



## **Soil Rhizosphere Microbial Properties of Selected Farmlands in Rumuokparali Community**

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### **Authors' contributions**

*This work was carried out in collaboration between all authors. Author HOS designed the study, performed the statistical analysis, wrote the protocol and wrote the first draft of the manuscript. Authors JA and CJU managed the analyses of the study. Author JA managed the literature searches. All authors read and approved the final manuscript.*

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### **ABSTRACT**

This study was conducted to determine the rhizosphere soil microorganisms associated with the cultivation of *Manihot esculentum*, *Comelina bengalensis*, *Talinum triangulare* and *Telfairia occidentalis*. The plants were obtained from newly cultivated, ready for harvest and fallowed farmlands. The rhizosphere microorganisms were enumerated and compared with bulk soil microorganisms. The heterotrophic bacterial count for newly cultivated farmland ranged from  $2.9 \times 10^7$ - $6.3 \times 10^8$  cfug<sup>-1</sup> and total fungal ranged from  $5.6 \times 10^4$ - $7.0 \times 10^6$  sfug<sup>-1</sup>, while the bulk soil total heterotrophic bacterial count was  $4.96 \times 10^9$  cfug<sup>-1</sup> and the total fungal count was  $5.87 \times 10^6$  sfug<sup>-1</sup>. The heterotrophic bacterial count for ready for harvest farmland ranged from  $1.82 \times 10^8$ - $1.80 \times 10^9$  cfug<sup>-1</sup> and total fungal ranged from  $2.3 \times 10^4$ - $3.57 \times 10^6$  sfug<sup>-1</sup>, while the bulk soil total heterotrophic bacterial count was  $1.90 \times 10^9$  cfug<sup>-1</sup> and the total fungal count was  $2.30 \times 10^6$  sfug<sup>-1</sup>. The heterotrophic bacterial count for fallowed farmland ranged from  $5.65 \times 10^8$ - $1.50 \times 10^9$  cfug<sup>-1</sup> and total fungal ranged from  $1.33 \times 10^6$ - $3.05 \times 10^6$  sfug<sup>-1</sup>, while bulk soil total heterotrophic bacterial count was  $1.74 \times 10^9$  cfug<sup>-1</sup> and total fungal count was  $1.07 \times 10^6$  sfug<sup>-1</sup>. The rhizosphere soil bacterial isolates belong to the genera: *Staphylococcus*, *Hafnia*, *Acinetobacter*, *Bacillus*, *Bacteroides*, *Klebsiella*, *Tatumella*, *Enterobacter*, *Corynebacterium* and *Pseudomonas* while fungal isolates belong to the

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genera: *Aspergillus*, *Epicocum*, *Chrysosporium*, *Trichosporon*, *Cryptococcus*, *Fusarium*, *Penicillium* and *Chaetomium*. The bulk soil bacterial isolates belong to genera: *Staphylococcus*, *Hafnia*, *Acinetobacter*, *Bacillus*, *Klebsiella*, *Tatumella*, *Corynebacterium* and *Pseudomonas* while the fungal isolates belong to genera: *Aspergillus*, *Epicocum*, *Chrysosporium*, *Trichosporon*, *Cryptococcus* and *Chaetomium*. Microbial diversity of rhizosphere soil was more compared to bulk soil.

**Keywords:** Rhizosphere; bulk soil; microorganisms; farmlands.

## 1. INTRODUCTION

The rhizosphere is a narrow region of soil that is at direct proximity to plants roots and is influenced by root secretions and actions of associated soil microorganisms [1]. The actual extent of rhizosphere is dependent on the influence zone of the plant's roots and associated microorganisms. Soil which is not part of rhizosphere is known as bulk soil. The rhizosphere is generally considered to be the most biodiverse and dynamic habitat on earth and also, a metabolically busier and more competitive environment than surrounding bulk soil [2]. Unlike the soil associated with rhizosphere, the bulk soil is not penetrated by plant roots, and generally has lower microbial communities [3].

