Microbial Population Dynamics Along a Toposequence in the Southern Guinea Savannah Zone of Nigeria

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ABSTRACT
A study was carried out at the Soil Science Laboratory of the School of Agriculture and Agricultural Technology, Federal University of Technology, Minna situated at Bosso in the month of June, 2009. The aim was to evaluate the population of bacteria, fungi and actinomycetes along a toposequence under four different land use positions (Teak, Gmelina, Cashew and Fallow) at three soil depths (0 - 5 cm,
5 -10 cm, 10 - 15 cm) representing a 4 x 3 factorial experiment in a complete randomized design (CRD). Soil samples were collected with auger and sterilized after each collection. Soil samples from the same position and depth were bulked, mixed and labeled. One part was air dried for physico-chemical properties while the other part was refrigerated for microbial counts using the plate count methods. Results revealed that the interactive effect of land use and depth significantly affected microbial counts (cfu x 10^n/g soil) at P = 0.05. Bacterial count (cfu x 10^8/g soil) and fungi count (cfu 10^4/g soil) decreased with depth in all the land uses. Fallow soils recorded the highest bacterial count, followed by Teak, Cashew and Gmelina in that sequence. Similarly, Fallow soils recorded the highest fungi count, followed by Teak, Gmelina and Cashew in that order. The trend observed for actinomycetes count (cfu x 10^7 / g soil) was same as those for bacteria and fungi counts, except that Gmelina soil was higher in actinomycetes count than Cashew soil. Present study clearly shows that land uses have significant effect on microbial population. Further studies should be carried out to include other forms of land uses in order to detect detrimental ecosystem changes and possibly prevent further degradation.

Keywords: Land use systems, Guinea savanna, Soil microbes.

1.0 Introduction

The advent of molecular genetics tools in microbial ecology has shown that we know only a very small part of the diversity of the microbial world. Much of this unexplored microbial diversity seems to be part of the apparently high amount of the yet uncultured bacteria. New direct methods, independent from cultivation, based on the genotype and phenotype of the microbes allow a deeper understanding of the composition of microbial communities. Nevertheless, the conventional methods of
culturing microbial organisms have remained relevant in elucidating our understanding of changes in microbial diversity due to variation in land-use and management practices. Some studies demonstrated clear effect of changes in farm management of a site on the total microbial community structures. They found a higher diversity in soil which was under organic farming management.

The number of bacteria in soil is influenced primarily by the amount and quality of food available. Other factors affecting their numbers include physical factors (moisture and temperature), biotic factors (predation and competition), chemical characteristics of the soil (acidity, dissolved nutrients and salinity). A similar range of fixed factors (like climate, stoniness, mineralogy, texture, cultivation) has been identified controlling the maximum potential of soil organic matter content (Siwana and Lucas, 2002). The number of microbial organisms varies with the habitat in which they are found. Despite these variations, there are a few generalization that can be made, for example, cultivated fields are generally lower than undisturbed native lands in numbers of soil organisms (Zelles *et al.*, 1996).

The current trend in global agriculture is to search for highly productive, sustainable and environmentally-friendly cropping systems (Crew arid Peoples, 2004) that do not only increase crop yield but also maintain soil health. For example, monocultures or even common crop rotations greatly reduce the number of species and so provide a much narrower range of plant material and rhizosphere environment than nature provides in the forest or grassland(Crew arid Peoples,2004). The main tropical cropping system is inter-cropping, where inter-specific competition or facilitation between plants may occur (Vandermer, 1989; Zhang *et al*., 2003). In such crop mixtures, the yield increases are not only due to improved nitrogen nutrition, but also to other causes (Connolly, *et al.,* 2001). Many of unknown and less researched processes occur in the rhizosphere of mixtures (Zhang *et at.,* 2003). So far, however, little attention has been paid to rhizosphere effect on crops grown in

mixtures, where interaction between different organisms is maximal (Connolly *et al.,* 2001).

The data on soil microorganism in several tropical soils are very limited and grossly underestimated (Ayanaba and Sanders, 1981). Most of the available reports did not consider the effect of some soil properties, cropping history, cropping system and waste disposal on microbial population (Isirimah *et al.,* 2006). In view of this, a study was conducted to estimate the microbial population in different cropping systems and to determine which cropping system has the highest microbial population distribution.

