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Assessment of Microbial Diversity and Abundance in Selected Sections of the Abattoir in Ozoro, Delta State, Nigeria.

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Abstract-* This study assessed the microbial diversity and abundance in selected sections of an abattoir in Ozoro, Delta State, Nigeria, with emphasis on the impact of abattoir waste on soil microbial communities. Soil samples were collected from blood-polluted, bone-polluted, and control (unpolluted) sites at depths of 0–15 cm and 15–30 cm. Standard microbiological techniques were employed for the isolation, enumeration, and identification of bacterial and fungal populations, while biochemical tests including IMViC and urease assays were used for bacterial characterization. The results showed that the control soil recorded the highest mean bacterial count ($7.50 \times 10^7 \pm 1.04 \times 10^7$ CFU/g), compared to blood-polluted ($4.73 \times 10^7 \pm 6.36 \times 10^6$ CFU/g) and bone-polluted ($4.90 \times 10^7 \pm 1.73 \times 10^6$ CFU/g) soils; however, these differences were not statistically significant ($p = 0.063$). Identified bacterial genera included Bacillus spp., Pseudomonas spp., Staphylococcus spp., Escherichia coli, Lactobacillus spp., and Micrococcus spp., while fungal isolates comprised Aspergillus spp., Penicillium spp., Rhizopus spp., Cladosporium spp., and Fusarium spp. Gram-positive bacteria constituted 60% of the total isolates, while Gram-negative bacteria accounted for 40%. Notably, only Gram-positive bacteria were recovered from the control soil, whereas both Gram-positive and Gram-negative bacteria were present in the polluted sites. Micrococcus spp. was highly abundant (+++), particularly in blood-polluted soil at the 0–15 cm depth, indicating its dominance in that environment. The detection of fecal indicator organisms such as E. coli and Staphylococcus spp. provided clear evidence of contamination associated with abattoir activities. Despite this, the presence of resilient indigenous microorganisms, including Bacillus, Pseudomonas, and decomposer fungi, suggests adaptive microbial responses to organic waste pollution. Overall, the findings demonstrate that improper disposal of abattoir waste alters soil microbial composition, introduces potential pathogenic organisms, and poses significant environmental and public health risks.

Index Terms-* Abattoir soil, microbial diversity, microbial abundance, soil contamination, bacterial and fungal isolates, abattoir waste,

I. INTRODUCTION

Soil is a dynamic and living system that plays a fundamental role in sustaining agricultural productivity, ecosystem stability, and overall environmental quality. Central to soil functionality is its microbial community, which comprises diverse groups of bacteria, fungi, archaea, and protozoa that drive essential ecological processes such as nutrient cycling, organic matter decomposition, nitrogen fixation, and maintenance of soil structure. Soil microorganisms also influence plant health, productivity, and resilience, making microbial diversity a reliable indicator of soil quality and ecological balance (Kozjek et al., 2021).

In recent years, abattoir waste pollution has emerged as a major environmental challenge, particularly in urban and peri-urban areas of developing countries where livestock processing activities are expanding rapidly and waste management systems remain inadequate. Abattoirs generate large volumes of organic wastes including blood, feces, urine, fat, bones, and intestinal contents, which are often discharged directly into surrounding soils and water bodies without proper treatment (Idu et al., 2023).

These wastes are typically rich in organic matter, nutrients, pathogens, and residual chemicals, and their uncontrolled disposal poses serious threats to environmental quality and public health.

The accumulation of abattoir waste in soil can significantly alter its physicochemical properties, including pH, moisture content, oxygen availability, and nutrient composition. Such changes directly influence soil microbial communities, often resulting in shifts in microbial diversity, abundance, and functional dynamics. High organic loading can stimulate excessive microbial respiration, leading to oxygen depletion and the selective proliferation of facultative and anaerobic microorganisms, while inhibiting oxygen-dependent species. Consequently, the natural balance of soil microbial populations may be disrupted, leading to reduced soil fertility, impaired plant growth, and increased risks of pathogen transmission to humans and animals (Ibeaja and Njoku, 2024; Yang et al., 2024).

Beyond ecological degradation, abattoir waste–polluted soils may serve as reservoirs for pathogenic and opportunistic microorganisms, including fecal indicator bacteria such as Escherichia coli and Staphylococcus species. The persistence of these organisms in soil environments raises serious concerns regarding food safety, groundwater contamination, and the spread of zoonotic diseases. However, despite these negative impacts, the nutrient-rich nature of abattoir wastes can also enhance microbial activity and promote the proliferation of certain indigenous microorganisms capable of adapting to organic pollution stress.

Notably, some soil microorganisms exhibit remarkable resilience and metabolic versatility, enabling them to survive and thrive in contaminated environments. These adaptive microbial populations may possess valuable traits such as antimicrobial production, enzymatic degradation of organic pollutants, and resistance to environmental stressors. Such characteristics highlight the potential of abattoir-polluted soils as reservoirs of beneficial microorganisms with applications in medicine, agriculture, and environmental bioremediation (Kumar et al., 2021; Akpan et al., 2020).

