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Impacts of Logging on Bacterial and Fungal Load of Tropical Moist Forest Soil - Implications on Forest Ecosystem Sustainability

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Abstract

Forest soil at Opor bush in Otuaba community Government Bayelsa State, was investigated after logging to evaluate if logging impacts on soil microbial populations and how this affect forest ecosystem sustainability, on the backdrop that logging alter soil activities with negative impacts on the environment. Three logging sites A, B, C were randomly selected, three transect lines measuring 100m were measured from a fixed point along logging sites. 20 points measuring 5m from the fixed point were marked along each transect lines. Five points were randomly chosen and at each point 2mx2m sample plots were demarcated for sample collection. In natural area adjacent to logged sites, five sample plots measuring 2mx2m were purposely demarcated for comparison. Soil samples were taken at 0-30cm depth for microbial analyses. Cultivation and isolation of bacteria associated with soil sample was carried out using pour plate method. Results shows that bacterial species encountered were higher (9;7) than fungal species. Bacterial isolates were higher in unlogged soil (326) than logged site (136). Fungal isolates were higher in unlogged soil (407) than logged soil (189). Bacterial and fungal counts was higher in unlogged soil ($7.6x10^5$ Tcfu/g) than the logged soil ($4.7x10^5$Tcfu/g). Bacterial and fungal load between the logged and unlogged soils were highly significantly different ($p < 0.01$, $F= 17.00161$; $p < 0.01$, $F=30.9$).
Logging reduces soil microbial loads which could affect sustainability of forest ecosystem. Alternative approach such as yarding is recommended.

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Introduction

Soil microorganisms are responsible for organic matter decomposition, nutrient cycling and maintenance of soil structure and degradation of pollutants and thus have great role in long-term sustainability of forest ecosystems (Duffkova and Macyrona, 2011). At the ecosystem level, the microbial communities mediate soil productivity and modulate the resilience of forest ecosystem to stress (Kuramae *et al*.,2001, Bardget *et al*., 2014). It is likely that the microbial community structure, metabolic activities and gene expression patterns can serve as indicators of forest ecosystem status, which is vital to monitor forest ecosystems, to evaluate effects of anthropogenic disturbances and to detect changes in energy and nutrient flow patterns before they have irreversible effects (Timbal and Viney, 2013).

Arunacham *et al*. (2000) observed that soil disturbed by tree removal often have reduced microbial diversity compared with undisturbed areas. Logging has been reported to decrease the fungal biomass and cause changes in the bacterial community structure (Ohtonen and Pennanen, 1999). Logging can exert direct effects on the soil microbial physiology and indirect effects by changing plants and soil properties (Camey and Matson, 2005., Stegen *et al*., 2012). Site organic matter (OM) and soil porosity (SP) are two vital properties directly affected by logging (Grigal,2000). Logging can cause severe soil compaction, especially in soils with low initial bulk density and high-water saturation (Powers *et al*.,2005). Compacted soil directly affects the prokaryotic communities by limited oxygen availability, altered water regimes and reduced pore sizes (Schnurr-Putz *et al*., 2006). Organic matter removal and soil compaction can change carbon and nitrogen content, nutrient availability, diversity of meso- and macrofauna, leading to a low resource environment (Keenan and Kimmins, 1993, Jugersen *et al*.,1997). All these changes can subsequently reduce soil microbial biomass and indirectly exert an influence on soil microbial community composition and structure (Carney and Matson, 2005).

Soil bacteria are highly responsive to soil nutritional changes (Carney and Matson, 2005), while archaea are more resilient to energy stress. Logging, as a disturbance event, kills or severely impacts numerous members of soil microbial community (Yao *et al*., 2014), which can be viewed as a 'reset' of the community assembly or as an 'environmental filter'. Logging creates a relatively low nutrition environment, thus, affecting the bacterial community. Removal of wood has an obvious influence on heterotrophic soil organisms. This loss of carbon, nitrogen, and associated minerals has a pronounced effect on the complex of micro-organisms dependent upon this material as a source of energy and nutrients. Thus, the removal of woody substrates would drastically alter the activity of fungi and other micro-organisms associated with wood decay.