2.0 Materials and Methods

The research was carried out in the Soil Science Laboratory of the School of Agriculture and Agricultural Technology, Federal University of Technology, Minna in the month of June, 2009. The experimental area is underlain by undifferentiated Basement Complex rocks (FDALR, 1990). Physico-chemical properties of the soils were determined using the methods of IITA (1989). The exchangeable Ca^{2+}. Mg^{2+} and K^{+} were low. The experiment was a 4 x 3 factorial experiment in a complete randomized block (CRD) with four land use systems of Gmelina, Teak, Fallow and Cashew and three soil depths of 0-15, 5-10, 10-15 cm. Microbial populations were determined by soil dilution plating technique using agar media. For each of six sub-samples from each composite soil sample, 10 g of soil was weighed and added to 90ml sterile deionized water, thoroughly stirred and serially diluted and plated on 1% nutrient agar for total bacteria counts and potato dextrose agar (PDA) with 1mg ml^{-1} of streptomycin for total fungal counts (Harrigan and Mc Cance, 1990). Serial dilution was 10- fold up to 10^{-7} dilution and aliquots (0.5 ml) of 10^{-5}, 10^{-6} and 10^{-7} dilutions were used for plating. Inoculated plates were incubated at 28ºC for 3 and 10 d prior to the enumeration of viable colonies of bacteria and fungi, respectively.

Statistical Analysis

Analysis of variance (ANOVA) was used to assess treatment difference. Least significant difference (LSD) was used to separate means where significant differences were observed at p=0.05 probability level.

Table 1: Chemical Properties of Soil and their Relationship with Different Land-Use Systems

Depth (cm)	m	pH $CaC1_2$	Acidity ($cmol\,kg^{-1}$)	OC ($g\,kg^{-1}$)	K ($cmol\,kg^{-1}$)	Na ($cmol\,kg^{-1}$)	Ca Mg	P ($mg\,kg^{-1}$) ($cmol\,kg^{-1}$)	Ca^{+} ($cmol\,kg^{-1}$)	N ($g\,kg^{-1}$)
					Teak					
0-5		5.93^{e}	6.40^{c}	13.80^{bc}	0.89^{c}	0.51^{cd}	23.47^{a}	37.33^{a}	7.47^{a}	3.20^{ab}
5-10		6.03^{d}	5.67^{cde}	12.50^{c}	3.32^{a}	0.31^{a}	18.29^{c}	22.53^{de}	5.20^{c}	2.80^{ab}
10-15		6.10^{c}	4.67^{def}	13.80^{bc}	0.55^{d}	0.63^{b}	22.20^{b}	36.17^{a}	6.60^{b}	3.10^{ab}
					Gmelina					
0-5		5.94^{e}	3.33^{f}	15.40^{ab}	0.48^{de}	0.87^{b}	2.87^{b}	19.50^{e}	4.87^{e}	3.00^{ab}
5-10		6.85^{f}	6.00^{cd}	12.60^{c}	1.96^{b}	0.19^{f}	22.40^{b}	32.67^{abc}	2.80^{d}	2.60^{ab}
10-15		6.07^{cd}	9.33^{ab}	12.90^{c}	0.83^{c}	0.39^{e}	14.00^{e}	28.37^{abcd}	1.27^{e}	1.70^{c}
					Cashew					
0-5		4.73^{f}	10.00^{a}	13.60^{bc}	0.48^{de}	0.27^{b}	21.87^{b}	31.50^{abc}	7.40^{ab}	3.30^{ab}
5-10		5.44^{g}	4.50^{ef}	13.60^{bc}	0.33^{f}	0.30^{gh}	16.80^{d}	23.83^{cde}	7.60^{a}	2.60^{ab}
10-15		5.42^{g}	6.00^{cd}	9.40^{d}	0.28^{f}	0.49^{d}	22.20^{b}	33.83^{ab}	6.87^{ab}	2.50^{ab}
					Fallow					
0-5		6.44^{a}	8.00^{b}	14.40^{bc}	0.38^{ef}	0.41^{e}	14.08^{e}	26.13^{cde}	5.27^{c}	3.50^{a}
5-10		6.22^{b}	9.00^{ab}	17.00^{a}	0.48^{de}	0.35^{f}	14.53^{e}	32.67^{abc}	4.67^{c}	2.50^{c}
10-15		5.26^{h}	5.33^{cde}	16.50^{a}	0.35^{ef}	0.54^{c}	13.33^{f}	31.97^{abc}	2.80^{d}	2.60^{ab}

Mean with the same letter are not significantly different $p < 0.05$

Table 2: Physical Properties of Soil and their Relationship with Different Land-Use Systems

