Degradation of Diesel by *Staphylococcus sciuri* Strain XB1 Isolated from a Dumpsite in Lagos State, Nigeria

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Abstract: *Staphylococcus sciuri* strain XB1, a diesel degrading bacterium, was isolated from Igando dumpsite by continuous enrichment technique on diesel mineral salt medium (MSM). The isolate was identified using cultural, morphological, biochemical characteristics and complemented with analytical profile index. The isolate is yellowish, Gram-positive cocci, catalase positive, oxidase and coagulase negative. The isolate fermented glucose, fructose, maltose, trehalose and xylose. The antibiotic susceptibility pattern revealed that XB1 was susceptible to ofloxacin, perfloxacin, ciprofloxacin, sparfloxacin, but resistant to streptomycin, gentamycin, augmentin, amoxacillin. The XB1 also tolerated 3% salinity and exhibit specificity for another hydrocarbon substrate aside diesel. The degradation kinetics showed that XB1 had a biphasic growth with generation times of 11.925 d^{-1} and 17.825 d^{-1} between day 0-12 and 12-30 respectively. Gas chromatographic analysis revealed 55% of diesel was degraded at day 15 and 85% at day 30 respectively with near disappearance of the major hydrocarbon peaks. The percentage hydrocarbon fractions degraded at day 15 and day 30 respectively were 75.79% and 100% for nonane, 34.8% and 77.99% for tetracosane, and 59.96% and 81.86% for hexacosane. Therefore, based on the isolate competent on diesel the findings posited that XB1 is a candidate for further study and optimization for clean-up of polluted sites.

Key word: Biodegradation, diesel, gas chromatography, continous-enrichment, *Staphylococcus scuiri*

INTRODUCTION

Pollution of natural environments by petroleum hydrocarbon is of global concerns. The total petroleum hydrocarbons (TPHs) that originate from the distillates of crude oil in the form of diesel, gasoline, lubricating oil, and other typical petroleum hydrocarbons have received much attention worldwide as contaminants due to their highly toxic, mutagenic, and carcinogenic nature (Kuppusamy *et al.,* 2020). Diesel is a contaminant of natural environments including soil and sea water (Vlaev *et al.,* 2011; Wang *et al.,* 2015 and 2016) that contains 74% of aliphatic, 24% of aromatic hydrocarbons. In addition to this, it also contains 2% of other smaller hydrocarbon fractions such asparrafins, oleifins and non-metallic substances such as sulphur, nitrogen and oxygen, while nickel, iron and vanadium could be added as additives. Global demand of diesel, and other derivatives of crude oil, has remarkably expanded petroleum hydrocarbon related activities including exploration, extraction, refining and transportation (Poland *et al.,* 2003; Obayori *et al.,* 2008a; Imron *et al.,* 2019) which in turn lead to release of about 1.7 million tons of diesel into the environment yearly (Dadrasnia and Agamuthu, 2013).

Contamination of natural environment with petroleum can also occur due to leakages, spill from oil wells, vandalization of pipelines, drilling rigs and accident during transportation of petroleum product. Small scale releases which are easily overlooked are a common problem in developing countries where the regulatory regime is poor, leading to cumulative impact on the environment. Notably, mechanic workshops and diesel generators are sources of such releases in Nigeria with consequent deposition in runoff, drainage and underground waters (Obayori *et al*., 2012).

Environmental contamination with petroleum or petroleum products can lead to loss of biodiversity. Borowik *et al*. (2019), reported that diesel pollution not only has the potential to reduce diversity of soil microbiome, but could also result in consequential shift in soil enzyme activity and bioactive substances, with implications for phytoremediation. In the natural environment, degradation of hydrocarbon compounds is usually by consortia of

