Microbiological and Physicochemical Characterization of Soil Samples from Dumpsites in Lagos, Nigeria

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Abstract

This study investigates the microbiological and physicochemical properties of soil samples collected from various dumpsites and corresponding garden controls in Lagos, Nigeria. Soil samples from UNILAG, Surulere, Ojota, and Oke Afa, alongside control samples, were analyzed for bacterial, coliform, and fungal populations, as well as the presence and identity of pathogenic microorganisms. Bacterial counts ranged from 4.00×10^{12} to 8.35×10^{12} CFU/mL, while total coliform counts varied between 2.30×10^7 and 3.67×10^7 CFU/mL. Fungal counts ranged from 1.12×10^9 to 3.24×10^9 CFU/mL, with Ojota showing the highest fungal load. Biochemical tests and Gram staining revealed the presence of various bacterial genera including *Escherichia coli*, *Bacillus* spp., *Klebsiella pneumoniae*, and *Pseudomonas* spp., indicating potential health and environmental risks. Fungal species such as *Aspergillus niger*, *Penicillium* spp., and *Rhizopus* spp. were also isolated. Soil pH levels ranged from moderately acidic (5.2) to near-neutral (6.9). The findings suggest that dumpsite soils harbor higher microbial loads and more diverse populations compared to control samples, underscoring the impact of anthropogenic waste disposal on soil microbial ecology and potential public health implications.

Keywords: Soil microbiology, dumpsites, coliform bacteria, waste pollution, public health

Introduction

Soil is a dynamic ecosystem that harbours a diverse assemblage of microorganisms, including bacteria, fungi, and protozoa, which play essential roles in nutrient cycling, organic matter decomposition, and the maintenance of soil fertility [1–2]. Numerous studies have shown that anthropogenic activities such as indiscriminate waste disposal, industrial effluents, and urban pollution significantly disrupt soil microbial communities, often resulting in increased microbial loads and the introduction of pathogenic organisms [3–4].

Urban dumpsites, particularly in developing countries, have been widely reported as major repositories of municipal solid waste. In Nigeria, inefficient waste management practices have contributed to environmental degradation and raised serious public health concerns, especially in densely populated urban centres such as Lagos [5–6]. Previous investigations have demonstrated that refuse dumpsites contain complex mixtures of biodegradable organic matter, plastics, metals, and other contaminants that alter soil physicochemical properties, including pH, moisture content, and nutrient availability, thereby influencing microbial abundance and diversity [7–8].

Several studies have documented the occurrence of pathogenic bacteria such as *Escherichia coli*, *Salmonella* spp., and *Klebsiella pneumoniae* in waste-contaminated soils, establishing a clear relationship between waste accumulation and microbial health risks [9–10]. Similarly, fungal genera such as *Aspergillus* and *Penicillium* have frequently been isolated from dumpsite soils, with some species known to produce harmful mycotoxins [11–12]. While these studies provide valuable insights, most have focused on single locations or relied primarily on culture-based identification methods, with limited integration of physicochemical parameters and molecular characterization.

The novelty of this study lies in its comparative assessment of multiple metropolitan locations within Lagos, the integration of physicochemical analysis with both conventional and molecular microbial identification methods, and the inclusion of garden soils as controls. This approach provides a more comprehensive understanding of the environmental and public health risks associated with urban waste dumping and offers data that may support effective remediation strategies and evidence-based policy formulation [13–14].

The aim of this study was to assess the microbiological quality and physicochemical characteristics of soils from selected urban dumpsites in Lagos, Nigeria. The specific objectives were to (i) determine bacterial and fungal loads in dumpsite and control soils, (ii) identify bacterial and fungal isolates using cultural, biochemical, and molecular techniques, and (iii) evaluate the influence of soil physicochemical properties, particularly pH, on microbial distribution.

Experimental

Study Area

The study was conducted in Lagos State, southwestern Nigeria (latitude ~6.45–6.65°N, longitude ~3.20–3.45°E), a highly urbanized coastal city characterized by a tropical wet climate, with mean annual temperatures of 26–30 °C and average annual rainfall of 1,500–2,000 mm. Four metropolitan locations with active or long-standing refuse dumpsites were selected:

1. UNILAG (Akoka, Mainland Lagos) – a university environment with moderate vehicular traffic and human activity, surrounded by academic buildings and hostels.

