Int J Pharm Bio Sci 2014 Jan; 5(1): (B) 21 - 36

Research Article **Microbiology**

International Journal of Pharma and Bio Sciences **ISSN 0975-6299**

MICROBIAL SOIL RESPIRATION AND IT'S DEPENDENCY ON SOIL MICROBIAL COMMUNITIES, ORGANIC CARBON & MOISTURE IN DIFFERENT DRY TROPICAL ECOSYSTEMS

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ABSTRACT

The relationship between environmental changes and microbial respiration is critical for projecting changes in soil carbon fluxes. The variation in OC, microbial-C and moisture among different soil profiles of Jharkhand, India were analyzed. The OC, microbial-C and moisture varied from (0.174-2.469)%, (55.586–646.703) μg/g soil and (6.643–11.329)% respectively. The OC was positively correlated with microbial-C (r=0.985; $p<0.01$) and moisture (r=0.979; $p<0.01$). The MB-C:OC ratio ranged from (2.6-3.9) %, and BSR:OC from (1.271-0.382)%. The basal soil respiration and microbial metabolic quotients ranged from (0.348-0.945) μg CO_2-C/g soil/hr and (6.2605-1.4612)x10^{-3} μg CO_2-C/g microbial-C/hr respectively. Microbial populations across the sites were estimated. Stepwise multiple regression analysis determines the degree of influence contributed by microbial community, OC, microbial-C and moisture on microbial soil respiration. Principal component analysis was able to discriminate different soil profiles, which correlated well with land degradation, and thus can serve as a biomarker of soil fertility.

KEY WORDS: **Organic carbon, Soil moisture, Microbial community, Basal soil respiration**

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INTRODUCTION

Ecosystem respiration provides energy, which is contributed by the components of an ecosystem (leaves, stems, roots and microorganisms). Small changes in ecosystem respiration may cause an ecosystem to switch from being a sink to a source of carbon[1]. Soil provides second largest carbon efflux to the atmosphere[2]. Soil respiration is an ecosystem-scale flux that integrates a multitude of component processes and fluxes[3] which includes both root and microbial respiration representing 60-90% of the total ecosystem respiration[4,5] and hence considered as the key component of carbon balance of whole ecosystem. It also reflects the intensity of soil organic matter decomposition, mineralization and the incidence of soil microbes, and often used for biomass determination[6]. As the ecosystem respiration will respond to environmental perturbations, it plays a crucial role in predicting past and future climates[7,8]. Thus, ecosystem respiration must consider its dependence on biotic and abiotic variables such as composition and activity of microbial community, quality and quantity of soil carbon pool, growth activity and soil moisture[9,10]. Besides, microbial biomass-C and basal respiration were also measured to assess changes in both microbial size and activity among different soil profiles. Microbial community constitute a major part of the biomass and play a fundamental role in establishing biogeochemical cycles[11], influencing soil physico-chemical and biological properties[12], controlling different soil processes[13,14,15]. Besides, the microbial population dynamics are also influenced by land use[16], as well as elemental composition in soils, which determines the characteristics of soil microbial community by providing habitats and nutrient sources for growth[17]. The change in OC strongly influence the soil microbial community composition[18,19]. However, the loss of soil biodiversity will make the soil type more vulnerable to other soil degradation processes. Soil biological and biochemical properties are responsive to small changes in soil, which is due to the microbial activity that directly influence the ecosystem stability[20], and hence considered as an index of soil fertility and indicator of soil quality. Rates of microbial respiration have been measured in a variety of ecosystems to examine the microbial activity, nutrient turnover, carbon cycling and other soil processes. Respiration activity is also used to evaluate soil quality or soil contamination with organic pollutants or heavy metals[21,22,23,24].

The rate of soil respiration is controlled primarily by the rate of CO_2 production by soil-biota, but is modified by various factors influencing CO_2 movement out of the soil[25, 26]. The other factors influencing the rate of soil respiration includes the physico-chemical properties of soil[27], physical and biochemical accessibility to substrate by the microbes[28,29,] water availability and substrate diffusion[30], microbial population dynamics[31,15]. Besides, soil moisture is considered as the most influential factor controlling soil respiration[32,33,34]. These gradients in resources and environmental stresses are likely to be the primary factors controlling the microbial communities residing in different soil profiles.

