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Microbiological Characteristics of Crude Petroleum Polluted Farmland Soils of Nweol Community in Rivers State, Nigeria

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ABSTRACT

Microbiological characteristics of Crude Petroleum polluted farmland soils in Nweol community of Rivers State, Nigeria were conducted to evaluate the effect of crude Petroleum on microbial populations and types. Standard microbiological procedures were employed during the experiments. Soil samples were collected from crude oil polluted sites, and unpolluted samples served as control. Ranges of mean values of total heterotrophic bacteria count (THB), total fungi (TF), hydrocarbon utilizing bacteria (HUB) and hydrocarbon utilizing fungi (HUF) in the polluted soils in: Baraol-Chara 1:THB between $1.17x10^6$ and $1.36x10^6$CFU/g, TF $0.83x10^6$ and $0.96x10^6$CFU/g, while HUB $0.51x10^4$ and $1.76x10^4$CFU/g, HUF $0.34x10^4$ and $0.38x10^4$CFU/g. Percentage mean HUB 28.41%, Percentage mean HUF 21.99%. Baraol-Chara 2: THB between $1.56x10^6$ and $1.98x10^6$CFU/g, TF $0.59x10^6$ and $0.73x10^6$CFU/g. While HUB ranged between $0.36x10^4$ and $0.63x10^4$CFU/g, HUF $0.31x10^4$ and $0.46x10^4$CFU/g with Percentage mean of 22.56% and 25.73% respectively. Baraol-Gor: THB between $1.23x10^6$ and $1.45x10^6$CFU/g, TF $0.43x10^6$ and $0.63x10^6$CFU/g. While HUB ranged between $0.35x10^4$ and $0.53x10^4$CFU/g, HUF $0.23x10^4$ and $0.43x10^4$CFU/g with Percentage mean of 17.27% and 35.27% respectively. The unpolluted Gava Area/control: THBC ranged between $0.43x10^6$ and $0.92x10^6$CFU/g, TF $0.24x10^6$ and $0.33x10^6$CFU/g, while HUB ranged between $0.23x10^4$ and $0.28x10^4$CFU/g, HUF $0.11x10^4$ and $0.17x10^4$CFU/g with Percentage mean of 31.76% and 17.01% respectively. Bacterial isolates were; *Staphylococcus aureus*, *Micrococcus roseus*, *Serratia marcescens*, *Pseudomonas aeruginosa*, *Pseudomonas fluorescens*, *Chromobacterium violaceum*, *Escherichia coli*, *Bacillus subtilis*. Fungal isolates were; *Aspergillus niger*, *Penicillium frequentans*, *Trichoderma viridae*, *Aspergillus nidulans*, *Fusarium moniliforme*, *Aspergillus terreus*. The very high indices for the Petroleum hydrocarbon utilizing bacteria and fungi recorded in this study is an indication for the lingering presence of Petroleum pollutants in the farmlands, and a remarkable evidence for health risk of crops grown in the farms to unsuspecting consumers.

Keywords: Crude Petroleum, Farmlands, Soil Pollution, Hydrocarbon Utilizing Bacteria, Fungi, Population.

Introduction

Petroleum is a complex mixture of both liquid and solid hydrocarbon (Akpor *et al*., 2007). Pollution of the environment by crude petroleum and oil spillages is an unavoidable result of Petroleum production, transportation and distribution (Kato *et al*., 2001). Pipeline vandalism and Oil theft also contribute to worsen the situation and can lead to very serious environmental problems (Eze *et al*., 2014).

Oil spillage is known to be a widespread form of crude petroleum source of pollution to our useful environments such as farmlands and water bodies (Olukunle, 2013).

It destroys soil fertility, causing shifts and alterations in the microbiological and chemical properties of the soil, to pose damaging effects on the terrestrial and aquatic habitats (Olukunle, 2013). Crude Petroleum molecules, in large concentrations are usually toxic to many organisms, and particularly to soil population of microorganisms and other soil dependent macro organisms, including humans. Oil spillage has caused consistent threat to useful and resourceful water bodies, agricultural viable farmlands, forest tree species, vegetable or crop gardens (Ogri, 2001). Pollution has major negative effects, as the pollutants enter the soil by spillages, to influence microbiological ecosystem balance, and affect soil productivity (Tamames *et al*., 2010; Dominati *et al*., 2010).

