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BACTERIAL DIVERSITY ON SELECTED DUMPSITE IN MADONNA UNIVERSITY, ELELE NIGERIA

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ABSTRACT

Improper waste disposal poses serious environmental and public health risks, as dumpsite serve as reservoirs for diverse microbial populations, including pathogenic bacteria. This study investigated the bacterial diversity of selected dumpsites in Madonna university with the aim of isolating, identifying and comparing the bacterial species present in soil samples collected from three dumpsites (A, B and C). A total of nine soil samples were collected aseptically from the three dumpsites and analyzed using standard microbiological techniques. Total heterotrophic bacterial counts (THBC), bacterial isolation and identification were carried out using conventional culture and biochemical techniques. The THBC ranged from 3.5 x 10^6 to 5.0 × 10^6 CFU/g, indicating substantial bacterial contamination and variation among the bacterial isolates. Dumpsite B consistently recorded the highest bacterial counts, whereas in Dumpsite C the lowest were determined, and differences among sampling sites were evaluated using one way analysis of variance (ANOVA) at $p \leq 0.05$. the study revealed a high diversity of bacteria, with predominant genera including *Escherichia*, *staphylococcus*, *Bacillus*, *pseudomonas*, Proteus specie and *klebsiella*, among the isolated bacteria species, *Bacillus specie* showed the highest frequency of occurrence (34.3%) while *Klebsiella specie* showed the lowest frequency occurrence (6.7%). The antibiotic susceptibility test indicated varying responses among the bacterial isolates. (Bacillus and Staphylococcus species) demonstrated a moderate (33%) susceptibility to (amoxicillin) while (*Escherichia coli, pseudomonas specie*, *Proteus specie* and *klebsiella specie*,) showed about 67% resistance to (gentamycin, zinnacef and amoxicillin). Some even indicated resistance to multiple antibiotics, which symbolizes the occurrence of multidrug-resistance bacterial populations within the environment of the dumpsite. The presence of these enteric pathogens indicates potential environmental contamination both from human and animal wastes, whereas the predominance of *Bacillus* and *Pseudomonas species* reflects their ability to survive under diverse environmental conditions and take part actively in the biodegradation of organic matter. The noticed antibiotic pattern of resistance is of environmental and public health significance as dumpsites may serve as sources of antibiotic-resistant bacteria and resistance determinant. The findings

therefore emphasized the need for proper waste management and continuous environmental monitoring to minimize microbial hazard associated with open dumpsites.

Keywords: Bacterial Diversity, Dumpsites, Bacterial Isolates, Soil Bacteria, Waste Disposal, Antibiotic Sensitivity Pattern, Antimicrobial Resistance, Madonna University.

1 INTRODUCTION

Bacterial diversity refers to the vast variety of bacteria found in different environments, shapes, genetic makeup, metabolic abilities, and ecological roles. Bacteria are among the most abundant and diverse organisms on Earth, occupying nearly every habitat, from soil and water to extreme environments like hot springs and deep-sea vents. Waste disposal has become a major environmental challenge in many developing communities. Dumpsites are common features of urban and semi-urban areas where domestic, industrial, and agricultural wastes are deposited. These sites provide favorable conditions for the proliferation of microorganisms, particularly bacteria, due to the abundance of organic matter and moisture. Bacteria present in dumpsites play essential roles in waste decomposition and nutrient recycling. However, some of these bacteria may be pathogenic, posing risks to human health and the environment. Madonna community, like many semi-urban settlements in Nigeria, relies on open dumping for waste disposal. The absence of sanitary landfill facilities increases the risk of environmental pollution and microbial spread. Investigating the bacterial diversity of a selected dumpsite in Madonna would provide baseline data on microbial composition, potential pathogenic bacteria, and environmental health risks. Such information is valuable for environmental monitoring agencies, public health authorities, and waste management planners.

