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Research Article

Impact of land-use change on soil microbial communities, organic carbon, and total nitrogen contents in Barkachha, Mirzapur District, India

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Abstract

Land-use change is a major driver of ecosystem degradation, particularly in the dry tropics, where forests are increasingly being converted into agricultural lands. This transformation not only reduces biodiversity and alters ecosystem functions but also significantly impacts soil health. This study assessed the effects of different land-use types, namely, natural forest, degraded forest, bamboo plantation, and agricultural land, on soil microbial community composition and biomass, and soil carbon and nitrogen contents in the dry area of Barkachha, Mirzapur District. A total of 24 composite soil samples were collected from all land use types. Soil organic carbon, total soil nitrogen, microbial biomass, and microbial community composition were determined by the oxidation and titration method, the micro-Kjeldahl method, the fumigation and extraction method, and FAME GC-MS, respectively. The results of the study showed a significant decline in the microbial community in agricultural and degraded lands compared to natural forest ($p<0.001$). In agricultural and degraded lands, the microbial community and biomass decreased by 28.8% and 22%, and 54.5% and 50%, respectively. Similarly, soil organic carbon and total nitrogen contents were markedly lower in converted land uses. Among all land use patterns, the highest organic carbon (0.84±0.054%), total nitrogen (0.123±0.013%), microbial biomass carbon (570.65±35.05μg/g), microbial biomass nitrogen (84.21±3.186μg/g), basal respiration (3.64±0.064μg/g), b-glucosidase (809.68±39.7μgμg PNP g^{-1} dry soil h-1) and microbial community composition were found under natural forest, followed by bamboo plantation, degraded forest, and agricultural land, in decreasing order. Among microbial groups, Gram-negative (G) bacteria and fungi showed similar decreasing trends across the land-use gradient, from natural forest to agricultural land. Conversely, Gram-positive (G^+) bacteria showed an increasing trend along the same gradient. The higher microbial and soil chemical properties in the bamboo plantation led to faster ecosystem recovery compared to either agricultural land or degraded lands. Therefore, bamboo plantation could be used for ecosystem recovery and sustaining soil health in response to disturbance, particularly in relation to land-use change in the dry tropics.

KEYWORDS: Soil microbial indicators; Ecosystem restoration; Soil nutrient; Bamboo Plantation; Degraded forest

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1 Introduction

Land-use change and unsustainable resource use have led to an annual global forest cover loss of approximately 0.6% (Hansen et al., 2010). Land-use change, particularly the conversion of natural forest to degraded and agricultural lands, leads to biodiversity loss, the alteration of ecosystem services, and the degradation of soil biological and physico-chemical properties (Ashagrie et al., 2007; Solomon et al., 2002; Tripathi & Singh, 2009). Recent studies have revealed that similar transformations significantly impact soil health and quality (Kotowska et al., 2015; Logah et al., 2010; Málaga et al., 2021). For instance, the expansion of agricultural land such as cacao (Emch, 2003), tea (Solomon et al., 2002), banana (Powers, 2004), oil palm and rubber (Kotowska et al., 2015; Málaga et al., 2021), and khat (Dessie & Kinlund, 2008; Mellisse et al., 2018; Wuletaw, 2018), frequently occurs at the expense of native forest and agroforestry systems, thereby reducing soil carbon and nitrogen stocks in Southeast Asia, Latin America, and East Africa (Bashir et al., 2021; Belete & Yadete, 2023). These changes in soil physico-chemical properties are intrinsically linked to a shift in the soil's biological engine: the microbial community (J. Zhang et al., 2020).

Even though tropical forests can sequester over 200 million tons of carbon each year, and are home to a diverse microbial community, land use change remains a major challenge (Keller et al., 2025; Lan et al., 2021). This challenge is particularly severe in the dry tropics, such as Mirzapur District, where ecosystems are characterized by seasonal water scarcity, higher temperatures, and often inherently lower soil fertility (Ashagrie et al., 2007; Tripathi & Singh, 2009) . These conditions make them highly sensitive to disturbances, and the recovery of such systems is often slow and challenging, creating a risk of permanent desertification. Several strategies have been designed to restore degraded lands. Among the several strategies, multipurpose tree plantation is considered an ideal measure for the restoration of degraded lands (Kumar & Ghoshal, 2017; M. K. Singh & Ghoshal, 2014). Bamboo, a fast-growing perennial, presents a promising candidate, offering both economic benefits and potential ecological restoration services. However, while its economic value is recognized, its capacity to restore soil biological integrity and nutrient cycling in degraded dry tropical landscapes remains critically understudied.

Soil microbes are important factors in terrestrial ecosystems. They drive numerous ecosystem services such as nutrient cycling, conservation of soil function (fertility and structure), and to mitigate global climate change, by acting as carbon sources and sinks, and by generating greenhouse gases (Chandra et al., 2016; Kumar & Ghoshal, 2017; D. M. Singh et al., 2018; Q. Zhang et al., 2016). The composition and activity of microbial communities in the soil are governed by foliage cover, nutrient availability, competition, humidity content, land use practices, and other physico-chemical parameters (Bashir et al., 2021; Belete & Yadete, 2023; N. K. Singh & Rai, 2024). Additionally, microbial properties are highly sensitive to environmental disturbances and frequently respond more rapidly than physical or chemical soil indicators, making them effective early warning signals of land use change, sustainability, and the restoration of ecosystems (M. K. Singh & Ghoshal, 2014; N. K. Singh & Rai, 2024). However, the degree and complexity of land-use-induced variations are highly variable and strongly dependent on the ecosystem. Although the impact of land-use changes on soil microbial community structure and function, and carbon-nitrogen dynamics has been widely studied, limited knowledge exists for the dry tropics, especially with reference to the restoration of degraded lands. Additionally, the specific response of soil microbial communities and carbon-nitrogen dynamics in the distinct geo-climatic context of Barkachha, Mirzapur, remains inadequately quantified. Thus, monitoring changes in microbial community structure and function can offer valuable insights for sustainable land management and ecosystem restoration (J. Zhang et al., 2020).

