Isolation and Characterization of Microorganisms Found in Dumpsite Soils in Federal University Oye-Ekiti (Oye-Campus), Ekiti State, Nigeria

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ABSTRACT

The increasing volume of unmanaged solid waste poses significant environmental and public health challenges, particularly within university environments. This study investigated the isolation and characterization of microorganisms present in dumpsite soils at the Federal University Oye-Ekiti (Oye Campus), Ekiti State, Nigeria. Soil samples were collected from residential halls, academic areas, and a control site, followed by physicochemical and microbiological analyses. Physicochemical parameters revealed higher values in dumpsite soils compared to the control, including electrical conductivity (0.0590 ± 0.0014 µS/cm), moisture content (0.0550 ± 0.0014%), and organic matter (1.8510 ± 0.0042%) in residential areas, while the control recorded 0.0215 ± 0.0021 µS/cm, 0.0280 ± 0.0014%, and 1.5835 ± 0.0050%, respectively. Soil pH ranged from 7.90 ± 0.02 to 8.18 ± 0.01, indicating a neutral to slightly alkaline environment favorable for microbial proliferation. Microbial analysis showed high bacterial and fungal loads, with bacterial counts reaching 1.4 × 10^7 CFU/g in academic areas and fungal counts peaking at 8.5 × 10^6 CFU/g in residential dumpsites. Identified bacterial isolates included Bacillus spp., Staphylococcus spp., Escherichia coli, and Pseudomonas spp., while fungal isolates comprised Aspergillus spp., Penicillium spp., and Rhizopus spp. These findings indicate the presence of diverse and metabolically active microbial communities adapted to waste-rich environments. The results demonstrate that dumpsite soils within the study area support abundant and diverse microorganisms, influenced by favorable physicochemical conditions. This study provides baseline data essential for environmental monitoring and highlights potential public health risks associated with improper waste disposal, while supporting the development of sustainable waste management strategies.

Keywords: *Dumpsites, Physicochemical analysis, Microbial diversity, Waste management, Solid waste*

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INTRODUCTION

Environmental pollution caused by improper waste management continues to be one of the major threats to ecological sustainability and public health, especially in developing countries like Nigeria. The rapid growth of cities, increasing population, and changing patterns of consumption have led to a sharp rise in the amount and complexity of solid waste generated, placing severe pressure on existing waste management systems (Ukala and Owamah, 2020; Omokaro *et al*., 2025). As a result, uncontrolled disposal methods such as open dumping and poorly managed landfill sites are common, contributing to soil degradation, surface and groundwater contamination, and increased health risks for surrounding communities (Omokaro *et al.,* 2025).

In many Nigerian towns and cities, waste is often deposited in open dumpsites that contain a mix of biodegradable and non-biodegradable materials, including food residues, plastics, metals, and electronic waste. These dumpsites pose ongoing threats to soil and water quality and create environments that favour the survival and proliferation of microbes (Ogunyemi *et al.,* 2025). Nigeria's steadily growing population, estimated to exceed 200 million people, further amplifies the waste management challenge. Weak infrastructure, inadequate funding, and limited enforcement of environmental laws have compounded the problem, resulting in persistent waste accumulation and environmental degradation in both urban and institutional settings such as university campuses (Ukala and Owamah, 2020; Omokaro *et al.,* 2025).

At the Federal University Oye-Ekiti (FUOYE), Oye Campus, the rapid increase in student numbers, academic activities, and campus expansion has strained existing waste disposal systems. Refuse generated from halls of residence, lecture theatres, laboratories, and commercial centers is often discarded in nearby open spaces, creating unsanitary conditions that threaten soil and water quality and may pose public health hazards. The dumpsites at FUOYE, characterized by a continuous influx of diverse organic and inorganic wastes, provide an opportunity to study the microorganisms that inhabit these soils. Other research in southwest Nigeria has shown that soils from waste disposal sites can host a wide range of bacteria, with diverse community structures when assessed using molecular techniques (Ogunyemi *et al*., 2025).

The types of waste generated within university environments are varied and include solid waste (e.g. paper, plastics, glass), food waste (e.g. kitchen residues and leftovers), electronic waste (e-waste such as discarded computers and batteries), laboratory waste, hazardous substances, and wastewater. Each category has distinct implications for environmental quality and health (Ukala and Owamah, 2020). Open dumping remains widely practiced due to its low cost and minimal regulation. When rainwater filters through waste piles, it can generate leachate that infiltrate soils and disrupt natural microbial communities, affect soil chemistry, and contaminate groundwater (Adedinni *et al.,* 2023; Ojoawo *et al.,* 2012). Despite these recognized environmental impacts, there is still limited published information on the specific microbial composition of soils at the dumpsites within the Federal University Oye-Ekiti (Oye Campus). Previous studies in other parts of Nigeria have documented bacteria and fungi in waste-impacted soils, indicating the ecological significance of these organisms in nutrient cycling and decomposition (Oni *et al.,* 2021). Given the important roles microorganisms play in waste decomposition and biogeochemical processes, it is necessary to investigate the microbial populations present in the dumpsite soils at FUOYE. Therefore, this study aims to isolate and characterize the microorganisms present in these soils.

METHODOLOGY

Study Area

The Federal Government of Nigeria founded Federal University Oye-Ekiti (FUOYE) in 2011 as part of a plan to increase access to high-quality postsecondary education (Figure 1). It is situated in the southwest part of Nigeria in Oye-Ekiti, Ekiti State. The university operates two main campuses: Oye (main campus) and Ikole. Geographically, the main campus of Federal University Oye-Ekiti is located at roughly latitude 7.7915° N and longitude 5.3245° E. The institution is situated within a semi-urban area, providing a mix of rural tranquility and access to urban infrastructure. The surrounding environment supports agricultural, educational, and socio-economic activities that contribute to student learning and research.

Sample Site

Soil samples were collected from two main dumpsites located within the Federal University Oye-Ekiti (FUOYE), Oye Campus. The first site was in the school residential halls (Latitude 7°6′28″N and Longitude 5°18′55″E) situated along Phase 2 and Phase 3 roads, while the second site was within the academic building environment (Latitude 7°6′45″N and Longitude 5°19′16″E) located along Phase 1 road. Additionally, an undisturbed area within the campus served as the control site (Latitude 7°6′32″N and Longitude 5°18′50″E).