Microbial biomass assessment in combination with OC and basal soil respiration provide an overall estimate of soil development and degradation[35]. Thus, the understanding of microbial respiration rate in different ecosystems and the factors that influence it has prime importance. The objectives of the investigation is to estimate the abundance and distribution of microbial communities in different soil samples (fresh mine spoil: FMS; 6yr mine spoil: MS; degraded wasteland soil: DWS; grassland soil: GS; pesticide treated soil: PTS; agricultural soil: AS and forest soil: FS). However, there have been few studies that quantitatively link microbial community characteristics and soil process rate. Therefore, emphasis has been given to evaluate the potential impact of microbial community composition, available organic carbon, moisture content and microbial biomass as predictors of basal soil respiration in order to link quantitatively, as interest grows in understanding

how microbial community might be related to ecosystem functioning.

MATERIALS AND METHODS

(i) Study site

The study was carried out in iron mines at Noamundi (85° 30' 33.61" east longitude and 22° 9' 49.96" north latitude), maintained by Tata Iron Steel Corporation limited (TISCO) located in the revenue district of West Singhbhum, Jharkhand, India (Figure 1). The study site is situated away from the mean sea level *i.e.* about 540m altitude. The natural vegetation of the study site exhibited tropical dry deciduous forest. However, rapid industrialization led to decline of forest cover. Besides, the different age series iron ore overburdens were observed as a consequence of the mining activity in the study site. Mean annual temperature and humidity is around 19.67°C and 20% respectively.

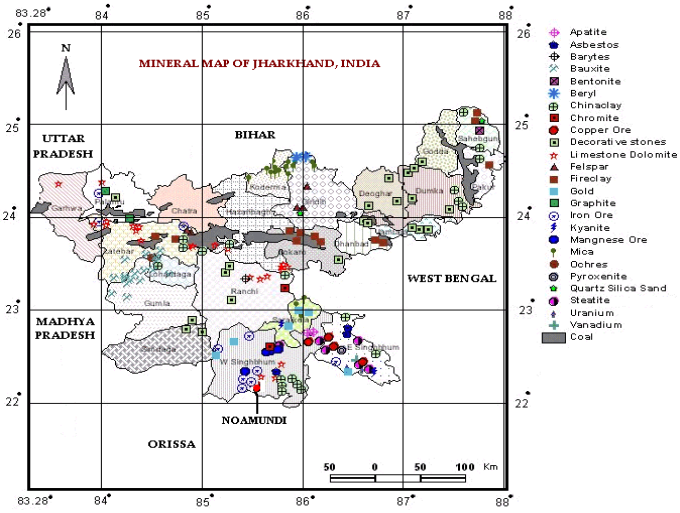

Figure 1

Geographical location and the mineral map of study site, Jharkhand, India.

(ii) Soil sampling

Sampling was done in accordance with the soil microbiological study[36]. Seven different samples [fresh mine spoil (FMS); 6yr old mine spoil (MS); degraded waste land soil (DWS); grassland soil (GS); pesticide-treated soil (PTS); agricultural soil (AS) and forest soil (FS)] were collected around the periphery of 10 Km from the mining area near Noamundi. Each site was divided into 3 blocks, and from each block, five samples were collected randomly from a soil depth of 0-15cm, which is referred to as 'sub-samples'. These sub-samples were brought to the laboratory and thoroughly mixed to form one 'composite sample'. Thus, three composite samples were obtained from each site. Further, the composite samples were subjected to sieving (2mm mesh size) for microbiological analysis.

(iii) Moisture content

The moisture content was determined following the protocol proposed by[37]. About 10g of soil sample (W_1) was taken and was oven dried at 105°C for 24hrs till a constant dry weight (W_2) was obtained. Soil moisture (%) = [(W_1-W_2)/10] x 100.

(iv) Soil Organic Carbon

Soil organic carbon (OC) was determined by partial oxidation method[38]. Oven dried soil sample of 5g was taken in a 500ml Erlenmeyer flask. To this 10ml of 1N $K_2Cr_2O_7$ and 20ml of concentrated H_2SO_4 were added. The flask was shaken and was allowed to stand for 30min. The content was then diluted with 200ml of distilled water, followed by addition of 10ml of 85%

H_3PO_4 and 1ml of diphenylamine indicator. The mixture was titrated against 1N ferrous ammonium sulphate solution until the colour of the mixture flashed to green.

(v) Microbial biomass-C

Soil samples were stored at (28 ± 2)ºC for a week to stabilize respiration, subsequently used for analysis. Microbial biomass carbon (MB-C) was determined by fumigation extraction method[39] through back titration with 0.04N $(NH_4)_2Fe(SO_4)_2.6H_2O$ using a ferroin indicator with K_{EC} = 0.38 (calibration factor) and expressed on oven dry weight basis.

(vi) Microbial basal respiration

Microbial basal respiration, an estimate of soil microbial activity was determined as the amount of CO_2 evolved by the soil following the alkali absorption technique[40,41].

