp. 723-730, 1993.
- [10] E. Baath, M. Diaz-Ravina and L. R. Bakken. "Microbial biomass, community structure and metal tolerance of a naturally Pb-enriched forest soil", *Microb Ecol*, vol. 50, pp. 496-505, 2005.
- [11] R. E. Drenovsky, K. L. Steenwerth, L. E. Jackson, K. M. Scow. "Land use and climatic factors structure regional patterns in soil microbial communities", *Glob Ecol Biogeogr*, vol. 19, pp. 27-39, 2010.
- [12] T. Pennanen, J. Liski, E. Baath, V. Kitunen, J. Uotila, C. J. Westman and H. Fritze. "Structure of the microbial communities in coniferous forest soils in relation to site fertility and stand development stage", *Microb Ecol*, vol. 38, pp. 168-179, 1999.
- [13] L. Zelles. "Fatty acid patterns of phospholipids and lipopolysaccharides in the characterization of microbial communities in soil: A review", *Biol Fertil Soils*, vol. 29, pp. 111-129, 1999.
- [14] K. M. Batten, K. M. Scow, K. F. Davies and S. P. Harrison. "Two invasive plants alter soil microbial community composition in serpentine grasslands", *Biol Invasions*, vol. 8, pp. 217-230, 2006.
- [15] D. B. Hedrick, A. Peacock, J. R. Stephan, S. J. Macnaughton, J. Bruggemann and D. C. White. "Measuring microbial community diversity using polar lipid fatty acid and denaturing gradient gel electrophoresis data", *J Microbiol Methods*, vol. 41, pp. 235-248, 2000.
- [16] H. Yao, Z. He, M. J. Wilson and C. D. Campbell. "Microbial biomass and community structure in a sequence of soils with increasing fertility and changing land use", *Micro Ecol*, vol. 40, pp. 223-237, 2000.
- [17] J. A. Harris. "Measurements of the soil microbial community for estimating the success of restoration", *Eur J Soil Sci*, vol. 54, pp. 801-808, 2003.
- [18] D. C. White, W. M. Davies, J. S. Nickels, J. D. King, R. J. Bobbie. "Determination of the sedimentary microbial biomass by extractable lipid phosphate", *Oecologia*, vol. 40, pp. 51-62, 1979.
- [19] X. Lie, L. Guo-bin, X. Sha and Z. Chao. "Soil microbial composition during natural recovery in the Loess plateau", *China J Intergrat Agri*, vol. 13, pp. 1-18, 2013.
- [20] R. D. Bardgett and E. McAlister. "The measurement of soil fungal:bacterial biomass ratios as an indicator of ecosystem self-regulation in temperate meadow grasslands", *Biol Fertil Soils*, vol. 29, pp. 282-290, 1999.
- [21] F. J. Calderon, L. E. Jackson, K. M. Scow and D. E. Rolston. "Microbial responses to simulated tillage in cultivated and uncultivated soils". *Soil Biol Biochem*, vol. 32, pp. 1547-1559, 2000.
- [22] R. E. Drenovsky, G. N. Elliott, K. J. Graham and K. M. Scow. "Comparison of phospholipid fatty acid (PLFA) and total soil fatty acid methyl esters (TSFAME) for characterizing soil microbial communities", *Soil Biol Biochem*, vol. 36, pp. 1793-1800, 2004.
- [23] Y. P. Wu, B. Ma, L. Zhou, H. Z. Wang, J. M. Xu, S. Kemmitt and P. C. Brookes. "Changes in the soil microbial community structure with latitude in eastern China, based on phospholipid fatty acid analysis", *Appl Soil Ecol*, vol. 43, pp. 234-240, 2009.
- [24] T. Pennanen, A. S. A. Frostegard, H. Fritze, E. Baath. "Phospholipid fatty acid composition and heavy metal tolerance of soil microbial communities along two heavy metal-polluted gradients in coniferous forests", *Appl Environ Microbiol*, vol. 62(2), pp. 420-428, 1996.
- [25] A. Frostegard, A. Tunlid and E. Baath. "Use and misuse of PLFA measurements in soil", *Soil Biol Biochem*, vol. 43(8), pp. 1621-1625, 2011.
