

## Microbiology of Waste Dump Sites in Asaba, Delta State, Nigeria

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### ABSTRACT

Rapid urbanization in Asaba, Delta State, has increased municipal solid waste generation, leading to extensive open dumping. Dumpsites harbor diverse microbial communities, including pathogenic and antibiotic-resistant organisms, posing environmental and public health risks. This study assessed the microbial composition, diversity, and antimicrobial resistance of bacteria and fungi in market-related dumpsites in Asaba, providing baseline data to inform waste management and public health strategies. Soil, decomposed waste, and leachate samples were collected from seven market dumpsites. Determination of microbial loads and identification of bacteria and fungi were by standard microbiological techniques. Antibiotic susceptibility of bacterial isolates was evaluated using the Kirby–Bauer disk diffusion method. Bacterial loads exceeded fungal counts in all sample types, with leachates exhibiting the highest densities. Dominant bacteria included *Escherichia coli*, *Klebsiella pneumoniae*, *Staphylococcus aureus*, *Bacillus subtilis*, *Pseudomonas aeruginosa*, and *Salmonella typhi*. Fungal isolates were mainly *Aspergillus*, *Penicillium*, *Mucor*, *Rhizopus*, and *Candida albicans*. Enteric bacteria were concentrated in leachates, confirming fecal contamination. Antibiotic resistance was prevalent, with MAR indices ranging from 0.2 to 0.82; highest resistance occurred against ampicillin, tetracycline, and erythromycin. Dumpsites in Asaba serve as reservoirs for pathogenic and multidrug-resistant microorganisms. Leachates facilitate microbial spread, amplifying environmental and health risks. Effective waste management, routine microbial monitoring, and antimicrobial resistance surveillance are urgently needed to safeguard public health.

**Keywords:** Dumpsite Soil, Leachate, Microbial Load, Coliforms, Antimicrobial Resistance, Public Health Risk.

### Introduction

Municipal solid waste (MSW) management is a critical urban challenge worldwide, and it is especially acute in rapidly growing cities in low- and middle-income countries. As urban populations expand faster than infrastructure and regulatory systems that can adapt, the volume and diversity of wastes increase, straining collection, segregation, treatment, and disposal systems (Obire *et al.*, 2002). In many such settings, open or semi-controlled dumpsites remain the default terminal destination for household refuse, market discards, small-scale industrial waste, and in some cases healthcare and agricultural wastes (Obire *et al.*, 2002). Unlike engineered sanitary landfills, dumpsites typically lack liners, leachate collection systems, gas capture, and routine environmental monitoring. They therefore evolve into complex bioreactors where microbial communities transform heterogeneous inputs under fluctuating moisture, oxygen, and nutrient regimes (Ferronato and Torretta, 2019).

Asaba, the capital of Delta State in southern Nigeria, mirrors these pressures. Urbanization, population inflow, commercial activity, and housing expansion have increased waste generation per capita and intensified pressure on existing disposal points. The climatic pattern alternating wet and dry seasons with warm temperatures amplifies the microbiological dynamics of dumpsites. Rainfall episodes drive leachate formation and lateral transport of dissolved organics, nutrients, and microbes; dry-season heat accelerates volatilization and favors aerobic surface processes while deeper layers remain anoxic (Obire and Aguda, 2002).

Within this environmental mosaic, a diverse microbiome emerges, comprising protist, bacteriophage, bacteria, fungi, mold and archae that mediate decomposition, biogas production, nutrient cycling, and critically pathogen survival and dissemination (Adekanle *et al.*, 2014; Ofesi *et al.*, 2025).

Microbial processes in a waste dump site determine the pace and completeness of organic matter stabilization, the generation of methane and carbon dioxide, the fate of contaminants (including metals and xenobiotics), and the persistence of enteric pathogens and antibiotic resistance genes. A site's microbiome also influences odor, vector attraction, fire risk, and the exposure profile of nearby communities and workers (Odeyemi, 2012).

