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Original Research Article

Impact Assessment of Gas Flaring on the Microbial Population of Mangrove Forest of Awoba Flow Station in Bille, Rivers State

Simbi-Wellington W. S. and *Chukunda F. A.

Department of Forestry and Environment, Faculty of Agriculture, Rivers State University, Nkoplu-Oroworukwo Port Harcourt, Nigeria

***Corresponding Author's E-mail: onyifrank2002@yahoo.com**
Tel.: 08037501179

Abstract

This research was conducted to determine the impact of gas flaring on the microbial population of mangrove forest around Awoba flow station in Bille, Rivers State. The experiment was laid in a randomized Complete Block Design (RCBD) in wet and dry seasons (months) and at different locations with three replications and the means were considered significant at (P≤ 0.05) and separated using Duncan Multiple Range Test. The results indicated that effects of gas flare on seasons and distance significantly (P≤ 0.05) affected the microbial population of bacteria and fungi found in the mangrove soil of Bille Awoba flare station. The total heterotropic bacterial count (THBC) appeared more in the month of March, 2018 (600,000cfu/ml) at the ET location followed by the month of September, 2017 while THFC, in the month of June, 2017 recorded the highest heterotropic bacterial (21,000cfu/ml) at the locations of WT and NT respectively. Hydrocarbon utilizing bacterial occurred more in the months of September and June, 2017 (143.333 – 187, 500cfu/ml) at ST and WT locations respectively and hydrocarbon utilizing fungi isolated from the mangrove soil was more in the months of March 2017 and 2018 respectively. Total heterotropic bacteria isolated included *Staphylococcus aureus* (Rosenbach), *Actinomyces* canis (Harz), *Corynebacterium amycolatum* (Lehmann and Neumann), *Acromonas aquariorum* (Stanier), *Bacillus* spp (Ehrenberg). Total heterotropic fungi isolated include: *Rhizopus stolonifer* (Ehrenb), *Candida albicans* (Berkh), *Aspergillus niger* (van Tieghem), *Fusarium solani* (Link), *Mucoramphibiorum* (Fresen) and *Penicillium bilaiae*, (Link). This research concluded that seasons and locations (distances) significantly (P≤ 0.05) affected the microbial population of the impacted soil due to gas flares from Awoba Bille flow station, Rivers State. The study recommended that some microbes in the soil are thermorphic while, some thrive in the crude oil polluted soil. Therefore, these organisms if properly harnessed could be used as soil biological remediating agents to boast agroforestry practices.

Keywords: Total heterotropic bacterial, Total heterotropic fungal, gas flaring, microbial population, mangrove, wetlands

INTRODUCTION

The mangrove is ecologically referred to as a taxonomically diverse assemblage of trees and shrubs which form the dominant plant communities in tidal saline wetlands of tropical and sub-tropical coasts (MAP, 2000).

Mangrove trees and shrubs are commonly known to thrive in shallow and muddy salt water or in brackish waters, mostly along shorelines and estuaries in tropical and sub-tropical regions because they cannot withstand the freezing temperatures of the temperate and polar regions. Mangrove is distinct structurally and functionally by its morphological and eco-physiological characteristics (Alongi, 2002).

Mangrove forests are found in nineteen West African countries including Nigeria. Nigeria is known to have the largest mangrove forest in Africa covering an area of about 7368km^2, which is about 22% of the mangrove cover in Africa. The Nigerian mangrove is also the third largest in the world following India and Indonesia (Macintosh and Ashton, 2003). The Nigerian Mangrove stretches along the coastal regions and can be found in nine states within the country. It extends from Badagry in the West to Calabar in the South covering a total area of 10,000km^2 along the coast and forms a vegetation band of 15 to 45km wide. (Abere and Ekeke, 2011).

There are three main mangrove families in Nigeria; Rhizophoraceae, Avicenniaceae and Combretaceae. These three families are comprised of six species namely: *Rhizophora racemosa, Rhizophora mangle, Rhizophora harrisonii, Languncularia racemosa, Avicennia germinans* and *Conocarpus erectus.* There are also palms associated with these species such as the *Nypafruitican*, *Prodococcus bateri* and *Ancistrophllum opacum.* Other associated plants include *Acrostichum aureum* (Obadimu *et al.,* 2016). The most abundant of the true mangrove species is the *Rhizophora racemosa* which makes up about 90% of the mangrove forests and occurs at the outer body of water. *R. racemosa* is also the biggest of the three species of the family Rhizophoraceae, attaining heights of up to 40m and diameter at breast height greater than 90 cm at maturity. *R. racemosa* is followed by *R. harrisonii* which attains heights of 5-10m and *R mangle* with less than 5m. In terms of distribution, *R harrisonii* occurs usually between *R racemosa* and *R mangle*. *R mangle* occupies the harder parts of the mangrove soil (Abere and Ekeke, 2011). The mangrove grass (*Paspalum vinatum*) and the mangrove fern (*Acrostichum aureum*) thrive in disturbed areas (World bank, 1995).