- [26] J. R. Vestal, D. C. White. "Lipid analysis in microbial ecology quantitative approaches to the study of microbial communities", *Biosci*, vol. 39, pp. 535-541, 1989.
- [27] D. C. White, J. O. Stair, D. B. Ringelberg. "Quantitative comparisons of in situ microbial biodiversity by signature biomarker analysis", *J Ind Microbiol*, vol. 17, pp. 185-196, 1996.
- [28] J. Steer and J. A. Harris. "Shift in the microbial community in the rhizosphere and non rhizosphere soils during the growth of *Agrostis stolonifera*", *Soil Biol Biochem*, vol. 32, pp. 869-878, 2000.

- [29] D. C. White. "Is there anything else you to understand about the microbiota that cannot be derived from analysis of nucleic acid?", *Microbiol Ecol*, vol. 28, pp. 163-166, 1994.
- [30] M. Diaz-Ravina, E. Baath, A. Martin and T. Carballas. "Microbial community structure in forest soils treated with a fire retardant", *Biol Fertil Soils*, vol. 42, pp. 465-471, 2006.
- [31] M. Lores, M. Gomez-Brandon and J. Dominguez. "Tracking down microbial communities *via* fatty acid and analysis: Analytical strategy for solid organic samples", *Curr resear*, technology and education topics in applied microbiology and microbial biotechnology (eds), Mendez-Vilas A, pp. 1502-1508, 2010.
- [32] S. J. M. Dickens, E. B. Allen, L. S. Santiago and D. Crowley. "Exotic annuals reduce soil heterogeneity in coastal sage scrub soil chemical and biological characteristics". *Soil Biol Biochem*, vol. 58, pp. 70-81, 2013.
- [33] J. A. W. Morgan and C. Winstanley. "Microbial biomarkers. In: Modern soil microbiology (eds)". J. D. van Elsas, J. T. Trevors, E. M. H. Wellington, M. Dekker. *Inc., New York*, pp. 331-348, 1997.
- [34] A. Frostegard and E. Baath. "The use of phospholipid fatty acid to estimate bacterial and fungal biomass in soil", *Biol Fertil Soils*, vol. 22, pp. 59-65, 1996.
- [35] R. T. Myers, D. R. Zak, D. C. White, A. Peacock. "Landscape-level patterns of microbial community composition and substrate use in upland forest ecosystems", *Soil Sci Soc Am J*, vol. 65, pp. 359-367, 2001.
- [36] M. Kroppenstedt. "Fatty acid and menaquinon analysis of actinomycetes and related organisms In: Chemical methods in bacterial systematics (eds) Googfellow M, Minnikin DE", *Academic Press, London*, pp. 173-199, 1985.
- [37] G. T. Hill, N. A. Mitkowski, L. Aldrich-Wolfe, L. R. Emele, D. D. Jurkonie, A. Ficke, S. Maldonado-Ramirez, S. T. Lynch and E. B. Nelson. "Methods for assessing the composition and diversity of soil microbial communities", *Appl Soil Ecol*, vol. 15, pp. 25-36, 2000.
- [38] A. Frostegard, A. Tunlid and E. Baath. "Microbial biomass measured as total lipid phosphate in soils of different organic content", *J Microbiol Method*, vol. 14, pp. 151-163, 1991.
- [39] S. Zhong, Y. Wu and J. Xu. "Phosphorus utilization and microbial community in response to lead/iron addition to a waterlogged soil", *J Environ Sci*, vol. 21, pp. 1415-1423, 2009.
- [40] J. P. Bowman, J. H. Skerratt, P. D. Nicholas and L. I. Sly. "Phospholipid fatty acid and lipopolysaccharide fatty acid signature lipids in methane utilizing bacteria". *FEMS Microb Ecol*, vol. 85, pp. 15-22, 1991.
- [41] J. V. Robie and D. C. White. "Lipid analysis in microbial ecology: Quantitative approaches to the study of microbial communities", *Biosci*, vol. 39(8), pp. 535-541, 1989.