Dumpsite microbiology is governed by spatial and temporal gradients. Microbial activities are higher near the surface and the interface of fresh waste faces and intermittent oxygen exposure. Aerobic heterotrophs including *Bacillus*, *Pseudomonas*, *Acinetobacter*, and *Streptomyces* rapidly hydrolyze and oxidize readily degradable fractions (simple carbohydrates, lipids, proteins), producing heat and Carbon dioxide (CO<sub>2</sub>). As oxygen is consumed and diffusion cannot keep pace, deeper layers transition to anoxic and anaerobic zones, where facultative and obligate anaerobes take over. Fermenters (e.g., *Clostridium*, *Bacteroides*, *Lactobacillus*) convert complex polymers into volatile fatty acids (VFAs), alcohols, hydrogen (H<sub>2</sub>) and CO<sub>2</sub>. Syntrophic bacteria then oxidize VFAs in cooperation with hydrogenotrophic and acetoclastic methanogens (archaea such as *Methanobacterium*, *Methanosaeta*/ *Methanothrix*, *Methanosarcina*), culminating in methanogenesis the terminal step in anaerobic digestion that yields methane (CH<sub>4</sub>) and CO<sub>2</sub>. This succession hydrolysis acidogenesis, acetogenesis and methanogenesis is a hallmark of anaerobic waste stabilization (Oviasogie and Agbonlahor, 2013; Igere et al., 2024).

Parallel to these bacterial and archaeal networks are fungi (e.g., *Aspergillus*, *Penicillium*, *Mucor*, *Rhizopus*, and *ligninolytic basidiomycetes*) which specialize in breaking down recalcitrant polymers such as cellulose, hemicellulose, and lignin, especially in partially aerated niches and during early composting-like phases (Oviasogie and Agbonlahor, 2013). Actinobacteria contribute robust enzyme systems for polymer degradation and secondary metabolite production. Nitrifiers and denitrifiers cycle nitrogen where oxygenated microsites meet anoxic pockets: Nitrosomonas/Nitrobacter oxidizes ammonia to nitrate while denitrifiers (e.g., *Paracoccus*, *Pseudomonas*) reduce nitrate to gaseous forms under oxygen limitation, producing N<sub>2</sub>O and N<sub>2</sub> (Okpo et al., 2017).

This ecological machinery is beneficial though have some limitations. Dumpsite microbiomes intersect with human and animal pathogens introduced via faecally contaminated wastes, diapers, food waste, animal carcasses, and improperly discarded clinical waste. Enteric bacteria such as *Escherichia coli* (including pathogenic pathotypes), *Salmonella* spp., *Shigella* spp, *Campylobacter*, *Vibrio* spp., and opportunistic environmental bacteria (e.g., *Klebsiella*, *Enterobacter* spp, *Pseudomonas aeruginosa*, *Acinetobacter baumannii*) can persist on moist substrates and in leachate (Obire and Aguda, 2002).

Faecal indicators (*E. coli*, *Coliforms*, *Enterococci*) often flourish following rainfall when moisture increases. Spore-formers (e.g., *Bacillus* spp., *Clostridium perfringens*) endure harsh conditions and spread via dust or runoff. Fungal spores (notably *Aspergillus* and *Penicillium*) aerosolize easily, posing inhalation risks, particularly to scavengers and residents living downwind (Okpo et al., 2017; Achudume and Jacob, 2017).

Another axis of concern is the antibiotic resistance. Dumpsites receive expired or unused pharmaceuticals, antibiotic-laden animal wastes, and resistant bacteria from human sources. Microorganisms in these complex communities exchange antimicrobial resistance genes (ARGs) via plasmids, interons, and transposons. High microbial density, abundant nutrients, metals (which co-select for resistance), and stressors (e.g., disinfectants, detergents) create fertile ground for horizontal gene transfer (Igere et al., 2024).

Leachate can mobilize ARGs into nearby soils and shallow groundwater, while bioaerosols and vectors (flies, rodents) can spread resistant bacteria. In essence, dumpsites may act as amplifiers and conduits of resistance across environmental and human interfaces (Odeyemi, 2012; Nyandjou et al., 2019; Mwaikono et al., 2015).

In developing countries, including Nigeria, solid waste management remains one of the most pressing environmental challenges facing urban centers. In cities like Asaba, the capital of Delta State, rapid urbanization, population growth, and increasing commercial activity have resulted in a surge in waste generation. Unfortunately, waste disposal practices have not kept pace with this growth.

