ISOLATION OF BACTERIAL ISOLATES FROM ENVIRONMENTAL HOTSPOTS IN OREDO L.G.A IN BENIN CITY, EDO STATE, NIGERIA.

BY

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CERTIFICATION

This is to certify that this project was carried out by **Ikharia Gold Yetunde**, with matriculation number **LSC2103947**, of the Department of Microbiology, Faculty of Life Sciences, University of Benin City, Nigeria.

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DEDICATION

This report is dedicated first to God Almighty, second to my parents and siblings and thirdly to my friends, I dedicate this report to God Almighty for His sufficient grace, consistent love, immeasurable faithfulness, and for sparing my life throughout the period of compiling this work.

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ABSTRACT

This study focused on the isolation and identification of bacteria from environmental hot spots using dumpsites located within Oredo Local Government Area of Benin City, Edo State, Nigeria, as reference points. The investigation aimed to assess the bacterial load, identify predominant microbial species, and evaluate their antibiotic susceptibility patterns. Ten samples were collected from various dumpsite points and analyzed using standard microbiological procedures. Total heterotrophic bacterial counts (THBC) ranged from 5×10^4 to 1.25×10^6 CFU/mL on MacConkey and EMB agars, indicating high microbial activity and organic contamination. Four representative isolates were further characterized biochemically and identified as *Escherichia coli* (three isolates) and *Pseudomonas spp.* (one isolate). Antibiotic susceptibility testing using the disk diffusion method revealed that all isolates were highly sensitive to fluoroquinolones (ofloxacin, ciprofloxacin, peflacine) and aminoglycosides (gentamicin, streptomycin) but exhibited strong resistance to β-lactam antibiotics such as ceporex and cefuroxime. The dominance of *E. coli* reflects fecal contamination of the dumpsites, while the presence of *Pseudomonas spp.* highlights the persistence of environmental opportunistic pathogens. The results suggest that these dumpsites represent potential reservoirs of antibiotic-resistant bacteria with implications for public health and environmental safety. This study emphasizes the urgent need for improved waste management, microbial monitoring, and enforcement of environmental sanitation standards to mitigate the spread of antimicrobial resistance in Benin City and other urban areas of Nigeria.

Keywords include Dumpsites, *Escherichia coli*, *Pseudomonas spp.*, antibiotic resistance, Benin City, heterotrophic bacterial count, and environmental hot spots.

CHAPTER ONE

INTRODUCTION

1.1 Background of the Study

The microbial world, often invisible to the naked eye, underpins nearly every ecological process on Earth, influencing nutrient cycling, biodegradation, and maintaining ecosystem health (Adeleke *et al*., 2022). Bacteria, in particular, are ubiquitous and highly adaptable, thriving in diverse environments from the most pristine to those heavily impacted by human activities. Environmental microbiology is therefore essential for understanding these complex microbial communities and their interactions with the environment and human health. One of the major anthropogenic activities that influences microbial dynamics is the improper disposal of waste, particularly in developing countries.

Dump sites are commonly regarded as environmental hot spots because they serve as reservoirs for diverse microorganisms, including pathogenic and opportunistic bacteria (Aliyu, 2010).

While some are beneficial, others pose serious health risks when present in significant concentrations in public spaces. Urban centers in developing countries like Nigeria frequently deal with high microbial loads in public areas due to ineffective sanitation, poor waste disposal practices, and overcrowding (Abiodun *et al*., 2016).

Urban environments, characterized by high population densities, intensive industrial activities, and significant waste generation, represent unique and often challenging ecosystems for microbial life. Within these urban landscapes, certain "environmental hotspots" emerge as focal points for concentrated microbial activity and potential dissemination. These hotspots, such as open sewage systems, stagnant water bodies, burgeoning refuse dumps, abattoirs, and industrial effluent discharge points, serve as reservoirs for a vast array of bacterial populations. While many environmental bacteria are benign or even beneficial, these anthropogenically influenced sites are also conducive to the proliferation and dispersal of pathogenic and opportunistic microorganisms, posing considerable public health risks (Brusseau *et al.*, 2019).

Previous microbiological studies in Benin City have identified *Escherichia coli*, *Staphylococcus aureus*, *Pseudomonas s*pp., and *Salmonella* spp. as dominant organisms in markets, water bodies, and food samples (Imarhiagbe and Eghomwanre, 2023). These organisms are commonly associated with gastrointestinal, dermatological, and respiratory infections, and are increasingly resistant to conventional antibiotics (Ologbosere and Ekhaise, 2023).

Nigeria, like many developing nations, faces significant challenges in urban planning, waste management, and sanitation infrastructure. This often leads to the widespread presence of environmental hotspots in densely populated areas.In Nigeria, particularly in Edo State, poor waste management practices have led to the creation of contaminated zones that promote microbial growth, threatening human health, groundwater quality, and the environment (Olowe *et al*., 2019). Benin City, the capital of Edo State, is no exception. As a rapidly growing urban center, Oredo Local Government Area (LGA) experiences a continuous influx of people and a corresponding increase in municipal and industrial waste. This expansion, coupled with inadequate waste disposal systems and informal economic activities (e.g., small-scale abattoirs, informal refuse collection points), creates ideal conditions for the accumulation of diverse bacterial communities, some of which may be of public health concern (Ibhadode and Anyata, 2009; Owoeje and Okojie, 2013). Environmental hotspots such as municipal waste dumpsites, mechanic workshops, and busy markets serve as reservoirs for diverse bacterial populations.

These bacteria play crucial roles in ecosystem functioning but can also pose significant health risks when pathogenic species proliferate. Urban areas, especially rapidly growing ones like Oredo Local Government Area (LGA) in Benin City, Nigeria, face increasing environmental contamination due to poor waste management, industrial activities, and high human population density. Major waste dump sites such as those located in Oredo (New Benin), Ikpoba Hill, and Uselu are characterized by indiscriminate waste accumulation, high organic matter content, and frequent exposure to human and animal traffic. These conditions promote bacterial growth and metabolic activities (Okunade *et al*., 2020).

Environmental surveillance and bacterial isolation from these hotspots not only provide insights into public health risks but also offer data for local health policy. Moreover, the emergence of antimicrobial resistance (AMR) genes in environmental isolates, as seen in recent studies from Benin City schools and hospitals, raises further concerns about the health implications of prolonged bacterial exposure (Abegunde *et al*., 2025).

The presence of these bacterial populations in environmental hotspots is not merely an academic curiosity; it has tangible implications for the health and well-being of the surrounding communities. Contaminated water sources, for instance, are a primary vehicle for the transmission of waterborne diseases such as cholera, typhoid fever, and dysentery, which remain prevalent in many parts of Nigeria (Atobatele and Owoseni, 2023; Simpa *et al*., 2024). Previous studies in Benin City have demonstrated the presence of various bacterial species such as *Bacillus* spp, *Escherichia* coli, *Staphylococcus* spp, *Pseudomonas* spp, and *Klebsiella* spp in soils, water, and air samples collected from environmental hotspots. These bacteria include both harmless environmental strains and potential pathogens that can cause infections in humans and animals. Moreover, environmental factors such as pH, temperature, and pollution levels influence bacterial diversity and abundance.

Similarly, unmanaged refuse dumps and unsanitary abattoir practices can facilitate the spread of zoonotic pathogens and contribute to respiratory and gastrointestinal illnesses among individuals living or working near these sites (Adeyemi and Adeyemi, 2014; Omusi *et al*., 2017). Furthermore, these environments are increasingly recognized as critical reservoirs for the emergence and dissemination of antimicrobial resistance bacteria (AMR) and their resistance genes, a global health crisis that threatens the efficacy of modern medicine (Larsson and Flach, 2022; Onwumere *et al*., 2024). Understanding the types of bacteria present, their abundance, and their potential resistance patterns in these specific hotspots around Oredo LGA is therefore paramount for effective public health intervention and environmental management.

1.2 Statement of the Problem

Despite the acknowledged importance of environmental microbiology in public health and ecological sustainability, there remains a significant knowledge gap regarding the specific bacterial diversity and prevalence, particularly of potentially pathogenic and antibiotic-resistant strains, within the various environmental hotspots of Oredo Local Government Area, Benin City. Existing studies in the broader Benin City area have highlighted concerns regarding heavy metal contamination in water bodies linked to industrial effluents and dumpsites, indirectly suggesting widespread environmental pollution (Ochu *et al*., 2023). However, comprehensive microbiological assessments specifically targeting various environmental "hotspots" like open dumps, untreated sewage channels, and abattoir discharge areas within Oredo LGA are limited or fragmented.

The indiscriminate disposal of solid waste and the discharge of untreated wastewater are common practices in urban centers like Benin City (Owoeje and Okojie, 2013).These practices create an environment where diverse bacterial communities thrive, including those of public health significance such as *Escherichia coli*, *Salmonella spp.*, *Klebsiella spp.*, *Staphylococcus aureus*, and *Pseudomonas aeruginosa* (Adewoye *et al*., 2013; Omusi *et al*., 2017; Ogu *et al*., 2017; Okonko *et al*., 2012). The absence of specific, localized data means that public health authorities and environmental managers in Oredo LGA lack the crucial baseline information needed to effectively identify contamination sources, assess health risks, and implement targeted interventions. Without a clear understanding of which bacterial species are prevalent in these hotspots, and whether they exhibit resistance to common antibiotics, the potential for widespread infections and the further spread of antimicrobial resistance within the community remains largely unquantified and unaddressed. This knowledge deficit impedes proactive measures for disease prevention, environmental protection, and the development of sustainable waste and water management strategies in the area.

1.3 Aim and objectives of the Study

The primary aim of this project is to isolate and detect bacterial species from selected environmental hotspots around Oredo Local Government Area, Benin City, to understand the microbiological landscape of these crucial urban interfaces.

1. To identify and enumerate bacterial isolates from some environmental hotspots in Oredo Local Government Area .
2. To enumerate the total heterotrophic bacterial counts and the counts of specific indicator bacteria (e.g., total coliforms, fecal coliforms, *Escherichia coli*) present in the collected samples.

