

Examination of bacteria content of leachate concentration in open dumpsites, at Gwagwalada, Federal Capital Territory, Abuja, Nigeria

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Abstract

The bacteria content of leachate concentration in open dumpsite is a threat to man and its environment if not properly managed. One of the negative impacts of bacteria in leachate is that it may pollute water system which may lead to diseases if not prevented. In this study, the leachate concentrates were collected from five different location of open dumpsite in Gwagwalada town and examined bacteriologically. Using pour plate method, bacteria were counted and isolated. Biochemical tests and Molecular identification of bacteria isolate based on DNA extraction, DNA quantification and 16S rRNA Amplification were carried out. The total coliform bacterial counts ranged from 4.1×10^5 cfu/ml - 4.8×10^5 cfu/ml. Isolated bacteria with percentage occurrence were *Staphylococcus* spp. (37.14%), *Klebsiella aerogenes* (25.71%), *Proteus* spp. (20%), *Priestia megaterium* (11.43%), *Pseudomonas stutzeri* (2.86%) and *Enterobacter hormaechei* (2.86%). Generally, both gram positive organisms showed 100% susceptibility to Pefloxacin and Cotrimoxazole and exhibited 100% resistance to Ampliclox while all gram negative bacteria showed 100% susceptibility to Ciprofloxacin. The biochemical test and molecular identification of bacteria isolates showed the presence of pathogenic bacteria which is hazardous to human health within the environment due to the possibility of contamination of drinkable water. As a result, the government and environmental agency should work together in preventing the situation of open dumpsite around residential areas through educational and awareness program.

Keywords: Bacteria; Leachate; Open dumpsite; Wastes; Public health; Environment.

1. Introduction

Leachate is produced when water percolates through waste deposited in a dumpsite. It is a discharge interface from leaching [4]. The accelerated pace of development, urbanization, industrialization, coupled with increase in population growth and pattern of consumption have compounded the problem of management of solid waste in Nigeria [5]. Across the world, the most used means of disposing solid waste is landfill [10]. The majority of wastes deposited in landfills are; paper, glass, metals, plastics, rubber, textiles, wood, food, leather, electronics, construction and demolition wastes.

In developing countries, open dumpsite remain the way solid waste are mostly disposed. These waste are disposed uncontrollably and posses great danger to the immediate environment. Poor waste management promotes the presence of pathogenic bacteria; it leads to the generation of hazardous leachate [4] capable of transmitting various diseases and health issues which are risk to human health. Domestic, industrial and clinic waste dumpsite contain numerous number of pathogenic and opportunistic bacteria [7]. Some of which include; *Athorobacter*, *Bacillus*, *E. coli*, *Kliebsiella*, *Micrococcus*, *Proteus*, *Serratia*, [13, 1].

Groundwater, soil, surface water supplies are being contaminated by dumpsite leachate when migrating from dumpsite into neighborhood land, and can cause offensive odor [8].

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Poor waste management has become a real danger to the wellbeing of local population particularly those living around the dumpsite. There is a need for proper disposal and treatment of waste materials in a designated environment that is considered safe for the wellbeing of the population.

This paper is aimed at examining the bacteriological content of leachate concentration in open dumpsite at Gwagwalada, Federal Capital Territory– Abuja, Nigeria.

2. Material and methods

2.1. Equipment

All the instruments used for this research includes; analytical weighing balance (Ohaus USA), Incubator, Autoclave, Biosafety cabinet laminar flow hood, Microscope, pH meter, biochromlibra s22 Spectrophotometer, Fridge, Centrifuge (thermo fisher scientific), Atomic Absorption Spectrophotometer (ICE 3000 series).

2.2. Media

All the media and regents used for this research includes; Nutrient agar and nutrient broth, Mannitol salt agar, Macconkey agar, Muller hinton agar , Nutrient broth - (himedia M173-500G, Mumbai Indian), Urea, Glucose, Sucrose, Lactose, Galactose, Mannitol (BDH laboratories supplies BH15 ltd, England), Eosin Methylene blue agar (Levine- Oxoid ltd, England), Agar agar (Titan Biotech ltd, Rajashan, India).

