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Original Research Article

Assessment of the Microbial Content of Abattoir Effluents Discharged into Swali River, Yenagoa, Bayelsa State

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Abstract

One of the greatest concerns for the environment and human health is the discharge of untreated effluents from abattoirs into aquatic environments with high microbial load and harmful pathogens. In this work, the microbiological content of abattoir wastewater released into Swali River was studied. Five sampling points were selected inside the abattoir environment; process water point, slaughter point, butcher point, disposal point and discharge point. Standard microbiological techniques were used to enumerate, isolate and characterise bacterial and fungal pollutants. The overall heterotrophic bacteria count was 1.4 × 106 to 7.2 × 106 CFU/ml and the enteric bacteria counts were 3.1 × 106 to 5.4 × 106 CFU/ml. Fungal counts varied from 7 × 10 3 to 4.3 × 10 4 CFU/ml. The maximum heterotrophic bacterial count was detected at the slaughter site and the highest fungal load was seen at the butcher point. Morphological and biochemical characterisation revealed the presence of pathogenic bacterial species including Salmonella spp, Escherichia coli, Klebsiella spp, Proteus spp, Pseudomonas spp, Staphylococcus spp, Clostridium spp and Bacillus spp. The discovered fungal isolates included Aspergillus spp., Aspergillus flavus, Penicillium spp., Fusarium spp. and yeasts such as Candida spp. and Saccharomyces spp.The preponderance of enteric bacteria and opportunistic fungal pathogens in the effluents implies high level of microbial pollution linked with poor sanitary practices and poor waste management within the abattoir environment. The direct dumping of these contaminated effluents into the Swali River may add to environmental contamination and raise the risk of water-borne infections among communities who depend on the river for domestic and economic activity. Therefore, the study proposes that appropriate wastewater treatment systems, rigorous hygiene procedures and routine microbiological monitoring of abattoir operations should be implemented to protect environmental and public health.

Keywords: *Abattoir effluent, microbiological pollution, enteric bacteria, fungal, pathogenic microorganism, Swali River, Bayelsa State.*

Introduction

River pollution is still a major environmental problem worldwide, especially in underdeveloped nations where untreated wastes are often released to natural water bodies. Rivers get contaminated through different sources include direct disposal of untreated home and industrial wastes, agricultural runoff containing fertilisers and pesticides and effluents from industrial and abattoir activities [1]. These pollutants negatively impact water quality and aquatic ecosystems resulting in severe environmental and health effects. Studies have shown that pollutants entering rivers can cause eutrophication, oxygen depletion and the loss of aquatic life, and harmful compounds such as heavy metals can accumulate and make water unfit for drinking, irrigation and other domestic uses [2].

Effluents from abattoirs are known to be a major source of water contamination due to their high organic and microbiological load. Abattoir effluent often contains blood, lipids, intestinal content, urine, faecal materials and suspended solids from animal killing and meat processing processes. The disposal of untreated effluents into the surrounding rivers leads to environmental pollution by increasing the biochemical oxygen demand (BOD) and chemical

oxygen demand (COD) of the receiving water bodies thereby causing a decline in the dissolved oxygen level for the aquatic life [3].