organisms in synergistic association. Reports abound of axenic cultures able to mineralize diesel, using it as sole carbon and energy source (Adebusoye *et al*., 2007; Zhang *et al.,* 2010; Panda *et al.,* 2013). Bacteria commonly isolated from hydrocarbon polluted environments span diverse phyla, classes, families and genera with members of the phyla Proteobacteria and Actinobacteria among the best reported as a result of their metabolic efficiency, robust gene framework and broad enzyme specificities (Salam *et al.,* 2017; Khan *et al.,* 2019). Others such as some Firmicutes owe their abundance in such environment to their ability to utilize vast number of hydrocarbon fractions. The genera *Pseudomonas*, *Flavobacterium* and *Bacillus* are notable for their adaptability, tolerance and survival during exposure to the contaminant (Chen *et al.,* 2017; Purwanti *et al.,* 2018) and have not only been reported from crude oil polluted sites but also from diesel polluted environments (Bhuvaneswar *et al.* 2012). Xu *et al*. (2018), identified close to 80 genera of bacteria that are capable of degrading hydrocarbons. Some of these bacteria play central role in utilization of petroleum hydrocarbon as a source of carbon and energy. These genera include: *Mycobacterium, Burkholderia, Kocuria, Pandoraea, Rhodococcus* and *Staphylococcus* amongst others. One of the characteristic features common to many petrochemical and petroleum refining industries is the high level of salt in their enormous wastewater effluents (Nouri *et al*., 2020). There is scarcity of information on biodegradation by halotolerant bacteria which leaves various issues unresolved (Arulazhagan *et al*., 2010). Biodegradation of hydrocarbons is known to decrease at higher salinities as a result of lower microbial diversity and reduced solubility of hydrocarbons and oxygen. However, biostimulation could increase the rate of hydrocarbon biodegradation by the autochthonous populations provided all other rate limiting factors are optimized. This present study reports the biodegradation of diesel by *Staphylococcus sciur*i strains XB1 isolated from an open dumpsite in Lagos, Nigeria.

MATERIALS AND METHODS

Sampling site: Soil samples used for this study were collected from Soluos dumpsites along Lagos State University-Igando Road, Lagos State, Nigeria. The site lies approximately between longitude 3°13'30"E to 3°17'15"E and latitude 6'28°N to 6'42°N. The dumpsites had served as a receptacle for all sort of wastes generated within Lagos State, Nigeria for more than three decades. Soil samples from the dumpsites were collected from depth 10-12 cm after clearing debris from the soil surface. Samples for physicochemistry were placed in clean container, while those meant for microbiological analysis was placed in sterile bottle and taken to the laboratory in ice-packed ziplock bag.

Physicochemical and microbiological analysis of soil sample: The pH of the soil sample was determined using table top Adwa pH meter (AD1040 pH/ mV Szeged, Hungary) in 1:1 soil solution in deionized water. Other parameters like total organic carbon, total hydrocarbon content, nitrate, phosphate and sulphate, were determined using standard analytical procedures as described by Chopra and Kanwar (1998). The total populations of various groups of microorganisms in the soil sample were enumerated using standard plate counts method. Total heterotrophic bacteria were enumerated on nutrient agar, while total heterotrophic fungi were plated on potato dextrose agar and mineral salt medium (MSM) described by Habe *et al.* (2003) was used for total hydrocarbon utilizing bacteria. The medium contained per liter: Na_2HPO_4: 2.2 g, KH_2PO_4: 0.8 g, NH_4NO_3: 3.0 g, $MgSO_4$. $7H_2O$: 0.2 g, $FeCl_3.6H_2O$: 0.05 g, $CaCl_2.2H_2O$: 0.01 g and yeast extract: 0.05 g. pH was adjusted to 7.2 and solidified with 20 g of purified bacteriological agar. Trace elements solution described by Bauchop and Elsden (1960) (1 ml^{-1}) was added separately to the medium. For fungal enumeration the

pH of the MSM was adjusted to 5.6 and fortified with 50 µg ml^{-1} of streptomycin to suppress bacterial growth. Aliquot (0.1 ml) of serially diluted sample were plated out on MSM medium supplemented with bacteriological agar and crude oil were made available to the bacterial culture in vapour phase as described by Raymond *et al.* (1976). Plates were incubated at room temperature (27 ± 2°C) for 5 –14 days.