2. Surulere – a densely populated residential and commercial area with heavy human traffic and indiscriminate waste disposal.

3. Ojota – a major transport hub with intense vehicular emissions, commercial activities, and mixed municipal waste accumulation.

4. Oke Afa (Isolo axis) – a peri-urban residential area with informal dumpsites receiving domestic and market waste.

Each dumpsite was paired with a nearby uncontaminated garden soil (approximately 50–100 m away from the dumpsite and not exposed to visible waste disposal) which served as the control.

Environmental Characteristics of the Sampling Sites

All dumpsites contained heterogeneous municipal solid waste comprising decomposing organic matter, food residues, plastics, paper, metals, and textile materials. The soils were predominantly sandy-loam to loamy in texture, visibly darkened at dumpsites due to organic matter accumulation, and moderately moist at the time of sampling. Control garden soils were vegetated, free from visible waste, and showed lighter coloration with minimal anthropogenic disturbance.

Sample Collection

Soil samples were collected during the dry season to minimize moisture-related variability. At each site, samples were obtained from the topsoil layer (0–15 cm depth)**,** which represents the biologically active zone and is most affected by waste deposition.

Using a sterilized soil auger, five subsamples were collected randomly within a 5 m radius at each location and pooled to form a composite sample. Approximately 500 g of soil was obtained per composite sample. The samples were placed into sterile, labelled polyethylene bags**,** sealed, and transported to the laboratory in an ice-packed container. All samples were processed within 24 hours of collection.

Sample codes were assigned as follows:

- SS I: UNILAG dumpsite
- SS II: Surulere dumpsite
- SS III: Ojota dumpsite
- SS IV: Oke Afa dumpsite
- SS CI: UNILAG control soil
- SS CII: Surulere control soil

Sample Preparation

In the laboratory, soil samples were air-dried at room temperature, gently crushed using a sterile mortar and pestle, and sieved through a 2-mm mesh to remove stones and debris. Portions of the processed soil were used immediately for microbiological analysis, while subsamples were stored at 4 °C for physicochemical analysis.

Experimental Design

A completely randomized laboratory design was employed. All analyses were conducted in triplicate to ensure reproducibility. Microbial enumeration, physicochemical assessment, and microbial identification were carried out under standardized laboratory conditions.

Microbial Enumeration

Total Bacterial and Coliform Count

One gram of soil was aseptically suspended in 9 mL of sterile distilled water and serially diluted. Aliquots were plated using the pour-plate technique. Nutrient Agar (NA) was used for total heterotrophic bacteria, while MacConkey Agar was used for total coliforms. Plates were incubated at 37 °C for 24–48 hours, after which colonies were counted and expressed as colony-forming units per milliliter (CFU/mL).

Fungal Count

Fungal enumeration was performed on Potato Dextrose Agar (PDA) supplemented with chloramphenicol. Plates were incubated at 28 °C for 3–5 days, and fungal colonies were counted and recorded as CFU/mL.

Physicochemical Analysis

Soil pH was determined using a calibrated digital pH meter. A soil–distilled water suspension was prepared in a 1:2.5 (w/v) ratio, stirred thoroughly, and allowed to equilibrate before measurement following standard protocols.

Isolation and Characterization of Microorganisms

Cultural and Morphological Characterization

Distinct colonies were purified by repeated subculturing. Colony characteristics such as color, shape, elevation, and margins were recorded.

Gram Staining

Bacterial isolates were Gram-stained and examined microscopically at ×1000 magnification to determine cell morphology and Gram reaction.

Biochemical Characterization

Bacterial isolates were subjected to standard biochemical tests including Indole, Methyl Red, Voges-Proskauer, Citrate utilization, Catalase, Oxidase, Urease, Starch hydrolysis, Nitrate reduction, Motility, Gelatin hydrolysis, and Sugar fermentation tests. Identification was based on Bergey's Manual of Determinative Bacteriology.

Fungal Identification

Fungi were identified using macroscopic colony features and microscopic examination following lactophenol cotton blue staining. Identification was based on hyphal structure, spore morphology, and conidial arrangement using standard taxonomic keys. Identified genera included *Aspergillus*, *Penicillium*, *Rhizopus*, and *Mucor* species.

Data Analysis

Microbial counts were expressed as CFU/mL. Descriptive statistics were used to compare microbial loads and physicochemical parameters across sampling locations.