3. To isolate and obtain pure cultures of distinct bacterial colonies from the environmental samples using selective and differential microbiological media.
4. To characterize the isolated bacterial species based on their macroscopic (colony morphology), microscopic (Gram staining, cell shape and arrangement), and biochemical properties (e.g., catalase, oxidase, IMViC tests, sugar fermentation) for presumptive identification.
5. To determine the prevalence and distribution of different bacterial genera/species across the selected environmental hotspots.
6. To determine the antibiotic susceptibility patterns of selected bacterial isolates against a panel of commonly used antibiotics to assess the presence of antibiotic-resistant strains.

CHAPTER TWO

LITERATURE REVIEW

2.1 Overview of Environmental Microbiology

Environmental microbiology is an expansive and interdisciplinary field that investigates the diversity, activities, and interactions of microorganisms within their natural and artificial habitats. It encompasses the study of bacteria, archaea, fungi, protists, and viruses in environments ranging from pristine natural ecosystems (e.g., oceans, soils, pristine forests) to human-impacted settings (e.g., wastewater treatment plants, landfills, urban air) (Madigan *et al .,* 2018). The core objective is to understand how microbial communities function, adapt, and influence their surroundings, and conversely, how environmental factors shape microbial life.

The result of industrialization is not just the alarming increase in wastes and pollutants, but also the generation of more complex non-biodegradable pollutants like hydrocarbons, highly potent pesticides and xenobiotics. Combined with the boom in human population, there is also the rapid increase in the generation of municipal wastes, leading to a dire need to scale processes of pollutant removal and break-down into non-toxic or less toxic compounds. If left untreated, these pollutants persist in the environment and threaten the health of all living organisms (Roychoudhury and Das 2022) .

Environmental hotspots are specific locations within a broader ecosystem that exhibit significantly higher levels of biological activity, contamination, or both, compared to surrounding areas. In urban contexts, these hotspots often include waste dumpsites, open markets, abattoirs, drainage channels, and mechanic workshops. These sites are characterized by the accumulation of organic and inorganic waste, high human traffic, and frequent interactions between humans, animals, and the environment.

2.2 Bacterial Diversity in Environmental Hotspots

Environmental "hotspots" in urban areas are localized sites characterized by concentrated human activity, waste accumulation, and often, poor sanitation. The soil been a highly complex environment that provides a habitat for a diversity of plants, animals, and microorganisms. Soil has a mean prokaryotic density of roughly 108 organisms per gram, with Proteobacteria, Acidobacteria, and Actinobacteria making up the majority of the biomass within the bacteria domain (Janssen, 2006; Delmont *et al*., 2011; Xavier and Naoise, 2014; Xu *et al*., 2014). The type and number of microorganisms in the soil are influenced by soil characteristics and wastes that flow into the soil, which either inhibits or stimulates their growth (Zhang *et al*., 2010; Tang *et al*., 2013). Microorganisms are an essential part of terrestrial ecosystems, playing important roles in soil biogeochemical cycles as well as in the fate of organic pollutants (Basu *et al*., 2021). In addition, there is enough evidence confirming the important role played by soil microorganisms in several ecosystem services such as erosion control, soil formation, nutrient cycling, and plant health (Nannipieri *et al*., 2003; Gardi *et al*., 2009; Ravi *et al*., 2019). However, microbes are potentially one of the most sensitive organisms to anthropogenic activities. Soil impacted by different pollutants would consequently have a significant detrimental effect on its quality and will also have a deleterious effect on the flora, fauna, and microorganisms. Soil microorganisms are generally considered the best indicators of soil pollution, as they are very responsive and provide important information about the changes occurring in soil (Sumampouw and Risjani, 2014). Studies have shown the alteration of soil microbial composition and diversity of dumpsites, revealing the dominance and loss of different microorganisms (Wang *et al*., 2017; Salam and Varma, 2019). Therefore, gaining in-depth knowledge of the impacts of pollution on the microbial communities and potential degraders in these environments is important. These areas provide unique ecological niches that foster the growth of diverse bacterial communities, some of which are of significant public health concern. Due to elevated concentrations of pollutants, microbial activity, or toxic substances compared to surrounding areas.

Such areas often include waste dumpsites, industrial discharge zones, and sewage-contaminated soils (Mahmoud, *et al*., 2020). These hot spots create unique ecological niches where microbes adapts and thrives under stressful conditions. In dumpsites, the abundance of organic materials and moisture supports bacterial proliferation, resulting in complex microbial ecosystems (Singh and Agrawal,2021). Hot spots are common in urban environments, where there is either improper waste management or population density, also population density exacerbates contamination. Globally, countries such as India, Brazil, and Nigeria are noted for having unregulated waste dumps that serve as microbial hot spots. Microbial activity within dumpsite environments facilitates the biodegradation of organic waste; however, it also leads to the emission of harmful gases such as methane and hydrogen sulfide, which contribute to greenhouse effects and air pollution (Zhou *et al*., 2019). The recognition of dumpsites as environmental hot spots therefore highlights their dual function as natural bioprocessors and significant sources of environmental contamination.

Municipal solid wastes are materials generated through man's daily needs and used for life sustainability that are presumably regarded as unwanted to individuals, although man has control over their generation and disposal (Odocha,1994); the challenge of waste management is increasingly becoming alarming due to some waste not being reused or recycled (Taiwo, 2009).

As a result of human anthropogenic engagements in manufacturing products and processing varieties of goods for consumption have resulted in the proliferation of solid waste generation; landfilling and dumpsites are simple, cost-effective means of managing municipal solid wastes; interestingly, most dumpsites and landfills in third-world nations run less than the recommended limits (Oyeku and , Eludoyin, 2010), in these countries, dumpsites and waste landfills are openly-sited around public institutions, estates and sometimes close to streams and water servicing the community (Alimba,*et al*.,2006). Microbial diversity in dumpsites are remarkably high due to the heterogeneity of waste materials and the varying physicochemical conditions of the environment. Bacteria and Protista dominates these ecosystems, followed by fungi and also a lesser extent of actionmycetes (Adeleke *et al*., 2022). Genera of Bacteria isolated from environmental hotspots such as dumpsites include, *Bacillus* spp, *Pseudomonas* spp, *Escherichia Coli*, *Enterobacter* Spp , *Klebsiella* Spp, (Ifeanyi *et al*., 2020).

The phyla Actinobacteria, Chloroflexi, Firmicutes, and Proteobacteria are in present in the soil communities. These bacteria are involved in organic matter decomposition, nitrogen cycling, and, in some cases, pathogenesis. Indicators of fecal contaminant such as E.coil, *Salmonella* spp, while *Pseudomonas aeruginosa* known for its antibiotic resistance traits (Nguyen *et al*., 2020). Environmental parameters such as temperature, pH, and moisture content influence microbial composition and activity in dump sites (Okunade *et al*., 2020).

Microbial communities are dynamic, responding rapidly to waste input and environmental fluctuations. Seasonal changes also affect bacterial abundance, with higher counts observed during the wet season when moisture enhances bacterial metabolism (Adebayo *et al*., 2021).

Dumpsite microbial populations often include extremophilic species capable of tolerating toxic metals, hydrocarbons, and plastic residues (Abioye *et al*., 2018). This adaptive ability makes dumpsites important sites for studying microbial resilience and potential biotechnological applications.

Understanding the specific bacterial profiles of these hotspots is crucial for assessing environmental risks and informing public health interventions. The significance of environmental hotspots lies in their dual role as both sources and sinks for various contaminants, including pathogenic microorganisms. These areas serve as focal points for the proliferation and dissemination of bacteria, some of which may be resistant to antibiotics or capable of causing disease outbreaks (Igbinosa, *et al* ., 2017). In urban centers like Benin City, environmental hotspots are integral to the local economy and daily life but also pose substantial risks to public health and environmental integrity. Understanding the microbial ecology of these hotspots is essential for developing effective strategies for pollution control, disease prevention, and sustainable urban management.

2.2.1 Microbial Ecology of Nigerian Dumpsites

The microbial ecology of dumpsites in Nigeria is characterised by a complex interplay between organic waste inputs, environmental pressures and microbial community responses. Open dumpsites often unmanaged and unlined receive mixed loads of domestic, industrial and often electronic-waste streams; these environments provide abundant substrates for microbial metabolism, yet also impose stressors such as heavy metals, persistent organic pollutants (POPs), leachate accumulation and fluctuating redox conditions (Igbinomwanhia, 2011) .Because microbial communities respond to both nutrient availability and toxic stressors, dumpsites become ecological niches where both biodegradation and pollutant generation occur in tandem. Microbes decompose wastes, producing methane (3% of Nigeria's emissions) and aiding nutrient recycling, but uncontrolled sites leach toxins into groundwater, bioaccumulating in chains. Health burdens: 1.27 million global ABR deaths annually, with dumpsites contributing via exposure. Bioprospecting potential: degraders for waste control.

In Nigerian dumpsites, studies of microbial community structure reveal substantial shifts in taxonomic composition in response to pollution load and site characteristics. For example, a metagenomic study of three Lagos municipal dumpsites (Cele, Computer Village, Solous) found that bacterial diversity (OTU richness and evenness) was lowest in the most polluted site, indicating that increased contaminant burden correlates with reduced microbial diversity (Adetunji, *et al.*, 2015;Saibu,*et al.*, 2020). At the phylum level, Proteobacteria, Actinobacteria and Bacteroidetes were identified as "core" taxa across the sites, though their relative abundance varied markedly according to contaminant type and concentration. These findings illustrate that dumpsite microbial ecology is dynamic and highly influenced by waste composition, pollutant load, and physical-chemical soil parameters (Ikpe, *et al.*,2019).