2.3. Area of study



Figure 1 Map of Nigeria showing the 36 states and capital (17)

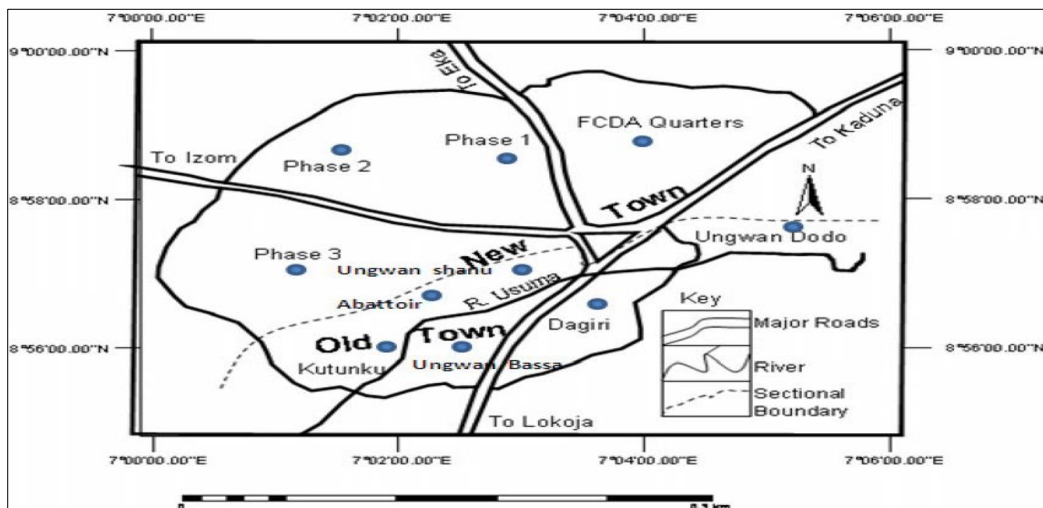


Figure 2 Map of Gwagwalada town [6]

The study area 'Gwagwalada is a town situated in the Federal Capital Territory of Nigeria with longitude of 07°10'E and latitude of 08°59'N. Gwagwalada town is greatly populated with a lot of economic and commercial activities. For the purpose of this study, five open dumpsites were selected to represent the geographical area of the town. This includes; Open dumpsite at Gwagwalada Old Kutunku, Gwagwalada main market road, University Kaida road, Gwagwalada Dukpa road and Gwagwalada Phase III.

2.4. Collection of samples

All leachate concentrate from the five open dumpsites (Open dumpsite at Gwagwalada Old Kutunku, Gwagwalada main market road, University Kaida road, GwagwaladaDukpa road and Gwagwalada Phase III open dumpsite) were collected aseptically at different sampling unit in duplicate. Collection was done using syringe into a well labeled sterile bottle and placed in an ice bag which was thereafter taken for research analysis at the Science and Technology Complex Laboratory (SHESTCO).

2.5. Bacteria Analysis / Enumeration

2.5.1. Serial dilution

10 fold Serial dilution of leachate sample was carried out up to dilution factor 10^{-8} . From the dilution of 10^{-5} , 0.1ml aliquot was aseptically transferred into sterile Petri dish; this was cultured in duplicate using nutrient agar by pour plate method. The plates were incubated at 37 °C for 24- 48 hours. After incubation, discrete colonies of culture developed on agar plates were counted and expressed in cfu/ml.

2.5.2. Identification of Bacteria

The bacteria isolates were identified morphologically by color, appearance, margin, shape e.t.c, biochemically by catalase test, citrate, indole, urease, starch hydrolysis, sugar fermentation test e.t.c. [10] and molecularly by DNA extraction, DNA quantification, 16S rRNA Amplification, Sequencing and Phylogenetic Analysis as described by Abimiku *et al.*, [9].

2.6. Antimicrobial Susceptibility Testing

The antimicrobial susceptibility test of bacteria isolates of leachate concentrate was carried out using the Kirby Bauer disk diffusion method. A single loop of each bacteria isolate was inoculated into sterile normal saline and standardized using McFarland standard. The standardized inoculum of each bacteria isolate were then inoculated in duplicate onto the surfaces of plain Muller – Hinton agar plates and were tested in vitro for susceptibility to the following commonly used antibiotics: Gentamycin (30ug), Streptomycin (30ug), Perfloxacin (30ug), Ciprofloxacin (30ug), Cotrimoxazole (30ug), Amoxicillin (30ug), Augumentin (10ug), Splaxocillin (10ug), Ofloxacin (10ug)and Chloramphenicol (30ug) disc ; these antibiotics disc were placed aseptically on the surface of agar plates and incubated at 37°C for 24hours. After incubation, zone of growth inhibited around each disc was measured and used to classify the organisms as sensitive, intermediate or resistant to the antibiotic used. This was done following the interpretive standard of the Clinical and Laboratory Standards Institute as earlier described by Asemota *et al.*, [3].