(vii) Microbial metabolic quotient

Microbial metabolic quotient (CO_2-C/g microbial carbon/hr) is defined as the amount of CO_2-C respired per unit MB-C per unit time, calculated from the mean MB-C and mean BSR.

(viii) Enumeration of soil microbes

The different microbial populations were enumerated using selective media by standard spread plate dilution technique. Azotobacter populations (AZB) in different soils were estimated using azotobacter mannitol agar and incubated for 48hr at 25-30ºC[42]. Arthrobacter populations (ARB) were enumerated using Arthrobacter selective media[43]. Rhizobia (RZB) were counted on yeast extract mannitol agar (YEMA) containing Congo red dye to distinguish them from other bacteria[44]. Total heterotrophic aerobic bacteria (HAB) were enumerated using nutrient agar[45]. Sulfur reducing bacterial population (SRB) was enumerated using sulphate reducing medium (Hi-Media[46]. Actinomycete counts (ACM) were determined using (CSA) starch-casein agar[47]. Streptomycin 40µl/ml and griseofulvin 50µl/ml were used to prevent bacterial and fungal contaminants respectively[48]. Yeast counts (YES) in different soils were estimated using potato sucrose agar[49]. Fungal count (FUN) was performed using Rose Bengal agar supplemented with streptomycin 50µl/ml to prevent bacterial contaminants[50].

(ix) Statistical analyses

Simple correlation analysis was performed to test the level of significance between MC, OC, MB-C, BSR and microbial populations among seven different soils using SPSS Statistics 17.0 software. Stepwise multiple regression analysis was performed to determine the quantitative contribution of microbial communities to microbial basal soil respiration using Minitab 16 software. Principal component analysis (PCA) was performed using Statistrix PC DOS Version-2.0 (NH Analytical software).

RESULTS AND DISCUSSION

(i) Moisture content

The moisture content in different soil samples indicated an increasing trend from FMS (6.643%) to FS (11.329%) (Table 1). Across the sites, significant fluctuation ($p<0.001$) in moisture content was exhibited. Reduced soil water loss by the canopy shading due to vegetation might contribute for higher moisture content in FS as compared to FMS[51]. The decrease in moisture level in DWS and GS may be due to the decrease in organic matter, and exposed surface soil that promote drying.

(ii) Organic carbon

The organic carbon content exhibited a wide variation from FMS (0.174%) to FS (2.469%) (Table 1). The increase in OC content with respect to seven different soil samples was found to be statistically significant ($p<0.001$). The increased accumulation of OC in FS as compared to FMS is due to the increase in clay percentage, which absorbed the organic complexes and physically protected it against decomposition[52]. Heavy metal pollution reduces the plant growth[53], a low input of plant and root litter is likely to decreases in OC content in FMS as compared to FS[54]. The higher level of OC in MS (0.307%) than FMS is due to the

vegetational development, micropore space, organic matter input, which influence soil aggregation, structural stability and nutrient retention[55,56]. Higher level of OC in AS (2.064%) as compared to PTS (1.667%) was estimated, which may be due to the increased use of pesticides (toxic chemicals) that led to contamination of PTS[57, 58].

(iii) Microbial biomass-C

Across the sites, the MB-C showed an increasing trend from 55.586 μg/g soil (FMS) to 646.703 μg/g soil (FS) (Table 1), which varied significantly ($p<0.001$) with respect to seven different soil samples.

Table 1

Soil moisture content, organic carbon content, microbial biomass-C and basal soil respiration in different ecosystems. (Values are mean ± SD; n = 3)

Soil types	MC (%)	OC (%)	MB-C (μg/g soil)	Basal Soil Respiration (μg CO_2-C/g soil/hr)
FMS	6.643 ± 0.103	0.174 ± 0.009	55.586 ± 3.383	0.348 ± 0.011
MS	7.422 ± 0.154	0.307 ± 0.011	120.883 ± 9.755	0.388 ± 0.019
DWS	7.541 ± 0.191	0.779 ± 0.042	258.373 ± 11.773	0.583 ± 0.016
GS	8.675 ± 0.097	1.256 ± 0.093	440.913 ± 8.729	0.883 ± 0.015
PTS	10.398 ± 0.158	1.667 ± 0.074	488.693 ± 12.776	0.904 ± 0.008
AS	10.509 ± 0.146	2.064 ± 0.081	541.476 ± 16.298	0.913 ± 0.012
FS	11.329 ± 0.183	2.469 ± 0.111	646.703 ± 18.215	0.945 ± 0.024

It is evident from the data that the MB-C was expectedly higher in FS as compared to FMS[55,59,60]. The major cause of such decline in MB-C in FMS was due to the lower input of OC[61]. The MB-C was found to be positively correlated (r = 0.985; $p<0.01$) with OC (Table 4). The difference in MB-C between FMS and MS was significant, reflecting a marked age effect[55]. Besides, the lower level MB-C in PTS (488.693 μg/g soil) as compared to AS (541.476 μg/g soil) may be due to the adsorption of small amount of pesticides on organic matter content, which could mask the affects of these agrochemicals on soil microbial biomass and subsequently led to lysis of microbial cells[57,58]. Further, higher level of MB-C was found in GS (440.913 μg/g soil) as compared to DWS (258.373 μg/g soil), which may be due to grazing that increase the turnover of fine roots and accelerates the leakage of labile organic matter[62].

