EFFECTS OF SOME PLANTATION CROPS ON MICRO-BIOLOGICAL PROPERTIES OF SOILS IN AKWA IBOM STATE, SOUTHEASTERN NIGERIA

ABERAGI, F. V.[1*], ATOYEBI, B.[2], OLIM, D. M.[3] AND AFANGIDE, A. I.[4]

[1,& 3]*Department of Soil Science, University of Calabar, Calabar.*

[2]*Department of Microbiology, University of Calabar, Calabar.*

[4]*Department of Soil Science, University of Technology, Owerri.*

**Corresponding author: aberagifidelis@gmail.com. GSM: 08033714972*

ABSTRACT

Tree crop plantations enhance the fertility of soil on which they grow by providing favourable micro-climate, massive organic litter and protection against erosion. Detailed quantitative scientific information on the soils under different tree species plantations are needed to guide management of the plantation to ensure soil conservation. This study investigated the effects of plantation crops on microbiological properties of soils of Uyo and Ibecikpo Asutan Local Government Areas in Akwa Ibom State. Soil samples were collected at 0 -15 cm depth in three plantations - oil palm (OPP), cashew (CAS) and Gmelina (GME). Total heterotrophic bacteria count (THBC) and total heterotrophic fungi count (THFC) were 14.58 x 10^5 $cfug^{-1}$ and 8.51 x 10^5 $cfug^{-1}$ during the wet season while during the dry season they were 17.50 x 10^5 $cfug^{-1}$ and 5.92 x 10^5 $cfug^{-1}$ respectively. THBC and THFC showed no significant difference ($p>0.05$) between seasons and plantations. THBC and THFC showed no significant ($p>0.05$) effect of plantation crop type and there was no significant difference between the seasons. The soils contained Bacillus, Achromobacter, Enterobacter, Clostridium perfringers, Microccocus, Flavobacteria sp, Penicillium, Aspergillus, candida, monilia, Mould sp, and Fusarium sp. THBC was found as 17.25 x 10^5, 18.63 x 10^5, and 12.25 x 10^5 $cfug^{-1}$, while THFC was 6.94 x 10^5, 5.58 x 10^5, and 9.13 x 10^5 $cfug^{-1}$, respectively for OPP, CAS and GME. It was concluded that the relative abundance and diversity of the microorganisms encountered in the different plantation sites was an indication that the seasonal fluctuations of microbial population are due to moisture content of the soils which affect the total number of microorganisms in the soils. The higher population of microorganisms during rainy season can be attributed to favorable moisture contents of the soils which favors rapid multiplication and growth of microorganisms.

Keywords: Micro-biological properties, plantation, soil, moisture content, seasons.

INTRODUCTION

The soil is one of the most dynamic sites of biological activity in nature. A very large population of microorganisms brings about biochemical reactions involved in decomposition of organic matter, weathering of rocks and nutrition of cultivated and uncultivated plants. It is based this fact that Essington (2015) opined that humans live on a roof top of a hidden world of cornucopia of microorganisms. A handful of soil can contain literally billions of bacterial cells, and tens of thousands of bacterial and hundreds of fungal species (Essington, 2015). Soil microbial population is the driving force that regulates soil processes and is governed by interactions between plant types, climate and management practices. Microorganism activities are one of the most important ecosystem components evaluated as an indicator of soil quality protection and sustainability (Bolat *et al.*, 2015; Oyedele *et al.*, 2015). Changes in climatic conditions such as fluctuations in the abundance and seasonality of

rainfall have important consequence at the ecosystem level. Seasonality can predict a reduced portion of the variation in microbial communities' distributions that is closely associated with climate factors; in this way, fast-changing soil attributes, such as soil moisture, soil processes, and nutrient pools, which are known to change over days or weeks, are likely better able to predict changes in microbial communities over shorter time periods (days to months). For example, soil moisture is well known to influence the community composition and activity of microbial communities in drying and rewetting processes (Manzoni *et al.,* 2012; Evans et al., 2014). Adenike and Olubukola (2019) reported that only a few studies have been done on the effect of different tree crop plantations and season on microbial population and diversity across the world. In Nigeria, and Akwa Ibom State in particular, no such study has been carried out.

The world population has kept increasing rapidly over time causing concern to several world economies and scholars all over the globe resulting in intensification of effort to increase yields per land area. Understanding microbial diversity and variation with land uses and seasons is of utmost importance in sustainable soil management and utilization for its overall productivity. This study sought to assess the effect of different plantation crops and season on microbial diversity in humid tropics of Nigeria.