Solid waste generation has increased tremendously due to rapid urbanization, industrialization, population growth, and changing lifestyles. The indiscriminate disposal of municipal, domestic, industrial, and agricultural wastes has resulted in the establishment of dumpsites in many communities. These dumpsites serve as reservoirs for diverse microorganisms, including bacteria, fungi, viruses and protozoa. Among these microorganisms, bacteria constitute the most abundant and metabolically active group because of their ability to utilize a wide range of organic and inorganic substances present in waste materials.

Dumpsites provide favorable environmental conditions such as moisture, nutrients, and suitable temperature that promote bacterial growth and multiplication. The bacterial communities present in dumpsites are involved in the decomposition of organic matter and nutrient cycling. However, some bacterial species are pathogenic and can pose serious health risks to humans and animals. These pathogenic bacteria may contaminate nearby soil, groundwater, surface water, crops, and the surrounding environment through runoff, wind dispersion, insects, rodents, and human activities.

Dumpsites are rich in biodegradable materials such as food remnants, plant residues, paper, and animal wastes. These materials serve as substrates for hetero-trophic bacteria, resulting in high microbial loads (Oyerinde et al., 2026). Studies have shown that dumpsite soils commonly contain bacterial genera such as Bacillus, Pseudomonas, Escherichia, Staphylococcus, Proteus, Klebsiella, and Enterococcus (Nwachukwu et al., 2010; Olayinka et al., 2015).

The bacterial diversity of dumpsites varies depending on the type of waste deposited, environmental conditions, geographical location, seasonal variations, and waste management practices. Common bacterial genera frequently isolated from dumpsites include Escherichia, Salmonella, Shigella, Staphylococcus, Pseudomonas, Bacillus, Proteus, Klebsiella, and Enterobacter. Some of these bacteria are opportunistic or pathogenic microorganisms capable of causing diseases such as gastroenteritis, typhoid fever, urinary tract infections, wound infections, pneumonia, and septicemia.

In developing countries such as Nigeria, poor waste management practices have contributed significantly to environmental pollution and the spread of infectious diseases. Open dumping remains the most common method waste disposal in many urban and rural communities. These dumpsites often lack proper engineering designs and environmental monitoring, thereby creating ideal habitats for disease causing microorganisms.

Investigating the bacteria diversity of selected dumpsite is essential for understanding the ecological distribution of bacteria and assessing the potential public health risks associated with waste disposal. Such information is valuable for environmental monitoring, waste management planning, disease prevention, and the development of effective environmental sanitation policies.

2 MATERIALS AND METHODS

2.1 Study Area

The research was carried out in Madonna University, Elele Campus, Rivers State, Nigeria. It is located in the South-South geopolitical region of Nigeria. Elele is one of the big towns in Ikwerre Local Government Area of Rivers State, Nigeria. It is a medium-sized town in the Niger Delta Region. It has a population of about 20,620. The distance between Elele and Port Harcourt, the capital of Rivers, is roughly about 42 kilometers (26 miles) distant.

2.2 Research Design

This study adopted a descriptive experimental research design to investigate the bacterial diversity present in selected dumpsites in Madonna University Elele Campus. The design involved systematic collection of soil samples from designated dumpsite locations, laboratory isolation of bacteria, and identification using standard microbiological techniques. Descriptive experimental designs are suitable for studies aimed at determining microbial distribution in environmental samples (Atlas & Bartha, 2009; Prescott et al., 2019).

2.3 Sample Collection

Soil samples were collected aseptically from the top 0–10 cm layer of each dumpsite using sterile spatulas and transferred into sterile sampling bags. Samples were transported immediately to the laboratory for analysis to prevent contamination and changes in microbial composition (Adeleke et al., 2018). Standard procedures were carried out for bacteriological assessments.

2.4 Media Preparation for Bacteriological Investigation

For the bacteriological analysis of pond water samples, standard microbiological media were such as Nutrient agar (NA), MacConkey agar, and *Salmonella-Shigella* agar (SS agar) were utilized, these culture media were prepared according to established protocols, by dissolving the appropriate amounts of powder in distilled water, followed by sterilization through autoclaving at 121°C for 15 minutes. The media were allowed to cool and poured into sterile Petri dishes under aseptic conditions. These media facilitated the isolation and enumeration of bacteria such as *Escherichia coli*, *Salmonella sp.*, and *Vibrio sp.* from the water samples (Ogbu et al., 2020).