Key environmental drivers shape microbial community composition in Nigerian dumpsites. In the Lagos study, canonical correspondence analysis linked heavy metals (e.g., Zn, Cu), polycyclic aromatic hydrocarbons (PAHs) and other organic pollutants with shifts in microbial taxa. For instance, Firmicutes (dominated by the genus Bacillus) were enriched in the site with intense open burning and high PAH burden, likely due to their spore-forming capacity and tolerance of extreme conditions. Conversely, soils with lower pollutant loads retained taxa more common in less-impacted soils (Acidobacteria, Chloroflexi, Planctomycetes) indicating that less-disturbed dumpsites may sustain microbial groups associated with normal soil biogeochemical cycling (Jaradat, and Al-khashman,2013). This demonstrates that the microbial ecology at Nigerian dumpsites is shaped by both contaminant-mediated selection and the legacy of waste management practices. Thus, microbial ecology in Nigerian dumpsites is neither uniform nor static — it reflects the local geochemistry, waste composition and redox micro-zones.

The structure of microbial communities in these dumpsites has significant functional consequences. In a study of solid waste leachates at the Olusosun dumpsite and Oke-Afa dumpsite in Lagos State, the authors detected 305 and 306 operational taxonomic units (OTUs) respectively in leachate samples, compared to 233 OTUs at a control site (Ogunyemi,*et al*., 2025).

Beyond taxonomic shifts, the microbial ecology of Nigerian dumpsites has important functional implications. Microbial populations in such settings are central to organic matter breakdown and the generation of key gases (e.g., methane, hydrogen sulfide) due to anaerobic or micro-aerobic zones that develop under decomposing waste layers. The dynamics of these metabolic processes depend on microbial consortium structure, availability of electron acceptors/donors, and substrate type (organic waste, leachate, etc.). This becomes highly relevant in the Nigerian context where open dumpsites dominate waste disposal. Furthermore, microbial taxa tolerant to heavy metals may contribute to pollutant transformation (e.g., metal sequestration or methylation) thereby influencing long-term fate of contaminants in both soil and groundwater.

Another layer of concern is the public health dimension: dumpsites in Nigeria serve not only as ecological processors but as microbial hotspots for pathogenic and antibiotic-resistant organisms. For example, air-sampling studies around dumpsites in Igando, Lagos revealed elevated counts of bacteria and fungi, including enteric bacteria and Staphylococcus aureus, with a proportion resistant to antibiotics such as cefuroxime and gentamicin. A similar investigation in Port Harcourt identified *Bacillus*, *Escherichia coli*, *Klebsiella*, *Proteus*, *Pseudomonas,* *Staphylococcus* and *Streptococcus* species in dump-site soils. These findings underscore the fact that microbial ecology at dumpsites is not purely environmental; it intersects with human exposure pathways, vector-host interactions, and potentially the spread of antimicrobial resistance. Yet a particularly alarming trend in Nigerian dumpsites is the role of leachate and adjacent surface/ground water in harbouring antibiotic-resistant bacteria (ARB) and antibiotic resistance genes (ARGs). For instance, a 2024 study of the Ajakanga Dumpsite in Ibadan found that 26 out of 32 *Escherichia coli* isolates from leachate and 9 out of 12 from surface water were ESBL-producers, carrying the bla_CTX-M gene, and many exhibited multidrug resistance (resistance to ≥3 antibiotic classes). This underscores that dumpsites function as important nodes in the environmental One-Health network: they link waste, microbial ecology, antimicrobial resistance and human/animal exposure. For your topic on ESBL-producing *E. coli* in hospital wastewater, this link is conceptually relevant: it shows how microbial ecology in waste management contexts (though not hospital wastewater per se) can drive ARG dissemination (Adekanmbi,*et al.,* 2024).

In the Nigerian context, the implication for biogeochemical cycling, waste management and environmental risk is multi-fold. Microbial communities in dumpsites support the breakdown of organic waste helping attenuate volumes and altering waste profiles but simultaneously contribute to pollutant release (e.g., via leachate, gas emissions) and act as reservoirs of harmful microorganisms (Uchegbu,2002). The state of microbial ecology is thus a barometer of dumpsite health and functionality: higher diversity and presence of soil-typical microbial groups may indicate less impacted conditions, whereas dominance of tolerant taxa (e.g.,Firmicutes, Bacillus) often signals severe contamination. From a management perspective, understanding microbial ecology offers pathways for engineered bioremediation (e.g., introduction of pollutant-degrading consortia), emission mitigation (targeting microbial processes that generate greenhouse gases), and public health oversight (monitoring resistant microbes)(HPA, 2016).

Given the paucity of longitudinal and functional studies in Nigeria, several gaps remain. There is limited data on archaea and fungal communities in dumpsites, minimal quantification of key gaseous emissions tied directly to microbial processes, and few studies linking leachate-microbe interactions with groundwater contamination. Future research should adopt high-throughput metagenomics, stable isotope probing and longitudinal monitoring of microbial activity to map temporal changes in community structure and function across dumpsites of varying age, waste profile and management status (Azubuike,*et al*., 2016).

Nigeria's waste management practices remain inefficient, resulting in widespread open dumping. Studies across several Nigerian cities have revealed that dumpsites harbor diverse bacterial species, many of which are opportunistic pathogens (Olowe *et al*., 2019).

Studies in Benin City, has shown that microbial analysis of dumpsites such as those in Oredo, Ikpoba Hill, and Uselu revealed the presence of *Bacillus subtilis*, *Staphylococcus aureus*, and *Pseudomonas aeruginosa* (Okunade *et al*., 2020).

These bacteria exhibit resilience to fluctuating environmental conditions and may contribute to antibiotic resistance dissemination. Another dimension is the airborne microbial ecology and pathogen-load dimension of Nigerian dumpsites. At Igando Dumpsite in Lagos, a study measured bacterial and fungal loads in air samples taken at increasing distances from the waste pile and found extremely high concentrations (total aerobic bacteria 2.6×10^7 cfu/m^3). *Staphylococcus* spp. was most prevalent among bacteria; fungi such as Rhizopus and Aspergillus were also isolated in significant proportions. These findings are significant because they illustrate that dumpsites are not only soil and leachate microbial habitats, but also airborne microbial emission sources with implications for respiratory exposure, allergenicity and pathogen transmission in adjacent human populations (Fashola, *et al*.,2019).

2.2.2 Sewage and Wastewater

Sewage and untreated wastewater are complex matrices rich in organic matter, nutrients, and a vast array of microorganisms originating from human and animal feces, domestic activities, and industrial discharges. They represent a primary conduit for the dissemination of enteric bacteria and pathogens into the environment. Wastewater typically harbors extremely high concentrations of bacteria, often exceeding 107 CFU/mL (Colony Forming Units per milliliter) (Akinbile *et al* ., 2016). The diversity is immense, including commensals from the human gut, environmental bacteria, and opportunistic pathogens. Indicator Organisms Coliforms, particularly fecal coliforms and *Escherichia coli*, are universally recognized as primary indicators of fecal contamination in water. Their presence suggests the potential for other, more virulent enteric pathogens (WHO, 2017). Studies in Nigeria frequently report high levels of coliforms and *E. coli* in untreated wastewater (Okonko *et al* ., 2012). Beyond indicators, sewage is a known reservoir for various human pathogens and the illness they cause and these include, *Salmonella spp.* Causative agents of typhoid fever and salmonellosis , *Shigella spp.* Responsible for bacillary dysentery, *Vibrio cholerae*: The bacterium causing cholera ,*Campylobacter spp* which is a leading cause of bacterial gastroenteritis.

Pseudomonas aeruginosa severs as an opportunistic pathogen, often associated with nosocomial infections, but also prevalent in aquatic environments, including sewage (Ogu *et al* ., 2017). *Staphylococcus aureus* While primarily a human commensal, it can be found in sewage, especially from healthcare facilities, and is a concern due to its potential for antibiotic resistance (Adegoke *et al* ., 2010).

- **Antibiotic Resistance:** Wastewater treatment plants, and by extension, untreated sewage, are considered "hotspots" for the development and spread of antibiotic resistance genes (ARGs) due to the high density of bacteria, presence of antibiotics/disinfectants, and opportunities for horizontal gene transfer (HGT) (Larsson and Flach, 2022). Studies in Nigeria have indeed isolated multidrug-resistant bacteria, including *E. coli*, *Klebsiella pneumoniae*, and *Pseudomonas aeruginosa*, from hospital wastewater and general sewage, posing significant public health concerns (Akinjogunla *et al* ., 2018; Onwumere *et al* ., 2024).

2.2.3 Stagnant Water Bodies (e.g., Ponds, Ditches, Urban Streams) as an Environmental hotspot

Stagnant water bodies in urban areas, often formed from poor drainage, overflowing gutters, or natural depressions, are characterized by low oxygen levels, accumulation of organic matter, and often, direct input of domestic waste and runoff. Water is the main transmission medium not only of algae but also of protists. Protists, particularly species from the genera Acanthamoeba, Naegleria, Saccamoeba, Hartmannella and Vexillifera, control the number of bacteria and, to a lesser extent, also of fungi (Zhang *et al*., 2016). Like algae, some represent hosts for pathogenic bacteria of the genera *Legionella* spp, *Burkholderia* spp, and *Mycobacterium* spp. Additionally, species from the genera Cryptosporidium, Microsporidia and Giardia can act as human pathogens, causing diarrhoea, nausea, keratitis, and encephalitis. Species that can form Oocysts represent particular problems, since they are less sensitive to water chlorination (Valster 2011; Novak Babic *et al*., 2020).

Stagnant water bodies such as ponds, ditches, and urban streams represent one of the most dynamic yet overlooked components of the urban and peri-urban environment. Despite their relatively small size and limited hydrological movement, these water bodies serve as critical zones of intense biological and chemical activity. The term *stagnant* refers to a lack of continuous flow or water exchange, which allows for prolonged interaction between organic matter, sediments, microorganisms, and chemical pollutants. Over time, these conditions transform stagnant water bodies into environmental hotspots sites where energy flux, microbial metabolism, and biogeochemical processes occur at rates disproportionate to their size. While they can function as important ecological buffers, their capacity to accumulate nutrients, waste, and microorganisms often leads to significant environmental and public health challenges.

