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Microbial population and diversity in four land use practices in Ekiti State, Nigeria

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Abstract

Increased specialized agricultural systems such as monocultures, mechanical cultivation and use of mineral fertilizers in developing countries in the recent times, has led to loss of biodiversity and reduced ecosystem resilience. This study examined the effect of land use practice on diversity and abundance of soil micro fauna. The study was carried out at the Teaching and Research Farm, Ekiti State University, Ado-Ekiti. Soil samples were collected from four (4) sites under different land use (natural forest, teak plantation, oil palm plantation and arable crop land). Three plots of 10 m x 10 m were randomly laid in each of the land use type. Soil samples were collected from three different points at two soil levels (0-15 cm and 15-30 cm) within each plot. Microbiological analysis of the soil samples revealed that land use significantly affect microbial population along the soil depth with natural forest having the highest value of 2.38 x 10^8 cfu/g followed by arable land (1.79x 10^8 cfu/g) and oil palm (1.66x 10^8 cfu/g) at 0-15 cm soil depth respectively. Soil under arable land has the greatest microbial diversity of 11 genera. It was suggested that land users (foresters and agriculturists) should embrace land use practice that will encourage biodiversity conservation for enhanced ecosystem stability.

Keywords: Microbial, Biodiversity, Population, Land Use, Ekiti State

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1. Introduction

Soil represents one of the most important reservoirs of biodiversity. It reflects ecosystem metabolism since all the bio-geochemical processes of different ecosystem component are combined within it. Soil micro-organisms occur in large number and display an enormous diversity of form and function. The roles and functions of soil fauna were recognized in soil formation and leaf litter decomposition in the tropical forest region for mixed leaf litter (Anderson et al., 1983). Microbial biomass is the most active fraction of soil organic matter, acting as a source or sink of available nutrients and plays important role in nutrient cycling and conversation in tropical ecosystem (Diaz-Ravina et al., 1993). Microbial biomass activity is used to characterize the microbiological status of a soil (Nanniperi et al., 1990). It also provides many regulatory services such as decomposition of soil organic matter (SOM), soil structure maintenance and nutrient cycling among others which ensure ecosystem sustainability (Kibblewhite et al., 2008).

Soil environment consists of a variety of physical, biological and chemical factors that affect the abundance and diversity of microbes found in the soil (Sylvia et al., 2005). On the other hand, microbial processes directly affect their environments by contributing to the carbon and nitrogen cycles, which are important for microbial and plant health (Ray and Brady, 2016). Soil harbors large part of the world's biodiversity, and it govern processes that are important components in the recycling of organic matter, energy and nutrients. Soil ecosystem generally contains large variety of animals, such as nematodes, micro-arthropods, mites, collembola, symphyla, chilopoda, pauropoda, enchytraeids and earthworm. Moreover, soil is a key player in several supporting and regulating ecosystem services (Jeffery et al., 2010).

The interactions between soil fauna are numerous, complex and varied. The degree of interaction between soil organisms in the soil ecosystem, usually differ among taxa and it is dependent on the part of the life cycle of the organisms that is been spent in the soil (Zeller et al., 2001). The impact of soil condition on the other hand is an important factor that regulates the size, activity, structure and diversity of microbial community (Fierer and Jackson, 2006). Decomposition of organic matter by soil organisms is crucial for the functioning of an ecosystem because the services provided by soil fauna plays important role in the conservation of edaphic biodiversity, plant growth and primary productivity (Maharning et al., 2008). Despite the importance of the activities of microbial communities in soils, information about how land use affects their population has not been fully explored. Consequently, knowledge of the effect of land use on soil microbial biomass population and diversity is essential which justifies the necessity for this study.

2. Materials and method

2.1. Study site

This study was carried out at the Teaching and Research Farm, Ekiti State University Ado-Ekiti, in South West Nigeria. Ado Ekiti is located between Latitude 7^0 6' and 7^0 7' North and Longitude 5^0 24' and 5^0 29' East of Greenwich meridian. The vegetation of the study area is tropical rain forest at an elevation of 250 m above sea level. The annual rainfall ranged from 1, 200 mm to 1, 500 mm. Temperature ranges between minimum of 24 ^{0}C and maximum of 35 ^{0}C with little variation throughout the year. The annual relative humidity ranged

between 65% and 90% during the raining season. The soil is an alfisol (Oxic- Tropudalf - USDA soil taxonomy). The soil is well drained with moderate fertility.

