

Bacteriological assessment of the impact of untreated abattoir effluents on the Okokpon Stream and Surrounding Groundwater, Edo State, Nigeria

Solanke EO ¹, Akpoka OA ^{1,*}, Adama TU ^{2,3}, Akinyeye AJ ¹ and Obi TE ^{1,4}

¹ Department of Biological Science, College of Natural and Applied Sciences, Igbinedion University.

² Department of Biological Science and Biotechnology, Caleb University, Imota, Lagos.

³ Department of Microbiology, Federal University Lokoja.

⁴ Department of Chemical Science, College of Natural and Applied Sciences, Igbinedion University.

World Journal of Biology Pharmacy and Health Sciences, 2026, 26(02), 232-238

Publication history: Received on 06 April 2026; revised on 22 May 2026; accepted on 25 May 2026

Article DOI: <https://doi.org/10.30574/wjbphs.2026.26.2.0284>

Abstract

The discharge of untreated abattoir waste into rivers and streams can adversely affect environmental and public health by increasing microbial contamination of receiving waters. This study assessed the spatial trend in the bacteriological quality of Okokpon Stream receiving raw abattoir waste. Water samples were collected over a period of four weeks from four points: upstream, the effluent discharge point, downstream, and a well servicing the abattoir. Samples were transported to the laboratory within three hours of collection for bacteriological analysis. Total aerobic viable count (TAVC), total coliform count (TCC), and *Escherichia coli* count (ECC) were determined using nutrient agar, MacConkey broth, and eosin methylene blue agar, respectively. TAVC and ECC were determined by the pour plate method, while TCC was determined by the Most Probable Number (MPN) presumptive test. Mean counts in the abattoir effluent were 7.45×10^3 cfu/mL for TAVC, 72.5 MPN/mL for TCC, and 9.25×10^1 cfu/mL for ECC. Corresponding downstream mean values were 4.67×10^4 cfu/mL, 18.3 MPN/mL, and 1.44×10^1 cfu/mL, compared with upstream values of 2.12×10^3 cfu/mL, 1.95 MPN/mL, and 3.75 cfu/mL, respectively. The abattoir well water also showed microbial contamination, with mean TCC and ECC values of 23MPN/mL and 5.38 cfu/mL. These findings indicate contamination associated with abattoir discharge and show that the microbiological status of Okokpon Stream poses environmental and health risks to residents who use the stream for domestic, recreational, and food-production purposes. To reduce contamination, it is recommended that to construct a simple sedimentation pond or vegetated buffer strip between the abattoir and the stream; Divert all liquid waste through a small biogas digester before discharge; Provide an alternative water source (borehole) for abattoir operations, separate from the well-used for washing; Enforce monthly microbial monitoring of the stream by the local government environmental health department. If possible, the stream water should be adequately treated before use and that regulatory agencies enforce strict control of abattoir waste disposal into surrounding water bodies.

Keywords: Abattoir Effluent; Bacteriological Quality; Coliforms; *Escherichia coli*; Stream Pollution; Public Health

1. Introduction

Water is fundamental to human health, food production, sanitation and ecological stability. However, the quality of available surface water is strongly influenced by surrounding land use and watershed activities. Human and animal wastes, sediments, nutrients and untreated effluents are among the most important anthropogenic factors that degrade stream quality and increase public health risk (Hamid et al., 2020; Kosek et al., 2003). In low- and middle-income settings, unsafe water and poor sanitation remain major contributors to diarrhoea disease burden. Kosek et al. (2003) showed that diarrhoea diseases account for substantial global morbidity and mortality, especially among children. More recent global assessments continue to emphasize the scale of the problem. At least 1.7 billion people were estimated to

* Corresponding author: Akpoka OA

use a drinking-water source contaminated with faeces in 2022. Microbiologically contaminated drinking-water is also estimated to cause about 505,000 diarrhoea deaths annually (World Health Organization [WHO], 2023). A broader global analysis further estimated that unsafe water, sanitation, and hygiene accounted for 69% of diarrhoea disease burden in 2019 (Wolf et al., 2023). In addition, contamination may occur both at source and after collection; Wright et al. (2004) demonstrated that microbiological quality often deteriorates between source and point of use in developing countries. These findings show the importance of protecting surface water at source and monitoring microbial contamination routinely.