Microbial contamination is one of the most important pollution features of abattoir effluents. The nature of slaughtering activities and the poor hygienic management of animal products, abattoir wastes contain microorganisms such bacteria, fungus, viruses and protozoa. Some bacteria are crucial in ecological functions of decomposition and nutrient recycling; while pathogenic species in abattoir effluents are severe hazards to human and animal health. Some research [4] have documented the existence of harmful microbes like Escherichia coli, Salmonella spp., and Staphylococcus aureus which are responsible for gastrointestinal illnesses, food poisoning and other communicable diseases in abattoir effluent. The organic content of abattoir waste is substantial, providing a good habitat for microbial growth and proliferation. Rivers that receive untreated abattoir discharges are usually characterised by increased microbial loads and the presence of faecal contamination indicators, therefore increasing the potential for transmission of waterborne diseases[5]. Coliform bacteria and other pathogenic microorganisms in polluted rivers are a significant indicator of poor water quality and possible threats to human health. Hence, regular monitoring and evaluation of microbiological contamination in water bodies receiving abattoir effluents is crucial for optimal environmental management and disease prevention [6, 7]. Various research have been carried out on the environmental effects of abattoir effluents in different places although information on the microbiological composition of abattoir waste water discharged into the Swali River is still scarce. Most of the studies available have mainly focused on physicochemical contaminants or generic findings across multiple geographical regions without proper consideration of the peculiar environmental and socio-economic characteristics of Yenagoa, Bayelsa State[8]. However, the local practices related to the operation of slaughterhouses, waste disposal and environmental cleanliness in the area have not been fully explored. This lack of information hinders the development of localised intervention strategies for efficient environmental protection and public health management. Therefore, this study was aimed at assessing microbiological contamination of abattoir effluents discharged into the Swali River in Yenagoa, Bayelsa State, Nigeria.

Materials and Methods

Study Design and Study Area

This study was conducted at the Swali Market Abattoir located in Yenagoa, the capital city of Bayelsa State, Nigeria. The abattoir is situated within the Swali Market area and serves as one of the major slaughtering and meat processing centers in the state. The study was designed to evaluate the microbial content of abattoir effluents discharged into the Swali River through microbiological assessment of effluent samples collected from different operational sections of the abattoir.

Ethical Approval

Ethical approval for this study was obtained from the Bayelsa State Ministry of Health prior to the commencement of sample collection and laboratory investigations.

Sample Collection

To assess the environmental and public health implications associated with abattoir operations, effluent samples were collected from five critical sections of the abattoir, namely the process water point, slaughter point, butcher point, discharge point, and disposal point.

The process water point represents the section where water is used for washing meat, cleaning equipment, and other processing activities. Effluents from this point are often contaminated with organic materials, detergents, and suspended particles. The slaughter point is the primary site where animals are slaughtered and dressed, contributing large quantities of blood, tissues, intestinal contents, and other animal wastes to the effluent. The butcher point involves meat cutting and processing activities and is characterized by the presence of fats, proteins, and microbial contaminants. The discharge point serves as the outlet through which combined wastewater exits the abattoir, while the disposal point represents the final site where the effluent is released into the environment or disposed of.

Effluent samples were collected aseptically using sterile sample bottles to avoid external contamination. Each sample was properly labeled and immediately stored in ice-cooled containers to preserve its microbiological integrity during transportation. The samples were transported to Wizlink Laboratory, Yenagoa, within 12–24 hours of collection for detailed microbiological analyses. Prompt transportation and preservation of samples were necessary to maintain their chemical and biological stability and to ensure accurate laboratory results.

Sample Preparation

Sample preparation was carried out using standard microbiological procedures under aseptic conditions. Exactly 1 ml of each effluent sample was aseptically collected using a sterile syringe and transferred into a sterile test tube containing 9 ml of normal saline. This initial mixture constituted the stock solution.

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Serial dilution of the stock sample was subsequently performed up to the fifth dilution (10^{-5}). The serial dilution process involved transferring 1 ml from the stock solution into another test tube containing 9 ml of sterile normal saline and repeating the procedure successively until the desired dilution factor was obtained. Serial dilution was necessary to reduce microbial concentration to a countable range suitable for microbial enumeration and isolation.

The diluted samples were homogenized by gently shaking and tilting the test tubes to ensure even distribution of microorganisms within the solution. Thereafter, the samples were allowed to stand for approximately 30 minutes prior to culturing to stabilize the microbial suspension.

Microbiological Assay

Enumeration of Microorganisms

Microbial enumeration was carried out using the spread plate technique to determine the total heterotrophic bacterial count, total enteric bacterial count, and fungal count. Dilutions of 10^{-3} and 10^{-5} were used for inoculation.