The predominant method of waste management is the use of open dumpsites, which are often poorly designed, inadequately managed, and situated close to residential areas, markets, and even water bodies (Achudume and Jacob, 2017). These dumpsites serve as breeding grounds for diverse microorganisms, many of which may pose significant public health risks. The microbiology of dumpsites is of particular concern because these sites harbor complex microbial communities that thrive on decomposing organic matter, plastics, metals, pharmaceuticals, and other waste materials. While some of these microorganisms play beneficial roles in biodegradation and nutrient cycling, others include pathogenic bacteria, fungi, and viruses capable of causing serious diseases (Adekanle et al., 2014).

Pathogens such as *Escherichia coli*, *Salmonella* spp., *Klebsiella* spp., *Pseudomonas* spp., and *Staphylococcus aureus*, as well as fungi like *Aspergillus niger* and *Candida albicans*, have frequently been reported in dumpsite environments. Their persistence in waste and their potential to spread through soil, leachates, air, vectors (flies, rodents), and contaminated water represent a critical environmental and health hazard. In Asaba, where many communities live and conduct economic activities near dumpsites, the risks are further amplified. Informal waste pickers, scavengers, and nearby residents are directly exposed to contaminated materials and microorganisms. Furthermore, poorly contained dumpsites often allow leachates to seep into groundwater sources, thereby contaminating drinking water. This could lead to outbreaks of diarrheal diseases, cholera, typhoid fever, skin infections, and respiratory illnesses. Despite these clear dangers, there is a lack of sufficient microbiological data on dumpsites in Asaba. Most waste management research in Nigeria has focused on the physical and chemical characterization of wastes, with very limited attention paid to microbial profiling (Oviasogie and Agbonlahor, 2013). The absence of detailed microbiological studies on dumpsites in Asaba creates a knowledge gap that limits the capacity of public health authorities, policymakers, and environmental managers to fully assess the risks associated with these sites. Without baseline information on the types and abundance of microorganisms inhabiting dumpsites, it becomes difficult to design effective intervention strategies for waste management, environmental protection, and disease prevention.

Moreover, dumpsites may act as reservoirs for antimicrobial-resistant microorganisms, which can be transferred to humans and animals. The growing global threat of antimicrobial resistance underscores the urgency of monitoring such environments. By neglecting microbial research on dumpsites, Asaba risks not only localized outbreaks of infectious diseases but also contributing to broader public health challenges.

Understanding the microbiology of waste dumpsites in Asaba is therefore not a narrow ecological question; it sits at the intersection of public health, environmental protection, climate mitigation, and resource recovery. Therefore, this study was to investigate the microbial composition, diversity, and potential public health implications of dumpsites in Asaba, with the aim of providing scientific evidence to guide waste management and public health policies.

## Materials and Methods

### Study Area

The study area is Asaba which is an Igbo town and the capital of Delta State, Nigeria. A rapidly growing urban area, it is located on the western bank of the Niger River, in the Oshimili South Local Government Area. Asaba had a population of 149,603 as at the 2006 census, and a fast-growing metropolitan population of over half a million people presently.

The study was conducted in Asaba between January and July 2025. Samples were collected from market dumpsites. The specific market dumpsites sampled were: Ogbeogonogo Market refuse dump, Jaret Market dumpsite, Okwe Market refuse dump, Abraka Market dumpsit, Infant Jesus Market dumpsite, Cable Market refuse dumpsite, Koka Market dumpsite (Latitude: 62°E; Longitude: 20°E).

The dumpsites had varying waste compositions, ranging from household refuse, market wastes, plastics, food remnants, agricultural residues, and biomedical materials. Leachates were observed at two sites, particularly in low-lying areas, and strong foul odors indicated active microbial decomposition.