The present study tested the following hypotheses: (i) land use change alters the concentration of microbial community soil and biomass, and carbon-nitrogen dynamics; (ii) shifting of microbial community structure in terms of PLFA occurs with the land-use change, and (iii) restoration of degraded lands can be achieved through plantation of bamboo. The present study was aimed at estimating the impact of various land-use patterns, i.e., natural forest, degraded forest, agricultural land, and bamboo plantation, in a dry tropical environment in the levels of soil microbial community and biomass, and carbon-nitrogen dynamics. We used a PLFA profiling analysis to quantify the microbial community across four land-use types and related these differences to measured edaphic properties in Mirzapur district in India.

2 Methods and Materials

2.1 Description of the study area

The study area, Barkachha, is in the southwest of Mirzapur District, Uttar Pradesh, along the Robertsganj Highway. Soil samples were collected from the Barkachha area located in Mirzapur district during the dry season. Barkachha is located at 25° 10' N latitude and 82° 37' E longitudes at an average elevation of 80 meters (masl) (Figure 1). It is a city in Uttar Pradesh, India, 650 km from both Delhi and Kolkata, 89 km from Allahabad, and 57 km from Varanasi. It has a population of 233,691 (2011 census). The climate in Bakachha in Mirzapur district is warm. In winter, there is much less rainfall than in summer in the district. The average annual temperature and rainfall are 26°C and 975 mm, respectively. The study area was classified into four sites based on their vegetation cover: Natural Forest (NF), Degraded forest (DF), Bamboo plantation (BP), and agricultural land (AL)(Figure 2). The collected soil samples were immediately brought to the laboratory of the Department of Botany, Institute of Science, Banaras Hindu University (BHU) for further analysis.

Mixed Forest

The forest site was the mixed dry deciduous type dominated by *Acacia nilotica, Tectona grandis, Butea monosperma, Madhuca indica, Dalbergia sissoo, Leucaena leaucocephala, Acacia catechu, Al-*

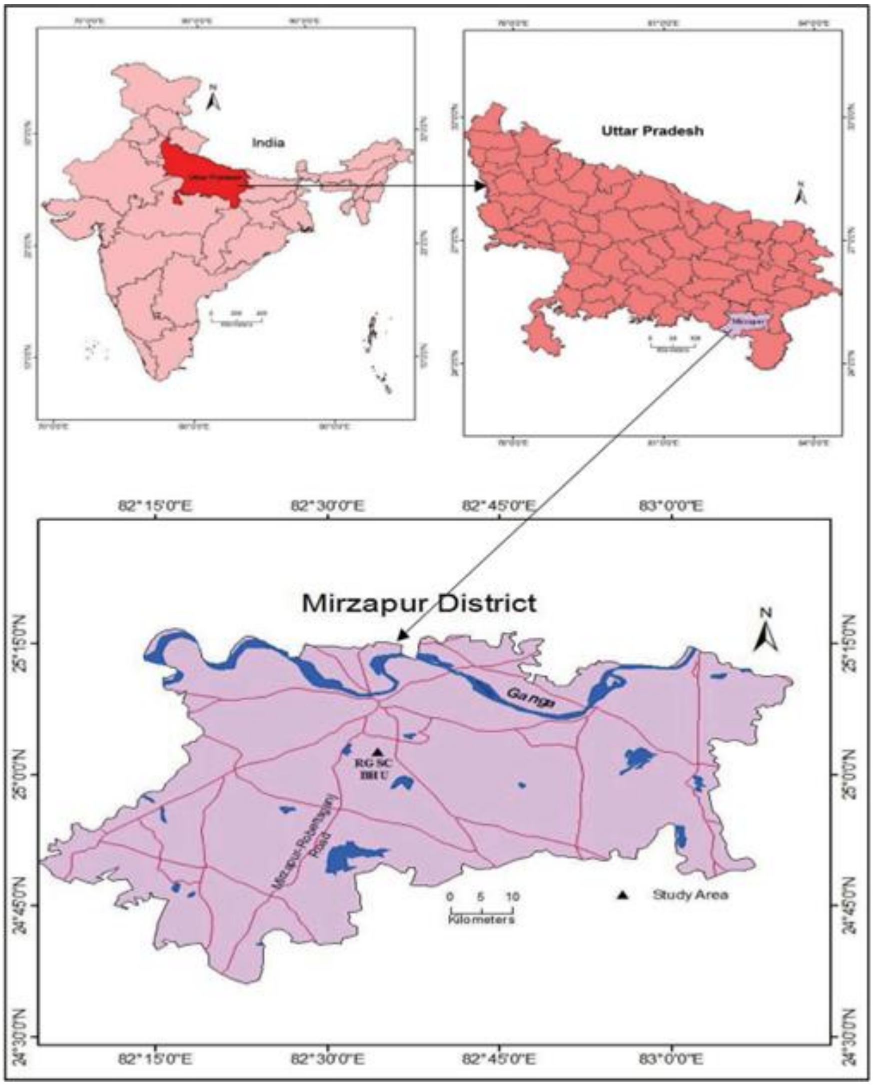

Figure 1: Map showing the location of the Study Area

bizia odoratissima, Boswellia serrata, Nyctanthes arbortristis, with scattered trees of Azadirachta indica Juss and Zizyphus glaberrima Santap. The forest floor was covered with herbaceous vegetation comprising *Ocimum americanum. L., Pisum arvense L., Rhynchosia minima (L.) DC., Cassia sophera(L.) Roxb., Acrocephalus indicus (Burm.f.) Kuntze, Cynodon dactylon (L.) and Oplismenus burmannii Ritz*. The total coverage of the forest area is 500 acres. The forest site is found in Barkachhakalan, Windom Fall Road, 4.8 km, Southwest, Rajiv Gandhi South Campus (RGSC), BHU. The forest site is located at 25° 1’ 41.6994” N latitude and 82° 36’ 40.842” E longitudes (Figure 2A).