2.5 Bacteriological analysis

Serial dilution of the soil sample was performed according the method described by Chukwu et al., (2022), to quantify bacterial populations in the in the soil obtained from selected dumpsites at Madonna University. Briefly 1gram aliquot of each water sample was mixed with 90 mL of sterile saline solution and shaken to dislodge the microbes from the soil particles to achieve a 1:10 dilution. Subsequent dilutions (10^{-1} to 10^{-6}) was prepared by transferring 1 mL of each diluted sample into 9 mL of sterile saline solution. For bacteriological analysis, 0.1 mL of each sample from the serial dilution was aseptically spread on the surface of selective agar media. Nutrient Agar (NA) was used for the enumeration of total bacterial counts, while MacConkey Agar was employed to isolate and quantify coliform bacteria, while *Salmonella-Shigella* Agar was used for detecting enteric pathogens such as *Salmonella* and *Shigella* species. The inoculated plates were incubated at 37°C for 24-48 hours to allow bacterial growth. All plates were prepared in duplicate. After incubation, colonies were counted and recorded as colony-forming units (CFU). Colonies were counted and recorded after incubation period. The different colonies on each plate were isolated, purified and stored on nutrient agar slants for further characterization and identifications.

2.6 Characterization and Identification of isolated bacterial Species

The bacteria isolates obtained were identified based on a combination of colonial, morphological and biochemical tests; these tests were conducted to determine the cultural characteristics of the isolates. The biochemical tests were conducted as described by Arbefeville, (2006) and include; catalase test, oxidase test, glucose test, glucose fermentation tests and hydrolysis of arginine.

2.7 Total Heterotrophic and Fecal Coliform Test

soil samples from the selected dumpsites were tested for the presence of fecal coliforms and heterotrophic bacterial species using the method described by ISO, (2014). The total heterotrophic count and fecal coliform test were assessed and determined on nutrient agar using the pour plate technique. One ml of each serially diluted sample was aseptically inoculated onto various sterile nutrient agar plates in triplicate; the inoculums were evenly distributed on the superficial layer of the media. Immediately, the plates were incubated at 37°C for 24 hours. Thereafter, the distinct colony growth of the isolates that developed were adequately counted using a counting chamber and expressed as colony-forming units per milliliter (CFU/ml) (Abasi 2024).

2.8 Antibiotic Susceptibility Test

Disc diffusion method as described by Haley et al., (2024) was used to determine the susceptibility of the bacterial isolates to selected antibiotics was tested on the Kirby- Bauer agar. The following antibiotic disk were used Augmentin (30µg), gentamicin (10 µg), ofloxacin (5µg), ciprofloxacin (5µg), ceftazidime (30µg), cefixime (30µg), erythromycin (15µg), and tetracycline (30µg). The prepared sterile Mueller Hinton agar was adequately dispensed into sterile petri dishes and allowed to solidify. Thereafter, 0.1ml of the bacteria isolates were streaked on the surface of the well- dried agar plates using a sterilized hockey stick. The multiple antibiotic discs were gently and firmly placed on the agar plates using a sterilized forceps. The plates were incubated at 35-37^0 C for 18-24hours. Zones of clearance or inhibition were observed, measured to the nearest millimeter and recorded accordingly. The zones clarity was interpreted as sensitive, intermediate or resistant for each of the assayed antimicrobial agent, based on the recommended standard (CLSI, 2017). The multiple antibiotic resistance index (MARI) was determined for each bacterial isolate by dividing the number of antibiotics, the isolates were resistant to the total number of antibiotics tested (Adenaike et al., 2016). Multi-Drug Resistant (MDR) bacterial isolates were determined based on the resistance to two antibiotics from different classes (Mandal et al., 2011).