The microbial ecology of stagnant water bodies is particularly complex and highly adaptive. These ecosystems are dominated by microbial communities that thrive in oxygen-deficient or low-flow environments. As organic matter from plant decay, domestic effluents, and surface runoff accumulates, microbial decomposers, particularly heterotrophic bacteria and fungi, begin the process of biodegradation. During this process, oxygen is rapidly depleted, creating anoxic or hypoxic conditions, particularly in deeper layers of the water or in sediments. Under such conditions, anaerobic microbes, including sulfate-reducing bacteria, methanogens, and denitrifiers, become dominant. Their metabolic activities drive crucial but sometimes harmful processes such as methane production, hydrogen sulfide emission, and nitrate reduction. These gases, especially methane (CH_4) and hydrogen sulfide (H_2S), are potent greenhouse gases and odorous compounds that influence both climate and local air quality.

In tropical and subtropical regions such as Nigeria, stagnant water bodies are ubiquitous in cities and rural areas alike. The combination of warm temperatures, heavy rainfall, poor drainage, and unregulated waste disposal creates numerous artificial ponds, ditches, and blocked drainage canals that retain water for extended periods. These features, often found along roadsides, residential estates, and industrial zones, act as *miniature reactors* of microbial and chemical transformation. Because they receive inputs from multiple sources, such as domestic sewage, agricultural runoff, market waste, and effluents, they become repositories of organic and inorganic pollutants. Nutrient enrichment, especially from nitrogen and phosphorus, promotes algal blooms and accelerates eutrophication. Once algal blooms die off, microbial decomposition consumes the remaining dissolved oxygen, creating a self-sustaining cycle of anoxia and pollution. This process transforms stagnant water bodies into persistent sources of greenhouse gases and pollutants that can leak into nearby soils and groundwater.

The microbial community structure within these environments reflects this ecological imbalance. Studies across Africa and Asia have shown that stagnant ponds and ditches host bacterial taxa such as *Bacillus*, *Clostridium*, *Pseudomonas*, *Escherichia*, and *Aeromonas*, many of which are known for their ability to degrade organic pollutants under anaerobic conditions. However, these same genera often include pathogenic or opportunistic species, some of which exhibit antibiotic resistance. The warm and nutrient-rich conditions of stagnant water provide an ideal breeding ground for these microbes, which can persist in sediments, biofilms, and suspended particulate matter. In addition, these environments serve as ecological "melting pots" where antibiotic-resistant genes can be exchanged among microbial populations, thereby increasing the risk of resistant infections in nearby human communities. In densely populated Nigerian cities such as Lagos, Port Harcourt, and Ibadan, stagnant drainage systems and urban streams have been found to harbor *Escherichia coli*, *Klebsiella*, *Proteus*, and *Enterococcus* species with multi-drug resistance, posing significant challenges to environmental and public health management.

Beyond their microbial significance, stagnant water bodies are hotspots of biogeochemical cycling. The sediments at the base of these systems act as both sinks and sources of nutrients and pollutants. When oxygen becomes depleted, microbial respiration shifts from aerobic to anaerobic pathways, promoting processes such as denitrification and methanogenesis. During these transformations, organic carbon is converted into methane, and nitrate is reduced to nitrogen gas, nitrite, or ammonia—depending on the redox potential of the environment. The cumulative effect of these microbially mediated reactions is the emission of greenhouse gases and the recycling of nutrients that would otherwise be locked in sediments. Yet, the same processes that sustain local nutrient cycles also exacerbate environmental problems by increasing emissions and deteriorating water quality.

Moreover, stagnant water bodies play a significant role in pollutant accumulation and transformation. Metals such as lead, cadmium, zinc, and copper from urban runoff or industrial effluents often settle into the sediments of ponds and ditches, where microbial interactions influence their speciation and mobility. Sulfate-reducing bacteria, for example, can convert metal ions into insoluble sulfides, effectively immobilizing them in sediments. Conversely, under changing redox conditions, these same metals can be remobilized, posing risks of recontamination to surface and groundwater systems. Similarly, hydrocarbons and polycyclic aromatic compounds deposited from oil residues, vehicle emissions, or industrial waste are degraded by hydrocarbon-oxidizing bacteria such as *Pseudomonas* and *Acinetobacter*, albeit sometimes incompletely, leading to the formation of intermediate compounds that may be more toxic than their precursors.

Human health risks associated with stagnant water bodies are multifaceted. The microbial and chemical characteristics of such systems create conditions conducive to the survival and transmission of pathogenic organisms. Many stagnant ponds and ditches in tropical cities double as breeding sites for mosquitoes, flies, and other disease vectors, thus linking microbial ecology to vector-borne disease transmission. In addition, human and animal contact with contaminated stagnant water can result in gastrointestinal and dermatological infections. The ingestion of untreated water from such sources, which occurs in some rural or peri-urban communities, exposes populations to pathogens such as *Vibrio cholerae*, *Salmonella typhi*, and *Shigella dysenteriae*. Furthermore, as antibiotic-resistant bacteria proliferate in these water bodies, the risk of horizontal gene transfer between environmental and clinical strains increases, compounding the threat of resistant infections.

From an environmental management perspective, stagnant water bodies embody the dual character of ecological systems they are both productive and hazardous. On one hand, they support microbial diversity and nutrient cycling; on the other, they function as reservoirs of pollution, greenhouse gases, and pathogens. The persistence of these water bodies in Nigerian cities is often tied to infrastructural challenges such as inadequate drainage, poor urban planning, and unregulated waste disposal. Consequently, addressing their environmental impact requires integrated management strategies that combine hydrological engineering, pollution control, and ecological restoration. Techniques such as dredging, aeration, vegetation planting, and controlled flow reintroduction can help restore oxygen balance and reduce microbial-driven emissions. Moreover, incorporating nature-based solutions such as constructed wetlands and vegetated buffer zones can harness microbial processes for pollutant removal while reducing the negative impacts of stagnation.

Stagnant water bodies in both natural and anthropogenic landscapes are critical yet underappreciated environmental hotspots. They embody the interconnectedness of microbial life, chemical transformations, and human activity. In Nigeria and other tropical countries, their ecological importance is amplified by socio-environmental realities rapid urbanization, inadequate waste management, and changing climate patterns that favour water stagnation. Understanding the microbial and biogeochemical dynamics of these systems is therefore essential not only for environmental protection but also for climate change mitigation and public health safety. As small and often neglected as they may appear, stagnant ponds, ditches, and urban streams are microcosms of global environmental processes—sites where life and pollution intersect in powerful and revealing ways.

According to US EPA, 2012, pathogenic microorganism is danger for human when it contaminates all types of water bodies. In developed and developing countries water supply networks in hospital, school and homes were identified as a hotspot for waterborne pathogen (Ling *et al*., 2018). Every year 3.4 million people die from water related diseases (WHO, 2014). Similarly, UNICEF (United Nations Children's Fund) reported every day 4000 children die due to contaminated water (UNICEF, 2014).

Fayomi *et al*., 2019, discussed in their study, the sewage disposal practice followed in Nigeria are release of septic tank in to soil will pollute soil and water environment (Nowak and Imperowicz, 2016), sewage water discarding into storm water can cause air pollution (Palamuleni,2002), sewage in to pond water is the source for vector diseases (Petrie et al., 2015) and direct dumping of sewage waste in river increase toxic substances in food chain through plants, animals and finally human (Ajibush and Terdoo, 2013). Similarly, a study said, potable water supply network harbours multifaceted microbial ecosystems, affecting the lives of 3.6

billion people living in urbanized areas (Fangqiong Ling *et al*., 2018). Diversity of microbes and germs are responsible for gastrointestinal infection which causes symptoms like fever, vomiting, diarrhoea and abdominal pain was recorded in 29.53% cases. Similarly,27% of cases were caused by *Shigella* sp., *Cryptosporidium parvum*,(10.99%), *Naegleria fowleri* (16.84%) Adenovirus 3(10.08%), E. coli 0157:H7 (12.63%), Leptospira (6.59%) and *Schistosoma* sp (29.53%) (Pandey *et al*., 2014).

According to Rajasulochana and Rebba, 2015 water contaminated with faecal coliform harshly affects the

performance of human; some of the main pathogen responsible for water contamination is *Campylobacter*,

Salmonella, *Staphylococcus aureus*, *Clostridium botulinum*, *Pseudomonas aeruginosa*, *Escherichia coli* and *Vibrio cholera*.

The lack of flow leads to oxygen depletion, favoring anaerobic and facultative anaerobic bacteria. High nutrient loads from pollution often lead to eutrophication, promoting algal and cyanobacterial blooms, which further contribute to organic matter and oxygen depletion upon decomposition.The presence of Indicator Bacteria Similar to sewage, the presence of total coliforms and fecal coliforms is a strong indicator of fecal contamination, often exceeding WHO guidelines for recreational or drinking water (WHO, 2017).

Opportunistic Pathogens present in stagnant water can harbor various opportunistic human pathogens, including *Pseudomonas aeruginosa* , Known for its ability to survive in diverse aquatic environments and cause infections in immunocompromised individuals *Aeromonas hydrophila* associated with gastroenteritis and wound infections, *Legionella pneumophila* while primarily associated with aerosols from cooling towers, it can proliferate in stagnant warm water and cause Legionnaires' disease.

Stagnant water is also a breeding ground for mosquitoes, which transmit diseases like malaria, dengue, and yellow fever, further exacerbating public health risks in these areas (Akinbile *et al* ., 2016). Studies in Benin City have shown concerns about the bacteriological quality of borehole water, which can be influenced by stagnant surface water infiltration (Atobatele and Owoseni, 2023).

2.2.3 Refuse Dumps/Landfills as Environmental Hotspots

A dumpsite can be referred to as an areas or a land site where material wastes from several sources and processes are deposited. The wastes include both municipal solid wastes and industrial wastes, including liquid effluents containing heavy metals (Ilusanya *et al*., 2023). Solid wastes are made up of all forms of waste arising from the byproducts of human and animal activities. Also industrial diversification and the provision of expanded health-care facilities have also contributed to a considerable quantity of industrial hazardous waste and biomedical waste into the waste stream, with potentially severe environmental and human health consequences (United Nations ESCAP 2020).