Microbiological contamination of streams is particularly important because indicator organisms such as total coliforms and *Escherichia coli* are widely used to assess faecal pollution and associated health risk. *E. coli* is regarded as one of the most reliable bacterial indicators of recent faecal contamination in water intended for domestic use (Odonkor and Ampofo, 2013; World Health Organization [WHO], 2011). Recent work on tributary monitoring has similarly emphasized that faecal indicator bacteria remain central to interpreting stream contamination patterns, even though source tracking may sometimes require supplementary tools (McMinn et al., 2024). The WHO guideline for drinking-water quality states that *E. coli* or thermotolerant coliform bacteria should not be detectable in any 100 mL sample of drinking water (WHO, 2011).

Abattoirs generate substantial volumes of solid and liquid wastes, including blood, manure, paunch contents, wash water, fats, and tissue residues. When such wastes are discharged untreated into nearby streams, they increase organic loading and create favourable conditions for the proliferation of coliforms and other microorganisms (Chaves et al., 2005; Adelegan, 2002). Nigerian studies have repeatedly shown that receiving water bodies downstream of abattoirs may contain bacterial loads far above recommended limits, posing environmental and public health threats (Adelegan, 2002; Anyata and Nwaiwu, 2000; Nafarnda et al., 2012; Akpoka et al., 2023). More recent evidence from Nigeria and other settings has added concern about the environmental dissemination of antibiotic-resistant bacteria from slaughterhouse wastewater, thereby broadening the public health significance of untreated abattoir discharge (Akpan et al., 2020; Chowdhury et al., 2025).

The Okokpon abattoir is situated directly on the bank of the stream, with no formal pre-treatment or containment facilities for liquid or solid waste before discharge. Evaluating the bacteriological quality of Okokpon Stream is therefore necessary to establish the extent of contamination and determine whether the water remains suitable for domestic and related uses. It is against this backdrop that this study assessed the bacteriological quality of Okokpon Stream receiving untreated abattoir effluent and the associated public health implications.

2. Materials and Methods

2.1. Study area and sample collection

The Okokpon Stream is a surface water body that flows through Okokpon Community in Ovia South West Local Government Area of Edo State, Nigeria. Its geographical coordinates are 6°38'0" N and 5°20'0" E. An abattoir is situated along the bank of the stream. At the Okokpon abattoir, an average of 10 cows and 20 sheep/goats are slaughtered daily, six days per week (Monday to Saturday). Samples were collected once weekly for four weeks during May and June [2025]. Water samples were collected in sterile bottles during the morning hours (8:00 a.m. to 10:00 a.m.). New sterile bottles were used for each sampling round. Four sampling points were investigated: abattoir effluent discharge, upstream, downstream, and the well water servicing the abattoir. The sterile bottles were dipped below the water surface to avoid air bubbles, corked below the surface, and transported to the laboratory within three hours of collection for analysis.

2.2. Bacteriological analysis

Bacteriological analyses performed on the samples included the pour plate method and the Most Probable Number (MPN) method. Total aerobic viable count (TAVC) and *Escherichia coli* count (ECC) were determined by the pour plate technique in accordance with APHA procedures, while total coliform count (TCC) was determined by the presumptive MPN method (APHA, 2000). Nutrient agar and EMB agar plates were incubated aerobically at 37 °C for 24 - 48 hours before colony enumeration. MacConkey broth tubes were incubated at 37 °C for 48 hours (presumptive test) and at 44.5 °C for a further 48 hours (confirmatory test). Pure cultures of bacteria isolated from the samples were subjected to morphological and biochemical characterization, including Gram staining, catalase, urease, oxidase, coagulase, citrate, indole, Voges-Proskauer, methyl red, and carbohydrate fermentation tests. Identification was carried out with reference to Bergey's Manual of Determinative Bacteriology (Buchanan and Gibbons, 1994).