2.2. Procedure of the experiment

2.2.1. Collection of soil samples

Soil samples were collected from four (4) sites under different land use practices (Natural Forest, Teak Plantation, Oil Palm Plantation and Arable Land), at the University's Teaching and Research Farm. Three plots of 10m x 10m were randomly laid in each of the land use type. Soil samples were collected at three different points along the diagonal laid within each plot at two different soil levels (0-15 cm and 15-30 cm). Soils from the same depth within a plot were bulked and collected into sample bottle for microbial analysis. The samples were covered with moistened sand to provide an environment similar to that of the field so as to prevent the soil from drying out there by preserving the microbial biomass. A portion of the soil samples from the plots for each land use were bulked for laboratory analysis to determine the physical and chemical properties of the soils.

2.2.2. Laboratory analysis

Physical and chemical properties of soil samples were determined using standard methods (AOAC, 2000). Microbiological analysis was carried out by diluting one gram (1 g) of each soil sample in test tube at 10^{-6}dilution. The samples were plated using Nutrient agar (NA) to determine the bacterial load. The colonies that developed on the plates were counted. The total bacterial loads for the samples were calculated by multiplying the colony counted with the dilution factor and expressed as colony forming unit per gram (cfu/g). Discrete colonies were streaked on agar plate to obtain pure culture which was stored on agar slants. Microbial isolates were characterized for identification using the following tests; gram stain, catalase, coagulase, spore stain and motility test.

2.3. Statistical analysis

One-way analyses of variance (ANOVA) procedure was used to compare the chemical and physical properties of soil under different land use practices using SPSS Version 17. Separation of the significant means of the soil properties was performed using Duncan significance test. Data obtained from the microbial test were also subjected to analysis of variance (ANOVA). A follow up test was conducted using Duncan Multiple Range Test (DMRT) to identify separate significant means.

3. Results

3.1. Chemical properties of the sampled soils

Result in Table 1 shows that soil under teak plantation had the least pH value and it is significantly different from the pH value of soils under other land use practices. Percentage organic carbon was highest in soil

under teak plantation and it is significantly different ($p<0.05$) from the values obtained in other land use practices. Percentage total nitrogen and potassium content among the various land use practices are not significantly different($p<0.05$).Phosphorus content of the various land use practices differed significantly ($p<0.05$) from one another, with oil palm plantation having the highest value while teak plantation had the least value.

Table 1. Chemical properties of the soils under different land use practices

Soil Variables	Values			
	TP	PP	AL	NF
pH (H_2O)	4.77 ± 0.83^{b}	6.18 ± 0.83^{a}	6.07 ± 0.83^{a}	6.72 ± 0.83^{a}
Organic Carbon (%)	2.10 ± 0.65^{a}	1.48 ± 0.65^{b}	0.60 ± 0.65^{c}	1.82 ± 0.65^{b}
Total Nitrogen (%)	0.17 ± 0.04^{a}	0.13 ± 0.04^{a}	0.07 ± 0.04^{a}	0.15 ± 0.04^{a}
Available Phosphorus (%)	5.81 ± 0.54^{d}	17.29 ± 0.54^{a}	6.63 ± 0.54^{c}	7.09 ± 0.54^{b}
Potassium (cmol)	0.26 ± 0.70^{a}	0.35 ± 0.70^{a}	0.29 ± 0.70^{a}	0.42 ± 0.70^{a}
Calcium (cmol)	4.86 ± 0.75^{b}	6.31 ± 0.75^{a}	5.58 ± 0.75^{a}	4.66 ± 0.75^{b}
Magnesium (cmol)	1.12 ± 0.39^{a}	1.80 ± 0.39^{a}	1.12 ± 0.39^{a}	1.80 ± 0.39^{a}
Sodium (cmol)	0.62 ± 0.10^{a}	0.69 ± 0.10^{a}	0.55 ± 0.10^{a}	0.80 ± 0.10^{a}
Manganese (mg/kg)	21.20 ± 0.16^{b}	51.00 ± 0.16^{a}	26.70 ± 0.16^{a}	52.65 ± 0.16^{a}
Iron (mg/kg)	16.7 ± 0.80^{a}	7.05 ± 0.80^{b}	7.60 ± 0.80^{b}	6.50 ± 0.80^{b}
Copper (mg/kg)	0.65 ± 0.04^{a}	0.75 ± 0.04^{a}	0.70 ± 0.04^{a}	0.70 ± 0.04^{a}
Zinc (mg/kg)	2.35 ± 0.13^{b}	3.30 ± 0.13^{ab}	1.70 ± 0.13^{c}	4.65 ± 0.13^{a}

Mean with the same superscript along the rows are not significantly different ($p>0.05$).