Open refuse dumps, common in many Nigerian cities, including Benin City, are heterogeneous environments teeming with diverse microbial life due to the decomposition of organic and inorganic waste (Ibhadode and Anyata, 2009; Owoeje and Okojie, 2013). Complex Microbial Ecosystems present at dumpsites are characterized by varying moisture content, temperature gradients, and oxygen levels, creating a mosaic of microbial niches. The decomposition processes generate leachate (a highly contaminated liquid) and landfill gas (rich in methane and carbon dioxide).

In urban areas, indiscriminate dumping of waste contaminates surface and ground water supplies, clogging drains, creating stagnant water for insect breeding and floods during the rainy.

Each year, over 5.2 million people (including up to 4 million children) have been reported to die from waste-related diseases (Uche *et al*., 2010). The disease burden associated with waste exposure in middle- and low-income countries has been shown to be increasing, although it remains largely unacknowledged (Landrigan *et al*., 2015). Numerous studies have identified inadequate waste management as a significant cause of soil and groundwater contamination globally (Marsilib *et a*l., 2009; Landrigan *et al*., 2015; Fazzo *et al*., 2017).In general, poor waste management leads to serious health hazards and contributes to the spread of infectious diseases. Unattended waste attracts flies, rats, and other disease-carrying creatures, while decomposing wet waste produces foul odors, creating unhygienic conditions that increase health risks (Mattiello *et al*., 2013).

Bacterial pathogens may develop in wastes undergoing decomposition in soils that suffer from environmental pollution as a result of indiscriminate disposal of pollutants. These bacterial pathogens, when

increased in population, pose great risk to human health (Onweremadu *et al*., 2009; Awisan *et al*., 2011).

Despite significant investments in the waste management sector, solid waste management remains one of the major environmental sanitation challenges facing the country today and has continually remained at the lowest level, because industrialization and rapid population growth in many cities and towns have led to wastes being generated faster than they are collected, and disposed. Dominant bacterial groups are in both aerobic decomposers and anaerobic decomposing bacterial, In the surface layers, aerobic bacteria like Bacillus spp., Staphylococcus spp., and various Gram-negative rods are active in the initial stages of decomposition (Abubakar *et al* ., 2019; Omusi *et al* ., 2017). Deeper within the dump, anaerobic conditions prevail, supporting fermentative bacteria such as *Clostridium spp.* and methanogens (archaea) (Madigan *et al* ., 2018). Several bacterial are of pathogenic concerns as attributed too refuse dump site, Refuse dumps are significant sources of human and animal pathogens due to the presence of fecal matter, food waste, and sometimes medical waste. Common isolates are *Escherichia coli* and other coliforms, *Salmonella* spp. and *Shigella* spp. *Staphylococcus aureus* (including MRSA) (Abubakar *et al* ., 2019), *Pseudomonas aeruginosa*, and *Proteus vulgaris*.

Public Health Risks as a result of urban wastes dumps and landfills are related to the Proximity to dumpsites wihich is associated with various health issues, including respiratory problems, gastrointestinal infections, and skin diseases, often linked to exposure to bioaerosols and contaminated leachate (Abubakar *et al* ., 2019; Ochu *et al* ., 2025). Studies in Sokoto, Nigeria, for instance, have isolated *Staphylococcus aureus*, *Bacillus licheniformis*, and *Staphylococcus caprae* from refuse dumps, highlighting the presence of potential pathogens (Abubakar *et al* ., 2019).

2.2.4 Abattoirs and Meat Processing Waste as Environmental Hotspot

Abattoirs are critical points for potential microbial contamination, as they handle large volumes of animal products and generate significant amounts of organic waste (blood, offal, faeces).

- **Rich Organic Substrate:** The waste from abattoirs provides an ideal, nutrient-rich environment for the rapid proliferation of diverse bacteria.
- **High Pathogen Load:** Abattoir environments are particularly concerning due to the presence of zoonotic pathogens originating from the animals themselves. Key bacterial isolates which could cause food borne illness includes *Escherichia coli* (including pathogenic strains like O157:H7), *Salmonella spp.* Which is mostly a major concern in meat products same as *Campylobacter spp.*

  Listeria monocytogenes then the likes of *Staphylococcus aureus* which can be noticed from animal skin, nasal passages, and human handlers and *Clostridium perfringens*.
- **Cross-Contamination Risk:** Poor hygiene practices in abattoirs can lead to cross-contamination of meat products, equipment, and the surrounding environment, posing direct risks to consumers and workers (Adewoye *et al* ., 2013). The discharge of untreated abattoir effluent into water bodies or land can further spread these pathogens into the wider environment.

2.3 Public Health Significance of dump site as an Environmental Hotspot

The interaction between humans and environmental bacteria is complex, with many beneficial aspects (e.g., nutrient cycling, bioremediation). However, environmental hotspots, particularly in urban settings with inadequate sanitation, can serve as significant reservoirs and transmission routes for pathogenic bacteria, posing substantial public health risks.

Contaminated water remains a leading cause of morbidity and mortality globally, especially in developing nations like Nigeria (Atobatele and Owoseni, 2023). Environmental hotspots such as stagnant water bodies, open sewage systems, and areas impacted by refuse leachate are primary sources of waterborne pathogens.

- **Cholera:** Caused by *Vibrio cholerae*, cholera is a severe diarrheal disease often linked to contaminated water sources. Outbreaks are common in areas with poor sanitation and inadequate access to safe drinking water (WHO, 2023).
- **Typhoid Fever:** *Salmonella typhi*, the causative agent of typhoid fever, is transmitted through the consumption of food or water contaminated with fecal matter from infected individuals. Environmental reservoirs, particularly contaminated water, play a crucial role in its spread (Crump *et al* ., 2015).
- **Bacillary Dysentery (Shigellosis):** Caused by *Shigella spp.*, this highly contagious disease leads to severe diarrhea and is primarily transmitted via the fecal-oral route, often through contaminated water or food.
- **Escherichia coli Infections:** While many *E. coli* strains are harmless commensals, pathogenic strains (e.g., enterotoxigenic *E. coli* (ETEC), enteropathogenic *E. coli* (EPEC), enterohemorrhagic *E. coli* (EHEC)) are significant causes of diarrheal disease, particularly in children. Their presence in environmental water bodies indicates fecal pollution and a risk of other enteric pathogens (Simpa *et al* ., 2024).
- **Other Waterborne Pathogens:** Other bacteria like *Campylobacter jejuni*, *Aeromonas hydrophila*, and even opportunistic pathogens like *Pseudomonas aeruginosa* can cause gastrointestinal illnesses or skin infections through contact with contaminated water (Ogunbiyi *et al* ., 2024).

2.3.2 Foodborne Illnesses Linked to dump site as an Environmental Hotspot

Environmental bacteria can easily enter the food chain, leading to foodborne illnesses. This often occurs through the use of contaminated water for irrigation or washing, direct contact with contaminated soil, or unsanitary practices in food processing and handling environments.

- **Contamination Pathways:** Vegetables and fruits can become contaminated if irrigated with polluted water or if they come into contact with fecal matter in the soil. Meat and poultry can be contaminated during slaughtering and processing if hygiene is poor (e.g., in abattoirs) or if equipment is unclean.
- **Key Foodborne Bacteria with Environmental Links:**
    - ***Salmonella spp.***: Commonly found in animal intestines and can contaminate meat, poultry, eggs, and produce.
    - ***Escherichia coli O157:H7***: A virulent strain that can cause severe gastrointestinal illness, often linked to contaminated meat or produce.
    - ***Listeria monocytogenes***: A ubiquitous environmental bacterium that can contaminate a wide range of foods, particularly ready-to-eat products, and can cause severe illness in vulnerable populations.
    - ***Staphylococcus aureus***: While often associated with human handlers, it can also persist in environmental surfaces in food preparation areas.

Impact: Foodborne illnesses range from mild gastroenteritis to life-threatening conditions, posing a significant public health burden and economic cost (WHO, 2015).

2.3.3 Dumpsite as Environmental Reservoirs of Antibiotic Resistance (AMR)

The environment, particularly those areas impacted by human and animal activities, is increasingly recognized as a critical reservoir and conduit for the emergence and dissemination of antibiotic resistance (AMR) (Larsson and Flach, 2022). This phenomenon is a cornerstone of the "One Health" concept, which acknowledges the interconnectedness of human, animal, and environmental health in addressing global health threats (NCDC, 2023).

- **The "One Health" Perspective:** Antibiotic resistance is not confined to clinical settings; it is a complex issue driven by antibiotic use in human medicine, agriculture, and its subsequent release into the environment. Environmental hotspots, with their high bacterial densities and exposure to residual antibiotics and disinfectants, act as "mixing vessels" where resistance genes can evolve and spread (Bengtsson-Palme *et al* ., 2018).
- **Mechanisms of Resistance Spread:**
    - **Horizontal Gene Transfer (HGT):** This is the primary mechanism by which bacteria acquire resistance genes from other bacteria. It occurs through:
- **Conjugation:** Direct transfer of plasmids (extrachromosomal DNA containing ARGs) between bacteria.
- **Transformation:** Uptake of free DNA (including ARGs) from the environment.
- **Transduction:** Transfer of ARGs via bacteriophages (viruses infecting bacteria).
- **Selective Pressure:** The presence of sub-inhibitory concentrations of antibiotics or other selective agents (e.g., heavy metals, disinfectants) in environmental hotspots favors the survival and proliferation of resistant bacteria, driving the evolution and spread of resistance (Perry & Wright, 2023).
- **Common Environmental ARB in Nigeria:** Studies in Nigeria have consistently reported the presence of multidrug-resistant bacteria in various environmental samples. For instance,

E. coli, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, and *Staphylococcus aureus* resistant to multiple antibiotics have been isolated from wastewater, soil, and even the air around dumpsites (Onwumere *et al* ., 2024; Akinjogunla *et al* ., 2018; Abubakar *et al* ., 2019). Specific resistance mechanisms, such as Extended-Spectrum Beta-Lactamase (ESBL) production and carbapenem resistance, are increasingly being detected in environmental isolates, mirroring clinical trends (NCDC, 2023). This poses a direct threat to public health, as these resistant strains can be transmitted back to humans through contaminated water, food, or direct contact, making infections harder to treat.

