

Culture and Molecular Profiling of Microorganisms Associated with Crops Grown on Abattoir Wastewater-Irrigated Soil in Agbor, Delta State, Nigeria

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Abstract: Untreated abattoir wastewater contains high microbial loads that may persist in irrigated soils and transferred to edible crops. This study investigated the culture and molecular profiles of microorganisms isolated from abattoir wastewater, its irrigated soils and crops cultivated on the receiving soils with particular emphasis on soil and crop-associated microbiomes in Agbor, Delta State, Nigeria. Effluents exhibited elevated bacterial ($6.94\text{--}7.02 \log_{10} \text{cfu ml}^{-1}$) and coliform counts ($5.38\text{--}5.52 \log_{10} \text{cfu ml}^{-1}$), with isolation of *Bacillus*, *Pseudomonas*, *Enterobacter*, *Escherichia coli*, *Aspergillus*, and *Penicillium* species. Wastewater-irrigated soils demonstrated significantly higher microbial population than the control, including heterotrophic bacteria (up to $7.46 \log_{10} \text{cfu g}^{-1}$) and enterococci (up to $5.08 \log_{10} \text{cfu g}^{-1}$). Soil communities were dominated by *Bacillus* (100%), *Pseudomonas* (90%), *Enterobacter* (70%), *E. coli* (70%), and *Aspergillus niger* (100%). Crops grown on abattoir wastewater-irrigated soils harboured similar microbial groups, confirming effluent–soil–crop microbial transmission. Molecular characterization using 16S rRNA gene sequencing for bacteria and Internal Transcribed Spacer (ITS) sequencing for fungi confirmed the identities of key isolates, including *Escherichia coli*, *Pseudomonas aeruginosa*, *Pseudomonas fluorescens*, *Enterobacter cloacae*, *Bacillus subtilis*, *Aspergillus niger*, and *Fusarium oxysporum*. The findings demonstrate that irrigation with untreated abattoir wastewater alters soil microbiome and facilitates the transfer of wastewater-borne microorganisms onto edible crops, raising significant food-safety and public-health concerns.

Key word: Abattoir wastewater, crop contamination, ITS sequencing, microbial profiling, microbiome, soil, 16S rRNA.

INTRODUCTION

The use of untreated wastewater for agricultural irrigation is a growing practice in many developing regions due to increasing water scarcity and poor waste management systems. Abattoir wastewater is particularly rich in organic matter, gut microorganisms, blood residues, fats, and suspended solids, making it a potent vehicle for the dissemination of environmental and enteric microbes (Olatunde *et al.*, 2020; Chukwu *et al.*, 2021). When discharged onto agricultural soils, these constituents can alter microbial communities, enhance pathogens survival, and facilitate transfer onto edible crops (Nwabor *et al.*, 2022).

Agbor, an agrarian community in Delta State, Nigeria, relies on wastewater reuse for vegetable farming. Previous studies have reported the presence of pathogenic and opportunistic microorganisms in abattoir effluents in Nigeria, including *Escherichia coli*, *Enterobacter* spp., *Salmonella*, *Staphylococcus aureus*, *Pseudomonas*,

Fusarium, and *Aspergillus* species (Akan *et al.*, 2022; Ezech *et al.*, 2023). However, limited information exists on how these organisms persist in irrigated soils leading to probable contamination of farm produce.

The increasing demand for water resources in agriculture, driven by population growth, urbanisation, and climate-induced water scarcity, has intensified the use of alternative water sources for irrigation in many developing countries. Among these alternatives, untreated wastewater has become a common option, particularly in semi-urban and urban farming systems where access to clean irrigation water is limited. While wastewater reuse may offer short-term agronomic benefits by supplying moisture and nutrients, its application without adequate treatment presents serious environmental and public-health risks due to the introduction of diverse microorganisms into soil–plant systems.