3. Results

3.1. Total bacterial counts

The total bacteria count of Leachate sample ranged from 4.1×10^5 - 4.8×10^5 cfu/ml for all five dumpsite with mean and standard deviation of 4.38 ± 0.23 . Site 2 (Gwagwalada main market road) recorded the highest total number of bacteria count of 4.8×10^5 cfu/ml, followed by Gwagwalada Phase III (site 3) with 4.4×10^5 cfu/ml, Old Kutunku (site 1) and Dukpa road (site 4) with 4.3×10^5 cfu/ml while site 5 (University Kaida road) had the least number of bacteria count of 4.1×10^5 cfu/ml. (Table 1).

3.2. Morphological, Biochemical and Molecular characterization of bacterial isolates from leachate concentrate

The morphological, biochemical (table 2) and molecular identification of bacteria from leachate concentrates revealed the following bacteria isolates; *Pseudomonas stutzeri*, *Priestia megaterium*, *Enterobacter hormaechei*, *Klebsiella aerogenes*, *Staphylococcus* spp., and *Proteus* spp (figure 3 – figure 6).

Table 1 Total bacterial counts in leachate concentrate of five open dumpsite at Gwagwalada, FCT – Abuja

Sampling location	Counts (x10 ⁵ cfu/ml)
Old Kutunku	4.3
Market road	4.8
Phase III	4.4
Dukpa road	4.3
University Kaida road	4.1
Minimum	4.1
Maximum	4.8
Range	4.1 – 4.8
Mean	4.38
S.D	0.2

3.3. Molecular characterization / identification of bacteria isolates

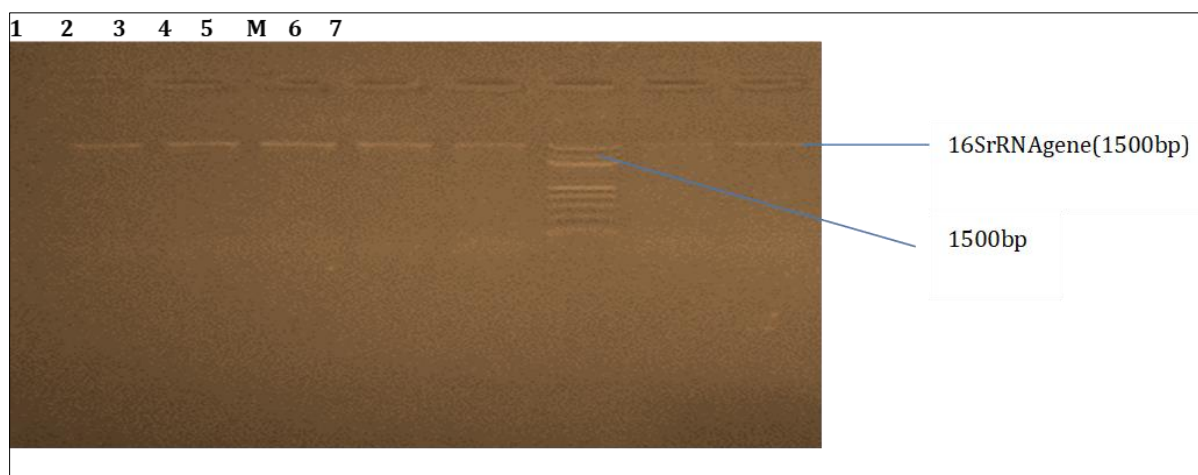


Figure 3 Agarose gel electrophoresis of the 16S rRNA gene of Bacteria isolates. Lanes 1-6 represent the 16SrRNA gene bands (1500bp), Lane M represents the 1500bp molecular ladder

Table 2 Morphological and Biochemical characterization of bacterial isolates from leachate concentration of open dumpsite at Gwagwalada FCT- Abuja.