Soil Sample Collection and Preparation

Soil samples were collected using a random sampling technique, to ensure representativeness and minimize spatial bias, from dumpsites containing mixed waste materials such as organic residues, plastics, metals, paper, and decomposed matter. At each site, samples were collected from three randomly selected points at a

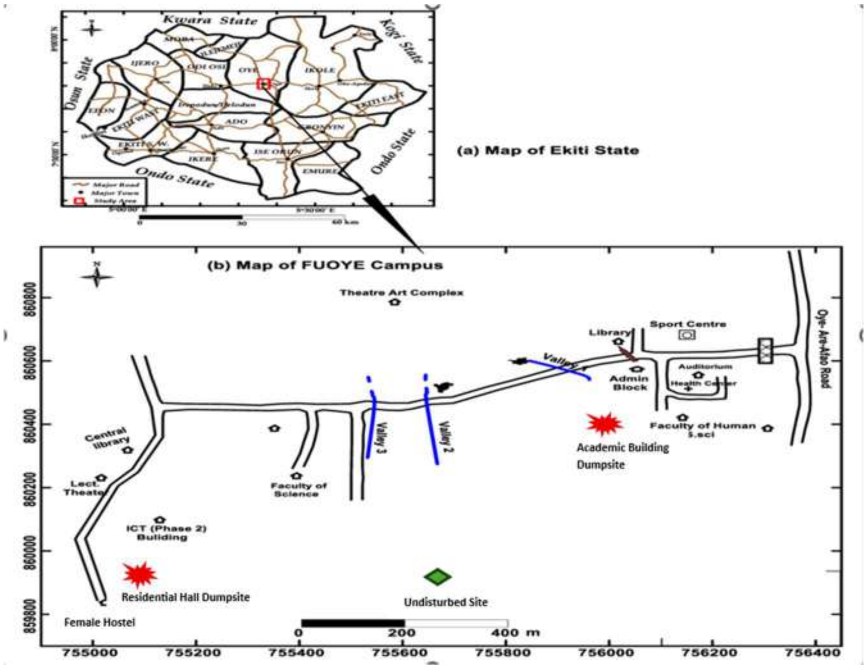

Figure 1: Map of Federal University Oye-Ekiti, (Oye-campus), Ekiti State, Nigeria.

depth of 0–15 cm using pre-sterilized soil augers and composited to obtain a representative sample per location. A control soil sample was collected from an undisturbed area away from dumpsite influence. Composite samples were placed in sterile, labeled sampling bags and transported to the Environmental Management and Toxicology Laboratory, Federal University Oye-Ekiti.

Physicochemical Analysis of Soil Samples

Physicochemical properties of the soil samples, including pH, electrical conductivity (EC), moisture content, and total organic matter, were determined using standardized procedures. Soil pH was measured potentiometrically in a soil–water suspension following ASTM D4972 (ASTM International, 2024). Moisture content was determined by oven-drying to constant weight, while total organic matter was quantified using the loss-on-ignition method in accordance with ASTM D2974 (ASTM International, 2021). Electrical conductivity (EC) was measured in soil extracts using a calibrated conductivity meter, based on ASTM D1125 (ASTM International, 2019), with methodological consistency ensured using internationally recognized protocols (ISO, 2018; APHA *et al*., 2017).

Microbial Analysis of Soil Samples

Bacterial Enumeration and Identification

Soil samples were analyzed for bacterial load and diversity using standard microbiological procedures. Nutrient Agar (NA) and Sabouraud Dextrose Agar (SDA) were prepared according to manufacturers' instructions and sterilized by autoclaving at 121 °C and 15 psi for 15 min. Sterile physiological saline (0.9% NaCl) was used as the diluent (Cheesbrough, 2000). Ten-fold serial dilutions of soil samples were carried out following the method described by Al-Mugren *et al*. (2025). Aliquots (1 mL) from appropriate dilutions (10^{-4} and 10^{-6}) were pour-plated on NA in triplicate and incubated at 37 °C for 18–24 h. Total viable bacterial counts were determined and expressed as colony-forming units per gram of soil (CFU/g) (Adeyemo *et al*., 2020). Distinct colonies were sub-cultured to obtain pure isolates. Preliminary identification was based on colony morphological characteristics, while further characterization was carried out using Gram staining and standard biochemical tests, including catalase, citrate utilization, indole, methyl red, and sugar fermentation tests, following established protocols (Cheesbrough, 2000; Holt *et al*., 1994).

Fungal Enumeration and Identification

Fungal populations in soil samples were determined using standard mycological methods. Ten-fold serial dilutions were prepared using sterile physiological saline following Al-Mugren *et al*. (2025). Aliquots (1 mL) from appropriate dilutions (10^{-4} and 10^{-6}) were pour-plated on Sabouraud Dextrose Agar (SDA), prepared and sterilized according to the manufacturer's instructions. All plates were incubated at 30 °C for 3–5 days. Soil samples from an undisturbed area were included as controls. Fungal colonies were enumerated and expressed as colony-forming units per gram of soil (CFU/g) by multiplying the mean colony count by the corresponding dilution factor (Adeyemo *et al*., 2020). Distinct colonies were sub-cultured on fresh SDA to obtain pure isolates. Identification of fungal isolates was based on cultural and microscopic characteristics. Colony morphology, including color, texture, and surface appearance, was assessed following Akinbobola *et al.* (2022). Microscopic examination was carried out using lactophenol cotton blue staining, and isolates were identified based on hyphal and spore structures with reference to standard fungal identification keys and atlases (Devi, 2011; *Kidd et al*., 2016).

Data Analysis

All physicochemical data were analyzed using IBM SPSS (version 19). Results were summarized using descriptive statistics (mean ± standard deviation). Differences between dumpsite soils and control samples were assessed using one-way analysis of variance (ANOVA). When significant differences were observed, Duncan's Multiple Range Test (DMRT) was applied as a post hoc test to separate mean values. Statistical significance was accepted at $p < 0.05$.