Exactly 1 ml of the appropriate dilution was inoculated onto the surface of solidified agar plates and evenly spread using a sterile disposable spreader. Nutrient agar was used for the enumeration of total heterotrophic bacteria, MacConkey agar for total enteric bacteria, and Potato Dextrose Agar (PDA) for fungal isolation and enumeration.

The inoculated bacterial culture plates were inverted and incubated at 37°C for 18–24 hours, while fungal culture plates were incubated at room temperature for 2–5 days without inversion. Following incubation, visible colonies were counted and expressed as colony-forming units per milliliter (CFU/ml) of the effluent sample.

Isolation and Identification of Bacteria

Distinct bacterial colonies obtained from Nutrient agar and MacConkey agar plates were aseptically picked using sterile wire loops and subcultured by streaking onto freshly prepared Nutrient agar plates to obtain pure isolates. The plates were incubated at 37°C for 24 hours.

Pure bacterial isolates were preliminarily identified based on colonial morphology, including colony shape, color, texture, elevation, and margin characteristics. The isolates were subsequently preserved on Nutrient agar slants for further characterization.

Further identification of bacterial isolates was carried out using Gram staining and biochemical tests including growth in Nutrient broth, growth in MacConkey broth, citrate utilization test, catalase test, Triple Sugar Iron (TSI) agar test, and growth on Salmonella–Shigella agar.

Isolation and Identification of Fungi

Fungal isolates obtained on Potato Dextrose Agar were preliminarily characterized based on colonial morphology, including surface appearance, pigmentation, texture, and reverse plate coloration. Distinct fungal colonies were aseptically picked and subcultured onto fresh PDA plates, followed by incubation at room temperature for 2–5 days to obtain pure cultures.

Further characterization and identification of fungal isolates were carried out using lactophenol cotton blue staining for microscopic examination and observation of growth patterns in Potato Dextrose Broth. Microscopic features such as conidia arrangement, hyphal structures, and spore morphology were used for fungal identification.

Results

Table 4.1: Total Heterotrophic bacteria and total enteric bacteria count of the abattoir effluent samples.

Sample ID	Total heterotrophic bacteria			Enteric bacteria			Fungi		
	Plate count		Cfu/ml	Plate count		Cfu/ml	Plate count		Cfu/ml
	10^{-3}	10^{-5}	10^{-5}	10^{-3}	10^{-5}	10^{-5}	10^{-3}	10^{-5}	10^{-3}
Process water (P)		72	7.2×10^{6}	70	50	5.0×10^{6}	8	3	8×10^{3}
Slaughter (S)	182	52	5.2×10^{6}	82	31	3.1×10^{6}	7	1	7×10^{3}
Butcher (B)	80	30	3.0×10^{6}		54	5.4×10^{6}	43	8	4.3×10^{4}
Disposal (DS)	53	14	1.4×10^{6}		35	3.5×10^{6}	24	3	2.4×10^{4}
Discharge (DC)	70	65	6.5×10^{6}		52	5.2×10^{6}	10	1	1.0×10^{4}

Key: P – Process water point, S – Slaughter point, B – Butcher point, DS – Disposal point, DC – Discharge point

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Table 4.2: Characterization of bacteria isolated from the effluents of the disposal and slaughter points of the abattoir