Texture	Colony Colour	Morphology Appearance	Elevation	Margin	Shape	Gram stain RXN	BioCAT	Test CT	IN	COG	UR	SH	H ₂ S	Sugar Fermentation					Presumptive Identity
														G	S	L	GA	M	
Mucoid	Cream On N.A Pink on MAC	Smooth	Raised	Entire	Rod	-	+	+	-	-	+	-	-	+	+	+		+	<i>Klebsiella</i> spp.
Moist	Colourless On MAC	Glistening	Raised	Irregular	Rod	-	+	+	+	-	+		+	+	-	-	-	-	<i>Proteus</i> spp.
Moist	Yellow On MAN	Glistening	Raised	Entire	Cocci	+	+	+	-	-	+		-	+	+	+	+	+	<i>Staphylococcus</i> spp.
Moist	Pale yellow on NA	Smooth	Raised	Irregular	Rod	-	+	-	-	-	-		-	+	-	-	+	-	<i>Enterobacter</i> spp.
Moist	Cream On N.A	Smooth	Flat	Irregular	Rod	-	+	+	-	-	-		-	-	-	-	-	+	<i>Pseudomonas</i> spp.
Dry	Off white On N.A	Smooth	Raised	Entire	Rod	+	+	+	-	-	-	+	-	+		-	-	+	<i>Priestia</i> spp.

KEY: CAT = Catalase, CT= Citrate, IN= Indole, SH=Starch Hydrolysis, COG = Coagulase, UR = Urease, H₂S = Hydrogen Sulfide production, G = Glucose, S = Sucrose, L = Lactose, GA = Galactose, M = Mannitol, + = Positive, - = Negative, RXN = Reaction.

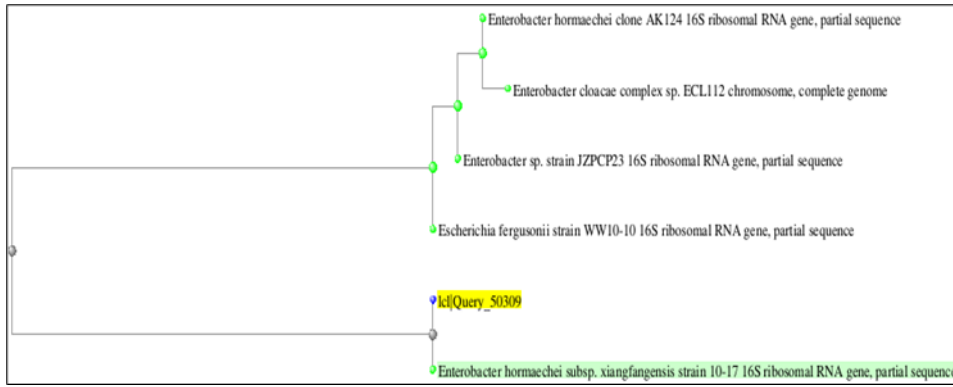


Figure 4 Phylogenetic tree of *Enterobacter hormaechei* showing the evolutionary distance between the bacteria isolates.

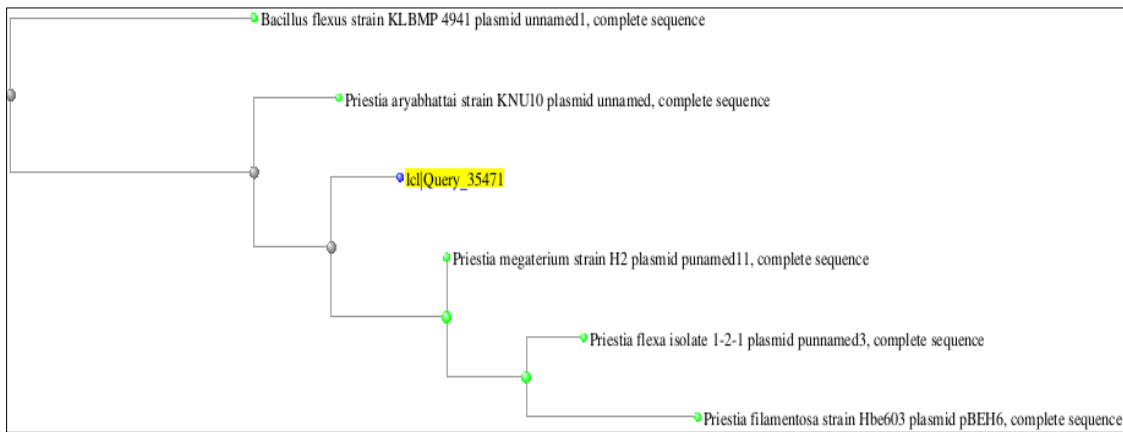


Figure 5 Phylogenetic tree of *Priestia megaterium* showing the evolutionary distance between the bacteria isolates.