Maintenance and identification of diesel oil degrader isolate: The best degrader of the diesel oil designated strain XB1 was selected and maintained in glycerol:nutrient broth (1:1). Strain XB1 was identified via colonial, and cellular phenotypic typing, biochemical characteristic according to the taxonomic schemes of Cowan and Steel (Barrow and Feltham, 1995). Analytical profile index (API V4.0) kit (BioMerieux, Durham, N.C) was further used to confirm XB1 identity

Substrate specificity of diesel oil degrader isolate: The Ability of strain XB1 to grow on different hydrocarbon substrates was evaluated on mineral salt medium supplemented with 50 mg/L of respective hydrocarbon or 0.1 % (V/V) in case of liquid substrate serving as carbon and energy source. Hydrocarbon degradation was determined by physical turbidity and gradual disappearance of the hydrocarbon as compared to the heat-killed control flask. The hydrocarbons examined include pyrene, phenanthrene, anthracene, crude oil, engine oil and kerosene.

Salt tolerance test of diesel degrader isolate: The ability of strain XB1 to tolerate different salt concentrations was determined on peptone broth. Different concentrations (1 to 10 %) of NaCl were prepared on peptone and inoculated with 24 h old culture. Incubation was carried out at room temperature (27±2ºC) for 3-5 days for visual observation of turbidity (Obayori *et al.*, 2009).

Antibiotic susceptibility test of isolate: The antibiotic susceptibility pattern of the bacterial strain was determined by the disk agar diffusion method described by Bauer *et al*. (1996). The antibiotics include amoxacillin (30 µg), augmentin (30 µg) chloramphenicol (30 µg), ciprofloxacin (10 µg), ofloxacin (10 µg), streptomycin (30 µg), sparfloxacin (10 µg) and septrin (30 µg). The antibiotics impregnated discs were placed on Mueller-Hinton agar plates already seeded uniformly with 0.5 McFarland of the cell suspension. Incubation of Petri plates was at room temperature (27 ± 2°C) 48 h and observed for zones of inhibition. Interpretation of susceptibility and resistant was by Clinical and Laboratory Standards Institute Guidelines (2018).

Growth of isolate on diesel: Replicate flasks containing 50 ml of MSM with 0.5 ml (1% v/v) of diesel were prepared and inoculated with the isolate. Control flasks contained heat killed cells. Total viable counts was determined at 3 days interval by plating out dilutions of cultures onto nutrient agar. Residual oil concentration and pH were also determined at the same interval. Amounts of hydrocarbon degraded were analyzed at 15 days interval (day 0, 15 and 30) using Gas chromatograph equipped with flame ionized detector (GC-FID). The extraction of residual oil and the running conditions for the gas chromatography were as described by Obayori *et al.*, (2018). The degradation rate constant was determined by fitting the residual oil data to the kinetics model of Yeung et al. (1997) $y = ae^{-kt}$ where *y* is the residual diesel oil in culture (mg/l), *a* is the initial diesel oil in culture (mg l^{-1}), k is the degradation constant (day^{-1}), and t is the time (day). Half-life ($t_{1/2}$) was then calculated as:

$$Half - life = \frac{ln(2)}{k}$$

RESULTS

The physicochemical and biological characteristics of the polluted soil sample are shown in Table 1. The soil recorded pH value of 6.63, total organic carbon of 5.10 mg kg^{-1}, while total hydrocarbon content was 42.10 mg kg^{-1}. The potassium content of the polluted soil was 25.28 mg kg^{-1}, total nitrogen of 25.20 mg kg^{-1} and phosphorus content of 30.29 mg kg^{-1}. The total heterotrophic bacteria enumerated was 1.53

x 10^9 cfu g^{-1}, while total heterotrophic fungi were 1.33 x 10^6 cfu g^{-1}, THUB and THUF recorded was 7.13 x 10^6 cfu g^{-1} and 3.77 x 10^3 cfu g^{-1}respectively.