3. Results

The quantitative bacteriological data are summarized in Table 1. The highest bacterial counts were recorded at the abattoir effluent discharge point, with mean total aerobic viable count (TAVC), total coliform count (TCC), and *Escherichia coli* count (ECC) of 7.45×10^3 cfu/mL, 72.5 MPN/mL, and 9.25×10^1 cfu/mL, respectively. Downstream of the discharge point, all three counts increased substantially: mean TAVC reached 4.67×10^4 cfu/mL, mean TCC was 18.3 MPN/mL, and mean ECC was 1.44×10^1 cfu/mL. In contrast, upstream values were lower (TAVC: 2.12×10^3 cfu/mL; TCC: 19.5 MPN/mL; ECC: 3.75 cfu/mL); however, *E. coli* was still detectable at this point in three of four sampling rounds. The abattoir well water also showed contamination, with mean TAVC of 7.2×10^1 cfu/mL, mean TCC of 23 MPN/mL, and mean ECC of 5.38 cfu/mL. All downstream and effluent TCC and ECC values substantially exceeded the WHO guideline that *E. coli* and thermotolerant coliforms should not be detectable in any 100 mL sample of drinking water (WHO, 2011).

The morphological and biochemical characteristics of bacterial isolates are presented in Tables 2 and 3. A total of 13 isolates were recovered from the four sampling locations. Organisms identified included *Escherichia coli*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Bacillus cereus*, *Bacillus subtilis*, *Serratia marcescens*, *Pseudomonas aeruginosa*, and *Chromobacterium violaceum*. *E. coli* was recovered from the abattoir effluent, the abattoir well water, and the downstream site. *S. aureus* was isolated exclusively from the abattoir effluent, while *S. marcescens* was recovered from the downstream site only. *P. aeruginosa* and *C. violaceum* were isolated from the upstream site, indicating background contamination at that sampling point.

Direct observations during sampling revealed that all blood from slaughtered animals was conveyed through a drainage channel into a sludge pond located approximately 5 m from the slaughter slab perimeter. A well dug within the slaughter slab area supplied water used to wash blood and paunch contents from the slaughter floor. Rendering of animal skins and internal organs was conducted outside the slaughter slab perimeter; organs were washed directly into the stream prior to boiling. Animal hair was removed by open burning, with soot entering the adjacent stream. Offensive odour was present throughout the site during all sampling visits, and mosquito breeding was observed in standing effluent near the abattoir.

Table 1 Bacteriological profile of Okokpon Stream and in-situ abattoir samples

Location of composite samples	Quantitative bacteriological parameter	Sample of abattoir and Okokpon Stream (bacteria count)				
		First visit	Second visit	Third visit	Fourth visit	Mean bacteria count
Abattoir effluent	TAVC (cfu/mL)	6.75×10^3	7.35×10^3	8.55×10^3	7.15×10^3	7.45×10^3
	TCC (MPN/mL)	46	110	110	24	72.5
	ECC (cfu/mL)	3×10^1	1.10×10^2	1.50×10^2	8×10^1	9.25×10^1
Abattoir well water	TAVC (cfu/mL)	9.05×10^1	6.6×10^1	7.65×10^1	5.5×10^1	7.2×10^1
	TCC (MPN/mL)	28	21	28	15	23
	ECC (cfu/mL)	4	2.5	9	6	5.38
Okokpon Stream (downstream)	TAVC (cfu/mL)	9.10×10^3	4×10^4	7.55×10^4	6.2×10^4	4.67×10^4
	TCC (MPN/mL)	9.2	15.0	28.0	21.0	18.3
	ECC (cfu/mL)	1.6×10^1	1.25×10^1	1.6×10^1	1.3×10^1	1.44×10^1
Okokpon Stream (upstream)	TAVC (cfu/mL)	3.95×10^3	1.65×10^2	9.15×10^2	3.45×10^3	2.12×10^3
	TCC (MPN/mL)	2.8	1.5	2.0	1.5	1.95
	ECC (cfu/mL)	0	2	6.5	6.5	3.75