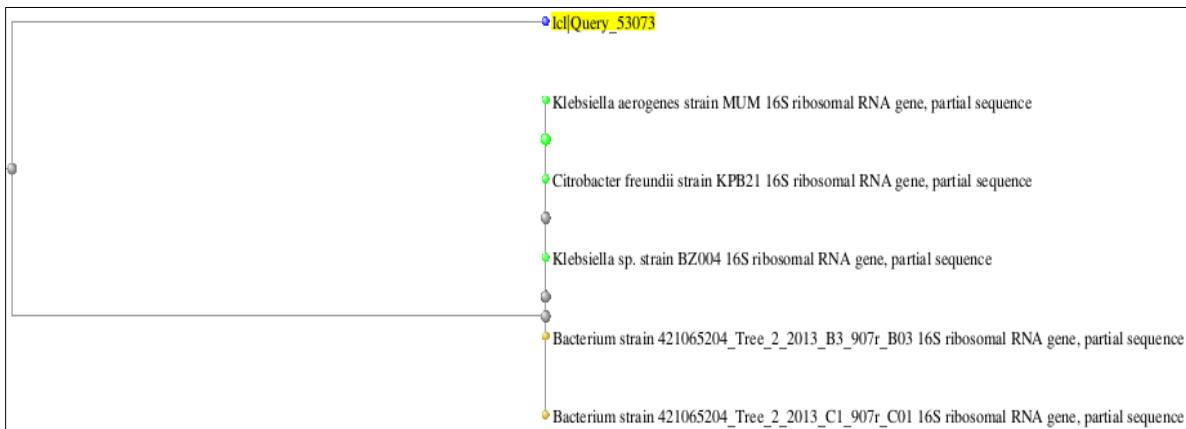


Figure 6 Phylogenetic tree of *Klebsiella aerogenes* showing the evolutionary distance between the bacteria isolates.

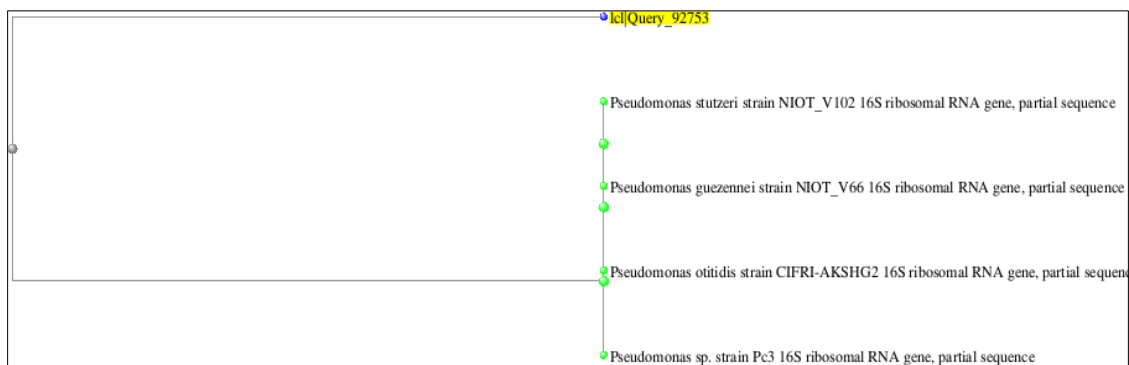


Figure 7 Phylogenetic tree of *Pseudomonas stutzeri* showing the evolutionary distance between the bacteria isolates.

3.4. Frequency of occurrence of bacterial isolates

The frequency of total bacteria isolate ranged from 2.86% - 5.71% at site 1 (Gwagwalada Old Kutunku), followed by 0.00% - 8.57% at site 2 (Gwagwalada main market road), 0.00% - 8.57% at site 3 (Gwagwalada Phase III), 0.00% - 8.57% at site 4 (GwagwaladaDukpa road) and 0.00% - 11.43% at site 5 (University Kaida road, Gwagwalada – Abuja) as shown in table 3.