Table 1: Physicochemical and microbiological characteristics of soil sample

Parameter	Value
pH	6.63
Moisture %	5.10
TOC (mg kg^{-1})	75.87
THC (mg kg^{-1})	42.10
Nitrogen (%)	25.20
Potassium (mg kg^{-1})	25.28
Phosphorus (mg kg^{-1})	30.29
THB (cfu g^{-1})	1.53 x 10^9
THF (cfu g^{-1})	1.33 x 10^6
THUB (cfu g^{-1})	7.13 x 10^6
THUF (cfu g^{-1})	3.77 x 10^3

Key TOC – total organic carbon; THC- total hydrocarbon content; THB- total heterotrophic bacteria, THF – total heterotrophic fungi; THUB – total hydrocarbon utilizing bacteria; THUF – total hydrocarbon utilizing fungi

Table 2: Colonial morphology and biochemical characteristics of XB1 from soil sample

Test	XB1
Cell shape	Cocci
Colour	Yellowish
Gram reaction	+
Oxidase	-
Catalase	+
Coagulase	-
Endospore	-
Glucose	+
Fructose	+
Mannose	+
Maltose	+
Lactose	-
Trehalose	+
Mannitol	+
Xylitol	-
Melibiose	-
Potassium nitrate	+
Naphthyl phosphate	+
Sodium Pyruvate	-
Raffinose	-
Xylose	+
Saccharose	+
Methyl α D-glucose pyroside	-
Acetyl-Glucosamine	+
Arginine	-
Urea	-
Putative Identity	*Staphylococcus sciuri*

Continuous enrichment of soil sample on diesel oil resulted in the isolation of strain XB1.The XB1 was Gram-positive non-motile coccus, oxidase negative, catalase positive, coagulase negative and endospore negative. The biochemical characteristics of the isolate are shown in Table 2. The isolate was able to utilise glucose, fructose, mannose, maltose, lactose, trehalose and mannitol. It tested negative to xylitol, mellibiose, sodium pyruvate, raffinose, methyl α-D-glucose pyroside, arginine and urea. Strain XB1 further tested positive to saccharose, acetyl glucosamine and was putatively identified as *Staphylococcus sciuri*. The antibiotic susceptibility pattern and salt tolerant is shown in Table 3. Strain XB1 was resistant to septrin, chloramphenicol, amoxacillin, gentamycin and streptomycin, but susceptible to sparfloxacin, ciprofloxacin, perfloxacin and ofloxacin. It was able to tolerate 3% NaCl concentration. Hydrocarbon specificity of strain XB1 is shown in Table 4. The isolate showed luxuriant growth on crude oil and kerosene, moderate growth on engine oil but was unable to utilize other hydrocarbons such as pyrene, phenanthrene and anthracene.

Table 3: GC-MS identified constituents of methanol seed extract of *M. myristca*

Antibiotic	**Strain XB1**
Septrin (30 µg)	R
Chloramphenicol (30 µg)	R
Sparfloxacin (10 µg)	S
Ciprofloxacin (10 µg)	S
Amoxacillin (30 µg)	R
Augmentin (30 µg)	R
Gentamycin (10 µg)	R
Perfloxacin (10 µg)	S
Ofloxacin (10 µg)	S
Streptomycin (30 µg)	R
Salt tolerant test	Turbidity
1%	+++
2%	+++
3%	+
4%	-
5%	-

Key: R: Resistant; S: susceptible. +++: luxuriant growth; ++: very good growth; +: poor growth; –: no growth. Susceptible: 21mm and above, Intermediate 11 -20 mm Resistance 0-10 mm

Table 4: Substrate susceptibility of isolate on different hydrocarbons

Substrate	Strain XB1
Crude oil	+++
Kerosene	+++
Engine oil	++
Diesel	+++
Anthracene	+
Phenanthrene	+
Pyrene	-

Key: +++: luxuriant growth; ++: very good growth; +: poor growth; –: no growth. Cultures were incubated for 7–30 day. All substrates were supplied at a concentration of 50 mg/L.