Abattoir wastewater represents a particularly complex and high-risk form of wastewater. It is generated during slaughtering and meat-

processing activities and typically contains blood, faecal matter, intestinal contents, fats, proteins, suspended solids, and wash water. These components collectively create a nutrient-rich medium capable of supporting dense and diverse microbial populations, including enteric bacteria, opportunistic pathogens, and saprophytic and toxigenic fungi. When such effluents are discharged untreated into the environment or reused for irrigation, they serve as efficient vehicles for microbial dissemination, altering the ecological balance of receiving soils and increasing the likelihood of crop contamination.

Soil is a dynamic reservoir of microorganisms and plays a central role in regulating microbial persistence and transmission within agricultural ecosystems. The introduction of untreated wastewater can profoundly modify the soil microbiome by increasing organic carbon availability, moisture content, and nutrient levels, thereby favouring the proliferation of heterotrophic and faecal-associated microorganisms. Several studies have shown that wastewater irrigation enhances microbial abundance and activity in soils, often leading to the dominance of metabolically versatile and stress-tolerant genera such as *Bacillus*, *Pseudomonas*, and members of the *Enterobacteriaceae*. While some of these microorganisms contribute to nutrient cycling, others are of public-health significance due to their pathogenic or opportunistic nature.

The contamination of crops cultivated on wastewater-irrigated soils is a major food-safety concern. Edible crops may acquire microorganisms through direct contact with contaminated irrigation water, soil splash, root uptake, or post-harvest handling. Vegetables and grains grown under such conditions have frequently been reported to harbour faecal indicators, enteric pathogens, and spoilage fungi. The presence of organisms such as *Escherichia coli*, *Enterobacter* spp., *Pseudomonas* spp., *Aspergillus* spp., and *Fusarium* spp. on edible plant tissues raises concerns not only

about acute foodborne infections but also about chronic exposure to mycotoxins produced by certain filamentous fungi.

In Nigeria, the disposal and reuse of abattoir wastewater remain poorly regulated, particularly in communities where slaughter facilities are often located close to farmlands. Agbor, an agrarian city in Delta State, exemplifies this challenge. Local abattoirs commonly discharge untreated effluents directly onto surrounding lands, which are subsequently used for cultivating crops such as maize, okra, and cowpea. Although several studies in Nigeria have documented high microbial loads in abattoir effluents, comparatively fewer investigations have examined the continuity of microbial transfer along the effluent–soil–crop pathway using both conventional microbiological and molecular approaches.

Traditional culture-based methods provide valuable information on microbial abundance and diversity but may underestimate community complexity. The integration of molecular techniques, particularly 16S rRNA gene sequencing for bacteria and Internal Transcribed Spacer (ITS) sequencing for fungi, offers a more robust framework for confirming taxonomic identities and understanding soil and crop-associated microbiomes. Molecular confirmation is especially important for distinguishing closely related species and identifying organisms of public-health relevance that may persist across environmental compartments.

Against this background, the present study investigated the culture and molecular profiles of microorganisms associated with abattoir wastewater, wastewater-irrigated soils, and crops cultivated in Agbor, Delta State, Nigeria. Specifically, the study aimed to (i) quantify microbial loads in abattoir effluents, irrigated soils, and crops; (ii) characterise the bacterial and fungal composition of the soil and crop microbiomes; and (iii) confirm the identities of representative isolates using 16S rRNA and ITS sequencing. By elucidating microbial transmission dynamics along the

effluent–soil–crop continuum, this study provides evidence relevant to environmental management, food safety, and public-health protection in wastewater-impacted agricultural systems.

MATERIALS AND METHODS

Study area: The study was conducted in Agbor, Delta State, Nigeria, a humid tropical City characterized by a bimodal rainfall pattern and an annual precipitation of about 2,200 mm. Temperatures typically range between 25–33°C, supporting year-round cultivation of crops such as maize, okra, and cowpea. Abattoir facilities within the city discharge untreated wastewater into adjoining farmlands, making the area suitable for investigating wastewater–soil–crop microbial interactions. Sample sites are represented in the map below (Figure 1).