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Oil spills hamper proper soil aeration, as oil film on the soil surface act as a physical barrier between air and the soil. It also reduces crop yield, land productivity and greatly depresses farm income (Odjuvwuederhie *et al*., 2006). Oil spillages have degraded agricultural lands leading to an increase in poverty indices, turning many productive farms into waste lands in most Niger Delta communities in Nigeria (Jackie *et al.,* 2001; Joseph and Sheu, 2015).

Soil has been described as the upper layer of earth, a mixture of organic remains, clay, rock and other particles in which crops and other plants grow. Soil is mixture of organic matter, minerals, gases, liquids and organisms that support life (Ugboma, 2014; Williams *et al*., 2020). A soil ecosystem is home to a large host of different plant and animal species. Many species rely entirely on soil ecosystems for both sustainable food and shelter from predators (Adnan and Fuying, 2018). Soil microorganisms play very important role in the soil ecosystems which could adjust energy flow and cycle of matter by digesting animal, plant and oil residues, and play a pivotal role in growth and development of agricultural crops, balance of soil ecosystem, organic matter transfer and bioremediation (Adnan *et al*., 2018). Plant roots are dynamic and the growth is strongly influenced by environmental conditions within the root zone. For the survival, growth and development of agricultural crops, plants need Air for free gas exchange, Water for uptake of soil nutrients, Carbohydrates, Minerals, Non-limiting temperature, Low soil density, Space, non-toxic soil chemistry and Rhizobial microbial associations within plants rhizosphere for any adequate production (Christopher, 2012).

Pollution of soil environments by anthropogenic activities, such as Oil spillages, and hydrocarbon effluents or other domestic wastes are of global concern, and potential health risk from increased soil or water nutrients, acidic and heavy metal indices to soil microbial shifts, and waterborne pathogens (Sadatipour *et al.,* 2004; Friends of the Earth International, 2019).

Certain extent of water and soil environmental contaminations by other pollutants can have natural recovery by simple attenuation over time, but high strength waste such as oil spills may take longer time to degrade (Aya and Nwite, 2016).

Most of the petroleum compounds are biodegradable, but the process may be very slow due to other environmental conditions.

Farm soil environments are usually fragile, very susceptible, and especially vulnerable to oil and petroleum spillages much like the coastal regions also are poorly containable and mitigation is often very difficult (Onwurah *et al.,* 2007). Deleterious effects of soil pollutants especially petroleum pollutants make it very compulsory for mitigation which is a counter measure to combat pollutants in our environments. Mitigation and controls in soil pollutions, may take many forms like, less use of chemical fertilizers in crop cultivation as these are more soil damaging than being beneficial, promoting reforestation and or afforestation of affected land, and by encouraging the use organic manures in planting.

In 1958 Shell Petroleum Development Company (SPDC) started Oil operations in Ogoni Kingdom of Rivers State, drilling a total of 96 Oil wells in Ogoniland alone to bring nine Oil fields on stream (Friends of the Earth International, 2019). Far above three decades ago Ogoni-land in Rivers State in Niger Delta of Nigeria has been on the spotlights for environmental pollutions by crude petroleum spillages, unguardedly perpetrated by the multinational oil producing companies as a result of their oil extraction activities. Pipelines operated by Shell still crisscross Ogoni farmlands, creeks, waterways and leakages caused by these corroded pipelines as well as bandits show that the area is still plagued by oil spills (Friends of the Earth International, 2019; Kolawole, 2022). In Gokana Kingdom several villages experienced environmental pollutions at various capacities, some affecting their farmlands, fresh water and marine environments, for those communities at the coastal region, while others, farmlands and fresh water streams were affected. Shell always insisted that most of the spills were cause by the saboteurs. Yet Amnesty International claims its researchers have found at least eighty nine (89) spills which might have been deliberately mislabeled as theft or sabotage (Friends of the Earth, 2019; Kolawole, 2022).

Friends of the Earth International, 2019, reported oil spillages in Gokana Local Government Area identified over twenty three years (23yrs). Many landmasses and previously agriculturally useful farmlands in Gokana communities have been lost for time.

