Journal of Advances in Microbiology Research

E-ISSN: 2709-944X
P-ISSN: 2709-9431
JRM 2024; 5(1): 221-226

www.microbiojournal.com
Received: 16-12-2023
Accepted: 25-01-2024

Chibuike PM
Department of Microbiology/ Rivers State University, Nkpolu-Oroworukwo, Port Harcourt, Nigeria

Nengi-Benwari AO
Department of Crop and Soil Science Faculty of Agriculture. University of Port Harcourt

Barika PN
Department of Microbiology/ Rivers State University, Nkpolu-Oroworukwo, Port Harcourt, Nigeria

Robinson VK
Department of Microbiology/ Rivers State University, Nkpolu-Oroworukwo, Port Harcourt, Nigeria

Correspondence
Chibuike PM
Department of Microbiology/ Rivers State University, Nkpolu-Oroworukwo, Port Harcourt, Nigeria

Antibiogram of bacteria isolated from oil-polluted soil in auto-mechanic workshops around a tertiary institution

Chibuike PM, Nengi-Benwari AO, Barika PN and Robinson VK

Abstract
The soil has been a vehicle in the transmission of multiple antibiotic resistant bacteria. This study is carried out to investigate the antibiogram of bacteria isolated from oil-polluted soil in auto mechanic workshops around Rivers State University. Total of thirty-six (36) soil samples were collected from different locations (Maingate, Backgate and Ikwerre Road) in Port Harcourt. The samples were collected using soil auger and subjected to standard microbiological procedures such as culturing, isolation and identification. The Kirby-Bauer disc diffusion method was used to test for antibiotic susceptibility patterns. Results showed that the heterotrophic bacteria count was $1.2\pm0.6 \times 10^8$ for backgate, $1.3\pm0.2 \times 10^8$ for maingate and $2.1\pm0.4 \times 10^8$ for Ikwerre Road while the Hydrocarbon utilising bacteria count was $2.7\pm0.9 \times 10^5$ for backgate, $2.7\pm0.9 \times 10^6$ for maingate and $2.2\pm0.5 \times 10^5$ for Ikwerre Road. Microorganisms isolated from oil polluted soil include *Bacillus* sp, *Staphylococcus* sp, *Micrococcus* sp, *Escherichia coli, Pseudomonas* sp, *Proteus* sp, *Klebsiella* sp and *Serratia* sp. *Pseudomonas* sp (33.33%) had the highest frequency of occurrence while *Escherichia coli* (3.52%) had the least frequency of occurrence. All the bacterial isolates were resistance to Amoxicillin, Ciprofloxacin, Erythromycin, Ceftazidime, Azithromycin (100%) and sensitive to Ofloxacin, Gentamincin and Streptomycin. Antibiotic resistance in soil bacteria can be an indirect consequence of exposure to pollutants, as certain genes that confer resistance to antibiotics may also enhance tolerance to environmental stressors like oil pollutants. Antibiotic resistance is an instance of the immense capacity for natural evolution and adaptation of bacteria to diverse ecosystems. While this process seems inevitable, humans have accelerated it through various anthropogenic activities. Automobile workshops contribute to the challenge of soil contamination with petroleum hydrocarbons in addition to toxic heavy metals as a result of indiscriminate disposal of oil.