Experimental Design and Sample Classification: Three matrices—abattoir wastewater, wastewater-irrigated soils, and edible crops—were examined to evaluate microbial transmission along the effluent–soil–crop pathway.

Effluent Sampling: Wastewater samples were obtained from three independent abattoirs, labelled, A, B, and C.

Collection of abattoir wastewater samples:

A Effluent: Edike market abattoir, Boji-Boji Agbor. **B Effluent:** New Boji-Boji market, Boji-Boji Agbor. **C Effluent:** Morning market, Umunede, Agbor. Effluent samples (1L each) were collected in sterile amber glass bottles directly from discharge points and immediately transported on ice (4 °C) to the laboratory for analysis within 24 hours (APHA, 2017). Composite soil samples (5–10 cm depth) were obtained using sterile augers from each treatment plot, air-dried at room temperature, homogenized, and sieved (2 mm mesh) for physicochemical analysis. Sub-samples were stored at 4 °C for microbiological and enzymatic assays (Cappuccino & Sherman, 2019).

Soil Sampling: Soil samples were grouped into the following treatments: Soil irrigated with distilled water designated as Control (C). Soils polluted with abattoir wastewater

for four weeks before planting, and irrigated with the same wastewater throughout cultivation cycle, assigned P-A, P-B, P-C. Another set of soil samples polluted throughout the cultivation cycle and left unplanted designated PUP-A, PUP-B, PUP-C. Another set of soil samples polluted four weeks without planting assigned P4-A, P4-B, P4-C.

Crop Sampling: Maize (*Zea mays*), okra (*Abelmoschus esculentus*), and cowpea (*Vigna unguiculata*) were cultivated on the soil treatments. At harvest, edible plant tissues were aseptically collected for analysis.

Soil Samples: Composite soil samples (8–10 cm depth) were collected using sterile augers. Five subsamples were pooled for each treatment, homogenized, and sieved through a 2 mm mesh. Soil portions for microbial analyses were stored at 4°C and processed within 24 hours (Cheesbrough, 2022).

Crop Samples: Ten grams of edible tissue were aseptically excised from each crop type, placed in sterile polyethylene bags, chilled during transportation, and analyzed the same day (APHA, 2017).

Microbiological Analysis of Samples

Sample Preparation: Serial ten-fold dilutions were prepared using sterile 0.85% physiological saline as described by Cheesbrough (2021). Effluent and soil samples were diluted up to 10⁻⁶; excised crop samples were analyzed qualitatively without dilution for organism detection.

Total Heterotrophic Bacterial Counts (THB): Aliquots (0.1 ml) were plated in triplicate on nutrient agar and incubated at 30 ± 2°C for 24–48 hours. Colony-forming units (cfu) were expressed as log₁₀ cfu/ml (effluent) or log₁₀ cfu/g (soil), following APHA (2017).

Total Fungal Counts (TFC): Fungal populations were enumerated on potato dextrose agar supplemented with chloramphenicol (50mg/l). Plates were incubated at 28 ± 2°C for 3–5 days (Pitt and Hocking, 2012).

Total and Faecal Coliforms: Total coliforms were enumerated using MacConkey agar incubated at 37°C for 24 h, while faecal coliforms were recovered on m-FC agar incubated at 44.5°C (APHA, 2017). Metallic-sheen colonies on Eosin methylene blue agar were presumptively identified as *Escherichia coli*.

Functional Microbial Groups (Soil): Functional groups were quantified to assess metabolic diversity: Lipolytic bacteria: Tributyrin Agar (halo zone formation). Amylolytic bacteria: Starch Agar + Lugol's iodine. Proteolytic bacteria: Skim Milk Agar (casein clearing). Phosphate-solubilizing bacteria: Pikovskaya's Agar (clear zones). Nitrifying bacteria: Winogradsky medium (nitrite/nitrate production) methods followed Cappuccino and Sherman (2019) and De Freitas et al. (1997).

Enterococci Enumeration: Enterococci were isolated on Bile Esculin azide agar incubated at 37°C for 24–48 h. Blackening indicated esculin hydrolysis (Facklam and Collins, 2020).