Quality Control

All media were prepared according to manufacturer instructions and sterilized at 121 °C for 15 minutes. Glassware and instruments were sterilized prior to use. Sterility controls were included during microbial analysis to ensure accuracy.

Results and Discussion

Table 1 shows the population of bacteria and coliform bacteria found in soil samples collected from different locations. The bacterial counts are expressed in colony-forming units per milliliter (Cfu/ml), with total bacteria measured in units of 10^{12} and total coliform in units of 10^7.

The soil sample from Ojota recorded the highest total bacterial count (8.35×10^{12} Cfu/ml) and total coliform count (3.67×10^7), indicating a relatively higher microbial presence. Surulere and Oke Afa samples also showed elevated bacterial and coliform counts, slightly lower than Ojota. Unilag and the control samples generally showed lower bacterial populations, with Unilag control being 5.19×10^{12} for total bacteria and 2.30×10^7 for coliforms. The control samples serve as baselines for comparison, representing either sterilized or less contaminated soil.

Table 1: Population of Bacteria and Coliform in Soil Samples

Sample Source	Total Bacteria (10^{12}) Cfu/Ml	Total Coliform (10^7)
Unilag	4.00	2.31
Surulere	7.60	2.67
0jota	8.35	3.67
Oke Afa	7.87	3.55
Unilag Control	5.19	2.30
Surulere Control	6.07	2.32

These data suggest variation in microbial contamination levels across different sites, with urban areas like Ojota showing higher bacterial and coliform counts in soil.

Table 2 presents the population of fungi in soil samples collected from dump sites and garden control areas, measured in colony-forming units per milliliter (Cfu/ml) $\times 10^9$. The highest fungal population was observed in the Ojota soil sample, with 3.24×10^9 Cfu/ml, indicating a greater fungal presence, likely due to organic matter in dump sites. Oke Afa and Surulere samples also showed relatively high fungal counts (2.55×10^9 and 2.01×10^9 respectively). The Unilag sample and the control samples from Unilag and Surulere gardens had lower fungal populations, with the lowest recorded in the Unilag control (1.12×10^9). Control samples represent less contaminated or natural garden soil, serving as a baseline for comparison.

Table 2: Population of Fungi in Soil Samples from Dump and Garden (Control)

Sample Source	Fungi (10^9) Cfu/Ml
Unilag	1.21
Surulere	2.01
Ojota	3.24
Oke Afa	2.55
Unilag Control	1.12
Surulere Control	1.44

Overall, fungi populations tend to be higher in dump sites compared to garden control areas, reflecting differences in soil conditions and organic content.

Table 3 shows the designation or coding system used for the soil samples collected from different locations. Each sample source is assigned a unique sample name or code for easy identification and reference throughout the study. UNILAG soil sample is labelled SS1, SURULERE soil sample is labelled SS11, OJOTA soil sample is labelled SS111, OKE AFA soil sample is labelled SS IV. Control samples from UNILAG and SURULERE gardens are labelled SS CI and **SS** CII respectively.

Table 3: Designation of Samples

Source	Sample Name
Unilag	SS1
Surulere	SS 11
Ojota	SS 111
Oke Afa	SS IV
Unilag Control	SS CI
Surulere Control	SS CII

This coding system helps streamline data management and analysis by providing concise, standardized sample identifiers.

Table 4 summarizes the cultural and biochemical characteristics of microbial isolates from soil samples. Each isolate is identified by a sample number and described based on four key colony features: Appearance: The colour or pigmentation of the colony (e.g., cream, grey and orange, white, yellow). Form: The general shape or outline of the colony (e.g., circular, irregular, punctiform, rhizoid, filamentous). Elevation: The profile or height of the colony surface (e.g., convex, flat, raised, umbonate, pulvinate). Margin: The edge or boundary of the colony (e.g., erose, entire, curled, lobate, undulate).

Table 4: Cultural and Biochemical Characteristics of Isolates

Sample Name	Appearance	Form	Elevation	Margin
2	Cream	Circular	Convex	Erose
3	Cream	Circular	Flat	Entire
4	Grey & Orange	Punctiform	Convex	Entire
6	Cream	Irregular	Flat	Curled
8	Orange	Circular	Raised	Erose
9	Cream	Irregular	Umbonate	Lobate
11	Cream	Irregular	Flat	Entire
12	Orange	Circular	Flat	Entire
15	Grey	Circular	Umbonate	Entire
16	Cream	Rhizoid	Flat	Entire
18	Grey	Circular	Raised	Entire
19	Orange	Irregular	Flat	Entire
23	White	Filamentous	Convex	Undulate
24	Cream & Grey	Circular	Pulvinate	Entire
25	Yellow	Circular	Pulvinate	Undulate

These characteristics help in the preliminary identification and differentiation of bacterial or fungal species isolated from the soil samples. Variations in colony morphology indicate diversity among microbial populations present in different soil environments.