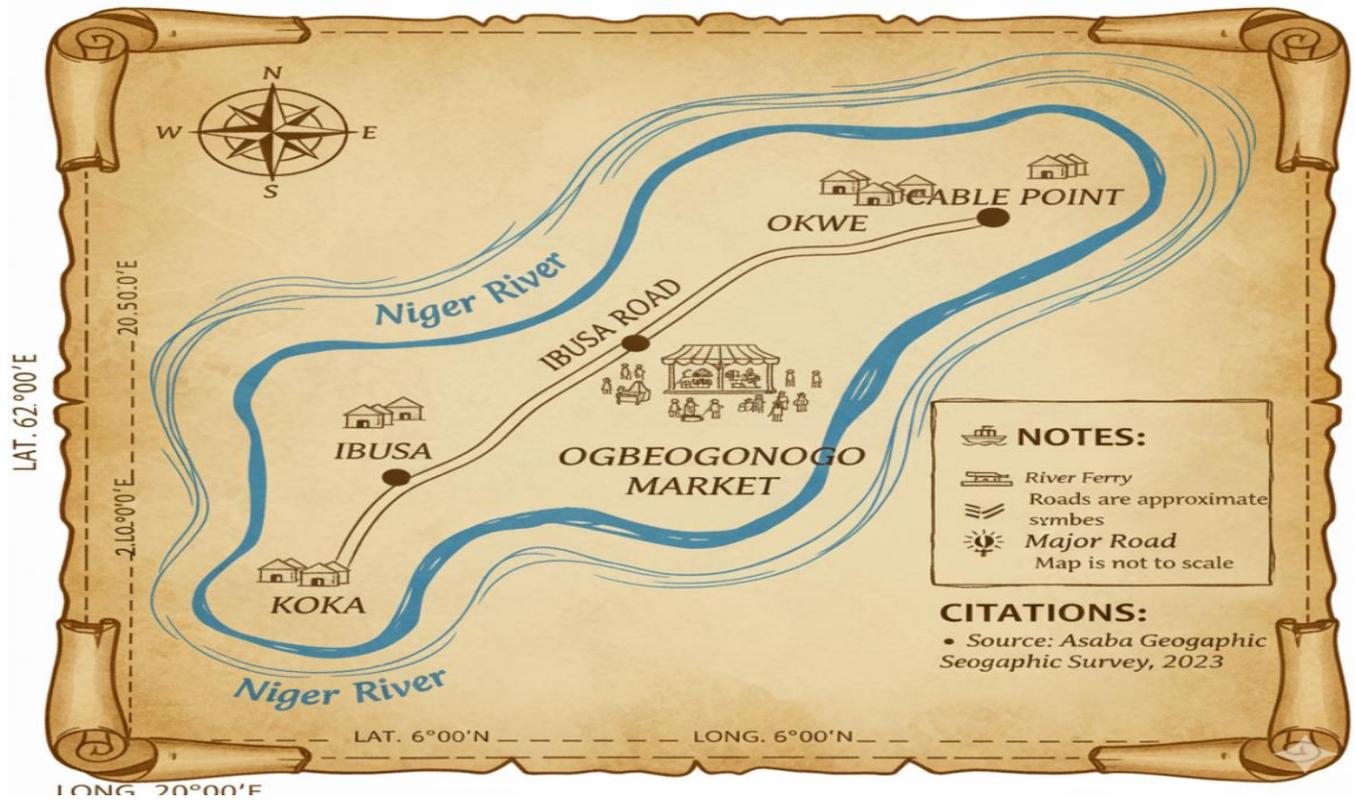


Fig. 1: Map of Asaba showing selected dumpsites (Asaba geographic seographic survey 2023)

### Collection of Samples

Soil samples were collected at depths of 0–15 cm using sterile augers. Leachate samples were collected in sterile screw-cap bottles from pooled liquid at dumpsite bases. Decomposed wastes were collected aseptically using sterile spatulas into sterile containers.

The samples were properly labeled with site/location code, sample type, and date. The samples were placed in iceboxes to preserve microbial viability and transported to the laboratory in iceboxes within 2–3 hours.

### Processing of Samples for Microbiological Analysis

Ten grammes (10g) of soil and decomposing waste samples were suspended in 90 ml sterile physiological saline and homogenized and Serial diluted ( $10^{-1}$  to  $10^{-6}$ ).

The Leachate samples were serially diluted directly ( $10^{-1}$  to  $10^{-6}$ ) in sterile saline.

### Determination of bacterial and Fungal Load

Bacterial load was determined using the pour plate technique on Nutrient Agar for total heterotrophic bacteria and MacConkey Agar for total coliforms. From appropriate serial dilutions ( $10^{-3}$  to  $10^{-6}$ ), 0.1 mL aliquots were aseptically transferred into sterile Petri dishes, after which molten agar (cooled to approximately  $45^{\circ}\text{C}$ ) was poured and gently swirled to mix. The plates were allowed to solidify and then incubated at  $37^{\circ}\text{C}$  for 24–48 hours. After incubation, plates showing 30–300 colonies were selected for counting. Colony counts were expressed as Colony-Forming Units per gram (CFU/g) of soil or decomposed waste samples, and Colony-Forming Units per milliliter (CFU/mL) of leachate samples.