Isolation and Preservation of Pure Cultures: Distinct bacterial and fungal colonies were repeatedly streaked on fresh media until pure colonies were obtained. Isolates were maintained on agar slants at 4°C and subcultured biweekly for viability (Cappuccino and Sherman, 2019).

Biochemical and Molecular Identification: Representative isolates were subjected to morphological, biochemical, and molecular tests. Selected bacterial isolates presented expected biochemical reactions: for example, *Bacillus* spp. were Gram-positive rods, catalase positive and motile; *Pseudomonas* spp. were Gram-negative rods, oxidase positive, citrate utilizing; *E. coli* isolates were indole positive and lactose fermenters. Molecular identification (16S rRNA for bacteria and ITS for fungi) resulted in high similarity matches for the following taxa: *Escherichia coli*, *Pseudomonas aeruginosa*, *Pseudomonas fluorescens*, *Enterobacter cloacae*, *Bacillus subtilis*, *Aspergillus niger*, and *Fusarium oxysporum*. Species-level alignment was

based on ≥ 98 % sequence identity with reference database entries.

Bacterial Identification: Bacterial isolates were subjected to: Gram staining, catalase and oxidase tests, Indole and citrate utilization tests, urease and hydrogen sulphide production, carbohydrate fermentation tests (glucose, lactose, sucrose, maltose, mannitol, galactose, cellulose). Identification was based on Bergey's Manual of Systematic Bacteriology and standard microbiological protocols (Holt et al., 1994; Cheesbrough, 2021).

Fungal Identification: Macroscopic characteristics (colour, texture, topography) and microscopic structures (conidia, vesicles, septation) were examined using lactophenol cotton blue mount. Fungal identification followed Barnett and Hunter (2006) and Samson et al. (2019).

Molecular Identification of Representative Isolates - DNA Extraction: Genomic DNA from selected bacterial and fungal isolates was extracted using a commercial soil/fecal DNA extraction kit following manufacturer's protocol.

PCR amplification of bacterial 16S rRNA gene: Amplified using universal primers (Lane, 1991): Molecular identification of bacterial isolates was performed by amplification of the 16S ribosomal RNA (rRNA) gene using universal primers: 27F: 5'-AGAGTTTGATCMTGGCTCAG-3' 1492R: 5'-TACGGYTACCTTGTTACGACTT-3' PCR reactions were carried out in a total volume of 25 μ L containing: 12.5 μ L of 2 $\times$ PCR Master Mix (Taq DNA polymerase, dNTPs, MgCl₂), 1.0 μ L each of forward and reverse primers (10 pmol), 2.0 μ L of template DNA, 8.5 μ L of nuclease-free water. Amplification was performed in a thermal cycler under the following conditions: Initial denaturation at 95 °C for 5 minutes, 35 cycles of denaturation at 95 °C for 30 seconds, Annealing at 55 °C for 30 seconds, Extension at 72 °C for 90 seconds, Final extension at 72 °C for 7 minutes.

Fungal ITS region: Amplified using universal primers (White et al., 1990):

Fungal identification was carried out by amplification of the Internal Transcribed Spacer (ITS) region using primers:

ITS1: 5'-TCCGTAGGTGAACCTGCGG-3'

ITS4: 5'-TCCTCCGCTTATTGATATGC-3'

PCR reaction mixtures and cycling conditions were similar to those used for bacterial amplification, except that annealing was performed at 52 °C. The ITS region was selected due to its high interspecific variability, making it a reliable DNA barcode for fungal identification.

PCR products were resolved on 1.5% agarose gel stained with ethidium bromide and visualized under UV illumination.

Sequencing and Data analysis: Sanger sequencing was performed using an Applied Biosystems 3500 Genetic Analyzer. Chromatograms were trimmed and aligned using MEGA X. Identification was confirmed through BLASTn comparison with reference sequences in the National Center for Biotechnology Information (NCBI) database, with $\geq 98\%$ similarity used as the species-level threshold.