Keywords: Antibiogram, bacteria, mechanic workshop, antibiotics

Introduction
Soil plays a major role as a source of nutrients in the environment, it serves as a shelter for plants and other species, and works as a big bioreactor, where pollutant decomposition as well as nutrient alteration occurs (Talukder *et al.,* 2021) [18]. Over the years, soil bacteria have been incrementally antibiotic resistant although more stringent antibiotic usage laws exist in medicine and agriculture (Kumar *et al.*, 2019) [8]. The soil ecosystem which is mainly influenced by human usage, where the interaction between clinical pathogenic isolates and environmental isolates occurs, and the presence of several antimicrobial selective pressure together, is ideal for exchanging and disseminating resistance genes (Pitondo-Silva *et al.*, 2014) [15]. Antibiotic resistance in soil bacteria can be an indirect consequence of exposure to pollutants; as certain genes that confer resistance to antibiotics may also enhance tolerance to environmental stressors like oil pollutants. Antibiotic resistance is an instance of the immense capacity for natural evolution and adaptation of bacteria to diverse ecosystems (Clarke *et al.,* 2020) [6]. While this process seems inevitable, humans have accelerated it through various anthropogenic activities (Wong, 2019) [22]. Automobile mechanic workshops in contribute to the challenge of soil contamination with petroleum hydrocarbons in addition to toxic heavy metals as a result of indiscriminate disposal of oil. Such contaminated soil environments can serve as reservoirs of bacteria which possess adaptive tolerance to these metals and hydrocarbons as well as resistance to antibiotics (Onovaye *et al.*, 2022) [13]. Recently, self-employed artisan auto-mechanics are relocating to agricultural lands to set up auto-mobile mechanic workshops as a result of limited space in urban areas parts of Nigeria (Musa, 2019) [9]. Oils are used as lubricating oils obtained after servicing and subsequently

draining from automobile and generator engines. This contains high percentage of aliphatic and aromatic hydrocarbons and other heavy metals such as nitrogen and sulphur. These metals are introduced into the oil as a result of wear and tear of the automobile and generator engine. The oil causes great damage to soil and soil microflora due to poor aeration, immobilization of soil nutrients and reduction of soil pH. It also alters the physical, chemical as well as microbiological properties of the soil. At low concentrations, some of these heavy metals are essential micronutrients for plants, on the contrary, they can cause metabolic disorders and growth inhibition when the concentration is high. (Musa, 2019) [9]. Several petroleum hydrocarbons contaminated sites are also contaminated with metals either as trace elements of crude oil or its derivatives. Metal contamination in soils also produces co-selection for bacteria conferring antibiotic resistance and the relationship between metal and antibiotic resistance in bacteria is also very well established (Poole, 2017) [17]. Even low concentrations of metals found in residential soils, assumed to have been free of antibiotic exposure showed a greater relative abundance of antibiotics resistant bacteria (Knap *et al.*, 2017) [7]. In establishing the application of bacteria in the bioremediation of hydrocarbon impacted environments, there is also a need to ascertain the antibiotics susceptibility of the bacterial isolates to overcome the spread of antibiotics resistant genes in the environment. Thus, the present study aims at evaluating the antibiotic resistant propensity among bacterial isolates from hydrocarbon impacted and pristine soil samples.

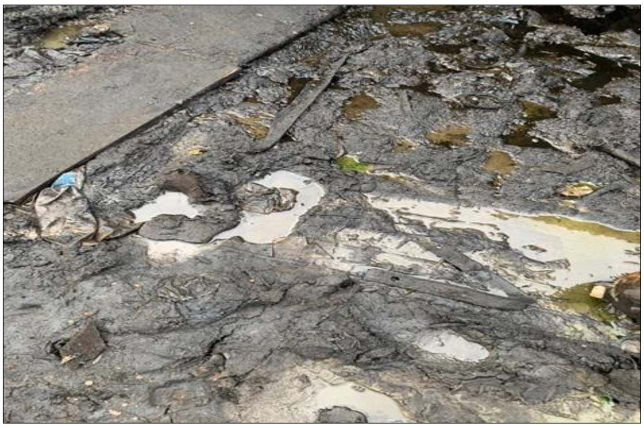
Materials and Methods

Description of Study area

The sample area was auto-mechanic workshops around Rivers State University, Port Harcourt. The sample stations were three major exits; Backgate (4.79552278,6.9843303), Maingate (4.8042420, 6.9843303) and Ikwerre Road (4.808841, 6.9860721). Table 3.1 shows the GPS Coordinates of the sample stations.

Table 1: Global Positioning System (GPS) coordinates of the sample stations

Sample stations	GPS Coordinates
BGM	Latitude: 4.79552278, Longitude: 6.9843303
MGM	Latitude: 4.8042420, Longitude: 6.986804
IRM	Latitude: 4.808841, Longitude: 6.9860721



Key: BGM (Back gate mechanic), MGM (Main gate mechanic), IRM (Ikwerre Road mechanic)

Plate 1: A picture showing oil polluted soil at the auto-mechanic workshop sampling station

Sample Collection

A total of thirty-six (36) soil samples were collected once every month from the auto-mechanic workshops for a period of four (4) months. The samples were labelled and placed in sterile polythene bags and then transported to Microbiology Laboratory in Rivers State University, Port Harcourt for bacteriological analyses.