Despite the growing environmental and health concerns associated with abattoir waste disposal, there remains limited empirical data on the microbial diversity and abundance of soils impacted by abattoir activities, particularly in many parts of Nigeria. Understanding how abattoir waste influences soil microbial communities is essential for evaluating soil health, assessing environmental risks, and identifying microbial taxa with potential biotechnological value. Therefore, this study aims to assess the microbial diversity and abundance in abattoir waste–polluted and non-polluted soils in Ozoro, Delta State, Nigeria, with a view to elucidating the effects of organic pollution on soil microbial ecology and highlighting the environmental and public health implications of improper abattoir waste management.

II. MATERIALS AND METHODS

Study Area

This study was conducted in Ozoro, a semi-urban town located in Isoko North Local Government Area, Delta State, in the Niger Delta region of Nigeria. Geographically, Ozoro is situated approximately at latitude 5.5469°N and longitude 6.2265°E. The town experiences a tropical climate with two major seasons: The rainy season (April to October) and the dry season (November to March). Average annual rainfall ranges between 2,000 mm and 2,500 mm, while temperatures typically vary between 24°C and 34°C throughout the year. Idheze community of Ozoro hosts a major abattoir site, which serves as the polluted site for this study. This abattoir is characterized by open slaughtering practices, poor waste disposal systems, and frequent discharge of organic waste including blood, fats, feces, and wastewater directly into the surrounding soil. This introduces a high load of biodegradable materials and potential pathogenic organisms into the environment, raising public health and ecological concerns.

A non-polluted (control) site was selected approximately 200 meters away from the abattoir site. This control site shares similar soil type, vegetation, and topography but is free from any visible anthropogenic pollution. Both sites fall within the same agro-ecological zone, allowing for reliable comparative analysis of microbial diversity and community structure. This choice of study area provides a practical model to examine the environmental implications of abattoir operations on soil microbiota, with potential applications in waste management, bioremediation, and public health policy formulation in similar rural and peri-urban settings across sub-Saharan Africa.

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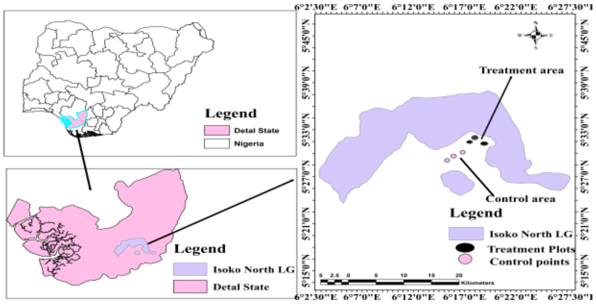


Figure 1: Map of Study Area

Research Design

This study employed an experimental and comparative research design aimed at assessing the microbial diversity in abattoir-polluted and non-polluted (control) soils in Ozoro, Delta State, Nigeria. This research was structured to evaluate:

1. The quantitative differences in microbial load between polluted and non-polluted soil samples.
2. The qualitative differences in microbial types (bacteria and fungi) are isolated from the two soil conditions.
3. The effects of soil depth (0–15 cm and 15–30 cm) on microbial diversity and population.

The design involved the following steps:

1. Field Sampling: Soil samples were collected from three abattoir-polluted locations (dung, blood, and bone disposal areas) and three control (non-polluted) sites.
2. Depth Variation: Each site was sampled at two depths: topsoil (0–15 cm) and subsurface soil (15–30 cm).
3. Laboratory Analysis: Samples were processed using serial dilution, pour plating, bacterial and fungal culturing, and colony enumeration on Nutrient Agar (NA) and Potato Dextrose Agar (PDA).
4. Microbial Identification: Morphological, microscopic, and Gram staining techniques were used to identify isolates.
5. Data Analysis: CFU/g was calculated, and results were statistically analyzed to determine significant differences in microbial load and diversity across sites and depths.

This design allowed for a controlled comparison between polluted and controlled soils under the same environmental conditions and helped reveal how abattoir waste affects soil microbial ecology.

Population of the Study / Size Determination

The study population of this study consists of the soil microbial communities present in both abattoir-polluted and non-polluted soils within the study area. Although the exact number of microbial organisms are not well defined due to their microscopic and abundant nature, representative samples were systematically collected to capture the diversity and abundance of these microbes. A total of 18 soil samples were collected (12 from polluted sites and 6 from control sites) across different depths and locations, ensuring adequate representation for microbial analysis. Two distinct polluted zones of the abattoir (blood and bone disposal areas). Three non-polluted control sites are located about 200 meters away from the abattoir. Each of these three sampling locations provided: Three replicates of soil samples at two different depths: 0–15 cm (topsoil) and 15–30 cm (subsurface soil). Giving a total sample size of 18 soil samples for microbial analysis.