Degraded Forest

The degraded forest site was dominated by Z. glaberrima, Chrysopogon fulvus, Heteropogon contortus, Adina cordifolia Roxb., and scattered trees of Bute amonosperma Lamk. Herbaceous vegetation in the degraded forest was dominated by Cassia tora L., Oldenlandia diffusa Roxb., Sporobolus spp., Panicum psilopodium Trin, and Alysicarpus varginalis (Figure 2B).

Agricultural Land

The farmers of the region depend mostly on rain for irrigation, rain-fed farming being the traditional farming practice of the area. Common crops grown are rice, wheat, lentil, chickpea, etc. Horticultural crops grown include guava, mango, custard apple, bael, karonda, etc. The soil of this region is red laterite and very poor in fertility status (Figure 2C).

Bamboo Plantation

The bamboo plantation consisted mostly of Dendrocalamus strictus, Bambusa nutans, B. tundra, and B. hamiltonii species of bamboo. This site was located in Barkachakhurd. The bamboo plantation site is found in Barkachhakalan, 2.9 km, Northwest, Southwest, RGSC, BHU, geographically located at 25° 4’ 28.1244” N latitude and 82° 35’ 24.1146” E longitudes (Figure 2D).

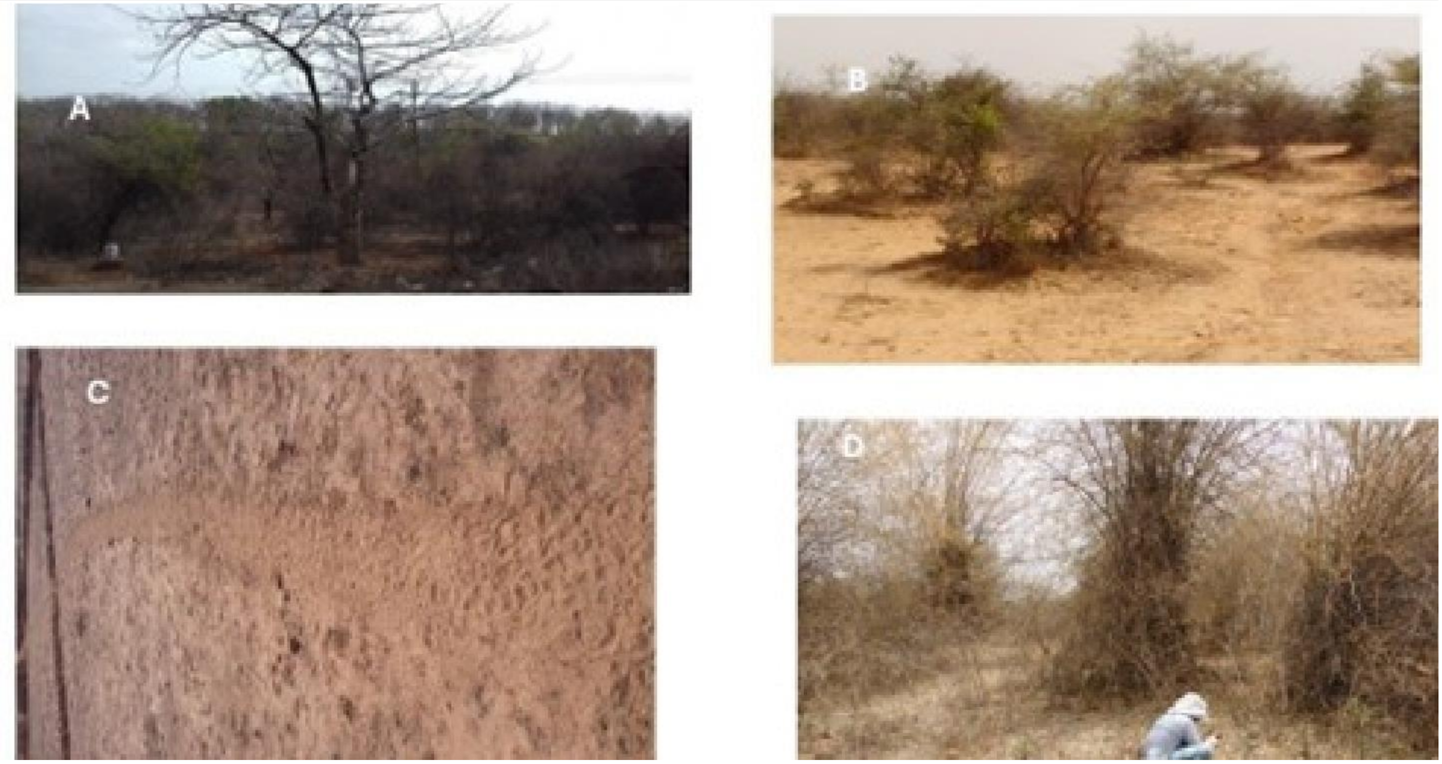

Figure 2: The study land uses (A) Natural Forest (NF), (B) Degraded forest (DF), (C) Agricultural land (AL), and (D) Bamboo plantation (BP) (Photo: Ghosha 2016)

