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Original Research Article

MICROBIAL CONTAMINATION AND ANTIMICROBIAL RESISTANCE PATTERNS IN ABATTOIR WATER SOURCES AND EFFLUENTS FROM JOS NORTH AND SOUTH LOCAL GOVERNMENT AREAS, PLATEAU STATE, NIGERIA

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ABSTRACT

Abattoir operations generate substantial microbial contamination that poses significant public health risks through water pollution and the dissemination of antimicrobial-resistant (AMR) bacteria. This study investigated microbial contamination levels and antimicrobial resistance patterns in water sources and effluents from the Jos Main Abattoir and four slaughter slabs located in Jos North and South Local Government Areas (LGAs). A total of 24 water and effluent samples were collected from the abattoir, slaughter slabs, and associated water sources. Total bacterial count, coliform enumeration, bacterial identification, and antimicrobial susceptibility testing against eight antibiotics were conducted using standard microbiological methods. All samples showed high levels of bacterial contamination, ranging from 8.0×10^3 to 2.34×10^5 CFU/ml. Coliform bacteria were detected in 58.3% of samples, with the highest count (1.9×10^4 CFU/ml) observed in abattoir effluents. Eight bacterial species were identified, with *Escherichia coli* (37.5%), Bacillus spp. (62.5%), and Pseudomonas aeruginosa (29.2%) being predominant. High levels of antimicrobial resistance were recorded, particularly to ampicillin (93.8%), sulfamethoxazole-trimethoprim (68.8%), and tetracycline (68.8%). Multidrug resistance was detected in 75% of isolates. These findings indicate that abattoir activities in Jos significantly contribute to environmental microbial contamination and the spread of AMR. The implementation of effective wastewater treatment systems and antimicrobial stewardship programs is urgently required to mitigate associated public health risks.

Keywords: Abattoir, Antimicrobial Resistance, Coliform bacteria, Public Health, Water contamination

INTRODUCTION

Abattoir operations are essential components of the meat supply chain but also generate substantial environmental contamination due to improper waste management and inadequate water treatment systems (Bello *et al*., 2019). The discharge of untreated or poorly treated abattoir effluents into water bodies poses significant public health risks, particularly in developing countries where regulatory oversight is often limited (Adelegan, 2002; Omole & Longe, 2008).

Nigeria's livestock industry is predominantly concentrated in the Middle Belt region of the country, within which Plateau State is located. Millions of animals are processed annually for meat in the numerous abattoirs and slaughter facilities across this region. The Plateau State capital, Jos, hosts the main abattoir and several slaughter slabs that serve both local and regional markets. However, many of these facilities lack adequate waste treatment infrastructure, resulting in the direct discharge of contaminated effluents into surface and groundwater systems (Bello & Oyedemi, 2009).

Microbial contamination of abattoir effluents typically includes pathogenic and indicator bacteria such as *Escherichia coli, Salmonella spp., Staphylococcus aureu*

and various environmental bacteria (Woolhouse *et al*., 2015). Of greater concern is the increasing prevalence of antimicrobial resistance (AMR) among these bacterial populations, driven by the widespread use of antibiotics in livestock production and the selective pressure exerted by antimicrobial residues present in abattoir waste (Marshall & Levy, 2011).

The World Health Organization (WHO) has identified antimicrobial resistance (AMR) as one of the top ten global public health threats, with environmental contamination playing a crucial role in the dissemination of resistant bacteria and resistance genes (WHO, 2019). Abattoirs represent potential hotspots for AMR development and transmission due to the convergence of antimicrobial residues, organic matter, and diverse bacterial populations (Capita & Alonso-Calleja, 2013).

Limited research has been conducted on microbial contamination and antimicrobial resistance (AMR) patterns in Nigerian abattoir systems, particularly within the Jos metropolis. This study aimed to assess the microbial quality of water sources and effluents from the Jos Main Abattoir and four major slaughter slabs located in Jos North and South Local Government Areas, and to characterize the antimicrobial resistance profiles of the isolated bacteria.

MATERIALS AND METHODS

STUDY AREA AND SAMPLE COLLECTION

This cross-sectional study was conducted in Jos North and South Local Government Areas of Plateau State, Nigeria. The Jos Main Abattoir, four major slaughter slabs, and their associated water sources were selected based on the operational scale of the slaughter facilities and their geographic distribution. A total of 24 samples were collected between June and July 2025, comprising nine abattoir effluent samples, five processing water samples, five borehole samples, four well samples, and one river water sample.