Sample Collection / Sampling Techniques

Soil samples were collected from two distinct locations within Ozoro, Delta State, Nigeria. A polluted site (abattoir soil) and a non-polluted site (control soil) located approximately 200 meters away from the abattoir.

In the polluted site (abattoir soil), samples were collected randomly from blood wastewater, and bone disposal zones. From each waste type location, three replica samples were collected making a total of six polluted samples. Each sample was taken at two depths: 0–15 cm and 15–30 cm, using a soil auger. In the control site, three soil samples were randomly collected from an adjacent area with no known history of pollution or human/animal waste contamination at depths of 0–15 cm and 15–30 cm. Soil samples were placed in sterile, labeled polyethylene bags and kept in an ice-cooled box during transport to the laboratory for analysis.

Methods of Data Collection

This section outlines the laboratory techniques used to isolate, enumerate, and identify the population and diversity of microorganisms in soil samples from both abattoir-polluted and control sites. The methods employed include serial dilution, culture media preparation, plating and incubation, and colony count.

Serial Dilution of Soil Samples

Each soil sample was homogenized and sieved, then 9.0 ml of distilled water was measured into 200 test tubes and properly sealed with cotton wool wrapped with foil paper before autoclaving to make it sterile. Exactly 1 g of soil was measured using weighing balance and added to each 9.0 ml of sterile distilled water in the test tube to make the 10^{-1} dilution and labeled S1 × 10^{-1}. After that, 1.0 ml of the first dilution was measured from S1 × 10^{-1} into the second test tube using a syringe and labeled S1 × 10^{-2}.

A tenfold serial dilution was performed up to 10^{-10} using sterile pipettes and test tubes containing 9.0 ml sterile water for each sample giving a total of 180 test tubes of serial dilutions in total. Each dilution was properly labeled and used for culturing.

Preparation of Culture Media

Culture media was prepared according to manufacturer's instruction, Nutrient Agar powder (NA) = 14g to 500 ml distilled water for bacteria and Potato Dextrose Agar powder (PDA) = 19.5g to 500 ml distilled water for fungi.

Procedure: The work bench was sterilized and disinfected using 70% ethanol, while spirit lamb was lit to keep the area sterile, 500 ml of distilled water was measured in a beaker using a measuring cylinder and 14g of Nutrient Agar powder was added to the 500 ml of distilled water in a conical flask for bacteria plates. 19.5g of Potato Dextrose Agar powder to 500 ml of distilled water in another conical flask for fungal plates. Both solutions were continuously stirred while gently heated on a magnetic sterile for about 5-10 minutes, boil gently until the agar is completely dissolved (the solution should become clear) for it to homogenize and prepare them for autoclaving .at 121°C for 15 minutes to sterilize both solutions. Both media were cool to 45–50°C before pouring into sterile Petri dishes.

Plating and Incubation

Plating was conducted using the prepared culture media to enumerate and isolate organisms from the serially diluted soil samples.

The bacteriological analyses of the soil samples were carried out according to the methods of Oyeleke and Manga (2008) and Rabah et al. (2008). From each serial dilution (10^{-1} to 10^{-10}), 1.0 ml of the diluted soil suspension was aseptically transferred into sterile petri dishes using a sterile syringe. 15 – 20 ml of cooled molten Nutrient Agar (NA), was poured into each petri dish. The contents were gently swirled to mix evenly (pour plate technique). Afterwards, allowed to solidify and then incubated at 37°C for 24 hours to support bacterial growth.

For fungi plating, each dilution level (10^{-1} to 10^{-10}), 1.0 ml of soil suspension was transferred into separate sterile Petri dishes. 15–20 ml of molten PDA was cooled to about 45–50°C and then poured into each plate. The plates were gently swirled and left to solidify to encourage fungal growth. The plates were incubated at room temperature (25–28°C) for 3–5 days. Fungal colonies (often fluffy, colored, or filamentous) were counted and described based on their growth pattern, texture, and pigmentation.

Colony Count and CFU Calculation

After incubation, colonies were counted manually using a colony counter. Colony Forming Units per gram (CFU/g) of soil were calculated using standard microbiological formulas based on colony count, dilution factor, and volume plated. The bacterial load in the original soil sample was calculated using the formula:

$$\text{CFU/g} = \frac{(\text{Number of colonies} \times \text{Dilution factor})}{\text{Volume plated (mL)}}$$

Colony morphology

After incubation, distinct colonies on plates were observed for physical characteristics such as: Colony shape (circular, irregular, rhizoid, filamentous), elevation (flat, raised, convex, umbonate), margin (entire, undulate, lobate), colors (white, cream, yellow, green, black especially for fungi) and surface texture (smooth, rough, mucoid, dry).

