

Enumeration, characterization and identification of bacteria in soils of selected waste dumpsites in Rivers State, Nigeria

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ABSTRACT

Rapid population growth and industrialization have led to increased waste generation, while effective waste management remains a major challenge in Nigeria, where solid wastes are often indiscriminately disposed of. This study investigated the diversity and abundance of bacteria in soils from selected solid waste dump sites in Rivers State, Nigeria. Soil samples were collected monthly from three dump sites and three control locations between May 2023 and April 2024. Samples were analyzed using standard microbiological techniques and cultured on Nutrient Agar, MacConkey Agar, Starch Casein Agar, Salmonella–Shigella Agar, Thiosulfate Citrate Bile Salts Sucrose (TCBS) Agar, and Mannitol Salt Agar. Purified isolates were identified using morphological and biochemical characterization. Mean bacterial counts ranged as follows: total heterotrophic bacteria (THB), $2.9 \pm 1.6 - 8.3 \pm 2.2 \times 10^5$ cfu/g; total coliforms, $4.1 \pm 1.2 - 12.5 \pm 2.4 \times 10^3$ cfu/g; total actinomycetes, $0.6 \pm 0.3 - 3.3 \pm 1.4 \times 10^3$ cfu/g; total *Staphylococcus*, $3.6 \pm 2.1 - 16.1 \pm 1.4 \times 10^3$ cfu/g; total *Salmonella*, $0.1 \pm 0.1 - 2.1 \pm 0.3 \times 10^2$ cfu/g; total *Shigella*, $0.0 \pm 0.0 - 0.9 \pm 0.1 \times 10^2$ cfu/g; and total *Vibrio*, $0.0 \pm 0.0 - 5.5 \pm 0.5 \times 10^2$ cfu/g. No significant difference ($p > 0.05$) was observed in THB populations among the study locations, whereas other bacterial groups showed significant variations ($p < 0.05$) in some locations. Identified bacterial genera included *Rhizobacter*, *Enterobacter*, *Citrobacter*, *Cronobacter*, *Kluyvera*, *Paraburkholderia*, *Serratia*, *Ralstonia*, *Vibrio*, *Aeromonas*, *Erwinia*, *Leclercia*, *Chryseomonas*, *Klebsiella*, *Pseudomonas*, *Salmonella*, *Shigella*, *Bacillus*, *Paenibacillus*, *Staphylococcus*, *Enterococcus*, *Salinococcus*, *Corynebacterium*, *Actinomyces*, *Rathayibacter*, *Microbacterium*, *Zhihengliuella*, *Sinomonas*, *Nesterenkonia*, and *Escherichia coli*. THB counts were highest at the Boskel dumpsite, followed by the Aluu dumpsite, and lowest at the Elijiji dumpsite. *Staphylococcus* spp. were the most prevalent isolates across the sites. The high bacterial load and diversity observed indicate that solid waste dumpsites may serve as reservoirs of potentially pathogenic microorganisms, posing environmental and public health risks to waste workers and nearby residents. These findings highlight the need for improved waste management practices and the siting of dumpsites at safe distances from residential areas to minimize potential health hazards.

Keywords: Bacteria, soil, dumpsites, population, waste.

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INTRODUCTION

Soil is an important natural resource composed of several interconnected components, including inorganic matter, organic matter, moisture, organisms, air, and soil solution (Chandak et al, 2017). Climatic and other abiotic factors influence soil properties and processes (Malik, 2017). However, human activities have continued to disrupt the

natural balance of soil systems. The disposal of wastes and other materials into the soil from various sources has resulted in soil pollution, which alters the microbiological and physicochemical characteristics of the soil (Jayara et al., 2021).

Waste generation is an inevitable consequence of

processes in which materials are utilized. The extraction of raw materials, manufacturing of products, and consumption of goods all generate waste. In recent years, the rate of raw material utilization has increased substantially, leading to a corresponding rise in waste generation. This trend has made conventional waste management practices increasingly challenging, and many communities are unable to effectively manage the volume of waste produced. Rapid industrialization and urbanization have further accelerated population growth, which ultimately contributes to increased waste generation (Douglas et al., 2020).

In many developing countries, the rate at which waste is generated exceeds the capacity for effective management during collection, transportation, and disposal (Mekonnen et al., 2020). Consequently, a large proportion of solid waste is disposed of on land in open dumps. These solid waste disposal sites are often located within or on the outskirts of urban areas. Such sites can significantly impact the surrounding environment, as they may serve as reservoirs for pathogenic microorganisms (Robinson et al., 2025). Open dumpsites therefore represent a major environmental concern, as they contribute to environmental pollution and may lead to illnesses among people living in or near these areas (Odum et al., 2020; Douglas et al., 2020).

Investigating the bacterial populations and diversity present in these waste dumpsites is therefore important for understanding the potential health risks associated with them and for developing strategies to mitigate diseases linked to such environments.