Mangrove is used traditionally and commercially worldwide. Coastal communities depend on the mangrove as a source of wood for building houses, for cooking and heating, for making huts and fences, matting and scaffolds. Timber gotten from the mangrove is widely used for charcoal production, fish cages and trap production, furniture making, bridge and boat construction, poles and many other products. While its tannin and resins are used for dying and leather making. The mangrove plants are also used for herbal medicines, (Kathirensan and Bingham, 2001). The mangrove provides ecosystem functions and several human utility benefits especially for coastal communities of the Niger Delta, Nigeria. They play a very important role in nutrient cycling, nutrient export, coastal protection, sediment trapping and also provide breeding and nursery grounds for marine and estuarine organisms (Mumby *et al.,* 2004). In the Niger Delta, mangrove forests act as sink for carbon dioxide playing an important role in sequestrating carbon and mitigating changes occasioned by atmospheric pollution (Ukwe *et al*., 2006). The halophytic nature of the mangrove and its ability to compensate for low oxygen in the soil aids its existence in the environment (Choudhry, 1997). However, the complex breathing roots of the mangrove are vulnerable to crude oil attack which can cause blockage of the openings of the breathing roots.

Sorensen (2002) has drawn attention to the fact that mangroves play a vital role in the coastal ecosystem because of their contribution to coastal fishery and their role in preventing coastal erosion, serving as nurseries for a variety of fish and prawns and as barriers to tidal and storm surges associated with tropical cyclones. Sorensen (2002) further estimated that the mangrove forest which once covered three quarters of the coastlines of tropical and subtropical countries is today less than 50% of that coverage and over 50% of the remaining forest is degraded and not in good productive condition.

In Nigeria crude oil plays a vital role in the national economy and about 70% of the oil exploration and exploitation activities take place in the mangrove forest of the Niger Delta, Nigeria. These activities have led to the loss of mangrove species and degradation of the mangrove ecosystem through clearing of the mangrove forest, oil spills from operational failures, vandalism of pipelines, oil well blowouts, tanker seepages/ accidents and de-blasting operations (Imevbore, 1979; Baker 1981a,b; Ekweozor 1985 and 1989; Snowden and Ekweozor, 1987; Nnyong and Anita, 1987, Amadi *et al.,* 1996). Ohimain, (2006a) reported that the Nigeria mangrove cover has been reduced by 26% since 1980. Some of the factors stated to be responsible for the decline include agriculture, industrialization and urbanization mostly timber and petroleum exploitation. Isebor and Awosika (1993) stated some associated environmental threats of petroleum exploitation which includes threats arising from gas flaring, oil spill, and installation of infrastructure.

Increase in industrialization has led to an increase in environmental pollution. Several researches have shown that the load of contaminants in air, soil and vegetation around gas flare sites are increases every year and negatively impacts on the forest ecosystems where the operating facilities are located. Regular assessment of the forest ecosystems where oil facilities are located and gas flared are essential for economic and environmental safety.

Research findings on the impact of gas flaring on the mangrove forest ecosystem around the Awoba Flow