Materials and Method

The study was carried out on the soils underneath cashew and gmelina along Uyo Village Road, Uyo, both on latitudes 5° 02′N and longitudes 7° 56′E and Eteidung John Thompson Udoh's oil palm plantation at Ibesikpo Asutan Local Government Area on latitudes 4° 55′N and longitudes 7° 58′E. The gmelina plantation was established in 2002 and covers about two and a half hectares. The trees were planted at 2 x 3 m distance. The cashew plantation was established in 1999 and covers about two hectares. The trees were planted at 8 x 7 m distance, and oil palm plantation was established in 1999 and covers about four hectares. The trees were planted at 9 x 9 m distance.

The experimental design used was completely randomized block design (CRBD), with the tree species as treatments and times (wet season, dry seasons: WS, DS) as blocks. Samples were collected from three different tree plantations. Two plantations located along Uyo City Road, and one at Ibesikpo area in Akwa Ibom State. The samples were collected at 0 - 15 cm depth for microbial analysis. Samples collections were carried out twice a month at 2 weeks interval from the month of September to December in 2014. Samples were placed in sterile polythene bags and immediately transported to the Microbiology Laboratory, University of Uyo for analysis.

The media used in this study were Nutrient agar for Total Heterotrophic Bacteria Counts and Potato dextrose agar for Total Fungal Counts. All the media were prepared and sterilized according to manufacturer's specifications.

The microbiological analysis was carried out based on the methods described by Atoyebi and Ekpo (2020). A measure of 1g of the soil sample collected from oil palm, cashew and gmelina plantations were serially diluted in tenfold up to 10^{-7} tubes. Then 1ml aliquots from the 10^{-4} tubes were aseptically inoculated onto already prepared plates of nutrient agar and potato dextrose agar using the pour plate method of inoculation. All plates were inverted and the nutrient agar (for bacteria) was incubated at 37°C for 24 hours while the potato dextrose agar plates (for fungi) were incubated at ambient laboratory temperature (28±2° C) for 72 hours. After the incubation, the total bacterial and fungal colonies on plate that contain 30 – 300 colonies were counted using a colony counter. The number of colonies on a plate was multiplied by the dilution factor to give the plate count per ml of the soil

sample and recorded as $cfug^{-1}$. E.g. if the counts for 2 plates of the 10^{-6} dilution were 55 and 65, the average is 60. Therefore, the original soil sample contains 60 x 10 x 10^6 = 6 x 10^8 $cfug^{-1}$. The colonies were also repeatedly subcultured onto fresh nutrient and potato dextrose agar media to obtain pure isolates. The bacterial isolates were identified and characterized using cultural, morphological and standard biochemical tests as described by Atoyebi and Ekpo (2020). The fungal isolates were identified according to the methods described by Oladele *et al.* (2019) based on their colour of aerial hyphae and substrate mycelium, arrangement of hyphae, and conidial arrangement.

Data Analysis

The data collected were subjected to analysis of variance. Significant means were separated using the Least Significant Difference (LSD).

Results and Discussion

THBC under OPP, CAS and GME was 17.25 x 10^5, 18.63 x 10^5, and 12.25 x 10^5 $cfug^{-1}$, respectively. There was no significant ($p>0.05$) effect of plantation crop type on THBC, but the trend was CAS > OPP > GME (Table 1). During the WS, THBC was 14.58 x 10^5 $cfug^{-1}$, while it was 17.50 x 10^5 $cfug^{-1}$ during the DS, but there was no significant difference between them. There was rainfall in the first week of the DS (sample 5) and a heavy down pour for three days during the third week of the DS (sample 6). This led to a significant increase in microbial biomass. The interaction of plantation crop type and season had no significant influence on THBC but the trend was as follows: CAS x dry, OPP x wet, OPP x dry, GME x wet, CAS x wet, GME x dry. The results of the different variety of bacteria isolated from the soil samples were identified as *Bacillus, Achromobacter, Enterobacter, Clostridium perfringers, Micrococcus, Flavobacteria sp,* as presented in Table 2. Variations in the population of THB (total heterotrophic bacteria) depends upon some factor such as rhizospheric positive interaction (due to release of fatty acid, protein, amino acids) and negative interaction (due to release of antimicrobial compounds, lack of suitable substrate as nutrition for microbes) between plant exudates and microbes (Adeleke and Babalola, 2021). Variation in heterotrophic population has also been reported by Ogbemudia & Ogboghodo (2020); Ubogu *et al.* (2019) in coastal areas of Nigeria.