Sample ID	Morphology Nut agar	Gram	MacConkey broth	Nutrient broth	Citrate	TSI Agar	SSA	Tentative isolate
Ds 1	Creamy mucoid in nutrient agar pink in MacConkey	-Rod	F/G	Turbid	+ yellow	R/Y	No growth	*Klebsiella* sp.
Ds 2	Creamy mucoid in nutrient agar pink in MacConkey	-Rod	F/G	Turbid	+ blue	R/Y, H_2S	No growth	*Salmonella* sp
Ds 3	Creamy mucoid in nutrient agar pink in MacConkey	-Rod	F/G	Turbid	-	Y/Y, H_2S, G	No growth	*Escherichia coli*
Ds 4	Creamy mucoid in nutrient agar pink in MacConkey	-Rod	F/G	Turbid	-	Y/Y, H_2S, G	No growth	*Escherichia coli*
Ds 5	Creamy mucoid in nutrient agar pale in MacConkey	-Rod	F/G	Turbid	+ blue	R/Y, H_2S	Black	*Salmonella* sp.
Ds 6	Creamy mucoid in nutrient agar pale in MacConkey	-Rod	F/G	Turbid	Positive [blue colour]	R/Y, H_2S, G	Black	*Salmonella* sp.
S 1	Creamy mucoid in nutrient agar pale in MacConkey	-Rod	NF/NG	Flocculant	negative	R/R	Pale	*Pseudomonas* sp.
S 2	Creamy mucoid in nutrient agar pale in MacConkey	-Rod	NF/NG	Flocculant	negative	R/Y	Pale	*Proteus* sp.
S 3	Creamy mucoid in nutrient agar pale in MacConkey	-Rod	F/G	Turbid	Positive [yellow colour]	R/R, H_2S	Black	*Salmonella* sp.
S 4	Creamy mucoid in nutrient agar pale in MacConkey	-Rod	F/G	Turbid	Positive [yellow colour]	R/Y, H_2S, G	Black	*Salmonella* sp.
S 5	Circular shiny creamy in nutrient pale in MacConkey agar	-Rod	F/G	Turbid	Positive [yellow colour]	R/Y, G	Pale	*Proteus* sp.
S6	Creamy mucoid in nutrient agar pink in MacConkey	-Rod	F/G	Turbid	negative	R/Y	No growth	*Escherichia coli*

Key: D – Disposal point, S – Slaughter point

Table 4.3: Characterization of bacteria isolated from the effluents of the discharge and butcher points of the abattoir

Sample ID	Morphology Nut agar	Gram	MacConkey broth	Nutrient broth	Citrate	TSI Agar	SSA	Tentative isolate
Dc 1	Creamy mucoid in nutrient agar pale in MacConkey	-Rod	F/G	Turbid	negative	R/Y, H2S	Black	*Salmonella* sp.
Dc 2	Circular shiny creamy in nutrient pale in MacConkey agar	-Rod	F/NG	Turbid	Positive [blue colour]	R/Y, H2S	Pale	*Proteus* sp.
Dc 3	Creamy mucoid in nutrient agar pale in MacConkey	-Rod	F/G	Turbid	Positive [yellow colour }	R/Y, H2S	Black	*Salmonella* sp.
Dc 4	Creamy mucoid in nutrient agar pale in MacConkey	-Rod	F/G	Pellicle	Positive [yellow]	R/Y, H2S	Black	*Salmonella* sp.
Dc 5	Creamy mucoid in nutrient agar pale in MacConkey	-Rod	F/NG	Turbid	Positive [yellow colour]	R/Y, H2S	Black	*Salmonella* sp.
Dc 6	Creamy mucoid in nutrient agar pale in MacConkey	-Rod	F/G	Turbid	Positive [yellow colour]	R/Y, H2S	Black	*Salmonella* sp.
B 1	Creamy mucoid in nutrient agar pale in MacConkey	-Rod	F/G	Pellicle	Negative	R/Y	Black	*Salmonella* sp.
B 2	Creamy mucoid in nutrient agar pink in MacConkey	+ Cocci	NF/NG	Pellicle	negative	R/Y	Black	*Salmonella* sp.

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B 3	Circular Creamy in nutrient agar yellow raised in mannitol salt agar	+ Cocci	NF/NG	Pellicle	Negative	R/Y		*Staphylococcus* sp.
B 4	Circular Creamy in nutrient agar	+Rod	NF/NG	Turbid	negative	R/Y		*Clostridium* sp.
B 5	Circular Creamy in nutrient agar	+Rod	F/G	Turbid	negative	R/Y		*Clostridium* sp.
B 6	Creamy mucoid in nutrient agar pink in MacConkey	-Rod	F/G	Turbid	negative	R/Y	No growth	*Klebsiella* sp.