2.2 Soil sampling and processing techniques

Soil samples were collected from the Barkachha area located in Mirzapur district during the dry season. The soil sample was taken from four land use types, namely NF, DF, BP, and AL. The NF was further divided into six sub-sites of 100m x 100m (Figure 3). From each subsite, four soil samples were collected from the corner (i.e., 24 composite soil samples in total from each study site) and mixed to represent the single composite sample to determine the soil microbial community, and soil organic carbon and nitrogen. The same procedure was followed by DF, BP, and AL. The soil samples were collected from one depth (0-15cm) using a core sampler. Then the collected soil samples were immediately brought to the laboratory (approx. 250g) in clean, dry, and sterile polythene bags for microbial properties, and organic carbon and nitrogen analyses (Allen et al., 1974, and Waksman, 1952). Separate plastic bags were used for soil samples for microbial and chemical analyses. Soil processing for organic carbon and nitrogen determination was initiated immediately after collection, whereas samples for microbial analysis were stored at 4 °C until the experiment commenced. The collected soil samples were air dried at room temperature, mixed well, grinded by using a mortar and pestle, and made to pass through a 0.5 mm sieve for soil organic carbon and total nitrogen analysis.

Soil Organic Carbon (SOC) and Total Nitrogen (TN)

The SOC content was analyzed by dichromate oxidation and back titration of unused dichromate (Kalembasa and Jenkinson, 1973), whereas TN concentration was measured by the micro Kjeldahl method (Jackson, 1973) by using a Gerhardt digester and distillation unit.

Microbial Biomass

The microbial biomass carbon (MBC) was estimated by the chloroform fumigation extraction method using purified CHCl3 treatment used by Brookes et al. (1985) and Vance et al. (1987). Microbial biomass nitrogen (MBN) concentration was measured by the micro-Kjeldahl method according to Jackson (1973) by using a Gerhardt digester and distillation unit. Microbial biomass determination involved a series of steps, including incubation, fumigation, extraction, and titration. Fresh soil samples (20 g) were incubated at room temperature in a closed container for 7 days. After incubation, two subsamples were prepared for each soil sample: Sample A (without chloroform/non-fumigated) and Sample B (with chloroform/fumigated) to estimate the microbial biomass. The fumigated and non-fumigated soil samples were extracted with 100 mL of K2SO4. Finally, 8ml and 4ml extracts were used for MBC and MBN analyses. Microbial biomass carbon (μg dry soil) and MBN (μg dry soil) are calculated by the following formulas:

$$MBC = \frac{NFu - Fu}{B} \times 3168 \tag{1}$$

$$MBN = (Fu - NFu) \times 207.407 \tag{2}$$

Where; NFu-non fumigated; Fu-fumugated; B-blank

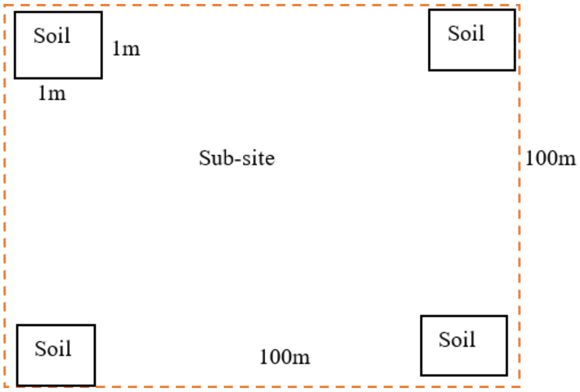

Figure 3: Sample layout for soil chemical and microbial properties

Basal Respiration (BR)

The basal respiration/metabolic activities of the soil microbial community were determined byNamipieri et al. (1990) method.

$$\mu\text{g } CO_2 \text{ oven dry soil/h at } 22^{\circ}\text{C} = \frac{(V_o - V) \times S \times 22 \times 12 \times 1000}{M \times \text{DWt.} \times t \times 44} \quad (3)$$

Whereas; Vo- volume of HCl used for titration of blank (mean of three replicates); V-Volume of HCl used for titration of sample (mean of three replicates); S- the strength of the HCl in normality; M- weight of soil g/sample; dwt- the oven dry weight of 1g sample; t- time of incubation in hrs.

Soil Enzyme

The β-Glucosidase activity was assayed by the method of (Eivazi & Tabatabai, 1988), using the substrate analogue para-nitrophenyl-β-d-glucopyranoside (pNPG). The activity of the enzyme is calculated by the following formula:

$$\text{EA} = \frac{\text{OD}}{\text{CF}} \times 100 + \frac{n(n-1)x^2}{2} \quad (4)$$

Soil Microbial Community Analysis

Soil microbial community was analyzed using phospholipid fatty acid assay (PLFAs) (Willers et al., 2015). The PLFAs include extraction, fractionation, methylation, and chromatography. Phospholipid fatty acids were extracted and quantified from 3g (dry weight equivalent) of soils using a procedure described by Bossio et al. (1998). The microbial community composition in terms of PLFA concentration was determined using the modified Bligh and Dyer (1959) and Willers et al. (2015) methods. Identification of peaks was based on the retention time against known standards (Supelco 37 Component FAME Mix 47885-U and Supelco BAME # 47080-U, Sigma-Aldrich, USA), with the peak area representing the abundance (%) of bacterial PLFAs (sum of gram-positive bacterial (G+) and gram-negative bacterial (G-) PLFAs) and fungal PLFAs.