THFC under OPP, CAS and GME was 6.94 x 10^5, 5.58 x 10^5, and 9.13 x 10^5 $cfug^{-1}$, respectively. There was no significant ($p>0.05$) effect of plantation crop type on THFC, but the trend was GME > OPP > CAS (Table 1). During the WS, THFC was 8.51 x 10^5 $cfug^{-1}$ while it was 5.92 x 10^5 $cfug^{-1}$ during the DS, but there was no significant difference between them. THFC increased in the first and third week of the DS (sample 5 and 6) due to heavy rainfall during these periods. The study indicated that fungi population decreased in the dry season. This agrees with the findings by Oladele *et al.* (2019) and Nwokolo *et al.* (2021) who reported that population of fungi during wet season could be due to favorable moisture contents of the rhizosphere soil which favors rapid multiplication and growth of microbes.

The interaction of plantation crop type and season had no significant influence on THFC, but the trend was as follows: GME x wet, OPP x wet, CAS x dry, GME x dry, OPP x dry, CAS x wet. Results of the different variety of fungi isolated from the soil samples were identified as *Penicillium sp, Aspergillus niger, candida, monilia, Mould sp, and Fusarium sp* (Table 2).

Table 1: Effect of plantation crop type and season on soil microbiological properties of coastal plain sands in Akwa Ibom State, Nigeria

	THBC	THFC
	cfug^{-1} ← →	
Plantation Type		
OPP	17.25 x 10^5	6.94 x 10^5
CAS	18.63 x 10^5	5.58 x 10^5
GME	12.25 x 10^5	9.13 x 10^5
LSD	16.73 x 10^5 ns	5.72 x 10^5 ns
Season		
Wet	14.58 x 10^5	8.51 x 10^5
Dry	17.50 x 10^5	5.92 x 10^5
LSD	13.66 x 10^5 ns	4.67 x 10^5 ns
Plantation x Season Interaction		
OPPxwet	17.75 x 10^5	8.38 x 10^5
OPPxdry	16.75 x 10^5	5.5 x 10^5
CASxwet	11.75 x 10^5	4.9 x 10^5
CASxdry	25.50 x 10^5	6.25 x 10^5
GMExwet	14.25 x 10^5	12.25 x 10^5
GMExdry	10.25 x 10^5	6.0 x 10^5
LSD	23.66 x 10^5 ns	8.09 x 10^5 ns

THBC = Total heterotrophic bacteria count, THFC = Total heterotrophic fungi count, OPP = oil palm plantation, CAS = cashew plantation, GME = gmelina plantation, LSD = Least significant difference, ns = not significant.

Table 2: Microbial isolates from each sample

Samples Wet Season	Bacterial Isolates					Fungal Isolates					
	OPP	Count (cfu/g)	CAS	Count (cfu/g)	GME	Count (cfu/g)	OPP	Count (cfu/g)	CAS	Count (cfu/g)	GME	Count (cfu/g)
1	Bacillus sp, Achromobacter, Enterobacter	7×10^5 5×10^5 5×10^5	Bacillus sp, Achromobacter, Micrococcus sp	5×10^5 3×10^5 2×10^5	Bacillus sp, Flavobacteria sp, Enterobacter Clostridium perfringers	4×10^5 3×10^5 4×10^5 2×10^5	Penicillium sp, Aspergillus niger, Candida, Monilia	10×10^5 9×10^5 2×10^5 2×10^5	Penicillium sp, Aspergillus niger, Mould sp,	3×10^5 1×10^5 1×10^5	Penicillium sp, Aspergillus niger, Fusarium sp	12×10^5 8×10^5 6×10^5
2	Bacillus sp, Achromobacter, Enterobacter	6×10^5 4×10^5 3×10^5	Bacillus sp, Achromobacter, Micrococcus sp	6×10^5 5×10^5 2×10^5	Bacillus sp, Flavobacteria sp, Enterobacter Clostridium perfringers	4×10^5 4×10^5 3×10^5 2×10^5	Penicillium sp, Aspergillus niger, Candida, Monilia	1×10^5 0.4×10^5 0.4×10^5 0.2×10^5	Penicillium sp, Aspergillus niger, Mould sp	4×10^5 2×10^5 2×10^5	Penicillium sp, Aspergillus niger, Fusarium sp	3×10^5 1×10^5 2×10^5
3	Bacillus sp, Achromobacter, Enterobacter	6×10^5 4×10^5 3×10^5 3×10^5	Bacillus sp, Achromobacter, Micrococcus sp	4×10^5 4×10^5 2×10^5	Bacillus sp, Flavobacteria sp, Enterobacter Clostridium perfringers	4×10^5 3×10^5 4×10^5 2×10^5	Penicillium sp, Aspergillus niger, Candida, Monilia	4×10^5 2×10^5 1×10^5 1×10^5	Penicillium sp, Aspergillus niger, Mould sp	3×10^5 2×10^5 1×10^5	Penicillium sp, Aspergillus niger, Fusarium sp	3×10^5 2×10^5 2×10^5
4	Bacillus sp, Achromobacter, Enterobacter	11×10^5 9×10^5 5×10^5	Bacillus sp, Achromobacter, Micrococcus sp	7×10^5 3×10^5 4×10^5	Bacillus sp, Flavobacteria sp, Enterobacter Clostridium perfringers	4×10^5 4×10^5 4×10^5 2×10^5	Penicillium sp, Aspergillus niger, Candida, Monilia	0.1×10^5 0.2×10^5 0.1×10^5 0.1×10^5	Penicillium sp, Aspergillus niger, Mould sp	0.3×10^5 0.2×10^5 0.1×10^5	Penicillium sp, Aspergillus niger, Fusarium sp	3×10^5 4×10^5 4×10^5