Table 3 Frequency of occurrence of bacterial isolates

Location	<i>Klebsiella aerogenes</i> (%)	<i>Proteus spp</i> (%)	<i>Staphylococcus spp</i> (%)	<i>Pseudomonas stutzeri</i> (%)	<i>Enterobacter hormaechei</i> (%)	<i>Priestia megaterium</i> (%)	Total no. of isolate location/ total% occurrence
Old Kutunku	2 (5.71)	1 (2.86)	1 (2.86)	1 (2.86)	1 (2.86)	1 (2.86)	7 (20)
Market road	3 (8.57)	1 (2.86)	2 (5.71)	0 (0.00)	0 (0.00)	1 (2.86)	7 (20)
Phase III	2 (5.71)	2 (5.71)	3 (8.57)	0 (0.00)	0 (0.00)	0 (0.00)	7 (20)
Dukpa Road	1 (2.86)	1 (2.86)	3 (8.57)	0 (0.00)	0 (0.00)	1 (2.86)	6 (17.4)
University Kaida Road	1 (2.86)	2 (5.71)	4 (11.43)	0 (0.00)	0 (0.00)	1 (2.86)	8 (22.8)
Total occurrence (%)	9 (25.71)	7 (20.0)	13 (37.14)	1 (2.86)	1 (2.86)	4 (11.43)	35 (100)
Minimum	1	1	1	0	0	0	
Maximum	3	2	4	1	1	1	
Range	1-3	1-2	1-4	0-1	0-1	0-1	
Mean	1.8	1.4	2.6	0.2	0.2	0.8	
S.D	0.74	0.49	1.02	0.40	0.40	0.44	

3.5. Antimicrobial susceptibility patterns of gram negative bacterial isolated from dumpsite leachate.

The antimicrobial susceptibility pattern of gram negative bacteria against 10 antibiotics; Gentamycin(30ug), Streptomycin(30ug), Pefloxacin(30ug), Ciprofloxacin(30ug), Cotrimoxazole(30ug), Amoxicillin(30ug), Augumentin(10ug), Splaxocillin(10ug), Ofloxacin(10ug) and Chloramphenicol(30ug) shown in table 4 revealed that *Klebsiella aerogenes* was susceptible to 9 antibiotics (Gentamycin, Streptomycin, Pefloxacin, Ciprofloxacin, Septrin, Amoxicillin, Splaxocillin, Ofloxacin, Chloramphenicol) at 90% and 10% intermediate to Augumentin with no resistance. *Pseudomonas stutzeri* showed susceptibility to 6 antibiotics (Gentamycin, Pefloxacin, Ciprofloxacin, Amoxicillin, Ofloxacin, Chloramphenicol) at 60% and was intermediate to the remaining 4 antibiotics (Streptomycin, Cotrimoxazole, Augumentin, Splaxocillin) at 40% with no resistance. *Proteus* spp. exhibited 10% susceptibility to Ciprofloxacin, 40% intermediate to Pefloxacin, Amoxicillin, Splaxocillin and Ofloxacin, while all other antibiotics were resistant at 50%. Also *Enterobacter hormaechei* was susceptible to 4 antibiotics (Pefloxacin, ciprofloxacin, Splaxocillin, Ofloxacin) at 40% but showed resistance to the remaining 6 antibiotics (Gentamycin, Streptomycin, Cotrimoxazole, Amoxicillin, Augumentin, Chloramphenicol) at 60% with 0% intermediary.

Generally, all gram negative bacteria showed 100% susceptibility to Ciprofloxacin. The degree of susceptibility of total gram negative bacteria against all 10 antibiotics showed that *Klebsiella aerogenes* had the highest susceptibility at 90% followed by *Pseudomonas stutzeri* at 60%, followed by *Enterobacter hormaechei* at 40% and lastly *Proteus* spp. at 10% susceptibility (table 4).

Table 4 Antimicrobial susceptibility patterns of gram negative bacterial isolated from dumpsite leachate.

Antibiotics	Zones	of inhibition	(mm)		General	(%)	
	<i>Klebsiella aerogenes</i>	<i>Pseudomonas Stutzeri</i>	<i>Proteus spp</i>	<i>Enterobacter hormaechei</i>	S	I	R
Gentomycin (30ug)	25.4	19.0	12.2	0.0	2(50.0)	0(0.0)	2(50.0)
Streptomycin (30ug)	25.2	14.3	7.2	0.0	1(25.0)	1(25.0)	2(50.0)
Pefloxacin (30ug)	30.0	28.6	16.6	28.6	3(75.0)	1(25.0)	0(0.0)
Ciprofloxacin (30ug)	27.0	28.6	26.2	31.0	5(100)	0.(0.0)	0(0.0)
Cotrimoxazole (30ug)	28.2	15.8	11.1	0.0	1(25.0)	2(50.0)	1(25.0)
Amoxicillin (30ug)	21.0	25.4	14.3	0.0	2(50.0)	1(25.0)	1(25.0)
Augumentin (10ug)	17.0	15.8	3.8	0.0	0(0.00)	2(50.0)	2(50.0)
Splaxocillin (10ug)	25.5	14.3	17.4	28.0	2(50.0)	2(50.0)	0(0.0)
Ofloxacin (10ug)	23.5	19.0	16.5	25.4	3(75.0)	1(25.0)	0(0.0)
Chloramphenicol (30ug)	22.3	17.5	7.5	1 2.7	2(50.0)	0(0.0)	2(50.0)
Average mean	24.5	19.8	13.3	12.6			
No. of Susceptibility (%)	9(90.0)	6(60.0)	1(10.0)	4(40.0)			
No. of intermediate (%)	1(10.0)	4(40.0)	4(40.0)	0(0.0)			
No. of Resistance (%)	0(0.0)	0.(0.0)	5(50.0)	6(60.0)			

