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ASSESSMENT OF IMPACT OF LAND USES AND SOME SOIL CHEMICAL PROPERTIES ON THE SPATIAL DISTRIBUTION OF BACTERIA IN SOUTHWEST NIGERIA

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Abstract
In recent decades, there has been a growing awareness of the need to understand how land use change and soil chemical properties impact on soil bacteria communities. This study was carried out to assess the spatial distribution of bacteria species as affected by land use changes and soil chemical properties. The study was conducted in Okitipupa and Irele local governments, southwest, Nigeria. Five land uses were identified in the study area: forest land, oil palm plantation, farmland, watershed and residential area. Soil samples were collected from each of the land uses at 0-30 cm, analysed for chemical properties and bacteria count. Data were analysed using ANOVA at 0.05 probability level. The results showed that, forest land recorded the highest bacteria counts with 1410.10 $cfug^{-1}$ and 1086.96 $cfug^{-1}$ in Okitipupa and Irele local governments. The least count of bacteria was found in the residential area with 990.21 $cfug^{-1}$ and 774.97 $cfug^{-1}$ in Okitipupa and Irele local governments respectively. It was also found that forest land with moderate to higher nitrogen and soil organic carbon recorded high bacteria over other land uses. Conclusively, land use changes and soil chemical properties impact some variabilities on the distribution of soil bacteria which could be used to monitor soil health either for agricultural or environmental purposes.
Keywords: Land use, Soil chemical properties, Soil bacteria

Introduction

Land use changes significantly impact the spatial distribution of microorganisms in various ecosystems. Microorganisms play a crucial role in maintaining ecological balance, nutrient cycling, and overall soil health. As anthropogenic activities alter land use, the structure, function, and diversity of microbial communities are also affected, leading to changes in ecosystem processes (Nannipieri *et al.*, 2017). Understanding these effects is essential for sustainable land management practices.

Microorganisms, including bacteria, fungi, archaea, and viruses, are fundamental to soil health and ecosystem functionality. They participate in key processes such as organic matter decomposition, nutrient mineralization, nitrogen fixation, and the suppression of soil-borne diseases (Garbeva

et al., 2018). The diversity and activity of microbial communities are influenced by various factors, including soil properties, climate, vegetation, and land management practices. Consequently, any change in land use can have profound implications for the microbial ecology of soils.

In recent decades, there has been a growing awareness of the need to understand how land use changes impact soil microbial communities. This is particularly important in regions undergoing rapid transformation due to human activities. Land use changes, such as deforestation, urbanization, and agricultural expansion, can lead to habitat fragmentation, loss of biodiversity, and alterations in soil structure and chemistry (Lauber *et al.*, 2013). These changes, in turn, influence the composition, diversity, and function of soil microbial communities, with potential consequences for ecosystem services and agricultural productivity.

Irele and Okitipupa Local Government Areas (LGAs) in Ondo State, Nigeria, have experienced considerable changes in land use over the past decades. These changes, driven by agricultural expansion, urbanization, and deforestation, have had significant impacts on the local environment and biodiversity. The region's reliance on agriculture, particularly the cultivation of cash crops like cocoa and oil palm, has led to extensive land conversion and habitat alteration (Ogunleye *et al.*, 2020).

Agricultural expansion in Irele and Okitipupa LGAs has primarily been driven by the need to increase food production and economic development. However, this has often come at the expense of natural ecosystems. The conversion of forests and natural grasslands to agricultural fields alters the physical and chemical properties of soils, which in turn affects the microbial communities that inhabit them (Ayangbenro and Babalola, 2021). Tillage, use of chemical fertilizers, pesticides, and monoculture practices disrupt the soil structure, reduce organic matter content, and create an environment that favors certain microbial taxa over others. This can lead to a decline in microbial diversity and changes in the functional capabilities of the soil microbiome (Gaston *et al.*, 2010).

Urbanization is another significant driver of land use change in Irele and Okitipupa LGAs. The expansion of urban areas involves the construction of buildings, roads, and other infrastructure, which leads to the sealing of soil surfaces and the disruption of natural habitats. Urban soils are often characterized by high levels of pollutants, compaction, and reduced organic matter, all of which negatively impact microbial communities (Gaston *et al.*, 2010). The introduction of exotic plant species in urban landscapes can also alter the composition of soil microbial communities by changing the types and amounts of organic matter inputs.

Deforestation, driven by logging and the need for land for agriculture and urban development, has led to the loss of forests in Irele and Okitipupa LGAs. Forest soils typically harbor diverse and complex microbial communities due to the high organic matter content and the presence of various plant species (Rodrigues *et al.*, 2013). The removal of forest cover reduces litter input, alters soil moisture regimes, and increases soil erosion, all of which affect the microbial communities. Deforestation often leads to the dominance of opportunistic and fast-growing microbial species that are less efficient in nutrient cycling and organic matter decomposition compared to the original forest microbial communities. This research is however to evaluate the significance of the impact of land use changes on the distribution of bacteria communities in the study area.

Study Area Description

Geography and Topography

The study focuses on Okitipupa and Irele Local Government Areas (LGAs) in Ondo State, Nigeria. This region is characterized by a tropical climate with specific topographical features. The terrain in this area is primarily undulating, with gentle slopes that influence both land use and soil properties. The topographic map will be utilized to identify and delineate the terrain features, including slopes and land use types, which are crucial for understanding the spatial distribution of microorganisms.

