ISSN (Online): 2349-1183; ISSN (Print): 2349-9265
TROPICAL PLANT RESEARCH
The Journal of the Society for Tropical Plant Research
6(1): 90–100, 2019
DOI: 10.22271/tpr.2019.v6.i1.013

Research article

Identification of soil microbial population under different land use

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[Accepted: 10 April 2019]

Abstract: Soil microorganism is important for the restoration, sustainability, balancing of soil ecosystem and organic matter transfer. The diversity of the microbial community in soil is closely related to the functions and structure of its surrounding ecosystem. The aim of this research work is principally on the identification of microbial population under different land use types in Akure, Nigeria. The land use types were oil palm, teak plantation, unclear forest, and cassava and sugar plantations. The soil samples were collected at depth of 0–15 cm, 15–30 cm and 30–75 cm on each land use area and were taken to the laboratory for microbial analysis. Microbial analysis was carried out using the dilution spread plates techniques of identification of microbial population. The bacteria isolates were identified by morphological and biochemical characterization using taxonomy scheme of Bergey's manual of determinative bacteriology. The fungal isolate were stained with lactophenol cotton blue and observed under the microscope for identification. The result showed that, there are 40 different species of bacteria and 10 fungal strains isolated from all the land use types. Some of the isolated bacterial species were from phylumactinobacter, bacteriodietes, firmicutes, proteobacter and that of fungi were representatives of phylum Ascomycota and Zycomycota. The data on bacteria and fungi were analyzed using ANOVA. The means of bacteria and fungi occurrence were separated using least significance difference at 5% level. It was found that the cassava land showed higher diversity of microbial population, this might be attributed to the effect of tillage on the land year by year which enhanced the free movement of air and encourages the availability of microbial population due to the presence of some microorganism in the tuber of cassava which had a great influence on soil organic matter contents via mineralization and decomposition.

Keywords: Soil ecosystem - Microbial population - Bacteria - Fungi - Land use types.

[Cite as: Akande GM & Adekayode FO (2019) Identification of soil microbial population under different land use. *Tropical Plant Research* 6(1): 90–100]

INTRODUCTION

Soil harbors over 109 microorganisms, soils are the most diverse habitat of microbes on earth and provide an ideal reservoir for microorganism (Dischinger *et al.* 2009). It's also a highly complex biological system that influenced the physical-chemical environmental parameters. The microorganism, which is sensitive indicators of the status of an ecosystem, can lose their resilience to ecosystem disturbances and become unable to perform their nutrients cycling functions. The importance of microorganism in ecosystem functioning has led to an increased interest in determining soil microbial population (Azam *et al.* 2003). The soil microbial communities are the active component ecosystem. It had been revealed that microorganism varied in and between soil types with bacteria being the most numerous (Girvan *et al.* 2003), It was reported that fungi in soil constituting a significant part of the soil biomass and served several important functions as decomposition of organic material, nutrient cycling, formation of soil aggregates and mycorrhizal symbiosis in soil (Kabir *et al.* 2003, Tahjib-Ul-Arif *et al.* 2018).

The land use types had been reported to play important roles in regulating microbial communities in tropical soils than in many temperate systems, where favorable climatic factors, combined with access to fertilizers and other soil amendments, helped to buffer changes in the soil environment (Buckley & Schmidt 2001). Land use

Received: 24 November 2018 Published online: 30 April 2019
https://doi.org/10.22271/tpr.2019.v6.i1.013

change affects the microbiota and their functions (Fierer *et al.* 2006). Change in land can affects the composition and function of microbial communities. Analysis of changes in microbial communities in tropical soils had hitherto been limited to a few land use types. These analyses had shown increases in microbial and fungal biomass as a result of differing organic matter inputs.

Particular the planting of different crops on the land, has led to decreases in soil microbial population throughout the world and has declined soil biodiversity of the microorganism (Liiri *et al.* 2012). Therefore, the need for identification of soil microbial population is becoming a rapidly growing concern. The study of soil microorganism through the world has yielded a lot of soil microbial species that are of a great value for the ecosystem. Microorganisms are easy to isolate, culture and maintain to improve their strain, microbes are omnipresent and exist in the environment. Bacteria are predominant because of their resistance endospore formation (Cafini *et al.* 2006). Therefore, determination of microbial population and identification of microbial population is a valuable tool for interpretation of microbial information in an ecological contexts and to examine how the abundances of major soil bacterial phyla corresponding to the biotic and abiotic characteristics of the soil environment. The absence of available data indicating the microbial population of soil types has led to assess the identification of soil microbial population in Akure, Nigeria.