Sample collection was carried out using sterile 500 ml bottles following standard procedures (APHA, 2017). The samples were transported in ice-cooled containers to the National Veterinary Research Institute, Vom, and analyzed within six hours of collection

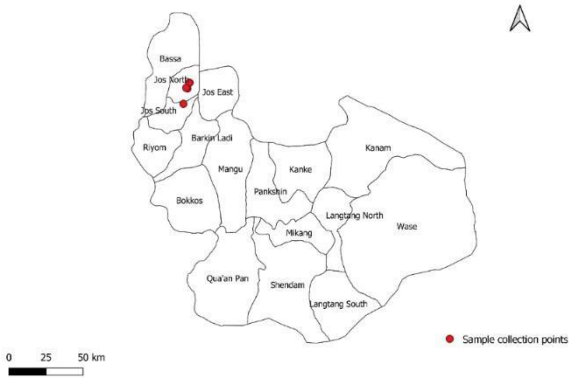

Figure. I: Map of Plateau State showing sample collection points

MICROBIOLOGICAL ANALYSIS

TOTAL BACTERIAL COUNT AND COLIFORM ENUMERATION

Serial dilutions (10^{-1} to 10^{-6}) were prepared using sterile normal saline. The total bacteria count was determined using Nutrient Agar plates which were incubated at 37°C for 24 hours. Coliform bacteria were enumerated using MacConkey Agar with incubation at 37°C for 24 hours. Results were expressed as colony forming units per milliliter (CFU/ml).

BACTERIAL IDENTIFICATION

Bacterial isolates were identified using conventional biochemical test, including Gram staining, catalase, coagulase, citrate utilization, gelatin hydrolysis, hemolysis, Triple Sugar Iron Agar (TSIA), indole production, motility, oxidase, urease, and carbohydrate fermentation tests (Cheesbrough, 2006).

ANTIMICROBIAL SUSCEPTIBILITY TESTING

Antimicrobial susceptibility testing was performed using the Kirby–Bauer disk diffusion method on Mueller–Hinton agar, following the guidelines of the Clinical and Laboratory Standards Institute (CLSI). Eight antibiotics were tested: sulfamethoxazole–trimethoprim (SXT, 25 µg), ciprofloxacin (CIP, 5 µg), cefepime (FEP, 30 µg), meropenem (MEM, 10 µg), ampicillin (AMP, 10 µg), chloramphenicol (C, 30 µg), streptomycin (S, 10 µg), and tetracycline (TET, 30 µg).

Zone diameters were measured and interpreted as susceptible (S), intermediate (I), or resistant (R) according to CLSI breakpoints. Multidrug resistance (MDR) was defined as resistance to three or more classes of antibiotics.

DATA ANALYSIS

Data were analyzed using descriptive statistics. Bacterial counts were $\log_{10}$-transformed prior to analysis. Resistance percentages were calculated for each antibiotic, and resistance patterns were evaluated across bacterial species and sample types.

RESULTS

BACTERIAL CONTAMINATION LEVELS

All 24 samples showed significant bacterial contamination, with total bacterial counts ranging from 8.0×10^3 to 2.34×10^5 CFU/ml (mean: 1.12×10^5 CFU/ml). The highest contamination levels were observed in abattoir effluents and processing water, while borehole and well water samples exhibited comparatively lower but still concerning bacterial loads.

Coliform bacteria were detected in 14 samples (58.3%), with counts ranging from 1.0×10^3 to 1.9×10^4 CFU/ml. The highest coliform contamination from the slaughter facilities sampled

were in BKK CE (1.9×10^4 CFU/ml) and Yanshanu Effluent (1.4×10^4 CFU/ml), indicating significant fecal contamination.

Figure IIa: Effluent Samples collected at the Jos Main Abattoir

Figure IIb: Effluent Samples collected at the Jos Main Abattoir

Figure III: Washing water collected at the Kara Market,

Figure IV: Borehole water sample collected at the Bukuru, Goat Section Jos Main Abattoir

Figure V: Borehole water collected at the cattle Slaughter floor of the Jos Main Abattoir