2.3.4 Other Environmental Health Impacts

Beyond direct infections, environmental contamination by bacteria can have other adverse health and ecological effects:

- **Bioaerosols:** Refuse dumps and wastewater treatment plants can release bioaerosols containing bacteria, endotoxins, and fungal spores, leading to respiratory issues and allergic reactions in nearby populations (Abubakar *et al* ., 2019).
- **Eutrophication and Ecosystem Disruption:** Excessive nutrient loading from sewage and agricultural runoff into water bodies can lead to eutrophication, causing algal blooms, oxygen depletion, and disruption of aquatic ecosystems, impacting biodiversity and water quality for human use .

2.4.2 Waste Management and Dumpsite Studies

The challenges of solid waste management in Oredo LGA and Benin City have been well-documented, often leading to indiscriminate disposal and the creation of numerous refuse dumps

(Ibhadode and Anyata, 2009; Owoeje and Okojie, 2013). These dumpsites are recognized as sources of environmental contamination.

- **Microbiological Quality of Dumpsites:** Research by Abubakar *et al* . (2019) on waste dumpsites in Keffi, Nigeria (a comparable urban setting), isolated *Escherichia coli*, *Pseudomonas aeruginosa*, *Staphylococcus aureus*, *Proteus vulgaris*, *Bacillus spp.*, and *Micrococcus spp.* from the air environment around these sites. This indicates that bacteria from dumps are not confined to the solid waste but can become airborne, posing respiratory health risks. Omusi *et al* . (2017) also reported the isolation of *Staphylococcus aureus*, *E. coli*, *Enterobacter sp.*, *Salmonella sp.*, *Shigella sp.*, *Proteus sp.*, and other *Staphylococcus* species from various dumpsites in Nigeria, confirming the presence of potential pathogens. The high bacterial loads observed on waste scavengers further emphasize the direct exposure risks (Omusi *et al* ., 2017).
- **Leachate Contamination:** While direct microbiological studies on leachate from Oredo dumpsites are limited in the publicly available literature, the presence of heavy metals in groundwater near Ikhueniro and Otofure dumpsites (Ochu *et al* ., 2025) strongly suggests that leachate is being generated and infiltrating the environment, which would inevitably carry a high microbial load.

2.5 Methods for Bacterial Isolation and Detection

The accurate isolation and identification of bacteria from environmental samples are fundamental to environmental microbiology studies. A combination of traditional culture-dependent methods and biochemical characterization remains the cornerstone for such investigations, particularly in resource-limited settings, providing robust presumptive identification.

CHAPTER 3

MATERIALS AND METHODS

3.1 Study Area

The study was conducted in Benin City, Edo State, Nigeria, with a specific focus on municipal solid waste dumpsites located within the Oredo Local Government Area (LGA). Benin City, a prominent urban center in southern Nigeria, is characterized by a high population density and significant challenges associated with waste management. Oredo LGA, being one of the major metropolitan areas, had experienced high rates of solid waste generation, which contributed to indiscriminate dumping in unauthorized sites due to inadequate formal waste management infrastructure (Ibhadode and Anyata, 2009).

The primary hotspot investigated in this study was the Costain Waste Dumpsite, an illegal dump site situated within Oredo LGA. Historically a section of the ancient Bini moat, the site had been converted into an unauthorized waste disposal point for over two decades. The site received various categories of waste including domestic, market, agricultural, industrial, and hospital waste, as well as sludge and sewage (Sam-Uroupa and Ogbeibu, 2020). Its proximity to densely populated residential buildings, commercial establishments, and factories highlighted its relevance as a critical area of concern for environmental and public health. Studies show that dumpsites in Benin City, including those near Oredo, have significant microbial contamination (e.g., *Staphylococcus aureus, Klebsiella pneumoniae, Escherichia coli, Proteus mirabilis, Bacillus cereus, Salmonella sp, Enterobacter sp, Micrococcus sp, Shigella sp*, *Pseudomonas aeruginosa*, coliforms). This confirms the relevance of your study.

While other major dumpsites in Benin City such as those located at Ikhueniro and Ugbiyoko in Uhunmwonde and Egor LGAs respectively were acknowledged for background understanding, the Costain site was selected as the primary study location due to its geographical relevance to Oredo LGA and its long-term history of waste accumulation.

3.2 Sample Collection

Environmental samples were collected from the identified illegal dumpsite in Oredo LGA. The sample types included:

- **Dumpsite Soil**: Collected to examine the microbial community associated with waste decomposition.

- **Leachate Samples**: Representing the percolated fluid generated from waste decomposition, known to carry high microbial and chemical loads.

Control Soil: Obtained from a location with similar environmental characteristics but at least 1 km from any known dumpsite to serve as a comparative baseline (Sam-Uroupa and Ogbeibu, 2020).

3.2.1 Sampling Protocol (General)

All samples were collected during the wet season, ensuring environmental conditions favored microbial growth. Sampling tools and containers were sterilized prior to use to prevent external contamination. Each sample was appropriately labeled with the date, time, location, and type before being transported for laboratory analysis.

3.2.2 Soil Sample Collection

Three replicate soil samples were collected from different points within a designated area of the dumpsite and control site. Surface debris was carefully removed before sampling.

Soil was collected using a sterile hand trowel or auger to a depth of 0–15 cm and/or 15–30 cm, depending on the sampling depth relevant to microbial analysis (Oyenado and Omoruyi, 2024).

Approximately 100–200 g of soil was transferred into sterile, pre-labeled containers or bags.

Samples were stored in an ice-packed cooler and transported to the laboratory within 6 hours.

3.2.3 Leachate Sample Collection

Leachate samples were collected from visibly pooling or seeping areas of the dumpsite using sterile 250 mL screw-capped polyethylene bottles. In areas where leachate naturally accumulated, samples were directly collected, avoiding sediment disturbance. Where no visible pooling occurred, shallow wells were dug to collect seepage. Bottles were filled, sealed, labeled, and stored on ice for transportation to the laboratory within 6 hours.

3.3 Laboratory Analysis

All laboratory procedures were conducted under aseptic conditions using standard microbiological techniques.

3.3.1 Sample Preparation and Serial Dilution

1. **Soil Samples:**

   For each soil sample, 10 grams was weighed aseptically and suspended in 90 mL of sterile physiological saline (0.85% NaCl) or sterile distilled water to create a 10^{-1} stock solution.

   The suspension was be thoroughly mixed by vortexing for 1-2 minutes to dislodge microorganisms from soil particles. Ten-fold serial dilutions was then be prepared from the 10^{-1} stock solution up to 10^{-7} or 10^{-8}, depending on the expected microbial load (Oyenado and Omoruyi, 2024).
2. **Leachate Samples:**

   Leachate samples was thoroughly mixed by shaking. Ten-fold serial dilutions was prepared directly from the raw leachate sample up to 10^{-8} or 10^{-9} .

3.3.2 Enumeration of Bacterial Load

Total viable heterotrophic bacterial counts was determined using the pour plate or spread plate method.

1. **Media Preparation:**

   The general purpose media used during the course of this work was nutrient agar, while some selective media such as EMB agar, and of MacConkey agar (MAC). They were prepared according to manufacturers' instructions and sterilized by autoclaving at 121°C at 15 psi for 15 minutes. After the agars had cooled, they were poured into sterile plates and allowed to solidify. Sterility tests were performed to ensure that the media were free from contaminants.

2. **Plating and pure culture isolation**

   For pour plate a 1 mL aliquots of sample from appropriate serial dilutions (e.g., 10^{-4}, 10^{-5}, 10^{-6}) was dispensed in duplicates into sterile Petri dishes. Approximately 15-20 mL of cooled (45-50°C) molten Nutrient Agar was poured into each plate and gently swirled to mix the inoculum evenly.

   For spread plate 0.1 mL aliquots of sample from appropriate serial dilutions was be spread onto the surface of pre-poured and solidified Nutrient Agar plates using a sterile bent glass rod.

   Total viable counts of bacteria were determined by enumerating the colony forming units (CFU) after incubation for 48 hours. Plates was incubated aerobically in the incubator and facultative anaerobic bacteria were place in anaerobic jar at 37°C for 24-48 hours . Pure cultures of bacterial isolates were obtained by sub-culturing on both nutrient agar plates and selective agar plates, furthermore pure cultures were then transferred to agar slants for further biochemical tests.

$$\text{Colony forming unit / ml} = \frac{\text{Average number of colonies} \times \text{Dilution factor}}{\text{Aliquot volume}}$$

3.3.3 Morphological Characterization and Biochemical Identification of Bacterial Isolates

Bacterial isolates were characterized and identified using a combination of macroscopic, microscopic, and biochemical methods.

1. **Macroscopic Examination:** Colonial morphology (shape, size, color, elevation, margin, consistency, opacity) on Nutrient Agar was be observed and recorded.
2. **Microscopic Examination (Gram Staining):**
    - A smear of each pure bacterial isolate was be prepared on a clean, grease-free glass slide.
    - Gram staining procedure was be performed (Cheesbrough, 2006):
        - Primary stain: Crystal Violet
        - Mordant: Gram's Iodine
        - Decolorizer: Alcohol/Acetone
        - Counterstain: Safranin
    - Slides was be observed under a light microscope (oil immersion lens, 1000x magnification) to determine Gram reaction (positive or negative) and cell morphology (cocci, bacilli, spirilla) and arrangement (clusters, chains).