2.9 Method of Data Analysis

Descriptive statistical methods such as mean and percentage distribution were used to analyze data. Identified bacterial species were compared across sampling sites to determine diversity and prevalence (Atlas & Bartha, 2009).

2.10 Ethical Consideration

Ethical approval was obtained from the relevant departmental committee before sample collection. Safety precautions were observed throughout the laboratory procedures to prevent exposure to pathogenic microorganisms. Proper disposal of microbial cultures and contaminated materials was carried out following standard bio-safety guidelines.

3 RESULTS

Table 1: shows the result of mean total viable bacterial count of soil samples from the three dumpsites, including the control site. The total heterotrophic bacterial count ranged from 3.5 x 10^{-5} to 5.0 x 10^{-5} CFU/g. Dumpsite A, recorded the highest Total Heterotrophic Bacterial Count (TVBC) (5.0 x 10^{-5} CFU/mL), In contrast, the control dumpsite had the lowest value for all bacteriological parameters, Overall, the results indicate that bacterial contamination was highest at Dumpsite A, followed by dumpsite B, and dumpsite C while the control exhibited the lowest microbial load, which further confirms the high bacterial population in dumpsite soil due to accumulation of organic waste.

Table 1: Mean Total of Heterotrophic Bacterial Counts of soil samples collected from three Dumpsites in Madonna University, Elele.

Sample location	Dilution factor	No of colonies	CFU/g
Dumpsite point A	10^{-4}	50	5.0×10^6
Dumpsite point B	10^{-4}	42	4.2×10^6
Dumpsite point C	10^{-4}	45	4.5×10^6
Control site	10^{-4}	35	3.5×10^6

Key: CFU/g = Colony Forming Unit per gram

Table 2: Distribution of Bacterial Isolates According to Dumpsites in Madonna University, Elele.

Bacterial Isolates	Dumpsite A	Dumpsite B	Dumpsite C	Total
Escherichia coli	3	4	4	11
Staphylococcus aureus	5	4	6	15
Bacillus spp.	8	7	6	21
Klebsiella spp.	2	2	2	6
Proteus specie	2	3	2	7
Pseudo. Spp.	4	5	3	12
Total	24	25	23	72

Table 3: Morphological and Biochemical Characteristics of bacterial isolates from three selected dumpsites in Madonna University, Elele Campus.

Gram rxn	Shape	Catalase	Coagulase	Motility	Starch hyd.	Citrate	Urease	MR	VP	Spore and hyphae	Dnase	Lip	Gala	Glucose	Malt	Xylose	Lactose	Fructose	Sucrose	Manitol	Galactose	Dextrose	Probable organisms
+ ve	Rods	+	+	-	-	-	-	-	-	**A**	+	-	-	**A**	**A**	**A**	**A**	**AG**	-	**AG**	**A**	**AG**	*Bacillus spp*
- ve	Rods	+	-	-	-	-	-	+	-	-	-	-	-	**A/G**	**A**	**A/G**	**A/G**	**A**	**A**	-	**AG**	**A**	*Pseudomonas spp*
+ ve	Cocci	+	-	+	+	-	-	-	+	±	-	-	-	**A**	**A**	**A**	**A**	**A**	**A**	-	**A**	**A**	*Staphylococcus aureus*
- ve	Rods	+	-	+	+	+	-	-	-	±	+	-	-	**A**	**A**	**A/G**	**A**	**A**	-	-	**AG**	-	*Klebsiella pnemoniae*
- ve	Rods	+	-	-	-	-	-	+	-	±	-	-	-	**A**	**AG**	**A/G**	**A/G**	**A**	**A G**	-	**A**	**A**	*Esherichia coli*
- ve	Rods	+	-	-	+	+	+	+	-	-	-	+	+	**A**	**A**	**A**	**A**	**A**	-	**A**	**A**	-	*Proteus spp*

Key: A = Acid production, G = Gas production, + = Positive, - = Negative reaction, VP = Voges Proskauer, MR = Methyl red,

Tables 2: shows the distribution of bacterial isolates recovered from the three dumpsites in Madonna University, Elele Campus. A total of 74 bacterial isolates were identified, with dumpsite B recording the highest number of isolates (25), followed by dumpsite A (24), while dumpsite C had the lowest (23). *Bacillus spp.* was the most frequently isolated bacterium (21 isolates), whereas *Klebsiella spp*. was the least frequently recovered (5 isolates). The findings indicate that Dumpsite B had a greater level of bacterial contamination than the other dumpsites.