Microbiological Analyses

Sample preparation and Bacterial Enumeration

reparation was done by weighing one (1g) gram of the soil samples in 9ml of the diluent. Serial 10-fold dilution was carried out to appropriate dilution of 10^{-6} for Total heterotrophic bacteria (THB) and 10^{-4} for hydrocarbon utilizing bacteria (HUB). Aliquot (0.1ml) from the appropriate dilutions were inoculated unto fresh agar plates in duplicate and spread using a glass spreader and plates were incubated at 37 °C for 24-48hours (Prescott *et al*., 2005) [6].

Enumeration of Hydrocarbon Utilizing Bacteria (HUB)

The vapour phase transfer method of Mills *et al*. (18) was adopted to determine the population of hydrocarbon utilizing bacteria (HUB). Aliquot (0.1ml) of the serially diluted soil sample was inoculated on Bushnell Haas Agar medium (Containing either Chloramphenicol or Fungosol) using the spread plate technique as described by Chibuike *et al*. (2023) [4]. Sterile filter paper discs soaked in filter-sterilized crude oil which served as the only carbon source in the mineral salt agar was placed aseptically in the cover of the inoculated agar plates in duplicates. The plates were incubated for 3-5 days at ambient temperature (37^0C). After the incubation period, the number of colonies was counted and recorded.

Bacterial Identification and Preservation

Pure cultures of bacteria were obtained by aseptically streaking representative colony of different morphological types on freshly prepared nutrient agar plates. Discreet colonies were transferred into 10% sterile glycerol solution and preserved for further analysis. Furthermore, biochemical test such as catalase, oxidase, citrate utilization, indole production, methyl red test, sugar fermentations and starch hydrolysis (Williams and Dimbu, 2015) [20]. The identification of bacterial isolates was confirmed by comparing them with Bergey's Manual of Determinative Bacteriology.

Antibiotic Susceptibility Test

The standard agar-disc-diffusion method (Kirby Bauer technique) was used to examine the antibiotic susceptibility pattern of the bacteria using Mueller-Hinton agar (Difco, Detroit, MI). Disc impregnated with Ampicillin, Erythromycin, Tetracycline, Gentamicin, Ciprofloxacin, Amoxicillin were used. After inoculation of the standardized bacteria the disc are placed on the plate allowing it to make contact with the agar. The plates were then inverted and incubated at 37° C for 24 h. After incubation, the plates were examined, and the zone of inhibition was measured in mm.

Data Analyses

The data obtained was analysed using analysis of variance (ANOVA) to test for significance and were differences occur, Duncan multiple range test was used to separate the means using the Statistical Package for Social Science (SPSS) version 25 (Bewick *et al*., 2004) [2].

Results

The results of the total heterotrophic (THB) and hydrocarbon utilizing bacterial (HUB) count of the soil samples isolated from the auto-mechanic workshops (MGM, BGM and IRM) are shown in Table 2. The highest total heterotrophic bacterial count was obtained in IRM ($2.1\underline{+}0.4\times10^8$) while the least count was obtained in BGM ($1.2\underline{+}0.6\times10^8$). MGM and BGM had equal population of hydrocarbon utilizing bacteria ($2.7\underline{+}0.9\times10^5$) while IRM had the least HUB population ($2.2\underline{+}0.5\times10^5$). There was no significant difference ($p\geq0.005$) in the hydrocarbon utilizing bacterial counts in the soil across the auto-mechanic workshops. Fig 1 shows the comparison of total heterotrophic bacterial count across the different locations.

Percentage occurrence of bacterial isolates

The total of fifty-seven (57) bacterial isolates belonging to eight (8) genera were isolated and identified from the soil sample, the isolates include *Bacillus sp*, *Staphylococcus sp*, *Pseudomonas sp*, *Micrococcus sp*, *Proteus sp*, *Klebsiella sp*, *Escherichia coli* and *Serratia sp*. Table 3 shows the percentage occurrence of the bacterial isolates. *Pseudomonas sp* (33.33%) had the highest frequency of occurrence while *Escherichia coli* (3.51%) had the least frequency of occurrence.