(iv) Basal soil respiration (BSR)

Basal soil respiration is considered as the reflection of the availability of slow flowing carbon for microbial maintenance, and thus can be used as a measure of basic turnover rate in soil[63]. Like MB-C, the basal respiration rate also exhibited significant variation ($p<0.001$) among different soil profiles, which ranged from 0.348 to 0.945 (μg CO_2-C/g soil/hr) with minimum in FMS and the maximum in FS (Table 1). A low basal soil respiration rate in FMS therefore evidences a low microbial turnover in comparison to FS. The low microbial turnover in FMS may be due to the low availability of substrate required for microbial growth, and the exposure of mine spoil to different environmental extremities. Gradual input of OC form vegetational component led to an increase in BSR[64]. The BSR was found to be positively correlated with OC (r = 0.932; $p<0.01$) and MB-C (r = 0.976; $p<0.01$) (Table 4). The ratio of microbial biomass nutrients to soil nutrients (MB-C:OC) otherwise represents the quantum of soil nutrients reflected in the microbial biomass[65,66]. The variation in MBC:OC ratio across the sites may be due to the prevalence of microbial species capable of utilizing the soil organic carbon as energetic substrate[67]. The major cause of such decline in MB-C was due to the lower input of OC into soil[61]. Differences among the soil profiles as well as the quantity of soil organic matter input from the overlying vegetation explain a wide range of ratios, which provides an insight into the soil

organic carbon status[68] and considered as the functional index of soil subsystem[69]. In the present study, the MBC:OC ranged from 3.9 to 2.6 (Table 2). The average percentage of OC in microbial biomass ranges from 2% to 4%[66]. The majority of microbial soil respiration in intact profiles is likely to come from the mineralization of more labile carbon pool[70,71]. The BSR: OC ratio displayed higher value in FMS (1.271%) as compared to FS (0.382%) (Table 2). Higher value of BSR: OC ratio confirms the higher use of native organic carbon by the microbial community inhabiting in FMS, which could also be ascribed to elevated stress conditions of the habitat[72].

Table 2

OC% present as microbial biomass-C (MB-C:OC); OC% evolved as CO_2-C (BSR:OC) and microbial metabolic quotients (qCO_2) in different soils.

Soil types	MB-C/OC (%)	BSR/OC (%)	Microbial Metabolic Quotients (CO_2-C/g microbial-C/hr)
FMS	3.1	1.271	6.2605×10^{-3}
MS	3.9	1.263	3.2097×10^{-3}
DWS	3.3	0.748	2.2564×10^{-3}
GS	3.5	0.703	2.0026×10^{-3}
PTS	2.9	0.542	1.8498×10^{-3}
AS	2.6	0.442	1.6861×10^{-3}
FS	2.6	0.382	1.4612×10^{-3}

(v) Microbial metabolic quotient

Amount of CO_2-C evolved for unit microbial biomass carbon per unit time is otherwise known as microbial metabolic quotient (qCO_2)[69]. In other words, it is an expression of the relationship between microbial function (respiration) to structure (biomass), and is analogous to R/B ratio used for the evaluation of ecosystem development[73]. Microbial metabolic quotient reflects the efficacy of the microbial community in terms of substrate/energy utilization[74]. The more efficient the microorganisms function the greater is the fraction of substrate C incorporated in their biomass, and relatively less carbon per unit biomass is lost through respiration resulting in a higher biomass and a low metabolic quotient. In the present study, the microbial metabolic quotient was observed to be maximum in FMS (6.2605×10^{-3}) and minimum in FS (1.4612×10^{-3}) (Table 2). Generally, more developed the soil; less CO_2-C is evolved per unit microbial biomass resulting a lower metabolic quotient[69, 74]. In FMS, in the absence of the detritus and with almost least amount of organic substrate, microbial community is expected to be of 'r'-strategy ecotype, which would respire more CO_2-C per unit of available substrate. As per the concept of "economic metabolism"[69], FS with the presence of complex detritus and organic substrate is expected to be predominated by 'k'-strategy ecotype, which respires relatively less CO_2-C per unit degradable substrate carbon[75]. In addition, more the labile C that is readily decomposable would favor opportunistic/cheaters 'r'-strategy ecotype over enzyme producers 'k'-strategy ecotype[76,77,64]. Usually disturbed soil habitat is colonized by the microbial ecotypes of 'r'–strategy and with the recovery of the disturbed soil habitat, 'r' strategy are substituted by 'k' strategy ecotypes[64]. Consequently, the progression of recovery of the soil is associated with the decline value of microbial metabolic quotient[78,74,79.] The difference in qCO_2 between FMS and FS can be explained on the basis of the qualitative change in microbial community specifically in terms of 'r' and 'k' ecotypes[64]. The study thus agrees with the view that the stressed soil habitat exhibited high qCO_2 due to the decline in the efficiency of microorganisms[74,80].