Table 3: shows the gram reaction and biochemical test of bacterial isolates from the three dumpsites. A total of seventy-four (74) bacterial isolates were recovered and presumptively identified as; *Staphylococcus aureus, Bacillus spp., Klebsiella pneumoniae, Proteus spp., Pseudomonas spp. and Escherichia coli.*

Table 4; presents the frequency and percentage occurrence of bacterial isolates recovered from the different dumpsites in Madonna University, Elele Campus, A total of 74 bacterial isolates were identified, with *Bacillus spp.* recording the highest occurrence (24 isolates; 34.3%), followed by *Staphylococcus aureus* (12 isolates; *(*13.3%)) and *Pseudomonas aeruginosa* (15 isolates; 18.0). *Escherichia coli*, and *Proteus spp*. accounted for 15.3%, and 12.3%, respectively, while *Klebsiella*, had the lowest occurrence (6 isolates; 6.7%). Overall, the predominance of enteric and opportunistic bacterial species suggests varying levels of microbial contamination within the dumpsite samples.

Table 4: Percentage Occurrence of Bacterial Isolates from recovered from the three dumpsites in Madonna University Elele Campus.

S/N	Probable Organisms	Number of Occurrence	Percentage of Occurrence
1	*Bacillus spp*	21	34.3%
2	*Pseudomonas spp*	15	18.0%
3	*Staphylococcus spp*	12	13.3%
4	*Escherichia coli*	11	15.3%
5	*Proteus spp*	7	12.3%
6	*Klebsiella pneumon.* Total	6 72	6.7% 100

Table 5; shows the gram reaction of bacterial isolates recovered from the three dumpsites in Madonna University, Elele. From the result obtained, about (47.8%) isolates were gram positive while (52.2%) were gram negatives. The results also indicated that the dumpsites had more gram-negative bacteria than gram positive bacteria which is evidence of fecal or organic contamination.

Table 5: Gram Reaction of Isolates Recovered from the Three Dumpsites

S/N	Gram Reaction	Number of Isolates	Percentage (%)
1	Gram positive	35	47.8
2	Gram negative	39	52.2
3	Total	74	100

Table 6: Antibiotic Susceptibility Test for Gram Positive Bacteria

	SXT	CH	SP	CPX	AM	AU	CN	PEF	OFX	S
Bacillus spp.	30mm	NIL	28mm	28mm	24mm	Nil	16mm	36mm	32mm	Nil
Staphylococcus spp.	30mm	30mm	32mm	32mm	32mm	28mm	24mm	30mm	39mm	24mm

Table 6: shows the antimicrobial susceptibility pattern of the probable bacteria in mm of positive disk with Bacillus specie having the zone of inhibition of 36mm on (PEF) pefloxacin followed by (OFX) tarivid 32mm, (SXT) septrin 30mm, (SP) sparfloxacin 28mm, (CPX) ciprofloxacin 28mm, (AM) amoxicillin 24mm, (CH) 16mm and resistance to (CH)

chloramphenicol, (AU) augmentin and streptomycin. Staphylococcus aureus with the zones of inhibition of 32mm on (SP) sparfloxacin, (CPX) ciprofloxacin, and (AM) amoxicillin, followed by (SXT) septrin 30mm, (CN) gentamycin 30mm, (PEF) pefloxacin 30mm, AU) augmentin 28mm, CN gentamycin 24mm. Staphylococcus showed no resistance to the antibiotics. From the result on Table 7: below shows the antimicrobial susceptibility pattern of the probable bacteria in mm of negative disk with Pseudomonas spp, Proteus species having the highest zone of inhibition of 30mm on (SXT) septrin, all the gram-negative isolates showed resistance to (AM) amoxicillin.