Key: Dc – Discharge point, B – Butcher Point

Table 4.4: Characterization of bacteria isolated from the process water point of the abattoir

Sample ID	Morphology Nut agar	Gram	MacConkey broth	Nutrient broth	Citrate	TSI Agar	SSA	Tentative isolate
P 1	Circular Creamy in nutrient agar	+Bacci	NF/NG	Turbid	Positive [blue colour]	R/Y		*Clostridium* sp.
P 2	Circular Creamy in nutrient agar	+Bacci	NF/NG	Flocculant	Positive [blue colour]	R/Y		*Clostridium* sp.
P 3	Circular Creamy in nutrient agar	+Bacci	NF/NG	Pellicle	Positive [blue colour]	R/Y		*Bacillus* sp.
P 4	Circular Creamy in nutrient agar	+Bacci	NF/NG	Pellicle	Positive [blue colour]	R/Y		*Bacillus* sp.
P 5	Circular Creamy in nutrient agar	+Bacci	NF/NG	Pellicle	Positive [blue colour]	R/Y		*Bacillus* sp.

Key: P – Process water point

Table 4.5: Characterisation of fungi isolates from Disposal and Discharge points of the abattoirs

Sample ID	Morphology on potato dextrose agar	Morphology on potato dextrose broth	Microscopy with lactophenol blue staining	Tentative isolate
DSI	Circular shiny raised entire perch [light pink] surface creamy backside	Sediment / turbid	Budding cells	Yeast *[Saccharomyces* spp / *candida* spp]
DS2	Circular shiny raised entire creamy surface creamy backside	Sediment / turbid	Budding cells	Yeast *[Saccharomyces* spp / *candida* spp]
DS3	Circular flat white surface white backside	Sediment	Budding cells	Yeast *[Saccharomyces* spp / *candida* spp]
DS4	Circular raised bluish green centre entire white edge surface brown backside	pellicle concave off white growth	Long chains of globose shapes arranged in columns. Conidiophores hyaline smooth walled and phialides is flask – shaped	*Penicillium* sp
DS5	Circular varicose whitish green surface creamy backside	pellicle concave off white growth	Long chains of globose shapes arranged in columns. Conidiophores hyaline smooth walled and phialides is flask – shaped	*Penicillium* sp
DC1	White circular raised hard surface creamy backside	Sediment / turbid	Budding cells	Yeast *[Saccharomyces* spp / *candida* spp]
DC2	Circular tiny raised white surface creamy backside	Circular white flocculant	Budding cells	Yeast *[Saccharomyces* spp / *candida* spp]
DC3	Circular granular dirty green surface creamy backside	Off white pellicle growth	Rough walled stripes, vesicles bearing phialides over their entire surface and conspicuous conidia	*Aspergillus flavus*
DC4	Circular raised slimy creamy surface creamy backside	Pellicle green dusty growth	Rough walled stripes, vesicles bearing phialides over their entire surface and conspicuous conidia	*Aspergillus flavus*
DC5	Circular dusty green surface varicose creamy backside	Pellicle dusty green growth rough meniscus	Rough walled stripes, vesicles bearing phialides over their entire surface and conspicuous conidia	*Aspergillus flavus*

Key: DS – Disposal Point, DC – Discharge Point

Table 4.6: Characterisation of fungi isolates from different butcher and slaughter points of the abattoirs