MATERIALS AND METHODS

Study area

The study area comprises Port Harcourt and Aluu in Rivers State, located in the South-South region of Nigeria within the Niger Delta. The area lies approximately 10 m above sea level and falls within latitudes 4°44'N to 4°56'N and longitudes 6°53'E to 7°08'E (Kpalap and Ajoku, 2021). Rivers State is rich in oil and gas resources, and numerous companies operate within the area due to direct or indirect relationships with the oil and gas industry, providing various services to these companies. The population of the area is estimated at 3.79 million people (Obenade et al., 2020; Adeyemo and Akpo, 2024).

The sampling locations consisted of three solid waste dumpsites and three control locations situated 100 m away from each dumpsite. The sampling locations and their coordinates are presented in Table 1.

Table 1. Sampling locations and the coordinates.

Sampling location	Location code	Coordinate
Aluuwaste dump	ARE	4.90702°N, 6.96342°E
Aluucontrol location	BIT	4.90478°N, 6.96352°E
Elijiji waste dump	CPS	4.83965°N, 7.0597°E
Elijiji control location	DUG	4.83994°N, 7.05767°E
Boskel waste dump	EDK	4.85888°N, 7.0821°E
Boskel control location	FIT	4.85861°N, 7.08197°E

Sample collection

Soil samples were collected monthly from May 2023 to April 2024 from three waste dump sites and three control locations using a soil auger at a depth of 0–15 cm. Surface debris was removed from the soil prior to sampling at each location. Control samples were collected from nearby sites located 100 m away from each dump site.

The soil samples were placed in sterile polythene bags, stored in ice-packed containers, and transported to the Microbiology Laboratory of Rivers State University for analysis.

Enumeration of bacterial population

The serial dilution method described by Douglas et al.

(2020) was used for the cultivation and enumeration of bacteria in the soil samples. One gram (1 g) of each soil sample was transferred into 9 ml of sterile normal saline to obtain a 10⁻¹ dilution. The mixture was thoroughly shaken to ensure proper mixing. One milliliter (1.0 ml) of the 10⁻¹ dilution was then transferred into 9 ml of sterile normal saline to obtain a 10⁻² dilution. Serial dilutions were subsequently prepared up to 10⁻⁴.

Aliquots of 0.1 ml from the selected dilutions were inoculated in duplicate onto sterilized media plates, including Nutrient Agar (NA), MacConkey Agar (MCA), Starch Casein Agar (SCA), Salmonella–Shigella Agar (SSA), Thiosulfate Citrate Bile Salts Sucrose Agar (TCBS), and Mannitol Salt Agar (MSA). A flame-sterilized glass spreader was used to evenly spread the inoculum on the surface of the media.

The inoculated plates were incubated at 37 °C for 24 hours. After incubation, plates containing between 30 and

300 colonies were counted, and the colony-forming units per gram (cfu/g) of soil were calculated (Odum et al., 2025).

Characterization and identification of bacterial isolates

Developed colonies were subcultured onto appropriate media using the streak plate technique until pure isolates were obtained. The purified isolates were subjected to Gram staining and a series of biochemical tests including motility, catalase, oxidase, indole, citrate utilization, methyl red, Voges–Proskauer, urease, salt tolerance, nitrate reduction, sulphate reduction, starch hydrolysis, and sugar fermentation tests for characterization (Cheesebrough, 2006).

Identification of the bacterial isolates was carried out using reference descriptions in *Bergey's Manual of Determinative Bacteriology* (Holt, 1994) and the Advanced Bacteriological Identification System (ABIS).

Statistical analysis

Bacterial counts were recorded using Microsoft Excel (Version 16). The mean and standard deviation of bacterial counts were calculated using SPSS version 27. Differences between means were analyzed using two-way analysis of variance (ANOVA). Means showing significant differences were separated using Duncan's

Multiple Range Test at a significance level of $p \leq 0.05$.

RESULTS

Figure 1 shows the mean Total Heterotrophic Bacterial (THB) population in soil samples from the different sampling locations. The THB counts at the Aluu dumpsite ranged from $3.0 \pm 1.4 \times 10^5$ to $16.7 \pm 6.1 \times 10^5$ cfu/g. At the Elijiji dumpsite, THB counts ranged from $1.9 \pm 0.4 \times 10^5$ to $11.1 \pm 6.1 \times 10^5$ cfu/g. The monthly mean THB population at the Boskel dumpsite ranged from $1.7 \pm 0.9 \times 10^5$ to $14.1 \pm 2.9 \times 10^5$ cfu/g. At the Aluu control location, THB counts ranged from $1.0 \pm 0.1 \times 10^5$ to $5.5 \pm 0.9 \times 10^5$ cfu/g. The THB population at the Elijiji control location ranged from $7.0 \pm 0.4 \times 10^4$ to $10.6 \pm 4.8 \times 10^5$ cfu/g, while the Boskel control location recorded monthly mean THB counts ranging from $1.1 \pm 1.3 \times 10^5$ to $9.0 \pm 2.9 \times 10^5$ cfu/g.