Depth (cm)	Sand (g kg^{-1})	Silt (g kg^{-1})	Clay (g kg^{-1})	Textural Class	Moisture Content (%)
			Teak		
0 - 5	700^{ab}	200^{ab}	100^{cd}	Sandy loam	4.02^{b}
5-10	720^{a}	170^{abc}	110^{cd}	Sandy loam	3.09^{c}
10-15	680^{b}	180^{ab}	140^{a}	Sandy loam	4.49^{b}
			Gmelina		
0 - 5	700^{ab}	210^{ab}	90^{d}	Sandy loam	2.92^{cd}
5-10	680^{b}	200^{ab}	120^{abc}	Sandy loam	2.88^{cd}
10-15	710^{a}	170^{bc}	1 20^{abc}	Sandy loam	2.64^{de}
			Cashew		
0 - 5	710^{ab}	170^{abc}	120^{abc}	Sandy loam	3.20^{c}
5-10	700^{ab}	170^{bc}	130^{ab}	Sandy loam	3.95^{b}
10-15	720^{a}	140^{c}	140^{a}	Sandy loam	4.46^{a}
			Fallow		
0 - 5cm	700^{ab}	200^{ab}	100^{bcd}	Sandy loam	2.28^{e}
5-10cm	720^{a}	170^{bc}	110^{bcd}	Sandy loam	1.25^{e}
10-15cm	700^{ab}	170^{abc}	130^{abc}	Sandy loam	1.79^{f}

Mean with the same letter are not significantly different p <0.05

Table 3: Relationship between soil physico-chemical properties and microbial population. (n=10^n in bact, fungi and Act = 10^8, 10^4, 10^7).

	Bact	Fungi	Actino	PHC	Acid	OC	MO	K	Na	CaMg	P	Ca	Sand	Silt	Clay	
Bact		0.79**	0.58*	0.18	0.30	0.35*	-0.25	-0.12	-0.003	-0.061	0.06	0.31	0.102	0.36*	-0.45	0.47**
Fungi			0.60**	0.34*	0.29	0.41*	-0.43	-0.29	0.01	-0.29	0.028	0.07	0.12	0.32	-0.33*	0.22
Act				0.29	0.10	0.21	-0.24	-0.05	0.07	-0.03	-0.18	0.15	0.03	0.39*	-0.42*	0.38*
PHC					-0.06	0.16	-0.20	0.23	0.18	-0.23	-0.12	-0.28*	-0.07	0.31*	-0.28	-0.037
Acid						0.05	-0.39*	-0.10	-0.51**	-0.31	0.25	-0.16	0.32*	-0.17	-0.03	-0.14
O.C							0.61**	-0.24	0.21	-0.42*	-0.10	-0.20	-0.04	0.29	-0.32	0.10
MO								-0.01	-0.39	0.07**	0.13	0.61**	-0.19	-0.15	0.37*	0.18
K									0.39*	0.14	-0.20	-0.21	-0.04	0.13	-0.27	0.05
Na										0.19	-0.09	0.07	-0.08	0.19	-0.18	0.15
CaMg											0.23	0.51**	-0.27	0.17	-0.01	0.31
P												0.13	-0.09	-0.16	0.32*	0.04
Ca													0.0005	-0.10	0.17	0.52**
Sand														0.64**	-0.18	-0.27
Silt															-0.58**	0.29
Clay																-0.01
N																