Table 2: Bacterial population from various workshops

Auto Mechanic Workshops	THBC × 10^8 (Cfu/g)	HUBC × 10^5 (Cfu/g)	HUB%
BGM	$1.2 \underline{+} 0.6^a$	$2.7 \underline{+} 0.9^a$	4.8
MGM	$1.3 \underline{+} 0.2^a$	$2.7 \underline{+} 0.9^a$	4.8
IRM	$2.1 \underline{+} 0.4^a$	$2.2 \underline{+} 0.5^a$	3.7

***Means with similar superscript down the group showed no significant difference ($p\geq0.05$)

Key: BGM (Back gate mechanic), MGM (Main gate mechanic), IRM (Ikwerre Road Mechanic), THBC (Total heterotrophic bacteria count), HUBC (Hydrocarbon utilising bacteria count).

Table 3: Percentage occurrence of bacterial isolates

Isolates	Percentage Occurrence (%)
Bacillus sp	17.54
Staphylococcus sp	19.30
Pseudomonas sp	33.33
Micrococcus sp	8.77
Proteus sp	5.26
Klebsiella sp	7..02
Escherichia coli	3.51
Serratia sp	5.26
Total	100

Antibiotic susceptibility pattern of the bacterial isolates

The result of the antibiotic susceptibility pattern is presented in Table 4. This indicates that a higher number of *Bacillus* isolates were 100% resistant to Amoxicillin, followed by Ciprofloxacin (60%) and Erythromycin (60%) while sensitive to Levofloxacin (100%), Streptomycin (80%), Cefalexin (80%). The susceptibility pattern of *Staphylococcus* sp isolated from oil-polluted soil, the majority of *Staphylococcus* isolates were 100% resistant to Amoxicillin, Ciprofloxacin, Gentamicin, Ceftazidime and Azithromycin while 100% sensitive to Levofloxacin, Rifampicin, Cefizox and Streptomycin. The susceptibility pattern of *Micrococcus* sp showed that *Micrococcus* isolates were 100% resistant to Amoxicillin, Ciprofloxacin, Erythromycin, Ceftazidime, Azithromycin while 100% sensitive to Levofloxacin, Rifampicin and Streptomycin. *Pseudomonas* isolates were 100% resistant to Ofloxacin, Augmentin, Ceftezole, and Ciprofloxacin followed by Pefloxacin (66.7%) and Streptomycin (66.7%) while 100% sensitive to Cephalothin, Thioredoxin and Gentamicin. All the bacterial isolates had a MAR index greater than 0.2.

Table 4: Susceptibility pattern of *Bacillus*, *Staphylococcus* and *Micrococcus* to antibiotics

Antibiotics	***Bacillus* sp**			***Staphylococcus* sp**			***Micrococcus* sp**		
	S	**I**	**R**	**S**	**I**	**R**	**S**	**I**	**R**
AMX	0	0	5(100)	0	0	1(100)	0	0	2(100)
CPX	2(40)	0	3(60)	0	0	1(100)	0	0	2(100)
E	2(40)	0	3(60)	0	1(100)	0	0	0	2(100)
LEV	5(100)	0	0	1(100)	0	0	2(100)	0	0
CN	4(80)	1(20)	0	0	0	1(100)	1(50)	1(50)	0
CEF	0	0	5(100)	0	0	1(100)	0	0	2(100)
RD	4(80)	1(20)	0	1(100)	0	0	2(100)	0	0
CTZ	2(40)	0	3(60)	1(100)	0	0	1(50)	0	1(50)
S	4(20)	1(20)	0	1(100)	0	0	2(100)	0	0
AZM	0	3(60)	2(40)	0	0	1(100)	0	0	2(100)

Key: S (Susceptibile), I (Intermediate), R (Resistant), AMX (Amoxicillin), CPX (Ciprofloxacin), E (Erythromycin), LEV (Levofloxacin), CN (Gentamicin), CEF (Ceftazidime), RD (Rifampicin), CTZ (Cefizox), S (Streptomycin), AZM(Azithromycin)

