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Original Article

Effect of Logging Activities on Soil Microorganisms in Selected Forest Reserve of Ondo State

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ABSTRACT

The study was carried out to assess the influence of logging on microbial population and soil properties in Akure forest reserve. The microbes were isolated and counted in agar plated composite soil samples collected from unlogged forest and two differently logged habitats in Akure forest reserve. The soil pH and soil structure of each selected habitat were also examined. The results show that the soil samples contain 18 species of bacteria and 13 species of fungi. However, 11 species of bacteria were found in the unlogged forest, 14 for lightly logged and 8 for heavily logged. Likewise 8, 9, 6 species of fungi were observed from unlogged, lightly logged and heavily logged forests respectively. Bacteria count was significantly higher ($p \leq 0.05$) in unlogged than other studied habitat. Unlogged forest had pH value of 5.85±0.17, lightly logged had 6.56±0.19 and heavily logged habitat had 6.40±0.15. The results of percentage sand composition shows that unlogged, lightly logged and heavily logged habitats had the value of 78.24±1.00, 76.99±1.79 and 77.24±1.00 respectively. The results further shows that the pH in unlogged is moderately acidic (5.85±0.17), while lightly logged forest and heavily logged forests were slightly acidic (6.56±0.19 and 6.40±0.15). The regression equation shows that a relationship exists between percentage sand content and bacteria, soil pH and fungi. But there is no relationship between the soil pH and bacteria and percentage sand content and fungi since their R^2 is very low. The implication of their relationship is discussed.

KEYWORDS: Bacteria, Fungi, Degraded, Diversity, and Abundance.

INTRODUCTION

Tropical rainforest ecosystems play a special role in global biodiversity conservation. It is estimated that about 70% of the world's plant and animal species (which consists of more than 13 million distinct species) are housed in tropical forest ecosystems (Anon, 1996; Onyekwelu *et al*., 2008). Generally, soil are natural resources of utmost importance for a number of ecosystem and biosphere processes such as plant production, cycling of organic matter and nutrients, storage of carbon and water and release of nitrous oxides, carbon(iv) oxide and methane. The role of soil fauna in mineralization cannot be over emphasized, mites and collembolans are known to fragment organic matter as they feed on soils micro flora. This fragmentation to finer particles creates new mineralization processes. Soil fauna tends to be greater in undisturbed natural lands compared to cultivated fields. However, the number and types of organisms vary from one system and environment to another and this is strongly influenced by agricultural practices (Gill, 1981).

Forest consists of many living micro organisms which are very helpful in recycling the forest soil nutrient through the decay and formation of humus soil. Humus has important physical and chemical properties such as water retaining ability and aeration. Micro organisms are also helpful in the replacement of lost nutrient to the soil. Such micro organisms include the nitrogen fixing bacteria, nitrifying bacteria and denitrifying bacteria (Badejo 1977). The decaying of the root of higher plants is achieved through micro organisms and this help continuously add organic matter to soil thereby changing the soil properties. Also, soil aggregation, cation exchange capacity, water and nutrient retention capacity of soil are improved (Biswas and Mukheateee, 1987). The complex physical and chemical nature of the soil, with a porous structure, immense surface area, and extremely variable supply of organic materials, food, water and chemicals mean that various animal, plant and microbial worlds can co-exist simultaneously and find appropriate niches for their development. Focusing on the litter decomposition process at the ecosystem level, soil mesofauna are involved in a variety of functions such as nutrition, litter microbial grazing and microbial dissemination. Most tropical soil fauna live in the top 10cm of mineral soil where organic matter is decomposed and the final products such as water, CO_2 and

mineral salt are available for crops through their roots. The identification of soil micro-organism magnification helps the observer to see and resolve their structures. The common divisions of the soil micro-organisms are the bacteria, fungi, yeast mold, protozoa e. t. c. and they have deoxyribonucleic acid (DNA) and the ribonucleic acid (RNA). Micro-organisms are present in high populations in the soil and in varying number in the air.