- [42] L. Zelles. "Phospholipid fatty acid profiles in selected members for soil microbial communities", *Chemosphere*, vol. 35, pp. 275-294, 1997.
- [43] H. C. Pinkart, D. B. Ringelberg, Y. M. Piceno, S. J. Macnaughton and D. C. White. "Biochemical approaches to biomass measurements and community structure analysis", In: C. J. Hurst, R. L. Crawford, G. R. Knudsen, M. J. McInerney, L. D. Stetzenbach, editors. *Manual of environmental microbiology. 2. Am Soc Microbiol. Press; Washington, DC*, pp.101-113, 1999.
- [44] A. Frostegard, A. Tunlid and E. Baath. "Use and misuse of PLFA measurements in soils". *Soil Biol Biochem*, pp. 1-5, 2010.
- [45] M. A. Arshad and S. Martin. "Identifying critical limits for soil quality indicators in agro ecosystems", *Agri Ecosys Environ*, vol. 88, pp. 153-160, 2002.
- [46] G. Renella, L. Landi, J. Ascher, M. T. Ceccherini, G. Pietramellara, M. Mench, P. Nannipieri. "Long-term effects of aided phytostabilisation of trace elements on microbial biomass and activity, enzyme activities, and composition of microbial community in the Jales contaminated mine spoils", *Environ Pollution*, vol. 152, pp. 702-712, 2008.
- [47] N. Chowdhury, P. Marschner and R. Burns. "Response of microbial activity and community structure to decreasing soil osmotic and metric potential", *Plant Soil*, vol. 344, pp. 241-254, 2011.
- [48] S. D. Veresoglou, A. P. Mamolos, B. Thornton, O. K. Voulgari, R. Sen, D. S. Vereogou. "Medium-term fertilization of grassland plant communities masks plant species-linked effects on soil microbial community structure", *Plant Soil*, vol. 344, pp. 187-196, 2011.
- [49] A. Halbritter and T. Mogyorossy. "Phospholipid fatty acid analysis of rhizosphere bacterial communities in a peat soil", *Agrokemiaes Talaj Tan*, vol. 51(2), pp. 123-128, 2002.
- [50] A. Kaur, R. Choudhary and R. Kaushik. "Phospholipid fatty acid: A bioindicator of environment monitoring assessment in soil ecosystem", *Curr Sci*, vol. 89, pp. 1103-1112, 2005.
- [51] E. Hackl, M. Pfeffer, C. Donat, G. Bachmann and S. Zechmeister-Boltenstern. "Composition of the microbial communities in the mineral soil under different types of natural forest", *Soil Biol Biochem*, vol. 37, pp. 661-671, 2005.
- [52] D. Parkinson, T.R.G. Gray, S. T. Williams. "Methods to study ecology of soil microorganisms", IBP Handbook No.19. *Oxford, Blackwell Scientific Publishing*, pp. 116, 1971.
- [53] J. S. Buyer, J. R. Teasdale, D. P. Roberts, I. A. Zasada and J. E. Maul. "Factors affecting soil microbial community structure in tomato cropping systems". *Soil Biol Biochem*, vol. 42, pp. 831-841, 2010.
- [54] D. C. White, H. C. Pinkart and D. B. Ringelberg. "Biomass measurements; Biochemical approaches", In: *Manual of environmental microbiology (Eds). C. J. Hurst and G. R. Knudsen ASM Press, Washington, DC*, pp. 91-101, 1997.
- [55] E. Baath and T. H. Anderson. "Comparison of soil fungal/bacterial ratios in a pH gradient using physiological and PLFA based techniques", *Soil Biol Biochem*, vol. 35, pp. 955-963, 2003.
- [56] K. L. Steenwerth, L. E. Jackson and F. J. Calderon. "Soil microbial community composition and land use history in cultivated and grassland ecosystems of coastal California", *Soil Biol Biochem*, vol. 35, pp. 489-500, 2003.
- [57] J. K. Maharana and A. K. Patel. "Microbial community PLFA responses to ecosystem restoration in a chronosequeces coal mine overburden spoil and implications of soil quality", *Int J Curr Microbiol Appl Sci*, vol. 3(6), pp. 45-71, 2014.