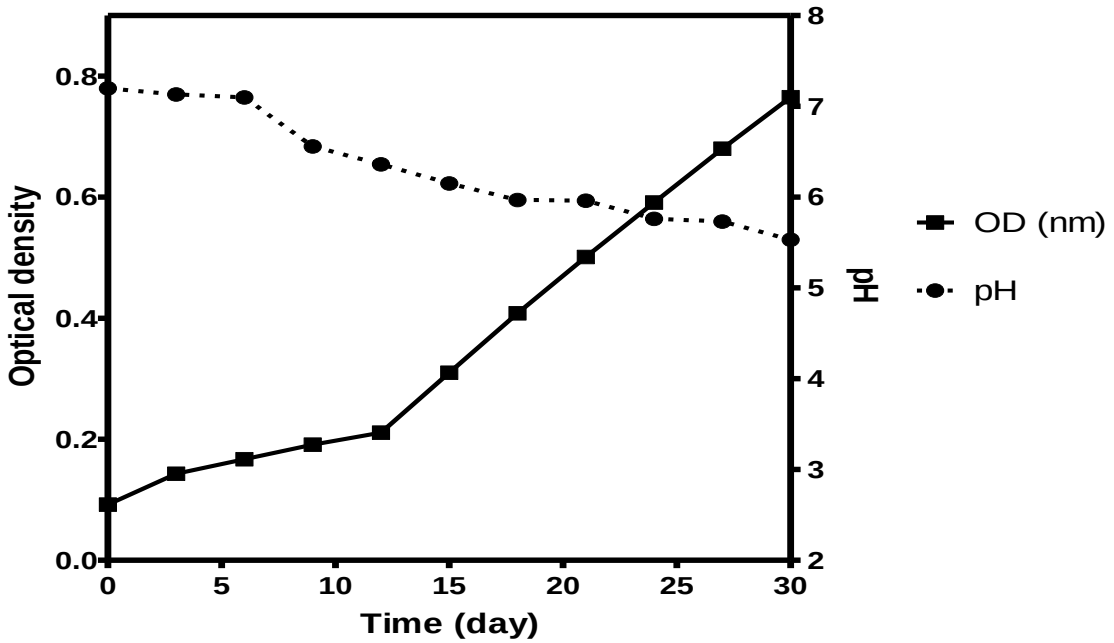

Figure 1: Growth curve of strain XB1 on diesel oil over a period of 30 days. The pH of the medium turns acidic as the growth rate increases indicating metabolite production by strain XB1.

The growth profile of strain XB1 is shown in Figure 1. Bacterial growth was monitored via optical density (OD) at 3 days interval. Strain XB1 exhibited a biphasic growth curve on diesel. The growth profile shows steady increase in optical density from 0.092 at day 0 to 0.191 at day 10 which was followed by second lag phase on day 12. At day 15 another logarithmic growth phase was observed at OD of 0.31 while increase in cell biomass was observed till day 30 with absorbance of 0.765. A slight decrease in pH of the medium was also observed from 7.2 at day 0 to 5.53 at day 30. The kinetics of degradation of strain XB1 is shown in Table 5. The chromatogram of the degradation of diesel by strain XB1 is shown in Figure 2. Readings from the chromatogram indicated that the isolate had a doubling time of 11.925 (d) between day 0 -12 and 17.825 (d) between day 12-30. The degradation rate was 0.042 $mgL^{-1}d^{-1}$ between day 0-12 and 0.072 $mgL^{-1}d^{-1}$ between day 12-30 respectively. The percentage overall hydrocarbon degraded was 55% at day 15 and 85 % at day 30.

Table 5: Kinetics of diesel oil degradation by strain XB1

Parameter	Value
T_d 12(d)	11.925
T_d 30(d)	17.825
DR 12 $mgl^{-1}d^{-1}$	0.042
DR 30 $mgl^{-1}d^{-1}$	0.072
$T_{1/12}$12	16.504
$T_{1/2}$ 30	9.627
PD15 %	55.000
PD 30 %	85.000

Key: Td12: doubling time between Day 0 and 12; Td30 doubling time between day 12 and 30; DR12: Degradation rate between day 0 and day 12; DR30: degradation rate between Day 12 and Day 30; $T_{1/2}$12: degradation half-life between Day 0 and Day 12; $T_{1/2}$30: degradation half-life between day 0 and Day 30; PD15: percentage of diesel degraded in the first 15 Day; PD30: overall percentage of diesel degraded during 30-day incubation.