Table 5: Susceptibility pattern of *Pseudomonas* to antibiotics

Antibiotic	*Pseudomonas* sp		
	S	I	R
CEP	3(100)	0	0
TRX	3(100)	0	0
S	1(33.3)	0	2(66.7)
CEF	0	0	3(100)
OFX	0	0	3(100)
AU	0	0	3(100)
PEF	0	1(33.3)	2(66.7)
CTZ	0	0	3(100)
CN	3(100)	0	0
CPX	0	0	3(100)

Key: S (Susceptible), I (Intermediate), R (Resistant), CEP (Cephalothin), TRX (Thioredoxin), S (Streptomycin), CEF(Ceftazidime), OFX (Ofloxacin), AU (Augmentin), PEF (Pefloxacin), CTZ (Ceftezole), CN (Gentamicin), CPX (Ciprofloxacin)

Table 6: MAR indices of the bacterial isolates

Organisms	MAR Index					
	0.1	**0.2**	**0.3**	**0.4**	**0.5**	**0.6**
Bacillus	0(0.00)	0(0.00)	0(0.00)	4(80)	1(20)	0(0.00)
Staphylococcus	0(0.00)	0(0.00)	0(0.00)	0(0.00)	1(100)	0(0.00)
Micrococcus	0(0.00)	0(0.00)	0(0.00)	0(0.00)	2(100)	0(0.00)
Pseudomonas	0(0.00)	0(0.00)	0(0.00)	1(33.3)	0(0.00)	2(66.7)
E.coli	0(0.00)	0(0.00)	0(0.00)	0(0.00)	1(100)	0(0.00)
Proteus	0(0.00)	1(100)	0(0.00)	0(0.00)	0(0.00)	0(0.00)
Serratia	0(0.00)	0(0.00)	0(0.00)	1(100)	0(0.00)	0(0.00)
Klebsiella	0(0.00)	0(0.00)	1(100)	0(0.00)	0(0.00)	0(0.00)

Discussion

Auto mechanic workshops are essential for vehicle maintenance and repair, but they often generate oil and petroleum-based waste which leads to soil pollution in the vicinity. Spent engine oil wastes in soils are currently considered one of the most serious environmental problems. After their introduction into the soil, hydrocarbons affect soil microorganisms directly or indirectly (Ogunte *et al*., 2021) [12]. In this study, Ikwerre road mechanic (IRM) had the highest total heterotrophic bacterial (THB) count which could be attributed to the nature of the environment, the age of the spill, the total petroleum hydrocarbon content and the high amounts utilizable organic matter present in the soil. The low population of heterotrophic bacteria in MGM and BGM could be as a result of pollution of soil samples in the mechanic workshops. Pollution of the soil samples in the mechanic workshops was due to indiscriminate release of various wastes such as spent engine oil, paints, hydraulic fluids, lubricants, solvents, carbides, batteries etc. this is an on-going practice in most mechanic workshops in Nigeria. Hydrocarbon utilizing microorganisms are ubiquitously distributed in oil polluted soil environments. According to Odukuma and Dickson (2004) [11], populations of hydrocarbon degraders normally constitute less than 1% of the total microbial communities. This study revealed that not all the members of the heterotrophic population could utilize the petroleum products spilled in the soil, hence a decrease in the count of hydrocarbon utilizing organisms compared to the heterotrophic microbial count which is in agreement with Chibuike *et al*., (2023) [4]. Back gate and Main gate mechanic workshops (BGM and MGM) had a higher population of hydrocarbon utilizing bacteria (HUB) compared to IRM. The high population of HUB in BGM and MGM could be attributed to the adaptation of the hydrocarbon utilizing bacteria to the amount of hydrocarbon in the environment. The hydrocarbon utilizing bacterial genera isolated from the oil contaminated soil were *Pseudomonas*, *Bacillus*, *Micrococcus*, and *Klebsiella*. Williams and Akemi (2020) [20] isolated similar hydrocarbon utilizing bacteria from major auto-mechanic workshops in Port Harcourt Metropolis. It has also been observed that some microorganisms are more abundant in areas of high concentration of hydrocarbons.