- [58] L. Zelles, Q. Y. Bai, R. X. Ma, R. Rackwitz, K. Winter and F. Beese. "Microbial biomass, metabolic activity and nutritional status determined from fatty acid patterns and poly hydroxybutyrate in agriculturally managed soils", *Soil Biol Biochem*, vol. 26, pp. 439-446, 1994.

- [59] J. C. Zak, M. R. Willig, D. L. Moorhead and H. G. Wildman. "Functional diversity of microbial communities: a quantitative approach", *Soil Biol Biochem*, vol. 26, pp. 1101-1108, 1994.
- [60] P. A. Olsson. "Signature fatty acids provide tools for determination of the distribution and interactions of mycorrhizal fungi in soil", *FEMS Microbiol Ecol*, vol. 29, pp. 303, 1999.
- [61] J. W. G. Cairney and A. A. Meharg. "Interaction between ectomycorrhizal fungi and soil saprotrophs: implications for decomposition of organic matter in soils and degradation of organic pollutants in the rhizosphere", *Can J Botany*. Vol. 80, pp. 803-809, 2002.
- [62] A. Frostegard, A. Tunlid and E. Baath. "Changes in microbial community structure during long term incubation in two soils experimentally contaminated with metals", *Soil Biol Biochem*, vol. 28, pp. 55-63, 1996.
- [63] C. Ratledge and S. G. Wilkinson. "Microbial Lipids". *Academic Press, London, England*. 1988.
- [64] J. H. Parker, G. A. Smith, H. L. Fredrickson, J. R. Vestal, D. C. White. "Sensitive assay, based on hydroxy fatty acids from lipopolysaccharide lipid A for gram-negative bacteria in sediments", *Appl Environ Microbiol*, vol. 44, pp. 1170-1177, 1982.
- [65] N. Rajendran, O. Matsuda, N. Imamura and Y. Urushigawa. "Microbial community structure analysis of euxinic sediments using phospholipid fatty acid biomarkers", *J Oceanography*, vol. 51, pp. 21-38, 1995.
- [66] G. E. Ekosse. "Spatial distribution of iron in soils and vegetation cover close to an abandoned manganese oxide ore mine, Botswana", *J Appl Sci*, vol. 8(1), pp. 14-25, 2008.
- [67] M. Pasayat and A. K. Patel. "Assessment of physico-chemical properties influencing mine spoil genesis in chronosequence iron mine overburden spoil and implications of soil quality", *Int J Curr Microbiol Appl Sci*, vol. 4(6), pp. 1095-1110, 2015.
- [68] R. J. Parkes and J. Taylor. "The relationship between fatty acid distributions and bacterial activity types in contemporary marine sediments", *Estuarine Coastal and Shelf Sci*, vol. 16, pp. 173-189, 1983.
- [69] J. B. Guckert, C. P. Antworth, P. D. Nichols and D. C. White. "Phospholipid ester-linked fatty acid profiles reproducible assays for changes in prokaryotic community structure of estuarine sediments", *FEMS Microbiol Ecol*, vol. 31, pp. 147-158, 1985.
- [70] M. Liao, C. L. Chen and C.Y. Huang. "Effects of heavy metals on soil microbial activity and diversity in a reclaimed mining wasteland of red soil area", *J Environ Sci*, vol. 17, pp. 832-837, 2005.
- [71] J. Moore-Kucera and R. P. Dick. "PLFA profiling of microbial community structure and seasonal shift in soils of a Douglas-fir chronosequences", *Microbiol Ecol*, vol. 55, pp. 500-511, 2008.
- [72] R. M. C. P. Rajapaksha, M. A. Tobor-Kaplon, E. Baath. "Metal toxicity affects fungal and bacterial activities in soil differently", *Appl Environ Microbiol*, vol. 70(5), pp. 2966-2973, 2004.
- [73] M. Pothoff, K. L. Steenwerth, L. E. Jackson, R. E. Drenovsky, K. M. Scow, R. G. Joergensen. "Soil microbial composition as affected by restoration practices in California grassland", *Soil Biol Biochem*, vol. 38, pp. 1851-1860, 2006.