Climate

The climate of Okitipupa and Irele LGAs are representatives of the hot and humid tropic climate typical of southwestern Nigeria. This region experiences seasonal rainfall, high temperatures, and high humidity. The total annual rainfall often exceeds 2000 mm, with a narrow range of soil temperatures between 27°C and 28°C (Esu, 2014). The area undergoes two distinct seasons: the rainy season, dominated by the southwest trade winds bringing moisture from the Atlantic Ocean between March and November, and the dry season, influenced by the northeast trade winds from December to February. The Inter Tropical Discontinuity (ITD) controls these seasonal variations, affecting other climatic parameters such as temperature, humidity, and wind patterns. The growing season in this region spans approximately 240 to 300 days annually (Reginster and Rounsevell, 2005).

Vegetation and Land Use

The study area is a forest zone featuring a mix of secondary forest, farm fallows, and arable farmland. Approximately 15% of the land is dedicated to arable farming, primarily growing cassava and maize, along with scattered oil palm trees and cocoa plantations. The secondary forest occupies about two-thirds of the area, characterized by a mix of woody trees and shrubs. The land use types present significant implications for soil microbial communities due to differences in vegetation cover, organic matter input, and land management practices.

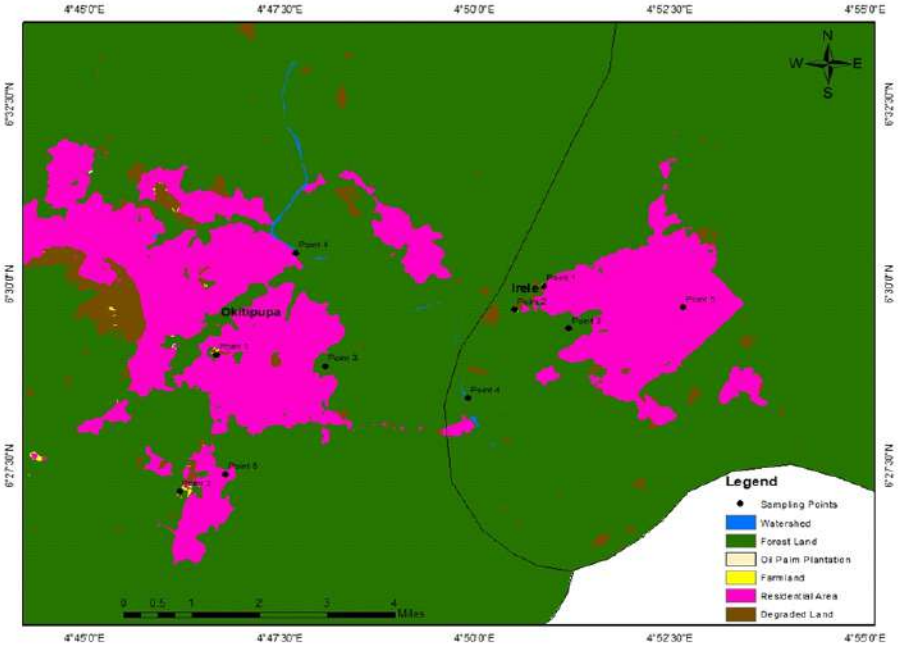

Figure 1: Map showing sampling points

Methods

Site Survey and Mapping

A general understanding of the topography was produced with the use of the site's perimeter and topographic maps, in addition to other data. An assessment was made of the topography's predominant slope.

Using transects, footpaths, and trunk C roads, the entire land area was traversed to visually identify and analyze the site's physical attributes on the spot. The basic map for establishing the terrain features, such as the kind of slope, the characteristics of erosion, the types and characteristics of land use and land cover, the man-made features that are currently in place, etc., will be the topographic/contour map. The base map displayed the approximate locations of these features, and the Geographic Positioning System (GPS) was utilized to capture the precise coordinates of these features (Adeyolanu *et al*, 2017).

Soil Survey and Mapping

With the use of topo-sheets when available, satellite photos, and cadastral maps, preliminary traverses of the whole research area were completed. Following permanent features such as roads, cart tracks, canals, streams, tanks, etc., the field borders and survey numbers listed on the cadastral sheet were located on the ground. Any modifications observed were then included in the cadastral map. If the previously listed resources are not available, the reference transects were established by conducting a reconnaissance assessment of the location. There were five transects created all with different lengths. Dutch Soil Auger used the global positioning system (GPS) to find the locations of each sampling point. For every sampling point, the physical properties of the soils were inspected and suitably documented between 0 and 30 cm and between 30 and 60 cm of depth. After removing coarse debris and roots, the auger samples were composited individually by bulking samples taken from the same plot and depth, air drying at room temperature, and sieving through a 2 mm sieve in preparation for analysis.

Preparation of Point Map

Coordinates of soil sample sites were recorded using a GARMIN GPS72H receiver. ArcGIS 10 software was employed to prepare point maps displaying the locations of soil samples. The spatial and non-spatial databases were integrated to generate spatial distribution maps, using MS Excel and ArcMap to link data points and visualize results (Basavaraj *et al.*, 2020).