The aim of this study therefore was to examine and compare the effect of different habitat or different forest landscape systems on the diversity and abundance of soil micro-organisms as well as to examine the relationship between them.

METHODOLOGY

STUDY AREA

This study was carried out at three different forest types selected within Akure forest reserve in Ondo State of Southwestern Nigeria. Akure forest reserve covers an area of 69.93 km^2. The reserve is under the management of the Department of Forestry, Ondo State, Nigeria. The reserve lies along Ondo – Akure road at about 20 km south of Akure, the capital city of Ondo State. It is located on Latitude 7^o 18'N and Longitude 5^o 02'E. The three forest types selected for this work are (unlogged, lightly logged and heavily logged forests), these forest types selected were in close proximity and similar in terms of forest type, altitude and topography to each other.

SAMPLE PLOT LOCATION

An area of one hectare was located in each of the three selected forests (unlogged, lightly logged and heavily logged). Five (25 m x 25 m) plots were randomly selected in each hectare and soil samples were collected at a depth of 0-10cm at three points were located within each plot. Soil samples collected at the three points in each plot were bulked to bridge the gap of non-uniformity within the plots. This same procedure was repeated for the three forest habitats. All soil samples collected were brought to the laboratory for microbial and mesofauna identification. Determination of soil pH and soil physical properties was carried out at each forest habitat.

POUR PLATE METHOD FOR BACTERIA CULTURE

Suspensions of the soil samples were prepared with sterile water and a serial dilution of five factors was made for accurate counting. One millimeter (1ml) of the appropriate dilution was carefully transferred to sterilized Petri dishes containing sterile molten nutrient agar at about 37°C. This was fixed and allowed to solidify. It was then incubated for 24 hours. The bacteria that grew into colonies were sub-cultured to obtain pure culture for easy identification.

POUR PLATE METHOD FOR FUNGI CULTURE

Serial dilution of the suspension was transferred into Petri dishes containing sterile molten malt extract agar. This was kept in an incubator at 30°C for 5 days. Fungi that grew were sub-cultured to obtain pure culture for easy identification. Microscopic characterization was done for identification.

DATA ANALYSIS

Data on bacteria and fungi counts were analyzed using Analysis of Variance procedure for completely randomized design (CRD) and the result was subjected to analysis of variance (ANOVA).

RESULTS

The bacteria diversity of the study area is presented in Table1 below. There are 18 different species of bacteria encountered in all the studied site, the highest abundance was encountered in lightly logged while the least was recorded in unlogged habitat. From the result, it was discovered that about 14 different bacteria was identified in lightly logged forest ecosystem, while in the unlogged possess about 11 different species of bacteria were identified. But, the least was recorded at heavily logged forest of 8 different species. It was discovered from the result of this study that only three types of bacteria species occurred in all the forest types, they are; *Bacillus magatarium, Eschericha coli* and *Kurthia spp.* But *Acinetobacter parapartusis, Actinomyces spp, Sereina flora* and *Strephylococcus faecolis* were found and identified within unlogged and lightly logged forest ecosystems. Also, in unlogged and heavily logged forest type, only two types of bacteria were found they are; *Bacillus cereus* and *Staphylococeus aereus*. In case of lightly logged and heavily logged, *Bacillus subtitles, Proteus vulgaris* and *Thiobacillus spp* bacteria species were common to these two ecosystems.

Likewise the highest Fungi diversity was recorded in lightly logged habitat of about 9 different species and followed by unlogged forest which has about 8 species of fungi and the least was recorded of 6 in number in heavily logged habitat (Table 2). From the results of this study revealed that these different types of fungi; *Fasarium spp, Gonotobotys simplex, Penicillum spp* and *Rhizopus nigricans* were found in all the ecosystems. But *Aspergillus niger*, *Borytritis cinera, Candia spp, Mucor spp, Streptomyces spp, Trichoderma vivide* and *Wardomyces spp* were only found in only one forest type.