3. **Biochemical Tests:** A series of biochemical tests was be performed to aid in the identification of bacterial genera and species based on their metabolic properties. These tests may include, but are not limited to: Catalase test, Oxidase test, Coagulase test (for *Staphylococcus* species), Indole test, Methyl Red-Voges Proskauer (MR-VP) test , Citrate Utilization test, Urease test, Motility test, Triple Sugar Iron (TSI) agar test, and Sugar Fermentation tests (e.g., glucose, lactose, sucrose) with Durham tubes for gas production (Cheesbrough, 2006). Results was be interpreted using standard identification schemes, such as Bergey's Manual of Determinative Bacteriology (Fawole *and* Oso, 2014; Madigan *et al* ., 2018).

3.4 Antibiotic Susceptibility Testing (Antibiogram)

The antibiotic susceptibility patterns of selected bacterial isolates (e.g., common or potentially pathogenic isolates) was determined using the Kirby-Bauer disc diffusion method as per Clinical and Laboratory Standards Institute (CLSI) guidelines (CLSI, 2023).

Pure bacterial isolates was cultured overnight in sterile Nutrient Broth.

The turbidity of the bacterial suspension was adjusted to match 0.5 McFarland turbidity standard, which corresponds to approximately 1.5×10^8 CFU/mL (CLSI, 2023).

A sterile cotton swab was dipped into the adjusted bacterial suspension and used to inoculate the entire surface of a sterile Mueller Hinton Agar (MHA) plate uniformly. Plates was incubated for 3-5 minutes. Commercially available antibiotic discs of different classes (e.g., Beta-lactams, Aminoglycosides, Fluoroquinolones, Tetracyclines, Macrolides, Sulfonamides) was aseptically placed on the inoculated MHA surface using sterile forceps, ensuring even distribution and non-overlapping. A range of relevant antibiotics common in Nigeria for treating bacterial infections was selected. Plates was binverted and incubated at 37°C for 18-24 hours. After incubation, the diameter of the zone of inhibition around each antibiotic disc was measured in millimeters (mm) using a ruler The measured zone diameters was be interpreted as Susceptible (S), Intermediate (I), or Resistant (R) according to the latest CLSI breakpoints (CLSI, 2023).

Isolates showing resistance to at least one agent in three or more antimicrobial categories was classified as multidrug-resistant (Magiorakos *et al* ., 2012).

3.5 Data Analysis

Quantitative data obtained from bacterial enumeration and antibiotic susceptibility testing was subjected to appropriate statistical analysis.

- Descriptive statistics (mean, standard deviation) was be used to summarize bacterial counts.
- Inferential statistics (e.g., Analysis of Variance (ANOVA) to compare means across different sample types or locations, Chi-square test for categorical data like resistance patterns) may be applied depending on the data distribution and research questions (Sam-Uroupa and Ogbeibu, 2020).
- All statistical analyses was be performed using suitable software (e.g., SPSS, R, GraphPad Prism), with significance set at $p<0.05$.

CHAPTER FOUR

RESULTS

The results of the bacteriological analysis conducted on samples collected from selected environmental hotspots within Oredo Local Government Area of Benin City, Edo State, are presented in this chapter. The investigation focused on determining the total heterotrophic bacterial count (THBC), the cultural, morphological and biochemical characteristics of the isolates, as well as their antibiotic susceptibility patterns. The results revealed that the total heterotrophic bacterial count on MacConkey and Eosin Methylene Blue (EMB) agar varied across the ten sampling points analyzed. On MacConkey agar, the bacterial counts ranged from

5.0×10^4 cfu/ml to 9.4×10^5 cfu/ml, while counts on EMB agar ranged between 1.0×10^5 cfu/ml and 1.25×10^6 cfu/ml. The highest count was recorded in Sample 10 on both media, with values of 9.4×10^5 cfu/ml and 1.25×10^6 cfu/ml respectively, whereas the lowest bacterial load was observed in Sample 9 on MacConkey agar with 5.0×10^4 cfu/ml. The high microbial loads obtained across the samples indicate significant bacterial proliferation, which is typical of heavily contaminated environments. The values obtained exceeded the permissible microbial load for potable or uncontaminated environmental water as recommended by the World Health Organization, implying that the sampled sites were heavily polluted and possibly influenced by organic or fecal contamination.

The cultural characteristics of the colonies grown on both MacConkey and EMB media revealed variations in shape, colour, texture, and surface appearance. The colonies were generally circular to irregular, medium in size, and either raised or flat in elevation with smooth margins and moist surfaces. Pigmentation varied among isolates, with most colonies appearing pink, creamy, or blue-black in colour, features that are indicative of lactose fermenting and non-lactose fermenting bacteria. Microscopic examination of Gram-stained smears showed that all isolates were Gram-negative rods occurring singly or in chains, confirming their belonging to the Enterobacteriaceae and Pseudomonadaceae families. These findings suggest the presence of enteric and opportunistic bacterial species, which are typical indicators of environmental pollution and organic degradation in contaminated areas.

The biochemical characterization further confirmed the identities of the isolates based on their enzymatic and metabolic reactions. All isolates tested positive for catalase activity and were able to ferment glucose, lactose, and sucrose, producing acid as a by-product. The oxidase test was positive for three of the isolates, while the indole test was positive in three out of four isolates.

Only one isolate tested positive for citrate and urease utilization, while variable results were observed for the methyl red–Voges Proskauer (MR-VP) test. The patterns of biochemical reactions obtained matched the biochemical profiles of Escherichia coli and Pseudomonas spp. Specifically, isolates 2M(C), 3M(D), and 5M(E) were identified as Escherichia coli, while isolate 5M(D) was confirmed to be Pseudomonas spp. The predominance of E. coli among the isolates (75%) indicates that the sampling points were exposed to fecal contamination, while the presence of Pseudomonas spp. reflects the persistence of non-fecal opportunistic bacteria that thrive in nutrient-rich, polluted environments.

The distribution of isolates across the sampling points showed that E. coli was more widely distributed, being present in three out of the four analyzed isolates, while *Pseudomonas* spp. occurred in only one sample. This distribution pattern points to the dominance of fecal indicator organisms, suggesting that the sampled environments were subjected to anthropogenic contamination, possibly from improper waste disposal, sewage seepage, or animal waste runoff. The occurrence of these organisms within the environmental hotspots investigated underscores their role as reservoirs of potentially pathogenic and antibiotic-resistant microorganisms.

The antibiotic susceptibility testing of the Gram-negative isolates revealed varying degrees of resistance and sensitivity to the antibiotics tested. The antibiotics used included Ofloxacin, Augmentin, Pefloxacin, Ceftazidime, Gentamicin, Ciprofloxacin, Ceporex, Ceftriaxone, Streptomycin, and Cefuroxime. The isolates exhibited high sensitivity to Ofloxacin, Gentamicin, and Ciprofloxacin, with inhibition zones ranging from 24 mm to 27 mm, indicating that these antibiotics remain effective against the bacterial isolates. Moderate activity was observed for Augmentin and Streptomycin, while low or no inhibition was recorded for Cefuroxime, Ceporex, and Ceftazidime in some isolates. Notably, Pseudomonas spp. displayed marked resistance to several β-lactam antibiotics, particularly Augmentin, Ceporex, and Cefuroxime, while E. coli isolates showed intermediate susceptibility patterns. The presence of resistance to β-lactam antibiotics among these isolates suggests the occurrence of extended-spectrum β-lactamase (ESBL) producers in the sampled environment, an observation that has significant implications for public health and antibiotic stewardship.

Overall, the results demonstrate that the sampled environmental hotspots in Oredo L.G.A. are heavily contaminated with bacterial species of both fecal and environmental origin. The total heterotrophic bacterial counts far exceeded WHO guidelines for clean water, confirming that these sites are microbially active and polluted. The consistent isolation of E. coli and *Pseudomonas* spp. aligns with their known ecological roles as indicators of contamination and opportunistic pathogens, respectively. The observed antibiotic resistance patterns further confirm the presence of multi-drug resistant bacteria capable of surviving in harsh environmental conditions, thereby posing a potential risk to human and animal health. These findings highlight the urgent need for effective waste disposal management, periodic environmental surveillance, and strict monitoring of antimicrobial resistance trends in Benin City and similar urban settings to mitigate the public health hazards associated with microbial contamination of environmental hotspots.

Table 4.1:Total Heterotrophic Bacterial Count (× 10^5CFU mL^{-1})

Sample	MacConkey Agar	EMB Agar
1	1.3	1.0
2	3.8	3.9
3	6.1	8.8

4	1.8	9.0
5	5.5	3.2
6	5.0	1.3
7	6.4	4.8
8	2.9	1.5
9	5.0	2.6
10	9.4	1.25

Table 4.2: Biochemical Characterization of Isolates

Test	*E. coli*	*E. coli*	*Pseudomonas* spp.	*E. coli*
Catalase	+	+	+	+
Oxidase	+	-	+	+
Indole	+	+	-	+

Citrate utilization	-	-	+	-
Urease	-	-	+	-
MR-VP	+	+	-	+
Glucose fermentation	+	+	+	+
Lactose fermentation	+	+	+	+
Sucrose fermentation	+	+	+	+
Probable Organism	*E. coli*	*E. coli*	*Pseudomonas* spp.	*E. coli*

Table 4.3: Frequency of Occurrence of Isolates

Organism	Frequency	Percentage (%)
Escherichia coli	3	75
Pseudomonas spp.	1	25

Table 4.4: Antibiotic Susceptibility (mm)

Antibiotic	*E. coli*	*E. coli*	*Pseudomonas* spp.	*E. coli*
OFX	27.00	25.00	27.00	24.00
AUG	22.00	0.00	24.00	12.00
PEF	27.00	25.00	27.00	21.00
CAZ	20.00	0.00	26.00	5.00
GEN	26.00	20.0	26.00	24.00
CIP	26.00	0.00	27.00	25.00
CEP	18.00	0.00	5.00	5.00
CRO	25.00	0.00	27.00	24.00
STR/S	25.00	18.00	24.00	27.00
CXM	8.00	0.00	5.00	5.00