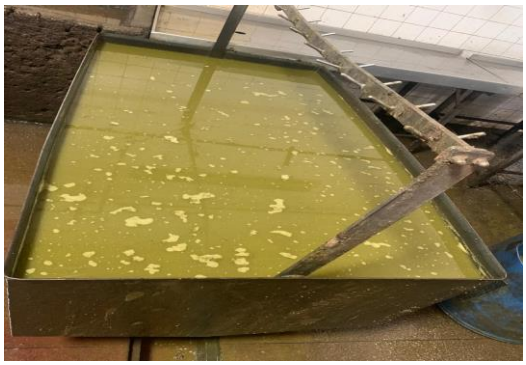

Figure VI: Water for washing viscera at the Jos Main Abattoir

Figure VII: Well used as a source of water for Kara Goat section, Bukuru

BACTERIAL SPECIES IDENTIFICATION

Eight bacterial species were identified from the 24 samples tested:

- Gram-positive bacteria: Bacillus subtilis (n = 7, 29.2%), Bacillus licheniformis (n = 6, 25.0%), Bacillus pumilus (n = 2, 8.3%), *Staphylococcus aureus* (n = 4, 16.7%), and coagulase-negative *Staphylococcus* spp. (n = 7, 29.2%).
- Gram-negative bacteria: *Escherichia coli* (n = 9, 37.5%), Klebsiella aerogenes (n = 6, 25.0%), and Pseudomonas aeruginosa (n = 7, 29.2%).

Escherichia coli was the most frequently isolated species, detected in 9 samples (37.5%), and followed by various Bacillus species collectively found in 15 samples (62.5%). The presence of E. coli in multiple samples indicates significant fecal

contamination of the water sources.

Table I: Bacterial Contamination Levels of the samples

S/N	Sample ID	Total Bacteria Count (CFU/ml)	Total Coliform Count (CFU/ml)	Bacterial Isolates
1	JMA CE 1	3.4×10^4	2.0×10^3	*Escherichia coli, Bacillus subtilis*
2	JMA CE 2	1.51×10^5	0	*CoNS, Bacillus licheniformis*
3	JMA CE 3	1.71×10^5	1.0×10^3	*Escherichia coli, Bacillus subtilis*
4	JMA GE	2.4×10^4	1.0×10^3	*Escherichia coli, CoNS*
5	JMA PE	5.7×10^4	0	*Bacillus subtilis*
6	JMA CT	1.8×10^4	1.0×10^3	*Escherichia coli, Bacillus licheniformis*
7	JMA GR	1.78×10^5	1.6×10^4	*Bacillus licheniformis, Klebsiella aerogenes*
8	JMA WW	2.09×10^5	0	*Bacillus pumilus*
9	JMA PT	1.1×10^4	3.0×10^3	*Escherichia coli, Bacillus subtilis, CoNS*
10	JMA BH 1	1.69×10^5	0	*Bacillus subtilis*
11	JMA BH 2	9.1×10^4	0	*Bacillus licheniformis*
12	JMA BH 3	1.94×10^5	0	*CoNS*
13	KWG 1	1.81×10^5	2.0×10^3	*Klebsiella aerogenes, Staphylococcus aureus, Pseudomonas aeruginosa*
14	KWG 2	9.3×10^4	1.0×10^3	*Escherichia coli, CoNS, Bacillus subtilis, Pseudomonas aeruginosa*
15	BKK CW	1.89×10^5	1.2×10^4	*Escherichia coli, Staphylococcus aureus*
16	BKK CE	1.97×10^5	1.9×10^4	*Klebsiella aerogenes, Bacillus licheniformis*
17	KEG 1	1.55×10^5	5.0×10^3	*Escherichia coli, Klebsiella aerogenes, CoNS, Pseudomonas aeruginosa*
18	YGW	8.0×10^3	0	*Pseudomonas aeruginosa*
19	YSB	5.9×10^4	1.0×10^3	*Bacillus pumilus*
20	KWWG 1	2.34×10^5	0	*Bacillus subtilis, Staphylococcus aureus*
21	YGR	8.1×10^4	3.0×10^3	*Bacillus licheniformis, CoNS, Klebsiella aerogenes, Pseudomonas aeruginosa*
22	YSE	9.6×10^4	1.4×10^4	*Klebsiella aerogenes, Staphylococcus aureus, Bacillus subtilis, Pseudomonas aeruginosa*
23	YGE	1.74×10^5	1.0×10^4	*Bacillus licheniformis, Escherichia coli, CoNS, Pseudomonas aeruginosa*
24	YGB	6.3×10^4	1.0×10^3	*Escherichia coli, Bacillus subtilis, CoNS, Staphylococcus aureus*