Figure 2 presents the mean total coliform population in soil samples from the different sampling locations. At the Aluu dumpsite, total coliform counts ranged from $3.5 \pm 0.1 \times 10^3$ to $26.3 \pm 2.1 \times 10^3$ cfu/g. Counts at the Elijiji dumpsite ranged from $2.6 \pm 0.8 \times 10^3$ to $28.6 \pm 0.3 \times 10^3$ cfu/g. At the Boskel dumpsite, the population ranged from 2.8×10^3 to 23.2×10^3 cfu/g. Total coliform counts at the Aluu control location ranged from $2.0 \pm 0.2 \times 10^2$ to $19.3 \pm 1.3 \times 10^3$ cfu/g. At the Elijiji control location, the counts ranged from $1.2 \pm 0.3 \times 10^3$ to $15.3 \pm 2.7 \times 10^3$ cfu/g, while the Boskel control location recorded monthly mean counts ranging from $7.0 \pm 0.4 \times 10^2$ to $12.4 \pm 0.6 \times 10^3$ cfu/g.

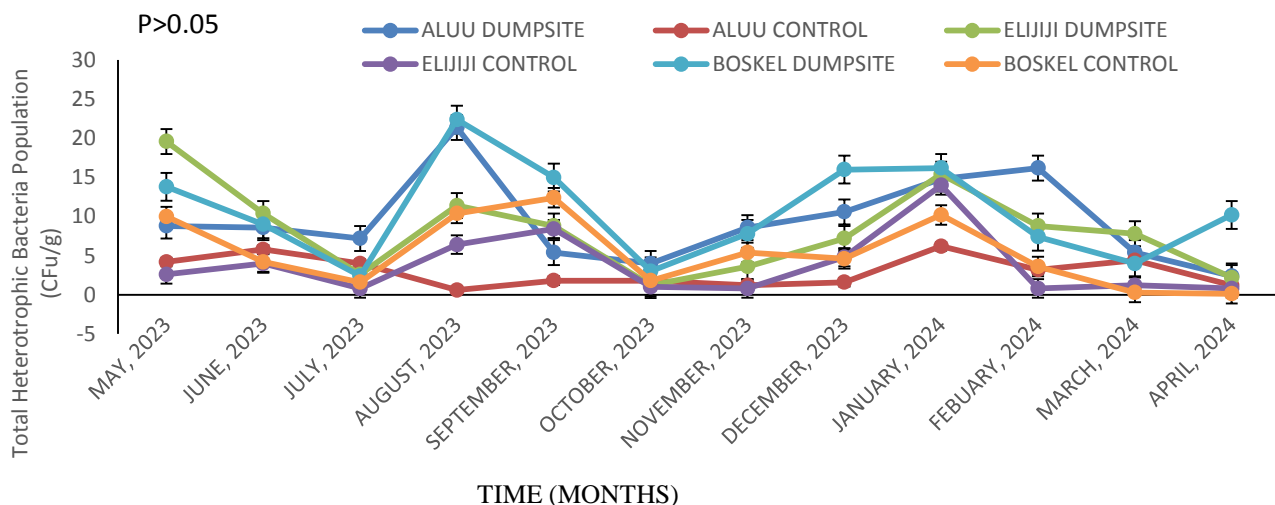


Figure 1. Mean total heterotrophic bacterial population in soil samples from different sampling locations as a function of time.

Figure 3 presents the mean actinomycete population in soil samples from the different sampling locations. Actinomycete counts at the Aluu dumpsite ranged from

$3.0 \pm 0.1 \times 10^2$ to $12.0 \pm 0.8 \times 10^3$ cfu/g. At the Elijiji dumpsite, counts ranged from $3.0 \pm 0.1 \times 10^2$ to $6.0 \pm 0.8 \times 10^3$ cfu/g. The monthly mean actinomycete counts at