RESULTS AND DISCUSSION

Physicochemical Analyses of Soil Samples

Electrical conductivity (EC) measures the soil's capacity to conduct electric current, which correlates with its ionic content, primarily from salts, dissolved organic compounds, and microbial by-products. Among the studied locations, EC was highest in the school residential halls (0.0590 ± 0.0014 μS/m), followed by the academic building environment (0.0510 ± 0.0014 μS/cm), and lowest in the control soils (0.0215 ± 0.0021 μS/m) (Table 1). The significant difference ($p < 0.05$) observed across these sites reflects varying levels of anthropogenic inputs, particularly from decomposing organic waste, detergents, and leachates commonly associated with residential activities. Similar trends have been reported in dumpsite soils, where elevated EC values were linked to the accumulation of electrolytes and organic leachates from municipal solid waste (Ogwuegbu and Muhanga, 2005; Gupta *et al.,* 2019). Elevated EC has also been associated with enhanced microbial metabolism and bioavailability of nutrients, thereby supporting the proliferation of bacteria and fungi (Brady and Weil, 2016). High EC in dumpsites also indicates enriched metabolic environments, potentially fostering the activity of hydrocarbon-degrading bacteria, such as *Pseudomonas aeruginosa* and *Bacillus subtilis* (Das and Chandran, 2011). Soil pH was generally neutral to slightly alkaline across all sites, ranging from 7.90 ± 0.0849 in the school residential halls to 8.1850 ± 0.0919 in the control soils (Table 1). Statistically, there was no significant difference ($p > 0.05$) in pH among the locations, suggesting that pH may not be a limiting factor for microbial diversity in this environment. Neutral to alkaline pH conditions are favorable for the growth of many bacterial taxa, especially *Bacillus subtilis, Staphylococcus aureus, Micrococcus luteus, Pseudomonas aeruginosa, Enterococcus faecalis*, which are commonly recovered from compost and organic waste-rich soils (Madigan *et al*., 2018; Fierer and Jackson, 2006). Previous studies have also demonstrated that many soil bacteria exhibit optimal growth within a pH range of 6.5–8.5, supporting high microbial diversity and metabolic activity under such conditions (Lauber *et al*., 2009). Therefore, the observed pH profile in this study provides a conducive environment for the isolation of metabolically versatile microbial strains from the sampled soils.

Moisture content varied significantly among sites. The school residential halls exhibited the highest moisture level (0.0550 ± 0.0014%), while the academic building environment had the lowest (0.0225 ± 0.0021%), with control soils falling in between (0.0280 ± 0.0014%) (Table 3.1). The statistically significant differences ($p < 0.05$) imply that moisture availability is influenced by site-specific conditions such as vegetative cover, waste accumulation, and water drainage patterns. Soil moisture plays a pivotal role in microbial survival by regulating nutrient solubility, enzymatic activity, and osmotic balance. Higher moisture levels support active microbial communities, particularly fungi and facultative anaerobes, by promoting substrate diffusion and organic matter decomposition (Paul, 2014; Prescott *et al*., 2017).

Organic matter content was significantly higher in the academic building environment (2.1865 ± 0.0050%) compared to the school residential halls (1.8510 ± 0.0042%) and control soils (1.5835 ± 0.0050%) (Table 3.1). Organic matter (OM) serves as the primary carbon source for microbial metabolism, and its abundance directly correlates with the richness of the microbial trophic network. OM enhances soil fertility, enzyme secretion, and biochemical cycling of nutrients such as nitrogen and phosphorus.

The elevated OM in the academic building environment dumpsite could be attributed to the disposal of paper materials, food remains, and laboratory waste, all of which serve as decomposable substrates. Studies have shown that soils with higher organic matter content typically support greater microbial biomass and colony-forming units due to increased nutrient availability (Wardle, 2002; Nguyen *et al*., 2018). These physicochemical conditions suggest that the dumpsite soils of Federal University Oye-Ekiti (Oye-campus) are nutrient-rich, microbially active environments.

The moderately alkaline pH, enhanced organic matter, and moisture variability create ecological niches conducive for the survival and function of indigenous microbial populations.

Table 1: Physicochemical Parameters of Selected Soil Samples in Federal University Oye-Ekiti (Oye-Campus).

Location	Electrical Conductivity (µS/cm)	pH	Moisture (%)	Organic Matter (%)
School residential halls	0.0590 ± 0.0014^{c}	7.9000 ± 0.0849^{a}	0.0550 ± 0.0014^{c}	1.8510 ± 0.0042^{b}
Academic building environment	0.0510 ± 0.0014^{b}	8.1250 ± 0.1061^{a}	0.0225 ± 0.0021^{a}	2.1865 ± 0.0050^{c}
Control soil sites	0.0215 ± 0.0021^{a}	8.1850 ± 0.0919^{a}	0.0280 ± 0.0014^{b}	1.5835 ± 0.0050^{a}

KEY: Results are means of duplicate treatments ± standard deviation.
Means followed by the same alphabet column wise indicate no significant difference ($p<0.05$)
Each superscript (a, b, c) represents a statistically distinct group as identified by post hoc (e.g., Duncan) tests at $\alpha = 0.05$