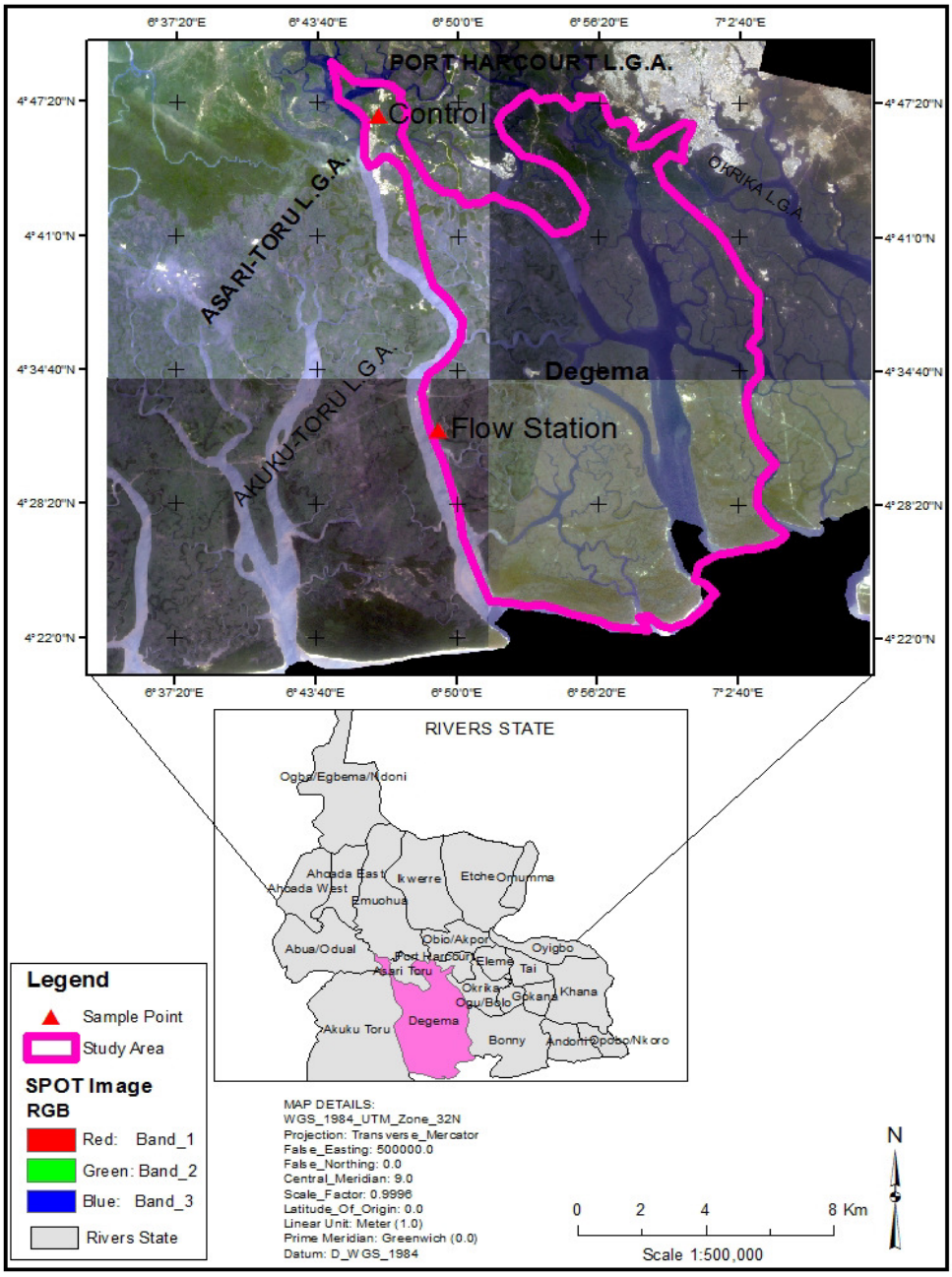

Figure 1. Map of Degema Local Government area of Rivers State showing study area

Station have not been adequately documented. Though Impact Assessment studies have been carried out by the companies operating in the study area, findings are not made available to the public and communities directly impacted this oil activities, hence this study aims at filling the gap by assessing the mangrove forest ecosystem especially the soil microorganisms following continued gas flaring at the Awoba flow station and providing information that could be used for environmental safety as well as informed forest management decisions on the host community.

The specific objectives are to determine the bacterial and fungi population in the mangrove soil at the study area and effects of seasonal variations on the bacterial and fungi population in the mangrove soil.

MATERIALS AND METHODS

Study Area

The study station (Awoba flow station) is located within

the Bille Territory. Bille is a low-lying coastal town in the vast mangrove forest region of the Niger Delta, Nigeria. It is a rural community in Degema Local Government Area of Rivers State. Its geographical coordinates are 4° 34' 37" North, 6° 53' 19" East (Wikipedia, 2014). Bille is an ancient autonomous community and is made up of 15 villages and 40 fishing settlements. The main occupation of the people is fishing. The community has a population of 30,000 people according to the Nigeria 1999 census (ERA, 1999). Figure 1

Determination of Bacteria and Fungi Population in Soil

Total heterotrophic bacterial count (THBC), Total heterotrophic fungi count (THFC), Hydrocarbon utilizing bacteria count (HUBC) and Hydrocarbon utilizing fungi count (HUFC) were determined for each of the study locations (NT, ST, ET, WT, CT). Samples were collected in four different months (March 2017, June 2017, September 2017 and March 2018) for this study. Microbial species observed were sub-cultured to obtain pure isolates which were further subjected to macroscopic, microscopic and biochemical tests for characterization and identification according to Cowan and Steel (1965).

Ten folds' serial dilution with sterile physiological saline as diluent was carried out with each sediment sample collected and inoculated on nutrient agar (NA) for total heterotrophic bacterial count (THBC). Mineral salt agar (MSA) was used for the determination of the hydrocarbon utilizing bacterial count (HUBC) using vapour-phase transfer technique as described by Okpokwasili and Amanchukwu (1987).

Experimental Design

Sampling locations were taken 20 meters away from the flow station. Four transects measuring 10m x 90m were laid, each on the North (NT), South (ST), West (WT) and East (ET) of the flow station and were sub-divided into three sampling units measuring 10m x 30m. A total of 12 sampling units were laid for the study. Samples were randomly collected in triplicates within each sampling unit. The wind direction was noted and considered as a factor. Samples were also collected at the control (CT) station which is a mangrove forest in Degema town, over 200km away from the study station.