In rhizosphere, symbiotic relationships exist between plant roots and microorganisms. Different water soluble nutritive compounds containing sugars and amino acids are exuded by plant roots which sustain and provide for microbial existence. Plants roots have strong impacts on physical and chemical environment in rhizosphere, such that a shift in this environment, which is influenced by manipulations of plant's roots, significantly impacts on the availability and forms of substances used for microbial metabolism, which in turn strongly affect the prevalence and diversity of different microbial species and functions, as well as their total biomass within the rhizosphere [1]. The microbial population in rhizosphere carries out processes, such as the transformation of carbon, nitrogen and other minerals, to plant benefit [4]. In addition to this, soil bacterial species produce biofilms which act as an aggregating mechanism for mineral particles and organic matter [5]. Also, mycorrhizal fungi have been shown to increase aggregation through the physical construction of fungal hyphae, as well through the secretion of their exopolymer deposit.

The rhizosphere is an environment that allows a diverse range of soil microorganisms to thrive.

This study aimed to determine both quantitatively and qualitatively, the rhizosphere soil microorganisms associated with certain plants from different farmlands.

## 2. MATERIALS AND METHODS

### 2.1 Sample Collection

Rhizosphere soil samples were collected from farmlands at Rumuokparali community in Obio Akpor Local Government Area of Rivers State, Nigeria. The rhizosphere soils were obtained from the plant roots, ranging from 0-10 cm depth. The control for each farmland was obtained from surface soil between 0-1 cm thickness. Using the composite sampling technique, rhizosphere soil samples were aseptically obtained with a sterile spatula from *Manihot esculentum*, *Talinum triangulare*, *Telfairia occidentalis* and *Comelina bengalensis* from newly cultivated and ready for harvest farmland. *Manihot esculentum*, *Talinum triangulare* and *Comelina bengalensis* rhizosphere soil samples were aseptically obtained from fallowed farmland. The bulk soils from farmlands, which served as controls, were collected using a composite sampling technique, with aid of a quadrat.

### 2.2 Microbiological Analysis

Soil samples were serially diluted to  $10^{-5}$  dilutions. These dilutions were used to carry out soil bacteria and fungi isolation and enumeration from the soil.

### 2.3 Enumeration of Total Heterotrophic Bacteria Count (THBC)

This test was done to screen for total viable aerobic, mesophilic and heterotrophic bacteria present in each soil sample. The rhizosphere soil samples were serially diluted to  $10^{-5}$  dilution using physiological saline. Aliquots 0.1ml from  $10^{-3}$ ,  $10^{-4}$  and  $10^{-5}$  dilutions were spread aseptically with a sterile glass rod on freshly

prepared dry nutrient agar plates. The plates were incubated at 37°C for 24 to 48 hours. After incubation, the THBC for each sample was recorded and expressed in colony forming unit per gramme (cfug<sup>-1</sup>) after colony count.

## 2.4 Enumeration of Total Fungal Count (TFC)

This test was carried out to enumerate total heterotrophic fungal species contained in effluent samples. Aliquots of 0.1 ml from 10<sup>-1</sup>, 10<sup>-2</sup> and 10<sup>-3</sup> dilutions were spread aseptically with a sterile glass rod on freshly prepared dry potato dextrose agar plates and incubated at 28°C for 3-5 days. After incubation, the TFC for each sample was recorded and expressed as spore-forming unit per gram (sfug<sup>-1</sup>) after colony count.

## 2.5 Purification and Characterisation

After incubation, distinct colonies observed on both nutrient agar plates and potato dextrose agar plates were isolated and purified by repeated sub-culturing. The bacterial isolates were characterised using their macroscopic, microscopic and biochemical attributes. The biochemical tests performed on bacterial isolates were: catalase, oxidase, motility, hydrogen sulphide production (H<sub>2</sub>S), indole, Voges-Proskauer (VP), Methyl red (MR), citrate, and sugar fermentation. The fungal isolates were characterised on basis of their macroscopic and

microscopic appearance with reference to the standard manual.