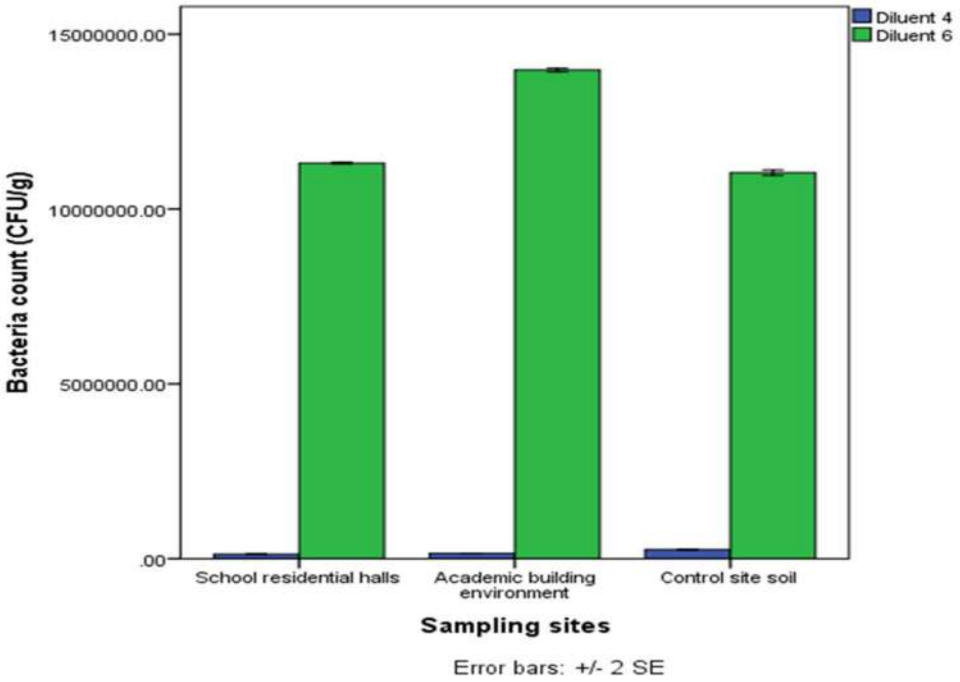

Figure 2: Bacterial Count of Selected Soil Sample in Federal University Oye-Ekiti, Ekiti State (Oye-Campus)

Microbial Analysis of the Soil Sample

Bacterial Count

The bacterial load in soil samples collected from different locations within the Federal University Oye Ekiti (Oye-Campus) varied markedly across the dilutions tested, indicating differences in microbial activity and potential organic loading. The measured colony-forming units per gram (CFU/g) at diluent 4 and diluent 6 levels provide insights into the viable bacterial populations within each environment. At the 10^{-6} dilution, the academic building environment exhibited the highest bacterial population with 1.4×10^{7} CFU/g, closely followed by the school residential halls (1.13×10^{7} CFU/g), while the control site soil had 1.1×10^{7} CFU/g (Figure 2).The relatively higher bacterial counts at the academic building environment suggest a rich microbial community possibly sustained by the presence of moderate organic residues, student and staff activities, and occasional waste discharge. Previous studies have shown that disturbed soils with greater organic inputs, such as those from human and animal activity, often support higher heterotrophic bacterial populations (Zhao *et al*., 2014; Xue *et al*., 2021). In contrast, the control soil site situated in a relatively undisturbed area showed a lower bacterial count, compared to other locations. This may suggest a stable but less densely populated microbial community, typical of less anthropogenically impacted soils. Lauber *et al.* (2023), noted that natural or fallow soils tend to maintain microbial populations adapted to nutrient cycling and soil structure maintenance, even with lower external inputs.

The school residential halls, despite housing students and being exposed to routine waste generation, recorded the lowest bacterial count at the 10^{-4} dilution and a mid-range count at 10^{-6} dilution. This pattern might indicate the presence of microbial inhibitory factors, such as heavy metals or detergents from domestic discharges. Research has demonstrated that urban soils exposed to pollutants, detergents, or heavy metals often exhibit altered microbial community structure and reduced culturable bacterial abundance at specific soil depths (Berg *et al*., 2005; Li *et al*., 2018).

The observed variations across the sites affirm the influence of human activity and environmental management on microbial abundance. Soils rich in biodegradable organic matter and with moderate moisture typically support greater bacterial populations, whereas less impacted soils show lower culturable counts under similar conditions. This pattern is consistent with studies showing that organic carbon content and anthropogenic disturbances are strong predictors of soil bacterial abundance and diversity (Fierer and Jackson, 2006; Hartman *et al*., 2018).

Morphological Characterization and Identification of Bacterial Isolates

Table 2 presents the morphological characterization of bacterial isolates recovered from the School Residential Halls (SRH), Academic Building Environment (ABE), and the Control Soil Site (CSS). The isolates exhibited considerable diversity in colony morphology, including variations in colony shape, margin, size, elevation, pigmentation, surface appearance, texture, and opacity. According to Bergey's Manual of Systematic Bacteriology, colonial morphology serves as an important preliminary criterion for bacterial identification because it reflects the physiological and adaptive characteristics of microorganisms within specific environments.

The isolates obtained from the School Residential Halls showed substantial morphological diversity, indicating the presence of heterogeneous bacterial populations within the residential environment. Isolate SRH.1 exhibited circular colonies with entire margins, convex elevation, cream coloration, smooth surfaces, and buttery texture. These characteristics are commonly associated with human-associated bacteria such as *Staphylococcus* species, which are frequently isolated from indoor environments due to continuous human contact. Similar findings were reported in hospital waste environments where smooth, creamy, and opaque bacterial colonies predominated among isolates recovered from highly populated environments (Adebowale et al., 2026). This suggests that environments with intense human activities encourage the proliferation of opportunistic and human-associated bacterial species.

SRH.2 displayed translucent grayish-white colonies with moist surfaces, suggesting the presence of bacteria adapted to humid environmental conditions. Moist and translucent colonies are often characteristic of environmental bacteria capable of surviving under high moisture conditions. This observation is consistent with the findings of morphologically diverse bacterial isolates with smooth and moist colonies recovered from borehole water systems (Oghonim et al., 2026). The similarity in colonial characteristics indicates that moisture availability significantly influences bacterial adaptation and colony formation.

The irregular green-pigmented and mucoid colonies observed in SRH.3 are suggestive of environmentally persistent bacteria such as *Pseudomonas* species. The glistening and mucoid appearance may indicate extracellular polysaccharide production associated with biofilm formation and enhanced environmental persistence. Similar adaptive characteristics, including pigmentation and mucoid growth patterns linked to stress tolerance, were reported among lead-resistant bacterial isolates from industrial discharge environments (Azhar & Shoukat, 2025).

Similarly, SRH.4 produced large mucoid cream colonies with very moist surfaces, suggesting the possible presence of encapsulated bacteria capable of resisting environmental stress conditions. Mucoid colonies are often associated with bacteria possessing protective extracellular structures that enhance survival in harsh environments. Comparable observations were reported among antimicrobial-producing bacteria isolated from organic waste dumpsites, where mucoid and rough colony morphologies were associated with stress resistance and environmental adaptability (Madukairo et al., 2026).