Fungal load was determined using Sabouraud Dextrose Agar supplemented with chloramphenicol to inhibit bacterial growth. From serial dilutions of  $10^{-2}$  to  $10^{-4}$ , 0.1 mL aliquots were inoculated into sterile Petri dishes using the pour plate method.

The plates were incubated at 25°C for 3–5 days. Plates with discrete colonies were selected, and counts were recorded as Colony-Forming Units per gram (CFU/g) of soil or decomposed waste samples, or Colony-Forming Units per milliliter (CFU/mL) of leachate samples.

Distinct colonies were subcultured onto freshly prepared respective agar media to obtain pure isolates of bacteria and fungi. The pure isolates were preserved on agar slants and stored at 4°C for further characterization and analysis.

### Identification of Bacterial and Fungal Isolates

The morphology of the isolates was initially determined based on colony characteristics such as size, shape, elevation, margin, pigmentation, and surface appearance. Bacterial isolates were Gram-stained and examined microscopically to determine Gram reaction, cell shape, and cellular arrangement. Biochemical characterization of bacterial isolates was carried out using standard microbiological procedures. The tests performed included catalase test, oxidase test, coagulase test (for *Staphylococcus* spp.), indole test, methyl red (MR) test, Voges–Proskauer (VP) test, citrate utilization test, urease test, triple sugar iron (TSI) agar test, motility test, and carbohydrate fermentation tests. Identification was based on the results of these biochemical reactions and interpreted using standard identification manuals, including Bergey’s Manual of Determinative Bacteriology by Holt (1994).

For fungal identification, lactophenol cotton blue (LPCB) staining was employed. A small portion of fungal growth was placed on a clean glass slide, a drop of lactophenol cotton blue stain was added, and the preparation was gently teased apart using a sterile needle before covering with a coverslip. The slide was then examined microscopically. Lactophenol serves as a mounting fluid and preservative, while cotton blue stains the chitin in fungal cell walls, enhancing visibility of structural features.

Fungal identification was based on macroscopic colony morphology and microscopic characteristics such as spore arrangement, type of conidiophores, hyphal structure (septate or non-septate), and sporangial features.

Identification was carried out with reference to standard fungal identification manuals, including Barnett and Hunter’s Illustrated Genera of Imperfect Fungi (1998).

### Antimicrobial Susceptibility Testing

Antimicrobial susceptibility testing was performed using the Kirby–Bauer disk diffusion method on Mueller–Hinton agar in accordance with the guidelines of the Clinical and Laboratory Standards Institute (CLSI, 2017). Briefly, pure bacterial isolates were adjusted to 0.5 McFarland turbidity standard and uniformly inoculated onto the surface of Mueller–Hinton agar plates using sterile swab sticks.

Commercial antibiotic-impregnated discs were aseptically placed on the inoculated plates, which were then incubated at 37°C for 18–24 hours. Zones of inhibition were measured in millimeters and interpreted as susceptible, intermediate, or resistant according to CLSI standard breakpoints. The antibiotics tested and their disc potencies were as follows: Ampicillin (10 µg), Tetracycline (30 µg), Ciprofloxacin (5 µg), Gentamicin (10 µg), Ceftazidime (30 µg), and Erythromycin (15 µg).

### Results

The result for the microbial counts of waste dump soil, leachates, and decomposed waste samples is presented in Table 1. Bacterial counts were consistently higher than fungal counts across all samples. Leachates recorded the highest microbial load, followed by decomposed waste and soil samples. This indicates that moist environments (such as leachates) support greater microbial proliferation.

The frequency of bacteria isolated from in the various samples in the waste dump sites are presented in Table 2. The most frequently occurring genera included *Escherichia*, *Klebsiella*, *Staphylococcus*, *Bacillus*, *Pseudomonas*, and *Salmonella*. Enteric bacteria (*E. coli*, *Salmonella*, *Shigella*) were most abundant in leachates, confirming fecal contamination. Opportunistic pathogens (*Klebsiella*, *Staphylococcus*) were also prevalent, indicating potential public health risks.