MATERIALS AND METHODS

Description of the study area

The study was conducted at the teaching and research farm of the Federal University of Technology Akure, Nigeria. Akure is located in the tropical rainforest area of southwestern Nigeria with a mean annual rainfall between 1300 mm and 1600 mm, which normally occurs between March to November and peaks in June/July. The dry season lasts about 3 months (December–February). It has a mean annual temperature of 27ºC (minimum) and 32ºC (maximum) with the elevation ranged from 255 to 381 meters above the sea level and the relative humidity during the raining season is between 85 and 100% and less than 60% during the dry season (Fasinmirin & Oguntuase 2008). The soils in these sites are classified as Alfisols by USDA soil taxonomy system and are characteristics of the variety found in the intensively weathered areas of basement complex formations in the tropical rainforest zone of south-western Nigeria (Onyekwelu *et al.* 2006).

Land use type

Land use types are oil palm, teak plantation, unclear forest, cassava and sugar. The teak plantation and unclear forest land is a natural forest which has not been disturbed for at least 100 years. Although shrubs and climbers are present in the unclear forest, the major plant species are trees such as bamboo (*Bambusa vulgaris* Schrad. ex J.C.Wendl.), oil bean (*Pentaclethra macrophylla* Benth.), and oil palm (*Elaeis guineensis* Jacq.). The arable and fallow land had been previously cultivated for 7 years with cassava (*Manihot esculenta* Crantz), and maize (*Zea mays* L.) either as sole crops or as crop combinations in various plots. Some of the crops cultivated during the previous years were cocoyam (*Colocasia esculenta* (L.) Schott), eggplant (*Solanum melongena* L.), pepper (*Capsicum* spp.), sweet potato (*Ipomoea batatas* (L.) Lam) and yam (*Dioscorea* spp.). At the time of sampling, both cassava and maize were cultivated on the land.

Soil sampling

Seven sample plots were demarcated on the ground in each land use. The size of the sample plots in oil palm, teak plantation, uncleared forest, cassava and sugar cane were 20 m × 20 m, 10 m × 10 m, 10 m × 10 m, 5 m × 5 m and 1 m × 1 m respectively. The experimental design for the investigation was split plot with each land use type as the main plot while the sub plots were soil depth at 0–15 cm, 15–30 cm and 30–75 cm.

Microbial Analysis

The soil samples were collected during the raining season at the depth of 0–15 cm, 15–30 cm and 30–75 cm at four locations in each sample plots and the soil was thoroughly mixed to obtain a composite sample. The soil samples were collected in separate sterilized samples bottles. Each sample bottle was labelled properly with land use types, location collection date and was taken to the laboratory for microbial analysis. The number of soil microorganisms was determined using the dilution spread plate technique. Nutrients agar (NA) and Potato Dextrose agar (PDA) were the culture media of choice used for bacteria and fungi. One milliliter aliquot of sample was pipetted into sterile test tube and serially diluted in another six set of test tubes each containing 9ml of sterile distilled water to dilution ratio10^{-6}, 0.1 ml portion of the diluents from the fourth (10^{-4}) and fifth (10^{-5}) dilution factors were pipette separately aseptically into different sterile petridishes and 20 ml of the cool (45ºC) sterile molten agar media was added under aseptic condition, swirled gently for even distribution of the inocula,

allowed to set and incubated at 30–37 ºC for 24 hours (for bacterial), and at 25–27 ºC for 72 hours for fungi. At the end of incubation (24 hours) microbial colony were counted and recorded appropriately for bacteria while after 72 hours microbial colony were counted and recorded appropriately for fungi.

Isolation and purification of bacteria strain

The strain of bacteria were selectively isolated by streak method to subculture the bacteria. An inoculating loop was sterilized using hot flame, allowed to cool before it was used to take part of a grown bacteria colonies from the cultured agar and streaked on the surface of fresh nutrient agar. The agar was incubated at 37ºC in an inverted position for 24–48 hours. Individual bacteria colonies were identified by morphological and biochemical techniques using the taxonomy scheme of Bergey's Manual of Determinative Bacteriology (Holt *et al.* 1994). The cultural characterization of bacteria colonies isolated was done by observing the colonies for color, shape, edge, elevation and surface appearance displayed on Nutrient agar while the following biochemical tests catalase test, motility test and oxygen- relation, methyl Red Tests, Fermentation of sugars (carbohydrates), gram's reaction, coagulate Test, were carried out for the identification according to Bergey's manual of determinative Bacteriology.

Isolation and purification of fungi strain

The fungi isolated were stained with lactophenol cotton blue and observed under the microscope for identification of mycelia and spore structures. The fungi species were classified based on cultural and microscopic spore characteristic.