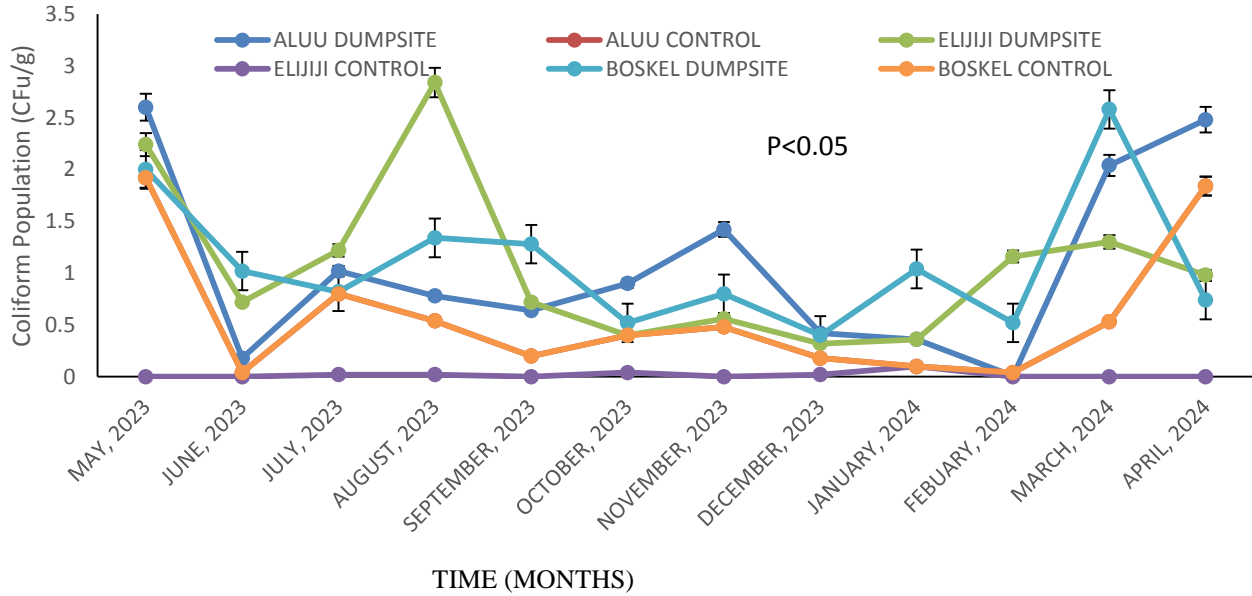


Figure 2. Mean total coliform population in soil samples from different sampling locations.

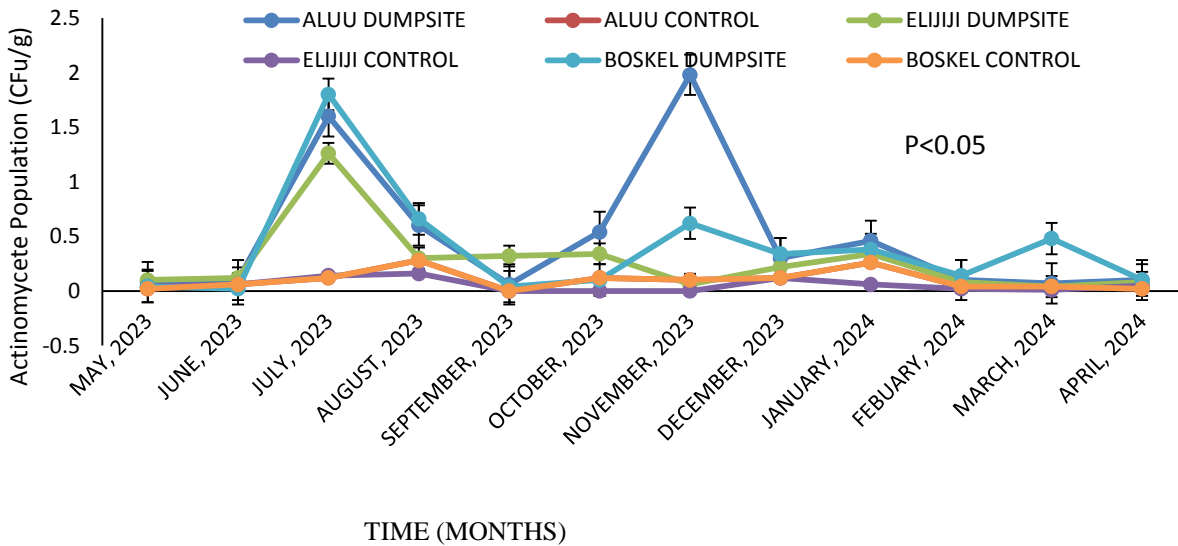


Figure 3. Mean actinomycete population in soil samples from different sampling locations.

the Boskel dumpsite ranged from $2.0 \pm 0.0 \times 10^2$ to $14.7 \pm 1.9 \times 10^3$ cfu/g. At the Aluu control location, the monthly mean ranged from $2.0 \pm 0.1 \times 10^2$ to $5.0 \pm 0.4 \times 10^3$ cfu/g. The Elijiiji control location recorded counts ranging from 5.0×10^1 to $2.5 \pm 0.2 \times 10^3$ cfu/g, while the Boskel control location had actinomycete populations ranging from $8.0 \pm 0.1 \times 10^2$ to $6.0 \pm 0.8 \times 10^3$ cfu/g.

Figure 4 presents the mean Salmonella population in soil samples from the different sampling locations. At the Aluu dumpsite, monthly mean Salmonella counts ranged from 2.0×10^1 to $2.7 \pm 0.9 \times 10^2$ cfu/g. The Salmonella

population at the Elijiiji dumpsite ranged from $3.0 \pm 0.1 \times 10^1$ to $1.3 \pm 0.4 \times 10^2$ cfu/g. At the Boskel dumpsite, monthly mean counts ranged from $1.0 \pm 0.1 \times 10^1$ to $7.7 \pm 4.4 \times 10^2$ cfu/g. At the Aluu control location, monthly mean Salmonella counts ranged from $7.0 \pm 0.4 \times 10^1$ to $2.9 \pm 1.6 \times 10^2$ cfu/g. The Elijiiji control location recorded counts ranging from $1.0 \pm 0.1 \times 10^2$ to $2.0 \pm 0.3 \times 10^2$ cfu/g, while the Boskel control location ranged from $1.0 \pm 0.1 \times 10^1$ to $1.1 \pm 0.1 \times 10^2$ cfu/g.