Table 5 presents the cultural characteristics of microbial organisms grown on MacConkey agar, a selective medium commonly used to isolate Gram-negative bacteria, especially coliforms. Each isolate, identified by a sample name (A, B, C, etc.), is described based on four colony features: Appearance: The color of the colonies, mostly shades of pink or cream, which indicates lactose fermentation ability (pink colonies typically ferment lactose). Form: The shape of the colonies (e.g., circular, rhizoid, irregular). Margin: The edge type of the colony (e.g., entire, erose, undulate). Elevation: The height or profile of the colony surface (e.g., flat, raised).

Table 5: Cultural Characteristics of Organisms on Macconkey Agar

Sample Name	Appearance	Form	Margin	Elevation
A	Pink	Circular	Entire	Flat
B	Orange	Rhizoid	Erose	Flat
C	Pink	Circular	Entire	Flat
D	Whitish Pink	Rhizoid	Undulate	Flat
E	Cream	Circular	Entire	Flat
G	Pink	Irregular	Raised	Flat
H	Light Pink	Circular	Entire	Flat
I	Pink	Irregular	Undulate	Raised

These morphological traits help differentiate bacterial species and give preliminary insights into their metabolic properties, such as lactose fermentation and motility, which are useful for identification and further biochemical testing.

Table 6 provides the cultural and morphological characteristics of fungal species isolated from soil samples. These descriptions help in identifying fungal genera based on observable traits such as colony colour, growth patterns, spore structures, and special features. *Aspergillus flavus*: Shows yellowish-green colonies with rough, globose conidia and forms dark brown sclerotia as it matures. *Aspergillus niger*: Characterized by fast-spreading black powdery colonies; begins white and darkens with age. The conidia are smooth and borne on phialides. *Penicillium* sp.: Displays greyish-blue colonies with branched conidiophores. The conidia are smooth, ellipsoidal to globose, sometimes not in chains. Mucor: Fast-growing with tall, white colonies that turn grey due to sporangia development. It lacks rhizoids and has uncollapsed columella. Rhizopus sp.**:** Fast-growing, fluffy colonies with black sporangia and extensive aerial mycelium. It rapidly covers the culture plate. *Aspergillus wentii*: Starts white at the edges, then turns light brown to deep brown with age.

Table 6: Cultural Characteristics of Fungi

Sample Name	Description
Aspergillus Flavus	The colonies had a yellowish green colouration; the conidia borne on the phialides, suspended by their conidiosphores were globose and finely roughened to echinulate; isolates produced dark brown sclerotia with old age.
Aspergillus niger	This species had typically black powdery conidia borne on phialides, which were suspended by their conidiophores. The colonies spread rapidly, with mycelium white at first and later become dark or black. The conidia were slightly smooth.
Penicillium sp.	The colonies had a greyish blue colouration. The conidiophores were branched into phailides, on which conidia were borne. There was no metulae present. The phialides form bisepetal chains of conidia. The conidia were smooth walled, ellispsoidal or globose to sub glubose. Some of the conidia were not in chain.
Mucor	The colonies were all fast growing and often several centimeters high. They were white and later became dark grey with development of the sporangia, which were suspended by their sporangiophore. The sponrangia had uncollapsed columella. The mycelia were wide spread in and on the substratum, but without rhizoids or especially membered stolons.
Rhizopus sp.	Hyaline fluffy with balck sporangium, aerial mycelium and very fast growing. It covered the plate very fast.
Aspergillus wentii	White at the boundary, light brown and turned deep brown as culture grew older.

These detailed morphological descriptions are essential for distinguishing fungal species in microbiological and environmental studies.