SRH.5 demonstrated irregular lobate colonies with dry, wrinkled surfaces and rough textures, characteristics commonly associated with spore-forming bacteria such as *Bacillus* species. Wrinkled colony morphology often reflects bacterial adaptation to nutrient limitation and environmental stress. Similar findings were observed among bacterial isolates recovered from cassava farmland soils, where rough and irregular colonies were associated with environmentally resilient soil bacteria (Afunwa et al., 2025).

The isolates from the Academic Building Environment also showed important morphological variations. ABE.1 and ABE.2 exhibited circular colonies with entire margins, smooth surfaces, buttery textures, and opaque appearances. These features suggest adaptation to relatively stable indoor environmental conditions and possible association with human skin flora. Comparable findings of smooth and opaque bacterial colonies influenced by anthropogenic contamination were reported by Nwachukwu et al. (2026), who emphasized the role of human activities in shaping microbial diversity within built environments.

Notably, ABE.3 and ABE.4 displayed bright yellow and golden-yellow pigmented colonies, respectively. Pigmented bacteria are often capable of surviving oxidative and environmental stress conditions because pigments provide protective functions against environmental damage. Similar pigmented bacterial isolates were reported among waste-associated bacterial populations from hospital environments (Adebowale et al., 2026). The authors suggested that pigmentation enhances bacterial survival under stressful environmental conditions. The isolate recovered from the Control Soil Site (CSS) exhibited circular, convex, and buttery colonies similar to some isolates recovered from indoor environments. This similarity suggests possible microbial transfer between outdoor soil environments and indoor environments through dust particles, air movement, and human activities. Soil environments have similarly been identified

Table 2: The Morphological Characterization and Identification of Bacterial Species Isolated from School Residential Halls and Academic Building Environment using Bergey's Manual of Identification.

Code	Colony Shape	Margin	Size	Elevation	Color	Surface	Texture	Opacity
SRH.1	Circular	Entire	Small	Convex	cream	Smooth	Buttery	Opaque
SRH.2	Circular	Entire	Small	Flat	Grayish-white	Smooth	Moist	Translucent
SRH.3	Irregular	Undulate	Large	Raised	Green	Mucoid	Glistening	Opaque
SRH.4	Circular	Entire	Large	Convex	Mucoid cream	Very moist	Mucoid	Opaque
SRH.5	Irregular	Lobate	Large	Flat	Dull white	Dry, wrinkled	Rough	Opaque
SRH.6	Circular	Entire	Medium	Raised	Off-white	Smooth	Dry	Opaque
ABE.1	Circular	Entire	Small	Convex	Grayish	Smooth	Buttery	Opaque
ABE.2	Circular	Entire	Small	Convex	White	Smooth	Buttery	Opaque
ABE.3	Circular	Entire	Small	Convex	Bright yellow	Smooth	Dry	Opaque
ABE.4	Circular	Entire	Medium	Convex	Golden-yellow	Smooth	Buttery	Opaque
CSS	Circular	Entire	Medium	Convex	White	Smooth	Buttery	Opaque

Table 3: Biochemical Characterization of Bacteria Isolates from School Residential Halls and Academic Building Environment.

Code	Gram staining	Catalase	Citrate	Indo	M. Red	Fru.	D-Man.	D-Mal.	Detected organisms
SRH.1	*+ve*	*+ve*	*+ve*	*-ve*	*+ve*	*-ve*	*+ve*	*-ve*	*Staphylococcus epidermidis*
SRH.2	*-ve*	*+ve*	*-ve*	*-ve*	*-ve*	*+ve*	*-ve*	*-ve*	*Neisseria spp.*
SRH.3	*-ve*	*+ve*	*-ve*	*-ve*	*+ve*	*+ve*	*-ve*	*-ve*	*Pseudomonas aeruginosa*
SRH.4	*-ve*	*+ve*	*+ve*	*+ve*	*-ve*	*+ve*	*+ve*	*+ve*	*Klebsiella pneumoniae*
SRH.5	*+ve*	*+ve*	*+ve*	*-ve*	*-ve*	*+ve*	*+ve*	*+ve*	*Bacillus subtilis*
SRH.6	*+ve*	*+ve*	*-ve*	*-ve*	*+ve*	*+ve*	*+ve*	*+ve*	*Bacillus pumilus*
ABE.1	*+ve*	*+ve*	*-ve*	*+ve*	*-ve*	*+ve*	*+ve*	*+ve*	*Enterococcus faecalis*
ABE.2	*+ve*	*+ve*	*-ve*	*-ve*	*-ve*	*-ve*	*+ve*	*-ve*	*Staphylococcus epidermidis*
ABE.3	*+ve*	*+ve*	*+ve*	*-ve*	*-ve*	*-ve*	*-ve*	*-ve*	*Micrococcus luteus*
ABE.4	*+ve*	*+ve*	*+ve*	*-ve*	*-ve*	*+ve*	*+ve*	*+ve*	*Staphylococcus aureus*
CSS	*+ve*	*+ve*	*-ve*	*-ve*	*+ve*	*+ve*	*+ve*	*+ve*	*Staphylococcus saprophyticus*

as important reservoirs of diverse microbial communities capable of dispersal into surrounding ecosystems (Muñoz-Muñoz et al., 2026). The morphological diversity observed in this study further supports the assertion that environmental conditions strongly influence microbial adaptation, survival, and persistence in contaminated environments (Napoli et al., 2025). The occurrence of mucoid, pigmented, and rough-textured colonies among the isolates indicates the presence of bacterial populations possessing adaptive mechanisms that enhance survival under stressful environmental conditions.

Furthermore, increasing environmental contamination and poor waste management practices have been associated with the proliferation and dissemination of environmentally persistent microorganisms (Fletcher et al., 2024). The presence of diverse bacterial populations within the school residential halls and academic buildings may therefore reflect the influence of human activities, overcrowding, and inadequate sanitation practices within the studied environments.

Similarly, environmental degradation and waste accumulation have been reported to create favorable conditions for microbial colonization and persistence (Inasaridze et al., 2025). This observation supports the present findings, which revealed substantial bacterial diversity within school environments where environmental contamination and anthropogenic activities may facilitate microbial survival and transmission.