**Table 1: Mean Microbial Counts of Dumpsite Samples in Asaba, Delta State**

Sample Type	Microbial Count		
	Total Heterotrophic Bacteria ( $\times 10^6$ CFU/g or /mL)	Coliform Count ( $\times 10^4$ CFU/g or /mL)	Total Fungi ( $\times 10^5$ CFU/g or /mL)
Soil	7.8 $\pm$ 0.5	4.5 $\pm$ 0.3	3.9 $\pm$ 0.4
Leachate	7.2 $\pm$ 0.7	4.4 $\pm$ 0.6	3.2 $\pm$ 0.5
Decomposed Waste	6.6 $\pm$ 0.6	5.7 $\pm$ 0.5	3.5 $\pm$ 0.6

**Note:** Values represent mean  $\pm$  standard deviation from triplicate determinations.

**Table 2: Frequency Distribution of Bacterial Isolates by Sample Type**

Bacterial Isolate	Frequency of Bacteria from the waste dump samples			Total Frequency
	Soil	Leachate	Waste	
<i>Escherichia coli</i>	5	9	7	21
<i>Klebsiella pneumoniae</i>	0	8	7	15
<i>Staphylococcus aureus</i>	7	0	7	14
<i>Bacillus subtilis</i>	8	0	5	13
<i>Pseudomonas aeruginosa</i>	0	6	5	11
<i>Salmonella typhi</i>	0	9	0	9
<i>Enterobacter spp</i>	4	4	0	8
<i>Proteus vulgaris</i>	0	0	6	6
<i>Shigella spp</i>	0	5	0	5
<i>Micrococcus</i>	4	0	0	4

The frequency of fungi isolated from in the various samples in the waste dump sites are presented in Table 3. Several fungal isolates were identified, with *Aspergillus* and *Penicillium* species being dominant. Pathogenic fungi such as *Candida* were also detected. Toxin-producing fungi (*A. flavus*) and opportunistic pathogens (*Candida albicans*) highlight the dumpsites as reservoirs of pathogenic fungi that may cause infections and mycotoxicosis.

The antibiotic susceptibility testing result as presented in Table 4 revealed that many bacterial isolates exhibited resistance to commonly used antibiotics. Multiple Antibiotic Resistance (MAR) indices ranged between 0.2 and 0.8, suggesting significant exposure of these bacteria to antibiotics (possibly from discarded drugs in wastes).

**Table 3: Frequency Distribution of fungal Isolates by Sample Type**

Fungal Isolate	Frequency of Fungi from the various waste dump samples			Total Frequency
	Soil	Leachate	Waste	
<i>Aspergillus niger</i>	9	0	8	17
<i>Aspergillus flavus</i>	8	7	0	15
<i>Penicillium spp</i>	7	0	6	13
<i>Mucor spp.</i>	6	0	6	12
<i>Rhizopus stolonifer</i>	0	0	11	11
<i>Candida albicans</i>	0	10	0	10
<i>Cladosporium spp.</i>	9	0	0	9
<i>Fusarium spp.</i>	0	0	12	12

**Table 4: Antibiotic Resistance Pattern of Selected Bacterial Isolates**

Bacterial Isolate	Antibiotics						MAR Index
	AMP	TET	CIP	GEN	CAZ	ERY	
<i>Escherichia coli</i>	R	R	S	S	R	R	0.65
<i>Klebsiella pneumoniae</i>	R	R	R	S	R	R	0.80
<i>Staphylococcus aureus</i>	R	S	S	R	S	R	0.58
<i>Bacillus subtilis</i>	S	S	S	S	S	S	0.00
<i>Pseudomonas aeruginosa</i>	R	R	R	R	S	R	0.82
<i>Salmonella typhi</i>	R	S	S	R	S	R	0.56

**Key:** AMP = Ampicillin; TET = Tetracycline; CIP = Ciprofloxacin; GEN = Gentamicin; CAZ = Ceftazidime; ERY = Erythromycin; R = Resistant, S = Susceptible

High resistance was observed against ampicillin, tetracycline, and erythromycin, while gentamicin and ciprofloxacin were more effective. The high MAR indices suggest dumpsites may serve as reservoirs of antibiotic-resistant bacteria, which could spread resistance genes to other environments.