2.3 Statistical Analysis

Soil organic carbon, total nitrogen, microbial biomass, and PLFA data were summarized, and mean values with standard deviations were calculated. Normality was evaluated with the Shapiro-Wilk test and homogeneity of variances with Levene's test. Analysis of variance (ANOVA) was performed to assess the effects of land use change on SOC, TN, SMB, and microbial community. For significant ANOVA results, Tukey's HSD post hoc (α=0.05) test was applied to determine pairwise differences among land use types. The Pearson correlation method was used to analyze the correlation between MBC, MBN, SOC, and TN. All statistical analyses were carried out using SPSS version 23.0. The figures were generated using Origin version 28. $\alpha = 0.05$ was statistically significant. Mean ±standard error mean was used by the software Statistic 10, shown in tables.

3 Results

3.1 Soil organic carbon and total nitrogen

Soil organic carbon (SOC) and TN differ significantly among the four land-use types (Table 1). Soil organic carbon ranged from 0.435% to 0.84%, while TN varied between 0.014% and 0.123%, with mean values of 0.635% and 0.0685%, respectively. The highest SOC and TN contents were observed in the NF, followed by BP, with the lowest values recorded in AL. Specifically, the NF showed the highest SOC (0.84±0.054%) and TN (0.123±0.013%), whereas the AL showed the lowest SOC (0.435±0.042%) and TN (0.014±0.0016b%). Analysis of variance indicated that soil TN in NF was significantly higher (α =0.05) than in the other land-use types, while the difference in SOC between the NF and BP was not statistically significant.

Table 1: Soil organic carbon (SOC), soil total nitrogen (TN), Microbial biomass carbon (MBC), Microbial biomass nitrogen (MBN), and soil basal respiration (BR) under different land use types

	Land use type					
	NF	DF	BP	AL	LSD	P-value
SOC (%)	0.84 ± 0.054^a	0.448 ± 0.113^b	0.72 ± 0.074^a	0.435 ± 0.042^b	0.21	< 0.001
TN (%)	0.123 ± 0.013^a	0.027 ± 0.003^b	0.033 ± 0.0034^b	0.014 ± 0.0016^b	0.021	< 0.001
MBC (μg/g)	570.65 ± 35.05^a	233.94 ± 60.36^b	479.03 ± 21.48^a	225.59 ± 20.84^b	114	< 0.001
MBN (μg/g)	84.21 ± 3.186^a	48.95 ± 2.506^b	63.05 ± 4.281^c	43.14 ± 1.784^b	9.23	< 0.002
BR (μg CO_2)	3.64 ± 0.064^a	2.69 ± 0.11^b	3.37 ± 0.067^a	2.56 ± 0.11^b	0.29	< 0.003
β-glucosidase (μg PNP g^{-1} dry soil h^{-1})	809.68 ± 39.7^a	380.50 ± 17.02^c	577.28 ± 84.39^b	492.88 ± 58.13^c	181.35	< 0.001
MBC/MBN	6.77	4.78	7.59	5.23		

Values are Mean ± SE. Different superscript letters (a, b, c) indicate significant differences among mean values at $\alpha = 0.05$ level.
(Source: Authors' own findings)

3.2 Microbial biomass

In this study, the values of MBC across the four land-use types ranged from 146.21 to 619.67μg/g soil, with mean values of 377.3μg/g soil. The MBC and MBN were highest in NF, with a mean of 570.65μg/g and 84.21μg/g, respectively (Table 1). While the BP showed a moderate decrease in MBC and MBN (mean 479.03μg/g, 63.05μg/g), DF and AL lands exhibited substantially lower levels, with mean values of 233.94, 48.95μg/g and 225.58, 43.14μg/g, respectively. Analysis of variance revealed that MBC in the NF and BP plantation was significantly higher than in AL and DF (α =0.05). However, there was no significant difference in MBC between NF and BP, nor between AL and DF.

3.3 Basal respiration (BR)

The values of basal respiration are presented in Table 1. Soil basal respiration (BR) across the four land-use types ranged from 2.36 to 3.75 CO_2/g soil with a mean value of 3.07 CO_2/g soil. Basal respiration (BR) was significantly higher in NF (3.64⊠μg CO_2/g soil), followed by BP (3.37⊠μg CO_2/g soil). In contrast, DF (2.69⊠μg CO_2/g soil) and AL (2.56⊠μg CO_2/g soil) exhibited significantly lower respiration rates (Table 1).

3.4 Enzyme activity

The results of b-glucosidase activity varied significantly among the land uses, and the activity ranged from 350.559 to 872.07µg PNP g^{-1} dry soil h-1, with a mean value of 565.08µg PNP g^{-1} dry soil h-1 (Table 1). The b-glucosidase activity under NF ranged from 735.88 to 872.07µg PNP g^{-1} dry soil h-1, with a mean value of 809.69µg PNP g^{-1} dry soil h-1; for BP, the values ranged from 408.55 to 665.24µg PNP g^{-1} dry soil h-1, with a mean of 577.29µg PNP g^{-1} dry soil h-1; and for AL, the values ranged from 432.93 to 609.13μg/g, with a mean value of 492.88μg/g soil. FFor DF, it ranged from 350.59 to 409.54µg PNP g^{-1} dry soil h-1, with a mean of 380.50µg PNP g^{-1} dry soil h-1. Analysis of variance revealed that b-glucosidase activity in the NF was significantly higher (α =0.05) than in all other land-use types. However, there was no significant difference in b-glucosidase activity between DF and AL.