Figure 5 presents the mean Shigella population in soil samples from the different sampling locations. At the Aluu

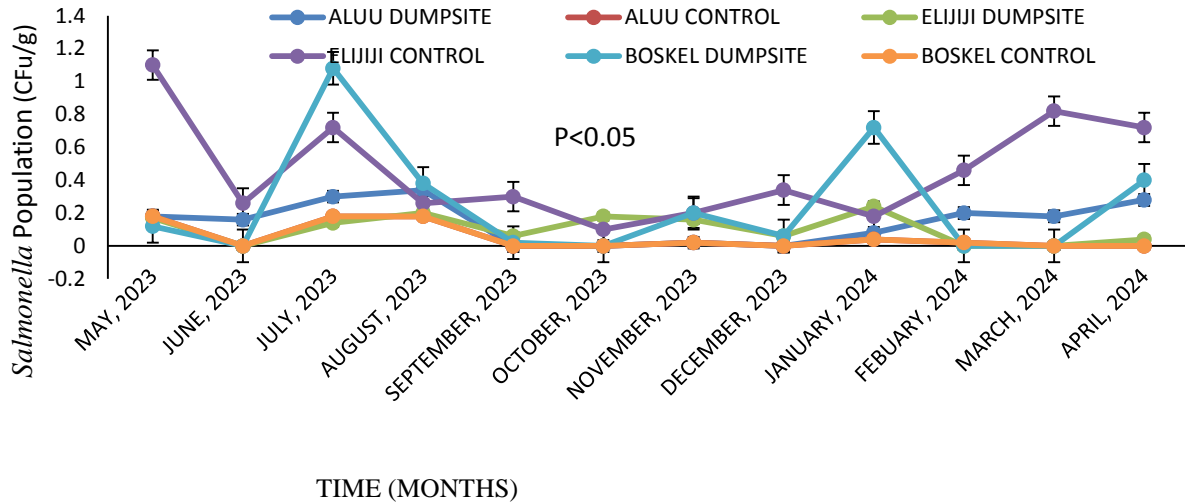


Figure 4. Mean *Salmonella* population in soil samples from different sampling locations.

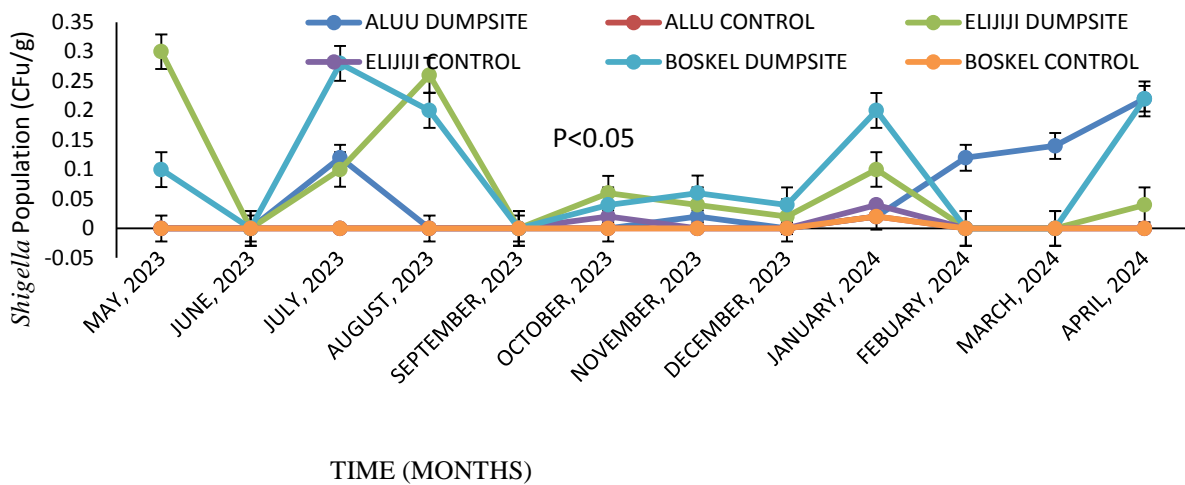


Figure 5. Mean *Shigella* population in soil samples from different sampling locations.

dumpsite, monthly mean counts ranged from $1.0 \pm 0.1 \times 10^2$ to $8.0 \pm 1.4 \times 10^2$ cfu/g. At the Elijiji dumpsite, counts ranged from $1.5 \pm 0.1 \times 10^1$ to $5.0 \pm 2.1 \times 10^2$ cfu/g. The Boskel dumpsite recorded monthly mean counts ranging from 1.9×10^1 to $17.0 \pm 0.3 \times 10^2$ cfu/g. *Shigella* spp. were detected at the Aluu control location only in January, with a monthly mean of $1.0 \pm 0.1 \times 10^2$ cfu/g. At the Elijiji control location, monthly mean counts ranged from $1.5 \pm 0.1 \times 10^1$ to $5.0 \pm 0.7 \times 10^2$ cfu/g. No *Shigella* growth was observed at the Boskel control location throughout the study period.

Figure 6 presents the mean *Vibrio* population in soil samples from the different sampling locations. The *Vibrio* population in soil samples from the Aluu dumpsite ranged from $1.0 \pm 1.0 \times 10^2$ to $12.0 \pm 1.1 \times 10^2$ cfu/g. At the Elijiji

dumpsite, monthly mean counts ranged from $1.0 \pm 0.1 \times 10^2$ to $24.0 \pm 2.6 \times 10^2$ cfu/g. At the Boskel dumpsite, counts ranged from $2.0 \pm 0.3 \times 10^2$ to $12.0 \pm 0.2 \times 10^2$ cfu/g. No *Vibrio* growth was detected at any of the control locations during the study period.