## 2.6 Physicochemical Analysis

The physicochemical parameters monitored for soil samples were temperature, pH, moisture content, total organic carbon and total nitrogen. The physicochemical parameters were assessed according to methods as described by American Public Health Association [6].

## 3. RESULTS

The results for the total heterotrophic bacterial count (THBC) and total fungal count (TFC) are shown in Table 1. The rhizosphere THBC ranged from 2.9 x10<sup>7</sup>-1.80x10<sup>9</sup> cfug<sup>-1</sup> while rhizosphere TFC ranged from 2.3 x10<sup>4</sup>-7.0x10<sup>6</sup> sfug<sup>-1</sup>. The bulk soil THBC ranged from 1.74-4.96.0x10<sup>9</sup> cfug<sup>-1</sup>, while bulk soil TFC ranged from 1.07 x10<sup>6</sup>-5.87.0x10<sup>6</sup> sfug<sup>-1</sup>.

Table 2 shows bacterial isolates from rhizosphere soil. The bacterial isolates belong to genera: *Staphylococcus*, *Hafnia*, *Acinetobacter*, *Bacillus*, *Bacteroides*, *Klebsiella*, *Tatumella*, *Corynebacterium*, *Pseudomonas* and *Enterobacter*. The fungal isolates were characterized to belong to genera: *Aspergillus*, *Epicoicum*, *Chrysosporium*, *Trichosporon*, *Cryptococcus*, *Chaetomium*, *Microsporium*, *Penicillium* and *Fusarium* (Table 3).

**Table 1. Bacterial and fungal counts obtained from rhizosphere soil samples**

S/N	Soil sample	Bacterial count (cfug <sup>-1</sup> )	Fungal count (sfug <sup>-1</sup> )
1.	NME	3.1 x10 <sup>8</sup>	1.91 x10 <sup>6</sup>
2.	NCB	1.55 x10 <sup>8</sup>	7.0 x10 <sup>6</sup>
3.	NTT	6.3 x10 <sup>8</sup>	5.6 x10 <sup>4</sup>
4.	NTO	2.9 x10 <sup>7</sup>	1.6 x10 <sup>6</sup>
5.	RME	18.2 x10 <sup>8</sup>	3.57 x10 <sup>6</sup>
6.	RCB	180 x10 <sup>9</sup>	2.0 x10 <sup>6</sup>
7.	RTT	9.0 x10 <sup>8</sup>	2.3 x10 <sup>4</sup>
8.	RTO	6.2 x10 <sup>8</sup>	3.32 x10 <sup>6</sup>
9.	FME	1.5 x10 <sup>9</sup>	1.83 x10 <sup>6</sup>
10.	FCB	6.55 x10 <sup>8</sup>	3.05 x10 <sup>6</sup>
11.	FTT	5.65 x10 <sup>8</sup>	1.33 x10 <sup>6</sup>
12.	NC	4.96 x10 <sup>9</sup>	5.87 x10 <sup>6</sup>
13.	RC	1.9 x10 <sup>9</sup>	2.30 x10 <sup>6</sup>
14.	FC	1.74 x10 <sup>9</sup>	1.07 x10 <sup>6</sup>

Keys: NME - Newly Cultivated *Manihot esculentum*; NCB - Newly Cultivated *Comelina bengalensis*; NTT - Newly Cultivated *Talinum triangulare*; NTO - Newly Cultivated *Telfairia occidentalis*; RME - Ready for Harvest *Manihot esculentum*; RCB - Ready for Harvest *Comelina bengalensis*; RTT - Ready for Harvest *Talinum triangulare*; RTO - Ready for Harvest *Telfairia occidentalis*; FME - Fallowed *Manihot esculentum*; FCB - Fallowed *Comelina bengalensis*; FTT - Fallowed *Talinum triangulare*; NC - Nearly Cultivated Control; RC - Ready for Harvest Control; FC - Fallowed Control