3.5 Soil Microbial PLFA Profiles

The composition and structure of the soil microbial community, as determined by phospholipid fatty acid (PLFA) analysis, varied significantly across the four land-use types (Table 2). The highest total PLFA was found in NF (73.55 nmol g^{-1}), followed by BP (63.23 nmol g^{-1}), DF (57.38 nmol g^{-1}), and AL (52.75 nmol g^{-1}). The trend of total PLFAs across all land-use types was in the order: NF BP DF AL. In terms of microbial groups, G bacteria and fungi were higher in NF, followed by BP, DF, and AL. However, G+ bacteria followed the reverse trend; NF< BP <DF< AL. Analysis of variance revealed that G⊠ bacteria differed significantly across all land-use types, whereas the pattern was not consistent for G⊠ bacteria and fungi. The ratio of G+/G- bacteria increased from NF to AL as the proportion of G+ bacteria rose, with a significant difference observed in AL. Conversely, the F/B ratio decreased along the same gradient, showing significant differences between NF and AL, NF and DF, and BP and AL.

Correlation

Pearson's coefficient correlation analysis revealed strong positive relationships among all measured soil variables (Table 3). Soil BR was highly correlated with SOC and MBC (r= 0.997**). MBC also showed near-perfect correlations with SOC (r = 1.00**) and strong associations with MBN (r = 0.955*). β-glucosidase activity was strongly correlated with SOC (r = 0.91), MBC (r = 0.903), STN (r = 0.901), and MBN (r = 0.924). Soil TN showed slightly lower but still strong correlations with carbon-related variables and MBN; r values ranged from 0.811 to 0.901.

Table 2: The amount of total phospholipid fatty acids (PLFAs), Gram-positive bacterial, Gram-negative bacterial, and fungal PLFAs (mg/g DW) under four land uses.

	Land use				
	NF	BP	DF	AL	P -value
G^-	37.43 ± 2.21^a	22.51 ± 1.75^b	15.78 ± 0.85^c	5.29 ± 0.477^d	< 0.001
G^+	15.61 ± 1.25^a	25.17 ± 2.02^b	30.64 ± 0.82^b	39.4 ± 3.73^c	< 0.001
Fungi	20.49 ± 1.24^a	15.55 ± 1.14^b	10.96 ± 0.86^c	8.06 ± 0.59^c	< 0.001
Total PLFA	73.55 ± 2.85^a	63.23 ± 1.8^b	57.38 ± 1.02^{bc}	52.75 ± 4.04^c	< 0.001
G^+/G^-	0.42 ± 0.01^a	1.12 ± 0.18^a	1.94 ± 0.15^a	7.44 ± 1.08^b	< 0.001
F/B	0.392 ± 0.046^a	0.326 ± 0.02^{ac}	0.236 ± 0.02^{cb}	0.18 ± 0.01^b	< 0.001

Values are Mean ± SE (mg/g dry weight). G^-: Gram-negative bacteria, G^+: Gram-positive bacteria, F/B: Fungi to Bacteria ratio. Different superscript letters within a row indicate significant differences at $\alpha = 0.05$ level.

Table 3: Correlation matrix for physical, chemical, and microbiological characteristics of soils from different land uses.

Soil variable	**BR**	**SOC**	**MBC**	**B-glucosidase**	**STN**	**MBN**
SOC	0.997^{**}	1				
MBC	0.997^{**}	1.000^{**}	1			
B-glucosidase	0.877	0.91	0.903	1		
STN	0.815	0.828	0.811	0.901	1	
MBN	0.960^{*}	0.963^{*}	0.955^{*}	0.924	0.944	1
BR	1	0.997^{**}	0.997^{**}	0.877	0.815	0.960^{*}

SOC: Soil organic carbon; STN: Soil total nitrogen; MBC: Microbial biomass carbon; MBN: Microbial biomass nitrogen; BR: Soil basal respiration.
*Significant at $\alpha = 0.05$, **Significant at $\alpha = 0.01$.
(Source: Authors' own findings)

4 Discussion

This study demonstrated that land-use change significantly affects soil microbial communities, microbial biomass, basal respiration, and the levels of soil SOC and TN in the dry tropics of India (Fig. 2, Tables 1,2, and 3). The conversion of native ecosystems, such as natural forests, to other land uses, particularly agricultural land, had a negative impact on both soil chemical and microbial properties in the study area. This agrees with the results of the studies conducted by Chen et al. (2010), Q. Zhang et al. (2016), and Zhou et al. (2002) who stated that land-use change alters soil chemical and biological properties by influencing key ecological processes.

Soil organic carbon (SOC) and TN are considered to be among the major attributes of soil fertility and agricultural sustainability (Paltineanu et al., 2024). The present results suggest that the conversion of NF to AL leads to significant declines in SOC and TN levels. The trend of SOC and TN across all land-use types was in the order: NF BP DF AL (Table 1). These findings are consistent with previous studies conducted in similar agroecological settings (Gol, 2009; Iqbal et al., 2014; Pereira et al., 2013). Another study also reported that native forest had higher SOC than pasture and agricultural lands, but the difference was not significant (Mazzetto et al., 2016). The superiority of SOC and TN in the NF relative to BP, DF and AL was associated with the regular addition of plant litter/greater total litter (above and below ground tree parts), root exudates and minimal anthropogenic disturbance, including the absence of tillage, low grazing pressure and high plant biodiversity (Iqbal et al., 2014; Srivastava & Singh, 1991). Additionally, the higher SOC and TN in BP, as compared to DF and AL were associated with the roughly twice as high leaf litter pool and fine roots in BP due to the bamboo ecosystem. The degradation of natural forests significantly decreased SOC and TN. The disturbances associated with deforestation might have led to a loss of vegetation, which in turn has resulted in land degradation, erosion, and subsequently, considerable losses of SOC and nutrients (Tripathi & Singh, 2009; Xiangmin et al., 2014). The least SOC and TN in AL, as compared to DF, could be due to continoues tillage, removal of crop residue and intensive grazing, all of which accelerate native soil organic matter oxidation by destroying soil aggregates and exposing newer sites to microbial attack, which in turn results in the loss of soil organic carbon (Chaudhary et al., 2008; Saha et al., 2010; S. Singh & Ghoshal, 2006; Tripathi & Singh, 2009).