Figure 7 presents the mean *Staphylococcus* population in soil samples from the different sampling locations. At the Aluu dumpsite, monthly mean counts ranged from $1.0 \pm 0.1 \times 10^2$ to $7.4 \pm 1.4 \times 10^3$ cfu/g. At the Elijiji dumpsite, the population ranged from $3.0 \pm 0.2 \times 10^2$ to $5.8 \pm 0.4 \times 10^3$ cfu/g. The Boskel dumpsite recorded monthly mean counts ranging from $1.0 \pm 0.1 \times 10^2$ to $6.5 \pm 4.9 \times 10^3$ cfu/g. At the Aluu control location, monthly mean counts ranged from $5.0 \pm 0.8 \times 10^2$ to $2.9 \pm 2.2 \times 10^3$ cfu/g. The Elijiji control location recorded counts ranging from

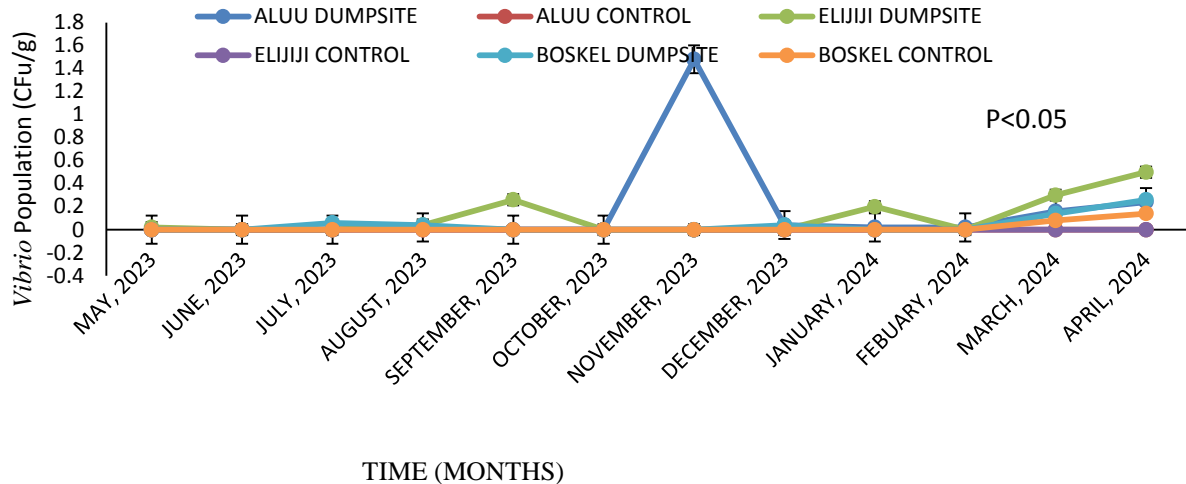


Figure 6. Mean *Vibrio* population in soil samples from different sampling locations.

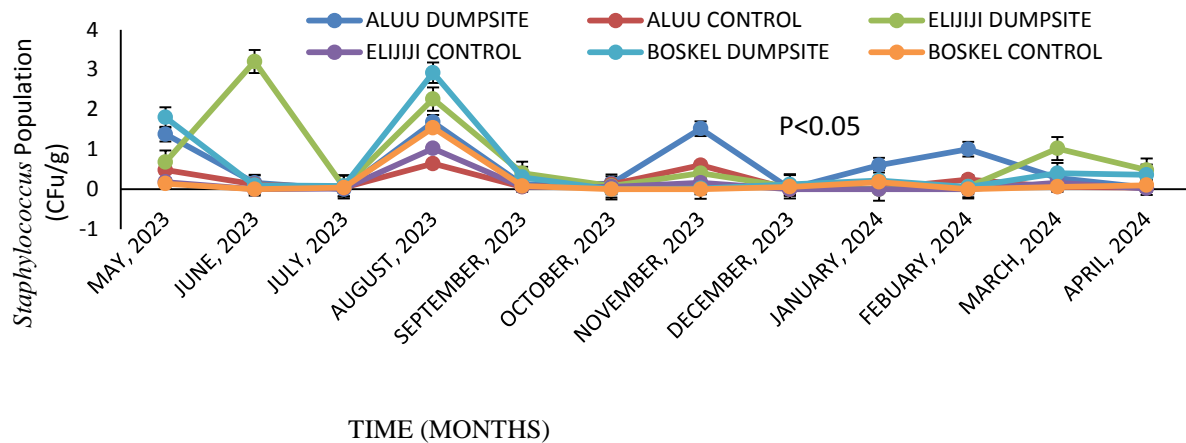


Figure 7. Mean *Staphylococcus* population in soil samples from different sampling locations.

$1.0 \pm 0.1 \times 10^2$ to $3.7 \pm 3.1 \times 10^3$ cfu/g, while the Boskel control location ranged from $2.0 \pm 0.2 \times 10^2$ to $4.1 \pm 3.4 \times 10^3$ cfu/g.