Key: TAVC = total aerobic viable count; TCC = total coliform count; ECC = *Escherichia coli* count; cfu/mL = colony-forming units per millilitre; MPN = most probable number.

Table 2 Identification of isolates using morphological methods

Location of isolates examined	Isolates	Colonial characteristics	Gram staining
Abattoir effluents	1	Purple pigmented mucoid colony	Gram-negative rods
	2	Dry colony with serrated margin	Gram-positive rods
	3	Yellow pigmented mucoid colony	Gram-positive cocci in clusters
	4	Mucoid colony with entire margin	Gram-negative rods
Abattoir well water	1	Large dry mucoid colony with serrated margin	Gram-positive rods
	2	Mucoid colony with entire margin	Gram-negative rods
Okokpon Stream (downstream)	1	Red pigmented colony	Gram-negative rods
	2	Purple pigmented colony	Gram-negative rods
	3	Mucoid colony with entire margin	Gram-negative rods
	4	Dry colony with entire margin	Gram-positive rods
	5	Pin-point mucoid colony	Gram-positive cocci in pairs
Okokpon Stream (upstream)	1	Purple pigmented mucoid colony	Gram-negative rods
	2	Mucoid colony with entire margin	Gram-negative rods
	3	Dry colony with serrated margin	Gram-positive rods

Table 3 Identification of bacterial isolates using biochemical methods

Location of isolates examined	Isolates	Biochemical tests										Probable bacteria
		Ox	Co	Ca	Ur	Ci	In	Mr	Vp	La	Ma	
Abattoir effluent	1	+	Np	+	-	+	-	-	+	-	-	<i>Chromobacterium violaceum</i>
	2	-	Np	+	-	+	Np	Np	Np	-	-	<i>Bacillus cereus</i>
	3	+	+	+	-	-	Np	Np	Np	-	+	<i>Staphylococcus aureus</i>
	4	-	Np	+	-	-	+	+	-	+	+	<i>Escherichia coli</i>
Abattoir well water	1	-	Np	+	-	+	Np	Np	Np	-	-	<i>Bacillus cereus</i>
	2	-	Np	+	-	-	+	+	-	+	+	<i>Escherichia coli</i>
Okokpon Stream (downstream)	1	-	Np	+	-	+	-	-	+	-	+	<i>Serratia marcescens</i>
	2	+	Np	+	-	+	-	-	+	-	-	<i>Chromobacterium violaceum</i>
	3	-	Np	+	-	-	+	+	-	+	+	<i>Escherichia coli</i>
	4	Np	+	+	-	+	Np	Np	Np	+	+	<i>Bacillus subtilis</i>
	5	+	-	+	-	-	Np	Np	Np	-	-	<i>Staphylococcus epidermidis</i>
Okokpon Stream (upstream)	1	+	Np	+	-	+	-	-	+	-	-	<i>Chromobacterium violaceum</i>
	2	+	Np	+	-	+	-	+	-	-	-	<i>Pseudomonas aeruginosa</i>
	3	-	Np	+	-	+	Np	Np	Np	-	-	<i>Bacillus cereus</i>

Key. +ve = positive reaction; -ve = negative reaction; Np = not performed; Ox = oxidase; Co = coagulase; Ca = catalase; Ur = urease; Ci = citrate; In = indole; Mr = methyl red; Vp = Voges-Proskauer; La = lactose; Ma = mannitol.