Key: CoNS: Coagulase Negative *Staphylococcus* species; JMA CE 1 – Jos Main Abattoir Cattle Effluent 1 ; JMA CE 2 – Jos Main Abattoir Cattle Effluent 2 ; JMA CE 3 – Jos Main Abattoir Cattle Effluent 3 ; JMA GE – Jos Main Abattoir Goat Effluent ; JMA PE – Jos Main Abattoir Pig Effluent ; JMA CT - Jos Main Abattoir Cattle Tank; JMA GR - Jos Main Abattoir Goat Reservoir; JMA WW - Jos Main Abattoir Well Water; JMA PT - Jos Main Abattoir Pig Tank; JMA BH 1 - Jos Main Abattoir Bore Hole 1; JMA BH 2 - Jos Main; abattoir Bore Hole 2; JMA BH 3 - Jos Main Abattoir Bore Hole 3; KWG 1 – Kara Well Goat 1; KWG 2 – Kara Well Goat 2; KEG 1 – Kara Effluent Goat 1; KWWG – Kara Washing Water Goat; BKK CW – Bukuru Cattle Washing water; BKK CE – Bukuru Cattle Effluent; YGW – Yanganda well; YGR – Yanganda River; YGE – Yanganda Effluent; YGB – Yanganda Borehole; YSB – Yanshanu Borehole; YSE – Yanshanu Effluent

Table II: Bacterial Species Identification

Biochemical Tests	*Bacillus lichenifor mis*	*Bacillus subtilis*	*Bacillus pumilus*	CoNS	*Staphyloco ccus aureus*	*Klebsiella aerogenes*	*Escherichia coli*	*Pseudomon as aeruginosa*
Gram stain	GPR	GPR	GPR	GPC	GPC	GNR	GNR	GNR
Catalase	+	+	+	+	+	+	+	+
Coagulase	NA	NA	NA	-	+			-
Citrate	+		+		+	+	-	+
Gelatin hydrolysis	+	-	-			-	-	+
Hemolysis	-	-	Weak			-	-	+
TSIA	NR	AAG	NR			AAG	AAG	ALK/ALK
H_2S	-	-				-	-	-
Indole	-	+	-		-	-	+	-
Motility	+	+			-	-	+	+
Oxidase	-	-	+		-	-	-	+
Urease	-	-	-		+	+	-	-
Arabinose	+	+	+			+	+	-
Dulcitol	-	-	-	-		+	-	
Glucose	+	+	+		+	+	+	-
Inositol	+	+	-			+	+	-
Lactose	+	+			+	+	+	-
Maltose	+	-	+			+	-	-
Mannitol	+	+	+			+	+	+
Mannose	+	-	+			+	-	-
Galactose	+	+	+			+		
Salicin	+	-	+			+	-	
Sorbitol	+	+	-			+	+	-
Sucrose	+	-	+		+	+	-	-
Trehalose	+	+	+			+	+	-
Xylose	+	+	+			+	+	-

KEY: TSIA= Tripple Sugar Ion Agar; CoNS= Coagulase Negative Staphylococcus species; D=Delayed, H_2S=Hydrogen sulphide production; AAG= Acid Acid Gas, ALK= Alkaline, NA=Not Applicable; NR=No Reaction, GPR Gram Positive Rod, GNR Gram Negative Rod, GPC Gram Positive Cocci

ANTIMICROBIAL RESISTANCE PATTERNS

Antimicrobial susceptibility testing was conducted on 16 representative isolates. High levels of resistance were observed across all tested antibiotics, as shown in the table IV

SPECIES-SPECIFIC RESISTANCE PATTERNS

Pseudomonas aeruginosa (n=6) exhibited the highest resistance rates, showing 100% resistance to ampicillin and tetracycline, and over 80% resistance to sulfamethoxazole-trimethoprim, cefepime, and ciprofloxacin.

Staphylococcus aureus isolates (n=3) demonstrated variable resistance patterns; one strain was completely susceptible to all antibiotics except sulfamethoxazole-trimethoprim, while the others exhibited multidrug resistance.

Escherichia coli isolates (n=2) exhibited contrasting patterns: one strain was completely susceptible to all tested antibiotics, whereas the other displayed high resistance to multiple antibiotic classes.

Bacillus species generally exhibited moderate resistance levels, showing higher susceptibility to newer antibiotics such as meropenem and cefepime.

MULTIDRUG RESISTANCE

Multidrug resistance (MDR) was detected in 12 of the 16 tested isolates (75%) across all locations and sample types, except in Yanshanu borehole, Bukuru cow water, and Bukuru cow effluent. The most common resistance patterns involved combinations of β-lactam antibiotics (ampicillin, cefepime), fluoroquinolones (ciprofloxacin), and older antibiotics such as tetracycline and sulfamethoxazole-trimethoprim.