- [74] S. Yu and J. G. Ehrenfeld. "Relationships among plants, soils and microbial communities along a hydrological gradient in the New Jersey Pinelands, USA", *Annal Bot*, vol. 10, pp. 185-196, 2010.
- [75] C. Ahn and R. M. Peralta. "Soil bacterial community structure and physicochemical properties in migration wetlands created in the Piedmont region of Virginia (USA)", *Ecol Engineer*, vol. 35, pp. 1036-1042, 2009.
- [76] S. M. Card and S. A. Quideau. "Microbial community structure in restored riparian soils of the Canadian Prairie pothole region", *Soil Biol Biochem*, vol. 42, pp. 1463-1471, 2010.
- [77] N. Fierer, J. P. Schimel and P. A. Holden. "Influence of drying rewetting frequency on soil bacterial community structure", *Micro Ecol*, vol. 45, pp. 63-71, 2003.
- [78] A. D. Peacock, M. D. Mullen, D. B. Ringelberg, D. D. Tyler, D. B. Hedrick, P. M. Gale, D. C. white. "Soil microbial community responses to dairy manure or ammonium nitrate applications", *Soil Biol Biochem*, vol. 33, pp. 1011-1019, 2001.
- [79] D. A. Bossio and K. M. Scow. "Impacts of carbon and flooding on soil microbial communities: phospholipids fatty acid profiles and substrate utilization patterns", *Microbiol Ecol*, vol. 35, pp. 265-278, 1998.
- [80] H. Insam and K. H. Domsch. "Relationship between soil organic carbon and microbial biomass on chronosequences of reclamation sites", *Microb Ecol*, vol. 15, pp. 177-188, 1988.
- [81] V. L. Bailey, J. L. Smith and H. J. Bolton. "Fungal to bacterial ratios in soils investigated for enhanced carbon sequestration", *Soil Biol Biochem*, vol. 34, pp. 997-1007, 2002.
- [82] A. Van der Wal, J. A. van Veen, W. Smant, H. T. S. Boschker, J. Bloem, P. Kardol, W. H. van der Putten and W. de Boer. "Fungal biomass development in a chronosequence of land abandonment", *Soil Biol Biochem*, vol. 38, pp. 51-60, 2006.
- [83] M, Pasayat and A. K. Patel. "Contribution of soil physico-chemical properties influencing microbial biomass used as biomarkers for mine spoil genesis", *Res J Pharma Biol Chem Sci*, vol. 7(5), pp. 738-747, 2016.
- [84] M. N. Hogberg, P. Hogberg and D. D. Myrold. "Is microbial community composition in boreal forest soils determined by pH, C:N ratio, the trees, or all three?", *Oecologia*, vol. 150, pp. 590-601, 2007.
- [85] M. N. Hogberg, E. Baath, A. Nordgren, K. Arnebrant, P. Hogberg. "Contrasting effects of N availability on plant C supply to mycorrhizal fungi and saprotrophs - a hypothesis based on field observations in boreal forest", *New Phytol*, vol. 160, pp. 225-238, 2003.
- [86] J. L. Smith, J. W. Doran. "Measurement and use of pH and electrical conductivity for soil quality analysis", In: *Methods for assessing soil quality*, J. W. Doran, A. J. Jones (eds), *Soil Sci Soc Am, Madison*, pp. 169-186, 1996.
- [87] K. Goupil, K. K. Nkongolo and S. Nasserulla. "Characterization of fungal communities in limed and unlimed lands contaminated with metals: Phospholipid fatty acid (PLFA) analysis and soil respiration", *Am J Biochem Biotechnol*, vol. 11(2), pp. 45-56, 2015.
- [88] U. Langer and J. Rinklebe. "Priming effect after glucose amendment in two different soils evaluated by SIR and PLFA technique", *Ecol Engineer*, pp. 37, pp. 465-473, 2011.
- [89] N. Fierer, J. A. Jackson, R. Vilgalys, R. B. Jackson. "Assessment of soil microbial community structure by use of taxon-specific quantitative PCR assays", *Appl Environ Microbiol*, vol. 71, pp. 4117-4120, 2005.