Zones of inhibition ≥ 18 mm (Sensitive), 13-17mm = (Intermediate), ≤ 13 mm (Resistance). S= Sensitivity, I= Intermediate, R= Resistance, spp = specie

3.6. Antimicrobial susceptibility pattern of gram positive bacterial isolated from dumpsite leachate

The antimicrobial susceptibility pattern of gram positive bacteria isolates against the following antibiotics; Gentamycin (30ug), Streptomycin (30ug), Pefloxacin (10ug), Ciprofloxacin (10ug), Cotrimoxazole (30ug), Amoxicillin (30ug), Ampiclox (30ug) as shown in table 5 revealed that *Priestia megaterium* was sensitive to 3 antibiotics (Gentamycin, Pefloxacin and Cotrimoxazole) at 42.9%, intermediate to three antibiotics (Streptomycin, Ciprofloxacin and Amoxicillin) at 42.9% but completely resistance to Ampiclox at 14.3%. In the case of *Staphylococcus* spp., it was also susceptible to 3

antibiotics (Pefloxacin, Ciprofloxacin and Septrin), intermediate to 2 antibiotics (Gentamycin and Streptomycin) at 28.6% and resistant to 2 antibiotics (Amoxicillin and Ampiclox) at 28.6 %.

Generally, both gram positive organisms showed 100% susceptibility to Pefloxacin and Cotrimoxazole. The degree of susceptibility of both gram positive bacteria against all 7 antibiotics showed that both isolates; *Priestia megaterium* and *Staphylococcus* spp. were 3(42.9%) susceptible as shown in table 5.

Table 5 Antimicrobial susceptibility pattern of gram positive bacterial isolated from dumpsite leachate

Antibiotics	Zone of inhibition (mm)		General (%)		
	<i>Priestia Megaterium</i>	<i>Staphylococcus Spp</i>	Sensitive	Intermediate %	Resistance %
Gentamycin (30ug)	20.0	15.8	1(50.0)	1(50.0)	0(0.0)
Streptomycin (30ug)	16.4	14.0	0(0.0)	2(100)	0(0.0)
Pefloxacin (10ug)	25.0	24.8	2(100)	0(0.0)	0(0.0)
Ciprofloxacin (10ug)	17.0	27.5	1(50.0)	1(50.0)	0(0.0)
Cotrimoxazole (30ug)	21.0	20.8	2(100)	0(0.0)	0(0.0)
Amoxacillin (30ug)	14.0	0.0	0(0.0)	1(50.0)	1(50.0)
Ampiclox (30ug)	0.0	0.0	0(0.0)	0(0.0)	2(100)
Average mean	13.2	14.7			
No. of Susceptibility (%)	3(42.9)	3(42.9)			
No. of Intermediate (%)	3(42.9)	2(28.6)			
No. of Resistance (%)	1(14.3)	2(28.6)			

Zones of inhibition \geq 18mm (Sensitive), 13-17mm = (Intermediate), \leq 13mm (Resistance).

4. Discussion of Findings

This present research examined the bacteriological content of leachate concentration in open dumpsite at Gwagwalada FCT - Abuja.