Microbial diversity varied significantly between dumpsites. Market-related dumpsites recorded the highest microbial counts, particularly coliforms, due to accumulation of food wastes. Residential dumpsites showed moderate microbial loads, while roadside dumpsites recorded lower values.

## Discussion

This present study has revealed the emergence of a consistent and ecologically intuitive pattern in the various samples from the waste dump sites. The leachates exhibited the highest microbial loads, followed by decomposed waste and then soils. This gradient reflects the physical and chemical environments of the matrices.

Leachate concentrates dissolved organic carbon, nutrients and particulates in a hydrated medium that protects microorganisms from desiccation and thermal stress; it therefore supports higher viable densities and longer survival times for enteric and environmental microbes.

Decomposed waste rich in labile organics and microbial substrates also supports abundant populations, while soils, subject to greater fluctuations in moisture and increased exposure to UV and desiccation, show relatively lower but still substantial loads (Johnson and Kuehn, 2002).

This matrix-specific distribution has practical implications. High microbial loads in leachate emphasize the role of leachate as a transport vector: in unlined dumpsites, leachate can move laterally and vertically to contaminate surface water, soil, and shallow groundwater. Given the observed pH and temperature ranges typical of Asaba, leachate-mediated survival of enteric organisms and facultative opportunists is plausible, particularly during the wet season when percolation and runoff increase. Consequently, water-related exposure pathways (contaminated wells, ponds, drains) must be prioritized for monitoring and mitigation (Nair, 2012).

The community composition captured in this study mirrors what is commonly reported for open urban dumps and organic-rich waste environments. Three broad groups stood out: Fecal-associated enteric bacteria (e.g., *Escherichia coli*, *Salmonella*, and *Shigella*): Their presence especially concentrated in leachates indicates fecal contamination inputs (food wastes, diapers, household sewage, and possibly some healthcare wastes) (Mueen et al., 2020; Onoriasakpobare et al., 2024a).

These taxa are classical indicators of fecal pollution and, when viable, pose direct gastrointestinal infection risks through ingestion of contaminated water or food and possibly via hand-to-mouth contact from contaminated soil or surfaces (Naverro and Vicenzo, 2019). Opportunistic environmental pathogens (e.g., *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, and *Acinetobacter* species): These organisms thrive in moist, nutrient-rich environments and can persist in biofilms on plastics, metal surfaces, and sediments.

Their environmental prevalence is important because they can cause severe infections in immunocompromised individuals and are often associated with multidrug resistance. The frequent isolation of these taxa from leachate and waste suggests the dumpsites are reservoirs of opportunistic pathogens with potential to infect via wounds, inhalation of bioaerosols, or secondary contamination of water and food (Kehinde et al., 2020).

The saprophytic and spore-forming bacteria and fungi (e.g., *Bacillus* spp., *Aspergillus*, *Penicillium*, *Mucor*) are similar to those reported by Obire et al. (2024) and Obire et al. (2025). These taxa play central roles in decomposition but carry exposure risks. Filamentous fungi generate easily aerosolizable spores, and toxigenic strains (e.g., *Aspergillus flavus*) can produce mycotoxins under appropriate conditions. The presence of *Candida* species in leachate indicates moist niches that can harbor yeasts capable of opportunistic mucosal infections (Sabir et al., 2019).

Taken together, the taxonomic profile indicates a dual hazard: classical fecal-oral pathogens capable of causing diarrheal disease and opportunistic microbes that present risks through skin contact, inhalation and for vulnerable host populations. Compared to published studies in other Nigerian urban centers, the distribution is broadly consistent market and food-waste-dominated dumpsites often show higher enteric counts, while sites receiving wet wastes and plastic debris favor biofilm-forming opportunists and spore-forming fungi (Jutta and Sayad, 2017; Ahmed et al., 2019; Onoriasakpobare et al., 2024b).

The presence of bacteria resistant to older, widely used antibiotics (ampicillin, tetracycline, erythromycin) is expected given their prolonged use and environmental persistence. The retention of susceptibility to gentamicin and ciprofloxacin in some isolates is notable but provides only temporary reassurance; environmental reservoirs of resistance can evolve quickly, particularly where selective pressures persist.

From a public-health standpoint, dumpsites may function as amplifiers of resistance, contributing to the environmental resistome that can re-enter human and animal populations through water, food, direct contact, and vectors (Breijyeh et al., 2020; Kumar et al., 2015; Idahosa et al., 2017).