4. Discussion

As shown in Table 1, the bacteriological counts were highest in the abattoir effluent and downstream sampling point, whereas upstream water showed lower counts. The mean downstream TAVC (4.67×10^4 cfu/mL) was markedly higher than the upstream value (2.12×10^3 cfu/mL). In the same way, mean TCC increased from 1.95 MPN/mL upstream to 18.3 MPN/mL downstream, while mean ECC increased from 3.75 cfu/mL upstream to 1.44×10^1 cfu/mL downstream. The abattoir effluent itself contained mean TAVC, TCC, and ECC values of 7.45×10^3 cfu/mL, 72.5 MPN/mL, and 9.25×10^1 cfu/mL, respectively, while the abattoir well water also showed contamination with mean TCC and ECC values of 23 MPN/mL and 5.38 cfu/mL. This pattern supports the view that the abattoir is an important source of microbial contamination to the receiving stream. Similar observations have been reported for abattoir-impacted water bodies in Nigeria, where downstream receiving waters showed bacterial loads comparable to raw effluent (Nafarnda et al., 2012; Akpan et al., 2020; Akpoka et al., 2023). All downstream TCC and ECC values exceeded the WHO guideline threshold for drinking water, which requires that *E. coli* and thermotolerant coliforms be undetectable in any 100 mL sample (WHO, 2011). Notably, a mean ECC of 3.75 cfu/mL was also recorded at the upstream site, with *E. coli* detected in three of the four sampling rounds. This upstream contamination suggests that faecal inputs from diffuse land-use activities or other pollution sources exist upstream of the abattoir, and it limits the extent to which the upstream site can serve as a truly uncontaminated baseline.

As described in the Results, substantial volumes of blood, wash water, paunch contents, and rendering residues entered the stream during operations, consistent with the high organic loads documented in similar abattoir-adjacent water bodies (Nafarnda et al., 2012; Adelegan, 2002). The discharge pathway, combining direct drainage to the sludge pond, overflow into the stream, and surface runoff from open rendering, provides multiple routes for bacteriological contamination of both the stream and the on-site well.

Published estimates indicate that only about 35% of a slaughtered cow's live weight constitutes edible meat, while approximately 65% consists of blood, bones, fat, hides, paunch contents, and other non-carcass materials (Omole and Longe, 2008). Previous studies further report that slaughter activities generate substantial quantities of blood, manure, paunch contents, and wastewater capable of contributing significant organic and suspended-solid loads to receiving water bodies when improperly managed. For an average 550 kg cow, approximately 13.6 kg (≈ 13 –14 L) of blood may be generated during slaughter (Gannon et al., 2004, as cited in Omole and Longe, 2008). Applying this estimate to the approximately 10 cattle slaughtered daily at the Okokpon abattoir suggests that slaughter operations could generate roughly 130–136 L of blood per day, alongside substantial volumes of wastewater and organic solid waste.

A large proportion of these wastes eventually reaches the nearby water body after only brief delay in the sludge pond. Since the bones are sold, the fat, grease, and some of the paunch contents contribute substantially to the suspended solids that pollute both the stream and the adjoining soil. The organisms identified from the effluent, well water, and stream samples (Tables 2 and 3) included *Escherichia coli*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Bacillus cereus*, *Bacillus subtilis*, *Serratia marcescens*, *Pseudomonas aeruginosa*, and *Chromobacterium violaceum*. The occurrence of *E. coli* in particular is epidemiologically important because it is an established indicator of recent faecal contamination in water intended for domestic use (Odonkor and Ampofo, 2013; WHO, 2011); its predominance in abattoir effluents in this region has been independently corroborated, with *E. coli* recording the highest frequency of occurrence in effluents from two Benin City abattoirs (Akpoka et al., 2023). The presence of *C. violaceum*, a Gram-negative rod native to tropical soils and freshwater environments, is consistent with the geographic setting of this study and further indicates the integration of environmental bacteria with faecal contaminants in the receiving stream. More recent studies have also shown that slaughterhouse wastewater may act as a reservoir of antimicrobial-resistant *E. coli* and other Gram-negative bacteria, reinforcing the public health significance of direct discharge into streams and shallow water sources (Akpan et al., 2020; Chowdhury et al., 2025).