Biochemical Characterization of Bacteria Isolates

Legend: SRH- School Residential Halls, ABE- Academic Building environment, CSS- Control Soil Site, Indo- Indole, Fru- Fructose, D-Man- D-Mannitol, D-Mal- D-Maltose, M.Red- Methyl-Red. + means positive and – means negative. Dumpsite soils in this study harbored a diverse population of both Gram-positive and Gram-negative bacteria. However, Gram-positive bacteria predominated, accounting for eight out of the eleven isolates, while only three were Gram-negative (Table 3). This dominance of Gram-positive bacteria may be attributed to their ability to withstand harsh environmental conditions, including desiccation, nutrient fluctuations, and exposure to toxic substances commonly found in dumpsite environments.

The predominance of Gram-positive organisms such as *Staphylococcus aureus, Staphylococcus epidermidis, Bacillus subtilis, Bacillus pumilus, Enterococcus faecalis,* and *Micrococcus luteus* suggests strong adaptive capabilities to polluted environments. Members of the genus *Bacillus* are known for their ability to form endospores, which enhances their survival under environmental stress (Nicholson *et al.,* 2000). Similarly, Enterococcus faecalis exhibits high tolerance to extreme conditions, including high salinity and antimicrobial agents, which may explain its persistence in dumpsite soils (Arias and Murray, 2012). The presence of *Staphylococcus aureus* and *Staphylococcus epidermidis* in the dumpsite is of public health concern. These organisms, commonly associated with human skin and waste materials, are known to exhibit multidrug resistance and biofilm-forming abilities, increasing their survival and pathogenic potential in contaminated environments (Otto, 2009; Tong *et al.*, 2015). Their occurrence in the study area may be linked to improper disposal of domestic and biomedical waste, which creates a selective environment for resistant strains (Oleksiuk *et al.,* 2021). Gram-negative isolates identified in this study, including *Pseudomonas aeruginosa*, *Klebsiella pneumoniae*, and *Neisseria spp.*, further highlight the potential health risks associated with dumpsite soils. *Pseudomonas aeruginosa* is a well-known environmental organism capable of surviving in nutrient-rich and contaminated habitats due to its metabolic versatility and intrinsic resistance mechanisms (Stover *et al.,* 2000). Its ability to tolerate harsh conditions and degrade complex organic compounds makes it well-suited for survival in dumpsite environments (Moradali *et al.,* 2017). The detection of *Klebsiella pneumoniae* suggests fecal or organic waste contamination, as this organism is commonly associated with human and animal waste. Its capacity to produce extended-spectrum beta-lactamases (ESBLs) further emphasizes the role of environmental reservoirs in antimicrobial resistance (Pitout and Laupland, 2008). Although *Neisseria spp.* is primarily a human-associated pathogen, its detection in environmental contexts has been linked to contamination from bodily fluids and signals concerns about its survival outside hosts (Tapsall *et al*., 2009).

Additionally, *Micrococcus luteus*, though generally considered non-pathogenic, was isolated in this study and may serve as an indicator of environmental contamination and poor hygiene conditions (Kumar *et al.,* 2012). The occurrence of *Staphylococcus saprophyticus*, commonly associated with urinary tract infections, further supports the likelihood of human-derived waste contributing to the microbial composition of the dumpsite (Naber, 2008). The diversity of microbial isolates observed in this study is consistent with previous findings that dumpsites serve as reservoirs of both environmental and opportunistic pathogenic microorganisms. The continuous deposition of organic, domestic, and possibly biomedical waste creates favorable conditions for microbial proliferation and selection of resistant strains (Zhang *et al.,* 2015).

Overall, the presence of these microorganisms highlights the environmental and public health implications of improper waste disposal practices at the study site. The coexistence of environmentally beneficial organisms and opportunistic pathogens suggests that dumpsite soils function not only as zones of active microbial metabolism but also as potential reservoirs for the spread of antimicrobial resistance.

Fungi Count

The fungal colony counts obtained from the soil samples at various locations within the Federal University Oye-Ekiti (Oye-Campus) indicate a varying degree of fungal load across the sites, which can be attributed to the level of anthropogenic activities, organic matter input, and ecological conditions. At the 10^{-4} dilution (Diluent 4), the school residential halls recorded the highest fungal population with 9.5×10^4 CFU/g, followed closely by the academic building environment at 8.5×10^4 CFU/g, while the control site soil recorded the lowest value of 6.0×10^4 CFU/g. This same trend is maintained at the 10^{-6} dilution (Diluent 6), where the fungal count was highest in the school residential halls (8.5×10^6 CFU/g), followed by the academic building environment (7.0×10^6 CFU/g) and then the control (5.0×10^6 CFU/g) (Figure 3).

The elevated fungal counts in the school residential halls may be attributed to increased nutrient availability from decomposed food waste, paper, textiles, and other biodegradable refuse common in residential waste streams. Such environments provide a favorable microhabitat for fungal colonization and proliferation, as organic matter and soil fungal abundance have been positively correlated in multiple ecosystem studies (Fracasso *et al*., 2026; Bonito *et al*., 2014). Fungi such as *Aspergillus*, *Penicillium*, and *Rhizopus* species are commonly isolated from such enriched soil environments, indicating the role of human activities in enriching the microbial diversity and load of the soil (Kashif *et al*., 2020). Similarly, the academic building environment, though less enriched than the residential halls, still showed higher fungal counts compared to the control site. This can be due to the presence of litter, paper debris, and foot traffic which moderately contribute organic residues, moisture, and aeration factors that enhance fungal survival and sporulation (van der Heijden *et al*., 2008).

The control site, presumably undisturbed and free from anthropogenic inputs, had the least fungal count. This confirms findings from previous research that undisturbed or fallow soils generally have lower microbial counts due to limited nutrient input and reduced organic matter content, with fungal communities significantly influenced by soil physicochemical properties and land use (Mayer *et al*., 2021).