Table 7 presents the pH values of various soil samples collected from dumpsites and control sites. pH is a critical indicator of soil acidity or alkalinity, influencing microbial activity, nutrient availability, and overall soil health. SSI (UNILAG): pH 6.3 – slightly acidic, SSII (Surulere): pH 6.0 – moderately acidic, SSIII (Ojota): pH 5.2 – strongly acidic, SSIV (Oke Afa): pH 5.5 – acidic, SSCI (UNILAG Control): pH 6.6 – near neutral and SSCII (Surulere Control): pH 6.9 – almost neutral. The control samples (SSCI & SSCII) have higher pH values, closer to neutral, indicating better soil conditions.

Table 7: Physico-Chemical Analysis Results (pH Values)

SAMPLES	pH
SSI	6.3
SSII	6.0
SSIII	5.2
SSIV	5.5
SSCI	6.6
SSCII	6.9

Dump site samples, especially SSIII and SSIV, show increased acidity, likely due to decomposition of organic waste and leachate from refuse, which can lower soil pH. Lower pH may negatively affect the diversity and activity of soil microorganisms and limit nutrient availability for plants.

Table 8 summarizes the Gram staining reactions and morphological characteristics of bacterial isolates grown on nutrient agar plates. Gram staining is a key microbiological technique used to classify bacteria into: Gram-positive: retain crystal violet stain (appear purple); have thick peptidoglycan cell walls. Gram-negative: do not retain the violet stain and take up safranin (appear pink); have thin peptidoglycan and an outer membrane.

Table 8: Gram Stain Results (Nutrient Agar Plates)

Sample	Description	Gram Stain
2	Streptococci	Gram positive
3	Cocci in chains	Gram negative
4	Coccoid shaped	Gram negative
6	Coccoid shaped in clusters	Gram positive
8	Coccoid shaped	Gram positive
9	Coccoid shaped in clusters	Gram positive
11	Coccoid shaped	Gram positive
12	Coccoid shaped	Gram positive
15	Elongated rods	Gram positive
16	Conccoid shaped	Gram negative
17	Short rods	Gram negative
18	Coccoid shaped	Gram positive
19	Coccoid shaped	Gram positive
23	Coccoid shaped	Gram positive
24	Coccoid shaped	Gram positive
25	Coccoid shaped	Gram positive

The variety in Gram reactions and shapes indicates a mixed bacterial population, common in soil environments. This microbial diversity reflects the richness of nutrient and waste decomposition processes occurring in the sampled soils.

Table 9 presents the Gram staining results of bacterial isolates grown on MacConkey agar, a selective and differential medium designed to isolate Gram-negative enteric bacteria and differentiate them based on lactose fermentation.

Table 9: Gram Stain Results (Mackonkey Agar Plates)

Sample	Description	Gram Stain
A	Coccoid shaped	Gram negative
B	Coccoid shaped	Gram negative
C	Coccoid shaped	Gram negative
D	Short rods	Gram negative
E	Elongated rods	Gram negative
G	Elongated rods	Gram negative
H	Coccoid shaped	Gram negative
I	Short rod shaped	Gram negative

The uniform Gram-negative reaction confirms that MacConkey agar effectively selected for Gram-negative organisms**,** mostly from the Enterobacteriaceae family. The presence of both coccoid and rod forms indicates a diverse coliform population, commonly found in contaminated soil or fecal-polluted environments**,** like waste dumps.

Table 10 presents the biochemical characteristics of various bacterial species isolated from soil samples. These tests are crucial for identification and classification of bacteria based on their metabolic activities and enzymatic functions.