Data Statistical Approach: Microbial counts were expressed as means $\pm$ standard deviation (SD) in $\log_{10}$ cfu. Prevalence data for microorganisms were presented as percentages across samples. Crop microbial data were reported qualitatively (presence/absence). Statistical analysis for microbial counts followed standard descriptive methods appropriate for microbiological enumeration (Madigan *et.al.*, 2021).

RESULTS AND DISCUSSION

The results revealed microbial transmission from contaminated effluent on agricultural soil and subsequently on edible crops cultivated on them. This pattern is consistent with previous reports of Akan *et.al.* (2022); Adekanmbi and Falodun (2021), highlighting the effects of untreated abattoir effluents as reservoirs and dispersal routes for environmentally persistent and enteric microorganisms. The study discovered that abattoir wastewater contained high microbial loads with isolation of several bacterial and

fungal species, indicating substantial faecal and organic pollution. Wastewater-irrigated soil showed elevated microbial counts compared with the control. Edible crops cultivated on polluted soils harboured multiple microbial taxa, confirming an effluent–soil–crop contamination pathway. Molecular analyses corroborated biochemical results by confirming the presence of key bacterial and fungal species, thereby strengthening the evidence for wastewater-driven microbial transmission.

The microbial counts of the three abattoir wastewater samples as presented in Table 1, showed consistently high levels of contamination across all samples. Total heterotrophic bacteria ranged from $6.94 \pm 0.08 \log_{10}$ cfu ml^{-1} in effluent A to $7.02 \pm 0.06 \log_{10}$ cfu ml^{-1} in effluent C, indicating a high samples pollution. Fungal presence was also substantial, with values between 5.59 ± 0.06 and $5.64 \pm 0.06 \log_{10}$ cfu ml^{-1} , suggesting the presence of organic matter capable of sustaining fungal growth. Total coliforms and faecal coliforms exceeded 5.3 and 5.0 $\log_{10}$ cfu ml^{-1} respectively. These values exceeded several national and international limits for irrigation water and reflect the organic richness of abattoir effluent, which typically contains blood residues, intestinal contents, gut flora, and decomposing tissue fluids (Olatunde *et.al.*, 2020). The detection of *E. coli*, *Enterobacter*, *Bacillus*, *Pseudomonas*, and *Aspergillus niger* further confirmed heavy faecal and environmental contamination. Similar microbial profiles have been reported in abattoir discharges in Ibadan, Port Harcourt, and Nairobi, underscoring the widespread microbiological risks associated with slaughterhouse wastewater according to Chukwu *et.al.* (2021); Njeru *et.al.* (2023).

The distribution of microbial genera presented in Table 2 shows isolation of *Bacillus* spp., *Pseudomonas* spp., *Enterobacter* spp., *Escherichia coli*, *Aspergillus niger*, and *Penicillium* spp. across all effluent samples. Opportunistic species such as *Staphylococcus aureus*, *Fusarium*, and *Trichosporon* spp. occurred,