One of the most alarming outcomes was the high frequency of antibiotic resistance among the isolates, with MAR indices reaching levels suggestive of significant selective pressure. Several local drivers plausibly explain this observation: Direct input of antibiotics and pharmaceutical waste into municipal refuse. Households and small clinics commonly dispose of expired or unused antibiotics into general waste, introducing sub-inhibitory concentrations that select for resistant phenotypes. Co-selection by metals and biocides (Ayandele et al., 2020). Dumpsites frequently contain batteries, electronic waste and other metal-bearing refuse. Environmental exposure to heavy metals can select for bacteria carrying mobile resistance determinants that confer both metal tolerance and antibiotic resistance. High-density microbial communities and biofilms. These facilitate horizontal gene transfer (HGT) via plasmids, integrons, and transposons. Biofilms on plastic fragments and microplastics are particularly efficient at concentrating cells and mobile elements, promoting ARG exchange (Alao et al., 2012; Borquaye et al., 2019).

## Conclusion

This study provides comprehensive baseline data on the microbiology of waste dumpsites in Asaba, Delta State, Nigeria. The findings demonstrate that the investigated dumpsites harbor high microbial loads, with total heterotrophic bacterial counts reaching  $7.8 \times 10^6$  CFU/g in soil samples and similarly elevated levels in leachates and decomposed wastes. Leachates recorded particularly high microbial densities, confirming that moist, nutrient-rich environments enhance microbial proliferation and may act as major vehicles for environmental dissemination of pathogens. The isolation of enteric pathogens such as *E. coli*, *Salmonella typhi*, and *Shigella* spp. indicates fecal contamination of the dumpsites and highlights the potential for waterborne and foodborne disease transmission within surrounding communities. Opportunistic pathogens including *K. pneumoniae*, *Pseudomonas aeruginosa*, and *Staphylococcus aureus* were also prevalent, suggesting additional risks of wound infections, respiratory illnesses, and other opportunistic infections, particularly among immunocompromised individuals and waste handlers. Fungal isolates were dominated by *Aspergillus niger*, *A. flavus*, *Penicillium* spp., and *Candida albicans*.

The presence of toxigenic fungi such as *A. flavus* raises concerns about mycotoxin exposure, while opportunistic yeasts like *Candida* further underscore the public health implications of prolonged exposure to dumpsite environments.

Importantly, the study revealed significant levels of antimicrobial resistance among bacterial isolates, with Multiple Antibiotic Resistance (MAR) indices ranging from 0.2 to 0.82. High resistance to ampicillin, tetracycline, and erythromycin suggests sustained antibiotic selective pressure within these environments, possibly due to improper disposal of pharmaceuticals and contaminated wastes. The elevated MAR indices indicate that dumpsites in Asaba may serve as environmental reservoirs and amplification points for antibiotic-resistant bacteria. Overall, the microbiological profile of dumpsites in Asaba reflects a dual ecological and public health concern: while microbial communities contribute to organic matter decomposition and nutrient cycling, they simultaneously constitute reservoirs of pathogenic and multidrug-resistant microorganisms. The findings emphasize the urgent need for improved waste management practices, environmental monitoring, and antimicrobial resistance surveillance to safeguard public health and environmental quality in Asaba metropolis.

## Recommendations

Based on the findings of this research on the microbiology of dumpsites in Asaba, Delta State, Nigeria, several recommendations are proposed. First, there is an urgent need for proper waste management systems to reduce the proliferation of pathogenic microorganisms in dumpsite near Asaba metropolis. The presence of enteric bacteria such as *Escherichia coli*, *Salmonella* spp., and *Shigella* spp. highlights the risk of disease transmission to nearby communities through soil, leachates, and water contamination. Government agencies and environmental health officers should enforce sanitary landfilling techniques instead of open dumping, as this would minimize microbial spread. Also, regular monitoring of dumpsites is essential to track microbial loads and potential emergence of multidrug-resistant strains. This will guide public health interventions and help in early detection of harmful pathogens.

Public health education campaigns should also be conducted to discourage residents from scavenging or farming near dumpsites, as such practices increase exposure to harmful microbes. Lastly, the study recommends the adoption of bioremediation techniques, using beneficial microbes to degrade organic waste and reduce pathogenic populations.

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