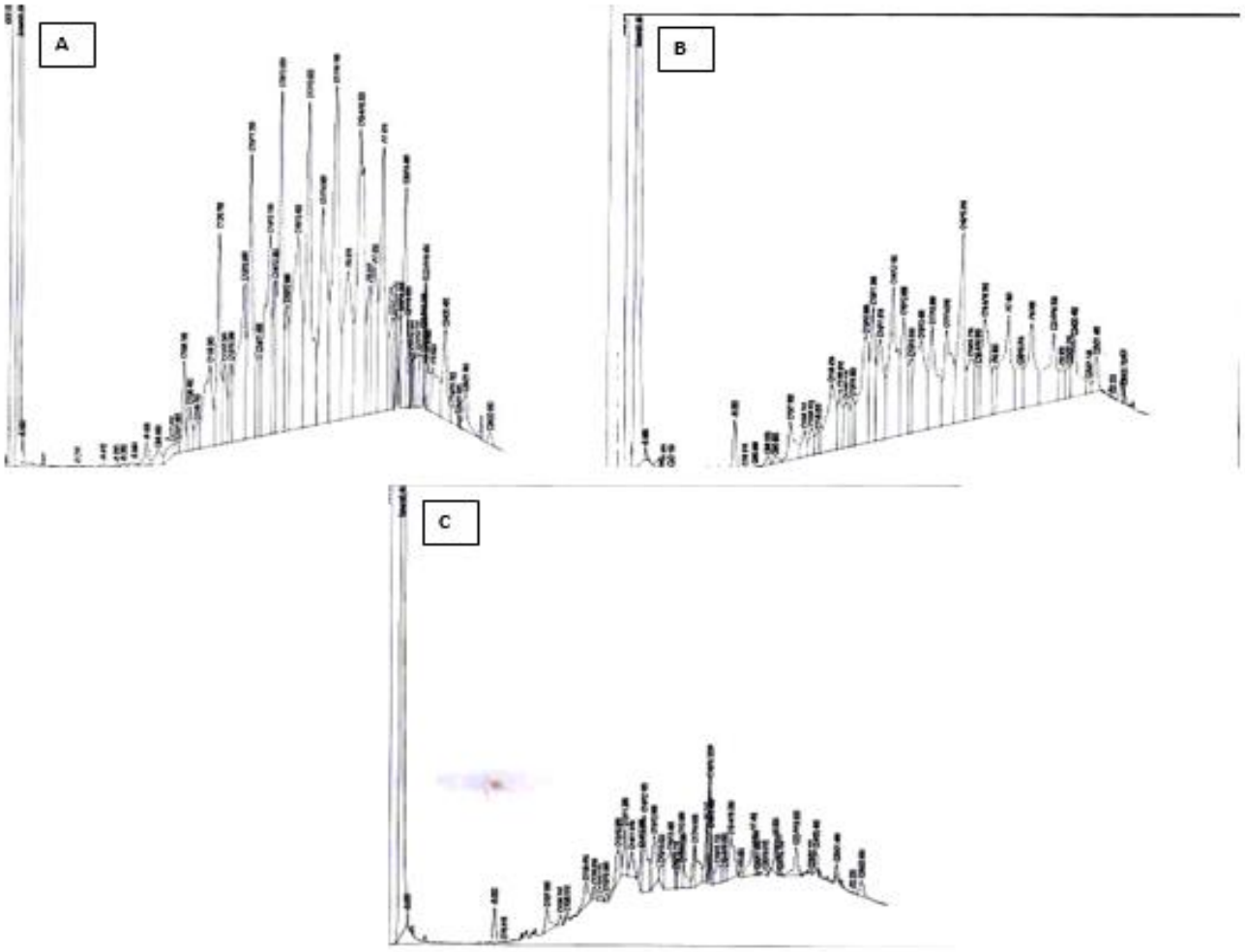

Figure 2: Gas chromatographic traces of n-hexane extract of fresh diesel oil from culture fluids of strain XB1 at day 0 (A) day 15 (B) and day 30 (C) on 1% diesel oil MSM. The oil components were separated on 30 m long HP-5 column (internal diameter, 0.25 mm; film thickness, 0.25 µm) in a Hewlett Packard 5890 Series II gas chromatograph equipped with flame ionization detector (GC-FID)