Experimental Design

The experiment was conducted in a randomized complete block design (RCBD),

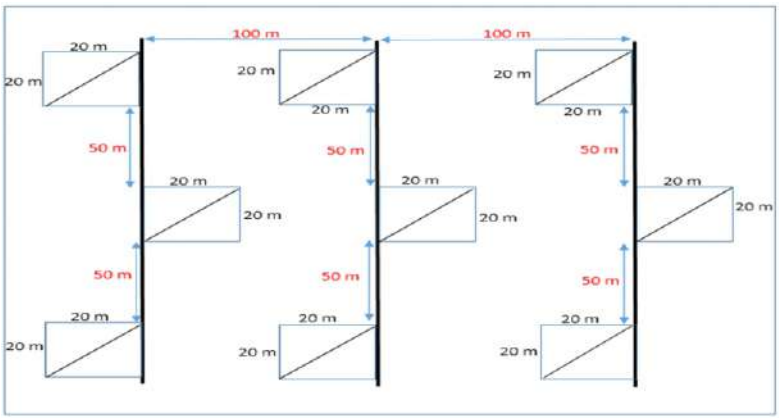

Figure 2: Plot layout and sampling technique adopted for each land use system

Soil Sample Collection and Sampling Procedure

In each of the land uses identified (forestland, Oil palm plantation, watershed, farmland and residential area) which represented the study sites, 250 m x 150 m rectangular was marked, partitioned into three blocks at 100 m apart and further sub-divided into three sub-plots of 20 m x 20 m at 50 m intervals using systematic strip sampling methods. Soil core samples were collected at depth of 0-30cm and 30 cm – 60 cm in each of the selected sub-plot within the three points along the diagonal of each plot using a 3cm diameter Dutch soil auger. The auger samples were composited separately by bulking samples collected from the same plot and depth, air dried at room temperature and sieved through a 2mm sieve in preparation for analysis after removing coarse fragments and roots. The composite soil samples were taken to the laboratory for analysis.

Soil Particle Analysis

Soil particle size analysis was conducted to determine sand, silt, and clay content using the hydrometer method. A 30-g sample of oven-dry soil was treated with Calgon solution, stirred, and transferred to a sedimentation cylinder. Hydrometer readings were taken after 40 seconds and 2 hours to measure the sand, silt, and clay fractions, with calculations performed to determine the percentage of each component (Basavaraj *et al.*, 2020).

Soil Chemical Properties Determination

The soil pH was determined by a pH meter in 1:2.5 soil: water (w/v) suspension (Anderson and Ingram, 1993). Total Organic Carbon (TOC) was determined using the Colorimetric method (Schulte and Hoskins, 2009). The Kjeldahl method was used to determine total Nitrogen (Sáez-Plaza *et al.*, 2013). Available phosphorus (Av. P) content in the soil was analyzed following the Bray-1 acid method (Sahrawat *et al.*, 1997). Potassium content was determined using a flame photometer (Rhoades, 1983). Ca, Mg, P, were determined by plasma-atomic emission spectroscopy (Hendershot *et al*, 1993). Effective Cation exchange capacity (ECEC) was estimated by summation of total exchangeable bases.

Soil Bacteria Analysis and Estimation

Enumeration of heterotrophic bacteria and fungi was carried out by pour plating technique. This was done by inoculating 0.1 ml tenfold serially diluted samples onto nutrient agar (Bacteria). The mineral salt media contains the following composition in gram per litre of distilled water NaCl 10g, MgSO4. $7H_2O$, 0.42g, KCl, 0.29g, K_2 HPO_4, 1.2g, KH_2 PO_4, 0.83g, $NaNO_2$, 0.42g, Agar –Agar, 15g, PH 7.2. The inoculated nutrient Agar plates were incubated at 370 C for 24 hours while the potato dextrose Agar plates were incubated at room temperature for 3-5 days.

Estimation of number of bacteria: No. of bacterial cells /1gm dry soil = No. of colonies ×inverted dilution Dry weight of 1gm soil sample

Data Analysis

Soil and bacteria data were compiled using Excel and analyzed with SPSS version 23. Descriptive statistics, including means and standard deviations were calculated for soil bacteria. Analysis of variance (ANOVA) was performed to identify significant differences between various land uses. Duncan's New Multiple Range Test was used for post-hoc comparisons at a 95% confidence level.

3.0. Results and Discussion

3.1. Results

Soil Chemical Properties and Land uses

pH of the study area was slightly acidic across all the land uses in Irele, it ranged from 5.83 to the least value of 4.92 in forestland and oil palm plantation land uses respectively, similar trend was also observed in Okitipupa,

the highest value of 5.23 to the least value of 4.95 in forestland and oil palm plantation respectively, however, there was no significant difference among the values in the two locations across the land uses Tables 1 and 2.