Antibiotic resistance, linked to oil polluted soil has been a worry worldwide, antimicrobial drugs and the development of resistance are now generally acknowledged to be related. The antibiotic sensitivity patterns of the bacterial isolates found in this study had a significant impact on public health Implications as there could be transmission of these bacteria into the food chain or the clinical settings. The susceptibility pattern of *Bacillus* sp was 100% resistant to Amoxicillin, Ceftazidime, followed by Ciprofloxacin (60%) and Erythromycin (60%) while sensitive to Levofloxacin (100%), Streptomycin (80%), Cefalexin (80%). The susceptibility pattern of *Staphylococcus sp* was 100% resistant to Amoxicillin, Ciprofloxacin, Gentamicin, CEF and Azithromycin while 100% sensitive to Levofloxacin, Rifampicin, Cefizox and Streptomycin. The susceptibility pattern of *Micrococcus* sp was 100% resistant to Amoxicillin, Ciprofloxacin, Erythromycin, Ceftazidime, and Azithromycin while 100% sensitive to Levofloxacin, Rifampicin and Streptomycin. The susceptibility pattern of *Pseudomonas* sp was 100% resistant to CEF, Ofloxacin, Augmentin, Ceftezole, Ciprofloxacin followed by Pefloxacin (66.7%) and Streptomycin (66.7%) while 100% sensitive to Cephalothin, Thioredoxin and Gentamicin. The high resistance of these organisms can be explained by the extensive and uncontrolled use of antibiotics. The susceptibility or resistance of Bacteria to antibiotics can be triggered or influenced by genes, ratio of antibiotic concentration to concentration of bacteria, strength of antibiotics (Wiedenbeck and Cohan, 2011) [19]. Also, a study by Oboh *et al*. (2006) [10] reported hydrocarbon-degrading and antibiotics resistance bacterial species from different sources. Some researchers from their studies have speculated and have shown this to be as a result of the likelihood that resistance genes to both antibiotics and heavy metals could be closely located on the same plasmid in bacteria and are thus more likely to be transferred together in the environment (Oyetibo *et al*., 2010 [14]; Akani *et al*., 2019) [1]. Bacteria isolated from oil polluted soil are becoming resistant to more antibiotics which is of great public health concern. The presence of multi-drug resistance strains shows how oil polluted soil bacteria is developing different methods to resist antibiotics making therapeutic options more limited and expensive. Multiple resistance to antibiotics is probably due to indiscriminate use of antibiotics.

Conclusion

Bacteria, which are important in maintaining the function and stability of the soil ecosystem, can also serve as vehicles for the dissemination of antibiotic resistance from the environment to the food chain. In this study, it was shown that several pathogenic bacteria associated with oil polluted soil were resistant to most antibiotics which could pose a serious threat to public health. The study identified the bacteria in oil polluted soil and determined the susceptible pattern of these isolated bacteria. This information provides baseline data for future references, the presence of antibiotic-resistant bacteria in oil polluted soils calls for a proactive approach to protect both public health and the environment. Addressing this challenge requires continued research as well as the implementation of sustainable remediation strategies.