Bacterial types isolated during the study

A total of 496 bacterial isolates were recovered from soil samples collected from the sampling locations during the study. Gram reaction and microscopic examination of the pure cultures revealed that 56.25% of the isolates were Gram-negative, while 43.75% were Gram-positive. Rod-shaped bacteria were the predominant cell morphology among the isolates, while the remaining isolates were cocci.

The bacterial isolates belonged to thirty (30) genera. The identified bacteria from the soil samples of the dumpsites and control locations included *Rhizobacter* spp., *Enterobacter* spp., *Citrobacter* spp., *Cronobacter*

spp., *Kluyvera* spp., *Paraburkholderia* spp., *Serratia* spp., *Ralstonia* spp., *Vibrio* spp., *Aeromonas* spp., *Erwinia* spp., *Leclercia* spp., *Chryseomonas* spp., *Klebsiella* spp., *Pseudomonas* spp., *Salmonella* spp., *Shigella* spp., *Bacillus* spp., *Paenibacillus* spp., *Staphylococcus* spp., *Enterococcus* spp., *Salinococcus* spp., *Corynebacterium* spp., *Actinomyces* spp., *Rathayibacter* spp., *Microbacterium* spp., *Zhihengliuella* spp., *Sinomonas* spp., *Nesterenkonia* spp., and *Escherichia coli* (Table 2).

The actinomycetes (filamentous bacteria) isolated during the study included *Actinomyces* spp., *Nesterenkonia* spp., *Rathayibacter* spp., *Sinomonas* spp., *Zhihengliuella* spp., and *Microbacterium* spp.

DISCUSSION

The mean bacterial counts in the soils from the waste dumpsites and the control locations were generally high,

Table 2. Percentage occurrence of the bacteria identified.

Bacteria	Percentage occurrence
<i>Staphylococcus</i> spp	15.3%
<i>Escherichia coli</i>	11.49%
<i>Bacillus</i> spp	10.08%
<i>Pseudomonas</i> spp	7.06%
<i>Vibrio</i> spp	5.65%
<i>Kluyvera</i> spp	5.65%
<i>Shigella</i> spp	4.64%
<i>Klebsiella</i> spp	4.44%
<i>Sinomonas</i> spp	4.44%
<i>Salmonella</i> spp	4.23%
<i>Nesterenkonia</i> spp	3.63%
<i>Rhizobacterdauci</i>	3.43%
<i>Paenibacillus</i> spp	3.02%
<i>Rathayibacter</i> spp	2.42%
<i>Actinomyces</i> spp	2.22%
<i>Cronobacter</i> spp	2.22%
<i>Chryseomonas</i> spp	2.02%
<i>Serratia</i> spp	1.61%
<i>Enterococcus</i> spp	1.41%
<i>Citrobacter</i> spp	1.21%
<i>Enterobacter</i> spp	1.01%
<i>Erwinia</i> spp	0.40%
<i>Leclercia</i> spp	0.40%
<i>Paraburkholderia</i> spp	0.40%
<i>Microbacterium</i> spp	0.40%
<i>Zhihengliuella</i> spp	0.40%
<i>Aeromonas</i> spp	0.22%
<i>Ralstonia</i> spp	0.20%
<i>Corynebacterium</i> spp	0.20%
<i>Salinococcus</i> spp	0.20%

although the populations were lower at the control sites than at the dumpsites. The highest mean Total Heterotrophic Bacterial (THB) population was observed at the Boskel dumpsite, followed by the Aluu dumpsite, while the Elijiji dumpsite recorded the lowest counts. The higher bacterial populations observed at the Boskel and Aluu dumpsites may be attributed to the composition of wastes present at these locations. These sites possibly contained higher proportions of household and organic wastes, which provide nutrients that enhance microbial growth (Douglas et al., 2020; Pondei and Okeke, 2024).

In contrast, bacterial populations at the control locations were lower than those observed at the dumpsites, possibly because wastes were absent and fewer nutrients were available to support microbial proliferation. This finding is consistent with the report of Omoigui and Onyeibor (2019), who also observed lower bacterial populations at control locations compared with dumpsites.

The THB counts recorded in this study ($2.9 \pm 1.6 - 8.3 \pm 2.2 \times 10^5$ cfu/g) were lower than those reported in some previous studies. For example, Williams and Hakam (2016) in Port Harcourt, Nigeria reported THB counts ranging from 2.4×10^7 to 1.2×10^8 cfu/g, while Wemedo et al. (2020), also in Port Harcourt, reported counts

ranging from $9.4 \pm 4.39 - 22.4 \pm 5.78 \times 10^5$ cfu/g. Similarly, Kapali et al. (2023) in India reported THB counts ranging from 1.2×10^8 to 2.8×10^8 cfu/g from soil samples. However, lower counts than those observed in the present study were reported by Eghomwanre et al. (2019) in Benin City, Nigeria, who recorded THB counts of $2.8 \times 10^4 - 6.4 \times 10^4$ cfu/g from dumpsite soils.

Variations in bacterial counts between this study and earlier studies may be attributed to differences in environmental conditions, types of waste deposited, and other ecological factors at the sampling locations (Obot et al., 2024). Differences in physicochemical characteristics of the soils, the proportion of organic materials present, and the levels of contamination may also contribute to these variations (Enerijiofi and Ekhaise, 2019).