Forestland recorded the highest total organic carbon with value of 3.36 and 3.03 g/kg-1 while the farmland has the lowest of 1.23 and 1.90 g/kg-1 in Irele and Okitipupa respectively, Organic matter (OM) followed a similar trend across all the land uses in the two locations. In the same vein, forestland recorded significantly highest total N of 0.23 gkg-1 while farmland recorded the lowest value of 0.12 gkg-1. Total P followed the same trend as the total N, the value of total P was statistically higher in the forestland with the value of 10.99 gkg-1 and 9.79 gkg-1 in Irele and Okitipupa while the lowest values of 7.83 gkg-1 and 7.78 gkg-1 were recorded in the residential area and farmland in Irele and Okitipupa respectively. Cation exchange capacity (CEC) was significantly higher in forestland over the other land uses and ranged between 10.77 gkg-1 to 8.73 gkg-1 in forestland and farmland respectively in Irele local government while it ranged from 11.87 gkg-1 to 9.76 gkg-1 in Okitipupa local government. The exchange acidity (EA) was significantly higher is oil palm plantation than in the forestland and ranged from 2.87 gkg-1 to 1.87 gkg-1 respectively in Irele Loca government. It also ranged from 2.47 gkg-1 to 1.79 gkg-1 in oil palm plantation and forestland in Okitipupa.

Bacteria Distribution across the Land Uses

The distribution of bacteria species is presented in Table 3, some of the identified bacteria are: *Zymomonas mobilis, Cellulomonas spp, Micrococcus spp, Bacillus subtilis, Bacillus linchemiformis, S. saprophyticus, Salmonella spp, Proteus mirbilis, Streptotoccus spp, Enterobacter spp, Arthrobacter spp, Chromoba. Lividum, Xanthomonas spp, Chromoba. Violaceum, Lactobacilius spp, Clostridium spp, Acinectobacter spp, Pseudo. Aeruginosa, Rhizobium spp, Citrobacter spp, Corynebacterium spp, Peptococcus spp, Flavobacterium spp, Diplococci spp, Alcaligenes spp.*

Zymomonas mobilis was higher in oil palm plantation with 23.00 $cfug^{-1}$ and 10.00 in Okitipupa and Irele local government respectively and dropped to 0.00 $cfug^{-1}$ in farmland and watershed in Okitipupa local government. *Cellulomonas spp* was in Okitipupa local government with 35.00 cfu in Watershed and 25.00 $cfug^{-1}$ in Irele local government also found in watershed land use. It dropped to 0.00 $cfug^{-1}$ in both local governments, these values were found in residential areas. As well as farmland in Okitipupa local government. *Micrococcus spp* has the highest counts of in oil palm plantation in Okitipupa and 20.66 cfu in forest land in Irele local government. *Bacillus subtilis* counts was higher in forestland with 152.00 $cfug^{-1}$ and 132.00 cfu in Okitipupa and Irele respectively. *Bacillus linchemiformis* counts was higher in forest land with 135.00 $cfug^{-1}$ in Okitipupa while in Irele local government, the count was 130.00 cfu also in forestland. *S. saprophyticus* had the highest counts in the forest land over other land uses, this trend follows similar trend recorded for some identified bacteria species. It also recorded higher count in Okitipupa. *Salmonella spp* count was higher in the watershed land uses over others with 30.00 $cfug^{-1}$ in Okitipupa and 20.00 in Irele. *Enterobacter spp* has the highest counts watershed with 62 $cfug^{-1}$ and 42 cfu in Okitipupa and Irele local government respectively. While the least counts of 37.00 cfu and 27.00 cfu were found in residential

area land uses. *Xanthomonas spp* count was higher in the farmland in the area under investigation with the highest count found in Okitipupa over that of Irele. *Chromoba. Violaceum* counts was higher in the oil palm plantation and highest in the farmland in Okitipupa and Irele respectively.

In total, forest land has the highest count of bacteria in both Okitipupa and Irele local governments. The total counts of bacteria counts were 1410.10 $cfug^{-1}$ and 1086.9 $cfug^{-1}$ and significant higher in Okitipupa local government over Irele local government. This was followed by oil palm plantation with 1180.07 $cfug^{-1}$ bacteria in Okitipupa and while watershed has 899.99 $cfug^{-1}$ in Irele local government. The residential area recorded the least counts of bacterial in both local governments with 990.21 $cfug^{-1}$ and 774.97 $cfug^{-1}$ in Okitipupa and Irele local government respectively.

Table 1: Chemical Characteristics of Soil Samples 0-30 Cm Depth (Irele)

	Farmland (0-30cm)	Oil Palm Plantation (0-30cm)	Forest Land (0-30cm)	Watershed (0-30cm)	Residential area (0-30cm)
pH	5.18 ^{a}	4.92 ^{a}	5.83 ^{ab}	5.42 ^{a}	5.47^{ab}
TOC gkg-1	1.23 ^{d}	3.07 ^{b}	3.36 a	2.08 ^{c}	1.57 ^{d}
TOM gkg-1	2.12^{d}	5.29 ^{b}	5.79 ^{a}	3.58 ^{c}	2.71^{d}
Total N gkg-1	0.12 ^{cd} 9.97 ^{b}	0.18 ^{ab} 8.20 ^{d}	0.23 ^{a} 10.99^{a}	0.14^{c} 9.06^{c}	0.20 ^{ab} 7.83^{d}
Total P gkg-1	0.32 ^{d}	0.80 ^{b}	0.88 ^{a}	0.69^{c}	0.62 ^{c}
Na gkg-1	1.29^{d}	1.62 ^{ab}	1.75^{a}	1.60 ^{bc}	1.50^{c}
K gkg-1	2.02^{c}	3.04^{b}	3.19^{a}	2.65^{b}	2.14 ^{c}
Ca gkg-1	3.15^{c}	2.91 ^{d}	3.47 ^{a}	3.10 ^{c}	3.23 ^{b}
Mg gkg-1	2.45 ^{a}	2.87 ^{a}	1.85 ^{c}	1.93 ^{b}	1.98 ^{b}
EA gkg-1	8.73 ^{d}	10.30 ^{b}	10.77 ^{a}	10.06^{b}	9.97 ^{c}
CEC gkg-1	77.66 ^{c}	81.62 ^{b}	89.97 ^{a}	80.83 ^{b}	71.13 ^{c}
BS gkg-1					