Mean colony count		**17.75 x 10^5**		**11.75 x 10^5**		**14.25 x 10^5**		**8.38 x 10^5**		**4.90 x 10^5**		**12.25 x 10^5**
Dry season												
5	Bacillus sp, Achromobacter, Enterobacter	10 x 10^5 4 x 10^5 5 x 10^5	Bacillus sp, Achromobacter, Micrococcus sp	6 x 10^5 4 x 10^5 2 x 10^5	Bacillus sp, Flavobacteria sp, Enterobacter Clostridium perfringers	4 x 10^5 2 x 10^5 2 x 10^5 2 x 10^5	Penicillium sp, Aspergillus niger, Candida, Monilia	3 x 10^5 1 x 10^5 1 x 10^5 1 x 10^5	Penicillium sp, Aspergillus niger, Mould sp	4 x 10^5 3 x 10^5 1 x 10^5	Penicillium sp, Aspergillus niger, Fusarium sp	5 x 10^5 4 x 10^5 2 x 10^5
6	Bacillus sp, Achromobacter, Enterobacter	14 x 10^5 8 x 10^5 10 x 10^5 6 x 10^5	Bacillus sp, Achromobacter, Micrococcus sp	44 x 10^5 24 x 10^5 14 x 10^5	Bacillus sp, Flavobacteria sp, Enterobacter Clostridium perfringers	11 x 10^5 8 x 10^5 4 x 10^5 3 x 10^5	Penicillium sp, Aspergillus niger, Candida, Monilia	4 x 10^5 3 x 10^5 2 x 10^5 1 x 10^5	Penicillium sp, Aspergillus niger, Mould sp	4 x 10^5 6 x 10^5 2 x 10^5	Penicillium sp, Aspergillus niger, Fusarium sp	5 x 10^5 4 x 10^5 1 x 10^5
7	Bacillus sp, Achromobacter, Enterobacter	3 x 10^5 1 x 10^5 1 x 10^5 1 x 10^5	Bacillus sp, Achromobacter, Micrococcus sp	3 x 10^5 1 x 10^5 1 x 10^5	Bacillus sp, Flavobacteria sp, Enterobacter Clostridium perfringers	1 x 10^5 1 x 10^5 0.5 x 10^5 0.5 x 10^5	Penicillium sp, Aspergillus niger, Candida, Monilia	2 x 10^5 1 x 10^5 0.8 x 10^5 0.2 x 10^5	Penicillium sp, Aspergillus niger, Mould sp	1 x 10^5 1.4 x 10^5 0.6 x 10^5	Penicillium sp, Aspergillus niger, Fusarium sp	0.3 x 10^5 0.8 x 10^5 0.9 x 10^5
8	Bacillus sp, Achromobacter, Enterobacter	2 x 10^5 1 x 10^5 1 x 10^5	Bacillus sp, Achromobacter, Micrococcus sp	2 x 10^5 0.5 x 10^5 0.5 x 10^5	Bacillus sp, Flavobacteria sp, Enterobacter Clostridium perfringers	0.6 x 10^5 0.5 x 10^5 0.5 x 10^5 0.4 x 10^5	Penicillium sp, Aspergillus niger, Candida, Monilia	0.9 x 10^5 0.4 x 10^5 0.5 x 10^5 0.2 x 10^5	Penicillium sp, Aspergillus niger, Mould sp	1 x 10^5 0.8 x 10^5 0.2 x 10^5	Penicillium sp, Aspergillus niger, Fusarium sp	0.5 x 10^5 0.3 x 10^5 0.2 x 10^5
Mean colon		**16.75 x 10^5**		**25.50 x 10^5**		**10.25 x 10^5**		**5.50 x 10^5**		**6.25 x 10^5**		**6 x 10^5**