Ns = Not significant; ** Significant at $p < 0.01$; * Significant at $p < 0.05$

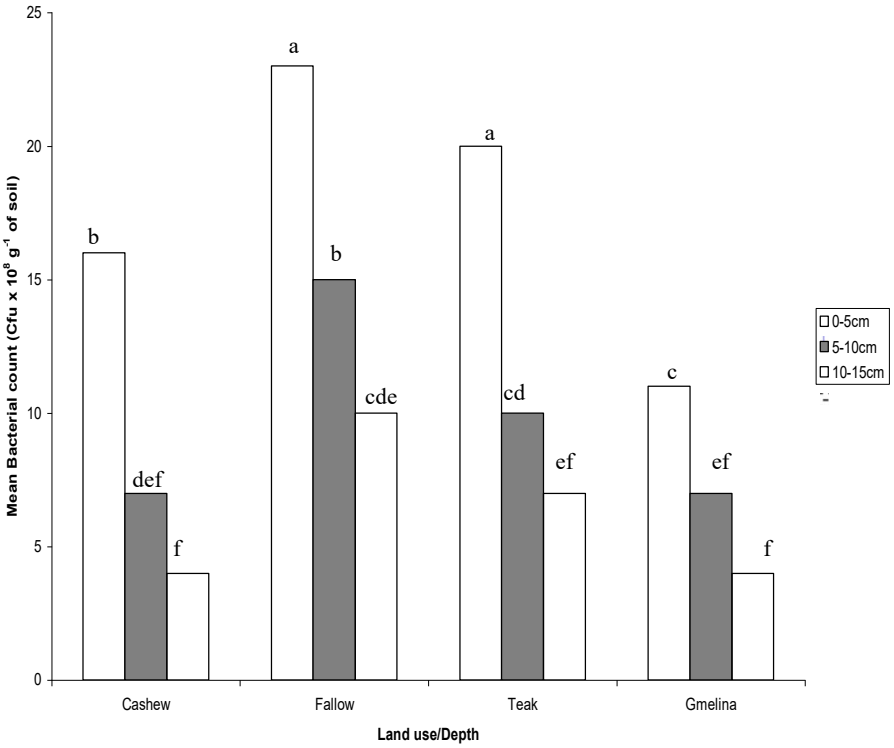

Fig. 1: Bacterial Population Count (Cfu x 10^8 g^{-1} of soil) as affected by land use systems at different soil depths.

Bars of the same depths with different letters are significantly different.

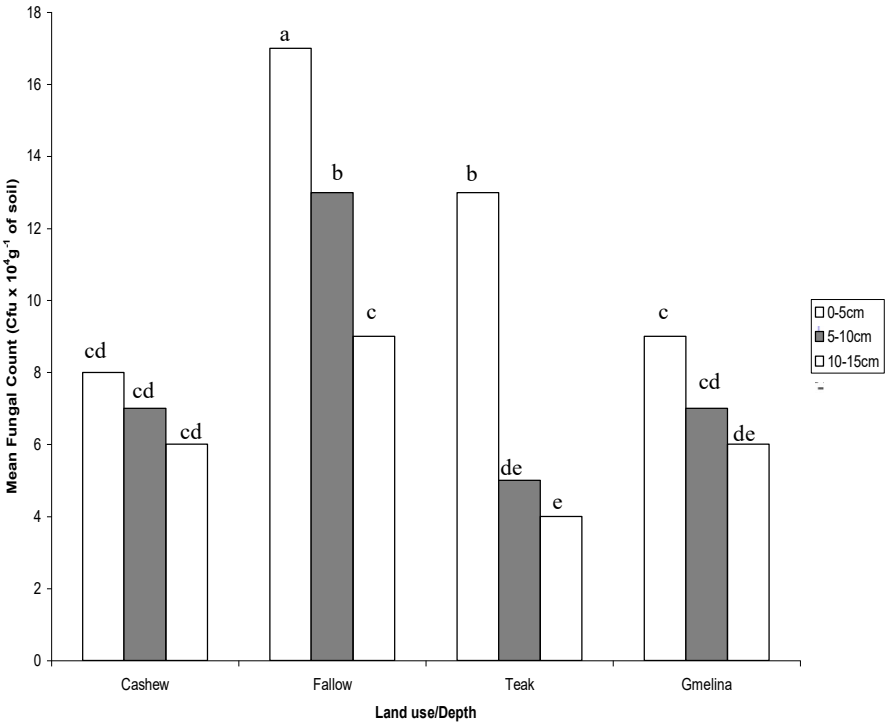

Fig. 2: Fungal Population Count (Cfu x 10^4 g^{-1} of soil) as affected by land use systems at different soil depths.

Bars of the same depths with different letters are significantly different.