Table 1. Diversity of Bacteria in the Study Area

S/N	Names	Unlogged forest	Lightly logged forest	Heavily logged forest
1	*Acinetobacter parapartusis*	*	*	-
2	*Acinetobacter luroffii*	-	*	-
3	*Actinomyces spp*	*	*	-
4	*Alcaligenes faecolis*	-	*	-
5	*Bacillus cereus*	*	-	*
6	*Bacillus magatarium*	*	*	*
7	*Bacillus polymysa*	*	-	-
8	*Bacillus subtites*	-	*	*
9	*Citrobacter freundii*	-	*	-
10	*Eschericha coli*	*	*	*
11	*Kurthia spp*	*	*	*
12	*Proteus vulgaris*	-	*	*
13	*Pseudomonas aeruginosas*	-	*	-
14	*Rhizobium leguminosarium*	*	-	-
15	*Sereina flora*	*	*	-
16	*Staphylococeus aereus*	*	-	*
17	*Strephylococcus faecolis*	*	*	-
18	*Thiobacillus spp*	-	*	*
	Total present	**11**	**14**	**8**

Table 2. Diversity of Fungi in the Study Area

S/N	Names	Unlogged forest	Lightly logged forest	Heavily logged forest
1	*Aspergillus niger*	*	-	-
2	*Borytritis cinera*	*	-	-
3	*Candian spp*	-	-	*
4	*Fusarium spp*	*	*	*
5	*Gonotobotys simplex*	*	*	*
6	*Mucor spp*	-	*	-
7	*Neurospora crassa*	-	*	*
8	*Penicillum spp*	*	*	*
9	*Rhizopus nigricans*	*	*	*
10	*Stachbotrys spp*	*	*	-
11	*Streptomyces spp*	-	*	-
12	*Trichoderma vivide*	-	*	-
13	*Wardomyces spp*	*	-	-
	Total present	**8**	**9**	**6**

Keys: * = Present, while - = Not present

Fungi abundance result obtained in this study was presented in Table 3. The counts are expressed as colony forming Unit per gram (cfu/g) with factor of 10^2. From the result the unlogged has, the highest values follow by lightly logged and heavily logged has the lowest values of $0.81x10^2$, $1.38x10^2$, and $0.61x10^2$ respectively. Also, the abundance of bacteria were recorded and their count were also treated as it was done to fungi as $43x10^4$, $47x10^4$, and $18x10^4$ in unlogged, lightly logged and heavily logged respectively (Table 4). These results shows that the higher the diversity of fungi and bacteria the higher the abundance.

Table 3. Abundance of Fungi in Colony Forming Unit (1g of Soil Sample)

S/N	Unlogged forest	Lightly logged forest	Heavily logged forest
1	$0.28x10^2$	$0.43x10^2$	$0.14x10^2$
2	$0.24x10^2$	$0.25x10^2$	$0.03x10^2$
3	$0.16x10^2$	$0.34x10^2$	$0.17x10^2$
4	$0.09x10^2$	$0.06x10^2$	$0.09x10^2$
5	$0.24x10^2$	$0.30x10^2$	$0.18x10^2$
TOTAL	$0.81x10^2$	$1.38x10^2$	$0.61x10^2$

Table 4. Abundance of Bacteria in Colony Forming Unit (1g of Soil Sample)

S/N	Unlogged forest	Lightly logged forest	Heavily logged forest
1	$4.0x10^4$	$9.0x10^4$	$3.0x10^4$
2	$5.0x10^4$	$13.0x10^4$	$5.0x10^4$
3	$12.0x10^4$	$8.0x10^4$	$3.0x10^4$
4	$13.0x10^4$	$8.0x10^4$	$4.0x10^4$
5	$9.0x10^4$	$9.0x10^4$	$3.0x10^4$
Total	$43x10^4$	$47x10^4$	$18x10^4$