Biochemical Characterization of Bacterial Isolates

Gram Staining Procedure: Using a sterile inoculating loop, collect a small amount of the bacterial culture then mix with a drop of sterile water on a clean slide to create a thin film and then spread evenly to allow the smear to air-dry completely. The air-dried slide was passed through the flame of a spirit lamp 2–3 times (smear side up) to heat-fix the bacteria to the slide. Then crystal violet was applied, then allowed to stand for 60 seconds and then rinse gently with distilled water. Gram's iodine was then applied using a pipette, left for 60 seconds and then rinse with distilled water. 95% ethanol was then applied for 10–20 seconds (until runoff is colorless). It was immediately rinsed with distilled water to stop the decolorization process. Drops of safranin were added, left for 60 seconds and then rinse off with distilled water. The slides were blot dried gently using blotting paper and then examined under a light microscope using oil immersion (100x objective lens).

Catalase Test: A drop of 3% hydrogen peroxide (H2O2) was added on a clean slide, a sterile loop was then used to add a colony of the test bacterium to the drop and the mixture was observed for the immediate production of bubbles.

Oxidase Test: A drop of oxidase reagent (1% tetramethyl-p-phenylenediamine) was added to a bacterial colony smeared on a clean slide to observe for a color change.

Citrate Utilization Test: Using a sterile loop, the bacterial isolate was streaked onto the surface of a Simmons' citrate agar slant. The inoculated slant was incubated at 37°C for 24–48 hours.

Indole Test: A test bacterium was inoculated into Tryptone broth and incubated for 24–48 hours. Following incubation, 5 drops of Kovac's reagent were added.

Methyl Red Test (MR): The test bacterium was inoculated into MR-VP broth and incubated for 48 hours. Following incubation, 5 drops of methyl red indicator were added.

Voges-Proskauer (VP) Test: A separate tube of the inoculated MR-VP broth was used, and after the incubation period, 15 drops of Barritt's A and 5 drops of Barritt's B were added.

Urease Test: Using a sterile loop, the surface of a Christensen's urea agar slant was streaked with the test bacterium. The inoculated slant was incubated at 37°C for up to 48 hours.

Analytical Tools

The data obtained from the microbiological analysis of soil samples were analyzed using a combination of descriptive, statistical, inferential, and graphical tools. These analyses were performed using GraphPad Prism, a robust statistical software widely used for scientific data interpretation and visualization. The following analytical tools and methods were employed:

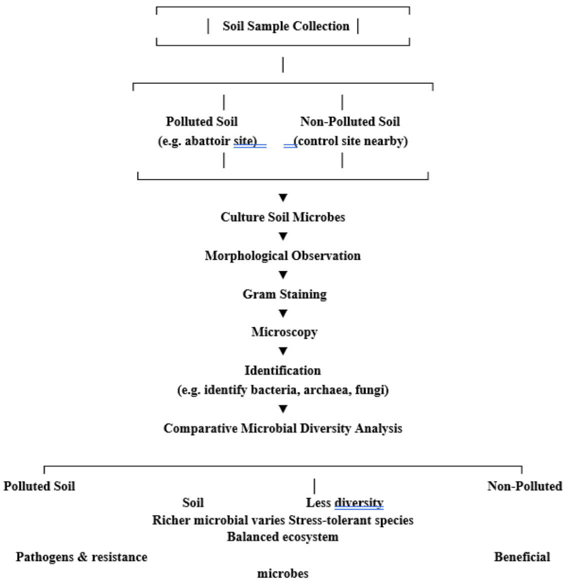
Descriptive Statistics: Descriptive statistical measures such as Mean, Standard deviation (SD) and Percentage composition were used to summarize bacterial colony-forming units per gram (CFU/g), frequency of distinct colonies, and distribution of microbial diversity across soil samples and depths.

Inferential Statistics: To evaluate the statistical significance of observed microbial variations a Two-Way Analysis of Variance (ANOVA) was conducted using GraphPad Prism to test the effects of Soil Depth (0–15 cm vs. 15–30 cm) and Site Condition (Polluted vs. Non-Polluted). The interaction between these two factors was also analyzed to determine whether microbial differences were influenced by both depth and pollution status simultaneously. Duncan multiple test was used to detect the mean difference and a significance level of $p < 0.05$ was used to determine statistical significance.

Graphical Tools: GraphPad was used to generate Bar Charts to compare microbial loads across samples and depths.

Microbial Identification Tools: Microscopy and Gram staining were used for basic identification of bacteria, biochemical tests (Catalase, Oxidase, MR-VP, Citrate, Indole, Urease) provided functional classification, and morphological observation on PDA was used for fungal identification.

Literature Comparison: Final identification of microbial genera was supported by comparing morphological and biochemical characteristics with standard taxonomic keys and previous microbiology literature. Figure 2 shows a schematic flowchart of the research methodology for investigating the microbial ecology of abattoir polluted and non-polluted soils. The diagram outlines the key stages from sample collection and microbial isolation to comparative analysis.



(Source: Madigan *et al.*, 2018).

Figure 2: A schematic flowchart of the research methodology for investigating the microbial ecology of abattoir polluted and non-polluted soils.