The total bacteria count of leachate concentrate from all site location (4.1×10^5 cfu/ml - 4.8×10^5 cfu/ml) indicates high bacteria load from leachate sample. Preliminary culture, morphological, biochemical and molecular (using DNA extraction, DNA quantification, 16S rRNA Amplification using the 27F: 5'-AGAGTTTGATCMTGGCTCAG-3' and 1492R: 5'-CGGTTACCTTGTTACGACTT-3' primers, sequencing and phylogenetic analysis to confirm bacteria isolates) identification of the bacteria isolates revealed the following bacteria; *Pseudomonas stutzeri*, *Priestia megaterium*, *Enterobacter hormaechei*, *Klebsiella aerogenes*, *Proteus* and *Staphylococcus*. Consequently, among bacteria isolated, *Klebsiella*, *Proteus* and *Staphylococcus* were isolated from all sample site. *Klebsiella* had the highest frequency of occurrence in site 1 (Old Kutunku) at 5.71% and site 2 (Market road) at 8.57% while *Staphylococcus* had the highest frequency of occurrence in site 3 (Phase III) at 8.57%, site 4 (Dupka road) at 8.57% and site 5 (University Kaida road) at 11.43%. Generally, the order of frequency of occurrence shows; *Staphylococcus* > *Klebsiella* > *Proteus* > *Priestia* > *Pseudomonas* and *Enterobacter*. Previous study reported by Arekemase *et al.*, [12] shows that *Enterobacter hormaechei* and *Priestia megaterium* were isolated from cassava peel dumpsite, *Pseudomonas stutzeri* was isolated from municipal waste [16] and from landfill leachate [11]. *Staphylococcus*, *Klebsiella*, *Proteus*, *Pseudomonas* and *Bacillus* species were reported by Obire *et al.*, [13]. This present investigation has revealed various bacteria that are associated with waste biodegradation which is in conformity with Obire *et al.*, [13] and Odeyemi *et al.*, [10]. As waste degrades, this intensifies the toxicity of leachate produced. A comparative study of this result being compare with other researchers shows similar bacteria isolates associated with waste and leachate biohazards as they are known to be potential pathogens [13,10, 4]. This may be linked to disposal of raw human waste/faeces at dumpsite as reported by Odeyemi *et al.*, [10]. This could be a risk factor on public health especially if runoff from this dumpsite leachate percolates into surface or ground water where population drinks from. People who drink from such water are at risk of contacting waterborne disease [4].

The antimicrobial susceptibility pattern of bacterial isolates revealed varying degree of susceptibility to the antibiotics used in screening as reported in table 4 and 5 for Gram negative and positive bacteria respectively. The degree of susceptibility of total gram negative bacteria against all 10 antibiotics showed that *Klebsiella aerogenes* had the highest susceptibility at 90% followed by *Pseudomonas stutzeri* at 60%, followed by *Enterobacter hormaechei* at 40% and lastly *Proteus* spp. at 10% susceptibility (table 4). Generally, both gram positive organisms showed 100% susceptibility to Pefloxacin and Cotrimoxazole while they exhibited 100% resistant to Ampliclox. The degree of susceptibility of both gram positive bacteria against all used antibiotics showed that both isolates; *Priestia megaterium* and *Staphylococcus* spp., were 3(42.9%) susceptible as shown in Table 5. Also, all gram negative bacteria showed 100% susceptibility to Ciprofloxacin. High susceptibility of bacteria isolates to Pefloxacin, Cotrimoxazole and Ciprofloxacin as shown in table 4 and 5, is a good relief since it's an indication of effectiveness [3]. However, the resistance of bacteria isolates to antibiotics as in the cuase of *Priestia megaterium* and *Staphylococcus* spp showing 100% resistance to Ampiclox, might be related to increased usage of a drug [2]. Moreso, it has been established that when bacteria undergo genetic change, it may become resistant to the antibiotics due to the production of enzymes which inactivates or modifies antibiotics [10].

Among the six bacteria isolated, four were gram negative bacteria, this conforms to a report cited by Imron *et al.*, [11], that gram negative bacteria are dominant among bacteria population isolated from leachate.

Bacterial contamination of dumpsite leachate is a great concern to the public health. The location of dumpsite closer to sensitive areas like market place, main roads and residential building (as recorded in this study) are not safe and should be considered a public health problem which needs to be properly addressed.

5. Conclusion

This study revealed the isolation of six bacteria from open dumpsite at Gwagwalada, Old Kutunku. They include: *Pseudomonas stutzeri*, *Priestia megaterium*, *Enterobacter hormaechei*, *Klebsiella aerogenes*, *Proteus* and *Staphylococcus* specie. The health risk assessment of these bacteria are threat to human health if not treated. Hence, the FCT government and the Environmental Agency should see to the restriction of open dumpsite within residential area through educational and awareness program.

Compliance with ethical standards

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Disclosure of Conflict of interest

I declare no conflict of interest.

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