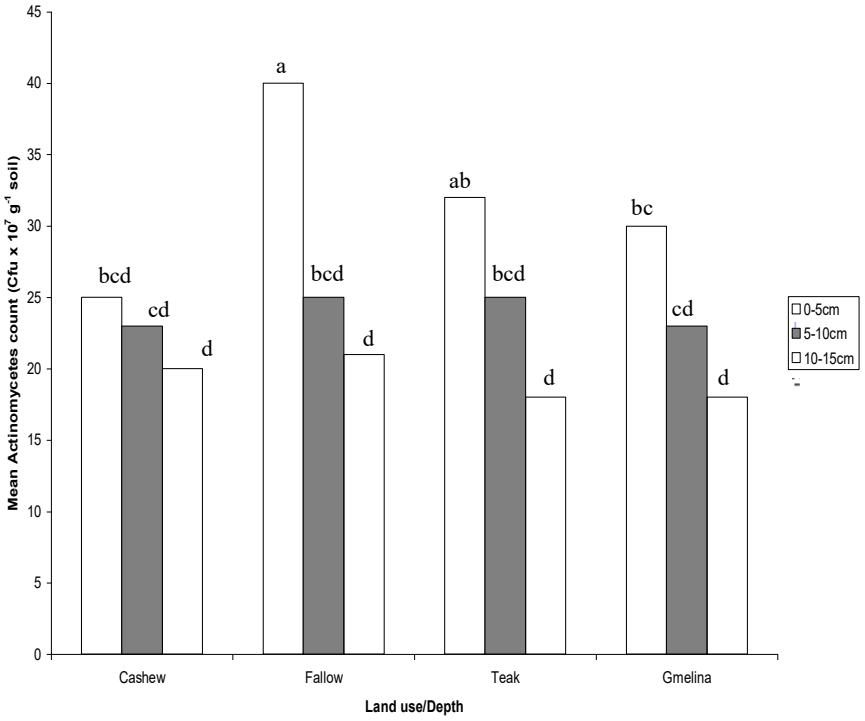

Fig. 3: Actinomycetes Population Count (Cfu x 10^7 g^{-1} of soil) as affected by land use systems at different soil depths.

Bars of the same depths with different letters are significantly different.

3.0 Result and Discussion

3.1 Soil Texture, Reaction and Exchangeable Bases.

Differences in physical and chemical properties of the soils of the land use systems were observed across depths (Tables 1 and 2). The textural class of soil did not however change because texture is a fixed properly of soil (Lim and Pong,1983). Soil physicochemical properties under the cropping systems shows that the soil was sandy loam, with the exception of rice field that was sandy clay loam. Soil reaction was slightly acidic, the organic matter was generally low and the available P was very low. The pH in $Cacl_2$ across vegetation type was in the range of 4.73 to 6.85 suggesting that vegetation increased the pH of soil probably as a result of the release of root exudates. At the top soil, fallow treatment had the highest organic carbon followed by Teak, Gmelina and cashew in that sequence indicating that a period of fallow allows for carbon accumulation and that depletion of carbon increases with use of land. Averagely, the N content (gkg^{-1} of soil) was highest under Teak vegetation followed by fallow treatment suggesting that most vegetation types will reduce soil N composed with that obtained under fallow unless they have inherent abilities through associations with root microorganisms to improve the supply of N (N-mineralization). The Ca Mg content (cmol Kg^{-1})of soil under vegetation was higher than that under fallow implying that leaf litter fall supplied their soil with Ca and Mg otherwise the root exudates must have improved the solubilization of Ca and Mg that were complexes as $CaHP0_4$ or $MgHP0_4$. Clay content increased with depth across land use system resulting to sandy loam textural class of soils which did not translate into higher moisture content of the soils across various land use; although soil under cashew vegetation was an exception (Table 1)

3.2 Soil physico chemical properties correlated with microbial population

The significant correlation of clay content with bacteria, actinomycetes and fungal counts (Table 3)

implied that clay probably served as a nutrient medium or moisture absorbent for the microbes. Similarly organic carbon correlated significantly bacteria and fungi suggesting that their strains were hetrotrophic therefore the carbon was only an energy source (Brady and Weil, 2002). In the same manner, total N correlated significantly with Bacteria and Actinomycetes content indicating that selection and proliferation was largely dependent on soil nitrogen content (Doran *et al*., 1996).

3.3 Microbial population as affected by land use

Fig. 1 to 3 shows the effect of land use on microbial population. Regardless of land use systems, at 0 – 5 cm depth, bacteria population was highest probably due to a higher accumulation of carbon and nitrogen at the soil surface (Table 1). This is consistent with the reports of Brady and Weil (2002) and Doran *et al*; (1996) who maintained at different times, the importance of carbon as energy source and nitrogen as a medium for qualitative selection of whole communities of micro organisms. Averagely, irrespective of soil depth, fallow treatment recorded the highest bacterial count followed by teak, cashew and Gmelina in that order probably due to higher organic carbon (OC) and total nitrogen (TN) content of the soil (Table 1). This probably explains why fallow treatments recorded the highest fungi and actinomycetes count compared with the rest treatments. Amongst the three vegetation treatments, teak soils especially at the top soil (0 – 5 cm) had always recorded a superior microbial count most likely because of a higher quality of its root exudates or a better association with microbes that mediate C and N transformations. Conversely, cashew soils, especially at the top soil recorded lower microbial counts probably due to its acid pH value of 4.73 (Table 1). Other vegetation treatments recorded a near neutral soil pH ideal for maximum microbial activities (Hutchinson and Collins, 1978; Acosta-Martinez, 2000).

Conclusion

The results have demonstrated that the population of bacteria was higher than that of actinomycetes and fungi. Fallow and Teak land use system recorded the highest soil microbial population, while cashew and Gmelina gave the lowest. Fallow and Teak land use systems are hereby considered healthier than cashew and Gmelina treatment and therefore provide essential baseline information regarding soil health maintenance reported previously in the tropics.

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