III. RESULTS AND DISCUSSION

RESULTS

This result of the findings from the microbial analysis of abattoir polluted and non-polluted soil samples from the study sites. The results of this study are presented in Table 1, Table 2 and Figure 3 to Figure 4.

Figure 3 shows the microbial counts (CFU/g) from each soil sample. The analysis revealed no statistically significant effect of Sample type (blood, bone, and control; p = 0.063) or depth (p = 0.127) on the overall bacterial counts, this means that the total number of bacteria in the topsoil (0-15cm) was not statistically different from the number in the subsurface (15-30cm). Furthermore, no significant interaction was observed between soil samples and depth (p = 0.921), This means the effect of depth on the bacterial count was the same for all three sample types, whether polluted or not. This indicates that while there may have been visual differences in the total bacterial load, these differences were not statistically significant and could not be definitively attributed to the abattoir waste or the sampling depth. The results revealed generally high counts of bacteria across all sampled soil types and depths, with culturable bacterial counts consistently observed in the order of 10^7 CFU/g (tens of millions).

plate 1, 2 and 3 represent the bacterial colonies isolated from the blood, bone and control samples of abattoir-polluted soil samples. Specifically, the highest mean bacterial count was recorded in the Control soil at 0-15cm depth, with $7.50 \times 10^7 \pm 1.04\times 10^7$ CFU/g. Similarly, high counts were also observed in the Bone 0-15cm samples ($4.90\times 10^7 \pm 1.73\times 10^7$ CFU/g) and Blood 0-15cm samples ($4.73\times 10^7 \pm 6.36\times 10^7$ CFU/g).

Table 1 presents the results of a wide variety of bacterial genera, with a notable presence of species such as Staphylococcus spp. and Escherichia coli in both contaminated and non-contaminated soils.

Table 2 details the presumptive identification of fungal species based on their colony morphology which were isolated from both polluted and non-polluted control soils. The most frequently observed genera included Aspergillus spp., Penicillium spp., Rhizopus spp., Cladosporium spp., and Fusarium spp. Plate 4, plate 5 and 6 shows colonies of fungi isolated from bone, blood and control respectively. The number of colonies was generally low, with most samples yielding only one or two colonies per plate. The microorganisms isolated from the polluted and non-polluted soil (control) in the study were: Bacillus spp, Pseudomonas spp, Staphylococcus spp, Escherichia coli, Lactobacillus spp, Enterobacter spp, Aspergillus spp. Or Fusarium spp, Rhizopus spp, Cladosporium spp, Trichoderma spp, Mucor spp.

Figure 4.2 shows the presence of both types of bacteria with distinct morphological features. The polluted samples showed a higher incidence of gram-negative bacteria like Pseudomonas, Escherichia coli, and Enterobacter, while gram-positive bacteria like Bacillus, Staphylococcus, and Micrococcus were also prevalent across all sample types.

Figure 3 shows a range of reactions consistent with the identified genera. For example, Escherichia coli was distinguished from Enterobacter by its positive Indole and Methyl Red tests and negative Voges–Proskauer and Urease tests, while Enterobacter showed the opposite reactions. Figure 5 shows a heatmap of the biochemical test results for the isolated bacterial species. A value of 1 indicates a positive result, and a value of 0 indicates a negative result.

Table 1: Relative Frequency and Qualitative Distribution of Bacterial Species Isolated from both Polluted and Non-Polluted Soil Samples

Bacterial Species	Blood (0-15cm)	Blood (15-30cm)	Bone (0-15cm)	Bone (15-30cm)	Control (0-15cm)	Control (15-30cm)
Bacillus spp.	+	+	-	++	-	-
Pseudomonas spp.	++	+	-	+	+	-
Staphylococcus spp.	+	++	++	+	+	+
Escherichia coli	+	+	++	+	+	++
Lactobacillus spp.	++	-	+	+	-	+
Enterobacter spp.	-	+	+	++	++	+
Micrococcus spp.	+++	+	+ +	+	+	++
Actinomyces spp.	+	+	++	+	++	+

Key: + = Present; ++ = Frequent; +++ = Highly Frequent; - = Absent

Table 2: Morphological characteristics and presumptive identification of fungal isolates from soil samples

Sample Type	Soil Depth (cm)	Number of Colonies	Presumptive Fungal Type	Colony Description	Texture	Growth Rate
Blood	0–15	2	Aspergillus spp. / Fusarium spp.	White, cotton-like, clustered	Fluffy	Fast
Blood	15–30	1	Penicillium spp.	Greenish, clustered	Powdery	Moderate
Bone	0–15	1	Rhizopus spp.	Grayish, clumsy	Cottony	Slow
Bone	15–30	1	Cladosporium spp.	Pure black	Velvety	Fast
Control	0–15	2	Fusarium spp.	Thick white cottony	Fluffy and cottony	Fast
Control	15–30	2	Penicillium spp.	White with green center	Fluffy	Fast