The significant difference in fungal populations among the different sites underscores the impact of human activity on the microbiological quality of soil. These findings align with earlier reports showing that areas subjected to waste accumulation and human interference tend to harbor higher loads of microorganisms, especially fungi, due to increased organic carbon and nutrient availability (Edwards *et al*., 2006). Furthermore, studies have highlighted that fungal abundance is often higher in soils with elevated organic carbon relative to soils low in organic matter, supporting enhanced fungal growth and community complexity (Chen *et al*., 2019). The increased fungal load in the school residential halls and academic building environment supports the hypothesis that waste-rich, human-influenced soils provide favorable ecological niches for fungal colonization and diversity (van der Heijden *et al*., 2008; Fracasso *et al*., 2026).

Morphological Characterization and Identification of Fungal Isolates

Fungal isolates obtained from the dumpsite soils in this study further demonstrate the ecological complexity and health implications of waste-contaminated environments

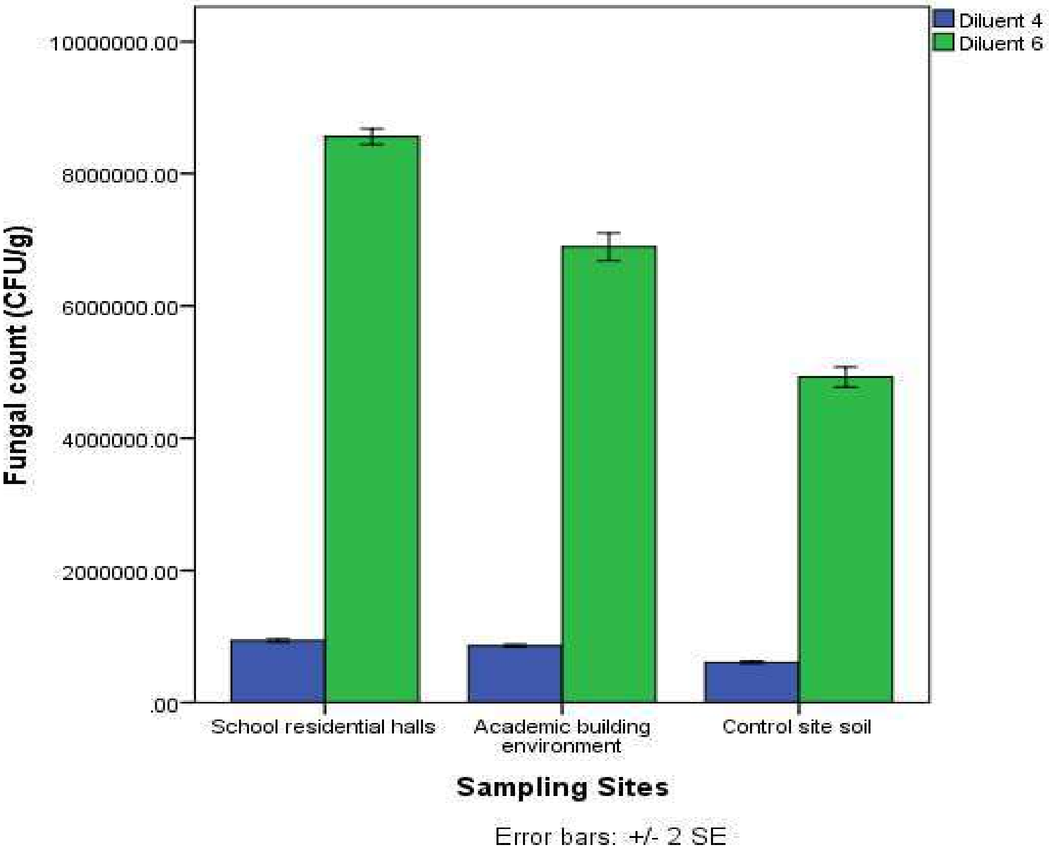

Figure 3: Fungal Count of Selected Soil Samples in Federal University Oye-Ekiti (Oye-Campus).

Table 4: Morphological Characterization and Identification of Fungal Isolates from School Residential Halls and Academic Building Environment.

Isolates	Colour (pigment)	Texture	Surface Appearances	Detected organisms
SRH. A	Pinkish center, pale to white margin	Velvety center, cottony	Circular, coned, regular margin	*Aspergillus Niger*
SRH.B	Dark-green	Powdery	Radial symmetry	*Fusarium solani.*
SRH.C	brown center	Cotton, woolly filamentous	Uniform, dense center, fluffy edge	*Fusarium solani.*
SRH.D	White (no pigmentation)	Cotton, fluffy, raised	Circular, regular, and uniform	*Mucor circinelloides.*
ABE.E	Dark gray with white margin	Velvety center, cotton margin	Circular, dense center, fluffy margin	*Penicillium citrinum.*
ABE.F	White to cream surface	Powdery	Slightly raised	*Trichophyton rubrum*
ABE.G	Dark-brown	Velvety	Slightly raised	*Cladosporium herbarum*
ABE.H	White (with a denser center)	Woolly	Uniform, dense center and fluffy edge	*Trichoderma longibrachiatum*
CSS	Pinkish center, pale to white margin	Cottony	Circular margin	*Aspergillus niger*

Legend: SRH- School Residential Halls, ABE- Academic Building environment, CSS- Control Soil Site

(Table 4). The dominance of filamentous fungi such as *Aspergillus niger, Fusarium solani, Mucor circinelloides, Penicillium citrinum, Trichophyton rubrum, Cladosporium herbarum,* and *Trichoderma longibrachiatum* reflects the high organic content and moisture availability typical of dumpsite soils. The frequent occurrence of *Aspergillus niger* in this study is consistent with its ubiquitous nature in soil and decaying organic matter, particularly in warm and humid environments. Its ability to produce extracellular enzymes such as proteases and ligninases enhances its role in the degradation of complex organic substrates, making it highly adapted to waste-rich environments (Rai *et al.*, 2018). However, its presence also raises public health concerns due to its association with respiratory infections and opportunistic diseases, especially in immunocompromised individuals (Kosmidis and Denning, 2015).