particularly in effluent B, indicating fluctuating microbial presence in the different slaughter sites. This finding is in agreement with earlier reports of Azuonwu and Ogbonna (2019). Microbial counts for control and polluted soils are presented in Table 3. The control soil demonstrated comparatively lower microbial population, with total heterotrophic bacteria (THB) at $5.86 \log_{10} \text{ cfu g}^{-1}$ and fungal counts (TFC) at $4.92 \log_{10} \text{ cfu g}^{-1}$. Total and faecal coliforms were similarly low at 4.21 and $3.76 \log_{10} \text{ cfu g}^{-1}$ respectively. In contrast, all wastewater-irrigated soils showed markedly higher microbial loads, reflecting the influence of continuous organic and faecal deposition from effluent irrigation. Total heterophilic bacteria values in the polluted samples were within the $7.14\text{--}7.22 \log_{10} \text{ cfu g}^{-1}$ range relative to the control. Fungal counts in P-C remained above $6.3 \log_{10} \text{ cfu g}^{-1}$, reflecting a consistent shift toward conditions favourable for fungal proliferation. Coliform counts in P-C exceeded $5.9 \log_{10} \text{ cfu g}^{-1}$ for total coliforms and $5.2 \log_{10} \text{ cfu g}^{-1}$ for faecal coliforms. Functional microbial groups—including nitrifiers, phosphate-solubilizing bacteria, amylolytic and proteolytic bacteria—were noticeably higher in P-C than in the control. These findings suggest intensified biochemical activity and nutrient transformation within wastewater-enriched soils. Enterococci levels in P-C remained high (approximately $4.9 \log_{10} \text{ cfu g}^{-1}$), demonstrating persistent faecal influence across the polluted soil treatments. Adesemoye et al. (2006), had similar report that abattoir wastewater polluted soil has higher microbial composition. The prevalence of bacterial taxa recovered from all soil samples, in Table 4, revealed dominance by *Bacillus* spp. (100 %), followed by *Pseudomonas* spp. (90 %), *Enterobacter* spp. and *E. coli* (70 %), and other opportunistic species such as *Staphylococcus* spp., *Serratia* spp., *Salmonella enterica*, and *Chromobacterium violaceum*. The bacterial diversity from this investigation is in agreement with the findings of Adesemoye et al. (2006). The

fungal profile (Table 5) was similarly enriched, with *Aspergillus niger* occurring in all polluted soils, followed by *Penicillium citrinum* (70 %), *Fusarium solani* (40 %), *Trichosporon faecale* (30 %), and *Geotrichum candidum* (20 %). These patterns collectively indicated that wastewater irrigation substantially altered soil microbial communities, favouring spore-forming and opportunistic genera adapted to nutrient-rich and moisture-variable environments. The isolation of these fungal species is similar to reports by Ire et al. (2017). The microorganisms detected on maize, okra, and cowpea grown on wastewater-irrigated soils are presented in Table 6. All three crop types exhibited colonization by multiple genera, many of which were also present in the effluent and soil samples. *Escherichia coli*, *Enterobacter* spp., *Pseudomonas* spp., and *Bacillus* spp. were isolated from maize, okra, and cowpea, confirming direct microbial transfer from polluted soil to crops. Fungal contaminants, including *Aspergillus niger*, *Penicillium* spp., and *Fusarium oxysporum*, were across the crops. The presence of both bacteria and fungi on edible plant tissues underscores the vulnerability of crops cultivated under wastewater irrigation. Adesemoye et al. (2006) reported higher microbial counts in crops grown on abattoir wastewater irrigated soil than in uncontaminated control soil. Soils irrigated with wastewater showed pronounced increases in total heterotrophic bacteria, fungi, coliforms, and functional microbial groups compared with the control. Elevated occurrence of amylolytic, proteolytic, and lipolytic bacteria are in total agreement with earlier report by Ezech et al. (2023). The dominant soil bacteria—*Bacillus* spp., *Pseudomonas* spp., *Enterobacter* spp., and *E. coli*—reflect organisms capable of surviving environmental fluctuations, competing for nutrients, and forming robust biofilms. *Bacillus* prevalence (100 %) is linked to endospore formation, which allows survival despite varying moisture and temperature. *Aspergillus niger* (100 %) and *Penicillium*

citrinum (70 %) were found in polluted soil samples. This is in consonance with reports of Samson *et.al.* (2019).