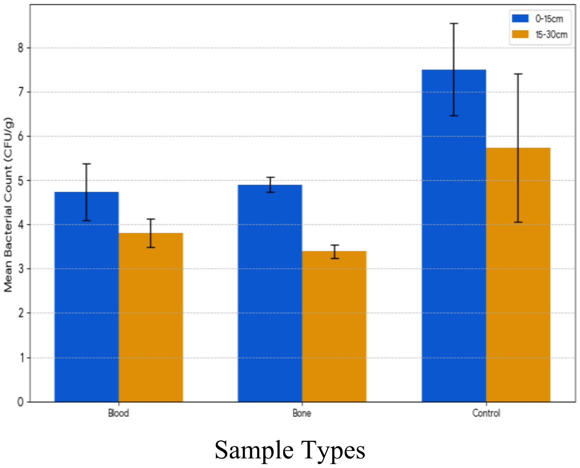


Figure 3 Microbial Counts (CFU/g) from each Soil Sample

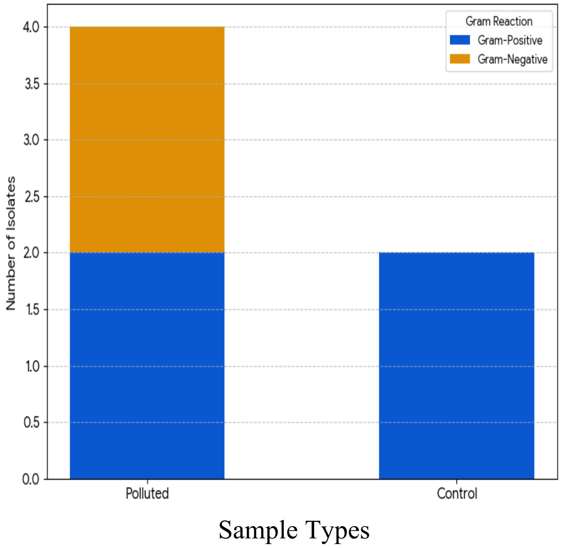
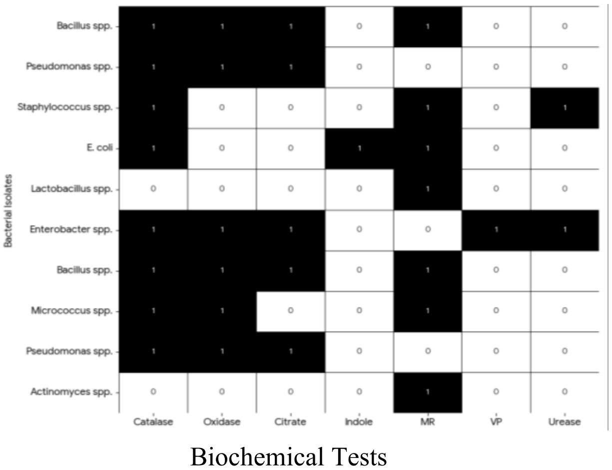


Figure 4. Gram staining and morphology of bacterial isolates



	Catalase	Oxidase	Citrate	Indole	MR	VP	Urease
Bacillus spp.	1	1	1	0	1	0	0
Pseudomonas spp.	1	1	1	0	0	0	0
Staphylococcus spp.	1	0	0	0	1	0	1
E. coli	1	0	0	1	1	0	0
Lactobacillus spp.	0	0	0	0	1	0	0
Enterobacter spp.	1	1	1	0	0	1	1
Bacillus spp.	1	1	1	0	1	0	0
Micrococcus spp.	1	1	0	0	1	0	0
Pseudomonas spp.	1	1	1	0	0	0	0
Actinomyces spp.	0	0	0	0	1	0	0

Figure 5 Heatmap of biochemical test results.