TP = Teak Plantation, PP= Oil Palm Plantation, AL = Arable Land, NF = Natural Forest

3.2. Physical properties of the sampled soils

Result in Table 2 shows that textural class of soils under teak plantation, arable land and natural forest are loamy sand, while soil under Oil palm plantation is sandy in texture.

Table 2. Particle size distribution and textural class of sampled soils

Land Use	Sand (%)	Silt (%)	Clay (%)	Textural class
Teak	84.60	10.8	4.60	Loamy sand
Oil Palm	87.60	5.8	6.60	Sand
Arable land	84.60	9.8	5.60	Loamy sand
Natural Forest	86.60	7.8	5.60	Loamy sand

3.3. Microbial population of soil samples

Table 3 shows that microbial population at 0-15 cm depth of the soil across the different land use practices are significant different($p<0.05$) with soil under natural forest having the highest value of 2.38 x 10^8cfu/g followed by arable land soil (1.79x 10^8cfu/g) and soil under oil palm (1.66x 10^8cfu/g) respectively. Soil under teak plantation had the least microbial population of 1.48 x 10^8cfu/g. At 15-30 cm depth of the soils, the microbial population followed the same pattern as the value obtained for 0-15 cm depth of the soils across the different land use practices.

Table 3. Microbial population (x10^8cfu/g) under different land use practice.

Soil Level	Land Use Types			
	Teak	**Oil-Palm**	**Arable Land**	**Natural Forest**
0-15 cm	1.48 ± 0.28^{d}	1.66 ± 0.28^{c}	1.79 ± 0.28^{b}	2.38 ± 0.28^{a}
15-30 cm	1.45 ± 0.18^{d}	1.61 ± 0.18^{c}	1.82 ± 0.18^{b}	2.34 ± 0.18^{a}

Means with the same superscript along the column are not significantly different, while means with different superscript along the row are significantly different.

3.4. Microbial diversity in teak plantation soil

Table 4 shows that five (5) different genera of microbes (*Providence, Arthrobacter, Staphylococcus, Pseudomonas* and *Bacillus*) were isolated from teak plantation soil. The result shows that at 0-15 cm soil depth, four (4) different genera of microbes (*Providence, Arthrobacter, Staphylococcus, Bacillus)* were present while at 15-30 cm soil depth two (2) different genera (*Pseudomonas* and *Bacillus*) were present.

Table 4. Morphological and Biochemical Characterization of Microbial Isolates

Teak plantation	GR	Spore	CT	CG	UR	MN	CR	ID	Microbes present
Depth (0-15 cm)	GPB	+	-	-	-	-	-	-	*Bacillus spp*
	GPC	-	+	-	-	+	-	-	*Staphylococcus spp*
	GPB	-	-	-	-	-	+	-	*Arthrobacterspp*
	GNB	-	+	-	-	-	+	+	*Providence spp*
Depth (15-30 cm)	GNC	-	-	-	-	-	-	-	*Psedomonasspp*
	GPB	+	-	-	-	-	-	-	*Bacillus cereus*

Key:

GR = Gram Reaction, CT = Catalase test, CG = Coagulase test, UR = Urease test,
MN = Mannitol test, CR = Citrate test, ID = Indole test, GPB = Gram Positive Bacilli
GPC = Gram Positive Cocci, GNB = Gram Negative Bacilli, GNC = Gram Negative Cocci

3.5. Microbial diversity in oil palm plantation soil

Table 5 shows five (5) different genera of microbes (*Aerobacter, Staphylococcus, Pseudomonas, Klebsiella* and*Bacillus*) were isolated and identified in oil palm plantation soil.At 0-15 cmsoil depth, four (4) different genera of microbes (*Aerobacter*, *Staphylococcus, Pseudomonas, Klebsiella)* were present while at 15-30 cm soil depth, only two (2) different genera (*Pseudomonas* and *Bacillus*) were present.