Samples were collected in four different months; two dry season months (March 2017/March 2018) and two wet season months (June 2017/September 2017). The experimental design used for this study is a 5 x 4 factorial in RCBD with three replications. The factors are months of data collections and sampling locations (North, South, East, West and control).

Data Analysis

Data analysis used was the multivariate analysis using General Line Model (GLM) of SPSS statistical package (2011), means were considered significant at P≤0.05 and were separated using Duncan Multiple Range Test.

RESULTS AND DISCUSSION

The results of the impact of gas flare on the microbial population in Awoba forest are presented in Table 1 and 2. The heterotrophic bacteria species isolated and identified in the mangrove soil were; *Staphylococcus aureus, Acromonas* aquariorum*, Bacillus* spp*., Pseudomonas* spp*., Streptococcus aureus, Micrococcus* spp*., Actinomyces canis, Citrobacter* spp*., Proteus* spp*. and Corynebacterium* amycolatum*.* The heterotrophic fungi species isolated and identified in the soil were; *Fusarium solani, Aspergillus niger*, *Mucoramphibiorum, Penicillium bilaiae, Rhizopus stolonifer* and *Candida albicans.* This result agrees with the report by Nwaugo *et al.* (2005) and Ukoima *et al.* (2016) that identified same species around gas flare locations.

Hydrocarbon utilizing bacteria species isolated and identified in the mangrove soil were; *Staphylococcus aureus, Actinomyces canis, Corynebacterium* amycolatum*, Acromonas* aquariorum*, Bacillus* spp*., Pseudomonas* spp*., Proteus* spp*., Micrococcus aureus, Staphylococcus aureus,* and *Citrobacter spp.* While the hydrocarbon utilizing fungi species isolated and identified were; *Rhizopus* spp*., Candida albicans, Aspergillus niger, Fusarium stolonifer Yeast* spp*., Mucoramphibiorum,* and *Penicillium bilaiae.* All the microbes isolated at the flare locations were also observed at the control location, which agrees with the report by Ezeigbo*et al.,* (2013) stating, that all the microbes isolated around the Izombe flare were also present at the control point.

The identification of the hydrocarbon utilizing bacteria; *Bacilli* spp*.* and *Pseudomona bilaiae*. around the flare location agrees with report by Ezeigbo *et al.* (2013) that the bacterial isolated within 10m distance from a flare site were species of *Pseudomonas* and *Bacillus*, which were hydrocarbon degraders while fungal isolates at the same distance were *Fusarium solani* and *Penicillium bilaiae.* which are also good hydrocarbon degraders (Prescot *et al.,*1999) and Chessbrough (1987) identified *Bacilli* as good spore formers that can survive very harsh environmental conditions, while *Pseudomonas bilaiae* are identified as major crude oil degrader.

Mean THB count was highest in location ET (600 $x10^3$cfu/ml) and lowest ST (425 $x10^3$cfu/ml) and NT (442 $x10^3$cfu/ml). The THB count recorded in CT (544 $x10^3$cfu/ml) and WT (478 $x10^3$cfu/ml) were not significantly (P≤0.05) different from the highest and lowest counts. Mean THF count was significantly (P≤0.05) highest in locations NT (22 $x10^3$cfu/ml) location

Table 1. Organisms isolated and identified in mangrove soil (Wet Seasons)