Table 5. Diversity and Abundance of Mesofauna in the Study Habitat

S/N	Forest Habitat	Diversity Index (H^1)	Evenness (E)	Abundance (M^2)
1	Unlogged forest	1.40	0.10	6100
2	Lightly logged forest	1.60	0.13	4000
3	Heavily logged forest	1.19	0.18	2600

H'- Shannon Weiner diversity index and M^2- Meters square

The Lightly logged forest has the highest diversity index (1.60) with least value in heavily logged forest (1.19). The evenness values ranges between 0.l0 to 0.18 (Table 5). But the result of total abundance observed in the studied site shows that unlogged forest had the highest value of 6100 m^2 while the heavily logged forest habitat had the least total abundance of 2600 $m^{2.}$ From the result of bacteria count, it was discovered that there is significant difference between lightly logged forests than unlogged forest, however there is no significant significant difference between lightly logged and heavily logged forest ecosystem as shown in table 6 below.

Table 6. Follow Up Procedures for Bacteria Count using Duncan Method

Source of variation	Mean ± SE
Lightly logged	5.96± 0.04a
Heavily logged	5.55± 0.04a
Unlogged	5.22 ± 0.16b

Means having the same alphabet are not significantly different ($P \leq 0.05$).

The relationship between sand and bacteria is negative and significant, while the relationship between sand and fungi, mesofauna, and pH are positive and not significant. The relationship between bacteria and fungi are negative and not significant while the relationship between bacteria and mesofauna and pH are negative and not significant.

The relationship between fungi and mesofauna is negative and not significant; while the relationship between fungi and pH is positive and not significant all these are for unlogged forest (Table 7).

Table 7. Correlations Matrices for Unlogged forest

		Correlations				
		% Sand	Bacterial	Fungi	Mesofaunna	pH
% Sand	Pearson Correlation	1				
	Sig. (2-tailed)					
Bacterial	Pearson Correlation	-0.986	1			
	Sig. (2-tailed)	0.002				
Fungi	Pearson Correlation	0.108	-0.050	1		
	Sig. (2-tailed)	0.863	0.936			
Mesofaunna	Pearson Correlation	0.843	-0.872	-0.048	1	
	Sig. (2-tailed)	0.073	0.054	0.938		
pH	Pearson Correlation	0.077	-0.113	0.704	0.313	1
	Sig. (2-tailed)	0.903	0.857	0.185	0.608	

The result of analysis in table 8 shows the relationship between percentage sand and bacteria and fungi in lightly logged and the result are positive and not significant, while the relationship between percentage sand and mesofauna is negative but significant. Likewise the relationship between percentage sand and pH is positive and not significant. The relationship between bacteria and fungi is positive but not significant, while the relationship between bacteria and mesofauna is negative but significant. Likewise the relationship between bacteria and pH is positive and significant.

The relationship between fungi and mesofauna and pH are positive and not significant (Table 8).
The percentage sand and bacteria and pH in heavily logged are positive and are not significant. While percentage sand in heavily logged and fungi and mesofauna are negative and not significant. The relationship between bacteria and fungi is negative and highly significant. While the relationship between bacteria and mesofauna and pH in heavily logged are positive and significant. The relationship between fungi and mesofauna and pH are negative and not significant (Table 8).

The relationship between percentage sand and bacteria and fungi in lightly logged are positive and not significant, while the relationship between percentage sand and mesofauna is negative but significant. Likewise the relationship between percentage sand and pH is positive and not significant. The relationship between bacteria and fungi is positive but not significant, while the relationship between bacteria and mesofauna is negative but significant. Likewise the relationship between bacteria and pH is positive and significant. The relationship between fungi and mesofauna and pH are positive and not significant (Table 9).

Table 8. Correlations Matrices for Lightly Logged Forest

		Correlations				
		% Sand	Bacterial	Fungi	Mesofaunna	pH
% Sand	Pearson Correlation	1				
	Sig. (2-tailed)					
Bacterial	Pearson Correlation	0.804	1			
	Sig. (2-tailed)	0.101				
Fungi	Pearson Correlation	0.718	0.463	1		
	Sig. (2-tailed)	0.172	0.432			
Mesofaunna	Pearson Correlation	-0.134	-0.463	0.423	1	
	Sig. (2-tailed)	0.830	0.433	0.478		
pH	Pearson Correlation	0.803	0.924*	0.650	-0.098	1
	Sig. (2-tailed)	0.102	0.025	0.235	0.875	

*. Correlation is significant at the 0.05 level (2-tailed).