Table 5. Morphological and Biochemical Characterization of Microbial Isolates

Oil Palm	GR	Spore	CT	CG	UR	MN	CR	ID	Microbes Present
Depth (0-15 cm)	GNC	-	+	-	-	-	-	-	*Pseudomonas geniculate*
	GNB	-	-	-	+	-	+	+	*Klebsiella oxytoca*
	GPC	-	+	+	-	+	-	-	*Staphylococcus aureus*
	GNB	-	-	-	+	-	-	-	*Aerobacter spp*
Depth (15-30 cm)	GNC	-	+	-	-	-	-	-	*Pseudomonas spp*
	GPB	+	-	-	-	+	+	-	*Bacillus megaterium*

Key:
GR = Gram Reaction, CT = Catalase test, CG = Coagulase test, UR = Urease test,
MN = Mannitol test, CR = Citrate test, ID = Indole test, GPB = Gram Positive Bacilli
GPC = Gram Positive Cocci, GNB = Gram Negative Bacilli, GNC = Gram Negative Cocci

3.6. Microbial diversity in arable soil

Table 6 shows that Eleven (11) different genera of microbes (Aerobacter, Arthrobacter, Nitrosomas, Serratia, Pseudomonas, Klebsiella, Providence spp, Bacillus, Clostridium, Lactobacillus and Staphylococcus) were isolated and identified in arable land soil. At 0-15 cm soil depth, eight (8) different genera of microbes (Aerobacter, Arthrobacter, Nitrosomas, Serratia, Pseudomonas, Klebsiella, Providence and Bacillus) were present while at 15–30 cm soil depth five (5) different genera (Bacillus, Pseudomonas, Clostridium, Lactobacillus and Staphylococcus) were present.

3.7. Microbial diversity in natural forest soil

Table 7 shows that seven (7) different genera of microbes (*Aerobacter*, *Serratia, Providence, Pseudomonas, Staphylococcus*, *Bacillus*and *Xanthomonas*) were isolated in natural forest soil. At soil depth of 0-15 cm, five (5) different genera of microbes (*Bacillus, Aerobacter, Xanthomonas, Pseudomonas and Staphylococcus)* were

present while at 15-30 cm soil depth, six (6) different genera (*Bacillus, Providence, Xanthomonas, Pseudomonas, Aerobacter and Serratia*) were present.

Table 6. Morphological and Biochemical Characterization of Microbial Isolates

Arable Land	GR	Spore	CT	CG	UR	MN	CR	ID	Microbes present
Depth (0-15 cm)	GNB	-	-	-	+	-	-	-	*Aerobacter spp*
	GNB	-	-	-	+	-	+	+	*Serratia spp*
	GPB	-	-	-	-	-	+	-	*Arthrobacter spp*
	GNC	-	-	-	-	+	-	-	*Nitrosomas spp*
	GNC	-	+	-	-	-	-	-	*Pseudomonas spp*
	GNB	-	-	-	+	-	+	+	*Klebsiella oxytoca*
	GNC	-	+	-	-	-	+	+	*Providence spp*
	GPB	+	-	-	-	-	-	-	*Bacillus cereus*
Depth (15-30 cm)	GNC	-	+	-	-	-	-	-	*Pseudomonas spp*
	GPB	+	+	-	-	-	+	-	*Bacillus subtilis*
	GPB	-	-	-	-	-	+	-	*Clostridium spp*
	GPB	-	-	-	-	-	+	-	*Lactobacillus spp*
	GPC	-	+	-	-	+	-	-	*Staphylococcus spp*

Key:
GR = Gram Reaction, CT = Catalase test, CG = Coagulase test, UR = Urease test,
MN = Mannitol test, CR = Citrate test, ID = Indole test, GPB = Gram Positive Bacilli
GPC = Gram Positive Cocci, GNB = Gram Negative Bacilli, GNC = Gram Negative Cocci

Table 7. Morphological and Biochemical Characterization of Microbial Isolates

Natural Forest	GR	Spore	CT	CG	UR	MN	CR	ID	Microbes present
Depth (0-15 cm)	GPB	+	-	-	-	-	-	-	*Bacillus cereus*
	GPB	-	-	-	-	+	-	-	*Bacillus megaterium*
	GNB	-	-	-	+	-	-	-	*Aerobacter spp*
	GNB	-	+	-	-	-	-	+	*Xanthomonas spp*
	GNP	-	-	-	-	-	-	-	*Pseudomonas aeruginoso*
	GPC	-	+	+	-	+	-	-	*Staphylococcus spp*
	GPB	+	+	-	-	-	+	-	*Bacillus subtilis*
Depth (15-30 cm)	GPB	+	+	-	-	-	+	-	*Bacillus subtilis*
	GPC	-	+	-	-	-	+	+	*Providence spp*
	GNB	-	+	-	-	-	-	+	*Xanthomonas spp*
	GPB	-	-	-	-	+	-	-	*Bacillus megaterium*
	GNC	-	+	-	-	-	-	-	*Pseudomonas spp*
	GNB	-	-	-	+	-	-	-	*Aerobacter spp*
	GNB	-	-	-	+	-	-	-	*Serratia spp*