Organisms (March 2017)				
Study Location	**THB**	**THF**	**HUB**	**HUF**
West (WT)	*Staphylococcus aureus* *Bacillus* sp. *Pseudomonas sp.*	*Mucoramphibiorum* *Fusarium solani* *Rhizopus stolonifer* *Aspergillus niger.*	*Pseudomonas spp.* *Staphylococcus aureus* *Bacillus subtilis* *Corynebacterium amycolatum*	*Penicillium bilaiae* *Aspergillus niger* *Rhizopus stolonifer* *Mucoramphibiorum*
South (ST)	*Staphylococcus aureus Proteus sp.* *Corynebacterium amycolatum* *Bacillus sp.*	*Mucoramphibiorum* *Aspergillus niger* *Rhizopus stolonifer*	*Bacillus subtilis* *Micrococcus spp.* *Proteus spp.* *Corynebacterium spp.*	*Fusarium solani* *Mucor spp.* *Penicillium bilaiae.* *Aspergillus niger*
East (ET)	*Proteus sp.* *Bacillus sp.*	*Fusarium solani* *Aspergillus niger*	*Staphylococcus aureus* *Bacillus subtilis*	*Rhizopus stolonifer* *Fusarium solani*
North (NT)	*Micrococcus sp.* *Proteus sp.* *Bacillus sp.* *Streptococcus sp.* *Pseudomonas sp.*	*Aspergillus niger.* *Mucoramphibiorum* *Fusarium solani* *Penicillium bilaiae*	*Pseudomonas spp.* *Bacillus subtilis* *Staphylococcus aureus*	*Penicillium spp.* *Aspergillus spp.* *Fusarium spp.* *Mucorspp.*
Control (CT)	*Staphylococcus aureus* *Aeromonas sp.* *Actinomycetes sp.* *Bacillus subtilis.*	*Candida albican* *Fusarium solani* *Rhizopus stolonifer* *Aspergillus niger* *Penicillium bilaiae*	*Corynebacterium amycolatum* *Streptococcus aureus* *Citrobacter spp.* *Bacillus spp.* *Actinomyces canis* *Micrococcus spp.*	*Aspergillus niger* *Candida albicans* *Penicillium bilaiae* *Rhizopus stolonifer*
		Organisms (June 2017)		
West (WT)	*Staphylococcus aureus* *Bacillus sp.* *Acromonas aquariorum* *Pseudomonas sp.* *Streptococcus sp.*	*Rhizopus stolonifer* *Aspergillus niger* *Penicillium bilaiae* *Fusarium solani* *Mucoramphibiorum*	*Staphylococcus aureus* *Achnomycescanis* *Corynebacterium amycolatum* *Acromonas aquariorum* *Bacillus spp.* *Pseudomonas spp.* *Proteus spp.*	*Aspergillus niger* *Fusarium solani*
South (ST)	*Pseudomonas sp.* *Staphylococcus* *Acromonas sp.* *Micrococcus* *Bacillus sp.* *Streptococcus sp.*	*Aspergillus niger* *Rhizopus stolonifer* *Fusarium solani* *Penicillium spp.* *Mucoramphibiorum*	*Staphylococcus aureus* *Bacillus stubtilis* *Acromonas aquariorum* *Micrococcus aureus*	*Rhizopus stolonifer* *Aspergillus niger* *Mucoramphibiorum*
East (ET)	*Bacillus subtilis.* *Achnomycescanis* *Staphylococcus aureus*	*Rhizopus stolonifer* *Aspergillus niger*	*Achnomycetes spp.* *Bacillus subtilis.*	*Rhizopus stolonifer*
North (NT)	*Bacillus subtilis.* *Staphylococcus aureus*	*Candida albicans* *Aspergillus niger* *Penicillium bilaiae*	*Staphylococcus aureus* *Bacillus spp.* *Corynebacterium amycolatum*	*Penicillium bilaiae* *Aspergillus niger* *Rhizopus stolonifer*
Control (CT)	*Acromonas aquariorum* *Pseudomonas sp.* *Citrobacter sp.* *Staphylococcus aureus* *Bacillus subtilis.* *Proteus sp.*	*Candida albicans* *Aspergillus niger* *Fusarium solani* *Penicillium albicans*	*Corynebacterium amycolatum* *Streptococcus aureus* *Pseudomonas spp.* *Bacillus spp.* *Citrobacter spp.* *Achnomyces canis*	*Aspergillus niger* *Fusarium solani* *Mucoramphibiorum*
Organisms (September 2017)				
Study Location	**THB**	**THF**	**HUB**	**HUF**
West (WT)	*Staphylococcus aureus* *Bacillus sp.* *Pseudomonas sp.* *Citrobacter sp.*	*Mucoramphibiorum* *Fusarium solani* *Rhizopus stolonifer* *Aspergillus niger* *Penicillium bilaiae*	*Staphylococcus aureus* *Bacillus spp.* *Pseudomonas sp.* *Corynebacteriumamycolatum* *Streptococcus aureus*	*Aspergillus niger* *Fusarium solani* *Mucoramphibiorum* *Rhizopus stolonifer*