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Nweol community farmlands experienced severe petroleum pollutions at Baraol-Chara and Baraol-Gor which may have emanated from oil-pipe outbursts due to the long abandonment of facilities, oil-pipe expiry and, or vandalism by disgruntled persons in the year 2000.

The aim of this study was Microbiological characteristics of Crude Petroleum Polluted farmland soils of Nweol community in Rivers State, Nigeria, so as to access the impact of crude petroleum pollution after several years on the microbial population and diversity of farmland soils.

Materials and Methods

Description of the Study Area

The study area are some farmlands contaminated with crude oil that resulted from an oil spillage about twenty-three (23) Years ago in Nweol, Gokana Local Government area, Rivers State, Nigeria. Two sampling stations**,** Baraol-Chara and Baraol-Gor that experienced oil spillages served for the three soil sampling locations namely; Baraol-Chara1, Baraol-Chara 2, and Baraol-Gor. While Gava Area where no oil spillage occurred served as unpolluted/control soil. These are two major farm areas that sustain farming activities and livelihood in Nweol. Major crops cultivated within these locations are; various species of Yams, Cocoyam, Cassava, three leaves yams, and different kinds of vegetables, including Pumpkins, garden eggs, Pepper, maize, melon, and tomatoes. Apart from other forest trees, such as Indian bamboo (*Panicum maximum*) which occupied part of the polluted sampling locations, all food crops cultivated within the area have root zones which thrive within 0-1meter, whereas oil spillages may go deeper below the rhizosphere of these vegetable or food crops.

Distances between these soil sampling locations are known. Distance between Baraol-Chara 1 and Baraol-Chara 2 is 14.31m, between Baraol-Gor and Baraol-Chara is 2363.10m. The distances between Gava area or unpolluted control location and the polluted sites are 1953.16m Baraol-Chara and 853.44m from Baraol-Gor. The Google Earth map Coordinates of Baraol-Chara 1: Latitude 514513N and Longitude 314651E, Baraol-Chara 2: Latitude 514514N and Longitude 314665E, Baraol-Gor: latitude 514773N and longitude 312302E, and Unpolluted Gava Area (Control): latitude 515381N and longitude 31290E. The Google Earth map .showing positions of the study area are as shown in Plate 1.