B1	Circular slimy cream surface creamy backside	Dusty concave creamy pellicle brownish meniscus	Smooth walled conidiophores and globose vesicles with phialides borne on metulae	*Aspergillus* sp
B2	Circular hard green surface in single and pairs dark brown backside	Off white pellicle growth	Smooth walled conidiophores and globose vesicles with phialides borne on metulae	*Aspergillus* sp
B3	Circular off white surface dark brown centre backside	Dusty concave green pellicle growth	Rough walled stripes, vesicles bearing phialides over their entire surface and conspicuous conidia	*Aspergillus* flavus
B4	Circular off white surface dark brown centre backside	Dusty concave pellicle growth with fluffy white meniscus dispatching into medium	Presence of characteristic macro-conidia and sickle shaped	*Fusarium* sp
B5	White circular raised hard surface creamy backside	Sediment growth	Budding cells	Yeast [*Saccharomyces* spp / *candida* spp]
S1	Circular dusty brown white edge surface varicose creamy backside	Jelly black droplet pellicle growth hard brown meniscus	Long chains of globose shapes arranged in columns. Conidiophores hyaline smooth walled and phialides is flask – shaped	*Penicillium* sp
S2	Circular raised entire shiny milky surface creamy backside	Creamy sediment growth	Budding cells	Yeast [*Saccharomyces* spp / *candida* spp]
S3	Circular white green centre surface creamy backside	Jelly black droplet pellicle growth hard brown meniscus	Long chains of globose shapes arranged in columns. Conidiophores hyaline smooth walled and phialides is flask – shaped	*Penicillium* sp
S4	Circular raised entire shiny creamy surface creamy backside	Creamy sediment growth	Budding cells	Yeast [*Saccharomyces* spp / *candida* spp]
S5	Circular raised entire dull white surface creamy backside	Creamy sediment growth	Budding cells	Yeast [*Saccharomyces* spp / *candida* spp]

Key: B (B1 to B5)– Butcher point, S (S1 to S5)– Slaughter point

Table 4.7: Characterisation of fungi isolates from process water points of the abattoirs

P1	Fluffy white surface creamy backside	Dusty green pellicle brownish hard meniscus white fluffy mycelium dispatching into medium	Presence of characteristic macro-conidia and sickle shaped	*Fusarium* sp
P2	Circular entire off-white surface creamy backside	Dusty green pellicle brownish hard meniscus white fluffy mycelium dispatching into medium	Presence of characteristic macro-conidia and sickle shaped	*Fusarium* sp
P3	Fluffy white surface creamy backside	Dusty green pellicle brownish hard meniscus white fluffy mycelium dispatching into medium	Presence of characteristic macro-conidia and sickle shaped	*Fusarium* sp
P4	Circular entire off-white surface creamy backside	Dusty green pellicle brownish hard meniscus white fluffy mycelium dispatching into medium	Presence of characteristic macro-conidia and sickle shaped	*Fusarium* sp
P5	Fluffy white surface creamy backside	Dusty green pellicle brownish hard meniscus white fluffy mycelium dispatching into medium	Presence of characteristic macro-conidia and sickle shaped	*Fusarium* sp

Key: P (P1 to P5) – Process water point

Discussion

Results of this analysis demonstrated extensive microbiological contamination of several parts of the abattoir indicating inadequate sanitary conditions and improper waste management techniques within the facility. The high total heterotrophic bacterial counts and enteric bacterial counts in the effluent samples were comparable to other studies of microbial contamination related with slaughtering activities. Similar results were reported by [8, 9] who studied bacterial contamination in slaughterhouses in Owerri, Nigeria and found high levels of heterotrophic and enteric bacteria in the abattoir environment. Similarly, substantial bacterial loads were found in abattoir effluents in several locations of Nigeria [10] which corroborate the findings of this investigation.

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The largest microbiological load was found in the slaughter site which can be due to accumulation of blood, intestinal contents, animal tissues and other organic wastes created during the slaughtering processes. The nutrients found in these organic materials promote the growth and spread of microbes. The high counts of enteric bacteria seen at the slaughter and butcher stations are strong indicators of faecal contamination due to incorrect handling of carcasses, contaminated equipment, and inadequate disposal of waste. [11] also observed widespread contamination by bacteria in the wastewater of abattoirs due to poor sanitary conditions and inadequate cleaning. The elevated fungal counts in the butcher section were in agreement with the results of [12] who found considerable fungal contamination in meat processing facilities due to moisture and organic matter which favour fungal growth and spore spread.