Table 1. Continue

South (ST)	*Staphylococcus aureus* *Staphylococcus aureus* *Achnomyces canis* *Bacillus subtilis.* *Pseudomonas aeroginase.*	*Aspergillus niger* *Rhizopus stolonifer* *Fusarium solani*	*Achnomyces canis* *Bacillus spp.* *Corynebacterium amycolatum* *Staphylococcus aureus* *Proteus spp.*	*Fusarium solani* *Penicillium spp.* *Rhizopus stolonifer* *Candida albicans* *Aspergillus niger*
East (ET)	*Staphylococcus aureus* *Bacillus subtilis*	*Penicillium bilaiae* *Fusarium solani*	*Bacillus subtilis* *Pseudomonas spp.*	*Mucoramphibiorum* *Aspergillusniger*
North (NT)	*Corynebacterium dipthera* *Bacillus subtilis* *Staphylococcus aureus* *Citrobacter spp.* *Proteus spp.*	*Mucoramphibiorum* *Candida albicans* *Aspergillus niger* *Fusarium solani* *Rhizopus stolonifer*	*Proteus spp.* *Bacillus spp.* *Achnomyces canis* *Staphylococcus aureus* *Corynebacterium amycolatum*	*Fusarium solani* *Aspergillus niger* *Penicillium bilaiae*
Control (CT)	*Staphylococcus aureus* *Staphylococcus aureus* *Bacillus spp.* *Pseudomonas spp.* *Acromonassp* *Micrococcus sp.*	*Penicillium bilaiae* *Fusarium solani* *Rhizopus stolonifer Aspergillus niger* *Mucoramphibiorum*	*Cirobacter spp.* *Bacillus spp.* *Pseudomonas spp.* *Micrococcus spp.* *Acromonas aquariorum* *Staphylococcus aureus*	*Mucoramphibiorum* *Candida albicans* *Aspergillus spp.* *Rhizopus stolonifer* *Fusarium solani*
Organisms (March 2018)				
West (WT)	*Staphylococcus aureus* *Bacillus subtilis.* *Pseudomonas spp.* *Achnomycetes spp.* *Proteus spp.* *Acromonas spp.*	*Fusarium solani* *Aspergillus niger* *Mucoramphibiorum*	*Staphylococcus aureus* *Aeromonas aquariorum* *Bacillus spp.* *Pseudomonas spp.*	*Rhizopus stolonifer* *Candida albicans* *Aspergillus spp.* *Fusarium spp.* *Mucoramphibiorum*
South (ST)	*Bacillus spp.* *Staphylococcus spp.* *Micrococcus spp.* *Aeromonas spp.* *Proteus spp.* *Actinomycetes spp.*	*Aspergillus niger* *Mucoramphibiorum* *Penicillium bilaiae* *Fusarium solani*	*Proteus spp.* *Bacillus stubtilis* *Staphylococcus spp.* *Citrobacter spp.*	*Mucoramphibiorum* *Aspergillus niger* *Rhizopus stolonifer* *Penicillium bilaiae* *Candida albicans*
East (ET)	*Bacillus subtilis.* *Micrococcus spp.* *Staphylococcus spp.*	*Rhizopus stolonifer* *Aspergillus niger* *Candida albicans*	*Micrococcus aureus* *Staphylococcus spp.*	*Aspergillus niger* *Fusarium solani*
North (NT)	*Proteus sp.* *Staphylococcus aureus* *Bacillus subtilis.* *Pseudomonas spp.*	*Fusarium solani* *Aspergillus niger*	*Bacillus subtilis.* *Staphylococcus aureus* *Aeromonas aquariorum* *Micrococcus spp.*	*Penicillium bilaiae.* *Aspergillus niger* *Rhizopus stolonifer* *Mucoramphibiorum* *Candida albicans*
Control (CT)	*Staphylococcus aureus* *Aeromonas sp.* *Actinomycetes sp.* *Bacillus subtilis.*	*Candida albicans* *Fusarium solani* *Rhizopus stolonifer* *Aspergillus niger* *Penicillium bilaiae*	*Corynebacterium amycolatum* *Streptococcus aureus* *Citrobacter spp.* *Bacillus spp.* *Actinomyces canis* *Micrococcus spp.*	*Aspergillus niger* *Candida albicans* *Penicillium bilaiae* *Rhizopus stolonifer*

Table 2. Mean counts (x 10^3cfu/ml) of bacteria and fungi in soil at the different locations

Location	THB	THF	HUB	HUF
WT	477.5000^{a,b}	21.0000^{a}	187.5000^{a}	6.3333^{a}
ST	425.0000^{b}	11.0000^{b}	143.3333^{a,b}	5.6667^{a}
ET	600.0000^{a}	12.0000^{a,b}	107.5000^{b}	6.5000^{a}
NT	441.6667^{b}	21.7500^{a}	101.0833^{b}	4.5833^{a}
CT	543.7500$^{a.b}$	20.50000^{a,b}	99.0625^{b}	4.7500^{a}

Mean with different superscripts within columns are significantly different at p≤0.05 using DMRT. WT – West Treatment, ST = South Treatment, ET = East Treatment, NT = North Treatment, CT = Control Treatment.