Data Analysis

The soil biological properties were subjected to analysis of variance (ANOVA) using the SPSS version 15. Treatments mean was separated using Duncan Multiple Range Test at $p< 0.05$.

RESULTS

Table 1. Colony forming units of microbial population under different land use types.

Land use	Bacteria population cfu g^{-1} Soil (10^4)	Fungi population cfu g^{-1} Soil (10^4)
Oil palm	6.72b	5.54c
Teak	6.57d	5.44d
Uncleared forest	6.64c	5.45d
Cassava	6.80a	5.59b
Sugar cane	6.78a	5.64a

Note: Mean followed by the same letter in each column are not significantly different from each other by Duncan's multiple Range Test (DMRT) at 5% level of probability.

Table 2. Colony forming units of microbial population with different soil depths.

Soil depths (cm)	Bacteria population cfu g^{-1} Soil (10^4)	Fungi population cfu g^{-1} Soil (10^4)
0–15	6.74a	5.61a
15–30	6.70b	5.52b
30–75	6.67c	5.46c

Note: Mean followed by the same letter in each column are not significantly different from each other by Duncan's multiple Range Test (DMRT) at 5% level of probability.

Colony forming units of microbial population under different land use types are shown in table1. Microbial population varied significantly *(p*< 0.05) across the land use types, the number of soil bacteria in the cassava land was significantly higher ($p < 0.05$) with 6.80×10^4 cfu g^{-1} compared to other land use types and lowest bacteria population was observed in teak plantation with 6.57×10^4 cfu g^{-1}. Significantly higher number of soil fungi was present in the sugarcane with 5.64×10^4 cfu g^{-1} compared to other land use type. Colony forming units of the microbial population with different soil depths was presented in table 2. Microbial population varied significantly *(p*< 0.05) across various soil depths (Table 2). Maximum number of microbes was recorded from surface soil (0–15 cm) as compared to other depths. The interaction effect of land use by soil depth was recorded in table 3. The highest microbial population of 6.83×10^4 cfu g^{-1} was recorded at the surface soil layer of the cassava land (0–15 cm), whereas the lowest 6.53×10^4 cfu g^{-1} was observed at subsoil layer of the teak land (30–75 cm) (Table 3). The fungi population was significantly high at the surface layer of cassava (30–75 cm) with 5.72×10^4 cfu g^{-1} and lowest value was recorded at subsoil layer of uncleared forest (30–75 cm) with 5.43×10^4 cfu g^{-1}.

Table 3. Colony forming units of microbial population under different land use types with different soil depths.

Land use	Depths (cm)	Bacteria population cfu g^{-1} Soil (10^{-4})	Fungi population cfu g^{-1} Soil (10^{-4})
Oil palm	0–15	6.76bcd	5.66a
	15–30	6.72de	5.53b
	30–75	6.68ef	5.43bc
Teak	0–15	6.61gh	5.51bc
	15–30	6.56hi	5.41d
	30–75	6.53i	5.40d
Uncleared forest	0–15	6.69e	5.49bc
	15–30	6.63fg	5.44cd
	30–75	6.63fg	5.43cd
Cassava	0–15	6.83a	5.72a
	15–30	6.81ab	5.57b
	30–75	6.77bcd	5.48bc
Sugarcane	0–15	6.81ab	5.69a
	15–30	6.78abc	5.66a
	30–75	6.74cde	5.56b

Note: Mean followed by the same letter in each column are not significantly different from each other by Duncan's multiple Range Test (DMRT) at 5% level of probability.

The Morphological characteristics of bacterial isolates from oil palm land were presented in table 4. These bacteria include *Pseudomonas aeruginosa*, *Flavobacterium* spp., *Actinobactera nitritus*, *Moraxella lacunata*, *Brucella* spp., *Bacteroides* spp., *Gemella* spp. and *Neisseria* spp.

Table 4. Morphological characteristics of bacterial isolates from oil palm land.

Isolate	Probable organism	Macroscopic characteristic	Microscopic characteristic
1	*Pseudomonas aeruginosa*	Green, Pairs and Chain	Gram negative, Rod
2	*Flavobacterium* spp.	Yellow and Round	Gram positive Cocci
3	*Actinobacter anitritus*	Creamy, Pairs and Chain	Gram negative, Cocco baccila
4	*Moraxella lacunata*	Pink , Chain and Clusters	Gram negative, Cocci
5	*Brucella* spp.	Off white, Pairs and Chain	Gram negative, Short rod
6	*Bacteroides* spp.	Dirty white, Bundles and Chains	Gram negative, Rod
7	*Gemella* spp.	Dirty white, Pairs and Chain	Gram negative, Cocci
8	*Neisseria* spp.	Creamy and Round	Gram negative, Cocco baccila

Table 5. Biochemical identification of bacterial isolates from oil palm land.