Table 10: Biochemical Test Result

	Indole Production	Methyl Red	Voges-Proskauer	Citrate utilization	Catalase test	Urease test	Oxidase	Starch hydrolysis	Nitrate utilization	Motility	Gelatin Hydrolysis	Acid and gas production	Lactose Fermentation	Sucrose Fermentation	Glucose Fermentation	Fructose Fermentation
Acetobacter sp.	-	+	-	-	+	-	+	-	+	+	-	-	-	+	+	-
Bacillus sp.	-	-	-	+	+	+	+	+	-	-	-	+	+	+	+	+
Campylobacter sp.	-	+	+	+	+	+	+	-	+	+	-	-	-	-	+	-
Escherichia coli	+	+	-	-	-	-	-	+	-	+	-	+	+	+	+	-
Klebsiella pneumonia	-	-	+	+	-	+	-	+	-	-	-	+	+	+	+	+
Micrococcus sp.	-	-	+	+	+	+	-	+	-	-	+	+	+	+	+	+
Proteus mirabilis	-	+	+	+	+	+	+	-	-	+	+	+	-	-	-	-
Actinomyces	+	-	+	-	-	+	+	-	-	-	-	-	+	-	+	+
Salmonella typhi	-	+	-	-	+	-	-	+	-	+	-	+	-	-	+	-
Serratia sp.	-	-	+	+	-	-	-	+	-	+	+	+	-	+	+	-
Shiella sp	-	+	-	-	-	-	-	-	-	-	-	+	-	+	+	-
Enterbacter sp	-	-	+	+	-	-	-	+	-	+	-	+	+	+	+	+
Flavobacterium sp	-	-	-	+	+	-	+	+	-	+	+	+	+	+	+	+
Pseudomonas sp	+	+	-	-	+	-	+	+	+	+	+	+	+	+	+	+
Streptococcus sp.	-	+	+	-	-	+	-	+	-	-	+	-	+	+	+	+
Clostridium sp.	-	-	-	-	-	-	-	-	+	+	-	-	-	-	+	-
Mycobacterium sp.	+	-	-	+	-	+	-	-	+	-	-	+	+	-	+	-

Table 11 summarizes the distribution of various bacterial species across different soil sample sites (coded as SSI to SSCII), including both dump sites and control (garden) soils.

Table 11: Soil Sample Locations and Micro-Organisms Found

	SSI	SS II	SS III	SS IV	SSC I	SSC II
Acetobacter sp	_	_	+	_	_	_
Bacillus sp.	+	+	+	+	+	+
Campylobacter sp	_	_	+	_	_	_
Escherichia coli	+	+	+	+	+	+
Klebsiella pneumoniae	+	+	+	+	_	+
Micrococcus sp	+	+	+	+	+	_
Proteus mirabills	_	+	+	+	_	+
Actinomyces	_	_	+	_	_	_
Salmonella typhi	_	+	+	+	_	+
Seratia sp.	+	_	+	+	_	_
Shigella sp.	_	_	+	+	_	_
Enterobacter sp	_	+	+	+	+	_
Flavobacterium sp	_	+	_	+	_	+

Pseudomonas sp	+	+	+	+	_	+
Streptococcus sp	+	+	_	+	_	_
Clostridium sp	_	_	+	+	_	+
Mycobacterium sp	_	+	+	_	_	+

Dump sites contain a greater diversity and abundance of pathogenic organisms than control soils, likely due to organic and fecal waste contamination. Control soils (SSC I & II) had fewer pathogens, showing relatively cleaner environments. The presence of pathogens like *Salmonella* and *Shigella* poses potential public health risks, especially in areas where dumps are close to residential zones or gardens.

The present study investigated the microbial composition and physicochemical characteristics of soil samples from dumpsites and control sites in Lagos, Nigeria. Results revealed significantly higher bacterial and coliform counts in dumpsite soils compared to their corresponding garden (control) soils. This aligns with previous findings that open dumpsites act as reservoirs for microbial proliferation due to the abundance of organic matter and moisture from decaying waste [17].

The highest total bacterial count (8.35×10^{12} CFU/mL) was recorded at Ojota, while the lowest (4.00×10^{12} CFU/mL) occurred at UNILAG. Similarly, total coliform counts were highest at Ojota (3.67×10^7 CFU/mL), indicating high fecal contamination levels, which is often linked to poor sanitation practices around open dumpsites [18]. Coliforms such as *Escherichia coli* were detected across all sites, both in dumpsite and control samples, suggesting environmental dissemination and persistence of fecal indicators.
The control soils (SS CI and SS CII) exhibited lower bacterial and coliform populations, likely due to reduced anthropogenic influence.

Fungal population trends followed a similar pattern, with Ojota (SS III) showing the highest count (3.24×10^9 CFU/mL), suggesting that organic waste favours fungal growth by providing abundant carbon sources [19]. Identified fungi included *Aspergillus niger*, *A. flavus*, *Penicillium* spp., *Rhizopus* spp., and *Mucor*, many of which are known for their capacity to degrade complex organic matter [20]. Cultural and biochemical analyses revealed a diversity of bacterial isolates, including *Bacillus* spp., *Pseudomonas* spp., *Klebsiella pneumoniae*, *Proteus mirabilis*, *Salmonella typhi*, and *Enterobacter* spp. The wide presence of *Bacillus* and *Pseudomonas* species, especially in all samples, suggests their environmental resilience and metabolic versatility. Their presence in control soils also aligns with their roles as natural soil inhabitants and biocontrol agents.