Table 6: Percentage of diesel oil fractions degraded by strain XB1 after 30 days of incubation in mineral salt medium at room temperature

Hydrocarbon fractions	Day 15	Day 30
C_9	75.790	100.000
C_{10}	20.100	66.805
C_{11}	40.160	86.547
C_{12}	86.870	97.932
C_{13}	62.040	87.851
C_{14}	7.500	73.103
C_{15}	95.780	98.012
C_{16}	62.910	90.748
C_{17}	70.786	93.433
C_{19}	83.108	92.934
C_{20}	39.511	95.79
C_{24}	34.800	77.988
C_{25}	28.430	64.864
C_{26}	59.960	81.861

Key: C_9 - Nonane; C_{10}- Decane - C_{11} – Undecane, C_{12} – Dodecane; C_{13} – Tridecane; C_{14} – Tetradecane; C_{15} – Pentadecane; C_{16} – Hexadecane; C_{17} – Heptadecane; C_{18} – Otadecane; C_{19} – Nonadecane; C_{20} – Icosane; C_{21} - Heinecosane, C_{22} – Docosane; C_{24} – Tetracosane; C_{25}- Pentacosane; C_{26}- Hexacosane.

Percentages of diesel oil fractions degraded by strain XB1 after 30 days of incubation in mineral salt medium at (27 ± 2°C) are shown in Table 6. The C_9 fraction of the hydrocarbon recorded percentage of 75.79% at day 15 and 100% at day 30, C_{10} had percentage degradation of 20.10% at day 15 and 66.81% at day 30. The C_{15} fraction recorded 95.78% and 98.01% degradation at day 15 and 30 respectively, while C_{19} recorded 83.11% and 92.93% at day 15 and 30 respectively. The long carbon chains hydrocarbon fractions (C_{25} and C_{26}) recorded 28.43%, 59.96% degradation rate at day 15 and 64.86%, 81.86% at day 30.

DISCUSSION

Petroleum hydrocarbons such as kerosene and diesel are some of the most abundant environmental pollutants; their non-polarity nature with affinity to binding to soil organic matter is often responsible for their high residual concentrations in soils (as compared to other more persistent, organic pollutants). The extensive utilization of diesel oil as a major source of energy has propelled the risks of accidental spills and hence, its pollution in the environment. As a result of the negative impacts of diesel oil pollution, several environmental biotechnological approaches are designed and tested so as to achieve sustainable environment.

Biodegradation is the major biological mechanism by which hydrocarbon pollutants including diesel are ultimately removed from the environment, even though physical and chemical weathering play important role especially at the initial stage. The key players in this regard are bacteria and fungi with the required genes for metabolism of the hydrocarbons as sources of carbon and energy. However, the enrichments and isolation of diesel oil degraders in pure culture is important in remediation of diesel polluted soil, paving the way for understanding of their physiology and in-depth appreciation of their genetic makeup (Hilyard *et al.,* 2008; Obayori *et al.,* 2012). The soil sample used in this study showed low levels of phosphorus and nitrogen. This could be attributed to their continuous use by the autochthonous microbial population for sugar phosphorylation and nucleic acid synthesis and other cellular activities (Andrew and Jackson, 1996; Obayori *et al.,* 2008a). Physicochemical properties of the environment often influence the type, number and metabolic activities of the microflora of any ecosystem (Adebusoye *et al.,* 2008). Andrew and Jackson (1996) reported that microorganisms require mineral nutrients from the environment to be metabolically active. Hence, if any of the required nutrients become limiting or lacking especially macronutrients, the degradation processes may proceed at a very slow rate despite the presence of carbon and nitrogen source (Giordani *et al.,* 1998; Lehtola *et al.*, 1998; Vidali, 2001).