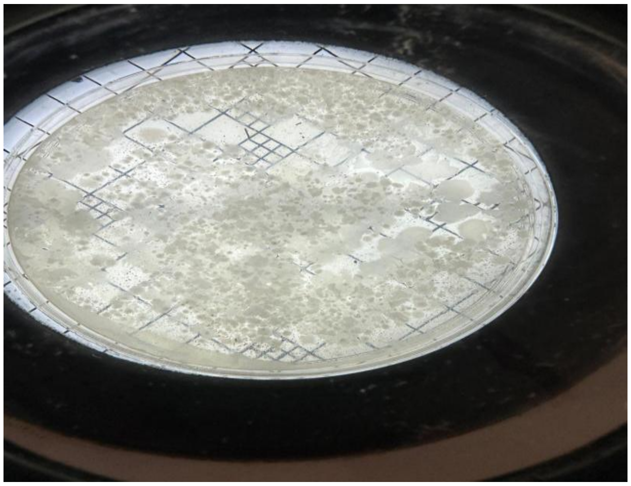


Plate 1: Representative bacterial colonies isolated from Bone

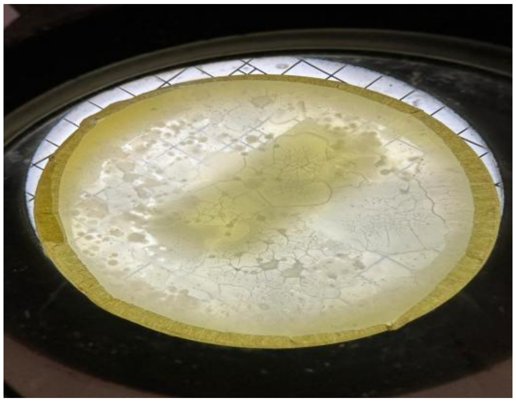


Plate 2: Representative bacterial colonies isolated from Blood

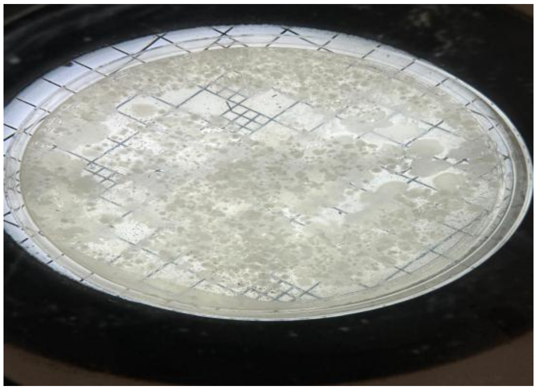


Plate 3: Representative bacterial colonies isolated from Control

Plate 4: Representative fungal colonies isolated from Bone

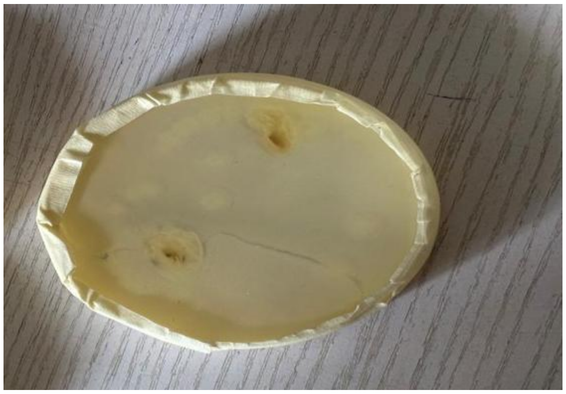


Plate 5: Representative fungal colonies isolated from Blood

Plate 6: Representative fungal colonies isolated from Control

IV. DISCUSSION

Microbial Counts and Statistical Analysis

The assessment of microbial abundance revealed that the control soil recorded higher mean bacterial counts compared to the abattoir-polluted (blood- and bone-contaminated) soils. This observation aligns with previous reports by Ayeni et al., (2024) and Adelowo (2012), who similarly documented higher microbial counts in non-polluted control sites relative to contaminated soils. Although abattoir wastes are rich in organic matter and nutrients capable of stimulating microbial growth, excessive organic loading can paradoxically suppress overall microbial abundance. High concentrations of organic substrates may lead to nutrient imbalance, accumulation of toxic metabolites, and oxygen depletion, thereby creating micro-anaerobic conditions unfavorable for many aerobic soil microorganisms (Oriomah et al., 2025; Adal, 2024).

In contrast, the control soil likely maintained a more stable physicochemical environment, characterized by balanced nutrient availability and adequate aeration, which supports a broader range of microbial taxa and promotes higher microbial abundance (Yang et al., 2024). The lack of statistically significant differences ($p > 0.05$) between the polluted and control soils suggests that while abattoir waste alters microbial composition, it does not necessarily increase total bacterial load. Rather, it selectively favors certain microbial groups capable of adapting to organic pollution stress.

Analysis of Isolated Bacterial Species

The bacterial species isolated in this study including Escherichia coli, Staphylococcus spp., Pseudomonas spp., Bacillus spp., and Micrococcus spp.are consistent with findings from similar studies conducted in abattoir-impacted environments (Emolade et al., 2025; Akinnibosun and Ayejuyomi, 2015 Adesemoye et al., 2006;). The detection of fecal indicator organisms such as E. coli and Staphylococcus spp. in polluted soils provides clear evidence of contamination originating from animal waste, blood, and intestinal contents commonly generated during slaughtering activities.

The presence of Bacillus spp. and Pseudomonas spp. in both polluted and control soils is not unexpected, as these genera are ubiquitous soil inhabitants known for their metabolic versatility and resilience. Their ability to degrade complex organic compounds enables them to thrive under both natural and polluted conditions (Idu et al., 2023). Their persistence in abattoir-polluted soils suggests that indigenous microbial communities remain active and are adapting to the altered environmental conditions by utilizing abattoir waste as a nutrient source. This coexistence of native soil microorganisms and pollution-associated bacteria highlights the dynamic nature of abattoir-impacted soils as complex microbial ecosystems (Kozjek et al., 2021).