The presence of multiple microbial taxa on maize, okra, and cowpea harvested from polluted soils indicated direct transfer of microbial pollutants from contaminated soil and/or wastewater on the crops. The consistent detection of *E. coli*, *Enterobacter*, *Pseudomonas*, *Bacillus*, and major fungal contaminants on all crop types confirmed soil-to-plant transfer. This agrees with Karanja *et.al.* (2021); Nwabor *et.al.* (2022). Molecular identification strengthened the reliability of culture-based findings. The 16S rRNA sequencing confirmed the presence of *E. coli*, *Pseudomonas aeruginosa*, *P. fluorescens*, *Enterobacter cloacae*, and *Bacillus subtilis*, all of which were previously identified through biochemical methods. Similarly, ITS region analysis verified *Aspergillus niger* and *Fusarium oxysporum*. The agreement between cultural and molecular identification supports the

correctness of the results obtained in this study. Importantly, several of the confirmed species—including *P. aeruginosa*, *E. coli*, and *Enterobacter cloacae*—are documented opportunistic pathogens with relevance to human health. The presence of the microbial isolates on edible crops highlights the public health implications of consuming produce grown with untreated wastewater. These findings indicated that untreated abattoir wastewater poses significant risks when used for crop irrigation. Pathogenic and opportunistic microorganisms can be transferred from the effluent to soil ecosystems and eventually reach food crops, potentially causing gastrointestinal infections, spoilage, or toxin exposure. This finding agrees with Azuonuwu and Ogbonna (2019). The results align with global reports that wastewater irrigation—without adequate treatment—can serve as a vehicle for transmitting enteric bacteria, antibiotic-resistant strains, and pathogenic fungi to the food chain (WHO, 2021).

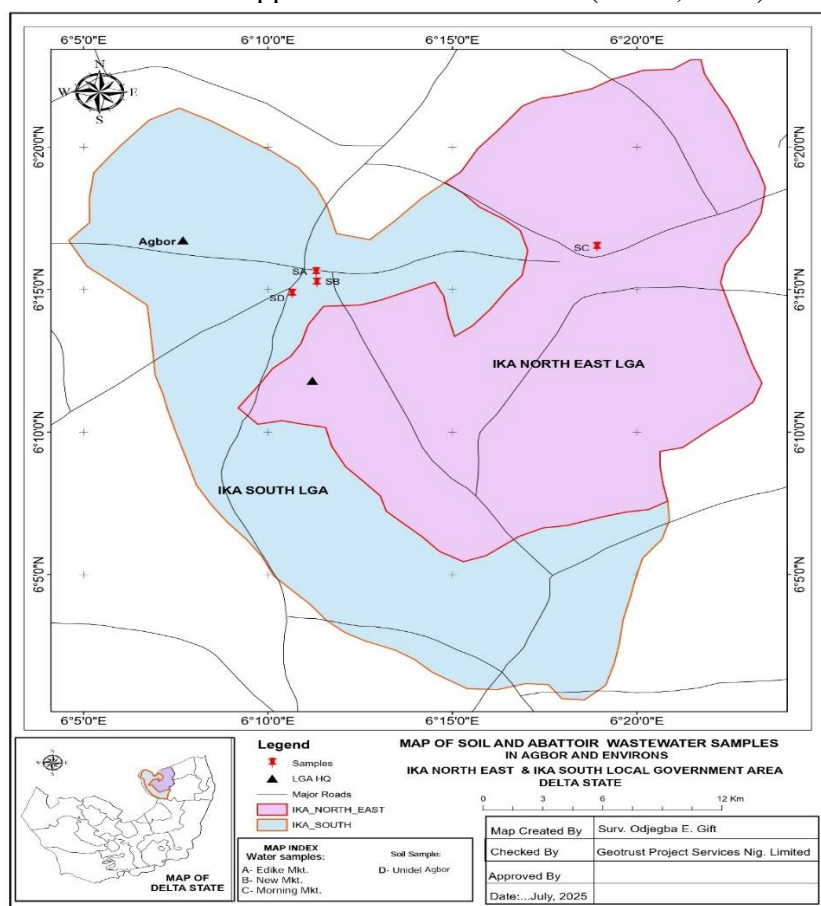


Figure 1: Samples map, Agbor, Delta State, Nigeria

Table 1: Microbial counts in abattoir wastewater ($\log_{10}$ cfu ml⁻¹ ± SD)