Note: Mean with same superscript along the rows are not significantly different at p>0.05

Table 2: Chemical Characteristics of Soil Samples 0-30 Cm Depth (Okitipupa)

	Farmland (0-30cm)	Oil Palm Plantation (0-30cm)	Forest Land (0-30cm)	Watershed (0-30cm)	Residential area (0-30cm)
pH	5.07^{a}	4.95^{a}	5.23^{a}	5.12 ^{a}	5.20 ^{a}
TOC	1.90 ^{d}	1.93 ^{d}	3.03 ^{a}	2.91 ^{c}	2.99 ^{b}
TOM	3.05 ^{d}	3.11 ^{d}	5.13 ^{a}	4.92 ^{c}	5.07b
Total N	0.09 ^{d}	0.12 ^{c}	0.25^{a}	0.12^{c}	0.20 ^{b}
Total P	7.78 ^{e}	9.07 ^{c}	9.79 ^{a}	8.96^{d}	9.23 ^{b}
Na	0.51 ^{d}	0.49 ^{d}	0.78^{a}	0.60^{c}	0.71 ^{b}
K	1.18 ^{c}	1.24 ^{c}	1.85 ^{a}	1.83^{b}	1.84 ^{b}
Ca	2.92 ^{c}	2.99 ^{c}	3.09^{a}	2.79^{d}	3.02 ^{b}
Mg	3.00 ^{c}	3.01^{c}	3.97 ^{a}	3.12 ^{b}	3.03 ^{b}
EA	2.05^{a}	2.47 ^{a}	1.79 ^{c}	1.93 ^{b}	1.82^{c}
CEC	9.76^{d}	10.03 ^{c}	11.87 ^{a}	9.96 ^{d}	10.89 ^{b}
BS	80.89^{b}	78.92 ^{c}	89.87^{a}	81.68 ^{b}	78.89 ^{c}

Note: Mean with same superscript along the rows are not significantly different at p>0.05