The presence of these bacteria in high counts constitutes a serious public health hazard because contamination of domestic water with enteric organisms increases the risk of waterborne disease transmission. This concern is reinforced by broader global evidence linking unsafe water, sanitation, and hygiene to a substantial preventable disease burden (WHO, 2023; Wolf et al., 2023). The offensive odour and mosquito breeding documented at the abattoir site further corroborate poor sanitary conditions in the study area. Overall, the findings indicate that untreated abattoir discharge is compromising the microbiological quality of Okokpon Stream and exposing nearby residents to avoidable health risks.

Several limitations of the present study should be acknowledged. The four-week sampling window may not capture seasonal variation in contamination levels, as rainfall patterns and stream flow fluctuate across the year in this region. Physicochemical parameters (pH, dissolved oxygen, turbidity, and temperature) were not measured, which limits

mechanistic interpretation of the bacterial distribution data. Finally, antibiotic resistance profiling of the isolates was not performed; given accumulating evidence that abattoir effluents harbour antimicrobial-resistant organisms (Akpan et al., 2020; Chowdhury et al., 2025), future studies at this site should incorporate resistance characterisation.

5. Conclusion

This study demonstrated that untreated abattoir effluent discharge is the primary driver of faecal bacteriological contamination in Okokpon Stream, with downstream counts for total coliforms, *E. coli*, and total aerobic viable bacteria all substantially exceeding WHO drinking-water guidelines; the abattoir well water was similarly impacted, extending risk to workers on site. The organisms identified, including *Escherichia coli*, *Staphylococcus aureus*, *Serratia marcescens*, *Pseudomonas aeruginosa*, and *Chromobacterium violaceum*, are of recognized public health significance, and their presence in water accessed by the surrounding community represents a preventable exposure risk. It is therefore recommended that primary treatment infrastructure be installed before effluent reaches the stream, the contaminated on-site well be replaced with a protected water source, and the local government environmental health department enforce routine microbial monitoring of Okokpon Stream in line with national environmental standards.

Compliance with ethical standards

Disclosure of conflict of interest

No conflict of interest to be disclosed.

References

- [1] Adelegan, A. J. (2002). Environmental policy and slaughterhouse waste in Nigeria. In Proceedings of the 28th WEDC Conference, Kolkata, India.
- [2] Akpan, S. N., Odeniyi, O. A., Adebawale, O. O., Alarape, S. A., and Adeyemo, O. K. (2020). Antibiotic resistance profile of Gram-negative bacteria isolated from Lafenwa abattoir effluent and its receiving water (Ogun River) in Abeokuta, Ogun State, Nigeria. *Onderstepoort Journal of Veterinary Research*, 87(1), e1-e8. <https://doi.org/10.4102/ojvr.v87i1.1854>
- [3] Akpoka, O. A., Solanke, E. O., Akinyeye, A. J., and Mekomah, H. U. (2023). Bacteria diversity of two abattoir effluents in Ikpoba Hill and Oluku, Benin City, Nigeria and their potential public health implications. *Microbes and Infectious Diseases*, 4(3), 954–959. <https://doi.org/10.21608/MID.2022.114174.1226>
- [4] American Public Health Association. (2000). Standard methods for the examination of water and wastewater (20th ed.). American Public Health Association.
- [5] Anyata, B. U., and Nwaiwu, C. M. O. (2000). Setting of effluent standards for water pollution control in Nigeria. *Journal of Civil and Environmental Systems Engineering*, 1(1), 47-66.
- [6] Adelegan, J. A. (2002). Environmental policy and slaughterhouse waste in Nigeria. In Proceedings of the 28th WEDC Conference, Kolkata, India.
- [7] Buchanan, R. E., and Gibbons, N. E. (Eds.). (1994). *Bergey's manual of determinative bacteriology* (9th ed.). Williams and Wilkins.
- [8] Chaves, P. C., Castillo, L. R., Dendooven, L., and Escamilla-Silva, E. M. (2005). Poultry slaughter wastewater treatment with an up-flow system. *Bioresource Technology*, 96, 1730-1736.
- [9] Chowdhury, N. S., Tasnia, R., Nahar, N., Hossain, Z. Z., Ferdous, J., Akhter, H., and Begum, A. (2025). Slaughterhouse wastewater as a reservoir of thermotolerant *Escherichia coli* with antimicrobial resistance and virulence potential in Dhaka, Bangladesh. *International Journal of Microbiology*, 2875935. <https://doi.org/10.1155/ijm/2875935>
- [10] Gannon, B., McGee, M., and O'Kiely, P. (2004). Beef production from two- and three-year-old bulls slaughtered at two live weights. Grange Research Centre, Teagasc.
- [11] Hamid, A., Bhat, S. U., and Jehangir, A. (2020). Local determinants influencing stream water quality. *Applied Water Science*, 10, Article 24.