**Table 2. Bacterial isolates obtained from different soil samples**

S/N	Soil sample	Bacterial isolates
1.	NME	<i>Staphylococcus</i> sp, <i>Hafnia</i> sp, <i>Acinetobacter</i> sp, <i>Bacillus</i> sp, <i>Bacteroides</i> sp
2.	NCB	<i>Staphylococcus</i> sp, <i>Hafnia</i> sp, <i>Corynebacterium</i> sp, <i>Klebsiella</i> sp, <i>Bacillus</i> sp
3.	NTT	<i>Klebsiella</i> sp, <i>Bacillus</i> sp, <i>Corynebacterium</i> sp
4.	NTO	<i>Bacillus</i> sp, <i>Enterobacter</i> sp, <i>Tatumella</i> sp
5.	RME	<i>Klebsiella</i> sp, <i>Hafnia</i> sp, <i>Acinetobacter</i> sp, <i>Tatumella</i> Sp, <i>Bacteroides</i> sp, <i>Bacillus</i> sp
6.	RCB	<i>Klebsiella</i> sp, <i>Tatumella</i> Sp, <i>Acinetobacter</i> sp, <i>Bacillus</i> sp
7.	RTT	<i>Bacillus</i> sp, <i>Hafnia</i> sp
8.	RTO	<i>Bacillus</i> sp, <i>Enterobacter</i> sp, <i>Tatumella</i> sp, <i>Klebsiella</i> sp, <i>Hafnia</i> sp, <i>Acinetobacter</i> sp
9.	FME	<i>Staphylococcus</i> sp <i>Bacillus</i> sp, <i>Corynebacterium</i> sp, <i>Hafnia</i> sp, <i>Tatumella</i> sp, <i>Klebsiella</i> sp
10.	FCB	<i>Pseudomonas</i> sp, <i>Klebsiella</i> sp, <i>Hafnia</i> sp, <i>Acinetobacter</i> sp, <i>Tatumella</i> Sp, <i>Bacillus</i> sp
11.	FTT	<i>Bacillus</i> sp, <i>Hafnia</i> sp, <i>Tatumella</i> sp, <i>Klebsiella</i> sp
12.	NC	<i>Bacillus</i> sp, <i>Acinetobacter</i> sp, <i>Staphylococcus</i> sp <i>Tatumella</i> Sp
13.	RC	<i>Bacillus</i> sp, <i>Acinetobacter</i> sp, <i>Staphylococcus</i> sp <i>Tatumella</i> Sp, <i>Klebsiella</i> sp
14.	FC	<i>Bacillus</i> sp, <i>Acinetobacter</i> sp, <i>Staphylococcus</i> sp <i>Klebsiella</i> sp, <i>Pseudomonas</i> sp, <i>Corynebacterium</i> sp, <i>Tatumella</i> sp