Three isolates obtained from Yanshanu borehole, Yanshanu effluent, and Bukuru cattle water showed resistance to six or more antibiotics, indicating extensive drug resistance (XDR) that severely limits therapeutic options.

This study revealed significant microbial contamination and concerning levels of antimicrobial resistance in water sources and effluents associated with abattoirs in Jos North and South LGAs. The bacterial contamination levels observed exceed

WHO guidelines for drinking water quality and pose substantial risks to public health and environmental integrity. The presence of bacterial contamination across all sample types, with counts reaching 2.34×10^5 CFU/ml, indicates widespread sanitary failures in abattoir operations and associated water systems. These findings are consistent with previous reports from Nigerian abattoirs (Bello et al., 2019; Ogbonnaya, 2008) and underscore the persistent nature of this public health challenge.

Snelling, 2009), burn wound infections (Azzopardi *et al.*, 2011), and otitis externa (Roland & Stroman, 2002). Isolated from 16.7% of samples, *Staphylococcus aureus* is a versatile pathogen responsible for a wide range of infections,

Table III: Antibiogram of identified Bacterial species

S/N	Sample ID	Organism(s)	**ANTIBIOTICS (ug/dL)/Diameters of Zones of Inhibition(mm)**							
			SXT (25)	CIP (5)	FEP (30)	MEM (10)	AMP (10)	C (30)	S (10)	TET (30)
1	JMA CE 1	*Escherichia coli*	6 (R)	28 (S)	6 (R)	12 (R)	6 (R)	30 (S)	10 (R)	10 (R)
2	JMA CE 2	*Bacillus licheniformis*	24 (R)	22 (S)	24 (S)	16 (S)	6 (R)	14 (R)	12 (I)	6 (R)
3	JMA CE 3	*Bacillus subtilis*	6 (R)	20 (I)	14 (R)	15 (I)	8 (R)	14 (R)	16 (S)	9 (R)
4	KWWG 1	*Staphylococcus aureus*	6 (R)	28 (S)	30 (S)	26 (S)	30 (S)	28 (S)	24 (S)	20 (S)
5	JMA GR	*Klebsiella aerogenes*	6 (R)	22 (I)	16 (I)	10 (R)	20 (S)	15 (I)	14 (I)	9 (R)
6	JMA GE	*Escherichia coli*	24 (S)	30 (S)	26 (S)	28 (S)	20 (S)	28 (S)	24 (S)	30 (S)
7	JMA BH 2	*Bacillus licheniformis*	22 (S)	6 (R)	32 (S)	30 (S)	14 (R)	30 (S)	14 (I)	26 (S)
8	KEG 1	*Pseudomonas aeruginosa*	6 (R)	20 (I)	10 (R)	28 (S)	6 (R)	6 (R)	6 (R)	6 (R)
9	Yanganda River	*Klebsiella aerogenes*	20 (S)	17 (R)	10 (R)	23 (S)	6 (R)	28 (S)	20 (S)	22 (S)
10	Yanshanu Effluent	*Pseudomonas aeruginosa*	22 (S)	16 (R)	9 (R)	24 (S)	6 (R)	24 (S)	24 (S)	26 (S)
11	Yanganda Effluent	*Pseudomonas aeruginosa*	6 (R)	10 (R)	20 (S)	14 (R)	6 (R)	10 (R)	12 (R)	10 (R)
12	Yanganda Borehole	*Staphylococcus aureus*	6 (R)	20 (I)	6 (R)	14 (I)	6 (R)	9 (R)	6 (R)	10 (R)
13	KWG 2	*Pseudomonas aeruginosa*	6 (R)	10 (R)	20 (S)	15 (R)	15 (R)	6 (R)	14 (I)	6 (R)
14	BKK CW	*Staphylococcus aureus*	20 (S)	30 (S)	22 (S)	11 (R)	9 (R)	22 (S)	22 (S)	16 (I)
15	KWG 1	*Pseudomonas aeruginosa*	20 (S)	22 (I)	6 (R)	22 (S)	10 (R)	24(S)	6 (R)	6 (R)
16	Yanganda Well	*Pseudomonas aeruginosa*	6 (R)	10 (R)	12 (R)	8 (R)	6 (R)	20 (S)	10 (R)	8 (R)

Key: SXT= Sulphamethaxazole/Trimethoprim, Streptomycin, FEP= Cepepime, MEM= Meropenem, Ampicilin, C= Chloramphenicol, CIP= Ciprofloxacin, TET= Tetracycline

The detection of coliform bacteria in 58.3% of samples, including water sources intended for human consumption, is particularly concerning. Coliforms serve as indicators of fecal contamination and the possible presence of enteric pathogens (WHO, 2011). The highest coliform counts observed in abattoir effluents (up to 1.9×10^4 CFU/ml) highlight the significant contribution of abattoir operations to environmental contamination.