- [12] Kosek, M., Bern, C., and Guerrant, R. L. (2003). The global burden of diarrhoea disease, as estimated from studies published between 1992 and 2000. *Bulletin of the World Health Organization*, 81(3), 197-204.
- [13] McMinn, B. R., Korajkic, A., Kelleher, J., Diedrich, A., Pemberton, A., Willis, J. R., Sivaganesan, M., Shireman, B., Doyle, A., and Shanks, O. C. (2024). Quantitative faecal pollution assessment with bacterial, viral, and molecular methods in small stream tributaries. *Science of the Total Environment*, 951, 175740. <https://doi.org/10.1016/j.scitotenv.2024.175740>
- [14] Nafarnda, W. D., Ajayi, I. E., Shawulu, J. C., Kawe, M. S., Omeiza, G. K., Sani, N. A., Tenuche, O. Z., Dantong, D. D., and Tags, S. Z. (2012). Bacteriological quality of abattoir effluents discharged into water bodies in Abuja, Nigeria. *ISRN Veterinary Science*, 2012, 515689.
- [15] Odonkor, S. T., and Ampofo, J. K. (2013). *Escherichia coli* as an indicator of bacteriological quality of water: An overview. *Microbiology Research*, 4(1), e2.
- [16] Omole, D. O., and Longe, E. O. (2008). An assessment of the impact of abattoir effluents on River Illo, Ota, Nigeria. *Journal of Environmental Science and Technology*, 1(2), 56–64.
- [17] Wolf, J., Johnston, R. B., Ambelu, A., Arnold, B. F., Bain, R., Brauer, M., Brown, J., Caruso, B. A., Clasen, T., Colford, J. M., Esteves Mills, J., Evans, B., Freeman, M. C., Gordon, B., Kang, G., Lanata, C. F., Medlicott, K. O., Prüss-Ustün, A., Troeger, C., Boisson, S., and Cumming, O. (2023). Burden of disease attributable to unsafe drinking water, sanitation, and hygiene in domestic settings: A global analysis for selected adverse health outcomes. *The Lancet*, 401(10393), 2060-2071. [https://doi.org/10.1016/S0140-6736\(23\)00458-0](https://doi.org/10.1016/S0140-6736(23)00458-0)
- [18] World Health Organization. (2011). *Guidelines for drinking-water quality* (4th ed.). World Health Organization.
- [19] World Health Organization. (2023, September 13). *Drinking-water*. <https://www.who.int/news-room/fact-sheets/detail/drinking-water>
- [20] Wright, J., Gundry, S., and Conroy, R. (2004). Household drinking water in developing countries: A systematic review of microbiological contamination between source and point-of-use. *Tropical Medicine and International Health*, 9(1), 106-117.