Keys: *Idem***Table 3. Fungal isolates obtained from different soil samples**

S/N	Soil sample	Fungal isolates
1.	NME	<i>Aspergillus</i> sp, <i>Epicocum</i> sp, <i>Chrysosporium</i> sp, <i>Trichosporon</i> sp, <i>Cryptococcus</i> sp
2.	NCB	<i>Trichosporon</i> sp, <i>Cryptococcus</i> sp, <i>Aspergillus</i> sp
3.	NTT	<i>Aspergillus</i> sp, <i>Epicocum</i> sp, <i>Trichosporon</i> sp, <i>Chaetomium</i> sp
4.	NTO	<i>Aspergillus</i> sp, <i>Chrysosporium</i> sp <i>Chaetomium</i> sp, <i>Trichosporon</i> sp, <i>Cryptococcus</i> sp, <i>Epicocum</i> sp
5.	RME	<i>Aspergillus</i> sp, <i>Trichosporon</i> sp, <i>Epicocum</i> sp, <i>Chrysosporium</i> sp, <i>Cryptococcus</i> sp, <i>Chaetomium</i> sp
6.	RCB	<i>Aspergillus</i> sp, <i>Microsporium</i> sp, <i>Epicocum</i> sp, <i>Chrysosporium</i> sp, <i>Trichosporon</i> sp, <i>Cryptococcus</i> sp, <i>Chaetomium</i> sp
7.	RTT	<i>Aspergillus</i> sp, <i>Epicocum</i> sp, <i>Trichosporon</i> sp, <i>Chaetomium</i> sp
8.	RTO	<i>Aspergillus</i> sp, <i>Microsporium</i> sp, <i>Epicocum</i> sp, <i>Chrysosporium</i> sp, <i>Trichosporon</i> sp, <i>Cryptococcus</i> sp, <i>Chaetomium</i> sp
9.	FME	<i>Aspergillus</i> sp, <i>Microsporium</i> sp, <i>Epicocum</i> sp, <i>Chrysosporium</i> sp, <i>Trichosporon</i> sp, <i>Cryptococcus</i> sp, <i>Chaetomium</i> sp
10.	FCB	<i>Aspergillus</i> sp, <i>Microsporium</i> sp, <i>Epicocum</i> sp, <i>Chrysosporium</i> sp, <i>Trichosporon</i> sp, <i>Cryptococcus</i> sp, <i>Chaetomium</i> sp <i>Penicillium</i> sp
11.	FTT	<i>Aspergillus</i> sp, <i>Epicocum</i> sp, <i>Chaetomium</i> sp, <i>Trichosporon</i> sp, <i>Cryptococcus</i> sp
12.	NC	<i>Aspergillus</i> sp, <i>Microsporium</i> sp, <i>Epicocum</i> sp, <i>Chrysosporium</i> sp, <i>Trichosporon</i> sp, <i>Cryptococcus</i> sp, <i>Chaetomium</i> sp
13.	RC	<i>Aspergillus</i> sp, <i>Microsporium</i> sp, <i>Epicocum</i> sp, <i>Chrysosporium</i> sp, <i>Trichosporon</i> sp, <i>Cryptococcus</i> sp, <i>Chaetomium</i> sp
14.	FC	<i>Aspergillus</i> sp, <i>Microsporium</i> sp, <i>Epicocum</i> sp, <i>Chrysosporium</i> sp, <i>Trichosporon</i> sp, <i>Cryptococcus</i> sp, <i>Chaetomium</i> sp

Keys: *Idem*

Table 4 shows the physicochemical parameters of farmlands. The rhizosphere soils from *Manihot esculentum* for the three farmlands had their temperature as 27°C, while pH ranged from 5.265-6.190; moisture content, 10.8-12.9%; total carbon content, 0.927-1.614 mgL<sup>-1</sup> and total nitrogen content, 1.40-1.68 mgL<sup>-1</sup>. The rhizosphere soils from *Comelina bengalensis* for the three farmlands had their temperature values as 27°C, while their pH values ranged from 5.901-6.682; moisture content, 41.0-43.6%, total carbon content, 12.232-17.001 mgL<sup>-1</sup>; total nitrogen content, 4.321-4.968 mgL<sup>-1</sup>. The rhizosphere soils from *Talinum triangulare* for the three farmlands had their temperature values as 27°C, while their pH values ranged from 4.987-6.230; moisture content, 16.29-33.20%, total carbon content, 8.002-12.280 mgL<sup>-1</sup>; total nitrogen content, 3.200-5.212 mgL<sup>-1</sup>. The rhizosphere soils from *Telfairia occidentalis* for the three farmlands had their temperature values as 27°C, while their pH values ranged from 4.890-6.009; moisture content, 28.2-32.0%, total carbon content, 3.210-7.980 mgL<sup>-1</sup>; total nitrogen content, 5.101-5.210 mgL<sup>-1</sup>. The bulk soil samples from the three farmlands had their temperature values as 27°C, while their pH values ranged from 6.628-6.983; moisture content, 6.69-7.21%, total carbon content, 10.01-11.29 mgL<sup>-1</sup>; total nitrogen content, 11.68-12.90 mgL<sup>-1</sup>.