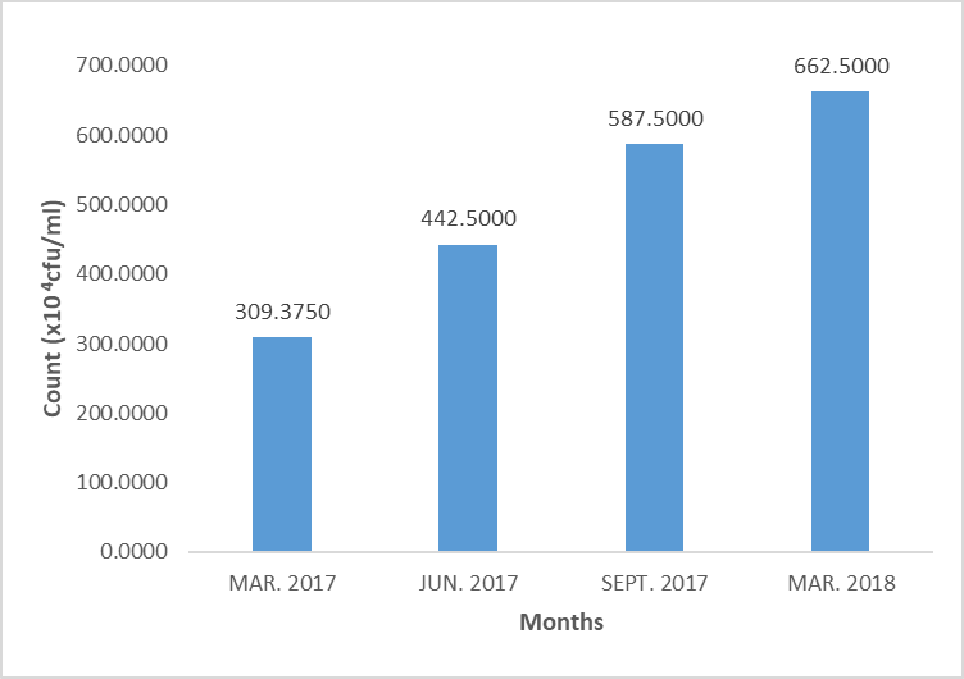

Figure 2. Total heterotrophic bacterial count in soil collected at different months of the year

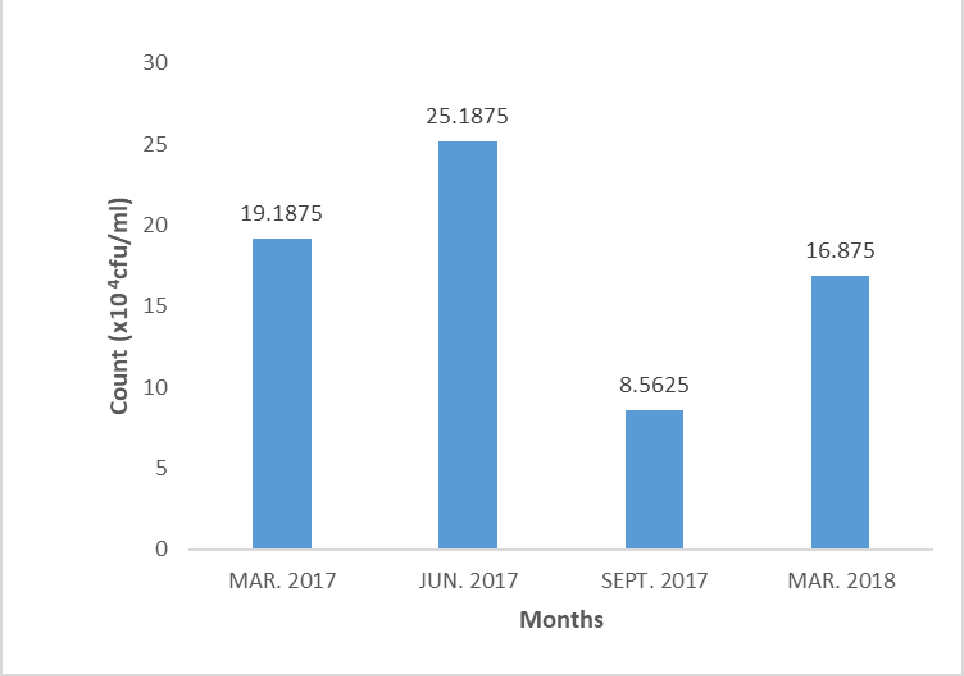

Figure 3. Total heterotrophic fungi count in soil collected at different months of the year