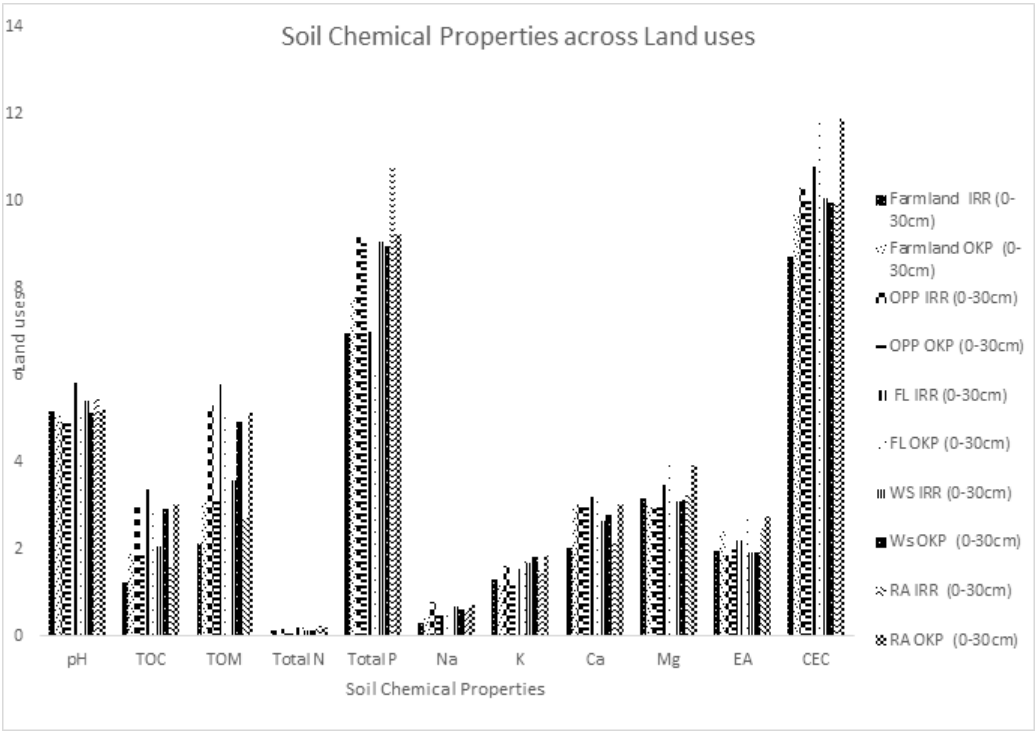

Figure 3: Soil Chemical across land uses

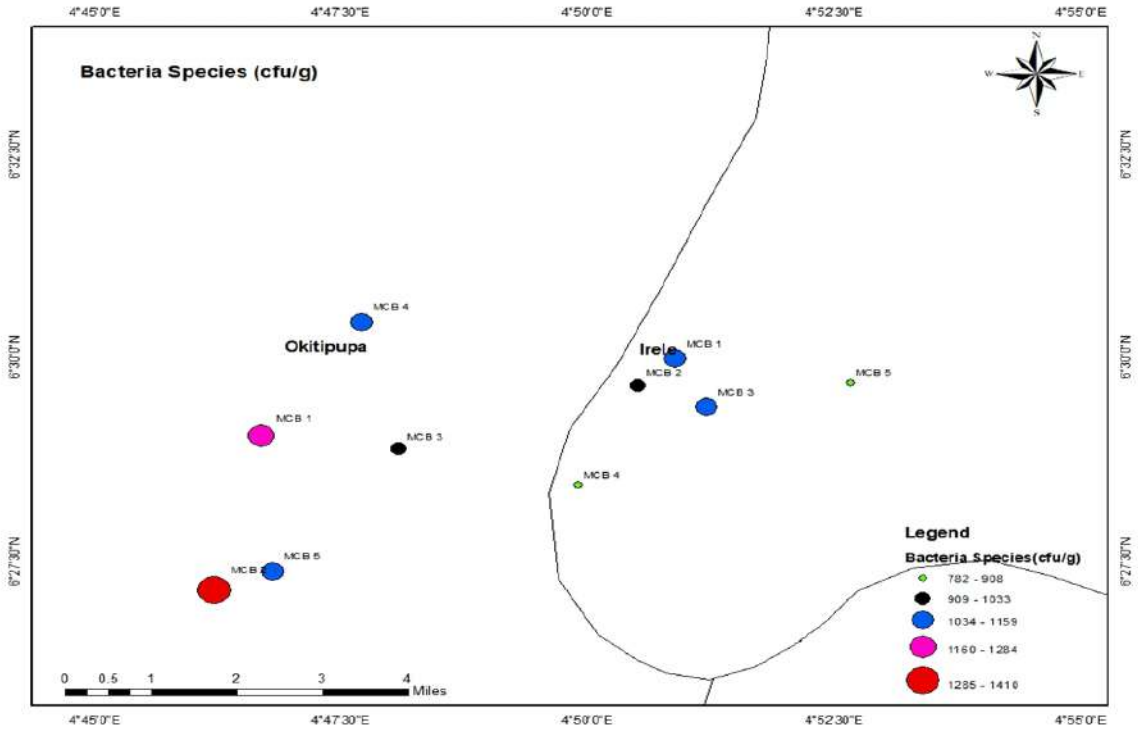

Figure 4: Map showing the bacterial species

Table 3: Comparison of Bacteria Population across the land uses in Irele and Okitipupa Local Government.