#### 4. DISCUSSION

This study was conducted to determine, both quantitatively and qualitatively, the diversity of rhizosphere soil microorganisms associated with

*Manihot esculentum*, *Comelina bengalensis*, *Talinum triangulare* and *Telfairia occidentalis* obtained from newly cultivated, ready for harvest and fallowed farmlands. The heterotrophic bacterial count obtained from different rhizosphere soils for different plant species in ready for harvest farmland ranged from 1.82 x10<sup>8</sup>-1.80 x10<sup>9</sup> cfug<sup>-1</sup> and total fungal count ranged from 2.3 x10<sup>4</sup>-3.57x10<sup>6</sup> sfug<sup>-1</sup>, while bulk soil heterotrophic bacterial count was 1.9 x10<sup>9</sup> and fungal count was 2.3x10<sup>6</sup> sfug<sup>-1</sup>. The ready to harvest soil had more bacterial load than the bulk soil which had a more fungal load. For fallowed farmland, heterotrophic bacteria count ranged from 5.65x10<sup>8</sup>-1.50x10<sup>9</sup> cfug<sup>-1</sup> and total fungi ranged from 1.33-3.05x10<sup>6</sup> sfug-1, while heterotrophic bacteria count for bulk soil sample was 1.74x10<sup>9</sup>cfug<sup>-1</sup> and total fungi count was 1.07x10<sup>6</sup> sfug<sup>-1</sup>. Just like in ready to harvest soil, fallowed farmland had more bacteria load than the bulk soil which had the more fungal load.

The microbial counts obtained from different rhizosphere soils of the different plant species at newly cultivated farmland ranged from 2.9x10<sup>7</sup>-6.3x10<sup>9</sup> cfug<sup>-1</sup> for heterotrophic bacteria and 5.6 x10<sup>4</sup>-7.0 x10<sup>6</sup> sfug<sup>-1</sup> for the total fungi, while bulk soil had a heterotrophic bacterial count of 4.96 x 10<sup>9</sup>cfug<sup>-1</sup> and total fungal count 5.87 x 10<sup>6</sup> sfug<sup>-1</sup>. Soil-root system affects soil microbial population [1]. The heterotrophic bacterial count range was lower compared to other farmlands. The lower heterotrophic bacterial content of rhizosphere soil could be as a result of regulatory mechanisms of the crop root system to maximise environmental properties to enhance their well being.

**Table 4. Physicochemical properties of farmland soil samples**

S/N	Soil sample	Temperature (°C)	pH	Moisture content (%)	Total carbon content (mgkg <sup>-1</sup> )	Total nitrogen content (%)
1.	NME	27	5.265	12.9	0.927	1.40
2.	RME	27	6.190	12.6	1.080	1.68
3.	FME	27	5.695	10.8	1.614	1.555
4.	NCB	27	6.682	43.6	12.232	4.968
5.	RCB	27	6.002	43.2	14.621	4.712
6.	FCB	27	5.908	41.0	17.001	4.321
7.	NTT	27	4.987	33.20	12.280	5.212
8.	RTT	27	6.230	16.29	8.002	3.200
9.	FTT	27	5.760	21.30	10.621	5.111
10.	NTO	27	4.890	32.0	3.210	5.210
11.	RTO	27	6.009	28.2	7.980	5.101
12.	NC	27	6.983	7.21	10.82	12.92
13.	RC	27	6.801	7.20	10.01	11.68
14.	FC	27	6.628	6.69	11.29	11.98

Keys: *Idem*

The newly cultivated bulk soil had the highest bacterial load compared to rhizosphere soils. This might be due to the organic load present in the soil before cultivation, rather than to microorganisms-plant roots interaction. Plant-derived compounds provide nutrients to a large variety of soil microorganisms [1]. The soil around *Manihot esculentum* at ready to harvest farmland had the highest bacterial load ( $1.8 \times 10^9$  cfug<sup>-1</sup>) among the rhizosphere soils. *Manihot esculentum* is a root crop with several branches, having a long duration for maturity before harvest. It follows that root exudates would have provided material for the proliferation of associated bacteria. The soil around *Comelina bengalensis* in newly cultivated farmland had the highest fungal load ( $7.0 \times 10^6$  sfug<sup>-1</sup>). The high fungal load from *Comelina bengalensis* a flowering plant and a common farmland weed in the area of study may be due to the plant material nature under decomposition within the soil vicinity.