(vi) Enumeration of microbes

Differences in microbial community composition were observed between different soil samples based on microbial enumeration (Table 3). The mean total azotobacter count

fluctuated from $8x10^{-1}$ (FMS) to $68x10^{-4}$ (FS); arthrobacter from $21x10^{-2}$ (FMS) to $39.9x10^{-4}$ (FS), rhizobia from $23x10^{-1}$ (FMS) to $23.8x10^{-4}$ (FS), heterotrophic aerobic bacteria from $32x10^{-2}$ (FMS) to $28.2x10^{-8}$ (FS), actinomycetes from $4x10^{-2}$ (FMS) to $45x10^{-3}$ (FS) respectively. However, the total cultural sulphur reducing bacteria ranged from $31.2x10^{-3}$ (FMS) to $10x10^{-1}$ (FS). Higher population of yeast and fungi were recorded in FS as compared to FMS, which ranged from $8x10^{-1}$ to $7.5x10^{-3}$, and $7x10^{-1}$ to $38x10^{-3}$ respectively.

Table 3
Distribution of microbial populations in different dry tropical ecosystems.

Microbial groups	CFU g^{-1} dry wt. soil						
	FMS	MS	DWS	GS	PTS	AS	FS
Azotobacter	$8 x10^{-1}$	$19x10^{-1}$	$26.2x10^{-2}$	$59x10^{-3}$	$48.9x10^{-4}$	$59.2x10^{-4}$	$68x10^{-4}$
Arthrobacter	$21x10^{-2}$	$27x10^{-2}$	$77x10^{-2}$	$10.8x10^{-3}$	$22.5x10^{-4}$	$31.5x10^{-4}$	$38.9x10^{-4}$
Rhizobia	$23x10^{-1}$	$34x10^{-1}$	$49x10^{-2}$	$9.6x10^{-3}$	$14.3x10^{-4}$	$16.8x10^{-4}$	$23.8x10^{-4}$
Heterotrophic Aerobes	$32x10^{-2}$	$42x10^{-2}$	$78x10^{-4}$	$94x10^{-6}$	$18.2x10^{-8}$	$22.6x10^{-8}$	$28.2x10^{-8}$
Sulphur reducing bacteria	$31.2 x10^{-3}$	$24x10^{-3}$	$8.9x10^{-2}$	$79x10^{-1}$	$56x10^{-1}$	$17.8x10^{-1}$	$10x10^{-1}$
Actinomycetes	$4x10^{-2}$	$13x10^{-2}$	$27x10^{-2}$	$11.8x10^{-3}$	$34x10^{-3}$	$39x10^{-3}$	$45x10^{-3}$
Yeast	$8x10^{-1}$	$15x10^{-1}$	$11x10^{-2}$	$22x10^{-2}$	$41x10^{-2}$	$69x10^{-2}$	$7.5x10^{-3}$
Fungi	$7x10^{-1}$	$11x10^{-2}$	$16x10^{-2}$	$21x10^{-2}$	$12.6x10^{-3}$	$25x10^{-3}$	$38x10^{-3}$