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Materials and Methods

Study Area

Otuaba is a rural community situated in Ogbia Local Government of Bayelsa State, in the Niger delta region of Nigeria. The community has a total population of 7,000 according to 2006 census, and lies within latitude of 4'51.23" N and longitude 6'20'19.8"E. It is bounded to the North by Elebele community to the east by Emeya II and kolo, to the west by Onuebum and otuogiri and to the south by Ewoi community. The existence of a tropical moist forest makes these communities rich in many economically important trees like African walnuts, *Colaedulis*, *Carcinacola*, *Irvingiagabonensis* etc. which generally contribute to the green vegetation. Otuaba shares similar climatic conditions with its neighboring communities, having rainfall generally every month of the year with heavy downpour between July through September. The mean temperature is in the range of 25^0C to 31^0C and the hottest months are December to April. Relative humidity is high in Otuaba throughout the year and decreases slightly in the dry season. Soil condition in the area is wet and moist throughout the year. Dominant economic activities carried out in the region include fishing, farming, boat making and lumbering.

Sampling

Three logging sites A, B and C were randomly selected in OPOR forest, a natural forest situated away from the settlement area and three transect lines measuring 100m were measured from a fixed point beginning from where cutting started along the logging sites A, B, C. 20 points measuring 5m from the fixed point were marked along each transect lines. 5 points were randomly chosen and at each point a 2mx2m sample plots were demarcated for sample collection. On the free area adjacent to the logging sites where no logging was done, five sample plots measuring 2mx2m were purposely demarcated for comparison.

Data Collection

Soil samples were collected using soil auger at the depth of 0-30cm from the logging sites A and B, C and from the uncut area. Samples were taken in their moist conditions in a polythene bag to the laboratory for microbiological analyses.

Data Analyses

The calculation of CFU was carried out as follows: - CFU = degree of dilution × aliquot × number of colonies. Morphology and cultural characteristic were analyzed by gram staining method, Biochemical characterization was analyzed using simple staining, Indole Production Test, Citrate Test, ant Oxidation Test. The SPSS package was used in analyzing the CFU.

The identified bacteria varied between $4.7x10^5$ to $7.6x10^5$Tcfu/g in the soil samples. They belong to the genera: *Pseudomonas, Klebsiella, Bacillus, E. coli, Proteus, Serratia, Micrococcus, Staphylococcus,* and *Erwinia*. Results in Table 1 shows that number of bacteria species isolated from unlogged forest soil were higher than in the logged forest soil. It also shows that of the nine bacteria species isolated in the unlogged forest soil, *Pseudomonas* species has the highest percentage (16.26%) while *Erwinia* species has the least percentage (5.52%). Under the logged forest soil, *Serratia* species has the highest percentage of occurrence where 13.80% were isolated, while *Erwinia* species has the lowest (2.20%). In all, the table show that number of bacteria isolates were higher in the undisturbed area than in the logged area.

Table 1: Number of Bacteria Isolates and Percentage in Logged and Unlogged forest Soil in Opor

Bacterial Species	**Logged Soil Isolates**	**%**	**Unlogged Soil Isolates**	**%**
Pseudomonas	12	8.82	53	16.26
Klebsiella	19	14.0	30	9.20
Bacillus	6	4.41	19	5.83
E.coli	17	12.50	39	11.96
Proteus	15	10.92	39	11.96
Serratia	33	24.26	45	13.80
Micrococcus	12	8.82	32	9.82
Erwinia	3	2.20	18	5.52
Total	**136**	**100**	**326**	**100**

Results in table 2 shows that percentage isolates of fungal species was higher in unlogged forest soil than under logged forest soil, with *Penicillin* species having the highest (19.16%) isolate, of the seven fungal species found in the unlogged forest soil. *Mucor* and *Fusarium* species have the same frequencies of occurrence (59), representing 14.50% each in unlogged soil. Under logged forest soil, *Fusarium* species has the highest percentage of isolate (22.75%) while *Aspergillus* species has the lowest (7.93%). In all, the number of fungal isolates were higher in unlogged forest soil than in soil under logging.