IRELE LOCAL GOVT						Okitipupa Local govt				
Parameters	**Oil palm plantation (0-30cm)**	**Forestland (0-30cm)**	**Residential area (0-30cm)**	**Watershed (0-30cm)**	**Farmland (0-30cm)**	**Oil palm plantation (0-30cm)**	**Forestland (0-30cm)**	**Residential area (0-30cm)**	**Watershed (0-30cm)**	**Farmland (0-30cm)**
Zymomonas mobilis	10.00 b	1.00e	7.00 c	1.0 e	1.00 e	23.00 a	0.00 e	11.00 b	2.66 d	0.00 e
Cellulomonas spp	1.00e	9.66 d	0.00 f	25.00 b	1.00 e	0.00 c	11.66 c	0.00 f	35.00 a	0.00 f
Micrococcus spp	20.00 e	20.66 e	17.33 f	47.00 a	0.00 g	45.00 b	32.66 c	27.33 d	67.00 a	0.00g
Bacillus subtilis	100.33 d	132.00 c	70.00 g	55.00 h	105.00 c	135.33 b	152.00 a	90.00 e	75.00f	115.00 c
Bacillus linchemiformis	36.33c	130.33 a	66.00 b	96.00 c	60.00 d	90.33c	135.33 a	76.00b	106.00b	68.00 d
S. saprophyticus	100.66 d	124.00 b	79.66 h	65.00 e	91.00 f	110.66 c	144.00 a	99.66 e	85.00g	90.00 f
salmonella spp	0.00 c	2.00 b	0.00 c	20.00b	0.00 c	0.00 c	4.00 b	0.00 c	30.00 a	0.00c
Proteus mirbilis	30.66 e	37.33 c	48.00 b	20.00 d	70.00 a	43.66 e	57.33 c	68.00 b	50.00 d	77.00 a
Streptotoccus spp	57.66 d	77.66 c	48.00 e	30.00 f	61.00 b	87.66 a	87.66 a	58.00 d	50.00 e	80.00 b
Enterobacter spp	40.00 f	40.66 e	27.66 d	42.00d	40.00 c	55.00 c	60.66 b	37.66 d	62.00 a	41.00 e
Arthrobacter spp	0.00 d	1.00 c	1.00 c	17.33 b	0.00 d	0.00 d	0.00d	0.00 d	27.33 a	0.00d
Chromoba. lividum	55.33 c	46.67 e	50.20d	18.00 e	60.33 c	65.33 a	56.67 c	50.00 d	28.00 e	63.33b
Xanthomonas spp	6.00 f	5.00c	0.00 a	20.00d	40.00 b	9.00 e	15.00 c	0.00 a	21.00 c	45.00 e
Chromoba. Violaceum	30.33d	36.33 c	25.00 b	45.00 b	17.66 a	50.33 a	46.33 b	35.00 c	40.00 c	20.66 a
Lactobacilius spp	35.66 a	28.33 c	30.33 e	40.00 d	53.33 b	65.66 a	58.33 c	40.33 e	45.00 d	60.33 b
Clostridium spp	30.33 e	95.66b	70.66 c	80.00 d	90.00 b	70.33 e	115.66a	90.66 c	81.00 d	96.00 b
Acinectobacter spp	0.00 d	5.33 c	35.33a	10.00 b	0.00 d	0.00 d	7.33 c	25.33 a	12.00 b	0.00 d
Pseudo. Aeruginosa	15.00 h	67.00 g	61.00 e	73.33 e	75.33 d	85.33 c	97.00 a	71.00 f	90.33 b	80.33 c
Rhizobium spp	0.00 e	48.00 a	4.00 c	20.00c	10.00 d	0.00 d	11.00 d	7.00 c	21.00 b	0.00 e
Citrobacter spp	0.00 e	0.00 e	3.00 c	4.00 a	10.00 a	0.00 e	0.00 c	2.00 d	8.00 b	0.00 e
Corynebacterium spp	42.00d	0.33g	68.00c	42.33 f	60.66 c	62.33 d	90.33 b	98.00 a	50.33 e	67.66c
Peptococcus spp	34.66 d	47.00 b	17.00 c	1.00 d	0.00 d	44.66 c	57.00 a	27.00 e	0.00 f	0.00 f
Flavobacterium spp	50.33 e	91.00 b	25.00 e	95.00 b	60.00 d	60.33 d	111.00 a	45.00 e	105.00 b	85.00 c
Diplococci spp	32.00 d	28.00 e	1.00 f	30.00 c	42.00 c	44.00 b	10.00 d	0.00 f	30.00 d	61.00 a
Alcaligenes spp	38.00 d	41.00 c	20.00 c	1.00 d	0.00 d	58.00 a	51.00 b	30.00 e	0.00 f	0.00 f
TOTAL	**851.29 g**	**1086.96 c**	**774.97 h**	**899.99 f**	**846.99 c**	**1180.07 b**	**1410.10 a**	**990.21 e**	**1120.32 c**	**1050.11 d**

*Mean with same superscript along the rows are not significantly different at p>0.05

Discussion

Bacteria distribution and soil chemical properties

The variations in soil bacterial communities are markedly influenced by soil chemical properties which encompass a range of factors, including soil pH, nutrient availability (particularly nitrogen, phosphorus, and organic matter), and cation exchange capacity. These properties directly affect the growth, diversity, and community structure of bacterial populations, which play crucial roles in biochemical processes, nutrient cycling, and overall soil health.

Soil pH is one of the most critical chemical properties affecting bacterial diversity and community composition. Research indicates that pH influences microbial processes significantly, as it governs the solubility and availability of various nutrients essential for bacterial growth (Bobuľská *et al.*, 2021; The

pH of the soil was slightly acidic which may promote the dominance of acidophilic bacteria such as the one found in the study area. The abundance of bacteria count in the forest land may be due to moderate to higher N found in this land use, for example, studies have demonstrated that total nitrogen content in soils strongly influences bacterial abundance; high nitrogen levels can enhance the growth of nitrogen-fixing bacteria and other microbial taxa that thrive in nitrogen-rich environments (Hua *et al.*, 2024; Sengupta *et al.*, 2020). However, low counts of bacteria in the farmland may be due to continuous nitrogenous fertilizer, although, this effect may vary depending on management practices and soil types (Sengupta *et al.*, 2020).

Many bacteria are found in the forestland over other land uses due to higher organic carbon content, soil organic carbon (SOC) provide energy sources for bacteria and influence the soil's physical and chemical properties, such as water retention and aggregate stability (Li *et al.,* 2020). High organic matter content typically correlates with greater bacterial richness and diversity, as diverse organic substrates in the soil foster the growth of various microbial populations (Hua et al., 2024). For instance, soils enriched with organic matter through composting or cover cropping practices demonstrate higher microbial abundance and diversity compared to intensively manage agricultural soils with low organic content (Zheng *et al.,* 2024; Hu *et al.,* 2022). The lowest bacteria counts in the farmland may be due to low level soil organic carbon found in the study area.

Cation exchange capacity (CEC) impacts soil nutrient retention and availability, thereby influencing bacterial communities. Soils with high CEC can retain more nutrients, provisionally providing a more favorable environment for diverse bacterial taxa (Ekero *et al.,* 2022). Research has shown that soils with enhanced nutrient retention capacities often support higher microbial activity levels, whereas soils with low CEC may experience more significant fluctuations in nutrient availability, potentially leading to reduced microbial diversity and dominance by resilient bacterial taxa capable of surviving adverse conditions (Kambai *et al.,* 2021; Ekero *et al.*, 2022) the conditions found in the forestland that makes bacteria more abundance in the area under forestland.. Changes in land use, such as transitioning from natural forests to agricultural systems or urban landscapes, typically lead to alterations in soil chemical profiles, often resulting in reduced microbial diversity due to the uniformity of inputs and management strategies (Bobuľská *et al.,* 2021; Yin *et al.,* 2021).