- [90] B. Wang, G. B. Liu, S. Xue, B. B. Zhu. "Changes in soil physico-chemical and microbiological properties during natural succession on abandoned farmland in the Loess Plateau", *Environ Earth Sci*, vol. 62, pp. 915-925, 2011.
- [91] R. D. Bardgett, D. K. Leemans, R. Coak and P.J. Hobbs. "Seasonality of the soil biota of grazed and ungrazed hill grasslands", *Soil Biol Biochem*, vol. 29, pp. 1285-1294, 1997.
- [92] N. Fierer and R. B. Jackson. "The diversity and biogeography of soil bacterial communities. Proceedings of the national academy of sciences of the United States of America", vol. 103, pp. 626-631, 2006.
- [93] C. L. Lauber, M. S. Strickland, M. A. Bradford and N. Fierer. "The influence of soil properties on the structure of bacterial and fungal communities across land-use types", *Soil Biol Biochem*, vol. 40, pp. 2407-2415, 2008.
- [94] P. Merila, R. Stromner, H. Fritze. "Soil microbial activity and community structure along a primary succession transect on the land uplift coast in western Finland", *Soil Biol Biochem*, vol. 34, pp. 1647-1654, 2002.
- [95] P. Hogberg, A. Nordgren, N. Buchmann, A. F. S. Taylor, A. Ekblad, M. N. Hogberg, G. Nyberg, M. Ottosson-Lofvenius, D. J. Read. "Large scale forest girdling shows that current photosynthates drives soil respiration", *Nature*, vol. 411, pp. 789-792, 2001.
- [96] M. William and C. W. Rice. "Seven years of enhanced water availability influences the physiological, structural, and functional attributes of soil microbial community", *Appl Soil Ecol*, vol. 35, pp. 535-545, 2007.
- [97] C. Meimei, C. Baodong and M. Petra. "Plant growth and soil microbial community structure of legumes and grasses grown in monoculture or mixture", *J Environ Sci*, vol. 20, pp. 1231-1237, 2008.
- [98] S. B. Gray, A. T. Classen, P. Kardol, Z. Yermakov, Michael and R. Mille. "Multiple climate change factors interact to alter soil microbial community structure in an old-field ecosystem", *Soil Sci Soc Am J*, vol. 75, pp. 2217-2226, 2011.
- [99] W. Zhou, D. Hui and W. Shen. "Effects of soil moisture on the temperature sensitivity of soil heterotrophic respiration: A laboratory incubation study", *Plos One*, vol. 9(3), pp. 92531-92540, 2014.
- [100] J. A. Ludwig and J. F. Reynolds. "Statistical Ecology: A primer in method and computing", John Wiley and Sons, pp. 337, 1988.
- [101] A. Arunachalam and H. N. "Pandey. Ecosystem restoration of Jhum fallows in Northeast India: microbial C and N along altitudinal and successional gradients", *Restor Ecol*, vol. 11, pp. 168-173, 2003.
- [102] S. S. An, Y. M. Huang and F. L. Zheng. "Evaluation of soil microbial indices along a revegetation chronosequence in grassland soils on the Loess Plateau, Northwest China", *Appl Soil Ecol*, vol. 41, pp. 286-292, 2009.
- [103] H. H. Zhu, X. Y. He, K. L. Wang, Y. R. Su and J. S. Wu. "Interactions of vegetation succession, soil biochemical properties and microbial communities in a Karst ecosystem", *Eur J soil Biol*, vol. 51, pp. 1-7, 2012.
- [104] L.E. Jackson, F. J. Calderon, K. L. Steenwerth, K. M. Scow, D. E. Rolston. "Responses of soil microbial processes and community structure to tillage events and implications for soil quality", *Geoderma*, vol. 114, pp. 305-317, 2003.
- [105] M. Welc, E. K. Bunemann, A. Fliebbach, E. Frossard, J. Jansa. "Soil bacterial and fungal communities along a soil chronosequence assessed by fatty acid profiling", *Soil Biol Biochem*, vol. 49, pp. 184-192, 2012.