Changes in land-use patterns from NF to BP, DF, and AL resulted in 1.19, 2.53, and 2.44-fold decrease in the level of MBC, respectively. Similarly, the MBN in NF was found to be higher and significant with other land use types except BP (Table 2). These findings are consistent with previous studies (Kara & Bolat, 2008; Q. Zhang et al., 2016). S. Singh et al. (2025) reported that a closed mixed Sal Forest had significantly higher MBC than the open mixed Sal Forest across the soil profile, with a strong seasonal effect. Lepcha and Devi (2020) also found that the annual mean MBC was highest in the forest (455.03μg/g), followed by cardamom agroforestry (392.86μg/g) and paddy cropland (317.47μg/g). The elevated MBC and MBN in NF soils are likely a result of increased input of soil organic matter, more diverse organic inputs, and enhanced biological processes. For instance, mixed forest systems have been shown to produce higher-quality litter, support faster litter decomposition, and enhance soil nutrient mineralization compared to other land use types. In addition, high levels of root biomass and root exudates in natural forests contribute to greater microbial activity and biomass (Bhuyan et al., 2013; Kara & Bolat, 2008). Similarly, increased availability of resources such as soil organic matter, more diversified organic matter input, and related processes are believed to be the cause of the higher MBC and MBN in diversified ecosystems. Bamboo plantation increased the MBC and MBN by 50% and 14%, respectively, over the DF and AL. Such arise in MBC and MBN indicate the trend of restoration of degraded land towards the NF occurring with bamboo plantation. Similarly, (Cheng et al., 2013) reported that the increase in the microbial biomass may be ascribed to the accumulation of soil organic carbon. The lower microbial biomass in DF and AL might be attributed to reductions in the vegetation cover, leading to lower levels of litter input, root necromass, and root exudates to the soil (M. K. Singh & Ghoshal, 2014).

Soil basal respiration (BR), quantified by the amount of CO2 produced /O2 consumed, varied significantly across the different land-use types. Similar findings were reported by. Soil BR in BP was 2% lower than NF, but 5% and 6% higher than DF and AL, respectively. The analysis of variance confirmed that BR in NF and BP were not significantly different from each other but were both significantly higher than in AL and DF. The similarity of the BR values between NF and BP, and AL and DF, suggested similar microbial activity (Pereira et al., 2013). The higher soil BR in NF and BP indicates the higher soil microbial activity due to the permanent and continuous addition of a source of labile organic matter to the soil and the consequent stimulation of heterotrophic microorganisms. Additionally, higher soil respiration is indicative of high biological activity, suggesting rapid decomposition of organic residues that make nutrients available for plant growth (Pereira et al., 2013) (Araújo et al., 2009). In contrast, the lower BR in AL and DF may reflect reduced microbial biomass or substrate availability, possibly due to soil degradation, lower organic inputs, or frequent soil disturbances such as tillage. This pattern aligns with the understanding that soil respiration is a sensitive indicator of soil biological activity and health, and its decline signals deteriorating soil quality under intensified or unsustainable land use.

This study demonstrated that changes in land-use impact the microbial community composition and enzyme activity under tropical conditions. The b-glucosidase activity in the NF was significantly higher than and significantly from other land use types at $p<0.05$. The trend of b-glucosidase activity across all land-use types was in the order: NF BP DF AL. This result is consistent with previous studies Bandick and Dick (1999) and Roldan et al. (2005). Sarto et al. (2020) reported that the higher β-glucosidase activity from ICLS (integrated crop-livestock system) as compared to native savanna, pasture, and maize. The higher β-glucosidase activity in the natural ecosystem was associated with the composition and quality of plant residues, because β-glucosidase is more active with less-complex residues (Lopes et al., 2013, 2015). The higher β-glucosidase activities in NF may be the consequence of both microbial growth and stimulation of microbial activity by enhanced resource availability (increase in the input of organic matter in the soil and improvement of soil physical properties), as well as of changes in microbial community composition (Bhattacharyya et al., 2005; Kong et al., 2007). On the other hand, the increment of enzyme activity in BP as compared to DF and AL may be due to the addition of leaf litter and root exudates from bamboo, which leads to stimulating microbial metabolism and decomposition rate (Masciandaro et al., 2003). Unlikely, the β-glucosidase activity was decreased as compared to NF may be due to the thinner canopy and greater soil exposure may have resulted in greater temperature and soil moisture fluctuation, as well as other factors that influence the decrease in microbial activity (Pereira et al., 2013).

The results of the present study showed that NF exhibited the highest microbial abundance in terms of total PLFAs, compared to BP, DF, and AL (Table 2). This finding is consistent with previous research (Mishra et al., 2024; Steenwerth et al., n.d.; Torsvik & Øvreås, 2002; Wang et al., 2025). For instance, García-Orenes et al. (2013) reported that native forest had the highest microbial PLFA concentration compared to various agricultural management systems in the Mediterranean Agro-Ecosystem. Similarly, Q. Zhang et al. (2016) found that higher microbial PLFA biomass from an afforested area as compared with cropland and uncultivated soils. In line with these findings, Steenwerth et al. (n.d.) also observed greater PLFA content in grasslands than in cultivated soils. These consistent patterns across studies suggest that natural and less-disturbed ecosystems support richer and more active microbial communities than intensively managed or degraded systems. The variation of total PLFA among the land use patterns could be due to soil pH, plant species diversity (Guo et al., 2016), and soil carbon and nitrogen availabilities (Q. Zhang et al., 2016). The higher total microbial PLFA in NF and BP is possibly attributed to increased litter input and soil organic carbon and nitrogen content. In contrast, the lower total microbial PLFA in DF and AL could be due to physical disturbance, mainly tillage, and limited levels of carbon and nitrogen input (M. K. Singh & Ghoshal, 2014).