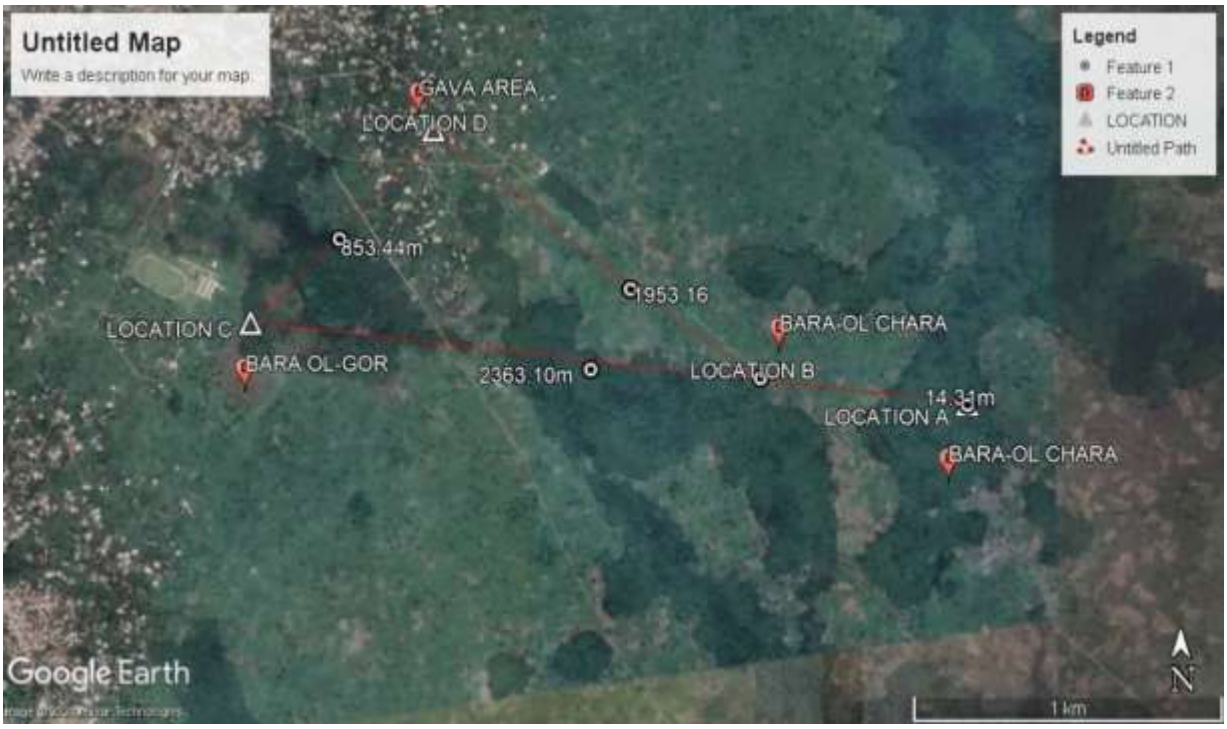

Plate 1: Google Earth Map Showing Positions of the Study Area and Sampled Locations

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Collection of soil Samples

Randomized samples of crude oil polluted farm soil samples were obtained from Baraol-Chara 1, Baraol-Chara 2 and Baraol-Gor. Unpolluted soil controls were obtained at the distances of 1953.16m and 853.44metres from the sites of pollution. Samples were scoped at three sampling times from surface, subsurface and deep-soil from petroleum polluted farm-sites, and an unpolluted site using a soil auger borer at depths of 0-15cm for surface samples, 16-30cm for subsurface samples, and 31-45cm for deep-soil samples, and composed into 12 sets of composite bulk. All samples were aseptically put into sterile plastic bags, labeled accordingly, and transported in cooled box with ice blocks to the laboratory for analysis.

Microbiological Analysis of Soils

All samples were serially diluted, by which 10g of each of the soil samples were separately dispensed into sterile test tubes containing 100ml of distilled water. A tenfold serial dilution was conducted in two sets on each homogenous mixtures to the 2^{nd} and 4^{th} steps respectively, by diluting 1ml of each homogenized mixture into 9ml of distilled water to have diluents in the steps of 10^{-1}, 10^{-2}, 10^{-3}, 10^{-4} (Keler *et al*., 2010; Ben-David and Davidson, 2014).

Laboratory preparation and composition of media

The media used in this study (Nutrient Agar and Potato Dextrose Agar) were all prepared by the manufacturer's specifications, while Mineral Salt Agar (MSA) was a laboratory preparation and was prepared by prescribed techniques designed and published by Rivers State University Institute of Pollution Studies IPS, (1990). By this method, 0.5 g of Ammonium chloride powder, 0.5g of Dipotassium hydrogen phosphate and 2.5 gram of Disodium hydrogen phosphate were dispensed into 1000ml of distilled water and mixed properly. After which 15g of Agar-Agar was added as hardener, 10ml of crude oil was added as hydrocarbon source, and finally Fungusol was also added to suppress and inhibit fungal growth against bacteria in test plates set for hydrocarbon utilizing bacteria (HUB), while antibiotics such as Tetracycline and Chloramphenicol were added to suppress and inhibit bacteria growth against fungi in test plates set for hydrocarbon utilizing fungi (HUF). All plates were autoclaved at 121^{o}C for 15min at 15atmosphere pressure. Exactly 0.1ml volumes of all homogenates were withdrawn from the 10^{-4} diluents of each set of the soil samples, and inoculated in duplicates to fresh plates of Nutrient agar (NA) and Potato Dextrose agar (PDA) by the spread plate technique, using sterile bent glass rod. Another 0.1ml volume of the same homogenates were withdrawn from the 10^{-2} diluents and inoculated in duplicates unto fresh plates of Mineral salt agar (MSA) for hydrocarbon utilizing bacteria HUB and hydrocarbon utilizing fungi HUF. A set of inoculated plates of the Mineral salt agar (MSA), and Nutrient agar (NA) were all incubated at 37^{o}C for 24 hours, while other set of inoculated plates of the Mineral salt agar (MSA) and Potato Dextrose Agar (PDA) were incubated at room temperature for 72 hours.