Biochemical test	Isolates							
	1	2	3	4	5	6	7	8
Coagulate test	-	-	-	-	-	-	-	-
Catalase	+	+	+	+	+	+	+	+
Oxidase	-	-	-	-	-	-	-	-
Mortility	+	-	-	-	-	-	-	-
Methy red	+	+	+	+	-	+	-	+
Starch hydrolysis	-	+	+	+	+	+	+	+
Sugar utilization								
Glucose	AG	AG	AG	-	-	AG	AG	AG
Lactose	-	-	AG	-	-	AG	AG	-
Sucrose	-	-	AG	-	-	AG	AG	-
Maltose	-	-	-	-	-	AG	AG	-
Manitol	AG	AG	-	-	AG	AG	AG	-
Inositol	AG	AG	-	-	AG	AG	AG	-
Xylose	-	-	AG	-	-	AG	AG	AG
Probable Organism	*Pseudomona aeruginosa*	*Flavobacterium* spp.	*Actinobacter antitritus*	*Moraxella lucunata*	*Brucella* spp.	*Bacteriodes* spp.	*Gemella* spp.	*Neissera* spp.

Note: +, Positive; -, Negatives; AG, Acid and gas fully produced; ND, Not indicate; A, Acid produce only.

The Biochemical identification of bacterial isolates from oil palm land were shown in table 5. The genera *Flavobacterium* spp., *Brucella* spp. are gram-positive bacteria while *Pseudomonas aeruginosa*, *Actinobactera nitritus*, *Moraxella lacunata*, *Bacteroides* spp., *Gemella* spp. and *Neisseria* spp. are gram-negative bacteria.

Table 6. Morphological characteristics of bacterial isolates from teak land.

Isolate	Probable organism	Macroscopic characteristic	Microscopic characteristic
1	*Bacillus cerus*	Creamy, Bundles and Chain	Gram positive, Ova
2	*Bacillus pumilus*	Creamy and Round	Gram positive, Long rod
3	*Bacillus subtilis*	Off white and Pairs	Gram positive, Rod
4	*Clostridium welchii*	Creamy, Chain and Pairs	Gram positive, Rod
5	*Clostridium septicum*	Dirty white, Chains and Clusters	Gram positive, Rod
6	*Clostridium carnis*	Off white, Pairs and chains	Gram positive, Rod
7	*Kurthia* spp.	Creamy and Round	Gram positive, Rod
8	*Corynebacterium murium*	Creamy, Pairs and Chains	Gram positive, Rod

Table 7. Biochemical identification of bacterial isolates from teak land.

Biochemical test	Isolates							
	1	2	3	4	5	6	7	8
Coagulate test	-	-	-	-	-	-	-	-
Catalase	+	+	+	+	+	+	+	+
Oxidase	-	-	+	-	+	+	+	-
Mortility	+	+	-	-	-	-	-	-
Methy red	+	+	+	-	+	+	+	-
Starch hydrolysis	+	+	+	+	+	-	+	+
Sugar utilization								
Glucose	AG	AG	+	+	+	+	+	+
Lactose	AG	AG	+	-	+	+	+	-
Sucrose	AG	AG	+	+	+	-	+	+
Maltose	AG	AG	+	-	+	+	+	-
Manitol	-	AG	+	-	+	-	+	-
Inositol	-	AG	+	-	+	-	+	-
Xylose	AG	AG	+	-	-	+	+	-
Probable Organism	*Bacillus cerus*	*Bacillus pumilus*	*Bacillus subtilis*	*Clostridium welchii*	*Clostridium septicum*	*Clostridium carnis*	*Kurthia* spp.	*Corynebacterium murium*

Note: +, Positive; -, Negatives; AG, Acid and gas fully produced; ND, Not indicate; A, Acid produce only.

Table 8. Morphological characteristics of bacterial isolates from uncleared forest.