Similarly, *Fusarium solani* was identified among the fungal isolates, suggesting the presence of plant-derived organic matter within the dumpsite. This species is known for its dual role as both a plant pathogen and an opportunistic human pathogen, capable of causing keratitis and systemic infections (Al-Hatmi *et al.*, 2016). Its resilience in polluted and metal-contaminated environments may contribute to its persistence in dumpsite soils (Jain *et al.*, 2022). The detection of *Mucor* *circinelloides* further highlights the suitability of dumpsite environments for fast-growing saprophytic fungi. Members of the genus *Mucor* thrive in decomposing organic matter and moist conditions, which are characteristic of unmanaged waste sites. Their clinical relevance has increased in recent years due to their association with mucormycosis, a severe fungal infection observed particularly in immunocompromised and diabetic individuals (Rodrigues and Nosanchuk, 2020).

In addition, *Penicillium citrinum* was isolated, indicating the presence of decomposing organic materials and stored waste components. While species of *Penicillium* are widely known for their beneficial applications, some strains produce mycotoxins with nephrotoxic effects, and airborne spores can contribute to environmental and indoor air contamination, posing potential health risks (Frisvad *et al.*, 2018). The presence of dermatophytic fungi such as *Trichophyton rubrum* suggests possible contamination from human or animal sources. This organism is a well-known causative agent of superficial fungal infections, including ringworm and athlete's foot, and its ability to survive on soil and contaminated materials enhances its transmission potential in waste-rich environments (de Hoog *et al.*, 2017).

Airborne fungi such as *Cladosporium herbarum* were also detected, further emphasizing the role of dumpsites as reservoirs of allergenic microorganisms. This species is commonly associated with respiratory allergies and asthma exacerbations and thrives in damp, organic-rich environments (Baxi *et al.*, 2016). Furthermore, *Trichoderma longibrachiatum*, typically recognized for its beneficial role as a biological control agent in agriculture, was identified in this study. Its presence reflects its strong adaptability and enzymatic capabilities, which enable survival in diverse and nutrient-rich environments; however, this species has also been documented to cause opportunistic infections in immunocompromised individuals (Harman *et al.*, 2012).

The diversity of fungal isolates observed in this study reflects the high organic load and favorable environmental conditions characteristic of dumpsite soils. Fungi are known to proliferate in environments rich in cellulose, lignin, and decomposing plant materials, where they contribute significantly to organic matter degradation processes (Tedersoo *et al.*, 2014). The presence of both environmentally beneficial and opportunistic pathogenic species suggests that dumpsite soils serve as active microbial ecosystems with important ecological and health implications. These observations are consistent with previous studies that identify dumpsites as reservoirs of diverse fungal communities adapted to waste-contaminated environments (Hyde *et al.*, 2019).

Environmental and Public Health Implications

The detection of potentially pathogenic microorganisms in soils surrounding school residential halls and academic building environments presents serious public health concerns within university environments. Students living in residential halls are regularly exposed to contaminated soil through physical contact with unpaved walkways, improperly managed refuse zones, and common recreational areas. This exposure increases their risk of contracting skin and soft tissue infections, allergic dermatitis, and other opportunistic conditions especially among immunocompromised individuals (Medeiros and Figueiredo, 2015).

Similarly, academic zones, frequented daily by both teaching and non-teaching staff as well as students, present risk pathways for the inhalation of airborne fungal spores. Species such as *Aspergillus niger, Cladosporium herbarum,* and *Penicillium citrinum* are commonly found in soil and air around waste dumps and have been associated with respiratory allergies, asthma exacerbations, and invasive infections in sensitive individuals (Baxi *et al.*, 2016; Kosmidis and Denning, 2015).

Additionally, the presence of bacteria such as *Staphylococcus aureus, Enterococcus faecalis,* and *Pseudomonas aeruginosa* in these environments suggests a risk of environmental transmission of antibiotic-resistant pathogens via contaminated surfaces, footwear, or skin contact especially during recreational activities or sanitation work. These species are known to persist in moist and organic-rich soils typical of campus dumpsites and can colonize surfaces in communal areas (Laxminarayan *et al.*, 2013; Magiorakos *et al.*, 2012).

Furthermore, the emergence of antimicrobial-resistant traits among soil-dwelling bacteria and fungi is of growing concern. Studies show that environmental exposure to pharmaceuticals, disinfectants, and metals in waste streams promotes the development and dissemination of resistance genes (World Health Organization, 2017; Wellington *et al.*, 2013). This microbial resistance can spread to clinical populations via contact or inhalation, increasing the burden on university healthcare services.

Given the high degree of human-soil interaction within both residential and academic areas, there is an urgent need for improved campus-wide sanitation infrastructure, designated waste disposal systems, and microbial monitoring strategies to mitigate the spread of infectious agents and safeguard community health (Prüss-Ustün *et al.*, 2019; Fewtrell *et al.*, 2005).

CONCLUSION

The study of dumpsite soils at the Federal University Oye-Ekiti (Oye Campus), Ekiti State, Nigeria, highlights the dynamic interplay between soil physicochemical properties and microbial populations in areas subjected to continuous waste disposal. The physicochemical analyses revealed elevated electrical conductivity, moisture content, and organic matter in soils from residential halls and academic zones, reflecting the influence of human activities and organic waste accumulation. These conditions create nutrient-rich microenvironments conducive to microbial survival and proliferation. Microbiological analyses confirmed the presence of dense and diverse bacterial and fungal communities across all sampled sites, with Gram-positive bacteria predominating. The bacterial isolates identified, including *Staphylococcus aureus, Staphylococcus epidermidis, Bacillus subtilis, Bacillus pumilus, Klebsiella pneumoniae,* and *Enterococcus faecalis*, demonstrate adaptive mechanisms that enable survival under the physicochemical stresses' characteristic of dumpsite soils. Fungal populations were similarly diverse, underscoring the role of both bacteria and fungi in organic matter decomposition and nutrient cycling within these disturbed environments.

These findings indicate that dumpsite soils at FUOYE possess physicochemical and microbiological profiles capable of supporting metabolically versatile microorganisms. Such indigenous microbial communities could serve as reservoirs of bioactive organisms for environmentally sustainable waste management strategies. The study reinforces the need for institutional and urban authorities to integrate microbial-based approaches alongside conventional waste management practices to mitigate environmental degradation, improve soil health, and reduce potential public health risks. The physicochemical enrichment and microbial diversity observed in FUOYE dumpsite soils highlight their ecological significance and present opportunities for leveraging native microbial populations in the development of low-cost, eco-friendly interventions for sustainable waste management.

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