Conflict of Interest

Not available

Financial Support

Not available

References

1. Akani NP, Barika PN, Nwankwo CEI. Prevalence and antibiogram of *Plesiomonas shigelloides* isolated from humans and some environmental sources. Indo American Journal of Pharmaceutical Sciences. 2019;6(10):13011-13018.
2. Bewick V, Cheek L, Ball J. Statistics review 12: survival analysis. Critical Care. 2004;8:01-06.
3. Chibuike PM, Ogbonna DN, Williams JO. Microbiology and heavy metal content of wetlands impacted by crude oil pollution in Rivers State, Southern Nigeria. Microbiology Research Journal International. 2021;31(2):53-63.
4. Chibuike PM, Wemedo SA, Williams JO, Ugboma CJ, Ogbonna DN. Effect of crude oil pollution on the microbiology of coastal wetlands in River State. Journal of Advances in Microbiology Research. 2023;4(2):92-105.
5. Chibuike PM, Ogbonna DN, Barika PN, Ihunwo RJ. Prevalence and antibiogram of bacteria isolated from *Tilapia zilli* sold in markets in Port-Harcourt Metropolis. Journal of Advances in Microbiology Research. 2024;5(1):189-196.
6. Clarke L, Pelin A, Phan M, Wong A. The effect of environmental heterogeneity on the fitness of antibiotic resistance mutations in *Escherichia coli*. Evolutionary Ecology. 2020;379-390.
7. Knap CW, Callan AC, Aitken B, Shearn R, Koenders A, Hinwood A. Relationship between antibiotic resistance genes and metals in residential soil samples from Western Australia. Environmental Science and Pollution Research. 2017;24:2484-2494.
8. Kumar M, Ram B, Honda R, Poopipattana C, Canh VD, Chaminda T, Furumai H. Concurrence of antibiotic resistant bacteria (ARB), viruses, pharmaceuticals and personal care products (PPCPs) in ambient waters of Guwahati, India: urban vulnerability and resilience perspective. *Sci Total Environ*. 2019;693:133-640.
9. Musa SA. Isolation and identification of diesel oil-degrading bacteria in used engine oil contaminated soil. Journal of Applied Sciences and Environmental Management. 2019;23(3):431-435.
10. Oboh B, Ilori M, Akinyeme J, Adebusuye B. Hydrocarbon degrading potentials of bacteria isolated from a Nigerian bitumen (tarsand) deposit. Nature and Science. 2006;4(3):3-9.
11. Odukuma LO, Dickson AA. Bioremediation of a crude oil polluted tropical mangrove environment. Journal of Applied Science and Environmental Management. 2004;7(2):191-199.
12. Ogunte UC, Owhonka A, Barika PN, Solomon IO. Isolation of heterotrophic and hydrocarbon-utilizing fungi from selected mechanic workshops in Port Harcourt. South Asian Journal of Research in Microbiology. 2021;11(4):10-18.
13. Onovaye AM, Ikhimiukor OO, Adelowo OO. Response of bacteria isolated from spent engine oil contaminated soil to hydrocarbons, metals and antibiotics. *Soil Sediment Contam: Int J*. 2022;1-16.
14. Oyetibo G, Ilori M, Adebusoye S, Obayori O, Amund O. Bacteria with dual resistance to elevated concentrations of heavy metals and antibiotics in Nigeria contaminated system. Environmental Monitoring and Assessment. 2010;168:305-314.
15. Pitondo-Silva A, Martins VV, Fernandes AFT, Stehling EG. High level of resistance to Aztreonam and Ticarcillin in *Pseudomonas aeruginosa* isolated from soil of different crops in Brazil. *Sci Total Environ*. 2014;473:155-158.
16. Prescott LM, Harley JP, Klein DA. *Microbiology*. 6th ed. London: McGraw Hill; 2005.
17. Poole K. At the nexus of antibiotics and metals: the impact of Cu and Zb on antibiotic activity and resistance. Trends in Microbiology. 2017;25(10):820-832.
18. Talukder A, Rahman MM, Chowdhury MMH, Mobashshera TA, Islam NN. Plasmid profiling of multiple antibiotic-resistant *Pseudomonas aeruginosa* isolated from soil of industrial area in Chittagong, Bangladesh. Beni-Suef University Journal of Basic and Applied Sciences. 2021;10:1-7.
19. Wiedenbeck J, Cohan FM. Origins of bacterial diversity

through horizontal genetic transfer. FEMS Microbiology Ecology. 2011;35:957-976.
20. Williams JO, Akemi PP. Microbiological and physicochemical evaluation of oil-polluted soil from major auto mechanic shops in Port Harcourt Metropolis, Rivers State, Nigeria. Journal of Advances in Microbiology. 2020;20(3):1-10.
21. Williams JO, Dimbu P. Research article: Effect of abbatoir waste water on soil microbial communities. Scholars Academic Journal of Biosciences. 2015;5:452-455.
22. Wong A. Unknown risk on the farm: Does agricultural use of iontophoresis contribute to the burden of antimicrobial resistance? Msphere. 2019;4(5):33-49.

How to Cite This Article
Chibuike PM, Benwari NAO, Barika PN, Robinson VKA. Antibiogram of bacteria isolated from oil-polluted soil in auto-mechanic workshops around a tertiary institution. Journal of Advances in Microbiology Research. 2024;5(1):221-226.