The qualitative frequency analysis further demonstrated a shift in microbial community structure rather than an overall increase in abundance. The high occurrence of Micrococcus spp. (+++) in blood-polluted soils, particularly at shallow depths, corroborates the findings of Pola (2025). This dominance suggests that Micrococcus spp. possess adaptive traits that enable them to exploit the nutrient-rich conditions created by blood contamination. Such shifts in dominance indicate selective pressure favoring organisms with efficient nutrient utilization and tolerance to organic pollution (Ibeaja and Njoku, 2023).

Analysis of Isolated Fungal Species

The fungal community exhibited a comparatively lower abundance than bacteria across all soil samples. This pattern may be attributed to competitive exclusion by faster-growing bacterial populations, especially in nutrient-rich environments such as abattoir-polluted soils. The fungal genera isolated Aspergillus, Penicillium, Rhizopus, Cladosporium, and Fusarium spp.—are well-known saprophytic fungi frequently reported in organically enriched soils (Wang et al., 2024).

Their presence, particularly in polluted soils, suggests active involvement in the decomposition of organic residues derived from abattoir waste. Fungi possess enzymatic systems capable of degrading complex organic materials and are often more tolerant of fluctuating pH and moisture conditions than many bacteria. This resilience allows them to coexist with bacterial populations and contribute meaningfully to organic matter mineralization, even at lower population densities (Ayeni et al., 2024).

Interpretation of Low Fungal Counts

The relatively low fungal counts observed in this study can be explained by several ecological factors. Bacteria typically exhibit faster growth rates and greater adaptability in environments with sudden organic enrichment, such as abattoir waste disposal sites. Consequently, bacteria may outcompete fungi for readily available nutrients, leading to a high bacterial-to-fungal ratio. Additionally, the culture media and incubation conditions employed may have been more favorable for bacterial proliferation than for a broader spectrum of fungal taxa.

Moreover, fungi are often primary decomposers of complex plant-derived polymers such as cellulose and lignin, which are less abundant in blood- and bone-dominated wastes. In contrast, bacteria are more efficient in utilizing proteins, lipids, and simple organic compounds, making them better suited for the initial stages of abattoir waste decomposition.

Interpretation of Gram Staining and Morphological Characteristics

Gram staining and colony morphology provided valuable insights into the structure and composition of the soil bacterial community. The recovery of both Gram-positive and Gram-negative bacteria from polluted soils reflects a diverse microbial population influenced by abattoir waste inputs. The presence of Gram-negative bacteria such as E. coli and Enterobacter spp. supports the assertion that abattoir activities introduce fecal contaminants into surrounding soils, as similarly reported by Pino-Hurtado et al. (2024).

Conversely, Gram-positive bacteria including Bacillus, Micrococcus, and Staphylococcus spp. are commonly associated with soil and organic matter decomposition. Their coexistence with pollution-indicator organisms suggests ongoing interactions between indigenous soil microbes and introduced contaminants, highlighting the adaptive capacity of soil microbial communities under pollution stress.

Analysis of Biochemical Characterization

Biochemical characterization was essential for confirming the identity of bacterial isolates and validating presumptive identifications based on morphology and Gram reaction. The biochemical profiles obtained in this study are consistent with reports by Eze and Phil-Eze (2020), who emphasized the reliability of classical biochemical tests in microbial identification. Positive catalase reactions observed in Bacillus, Staphylococcus, and Pseudomonas spp. align with their established physiological characteristics.

Furthermore, IMViC tests effectively differentiated closely related enteric bacteria, clearly distinguishing Escherichia coli (Indole and Methyl Red positive) from Enterobacter spp. (Voges-Proskauer and Citrate positive). Positive urease reactions further strengthened the identification of Staphylococcus and Enterobacter spp. This systematic approach from morphological observation to biochemical confirmation provided robust and reliable evidence for microbial identification and enhanced the credibility of the study's findings (Adelowo, 2012).

V. CONCLUSION

The study identified a wide range of bacterial genera, including Bacillus, Pseudomonas, Staphylococcus, Escherichia, Actinomyces, Lactobacillus, and Enterobacter spp., with variations in species distribution observed between surface and subsurface soil layers. This depth-related variation suggests that different microbial taxa have adapted to distinct physicochemical conditions within the soil profile.

Fungal genera such as Aspergillus, Fusarium, Penicillium, Rhizopus, and Cladosporium spp. were also isolated, reflecting their role as key decomposers of organic residues. The findings demonstrate that abattoir operations alter soil microbial balance, introduce pathogenic and indicator organisms, and pose significant environmental and health concerns if waste is not properly managed.

Abattoir operators should implement effective waste management systems, including proper collection, treatment, and disposal of blood, bone, and other organic wastes, to prevent direct discharge into surrounding soils and reduce microbial contamination. Further studies should explore the potential application of resilient microbial taxa identified in this study for bioremediation, waste degradation, and antimicrobial production, thereby transforming environmental challenges into sustainable biotechnological opportunities.

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