Table 9. Correlations Matrices for Heavily logged area

		Correlations				
		% Sand	Bacterial	Fungi	Mesofaunna	pH
% Sand	Pearson Correlation	1				
	Sig. (2-tailed)					
Bacterial	Pearson Correlation	0.623	1			
	Sig. (2-tailed)	0.261				
Fungi	Pearson Correlation	-0.498	-0.975**	1		
	Sig. (2-tailed)	0.393	0.005			
Mesofaunna	Pearson Correlation	-0.141	0.016	-0.167	1	
	Sig. (2-tailed)	0.821	0.980	0.788		
pH	Pearson Correlation	0.478	0.630	-0.716	0.268	1
	Sig. (2-tailed)	0.415	0.254	0.174	0.663	

**. Correlation is significant at the 0.01 level (2-tailed).

Table 10. Average Soil Properties

Forest type	% Sand composition	% Clay	% Silt	Soil pH
Unlogged	78.24± 1.00	15.87± 0.67	5.84± 1.45	5.85± 0.17
Lightly logged	76.99± 1.79	15.70± 0.29	7.31± 1.70	6.56± 0.19
Heavily logged	77.24± 1.00	18.20± 1.00	4.56± 1.00	6.40± 0.15

DISCUSSION

Results presented in Table 1 shows that there are some bacteria which are common in the three selected forest types. It implies that such bacteria have high resistance to environmental changes for instance *Bacillus cereus, Bacillus magatarium* and *Kurthia spp.* Similar findings were observed by Adekunle *et al* (2005) who reported that *Bacillus spp* were able to withstand adverse environmental conditions due to the fact that they are able to produce drought resistant endospore. They were thereby referred to as habitat generalist. *Alcaligenes*

faecolis were found in the lightly logged forest alone. The diversity of bacteria was found to be higher in the lightly logged forest (Table 4) while the heavily logged forest had the lowest diversity.

The analysis of variance shows that there is significant difference ($p<0.05$) in the bacteria count encountered in the study area whereby the lightly logged forest has the highest bacteria count being the one with highest mean value (5.96±0.04) followed by unlogged and heavily logged forest. The variation may be as a result of the opening up of canopy which allowed slight penetration of light and also due to availability of food, temperature, moderate soil pH etc.. As this was supported by the work of Adekunle *et al* (2005) and Jim-Bauda and Bozeman (2006) who reported that microorganisms needs slight penetration of sunlight to survive. The results presented in Table 2 shows that *Fusarium sp, Penicillium sp, Rhizopus nigircans* were found in the three forest habitats. This could be attributed e to the fact that they have high resistance to environmental changes. *Candian sp* was found in the heavily logged forest only.

However, out of fourteen species of fungi isolated the highest diversity were found in the lightly logged forest, and this implies that fungi concentrated much where there is slight penetration of sunlight (Adekunle *et al* 2005). The analysis of variance shows that there is no significant difference ($p<0.05$) in the three selected habitat for fungi abundance.

The relationship between percentage sand in unlogged habitat and mesofauna, likewise bacteria and mesofauna are negative and significant (Table 7) this implies that as percentage sand increases the bacteria count decreases, likewise as mesofauna increases bacteria decreases. Likewise as pH increases bacteria decreases (Table 7).

All relationship in table 8 are not significant except relationship between bacteria and pH The relationship between percentage sand and mesofauna , likewise bacteria and mesofauna in lightly logged habitat are negative. This implies that as percentage sand increases the mesofauna abundance decreases, as well as mesofauna abundance increases bacteria abundance decreases, this is because mesofauna in the soil depend on bacteria as food.