Isolate	Probable organism	Macroscopic characteristic	Microscopic characteristic
1	*Vibrio* spp.	Dirty white, Bundles and Chains	Gram negative, Long rod
2	*Bordetella* spp.	Dirty white, Pairs and Chains	Gram negative, Short rod
3	*Acinetobacter pertussis*	Creamy, Bundles and Chain	Gram negative, Short rod
4	*Morganella iwoffi*	Creamy, Pairs and Chains	Gram negative, Long rod
5	*Chromobacterium morganii*	Creamy Chains and Clusters	Gram negative, Short rod
6	*Necromonas lividum*	Creamy and Round	Gram negative, Long rod
7	*Moraxella bovis*	Creamy and Ova	Gram negative, Rod
8	*Eubacterium letitum*	Creamy, Chains and Clusters	Gram positive, Long rod

The Morphological characteristics of bacterial isolates from teak land were presented in table 6. These bacteria include *Bacillus cerus*, *Bacillu pumilus*, *Bacillu subtilis*, *Clostridium welchii*, *Clostridium septicum*, *Clostridium carnis*, *Kurthia* spp. and *Corynebacterium murium.* The Biochemical identification of bacteria species isolated from teak land was shown in table 7. *Bacillus cerus*, *Bacillu pumilus*, *Bacillu subtilis*, *Kurthia* spp. and *Corynebacterium murium* are gram-positive bacteria while the spore fo-rmers include *Clostridium welchii*, *Clostridium septicum*, *Clostridium carnis*, *Corynebacterium murium*. *Bacillus cerus*, *Bacillus pumilus* and *Bacillus subtilis*. The morphological characteristics of bacterial isolates from the uncleared forest were presented in table 8. These bacteria include *Vibrio* spp., *Bordetella* spp., *Acinetobacter pertussis*, *Morganella*

iwoffi, *Chromobacterium morganii*, *Necromonas lividum*, *Moraxella bovis* and *Eubacterium letitum*. The Biochemical identification of bacteria species isolated from the uncleared forest was shown table 9.

Table 9. Biochemical identification of bacterial isolates from uncleared forest land.

Biochemical test	Isolates							
	1	**2**	**3**	**4**	**5**	**6**	**7**	**8**
Coagulate test	-	-	-	-	-	-	-	-
Catalase	+	+	+	+	+	+	+	+
Oxidase	-	+	-	-	+	+	-	-
Mortility	+	-	-	+	+	-	-	-
Methy red	+	-	-	+	+	+	+	+
Starch hydrolysis	+	+	+	+	+	+	+	+
Sugar utilization								
Glucose	+	-	-	-	-	-	-	-
Lactose	+	-	-	-	-	-	-	-
Sucrose	+	-	-	-	-	-	-	-
Maltose	+	-	-	-	-	-	-	-
Manitol	+	-	-	-	-	-	-	-
Inositol	+	-	-	-	-	-	-	-
Xylose	+	-	-	-	-	-	-	-
Probable Organism	*Vibrio* spp.	*Bordetella* spp.	*Acinetobacter Pertussis*	*Morganella iwoffi*	*Chromobacterium morganii*	*Necromonas lividum*	*Moraxella bovis*	*Eubacterium letitum*

Note: +, Positive; -, Negatives; AG, Acid and gas fully produced; ND, Not indicate; A, Acid produce only.

Eubacterium letitum is the only gram-positive bacterium that was identified in the forest land while *Vibrio* spp., *Bordetella* spp., *Acinetobacter pertussis*, *Morganella iwoffi*, *Chromobacterium morganii*, *Necromonas lividum* and *Moraxella bovis* are gram-negative bacteria.

Table 10. Morphological characteristics of bacterial isolates from cassava land.

Isolate	Probable organism	Macroscopic characteristic	Microscopic characteristic
1	*Peptococcus* spp.	Off white, Pairs and Chain	Gram positive, Cocci
2	*Streptococcus epidermicus*	Creamy, Clusters and Chains	Gram positive, Cocci
3	*Streptococcus equisimillis*	Creamy, Chains and Clusters	Gram positive, Cocci baccila
4	*Micrococcus roseus*	Creamy and Pairs	Gram positive, Cocci
5	*Micrococcus varius*	Creamy, Pairs and Chains	Gram positive, Cocci
6	*Salmonella pullorium*	Off white, Pairs and Chains	Gram negative, Rod
7	*Proteus murabillis*	Creamy and Round	Gram negative, Long rod
8	*Serratia rubidaea*	Pink and Pairs	Gram negative, Rod

Table 11. Biochemical identification of bacterial isolates from cassava land.

Biochemical test	Isolates							
	1	**2**	**3**	**4**	**5**	**6**	**7**	**8**
Coagulate test	-	-	-	-	-	-	-	-
Catalase	+	+	+	+	+	+	+	+
Oxidase	-	-	ND	ND	-	-	-	-
Mortility	-	-	-	-	-	+	+	+
Methy red	+	+	+	+	-	+	-	+
Starch hydrolysis	+	+	+	+	+	+	+	+
Sugar utilization								
Glucose	-	-	+	+	-	-	-	+
Lactose	-	-	-	-	-	-	-	-
Sucrose	-	+	+	+	-	-	+	+
Maltose	-	-	-	+	-	-	-	-
Manitol	-	-	-	-	-	-	-	-
Inositol	-	-	-	-	-	-	-	-
Xylose	-	-	-	-	+	+	-	-

Probable Organism	*Peptococcus* spp.	*Streptococcus epidermicus*	*Streptococcus equisimillis*	*Micrococcus roseus*	*Micrococcus varius*	*Salmonella pullorium*	*Proteus murabillis*	*Serratia rubidaea*

Note: +, Positive; -, Negatives; AG, Acid and gas fully produced; ND, Not indicate; A, Acid produce only.