Key:
GR = Gram Reaction, CT = Catalase test, CG = Coagulase test, UR = Urease test,
MN = Mannitol test, CR = Citrate test, ID = Indole test, GPB = Gram Positive Bacilli
GPC = Gram Positive Cocci, GNB = Gram Negative Bacilli, GNC = Gram Negative Cocci

4. Discussion

The observed improvement in texture of soils under teak plantation, natural forest and arable land from sand to loamy sand texture, might be due to addition of humus into the soil from decomposed leaf litter through the activities of soil fauna. This observation is in agreement with the reports by Audu et al. (2009). Observed sandy nature of the soil under oil palm could be attributed to the bear floor of the plantation as the palm trees does not shed leaf. The poor litter quality of palm leaves, coupled with the fact that when the leaf is cut, it is usually arranged on a spot could have further been responsible for low percentage of silt in soil under oil palm. This assertion is in agreement with the submission of Ogunwole (2005) and Olujobi (2016) who in separate studies reported that improvement in soil physical property depends on the quality of residue cover. The significantly ($p < 0.5$) least value of pH obtained in soil under teak plantation compared to other land use despite the high organic matter content (Table 2), may largely be due to secretion of acid from the fruit of the plant that littered the floor of the plantation.

The significantly ($p < 0.5$) least microbial count obtained in soil under teak plantation (Table 4) compared to other land use might be due to low pH value of the soil, while the highest microbial population in natural forest soil could also be as a result of more or less neutral nature of the soil. This observation further confirms the submission of Fierer et al. (2006) who's study revealed that most micro-organism thrives in pH value close to neutral, Also, observed highest microbial population in soil of natural forest may be attributed to high percentage of organic matter, while low microbial diversity in soil under oil palm plantation may be as a result of the sandy texture of the soil with low humus content.

Observed greater microbial diversity in soil of arable land could probably be attributed to frequent tilling of the soil which has brought about finer textured sand especially at the surface level thereby making the soil to be well aerated. This condition gives room for more microbial colonization. This assertion corroborates the submission made by Ray and Brady (2016) who reported that Oxygen (O_2) is an important element for the productivity of both microbes and plant roots. Also greater microbial diversity observed in arable land may be due to the fact that the soil is well exposed to solar radiation, resulting in higher temperature and consequently higher microbial activity. This observation further confirms the assertion of Sylvia et al. (2005), who reported that microbial activity increases with increasing temperature.

The presence of *Clotrisimma spp.* and *Lactobacillus spp.* which are anaerobic bacteria at 15-30 cm soil depth of arable land (Table 7) may be due to the higher degree of soil compaction brought about by the use of tractors and other farm implements. This compaction results in reduction of soil pore spaces thereby limiting oxygen circulation, this phenomenon may in turn favour the growth and colonization of anaerobic bacteria at this soil level. Also the presence of *Nitrosomonas spp.*in soil under arable land suggests the use of fertilizer on the land during cropping season. *Nitrosomonas* is a nitrifying bacterium that oxidizes ammonia to nitrite in

Nitrogen containing fertilizer. *Nitrosomonas* play an important role in providing Nitrogen to plant and it can pose a problem as it can make the nitrate in the soil more susceptible to leaching and therefore less available to plant.

5. Conclusion and recommendation

Result from this study has revealed that land use practice significantly affect chemical properties of soil of the study sites. The study also showed that textural class of soils under teak plantation, arable land and natural forest improved from sand to loamy sand as the texture of the soil in the study area is generally sand in nature. Also the study further revealed that land use significantly affected microbial population along the soil depth with natural forest having the highest microbial colony count followed by the soils under arable land and oil palm respectively at 0-15 cm soil depth. Result from this study has also revealed that land use practice significantly influence diversity of soil microbes along the soil depth in the study sites. In view of the above results, it was recommended that land users at all level; most especially Foresters and Agriculturist should embrace land use practice that will be capable of increasing the organic matter content of the soils thereby improving the soil for microbial colonization. In addition, farmers should be educated on the services and environmental functions of soil microbes, so that they could desist from the use of chemicals that could lead to soil poisoning. Conclusively, relationship between land use practice and soil fauna is an important factor to be considered in the process of biodiversity conservation, soil reclamation and ecosystem stability.

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