The azotobacter, arthrobacter, rhizobia, actinomycetes, yeast and fungal count showed an increasing trend from FMS to FS, which depend on the degree of available substrate, OC content, microclimatic conditions and the heterogeneity of vegetational cover. Azotobacter belongs to family *Azotobacteraceae*, which is typical obligately aerobic, chemoheterotrophic, dinitrogen-fixing bacteria. Being the nutrient deficient profile of FMS, the azatobacter count increases from FMS to FS. The soil arthrobacters can use a wide and diverse range of organic substrates as principal sources of carbon and energy[43] and was also capable of dinitrogen fixation. However, both the numbers and the proportions of arthrobacters in "total" counts decreases with increasing soil acidity[43], which may be the reason of minimal count in FMS as compared to FS. Their numerical predominance varied among soils because of their nutritional versatility of extreme resistance to drying[81] and starvation[82]. The predominant soil arthrobacters in PTS may be due to its ability to degrade herbicides[83,84]. The genus *Rhizobium* engages in a symbiotic relationship with leguminous plants to assimilate gaseous nitrogen (nitrogen-fixing). Besides, these are highly specific for their plant host. The association of the nitrogen-fixing Rhizobium sp. with leguminous plant influences the structure and function of ecosystems[85,86,87], which may be the possible explanation of higher rhizobia counts in FS as compared to FMS. The total heterotrophic aerobic bacterial count was much higher than other microbial groups. The data suggested that the HAB population in FMS was less as compared to non-contaminated soil (FS), which could be regarded as the destabilization of soil ecological balance arising from contamination. Environmental stresses brought by the contamination could be adducted for the reduction in microbial population and diversity[15]. Further, the microbial population in PTS was found to be comparatively less than AS, which may be due to the adsorption of microbes onto agrochemicals, which did not protect against pesticides[57,58].

However, the total sulphur reducing bacterial counts showed a decline trend from FMS to FS. As FMS represents an altered geomorphic system with OC deficient situation, but enriched with pyrite (FeS_2) contamination, it favours the enrichment of SRB in FMS as compared to FS[55,59]. SRB are anaerobic, widespread in anoxic habitats, where they use sulphate as a terminal electron acceptor for degradation of organic compounds resulting in the production of sulphide. Subsequently, the sulphide can be oxidized under oxic conditions by chemolithotrophic sulphur bacteria or under

anoxic conditions by phototrophic sulphur bacteria. Utilization of the sulfur compound[88], oxidation of reduced inorganic phosphorous compound[87] was demonstrated with several SRB. It has been estimated that sulphate reduction can accounted for about 50% of OC mineralization[89], which indicates the importance of sulphate reducers in both the sulphur and carbon cycles, and consequently why SRB have been studied extensively[90].

Actinomycetes are aerobic, gram-positive bacteria. This is one of the major groups of soil population, which are widely distributed[91]. The number and dominance in a particular soil would be greatly influenced by geographical location such as soil temperature, pH, organic carbon content, aeration and moisture content[92]. This may be the possible reason of higher ACM counts in FS as compared to FMS. Besides, actinomycetes populations are comparatively lower than other soil microbes, and are relatively acid-tolerant[93], which explained the least ACM counts in FMS. Fungi are important in stabilizing soil structure. The basic unit of a fertile soil is the soil aggregate, which is held together by microbial polymers, while fungal hyphae bind the microaggregates into macroaggregates. Soil fungi may occur as free-living organisms or in mycorrhizal association with plant roots. Fungi are found primarily within the top 10 cm soil depth, but rarely found below 30 cm. Most fungi in soil are opportunistic (zymogenous). The distribution of fungal population is influenced by a number of environmental factors like pH, moisture content, soil organic carbon content[94], aeration and concentration of utilizable substrates[95]. Higher fungal population in FS was due to prevailing favourable moisture, sufficient organic matter and humus accumulation that enhanced colonization of soil microbes[96]. Besides, presence of fungal population in acidic soils like FMS has also been reported[97]. Each soil type develops its own physical, chemical, microbiological, and mineralogical characteristics due to addition, losses, transfer and transformations of energy and matter occurred during the formation and development of soil, which can determine various microbial environments within the soil. Such difference could have sorted a segregation of the microbial communities in function of the variable availability of nutrient and energy[98], which could bring to 'a shift in the population structure of the microbial community'[15,98,99]. A simple correlation analysis between microbial populations and different soil parameters was calculated (Table 4).

Table 4
Simple correlation coefficients of microbial counts and soil properties.

Parameters	AZB	ARB	RZB	HAB	SRB	AMC	YES	FUN	MC	OC	MBC	BSR
MC	0.960**	0.940**	0.948**	0.949**	-0.736*	0.985**	0.958**	0.894**	1.000			
OC	0.932**	0.924**	0.927**	0.924**	-0.795*	0.964**	0.976**	0.908**	0.979**	1.000		
MBC	0.868**	0.848**	0.857**	0.853**	-0.860**	0.920**	0.926**	0.829*	0.961**	0.985**	1.000	
BSR	0.787*	0.746*	0.755*	0.758*	-0.889**	0.857**	0.848**	0.699*	0.910**	0.932**	0.976**	1.000