The discrete colonies of total heterotrophic bacteria, hydrocarbon utilizing bacteria, total fungi and hydrocarbon utilizing fungi that developed were counted. The values were represented in colony forming unit/gram (CFU/g) soil (Martin *et al*., 2004).

Microbial purifications were conducted as described by Martin *et al*., (2004), by way of isolation and subculture of discrete colonies unto fresh plates of Nutrient agar, to obtained pure cultures. Bacteria colonial, morphological and biochemical tests were carried out by the conventional methods as described by Peekate, (2022), and by molecular analysis for identification of isolates. Morphology and microscopy of Fungi were used for identification using the method described by Alexopoulus *et al* (2001), by which wet-mounting of fungal spores were made in lacto phenol cotton blue upon clean glass slides, and then observed under x40 objectives. Features of importance such as vesicle shape, length, colour or stripe, type of conidia and the separation were considered. More features such as colour of the fungi on plate, diameter of fungi, and the reverse colour on the plates were also considered.

Results

The results of the mean values of various microbial populations of duplicate samples in the polluted and unpolluted (control) soil samples are as shown in Table 1.

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Table 1: Mean values of various microbial populations of duplicate samples in the polluted and unpolluted (control) soils

Soil Code	Total Microbial Count in Colony Forming Unit per Gram Soil (CFU/g Soil)			
	Total Heterotrophic Bacteria (THB)	**Hydrocarbon Utilizing Bacteria (HUB)**	**Total Fungi (TF)**	**Hydrocarbon Utilizing Fungi (HUF)**
PSBC1	$1.36 \times 10^6 \pm 3.57 \times 10^6$	$0.76 \times 10^4 \pm 2.65 \times 10^4$	$0.83 \times 10^6 \pm 2.88 \times 10^6$	$0.34 \times 10^4 \pm 1.37 \times 10^4$
PSBC1	$1.17 \times 10^6 \pm 3.25 \times 10^6$	$0.51 \times 10^4 \pm 2.35 \times 10^4$	$0.96 \times 10^6 \pm 2.65 \times 10^6$	$0.38 \times 10^4 \pm 1.65 \times 10^4$
PSBC2	$1.56 \times 10^6 \pm 3.75 \times 10^6$	$0.63 \times 10^4 \pm 2.55 \times 10^4$	$0.73 \times 10^6 \pm 2.61 \times 10^6$	$0.46 \times 10^4 \pm 1.85 \times 10^4$
PSBC2	$1.98 \times 10^6 \pm 3.95 \times 10^6$	$0.36 \times 10^4 \pm 1.65 \times 10^4$	$0.59 \times 10^6 \pm 2.65 \times 10^6$	$0.31 \times 10^4 \pm 1.49 \times 10^6$
PSBG	$1.45 \times 10^6 \pm 3.75 \times 10^6$	$0.35 \times 10^4 \pm 3.54 \times 10^4$	$0.63 \times 10^6 \pm 2.55 \times 10^6$	$0.43 \times 10^4 \pm 3.45 \times 10^4$
PSBG	$1.23 \times 10^6 \pm 3.35 \times 10^6$	$0.53 \times 10^4 \pm 2.65 \times 10^4$	$0.43 \times 10^6 \pm 1.45 \times 10^6$	$0.23 \times 10^4 \pm 1.35 \times 10^4$
(Control)	$0.92 \times 10^6 \pm 2.75 \times 10^6$	$0.23 \times 10^4 \pm 1.55 \times 10^4$	$0.33 \times 10^6 \pm 1.65 \times 10^6$	$0.17 \times 10^4 \pm 1.25 \times 10^4$
(Control)	$0.43 \times 10^6 \pm 1.75 \times 10^6$	$0.28 \times 10^4 \pm 1.65 \times 10^4$	$0.24 \times 10^6 \pm 1.65 \times 10^6$	$0.11 \times 10^4 \pm 1.05 \times 10^4$

Key: PSBC1=Polluted soil Baraol-Chara 1; PSBC2=Polluted soil Baraol-Chara 2; PSBG=Polluted soil Baraol-Gor; Control=Unpolluted soil Gava Area

In polluted soils from Baraol-Chara 1, the mean value of total heterotrophic bacteria count (THBC) ranged between 1.17×10^6 and 1.36×10^6CFU/g, TF between 0.83×10^6 and 0.96×10^6CFU/g, while HUB were between 0.51×10^4 and 1.76×10^4CFU/g, and HUF between 0.34×10^4 and 0.38×10^4CFU/g.