The Morphological characteristics of bacterial isolates from cassava land were presented in table 10. These bacteria include *Peptococcus* spp., *Streptococcus epidermicus*, *Streptococcus equisimillis*, *Micrococcus roseus*, *Micrococcus varius*, *Salmonella pullorium*, *Proteus murabillis* and *Serratia rubidaea.* The Biochemical identification of bacteria species isolated from cassava land was shown in table 11. The bacteria, *Peptococcus* spp., *Streptococcus epidermicus*, *Streptococcus equisimillis*, *Micrococcus roseus* and *Micrococcus varius* are gram-positive bacterium while *Salmonella pullorium*, *Proteus murabillis* and *Serratia rubidaea* are gram-negative bacteria.

Table 12. Morphological characteristics of bacterial isolates from sugar cane land.

Isolate	Probable organism	Macroscopic characteristic	Microscopic characteristic
1	*Enterobacter cloacae*	Creamy, Chains and Clusters	Gram negative, Rod
2	*Proteus inconstsus*	Dirty white, Chains and Clusters	Gram negative, Ova
3	*Klebsiella oxytoca*	Off white, bundles and Chains	Gram negative, Cocco baccila
4	*Serratia marcescens*	Red, Pairs and Chains	Gram negative, Cocci
5	*Enterobacter aerogenes*	Off white, Pairs and Chain	Gram negative, Short rod
6	*Klebsiella aerogenes*	Creamy, Pairs and Chains	Gram negative, Rod
7	*Leuconostoc* spp.	Creamy, Bundles and Chain	Gram positive, Cocci
8	*Nocardia caviae*	Creamy, Pairs and Chains	Gram positive, Ova

The Morphological characteristics of bacterial isolates from sugar cane land were presented in table 12. These bacteria include *Enterobacter cloacae*, *Proteus inconstsus*, *Klebsiella oxytoca*, *Serratia marcescens*, *Enterobacter aerogenes*, *Klebsiella aerogenes*, *Leuconostoc* spp. and *Nocardia caviae*.

Table 13. Biochemical identification of bacterial isolates from sugar land.

Biochemical test	Isolates							
	1	2	3	4	5	6	7	8
Coagulate test	-	-	-	-	-	-	-	-
Catalase	+	+	+	+	+	+	+	+
Oxidase	-	-	-	-	-	-	-	-
Mortility	+	-	-	-	-	-	+	-
Methy red	+	-	+	-	+	+	+	+
Starch hydrolysis	+	+	+	+	+	+	+	+
Sugar utilization								
Glucose	+	+	+	+	+	+	+	+
Lactose	+	+	+	+	+	+	+	+
Sucrose	+	-	+	+	+	+	+	+
Maltose	+	+	+	+	+	+	+	+
Manitol	+	+	+	+	+	+	+	+
Inositol	+	+	+	+	+	+	+	-
Xylose	-	-	-	-	-	-	-	-
Probable Organism	*Enterobacter cloacae*	*Proteus inconstsus*	*Klebsiella oxytoca*	*Serratia marcescens*	*Enterobacter aerogenes*	*Klebsiella aerogenes*	*Leuconostoc* spp.	*Nocardia caviae*

Note: +, Positive; -, Negatives; AG, Acid and gas fully produced; ND, Not indicate; A, Acid produce only.

The Biochemical identification of bacteria species isolated from sugar cane land was shown in table 13. *Leuconostoc* spp. and *Nocardia caviae* are gram-positive bacterium while *Enterobacter cloacae*, *Proteus inconstsus*, *Klebsiella oxytoca*, *Serratia marcescens*, *Enterobacter aerogenes* and *Klebsiella aerogenes* are gram-negative bacteria.