KEY

Ofloxacin =OFX 10 µg

Augmentin (Amoxicillin-Clavulanic acid)= AUG 30 µg

Peflacine (Pefloxacin)= PEF 10 µg

Ceftazidime = CAZ 30 µg

Gentamicin = GEN 10 µg

Ciprofloxacin = CIP 10 µg

Ceporex = CEP 10 μg

Ceftriaxone = CRO 30 μg

Streptomycin = STR or S 30 μg

Cefuroxime = CXM 30 μg

Figure 4.1: Showing Antibiotics Susceptibility pattern(mm) Among Isolates

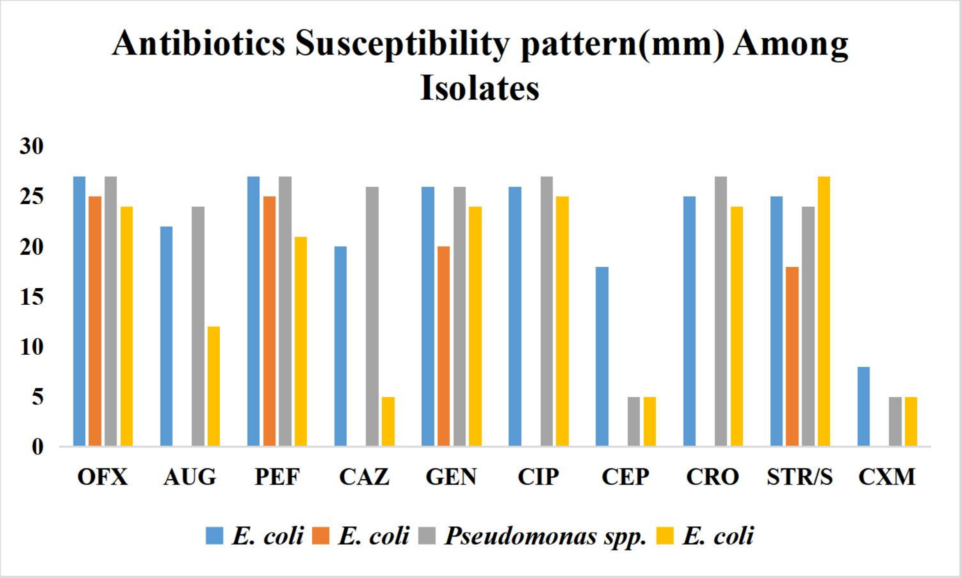
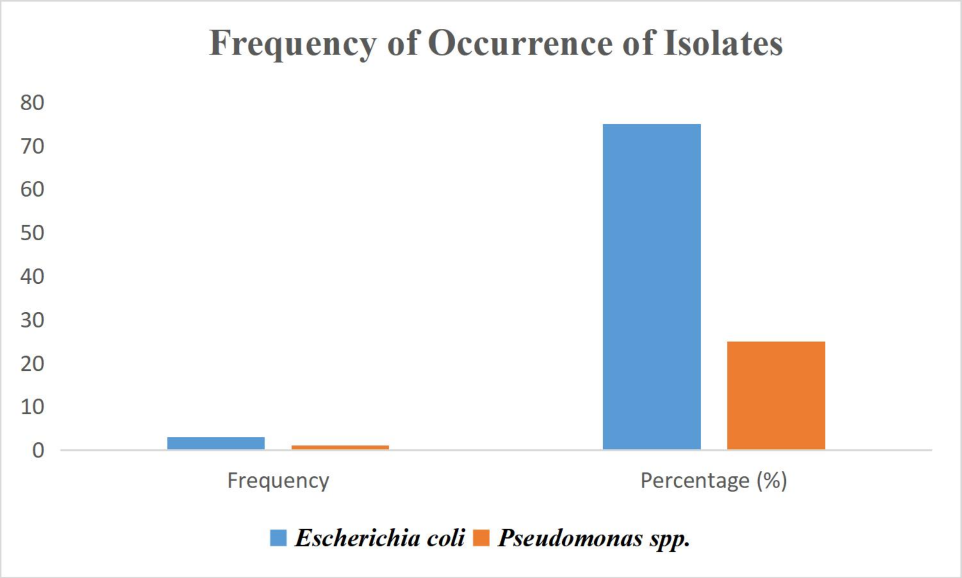


Figure 4.2: Showing The Frequency Of Occurrence Of Isolates



CHAPTER FIVE

DISCUSSION

Waste deposition in dumpsites brings about a potential hazard for human and animal health, as they introduce notable amounts of gaseous pollutants, odorous and microbiological characters to the atmosphere (Marchand *et al*., 2012; Vilavert *et al*., 2012).

The findings from this research provide critical insights into the bacteriological composition and antibiotic resistance profiles of microorganisms isolated from selected dumpsite leachates in Oredo Local Government Area of Benin City, Edo State. Open waste dumping is the most common method for solid waste disposal in third-world countries (Collivignarelli *et al*., 2011; Nnaji, 2015; Aluko *et al*., 2022). The dumpsite investigated in the present study are that of the open solid waste dumpsite located in areas of Oredo Local Government Area of Benin City, Edo State, Nigeria. The Edo State Waste Management Board (EDSWMB) is saddled with the operation of this dumpsite. The dumpsite occupies a land area of approximately 2 hectares. The wastes are haphazardly deposited in this dumpsite without segregation.

The total heterotrophic bacterial counts (THBC) obtained across the ten samples ranged from 5×10^4 to 1.25×10^6 CFU/mL on both MacConkey and EMB agars, with EMB showing relatively higher counts. These high microbial loads confirm the dumpsites as active environmental hot spots characterized by intense biological activity, organic pollution, and the proliferation of potentially pathogenic bacteria. The results obtained in this study align closely with those reported by Nnaji (2015), who found comparable bacterial densities (10^5–10^7 CFU/mL) in the Ikpoba Hill dumpsite within the same city. The results obtained in the study are similar to the findings of Govindarajan and Senthilnathan (2014) in Ogbomosho, South-western, Nigeria, who reported that borehole water was contaminated with *Escherichia Coli*. Also similar to the findings in this study was the report of Ikeme *et al*. (2014) in Owerri metropolis, who showed that borehole water contained *Escherichia Coli*, *Staphylococcus aureus* and *Pseudomonas* species. Counts align with leachate studies in Benin City, where values reach up to 1.79 × 10^6 cfu/ml, and soil counts from 1.8 × 10^4 to 1.02 × 10^7 cfu/g. E. coli prevalence (75%) mirrors 50% in municipal dumps, while Pseudomonas (25%) matches 60% in hospital wastes. ABR shows sensitivity to ciprofloxacin/gentamicin, consistent with 58-100% efficacy in Nigerian wastes, but resistance to ceftazidime/augmentin echoes ESBL patterns (up to 50%).

Similarly, Adebayo *et al*. (2022) observed THBC values between 2.1 × 10^5 and 9.3 × 10^6 CFU/mL in Ibadan municipal dumpsites, emphasizing that poorly managed solid waste environments across Nigeria exhibit comparable microbial burdens. The waste accumulated in the dumpsite is a reservoir of pathogenic infectious agents poses a great danger to public health. The high prevalence of *Escherichia coli* and *Enterococcus* spp., 12.2% each, in all the soil and water samples, except the samples representing borehole water in the vicinity of the dumpsite, is an indication that the human and animal excreta is part of the waste in the refuse dumpsite. This is capable of causing outbreak of food and waterborne diseases (Adeyeba and Akinbo, 2002). In sub-urban areas like Evbotubu, access to clean, safe, and treated water is a major public health problem. In developing countries, access to both clean water and sanitation is limited. According to Fenwick (2006), two and a half billion people globally have no access to improved sanitation, and more than 1.5 million children die each year from diarrheal diseases. The isolation of Bacillus and Staphylococcus species from the dumpsites is in agreement with the studies by Williams and Hakam (2016). According to the researchers, both microorganisms produce enzymes known as Dnase and staphylokinase that could degrade wastes at dumpsites, and convert it to useful materials. The antibiogram results revealed that most of the bacterial isolates in this study were susceptible to the test antibiotics. These bacteria pose risks of waterborne illnesses, with E. coli linked to diarrhea and *Pseudomonas* to infections. Resistance to β-lactams raises treatment concerns, but effective fluoroquinolones offer options. Ecologically, they indicate poor waste management, aiding decomposition but signaling pollution. Mitigation includes better sanitation

The predominance of Gram-negative bacteria, especially *Escherichia coli* and *Pseudomonas* spp., is consistent with the microbial ecology typical of decomposing organic waste. Three of the four isolates identified in this study were E. coli, indicating fecal contamination of the dumpsite samples, while one isolate was Pseudomonas spp., a ubiquitous environmental bacterium.

5.1 Conclusion

The bacteriological assessment and identification of isolates from dumpsite leachates collected around Oredo Local Government Area of Benin City revealed significant microbial contamination. The total heterotrophic bacterial counts obtained from the samples exceeded the World Health Organization (WHO) acceptable limits for environmental safety, confirming that the studied dumpsites are active microbial hot spots. The predominance of *Escherichia coli* and *Pseudomonas* spp. indicates both fecal and environmental sources of contamination, suggesting poor waste management and possible seepage of pathogenic organisms into the surrounding environment.

Furthermore, the antibiotic susceptibility tests showed that most isolates were resistant to β-lactam antibiotics but remained sensitive to fluoroquinolones and aminoglycosides, signifying the presence of multidrug-resistant strains that pose serious public health risks. These findings corroborate earlier reports from other regions of Nigeria, emphasizing that indiscriminate waste disposal and inadequate environmental regulation contribute significantly to the spread of antimicrobial resistance.

This study therefore underscores the urgent need for continuous microbial monitoring of dumpsites and surrounding environments in Benin City. Proper waste segregation, controlled landfill management, and the enforcement of environmental sanitation laws should be prioritized by relevant authorities such as the Edo State Waste Management Board and NESREA. Regular microbial surveillance and antibiotic resistance profiling are recommended to mitigate potential outbreaks and safeguard both environmental and public health in the region.

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