***** Correlation is significant p < 0.01 and * correlation is significant p < 0.05.***

The data suggested that not only the microbial populations in FS, but also the potential activity in terms of basal soil respiration rate contributed by microbial communities was estimated to be higher than FMS. Such variation in microbial communities is due to the adsorption of soil microbes onto organo-mineral aggregates, which did not protect them against heavy metal pollution. Microorganisms and heavy metal seems to occupy same binding sites, but the spatial separation of toxic heavy metals from soil microorganisms did not occur[54]. The fluctuations in microbial communities were positively correlated with available soil OC[100,101]. The soil profiles with its strong gradient in productivity as evidenced by the decline in MB-C from FS to FMS provides an unique system in which the abundance and distribution of different microbial

communities can be used to test these competing diversity-productivity relationship[100]. Microbial biomass is assumed to be proportional to the basal soil respiration rate measured after the addition of a labile C substrate to a soil sample[102]. The variation in MB-C was positively correlated with the fluctuation in soil microbial communities across the sites (Table 4). Besides the variability in moisture content can influence the microbial community composition[103,104,105]. Soil moisture is the second most important abiotic variable for predicting microbial soil respiration[64], as it strongly influences the physiological activity of vegetation and soil microbes[33]. Moisture variability is likely to be an important control on microbial populations among different soil profiles, where significant fluctuation in moisture content are frequent and rapid enough to select specific microbial groups with high tolerance of moisture stress[106].

(vii) Contribution of microbial communities, OC, MB-C, MC to BSR

Variation in microbial respiration caused by the changes in intrinsic respiration of the existing microbes (low efficiency) or changes in soil microbial community composition (adaptation and higher efficiency), which may be affected by carbon inputs, microbial biomass and moisture content[15,64]. The stepwise multiple regression analysis using microbial communities as dependent variables are summarized (Table 5).

Table 5

Stepwise multiple regression analysis of microbial soil respiration using microbial communities exhibited in different dry tropical ecosystems as dependent variables.

Parameter	Equations	*R^2
Microbial soil Respiration	0.536 + 0.000001 AZB	0.619
	0.4874 + 0.00001 AMC	0.734
	0.3471 – 0.000001 AZB + 0.00006 AMC	0.976
	0.4669 – 0.000001 AZB + 0.00005 AMC – 0.000001 SRB	0.996
	1.0356 – 0.000001 AZB + 0.00006 AMC – 0.00001 SRB -0.0792 MC	0.999
	0.5515 + 0.000001 ARB	0.556
	0.2445 – 0.000001 ARB + 0.00144 MB-C	0.976
	0.261 – 0.000001 ARB + 0.0013 MB-C + 0.000001 AZB	0.995
	0.8502 – 0.000001 ARB + 0.00166 MB-C + 0.000001 AZB – 0.089 MC	0.999
	0.5491 + 0.000001 RZB	0.570
	0.2414 – 0.000001 RZB + 0.00146 MB-C	0.977
	0.2657 – 0.000001 RZB + 0.00111 MB-C + 0.0000AMC	0.994
	0.5499 + 0.000001 HAB	0.575
	0.2466 – 0.000001 HAB + 0.00143 MB-C	0.972
	0.2591 – 0.000001 HAB + 0.00125 MB-C +0.000001 AZB	0.996
	0.8532 – 0.00002 SRB	0.790
	0.3914 – 0.000001 SRB + 0.00096 MB-C	0.962
	0.1517 + 0.000001SRB + 0.00171 MB-C – 0.00001 FUN	0.994
	0.4822 + 0.00007 YES	0.719
	0.2382 – 0.00003 YES + 0.00158 MB-C	0.974
	0.2509 + 0.00003 YES + 0.0013 MB-C – 0.00001 FUN	0.996
	0.5662 + 0.00001 FUN	0.488
	0.2458 – 0.00002 FUN + 0.51081 OC	0.993
	0.1419 – 0.00002 FUN + 0.60442 OC + 0.000001 SRB	0.997

All R^2- values are significant at p<0.001.

About 61.9% and 73.4% of variability in BSR was explained by AZB and AMC independently. With AZB as 1st variable, an additional 35.7% and 2% of variability in BSR was explained by AMC and SRB as 2nd and 3rd variable respectively, and a marginal effect (0.3%) by MC. With ARB as 1st variable explained 55.6% of variability in BSR, and an additional 42% by MB-C as 2nd variable. Only a marginal effect on BSR variability was explained by AZB (1.9%) and MC (0.4%). With RZB as 1st variable explained 57% of variability in BSR. The