Isolation of Escherichia coli and Klebsiella species from disposal and slaughter points also confirmed the microbiological dangers associated with untreated abattoir effluents. These organisms are widely known markers of faecal pollution and poor sanitation. Similar observations were reported by [14] who attributed the presence of faecal coliforms in abattoir effluent to poor disposal of animal waste and unhygienic slaughtering procedures. Also, E. coli and Klebsiella species were reported as prevalent pollutants of untreated abattoir effluent and their public health importance was stressed due to their pathogenic potentials [15].

The dominance of Salmonella species in this investigation is in agreement with previous studies by [16] who regularly isolated Salmonella species from abattoir environments due to contamination of carcasses, processing water and slaughtering equipment. The black colour seen in this work on Salmonella-Shigella agar as a characteristic hydrogen sulphide generation is a well known diagnostic hallmark of Salmonella species [17]. The presence of Salmonella in abattoir effluents is of special concern because of its link with foodborne illnesses, gastroenteritis and outbreaks of waterborne sickness.

Similarly, the isolation of Pseudomonas and Proteus species from the slaughter and discharge locations agrees with previous research that recognised these organisms as opportunistic pathogens generally present in damp and nutrient-rich environments like as abattoirs [18]. Pseudomonas species are characterised by their resistance to disinfectants and their ability to live in difficult environmental circumstances [19], whereas Proteus species have high adaptive capacities that enable them to remain in contaminated settings [20]. Thus, their existence suggests bad hygienic conditions in the abattoir and absence of proper microbial control methods.

Also, the presence of Staphylococcus species at the butcher point is of public health concern since representatives of this genus are often implicated in food poisoning and contamination of meat products . Colonial morphology on nutritional agar and mannitol salt agar in this study is comparable with studies of [21] who identified Staphylococcus aureus from abattoir settings. Also, the presence of Clostridium species in the effluents is in agreement with previous findings that poorly managed abattoir wastes create anaerobic conditions that are favourable for the survival of spore-forming bacteria [22]. The ability of such organisms to survive in the environment increases the risk of toxin generation and disease transmission.

The detection of Bacillus and Clostridium species in the process water samples implies contamination of the water used in the meat processing activities. Similar results were reported by [23] who recognised abattoir process water as a large reservoir of harmful bacteria. Bacillus species are capable of forming resistant endospores, which allow them to live under extreme environmental circumstances, such as poor cleaning and disinfection processes [24]. The turbid and flocculant appearances in the nutrient broth cultures found in this investigation further indicate the substantial microbial burdens in the process water samples.

Fungal characterisation confirmed the presence of yeast species, Penicillium, Aspergillus, Aspergillus flavus and Fusarium species in the effluent samples. The isolation of yeast species such as Candida and Saccharomyces spp. from disposal and discharge locations is consistent with other results stating that yeasts are the predominant fungus in organic matter-rich settings [25]. Isolation of Penicillium spp. from disposal and slaughter points is also in agreement with results reported in earlier studies on fungal contamination in agricultural and industrial wastes. The bluish-green colonies and flask-shaped phialides reported in this study are typical features of Penicillium species [26].

The prevalence of Aspergillus flavus at the input and discharge locations is particularly noteworthy since the fungus is capable of producing aflatoxins which are toxic secondary metabolites linked to food poisoning and serious health problems. Comparable findings were reported by [27] who also identified Aspergillus spp. in abattoir environments and stressed their importance in food deterioration and mycotoxin generation. Furthermore, the constant recovery of Fusarium spp. from process water supports the notion of widespread fungal contamination of water utilised in the abattoir. Fusarium species are well recognised environmental fungus able to produce mycotoxins and cause opportunistic infections [28].

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Conclusion

The findings of the present study showed that abattoir environment is a significant reservoir of harmful bacteria and fungus that may contaminate the nearby water bodies including the Swali River. The direct discharge of abattoir effluents without treatment into the river creates major environmental and public health problems especially for communities that depend on the river for domestic and economic activity. Thus, the study emphasises the importance of improving sanitation practices, wastewater treatment systems, regular microbiological monitoring, and regulatory enforcement to reduce microbial pollution and preserve public health.

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