Table 7: Result of Antibiotic Susceptibility Test for Gram's Negative Bacteria.

Organisms	**PEF**	**CN**	**APX**	**Z**	**AM**	**R**	**CPX**	**S**	**SXT**	**E**
Pseudomonas spp.	20mm	Nil	14mm	18mm	Nil	20mm	28mm	20mm	32mm	20mm
Klebsiella spp.	30mm	16mm	28mm	22mm	Nil	24mm	30mm	16mm	30mm	28mm
Escherichia coli	20mm	18mm	14mm	Nil	Nil	18mm	32mm	24mm	28mm	24mm
Proteus spp.	22mm	20mm	18mm	20mm	Nil	20mm	30mm	22mm	32mm	26mm

Table 8: Antibiotics Used and their Different Abbreviations

GRAM NEGATIVE		**GRAM POSITIVE**	
SXT	Septrin	PEF	Pefloaxin
CH	Chloramphenicol	CN	Gentamycin
SP	Sparfloxacin	APX	Ampiclox
CPX	Ciprofloxacin	Z	Zinnacef
AM	Amoxacillin	AM	Amoxacillin
AU	Augmentin	R	Recephin
CN	Gentamycin	CPX	Ciprofloxacin
PEF	Pefloxacin	S	Streptomycin
OFX	Tarivid	SXT	Septrin
S	Streptomycin	E	Erythromycin

4 DISCUSSION

The bacterial diversity of soil collected from three selected dumpsites in Madonna University Elele Campus, revealed that all the dumpsites contained considerable bacterial populations, although the level of contamination differed among the various dumpsites. The Total Heterotrophic Bacterial Count (THBC) ranged from 3.5×10^{-5} CFU/g at dumpsite A to 5.0×10^{-5} CFU/g at dumpsite C. Dumpsite A consistently recorded the highest microbial counts, whereas dumpsite C had the lowest values. These findings indicate that microbial contamination was not evenly distributed across the dumpsites and may have resulted from differences in dumpsite management practices. The disparity in bacterial diversity among the selected dumpsites may be due to variation in waste composition, age of the dumpsites, water content, pH, temperature, and human activities. Dumpsites that receive a larger quantity of biodegradable waste usually support greater microbial diversity than those dominated by inorganic materials. Similar observation was made by Saibu et al., (2023), in a metagenomic studies, where the kind of waste and environmental conditions seriously affects bacterial community make up. The huge bacterial load noticed in the present study supports the view that dumpsites act as crucial reservoirs of microorganisms that fronts the decomposition and recycling of organic matter and thus these microorganisms are highly beneficial because they contribute to nutrient waste break-down and nutrient cycling, the presence of pathogenic species like Escherichia coli, Klebsiella spp. and Staphylococcus aureus is a major public health concern. Exposure to polluted soil, dust, or leachate from poorly managed dumpsites may increase the risk of infectious diseases among waste handlers and nearby residents. Same concern was highlighted in previous studies by Achuba et al., (2026), on dumpsite microbiology and environmental health.

This present research shows that selected dumpsites accommodated a wide diversity of bacterial species, with *Bacillus spp., Staphylococcus spp., Pseudomonas spp., Escherichia coli., Klebsiella spp., Proteus spp.* being among the predominant

isolates. Overall, the predominance of enteric and opportunistic bacterial species suggests varying levels of microbial contamination within the dumpsite samples. The gram reaction of bacterial isolates recovered from the three dumpsites, (47.8%) isolates were gram positive while (52.2%) were gram negatives. The results also indicated that the dumpsites had more gram-negative bacteria than gram positive bacteria which is evidence of fecal or organic contamination. The immerse bacterial diversity noticed can be ascribed to the abundance of biodegradable organic matter, favorable moisture content, and the continuous deposition of household and commercial waste, which provide nutrients that aid microbial growth. Similar findings have been reported in studies of Nigerian dumpsites, where organic-rich waste environments supported a wide range of culturable bacteria Wilcox et al., (2026).