OPP = oil palm plantation, CAS = cashew plantation, GME = gmelina plantation

Conclusion

Result presented here showed that microbial properties of the investigated soils changed in response to season. Therefore, the organisms are neither uniformly distributed through the soil nor uniformly present all year. The study demonstrated that bacteria and fungi population increased significantly in wet condition. The central role of microbial biomass in the soil nutrient cycling facilitated the use of microbial biomass as an indicator for healthy soil. Cashew had the highest soil microbial biomass followed by oil palm, then gmelina. In other words, the soil health of the plantations is in the order of cashew, oil palm and gmelina.

REFERENCES

Adeleke, B. S., & Babalola, O. O. (2021). Roles of plant endosphere microbes in agriculture-a review. *Journal of Plant Growth Regulation*, 1-18.

Adenike, E. A., & Olubukola, O. B. (2019) Effect of land use on bacterial diversity and community structure in Temperate Pine and Indigenous Forest Soils. *Diversity, 11*(117), 1-12.

Adesemoye, A. O., Opere, B. O., & Makinde, S. C. O. (2006). microbial content of abattoir wastewater and its contaminated soil in Lagos, Nigeria. *African Journal of Biotechnology, 5*(20), 1963-1968.

Atoyebi, B., & Ekpo, M. A. (2020). Microorganisms and Physico-chemical Profile of Aquatic Ecosystem in Akwa Ibom State. *Journal of Applied Life Sciences International*, 23(6), 15-22.

Bolat, I., Kara, O., & Tunay, M. (2015). Effects of seasonal changes on microbial biomass and respiration of forest floor and topsoil under Bornmullerian Fir Stand. *Eurasian Journal of Forest Science 3*, 1-13.

Essington, M. E. (2015) Soil and water chemistry: An integrative approach. CRC press.

Evans, S. E, & Wallenstein, M. D. (2014). Climate change alters ecological strategies of soil bacteria. *Ecol Lett 17*, 155–164.

Manzoni, S., Schimel, J. P., & Porporato, A. (2012). Responses of soil microbial communities to water stress: results from a meta-analysis. *Ecology 93*, 930–938.

Nwokolo, N. L., Enebe, M. C., Chigor, C. B., Chigor, V. N., & Dada, O. A. (2021). The contributions of biotic lines of defense to improving plant disease suppression in soils: A review. *Rhizosphere*, *19*, 100372.

Ogbemudia, I., & Ogboghodo, I. A. (2020). Soil chemical properties and heterotrophic bacterial population in the rhizosphere of oil palm plantations under different ages. *ADAN JOURNAL OF AGRICULTURE*, *1*(01), 74-81.

Oladele, S., Adeyemo, A., Adegaiye, A., & Awodun, M. (2019). Effects of biochar amendment and nitrogen fertilization on soil microbial biomass pools in an Alfisol under rain-fed rice cultivation. *Biochar*, *1*(2), 163-176.

Oyedele, A. O., Olayungbo, A. A., Denton, O. A., Ogunrewo, O. M., & Momodu, F.O. (2015). Assessment of the microbial biomass carbon, nitrogen and phosphorus in relation to physico-chemical properties of Acric Luvisols in Ibadan South West, Nigeria. *Journal of Agriculture and Environment for International Development (JAEID) 109*, 179-187.

Ubogu, M., Odokuma, L. O., & Akponah, E. (2019). Enhanced rhizoremediation of crude oil–contaminated mangrove swamp soil using two wetland plants (Phragmites australis and Eichhornia crassipes). *Brazilian Journal of Microbiology*, *50*(3), 715-7