Table 2: Number of Fungal Isolates and Percentage in Logged and Unlogged forest Soil in Opor Forest

Fungal Species	**Logged Soil Isolates**	**%**	**Unlogged Soil Isolates**	**%**
Aspergillus	15	7.39	48	11.80
Rhlopu	34	18.00	56	13.75
Penicillin	11	5.82	78	19.16
Saccharomyces	33	17.46	55	33.51
Mucor	23	12.17	59	14.50
Fusarium	43	22.75	59	14.50
Aspergillus fumigatus	30	15.87	52	12.78
Total	**189**	**100**	**407**	**100**

A stable forest ecosystem is one that is productive, can recover from disturbances; provide the needed good and services, and self –regenerating. However, for the forest ecosystem to exhibits these qualities, it must subsist on a stable and constantly interactive and undisturbed soil environment.

Results on table 1, and 2 shows that bacterial and fungal loads were higher in unlogged forest soil than in soil under logging operation. The soil type and properties investigated were the same meaning that soil fungal and bacterial loads should normally follow the same trend in occurrence, but for the logging operation that has taken place in site A and B. The number of bacterial and fungal isolates were higher in unlogged forest soil than in the logged forest soil, and the total microbial counts for bacterial and fungal between logged and unlogged forest soil was highly significantly different (($p < 0.01$, $F= 17.00161$; $p < 0.01$, $F=30.9$) Table 3, and 4.Soil disturbance such as compaction by heavy machines and trucks compresses the soil structure thus reducing or closing up the pore space for water and air thereby limiting soil air, aeration and soil water for the below ground microbes which reflects on species occurrence and abundance, and eventually on the soil fungal and bacteria population, as some will either migrate or die off as bacteria are said to be highly responsive to soil nutritional changes Siera (Forest Legacy, 2008). Soil microorganisms are responsible for organic matter decomposition, nutrient cycling and maintenance of soil structure and degradation of pollutants and therefore pivotal to sustainability of the forest ecosystem.

Forest productivity is a site index predictor, meaning that if the soil loses all or some of its functional integral components, this will reflect on the forest stands. Soils with low or devoid of robust microbial populations could be termed a poor soil because such soil will be poor in nutrients resulting to poor forest stands. Low soil fungal and bacteria load could influence important processes like nitrogen cycle and biogeochemical cycles which keep the soil ecosystem dynamic and stable.

A functional soil ecosystem will give rise to a functional forest ecosystem because greater components of what make the forest ecosystem stable and sustainable is a derivative of the soil on which forest stand subsist. Soil bacteria and fungi play a major role in enhancing soil quality because many soil processes flow through these organisms. Soil bacteria community and the community's biodiversity, are pivotal in soil quality determination, biodiversity, and agro- ecosystem stability for sustainability. There is therefore a strong implication that a sustainable forest ecosystem can only result from a dynamic, microbial rich soil ecosystem. It is on this premise we carried out this research to ascertain whether soil disturbance through logging operation affect soil bacterial and fungal load of a moist tropical forest soil. The findings suggest logging of forested areas can have negative impacts on soil microbial community which in turn will negatively impact on the forest stand.

Our results indicate that logging negatively affect soil fungal and bacterial load which could lead to poor soil functions, bearing in mind that soil functionality is a conglomeration of microbial activities going on in the soil. It therefore means that forest logging will impact negatively on the forest ecosystem. Under a disturbed soil environment, forest cutting, particularly logging will result in poor forest regeneration due to trampled wildlings. Poor seed germination due to trampled seeds on soil surface, which have become buried deeply below the top soil will also occur. Tree removal by logging will create gaps in the canopy layers giving room for penetration of more radiation from the sun as well as rain drops, causing the forest ecosystem to experience a phenomenon that is entirely new to its dynamics in which case, will affect its functions and services as it reacts to these changes.

Conclusion

Sustainable forest ecosystem is the anchor of conducive environment and since environmental sustainability is rooted in the activities of soil microorganisms, the protection of forest soil and its microorganisms cannot be overlooked. Logging impacts on soil bacterial and fungal loads in moist forest soil as is with dry upland soils. Heavy trucks should not go beyond the landing while cable transport of log is suggested in other to have minimal impact on the forest soil.

Conflict of Interest: There is no conflict of interest in this manuscript.

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