Bacteria were the most dominant in soil given their population and diversity. The rhizosphere bacteria differ with the plant species. The bacteria isolated from the different rhizosphere soils belong to ten genera namely: *Staphylococcus*, *Hafnia*, *Acinetobacter*, *Bacillus*, *Bacteroides*, *Klebsiella*, *Tatumella*, *Corynebacterium*, *Pseudomonas* and *Enterobacter*. Seven bacterial isolates were obtained at bulk soils which were *Staphylococcus* sp, *Acinetobacter* sp, *Bacillus* sp, *Klebsiella* sp, *Tatumella* sp, *Corynebacterium* sp and *Pseudomonas* sp. The most common rhizosphere bacteria genera are *Pseudomonas*, *Bacillus*, *Arthrobacter*, *Rhizobia*, *Agrobacterium*, *Alcaligenes*, *Azotobacter*, *Mycobacterium*, *Flavobacter*, *Cellulomonas* and *Micrococcus* [7]. Panaiyadiyan and Chellaia [8] reported *Acinetobacter* sp, *Klebsiella* sp, *Staphylococcus* sp, *Bacillus* sp and *Pseudomonas* sp among the 18 bacterial species isolated from rhizosphere soil. *Bacillus* sp and *Pseudomonas* sp are generally found in most rhizosphere soil, with their composition dependent on plant species [9]. In this study, *Bacillus* sp was dominant and present in both rhizosphere and bulk soil. *Bacillus* sp had been reported as most numerous rhizobacteria associated with rice and wheat [10].

The fungal rhizosphere isolates at bulk soil belong to genera *Aspergillus*, *Epicocum*, *Chrysosporium*, *Trichosporon*, *Cryptococcus*, *Chaetomium*, *Microsporium*, *Penicillium* and *Fusarium*. There were nine fungal isolates in

total. Fungi are more tolerable to acidic soil. The rhizosphere soil had more fungal diversity, with all the fungal genera represented. The bulk soil had *Microsporium* sp, *Aspergillus* sp, *Epicocum* sp, *Chrysosporium* sp, *Trichosporon* sp, *Cryptococcus* sp, *Chaetomium* sp, with *Penicillium* and *Fusarium* not detected. *Aspergillus* sp was a dominant fungal isolate. Panaiyadiyan and Chellaia [8] similarly isolated *Aspergillus* sp from rhizosphere soil, which they described as one of the most important soil fungi because of their benefits to plants.

The results of physicochemical analyses of the samples showed variations. The pH values were generally mildly acidic. Soil pH affects soil chemistry and extends to virtually all characteristic of soil that is affected by multiple interactions within the rhizosphere. Respiration by roots macro and microorganisms releases carbon dioxide which generates bicarbonate/carbonic acid which impact on soil acidity. The increased microbial activity also increases microbial transformations of chemical species to nitrate acid and sulphuric acid production [11]. The soil contributed to soil microbial population and diversity. According to Kent and Triplett [5], soil pH affects the nutrients availability and influence the abundance and diversity of associated microorganism. The soil temperature (27°C) supported the mesophilic microorganism present at the soil. The soil moisture content which ranged from 16.29-33.20% was adequate for both bacteria and fungi to thrive.

## 5. CONCLUSION

It has been established that rhizosphere soil microbes play various roles in the development of plants, and these roles confer additional benefits to plants. Several bacteria and fungi species are closely associated with plant roots, which together with soil environment influence microbial population and diversity.

## COMPETING INTERESTS

Authors have declared that no competing interests exist.

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