2nd and 3rd variables of importance in explaining the variability in BSR were MB-C (20.7%) and MC (1.7%) respectively. The stepwise multiple regression analysis suggested that 57.5% of variability in BSR was explained by HAB as 1st variable, and an additional 39.7% and 2.4% by MB-C and AZB respectively. The SRB explained about 79% of variability in BSR, an additional 17.2% by MB-C as 2nd variable, and a marginal effect by FUN (3.2%). With YES as 1st variable explained 71.9% of variability in BSR. The 2nd and 3rd variables explaining the variability in BSR were MB-C (25.5%) and FUN (2.2%) respectively. About 48.8% of variability in BSR was explained by FUN, an additional 50.5% by OC as 2nd variable, and a marginal effect by SRB (0.4%). The stepwise multiple regression analysis using OC, microbial biomass-C and moisture as dependent variables are summarized (Table 6). Positive correlation between BSR and OC (86.9%; $p<0.001$) was observed. About 12.4% of variability in BSR was explained by FUN as 2nd variable, and a marginal effect by SRB (0.4%). The multiple regression analysis suggested that 95.2% of variability in BSR was explained by MB-C as 1st variable and an additional 3.9% by FUN as 2nd variable. With MC as 1st variable explained 82.8% of variability in BSR. The 2nd and 3rd variables of importance were MB-C (13.4%) and FUN (3%) respectively.

Table 6

Stepwise multiple regression analysis of microbial basal soil respiration using organic carbon, microbial biomass-C and moisture content as dependent variable.

Parameter	Equations	R^2
Microbial basal soil respiration	0.3602 + 0.28023 OC	0.869
	0.2458 + 0.51081 OC – 0.00002 FUN	0.993
	0.1419 + 0.60442 OC – 0.00002 FUN + 0.000001 SRB	0.997
	0.2894 + 0.00115 MB-C	0.952
	0.2355 + 0.0015 MB-C – 0.00001 FUN	0.991
	-0. 46426 + 0.1314 MC	0.828
	0.60243 – 0.0516 MC + 0.00156 MBC	0.962
	0.09546 + 0.0219 MC + 0.00137 MB-C – 0.00001 FUN	0.992

All R^2- values are significant at p<0.001.

Further, in order to view the differences among seven different soils, principle component analysis was performed to discriminate different sites on the basis of MC, OC, MB-C, BSR as well as microbial population dynamics[107]. Principal component analysis indicated that Z_1 and Z_2 components explained the maximum variance with respect to different soil parameters and their cumulative percentage of variance was estimated to be 99%, which can able to segregate seven soil profiles into independent clusters (Figure 2).

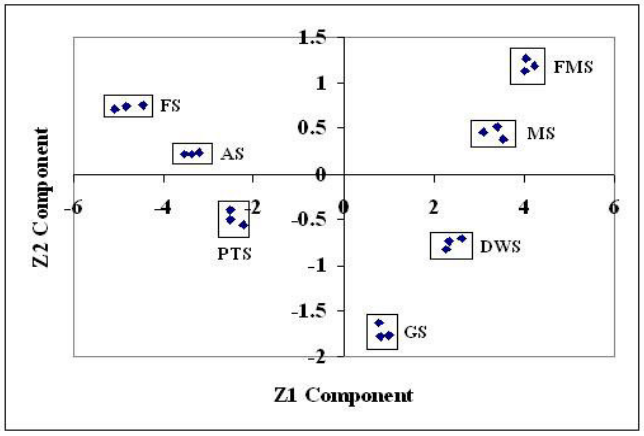

Figure 2
Principal component analysis based on microbial populations, organic carbon, moisture, and microbial basal soil respiration in different soil profiles.

CONCLUSION

Spatial heterogeneity in microbial basal soil respiration within the landscape is related to abundance and distribution of microbial communities. Possible reasons for such differences among soil profiles may be attributed to microbial activity, which is confounded with soil OC and moisture. On the basis of data sets of soil microbial communities, OC, microbial biomass-C and moisture in different soil profiles, how microbial basal soil respiration responds to microbial communities, and fluctuation in soil properties has been presented. The degree of contribution attributed by microbial communities, OC and moisture towards basal soil respiration was estimated. The gradual OC accumulation and an increase in moisture shift the microbial population across the sites supplemented to higher microbial respiration. However, the complete soil C budgets that differentiate between root and microbial processes that include the effect of soil OC, temperature, water content and gaseous transport are needed to refine our current understanding of soil respiration. Due to the dispersed nature of soil profiles, a consistent and economically appealing approach to its protection is pre-requisite for sustainable development.

ACKNOWLEDGEMENT

The authors are indebted to Ms. Sarita Nayak, who helped with field, laboratory and computational analyses during the course of the study. The authors are thankful to the Head, School of Life Sciences, Sambalpur University, Odisha, India for providing the necessary laboratory facilities. Authors are also thankful to UGC, Government of India for financial support in terms of Rajiv Gandhi National Fellowship (RGNF) scheme.

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