Several bacterial strains that are widespread in oil polluted environments with great potential to utilize diesel oil as sole source of carbon and energy have been reported in literature (Panda *et al.*, 2013; Zhang *et al.*, 2013). Nwinyi *et al.* (2014), confirmed effective utilization of diesel oil by *Bacillus, Pseudomonas and Mycobacterium* species isolated from diesel oil contaminated soil. Equally, Tudararo-Aherobo *et al.* (2017) reported isolation of *Staphylococcus* sp., *Acetobacter* sp., *Acinetobacter* sp. and *Marinococcus* sp. from diesel contaminated water. The isolation of *S. scuri* in this study is of interest because this organism belongs to a group of coagulase negative *Staphylococcus* commonly reported as animal-associated commensals with potential for causing infection in plants and animals (Beims *et al*. 2016). The isolate from this study (*S. scuiri* XB1) indicated resistance to six different antibiotics. This is not surprising as coagulase-negative *Staphylococcus* species are known to usually resist ofloxacin and fluoroquinolone antibiotics (Pegues *et al.,* 1998). The ability of the isolate to resist septrin, chloramphenicol, amoxacillin, augmentin and streptomycin may be due to continual release of such antibiotic into the environment where exposure may lead to the

acquisition of resistance by microorganisms thus, given organisms due advantage over other members in their natural environment.

The ability of strain XB1 to tolerate 3% salt concentration makes it a better candidate for bioremediation purpose because salinity is one of the important factors that determined survival of organism in soil when used in bioaugmentation process (Kastner *et al.* 1998). The ability of strain XB1 to utilize broad spectrum of hydrocarbons could be due to relative abundance of this contaminant in the polluted environment. Biphasic growth curve was observed in the growth experiment of strain XB1 on diesel. This could be due to utilization of more readily available hydrocarbon fraction by the isolate before utilization of the more recalcitrant fractions. The gradual reduction observed in the medium pH over a period of 30 days could be due to production of acidic metabolites by hydrocarbon degrading bacteria (Adebusoye *et al.,* 2007). Initially, a drastic reduction in pH value may have been observed but, buffering the medium prior to inoculation of bacteria could be responsible for slight reduction in pH value over the 30 days experimental period.

The overall percentage hydrocarbon degradation of 85% recorded for strain XB1 points to the fact that the bacterium exhibits strong degradation potential for the hydrocarbon contaminant making this isolate a better candidate for bioremediation experiments. The percentage hydrocarbon degraded by strain XB1 obtained in our study is higher than that obtained by Tudararo-Aherobo (2017), where degradation percentage of 77.5% was recorded with *Acetobacte*r sp. and 81.34% with *Acinetobacter* sp on diesel over a period of 14 days incubation period. Generation time (tg) of 11.925 $d^{-1}$and 17.825 d^{-1} was recorded for the dual growth phases.

The drastic reduction in hydrocarbon fractions from C_9, C_{12}, C_{15}, C_{19} over 15 days incubation period could point to the fact that the hydrocarbon fractions are saturated non-linear alkane fractions which are readily more degradable when compared with the aromatic counterpart. Hydrocarbon fractions such as C_{10}, C_{11}, C_{14} and C_{20} showing little degradation value over 15 days incubation period could be suggested to be aromatic portions of the diesel contaminants. The complete and almost complete disappearance of the hydrocarbon fractions over 30 days incubation period point to the fact that strain XB1 is a potent hydrocarbon degrader showing strong degradation capacity for diesel oil.

CONCLUSION

This study shows that dumpsite could be an excellent source for potent oil degrading bacteria. *Staphylococcus scuiri* strain XB1, an indigenous bacterium isolated from dumpsite polluted soil showed effective utilization of diesel oil and different hydrocarbon fractions in this study. However, further studies to determine the optimal environmental conditions suitable for utilization of this isolate as an inoculant in large-scale hydrocarbon polluted environments will be our focus in our future studies.

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