Bacteria distribution and land uses

The higher count of bacteria in the forest land showed that forestland serves as a benchmark for microbial diversity due to its rich organic matter and complex rooting systems that provide diverse habitats for soil bacteria. Research shows that forest ecosystems support higher bacterial diversity compared to agricultural systems, primarily due to the presence of multiple plant species contributing varied organic material to the soil (Wıbowo *et al.,* 2022; The distinct microclimatic conditions found within forests, such as stable moisture levels and nutrient availability, promote a rich array of microbial species and functional groups (Enaruvbe *et al.,* 2021). Forests are observed to harbor diverse Proteobacteria and Acidobacteria, which are crucial for organic matter decomposition and nutrient cycling (Behera *et al.,* 2020). The undergrowth and litter layer of forests also foster complex interactions among bacterial communities, making them resilient to environmental changes (Devi,

2021). On the contrary, land-use conversion to Oil palm plantations significantly disrupts these microbial communities. Although oil palm plantations can yield economic benefits, they often replace biodiverse forest ecosystems, leading to decreased microbial richness and altered community structures. Studies indicate a marked decline in bacterial diversity within oil palm plantations compared to adjacent forest ecosystems, primarily due to soil compaction, altered nutrient cycles, and homogenized organic inputs (Wıbowo *et al.*, 2022; Ramadhan *et al.*, 2022). The cultivation practices involved in oil palm farming, such as the application of fertilizers and pesticides, can further select for specific bacterial taxa, often leading to a reduction in functional diversity that is essential for ecosystem stability and resilience (Behera *et al.,* 2020; Ramadhan *et al.,* 2022). Moreover, oil palm plantations are characterized by a unique set of soil properties influenced by management practices, including pH elevation and increased soil salinity, which in turn shape the bacterial communities inhabiting these environments (Behera *et al.*, 2020). For instance, the soil bacterial community in oil palm areas tends to be dominated by genera like Pseudomonas and Rhizobium, which are associated with nutrient cycling under agricultural conditions (Ramadhan *et al.,* 2022; Ashraf *et al.*, 2023). This dominance signifies a shift from the complex interactions found in forest soils to simpler, highly managed microbial communities in oil palm systems.

Watersheds present another critical land-use type, as they encompass various land-use patterns affecting soil bacterial distribution. Soil bacteria in watersheds experience fluctuations in moisture and nutrient availability due to runoff and soil erosion from surrounding agricultural practices and urban areas. Research indicates that watershed management practices that promote vegetation cover can enhance soil microbial communities by maintaining moisture levels and reducing nutrient loading, thus promoting a more diverse and functional soil microbiome (Manar *et al.,* 2023; Greenshields *et al.*, 2023). The interactions between soil and water are key in determining the resilience of microbial communities, as they are sensitive to changes in hydrology and sediment movement (Manar *et al.*, 2023). Farmland is often marked by intensive agricultural practices that can drastically alter soil properties and, consequently, bacterial communities. Soil compaction, shift in pH, and nutrient excesses from fertilizers are common characteristics of agricultural land-use, leading to a decline in bacterial diversity and shifts in community structure (Supriyanto *et al.,* 2022). Research indicates that monoculture practices dominate farmland, often resulting in the loss of critical microbial functions needed for organic matter decomposition and nutrient cycling (Brindis-Santos *et al.,* 2021). The high presence of *S. saprophyticus* and *Xanthomonas spp suggests* bacterial communities found in this study in farmland are frequently found to be dominated by nitrate-utilizing and phosphorus-solubilizing bacteria, adapting to the nutrient-rich conditions created by fertilizers, yet such adaptation might compromise overall soil health and fertility in the long term (Brindis-Santos *et al.,* 2021). The lowest counts of bacteria in residential areas in this study often embody different land use characteristics, including impervious surfaces and landscaping practices that influence soil properties. Soil disturbance and the introduction of synthetic chemicals can lead to distinctly different microbial populations compared to those found in natural ecosystems or agricultural

lands. Recent studies indicate that bacterial communities in urbanized areas may exhibit lower diversity and are sometimes dominated by opportunistic pathogens due to higher nutrient loads such as nitrogen and phosphorus from urban runoff (Abiodun *et al.,* 2021). Furthermore, residential landscaping practices can lead to further alterations in soil properties, impacting soil structure and microbial habitat availability (Irvanto *et al.,* 2022).

Conclusion

This study provides a comprehensive analysis of bacteria population characteristics across different land use types, revealing patterns that align with findings from similar tropical and urban environments while differing from those in arid, rural, and industrial regions. The study shows that forestland recorded the highest bacteria counts while the residential area recorded least count of bacteria. The study highlights the influence of environmental conditions, land use practices, and human activities on bacteria communities, with important implications for soil health, plant growth, and public health. Future research should focus on expanding the scope of such studies to include a broader range of land use types and environmental conditions, as well as investigating the long-term trends in microbial populations in response to changing land use and environmental factors.

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