The high occurrence of Bacillus species aligns with the investigation of Pondei et al., (2024), who reported that Bacillus species were among the most frequently isolated bacteria isolated from Yenagoa central dumpsite due to their ability to produce resistant endospores and survive harsh environmental conditions. Moreover, Wilcox et al., (2026) found *Bacillus species* to be common in dumpsite soils in Rivers State, suggesting that they play an important role in the biodegradation of organic wastes.

The isolation of *Escherichia coli* and *Proteus spp* is a major red flag of fecal contamination of the dumpsite, which could be arising from house hold refuge, animal waste and sewage-contaminated materials. Similar observations were made by Achuba et al., (2026). Who isolated the enteric organism from dumpsites in Asaba and indicated their public health significance because they function as source of gastrointestinal infections, the presence of *Staphylococcus spp*. aligns with the investigation of Odum et al., (2020), where *Staphylococcus spp*. was isolated from dump soil in Abraka, Delta state. The isolates are commonly introduced into dumpsites through the activity and unused personal materials. Their occurrence suggests that the dumpsites may serve as reservoirs for opportunistic pathogens that are capable of causing infections, mostly in immune-compromised individuals.

Moreover, in this study, all antibiotic disc diffusion were tested using the disc diffusion method using a separated disk (positive and negative disk), among the strains tested, about 67% were persistent to streptomycin, zinnacef, gentamycin and amoxicillin respectively, while about 33% were susceptible to amoxicillin and this is in line with the report of Adamson et al., (2019). The majority of Bacillus and Staphylococcus species susceptibility to amoxicillin though not commonly expected, portrays that the isolates are likely non-β-lactamases producers or have limited exposure to β-lactam antibiotics, allowing them to retain intrinsic sensitivity to β-lactam drugs, this often occur in environmental strains, such as those from abattoir wastewater and dumpsites in which their exposure to lower antibiotic pressure compared to hospital strains (Verdu-Exposito et al., 2020). Furthermore, other studies report high resistance of these microorganisms to amoxicillin, especially among clinical and food isolates, due to β-lactam production and gene transfer (Isaiah et al., 2025). In this present research, susceptibility indicates possible environmental sensitivity, amoxicillin is still not recommended as a first-line treatment due to widespread resistance and more stable β-lactams such as cloxacillin or amoxicillin-clavulanic acid are preferred. Environmental bacterial strains can be utilized in conducting population-based investigation by identifying the major parts these organisms play in posing health risks to human, animals and in the spread of antibiotic resistance and monitoring a wide range of pollutants in water and soil contaminated with waste.

5 CONCLUSION

Finally, the results obtained from this study aligns with earlier findings that demonstrated that solid waste dumpsites support different bacterial populations consisting of both beneficial decomposer and potentially pathogenic microorganisms. The results highlight the need for proper waste management practices, frequent microbiological supervision and public health interventions to bring down the level of environmental contamination coupled with the spread of disease-causing bacteria.

STATEMENTS ON COMPLIANCE WITH ETHICAL STANDARDS

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Disclosure of conflict of interest

Authors have declared that no competing interest exist.

REFERENCES

[1] Abasi, T. B., Sampson, T., & Aleruchi, O. (2024). Impact of solid waste disposal on the bacteriological quality of soil around hostels of tertiary institution in Port Harcourt, Nigeria. South Asian Journal of Research Microbiology, 18(10), 14-22.

[2] Achuba, I., Onoriasakpobare, F. O., Chukwurah, A. I., & Daniels, A. K. (2026). Microbiology of Waste dump sites in Asaba, Delta State, Nigeria. International Journal of Microbiology and Applied Sciences, 5(1), 111-121.

[3] Adamson, O. O., Adeyemi, M. O., Gbotolorun, O. M., Oduyebo, O.O., Oeniyi O., & Adeyemo, W. L. (2019). Comparison of sensitivity of bacteria isolated in odontogenic infections to ceftriaxone and amoxicillin-clavulanate. African Health Sciences, 19(3), 2414-2420.