Different bacterial species were isolated from both the dumpsite and control soil samples; however, a greater diversity and abundance of bacteria were observed in the dumpsite soils, indicating that these locations were more contaminated than the control sites. This observation agrees with the findings of Nyandjou et al. (2018), who reported higher bacterial populations in dumpsite soils compared with control locations.

The wide variety of organisms isolated from the dumpsites suggests a high level of contamination of the

soils. The presence of organisms such as *Escherichia coli*, *Shigella* spp., *Salmonella* spp., *Vibrio* spp., *Staphylococcus* spp., *Klebsiella* spp., *Enterobacter* spp., and *Citrobacter* spp. indicates significant microbial contamination of the dumpsite soils. The isolation of these bacteria suggests the presence of faecal contamination at the dumpsites. Furthermore, the presence of *Bacillus* spp., which are spore-forming bacteria capable of contaminating food and causing food poisoning and other diseases, represents a potential threat to public health (Haque et al., 2022).

The diversity of organisms isolated in this study indicates that dumpsites provide favorable environments that support the survival and proliferation of a wide range of microorganisms. The potential pathogenic organisms isolated from the soils may result from faecal contamination associated with domestic wastes deposited at the dumpsites. These pathogens may cause infections such as dysentery, typhoid fever, gastroenteritis, and urinary tract infections (Obueh et al., 2024).

Some pathogenic bacteria observed in this study, including *Staphylococcus* spp., *Escherichia coli*, *Shigella* spp., *Salmonella* spp., *Vibrio* spp., and *Klebsiella* spp., were isolated from all dumpsites, although their distribution varied among the locations. The Aluu dumpsite had the highest diversity of bacterial species, while the Elijiji dumpsite had the lowest. Dumpsites in Rivers State, as well as in many other parts of Nigeria and developing countries, are often located close to residential communities. The presence of these organisms at such locations represents a potential environmental hazard and constitutes a health risk to waste workers at the dumpsites as well as residents living in nearby communities (Kasarawa et al., 2020).

Some of the bacterial species identified in this study have also been reported in previous investigations. Wemedo et al. (2020) isolated *Bacillus* spp., *Pseudomonas* spp., *Staphylococcus* spp., *Escherichia coli*, and *Raoultella* spp. from soil samples collected from active dumpsites in Port Harcourt, Nigeria. Similarly, Kasarawa et al. (2020) reported the presence of *Staphylococcus* spp. and *Bacillus* spp. in dumpsite soils in Sokoto, Nigeria. Douglas et al. (2020) isolated *Bacillus*, *Pseudomonas*, *Klebsiella*, *Staphylococcus*, *Enterobacter*, and *Escherichia coli* from dumpsite soils, while Emmanuel-Akerele and Peter (2021) reported the presence of *Escherichia coli*, *Klebsiella* spp., *Salmonella* spp., *Enterobacter* spp., and *Pseudomonas* spp. in soil samples from dumpsites in Lagos, Nigeria.

The percentage occurrence of bacterial isolates in this study differed from the findings of Obueh et al. (2024), who reported the following percentages: *Bacillus cereus* (22.4%), *Escherichia coli* (12.2%), *Enterococcus* spp. (12.2%), *Staphylococcus aureus* (10.2%), *Pseudomonas aeruginosa* (8.2%), *Streptococcus* spp. (8.2%), and *Corynebacterium* spp. (8.2%). Differences in the frequency of occurrence of bacterial isolates may be

attributed to variations in sample size, environmental conditions, geographical location, and the types of wastes present at the dumpsites (Oni et al., 2021). Additionally, human and animal activities at the dumpsites, including the disposal of domestic waste and sewage, may contribute to increased nutrient availability, thereby supporting microbial growth and proliferation.

CONCLUSION

This study revealed that the mean bacterial counts in soils from the waste dumpsites were generally high. The annual mean Total Heterotrophic Bacterial (THB) counts were highest at the Boskel dumpsite ($8.3 \pm 2.6 \times 10^5$ cfu/g), followed by the Aluu dumpsite ($7.5 \pm 3.1 \times 10^5$ cfu/g), while the Elijiji dumpsite recorded the lowest counts ($5.8 \pm 1.6 \times 10^5$ cfu/g). The bacterial isolates identified in this study indicate that dumpsites harbor a wide variety of microorganisms, some of which may be pathogenic. The diversity and abundance of these bacteria suggest a high level of contamination of dumpsite soils.

The high bacterial populations observed at the waste dumpsites, particularly the presence of *Escherichia coli*, *Staphylococcus* spp., *Salmonella* spp., *Shigella* spp., *Vibrio* spp., and *Klebsiella* spp., may contribute to environmental pollution and pose potential health risks. These microorganisms constitute a hazard to waste workers at the dumpsites as well as residents living in nearby communities, thereby representing a significant public health concern.

Therefore, it is recommended that waste dumpsites be properly located at safe distances from residential areas. In addition, waste management authorities should implement effective waste management practices to reduce environmental contamination and associated health risks.

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