In polluted soils from Baraol-Chara 2, the mean value of total heterotrophic bacteria count (THBC) ranged between 1.56×10^6 and 1.98×10^6CFU/g, TF between 0.59×10^6 and 0.73×10^6CFU/g, while HUB were between 0.36×10^4 and 0.63×10^4CFU/g, and HUF between 0.31×10^4 and 0.46×10^4CFU/g.

In polluted soils from Baraol-Gor, the mean value of total heterotrophic bacteria count (THBC) ranged between 1.23×10^6 and 1.45×10^6CFU/g, TF between 0.43×10^6 and 0.63×10^6CFU/g, while HUB were between 0.35×10^4 and 0.53×10^4CFU/g, and HUF between 0.23×10^4 and 0.43×10^4CFU/g.

In unpolluted/control soils from Gava area, the mean value of total heterotrophic bacteria count (THBC) ranged between 0.43×10^6 and 0.92×10^6CFU/g, TF between 0.24×10^6 and 0.33×10^6CFU/g, while HUB between 0.23×10^4 and 0.28×10^4CFU/g, and HUF were between 0.11×10^4 and 0.17×10^4CFU/g.

Percentage mean Hydrocarbon utilizing bacteria (HUB), and the Percentage mean Hydrocarbon utilizing fungi HUF were as shown in Table 2.

In polluted soils from Baraol-Chara 1, Percentage mean Hydrocarbon utilizing bacteria (HUB) was 28.41%, while the Percentage mean Hydrocarbon utilizing fungi (HUF) was 21.99%.

In polluted soils from Baraol-Chara 2, Percentage mean HUB was 22.56%, and percentage mean HUF was 25.73%.

In polluted soils from Baraol-Gor, Percentage mean HUB was 17.27%, and Percentage mean HUF was 35.27%.

In unpolluted/control soils from Gava area, the Percentage mean HUB was 31.76%, while the percentage mean HUF was 17.01%.

The results of the colonial, morphological and biochemical characteristics of the bacteria isolated from the soils during the study showed that, the most predominant bacterial isolates identified by conventional methods were; *Staphylococcus aureus*, *Micrococcus roseus*, *Serratia marcescens*, *Pseudomonas aeruginosa*, *Pseudomonas fluorescens*, and *Chromobacterium violaceum*.

From the macroscopy and microscopy results, the most encountered fungi identified were; *Aspergillus niger*, *Penicillium frequentans*, *Trichoderma viridae*, *Aspergillus nidulans*, *Fusarium moniliformes*, and *Aspergillus terreus*.

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Table 2: Percentage mean Hydrocarbon Utilizing Bacteria and Hydrocarbon Utilizing Fungi in polluted and unpolluted soils