The relationship between bacteria and fungi is negative and highly significant; all other correlations in table are not significant. The relationship between percentage sand and fungi, and mesofauna are negative and not significant, which implies that as percentage sand increases the fungi count and mesofauna abundance decreases. Also as the mesofauna abundance increases the fungi count decreases. This is because mesofauna depend on fungi for food as food in the soil; hence they regulate the abundance of fungi in the soil. Also as pH value increases fungi count decreases this observation is supported by king (2002) who reported that microorganisms grow in soil that is moderately acidic and slightly acidic.

CONCLUSION

Logging has effect on the soil properties by exposing the soil to high temperature and wind thrown which in turn leads to reduction in soil fertility and increases the level of disease outbreak by destroying the microorganisms that aids plant diseases suppression thereby exposing the habitat organisms to diseases and intense temperature.

Furthermore, logging of our forest ecosystems disrupts variety of life forms in the forest ecosystems. However, the intensive site disturbance activity may decrease site productivity by altering the soil physical environment directly and species composition of soil microorganisms.

REFERENCES

Adeduntan S .A, Fuwape J.A and Ofuya T.I (2005): Environmental effects of insect herbivours and logging on tree species diversity in Akure forest reserve (Aponmu) Journal of applied tropical agriculture Vol 9 pg12-18.

Adekunle, V. A. J. Dafiewhare H. B and Ajibode O. F. (2005) Microbial population and diversity as influenced by soil pH and organic matter in different forest ecosystems. In Pakistan journal of biological sciences VOL 8 Number 10.

Akinyosoye (1976): Principles of microbial spoilage. Journal of Microorganisms. Vol 3 pg 79-82

Alexander M. (1997): Introduction to soil microbiology,2nd edition,Pg 467.

Anderson, R.V., D.C.Coleman and C.V. Cole. (1992): Effect of saprophitic grazing on net miniralization,pg 201-217. In: F.E.Clark and T. Rosswall (Editors). Terrestrial Nitrogen Cycles. Ecol. Bull. (Stockholm) 33.

Badejo A.M (1977): Ecological role of soil microflora and microfauna.Nigeria Journal of forestry Vol 2 pg 29-21.

Badejo, M.A. Tian G. and.Okoh I.O. (2005): Litter transformer as ecosystem engineers in sustainable agroecosystems Vol 2 Pg 91-94.

Biswas and Mukheatee (1987): In weed and microbial diversity assessment in chronosequence stands of Gmelina and Teak in Oluwa forest reserve. A B-Agric Tech Thesis submitted to Department of Forestry and Wood Technology, Federal university of Technology Akure, Nigeria. Pg2.

Crossley D.A, And Blumberg, A.Y. (1983): Comparison of of soil surface arthropod populations in conventional tillage, no-tillage and old field systems. Agro-Ecosystems. Vol 8 pg 247-253.

Cullen, S. J., Montagne, C. and Ferguson, H (1991): Timber harvest trafficking and soil

compaction in western Montana.pg 1418–1420.

Harvey, A. E., Page-Dumroese, D. S., Jurgensen, M. F., Graham, R. T. and Hill J.K and Harmer K C,Lace I.A. and Banham W.M.T. (1995): Effect of selective logging on tropical forest butterflies on Buru, Indonesia journal of applied ecology Vol 32 pg 54-760.

Jim-Bauda and Bozeman (2006): What do fungi and bacteria do in the soil. In Montana state University Communications Services Journal.Vol 2 pg 10-15.

Rapport (1983): In soil fauna and agriculture: past findings and future priorities. EAP Publication-25

Taggart (1970): In weed and microbial diversity assessment in chronosequence stands of gmelina and teak in Oluwa forest reserve. A B-Agric Tech Thesis submitted to Deparetment of Forestry and Wood Technology, Federal University of Technology Akure, Nigeria. Pg1.

William. L. Pritchett and Richard. F. Fisher (1987): Properties and management of forest soil.2nd Edition.