Characteristic of fungi isolated from the soil sample collected from all the land use areas were shown in

table 14. The fungi identified were as follows: *Rhizopus stolonifer*, *Aspergillus funmigatus*, *Ulocladium lanuginosum*, *Aspergillus ustus*, *Gliocladium rosum*, *Alternaria alternate*, *Aspergillus niger*, *Penicillium italicum*, *Mucor* spp. and *Candida* spp. Most of the fungi appeared in different colors on the agar media (PDA). *Rhizopus stolonifer* appeared White cotton-like mycelia at 24 hrs, turning dirty with development of black spores' mycelium on Potato Dextrose Agar (PDA), *Aspergillus funmigatus*, appeared white base with brown conidiophores which make it appears brown in color on PDA, *Ulocladium lanuginosum*, appeared Dark on Potato Dextrose Agar with dictyosporus, usually without constriction at major septum, borne singly, apical and on new sympodial growing points saprophytic, *Aspergillus ustus* appeared brown in color on Potato Dextrose Agar with White base with brown conidiophores. *Gliocladium rosum* appeared Hyaline or brightly colored in mass on the PDA, one-celled, produced successively apically and collecting in mucilaginous droplets, saprophytic, common in soil, they also produced a verticillium state. *Alternaria alternate have a dark* Conidiophores, mostly simple, rather short or elongate, typically bearing a simple or branched chain of conidia on PDA. *Aspergillus niger* appeared on PDA in Black mycelium. *Penicillium italicum* appeared Yellowish green to dark green hyphae on PDA. *Mucor* spp. appeared in a White to grayish brown colors on PDA, wooly to cotton spreading colonies and darkens with time and *Candida* spp., appeared Creamy to white color, circular, mucold, raised and opaque colonies with entire margin on PDA.

Table 14. Characteristic of some fungi isolated from soil sample collected from all the land use.

Isolate	Cultural characteristics	Spores/conidia arrangement under the microscope	Name of organism present
01	White cotton-like mycelia at 24 hrs, turning dirty with development of black spores mycelium	Non-septate hyphae and coenecytic, thin sporogiophores, sporangium have well developed collumelium which is umbrella like, spores are of various shape but are generally oval.	*Rhizopus stolonifer*
02	White base with brown conidiophores which make it appears brown in color.	Upright conidiophores that terminated in a clavate swelling bearing phialides at the apex. Conidia are one-celled and vesicles globose, non-septiate and non collumella.	*Aspergillus funmigatus*
03	Dark, dictyosporus, usually without constriction at major septum, borne singly, apical and on new sympodial growing points saprophytic.	Conidiophores arising as upright branches of mycelium, conidia (porospores).	*Ulocladium lanuginosum*
04	White base with brown conidiophores which make it appears brown in color.	Conidiophores upright, simple, terminating in aglubose or clavata swelling, bearing phialides at the apex or radiating from the entire surface, conidia (philalospores) one-celled globose, often variously colored in mass in dry basipetal chains.	*Aspergillus ustus*
05	Hyaline or brightly colored in mass, one-celled, produced successively apically and collecting in mucilaginous droplets, saprophytic, common in soil. They also produced a verticillium state.	Corda, conidiophores portion bearing penicillate branches, forming a compact ‘’brush” as in penicillum, conidia (phialaspores).	*Gliocladium rosum*
06	Conidiophores dark, mostly simple, rather short or elongate, typically bearing a simple or branched chain of conidia.	Conidia (porospores) dark, typically with both cross and longitudinal septa, variously shaped,obclavate to elliptical or ovoid, frequently borne acropetally in long chains.	*Alternaria alternate*
07	Black mycelium	Conidiophores were upright, unbranched simple and terminating in a globose swelling bore phialides at apex.	*Aspergillus niger*
08	Yellowish green to dark green hyphae	Conidiophores arranged singly form the mycelium, they were mostly ovoid or globose near the apex.	*Penicillium italicum*

09	White to grayish brown, wooly to cotton spreading colonies and darkens with time	Broad non septate hyphae, sporongiophores are long terminates in a round spore filled sporangium absence of rhizoids.	*Mucor spp* (Scholer, 1983)
10	Creamy to white, circular, mucold, raised and opaque colonies with entire margin	Round to oval shaped ellipsoidal budding cells with blastoconidia and pseudohyphae, some cell appeared singly and others in pairs.	*Candida spp* (C-P Robin Berkhout, 1923)

Note: Some of the fungi identified in table .14 are similar to those identified by Olukunle *et al.* (2011) in determination of degrading activity of fungi on kerosene, diesel and petrol using classical selective enrichment method.