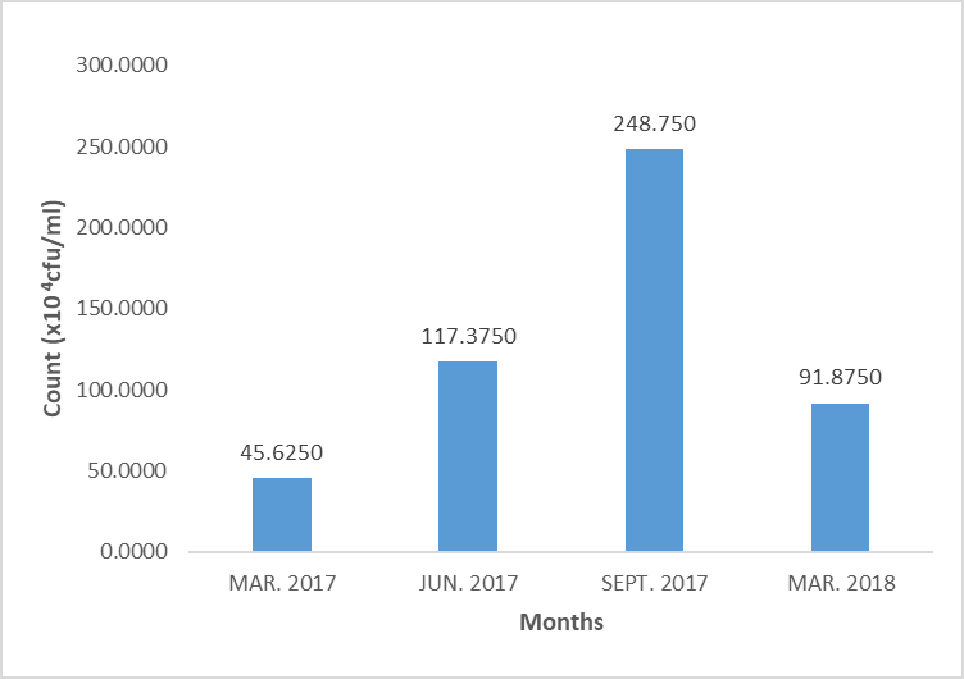

Figure 4. Hydrocarbon utilizing bacterial count in soil collected at different months of the year

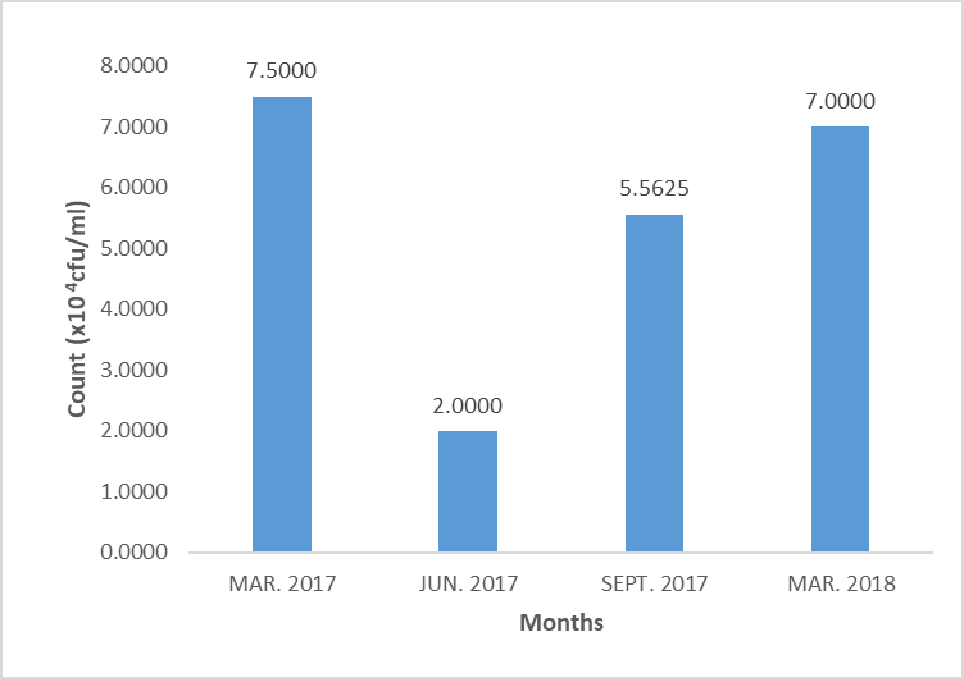

Figure 5. Hydrocarbon utilizing fungi count in soil collected at different months of the year

WT (21 x10^3cfu/ml). The lowest THF counts were observed in location ST (11 x10^3cfu/ml). Mean THF count observed in locations CT (21 x10^3cfu/ml) and ET (12 x10^3cfu/ml) were not significantly different from the highest mean and lowest mean counts. Highest mean HUB count was observed in location WT (188 x10^3cfu/ml). The lowest mean count was observed in location CT (99 x10^3cfu/ml), NT (101 x10^3cfu/ml) and location ET (108 x10^3cfu/ml). No significant differences were observed for mean HUF count in all the study locations. This is consistent with findings of Chukunda *et al.,* 2019.

The effects of season (months) on the Total heterotrophic bacterial counts (THBC), Total heterotrophic fungi

counts (THFC), hetrotrophical utilizing bacterial counts (HUBC) and heterotrophic utilizing fungi counts was significantly (P≤ 0.05) different due to monthly variations. The THBC organism occurred more in the month of March, 2018 followed by September, 2017 whereas, THFC organism were more prevalent in the month of June, 2017 followed by the month of March, 2017. However, the amount of HUBC organism found at the experimental mangrove soil sampled recorded more bacterial at the month of September, 2017 followed by the June, 2017 whereas HUFC micro-organisms were found more in the month of March 2018. This findings conforms that season significantly affect the amount of micro-organisms that will be isolated from a given soil sample. This is consistent with the findings of Chukunda *et al.,* (2019).

CONCLUSION AND RECOMMENDATION

This research has provided evidence on the distribution of pollutants in the vegetation, soil and air in the mangrove forest around Awoba flow station. Some of the microbes identified thrives in crude oil polluted soil and be used as soil biological remediating agents if properly harnessed.

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