Land-use change not only influenced the overall microbial community but also affected the composition of specific microbial taxonomic groups (Guo et al., 2016; Mishra et al., 2024; Nagendran et al., 2014). In this study, three major soil microbial groups were considered: Gram-negative bacteria (G-), Gram-positive bacteria (G+), and fungal communities. The abundance of G- G-bacteria and fungal communities declined sharply along the land-use gradient from NF to AL, indicating a reduction in microbial diversity with increasing disturbance. In contrast, G+ bacteria exhibited a reverse trend, increasing in relative abundance from NF to AL. The same result has been reported by Kumar and Ghoshal (2017), Mishra et al. (2024), Steenwerth et al. (n.d.), and Torsvik and Øvreås (2002). Similar findings were reported by Bossio et al. (2005) and Moore-Kucera and Dick (2008), who observed an increase in G+ bacterial dominance following deforestation and the conversion of forest to cropland.

The relatively higher abundance of G– bacteria in NF may be attributed to the presence of diverse vegetation and continuous organic matter inputs that provide labile carbon substrates, which favor fastidious microorganisms (Moore-Kucera & Dick, 2008). In contrast, AL and DF, characterized by reduced litter input, physical disturbance (tillage), and greater environmental stress (e.g., fluctuating moisture and temperature), tend to favor G+ bacteria, which are more resistant to nutrient limitation and desiccation (Boylen & Ensign, 1970). Additionally, G– bacteria were associated with simple carbon compounds (alkyls), whereas G+ bacteria were more strongly associated with more complex carbon forms (carbonyls) (Fanin et al., 2019). The drop in the fungal community in DF could be because filamentous fungi are more sensitive to physical disturbance than single-celled bacteria (Kabir et al., 1999; Mishra et al., 2024). In AL, physical disturbance, substantially tillage, destroyed fungal mycelium networks, and the combination of mechanical destruction, soil contraction, and reduced severance volume inclusively led to the smallest fungal PLFA values (Bardgett et al., 2001; García-Orenes et al., 2013). This might be due to changes in litter quantity and quality, which conceivably accounts for the changes in fungal PLFAs (Denef et al., 2009).

The fungal: bacterial PLFAs (F:B) ratio is used to evaluate the responses of the soil microbial community to soil carbon and nitrogen dynamics and environmental changes (Fanin et al., 2019; Q. Zhang et al., 2016). The G/G ratio increased with land-use disturbance, from 0.42 in natural forest to 7.44 in agricultural land, indicating a shift toward microbial communities more tolerant of environmental stress. Likewise, the fungi-to-bacteria (F/B) ratio declined from 0.386 in NF to 0.18 in AL, suggesting a transition from fungal-dominated communities associated with stable carbon-rich systems to bacterial-dominated communities with faster nutrient cycling and reduced carbon retention. This result is consistence with a former study (García-Orenes et al., 2013), the ratio of bacteria: fungi was higher in wild forest coverage and land abandoned systems, as well as in the soil treated with oat straw. These patterns collectively highlight the adverse effects of land-use change on microbial community composition, soil biological functioning, and ecosystem resilience.

According to Oyedele et al. (2015), MBC and MBN were significantly correlated with the SOC and TN. In this study, on average, 95% of the microbial biomass and activities were governed by the SOC and TN (Table 3). The significant positive relations between the soil MBC and SOC agree with earlier reports by Bhuyan et al. (2013), Cheng et al. (2013), Makova et al. (2011), and Yang et al. (2010). This might be due to microbial biomass concentration depending on the organic matter availability to microbial activity (Anderson & Domsch, 1989); however, Insam et al. (1989) found no correlation between the biomass carbon and organic carbon. Similarly, SOC was significantly correlated to TN Bhuyan et al. (2013), Cheng et al. (2013), Kara and Bolat (2008), and Yang et al. (2010), while TN was strongly related to MBN agrees with the results by (Yang et al., 2010). These results indicate that MBN levels in the soils were determined by SOC and TN (Adeboye et al., 2011). The results of many studies showed a close correlation between MBC and SOC or TN because most microorganisms are heterotrophic and their distribution and biological activity often depend on organic matter (Kara & Bolat, 2008; M. K. Singh & Ghoshal, 2014; Xiangmin et al., 2014). Several studies have found strong correlations between MBN and TN (Anderson & Domsch, 1989; Insam et al., 1989).

5 Conclusions

This study demonstrated that land-use change significantly affects soil microbial biomass, SOC, and TN contents in the study area. The most severe impacts of natural forest conversion were observed in the DF and AL, where soil PLFA, microbial biomass, enzyme activity, SOC, and TN levels were the lowest. Following the NF, the BP exhibited higher levels of SOC, TN, BR, β-glucosidase activity, microbial biomass, and PLFA content, indicating a healthier and more functionally diverse soil ecosystem, which favoured the restoration of degraded forests toward natural forests. Significant variations in microbial PLFA composition and biomass among land-use types suggest that these parameters can serve as reliable indicators of ecosystem recovery. Based on the higher soil PLFA content, microbial biomass, and faster recovery rates, it is suggested that bamboo plantation could be adopted as a major strategy for restoring degraded lands in the dry tropics.

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Availability of data and materials

All data generated or analysed during this study are included in this manuscript

Competing interests

The authors declare that they have no conflicts of interest.

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