[4] Adeleke, R. A., Adepoju, A. G., & Ojo, D. A. (2018). Microbial diversity and public health implications of municipal waste dumpsites in Nigeria. Journal of Environmental Microbiology, 12(3), 45–58.

[5] Atlas, R. M., & Bartha, R. (2009). Microbial Ecology: Fundamentals and Applications (5th ed.). Benjamin Cummings.

[6] Arbefeville, S. S., Timbrook, T.T., & Garner, C. D. (2024). Evolving Strategies in microbe identification-a comprehensive review of biochemical, MALDI-TOF MS and molecular testing methods. Journal of Antimicrobial Chemotherapy, 79 (Suppl. 1), 12-18.

[7] Clinical and Laboratory Standards Institute. (2017). Performance standards for antimicrobial susceptibility testing (27th ed; CLSI supplement M100). Clinical and Laboratory Standards Institute.

[8] Cheesbrough, M. (2006). District laboratory Practice in tropical countries. Part 1, second edition, Pp. 12-17.

[9] Chukwu, L. E., Ogbogu, N., & Eze, C. M. (2022). Bacteriological water quality analysis infresh water aquaculture ponds: A comparative study of membrane filtration and plate count methods. Journal of Environmental Management, 107, 67–73.

[10] International Organization for Standardization. (2014). Water quality – Enumeration of Escherichia coli and Coliform bacteria-Part1: Membrane filtration method for water with low bacterial background flora (ISO Standard No. 9308-1:2014)

[11] Isaiah, D. O., Otokunefor, K., & Agbagwa, O. E. (2025). Multiple antibiotic resistance indexing and molecular identification of Escherichia coli isolated from clinical and non-clinical sources in Port Harcourt Metropolis, Nigeria. Pan African Medical, 51, Article 11.

[12] Nwachukwu, N. C., Orji, F. A., & Ugbogu, O. C. (2010). Health care waste management and microbial assessment of dumpsites in Nigeria. African Journal of Environmental Science and Technology, 4(11), 795–799.

[13] Odum, E. I., Idise, O. E., & Ogogo, D. I. (2020). Multidrug resistant bacteria in dumpsite soils within Abraka, Delta State, Nigeria. FUDMA Journal of Sciences, 4(2), 639–644.

[14] Oyerinde, K. K., & Ogunsola, A. D. (2026). Estimation of municipal solid waste generation trends from selected dumpsite in Ibadan from 2018-2024. LAUTECH Journal of Engineering and Technology, 20(2), 30-39.

[15] Ogbu, F. A., Okenwa, S. O., & Ibeh, A. F. (2020). The role of coliform bacteria as indicators of fecal contamination in aquaculture water quality. Aquaculture Research, 52(2), 88 94.

[16] Pondei, J. O., & Okeke, C. C. (2024). Bacterial isolates of soils of different waste types in Yenagoa Central Solid Waste Dumpsite, Nigeria. Research journal of Biotechnology and Life Science., 4(1), 12–22.

[17] Prescott, L. M., Harley, J. P., & Klein, D. A. (2019). Microbiology (11th ed.). McGraw-Hill Education.

[18] Wilcox, O. A., Wemedo, S. A., Douglas, S. I., & Ugboma, C. J. (2026). Enumeration, Characterization and Identification of Bacteria in Soils of Selected Waste Dumpsites in Rivers State, Nigeria. Microbiology Research international, 14(1),8-16.

[19] Saibu, S., Adebusoye, S. A., Oyetibo, G. O., & Rodrigues, D. F. (2023). Metagenomics analyses of bacterial community structure in selected waste dumpsites in Lagos Metropolis, Nigeria. Frontiers in Environmental Science, 11, Article 130433.

[20] Williams, J. O., & Hskam, K. (2016). Microorganisms associated with dumpsite in Port Harcourt Metropolis, Nigeria. Journal of Ecology and Natural Environment, 8(2), 9-12.