Parameter	Effluent A	Effluent B	Effluent C
Total heterotrophic bacteria	6.94 ± 0.08	6.96 ± 0.07	7.02 ± 0.06
Total fungi	5.59 ± 0.06	5.61 ± 0.05	5.64 ± 0.06
Total coliforms	5.38 ± 0.05	5.46 ± 0.05	5.52 ± 0.06
Faecal coliforms	5.04 ± 0.06	5.18 ± 0.05	5.21 ± 0.05

Table 2: Occurrence of microbial isolates in effluent samples

Microorganism	A	B	C	Prevalence (%)
<i>Bacillus</i> spp.	+	+	+	100
<i>Pseudomonas</i> spp.	+	+	+	100
<i>Enterobacter</i> spp.	+	+	+	100
<i>Escherichia coli</i>	+	+	+	100
<i>Aspergillus niger</i>	+	+	+	100
<i>Penicillium</i> spp.	+	+	+	100
<i>Staphylococcus aureus</i>	—	+	—	33.3
<i>Fusarium</i> spp.	—	+	+	66.7
<i>Trichosporon</i> spp.	—	+	—	33.3

Table 3: Microbial counts in control and wastewater-irrigated soil treatments ($\log_{10}$ cfu g⁻¹)

Sample	THB	TFC	Total Coliforms	Faecal Coliforms	Nitrifiers	PSB	Amylolytic	Proteolytic	Enterococci
C (Control)	5.86	4.92	4.21	3.76	3.64	3.78	3.94	4.10	3.42
P-A	7.22	6.46	6.03	5.27	5.23	5.30	5.52	5.64	4.98
P-B	7.14	6.38	5.96	5.21	5.17	5.25	5.47	5.59	4.92
P-C	7.18	6.40	5.98	5.24	5.19	5.27	5.50	5.61	4.95

Table 4: Prevalence of bacterial genera in soil samples

Taxon	Prevalence (%)
<i>Bacillus</i> spp.	100
<i>Pseudomonas</i> spp.	90
<i>Enterobacter</i> spp.	70
<i>Escherichia coli</i>	70
<i>Staphylococcus</i> spp.	60
<i>Serratia</i> spp.	40
<i>Salmonella enterica</i>	30
<i>Chromobacterium violaceum</i>	20

Table 5: Prevalence of fungal taxa in soil samples

Taxon	Prevalence (%)
<i>Aspergillus niger</i>	100
<i>Penicillium citrinum</i>	70
<i>Fusarium solani</i>	40
<i>Trichosporon faecale</i>	30
<i>Geotrichum candidum</i>	20

Table 6: Morphological identities of microorganisms on edible crops grown on wastewater-irrigated soils

Microorganisms	Maize	Okra	Cowpea
<i>E. coli</i>	+	+	+
<i>Enterobacter</i> spp.	+	+	+
<i>Pseudomonas</i> spp.	+	+	+
<i>Bacillus</i> spp.	+	+	+
<i>Staphylococcus aureus</i>	+	—	—
<i>Aspergillus niger</i>	+	+	+
<i>Penicillium</i> spp.	+	+	+
<i>Fusarium oxysporum</i>	—	+	+

CONCLUSION

This study established clear microbial transmission from abattoir wastewater to soil and subsequently to crops grown on polluted fields. Effluents contained high loads of heterotrophic bacteria, coliforms, and fungi. Wastewater-irrigated soil showed significantly elevated microbial counts and dominance of *Bacillus*, *Pseudomonas*, *Enterobacter*, *E. coli*, and *Aspergillus* species. Crops cultivated on these soils harboured similar organisms, confirming effluent–soil–crop contamination pattern. Molecular identification validated the presence of key bacterial and fungal species

of public health relevance. Overall, untreated abattoir wastewater poses considerable risks to crop hygiene, soil quality, and consumer safety. Monitor irrigation water sources for contaminants before use. Practice proper sanitation on farm produce before consumption. Provide public awareness campaigns. Antibiotic stewardship. Adoption of remediation strategies. Regular environmental monitoring. Installation of wastewater treatment facilities. Practice integrated waste management. Adopt alternate irrigation practices.

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