DISCUSSION

The total microbial count in this study range from a low of 6.57×10^4 cfu g^{-1} in the teak plantation to 6.80×10^4 cfu g^{-1} in cassava land, with significantly higher number of soil fungi was present in the sugarcane with 5.64×10^4 cfu/g^{-1} compared to other land use type. The population of bacteria was higher in cassava land use types, than in other land use area. and this suggested that microbial population variation in cassava land might be attributed to the effect of tillage on the land year by year which enhanced the free movement of air, which encourage the availability of microbial population and as a result of presence of some microorganism in the tuber of cassava which had a great influence on soil organic matter contents through mineralization and decomposition. This research was in agreement with research conducted by (Uzochukwu *et al.* 2001) on the evaluation of microorganism from cassava waste water. He revealed that the presence of sugar and starch in cassava tuber stimulate microbial growth.

The high population of fungi in sugarcane land might be as a result of longtime cultivation of the sugarcane land, which might homogenize the soil resources and increases the fungi population in sugarcane land (Cotty *et al.* 1994) The microbes in the soil also decreases with increase in soil depths, in which the counts were higher in surface soil at 0–15 cm, this is due to the presence of more organics and nutrients at the surface layer of the soil. Organic matter generally decreases from the surface to the bottom of the soil profile (Trumbore 2000). The decreasing trend of microbial abundance in the downward direction is commonly seen and is naturally obvious because the majority of soil microorganisms are heterotrophs.

From table 4 to table 13, eight isolates were obtained from each land use, make it up to 40 isolates in all the land use area, this study was in line with Borneman *et al.* (1997) which suggested that, land use soils contained high levels of microbial diversity composed of some unusual microorganisms. This same author also investigated the effects of vegetative cover and land-use changes on microbial communities and he indicated that distinct microbial communities were present under each form of land use. It was observed that, there were more Gram-negative type bacteria in the land use than Gram-positive bacteria. *Flavobacterium*, *Bacillus*, *Clostrium*, *Kurthia*, *Corynebacterium*, *Eubacterium*, *Peptococcus*, *Streptococcus*, *Micrococcus*, *Leuconostoc* and *Nocardia* are gram-positive bacteria while *Pseudomonas*, *Atinobacter*, *Moraxella*, *Bacteroides*, *Gemella*, *Neisseria*, *Vibrio*, *Bordella*, *Acinetobacter*, *Morganella*, *Chromobacterium*, *Necromonas*, *Salmonella*, *Proteus*, *Serratia*, *Enterobacter* and *Klebsiella* are gram- negative bacteria. The spore forming bacteria include *Clostridium* spp., *Corynebacterium* spp. *and Bacillus* spp.

The macroscopic and cultural characteristics of fungi isolated from all the land use area are presented in table 14. They appeared in various colors' of Yellow, black, brown, white and green on the Potato Dextrose Agar (PDA). The fungi identified were as follows: *Rhizopus stolonifer*, *Aspergillus fumigates*, *Ulocladius lanuginosum*, *Mucor* spp., *Aspergillus ustus*, *Canadida* spp., *Gliocladium rosum*, *Alternaria alternate*, *Penicillum italicum* and *Aspergillus niger*. These results was in agreement with previous work of Amir & Pineau (1998), That revealed the level of root colonization of soil microbial characteristics with highest biomass and activity under land use type and vegetation. Results showed that the microbial population is higher in cultivation area of the land use; this might be attributed to the fact that cropping appeared to affect microbial communities positively, as bacterial and fungal diversity increased under cultivation. Knowles (1998) and Ehiagbonare *et al.* (2009) discovered that the presence of bacteria and fungi diversity increased under cultivation. The soil of the land use types contained more bacteria than fungi which could be corroborated by the previous observation that soil usually contained greater amounts of soil bacteria than fungi. This was because bacteria are less susceptible to changes in soil and environmental conditions, unlike fungi which are easily restricted by soil pH, nutrient and harsh environmental conditions (Zhang *et al.* 2002).

CONCLUSION

Results from the present study demonstrate that land use types exert a profound influence on microbial populations; the microbial population was greatly influenced by land use type. Among the land use types, the cassava land harbors more microbes due to the availability of some microorganism in the tuber of cassava which had a great influence on soil organic matter contents through mineralization and decomposition. The dilution spread plates techniques of identification of microbial population enable the soil pathologist to understand the basic principles of identification of microbiological and physiologic traits. The information from the techniques employed in this study showed that there could be more novel bacterial and fungal species that could be recovered in future studies by using the recently developed technique that allows quick and detailed analysis of the microbial diversity in different land use types.

ACKNOWLEDGMENTS

I wish to express my deep appreciation to my supervisor, Professor F. O Adekayode is highly acknowledged. My heartfelt thanks go to Mr. Hassan, Soil Laboratory technicians of Federal University of Technology, Akure Nigeria, for offering his all possible helps in all aspects of the laboratory work. The management of Teaching and Research Farm of Federal University of Technology is highly acknowledged.

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