Soil Code	SD (cm)	Hydrocarbon Utilizing Bacteria (CFU/g)	% Mean	SD (cm)	Hydrocarbon Utilizing Fungi (CFU/g)	% Mean
PSBC1	0-15	$0.31x10^4$ $\pm1.49x10^4$	**28.41**	0-15	$0.15x10^4$ $\pm0.39x10^4$	**21.99**
		$0.34x10^4$ $\pm1.37x10^4$			$0.17x10^4$ $\pm0.57x10^4$	
	16-30	$0.37x10^4$ $\pm1.73x10^4$		16-30	$0.21x10^4$ $\pm0.73x10^4$	
		$1.02 x10^4$			**$0.53x10^4$**	
	31-45	$\pm$ 3.25 x 10^4		31-45	$\pm$ 2.65x 10^4	
PSBC2	0-15	$0.24x10^4$ $\pm0.89x10^6$	**22.56**	0-15	$0.17x10^4$ $\pm0.39x10^6$	**25.73**
		$0.27x10^4$ $\pm0.47x10^4$			$0.21x10^4$ $\pm0.57x10^4$	
	16-30	$0.31x10^4$ $\pm1.49x10^4$		16-30	$0.24x10^4$ $\pm0.73x10^4$	
		$0.82 x10^4$			**$0.62x10^4$**	
	31-45	$\pm$2.85 x 10^4		31-45	$\pm$2.65 x 10^4	
PSBG	0-15	$0.17x10^4$ $\pm0.39x10^6$	**17.27**	0-15	$0.26x10^4$ $\pm0.39x10^6$	**35.27**
		$0.21x10^4$ $\pm0.57x10^4$			$0.28x10^4$ $\pm0.57x10^4$	
	16-30	$0.24x10^4$ $\pm0.73x10^4$		16-30	$0.31x10^4$ $\pm0.73x10^4$	
		$0.62x10^4$			**$0.85x10^4$**	
	31-45	$\pm$ 2.65x 10^4		31-45	$\pm$ 2.65x 10^4	
Control	0-15	$0.35x10^4$ $\pm1.49x10^6$	**31.76**	0-15	$0.11x10^4$ $\pm0.39x10^6$	**17.01**
		$0.38x10^4$ $\pm1.37x10^4$			$0.14x10^4$ $\pm0.57x10^4$	
	16-30	$0.41x10^4$ $\pm1.73x10^4$		16-30	$0.16x10^4$ $\pm0.73x10^4$	
		$1.14 x10^4$			**$0.41x10^4$**	
	31-45	$\pm3.45x10^4$		31-45	$\pm1.45x10^4$	
Total	**0 – 45**	**3.59**	**100**	**0-45**	**2.41**	**100**

Key: PSBC1=Polluted soil Baraol-Chara 1; PSBC2=Polluted soil Baraol-Chara 2; PSBG=Polluted soil Baraol-Gor; Control=Unpolluted soil Gava Area; SD=Soil depth.

Discussion

The study revealed high incidence of hydrocarbon utilizing bacteria and fungi with Percentage mean Hydrocarbon utilizing bacteria ranging between 17.27% and 31.76%, while the Percentage mean Hydrocarbon utilizing fungi ranged between 17.01% and 35.27%. These are indications for lingering persistence of pollution by Petroleum hydrocarbon spillages in the farm soils. Study also revealed high indices for microbial populations in both polluted and unpolluted/control soils by mean total heterotrophic bacteria, total fungi showing high significant microbial population counts for bacteria and fungi. This is in agreement with previous reports by Obire and Wemedo (1996) and Elise *et al.,* (2012) who stated that, heterotrophic bacteria and fungi have evolved tremendous ability to metabolize simple and complex hydrocarbon contaminants, and harnessing their metabolic ability to remediate contaminated environments as petroleum polluted soils, by a technique referred to as bioremediation.

Bacterial isolates identified from the farm soils were, *Staphylococcus aureus*, *Micrococcus roseus, Serratia marcescens*, *Pseudomonas aeruginosa*, *Pseudomonas fluorescens,* and *Chromobacterium violaceum*. These bacteria are major indicators for Petroleum hydrocarbon biodegradation in soils polluted by Petroleum spillages. This result is in agreement with previous reports revealing that *Pseudomonas, Staphylococcus* and *Micrococcus* species have also been found very useful in the biodegradation and decomposition of petroleum and oil spills (Bello, 2007).

Fungal isolates identified from the farm soils were *Aspergillus niger*, *Penicillium frequentans*,

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Penicillium expansum, *Trichodema viridae*, *Aspergillus nidulans*, *Fusarium moniliforme*, and *Aspergillus terreus* all of which biodegrades petroleum hydrocarbon, which also agree with reports by Obire and Wemedo (2002); and Anwar, (2015) stating that, heterotrophic microorganisms found in oil polluted soils include the naturally occurring soil microbial populations that have the ability to biodegrade petroleum products, and contributing to soil microbiological petroleum biodegradation for soil bioremediation.

In conclusion, this study revealed high indices for Petroleum hydrocarbon utilizing bacteria and fungi, which are indications for still lingering presence of the Petroleum hydrocarbon pollutants in the farm soils. This is a remarkable evidence for crude petroleum soil pollution, making it unsuitable for farming and Agriculture, and also of health risk in persons who may consume crops grown in these affected farms.

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