The presence of pathogenic bacteria like *Salmonella typhi*, *Shigella* spp., and *Campylobacter* spp. predominantly in dumpsite soils highlights the public health implications of poor waste management. These organisms are often associated with gastrointestinal infections and indicate fecal contamination from human or animal sources [21].

Gram staining and cultural characterization revealed a predominance of Gram-positive cocci in nutrient agar plates and Gram-negative rods on MacConkey agar. This reflects the selective nature of the media and is consistent with previous studies on soil microbial composition [22]. The high number

of Gram-negative isolates on MacConkey agar, such as *E. coli* and *K. pneumoniae*, confirms the high coliform content and fecal contamination.

Biochemical test profiles supported the identification of multiple genera. For example, *E. coli* was positive for indole and methyl red tests but negative for citrate utilization, matching standard diagnostic profiles [23]. *Klebsiella pneumoniae* was identified by its positive citrate utilization and urease activity, consistent with its enteric characteristics.

The soil pH values ranged from 5.2 (Ojota) to 6.9 (Surulere control), indicating that most soils were slightly acidic. This pH range supports microbial growth, although some bacteria, like *Clostridium* and *Actinomyces*, may favour more neutral conditions [24]. Dumpsite soils, particularly Ojota and Oke Afa, had more acidic pH values, possibly due to organic acid production from decomposing waste [25].

Microbial diversity was greater in dumpsite soils than control soils, aligning with the hypothesis that increased organic content and nutrient influx support complex microbial ecosystems [8]. However, this diversity includes many opportunistic and pathogenic organisms, underscoring environmental and health hazards [13].

The detection of multiple bacterial and fungal genera across all sites, including controls, also suggests possible leaching or windborne dispersion of contaminants from dumpsites to surrounding areas [26]. This calls for strict regulations on waste disposal to prevent soil and groundwater contamination.

Conclusion

This study set out to evaluate the microbial diversity and loads of dumpsite soils in selected metropolitan areas of Lagos, identify bacterial and fungal isolates of public health and environmental significance, and assess the influence of physicochemical factors particularly soil pH on microbial distribution. The results obtained directly address these objectives, as dumpsite soils consistently exhibited higher total bacterial, coliform, and fungal counts compared to the control garden soils. This confirms the objective of determining microbial load differences between waste-impacted and uncontaminated soils.

The identification of pathogenic bacteria such as *Escherichia coli*, *Salmonella typhi*, and *Shigella* spp. exclusively in dumpsite soils fulfills the objective of characterizing potentially harmful microorganisms associated with urban waste disposal. Conversely, the isolation of beneficial and industrially relevant bacteria, including *Bacillus*, *Pseudomonas*, and *Flavobacterium* species, supports the objective of assessing overall microbial diversity and highlights the dual ecological and applied significance of dumpsite soils. The observed variation in microbial populations across sampling sites further demonstrates the influence of local environmental conditions and soil physicochemical properties on microbial distribution, thereby addressing the objective related to physicochemical–microbial interactions.

Despite these findings, the study has certain limitations. The investigation relied largely on culture-dependent techniques, which may underestimate total microbial diversity by excluding non-culturable organisms. Additionally, physicochemical analysis was limited primarily to soil pH, without incorporating other influential parameters such as organic matter content, moisture level, heavy metal concentration, or nutrient availability. The study was also cross-sectional, representing a single

sampling period, and therefore does not account for seasonal variations that may affect microbial dynamics.

Future studies should adopt culture-independent molecular approaches, such as metagenomic or 16S rRNA sequencing, to provide a more comprehensive assessment of microbial communities in dumpsite soils. Expanding physicochemical analyses to include heavy metals and other pollutants would enhance understanding of environmental drivers of microbial distribution. Longitudinal studies covering both dry and wet seasons are also recommended to capture temporal variations. Furthermore, risk assessment studies linking soil microbial contamination to human exposure pathways would provide valuable data for public health planning and policy formulation.

Overall, this study contributes baseline data on the microbial ecology of urban dumpsites in Lagos and reinforces the need for improved waste management practices, regular environmental monitoring, and informed land-use policies to reduce environmental and public health risks associated with indiscriminate waste disposal.

Conflict of Interest

The authors hereby declare that there is no conflict of interest concerning this manuscript.

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