The bacterial species identified in this study represent important human pathogens associated with diverse clinical manifestations and disease outcomes. Understanding the pathogenic potential of these organisms is essential for accurately assessing the public health risks posed by contaminated water sources.

Escherichia coli was isolated from 37.5% of samples, confirming significant fecal contamination. Although most *E. coli* strains are harmless commensals, pathogenic variants can cause severe diseases, including gastroenteritis (Qadri et al., 2005), hemorrhagic colitis (Karmali et al., 2010), urinary tract infections (Foxman, 2010), and neonatal meningitis (Kim, 2003).

Detected in 29.2% of samples, Pseudomonas aeruginosa is a notorious opportunistic pathogen responsible for various infections, including respiratory infections (Gellatly & Hancock, 2013), healthcare-associated infections (Kerr & Snelling, 2009), burn wound infections (Azzopardi *et al*., 2011), and otitis externa (Roland & Stroman, 2002).

Isolated from 16.7% of samples, *Staphylococcus aureus* is a versatile pathogen responsible for a wide range of infections, including skin and soft tissue infections (Miller et al., 2005), foodborne illness (Le Loir et al., 2003), invasive infections (Tong et al., 2015), and toxic shock syndrome (McCormick et al., 2001).

Table IV: Antimicrobial Resistance Patterns

Antibiotic	Number of Resistant Isolates (n=16)	Resistance (%)
Ampicillin	15	93.8%
Sulfamethoxazole-trimethoprim	11	68.8%
Tetracycline	11	68.8%
Cefepime	9	56.3%
Streptomycin	9	56.3%
Ciprofloxacin	8	50.0%
Meropenem	7	43.8%
Chloramphenicol	6	37.5%

Present in 25% of samples, *Klebsiella aerogenes* is associated with several clinical conditions, including healthcare-associated infections (Davin-Regli & Pagès, 2015), neonatal infections (Dalben et al., 2008), and respiratory tract infections (Mezzatesta et al., 2012).

Bacillus species were found in 62.5% of samples and are known to cause various opportunistic infections, including *B. subtilis* infections (Oggioni et al., 1998), *B. licheniformis* infections (Salkinoja-Salonen et al., 1999), and *B. pumilus* infections (Tena et al., 2007).

Coagulase-negative Staphylococci (CoNS) was found in 29.2% of samples, these organisms are known to cause device-related infections (Von Eiff et al., 2002), neonatal sepsis (Dong & Speer, 2015), and urinary tract infections (Hooton et al., 1996).

The high levels of antimicrobial resistance observed in this study are alarming and mirror global trends in the emergence and spread of AMR. The 93.8% resistance rate to ampicillin is particularly concerning, given the drug's widespread use and its importance in treating a variety of bacterial infections in both humans and animals.

The elevated resistance to sulfamethoxazole-trimethoprim (68.8%) and tetracycline (68.8%) likely reflects the extensive use of these antibiotics in veterinary practice and their persistence in environmental matrices (Kümmerer, 2009). These findings align with previous studies in Nigeria that reported high antimicrobial resistance prevalence in environmental samples (Adelowo et al., 2014).

The detection of resistance to newer antibiotics such as cefepime (56.3%) and meropenem (43.8%) is particularly concerning, as these drugs serve as last-resort therapeutic options for treating severe infections. This finding suggests ongoing selective pressure and possible horizontal gene transfer that facilitates the dissemination of resistance genes (Davies & Davies, 2010).

The combination of high bacterial contamination and widespread antimicrobial resistance creates a significant public health threat through multiple exposure pathways:

1. **Direct consumption** of contaminated water from wells and boreholes
2. **Foodborne transmission** through consumption of meat products processed with contaminated water
3. **Environmental exposure** through contact with contaminated surface water
4. **Occupational exposure** for abattoir workers and nearby communities

The presence of multidrug-resistant (MDR) bacteria in water sources used for domestic purposes poses a serious risk of treatment failure for bacterial infections in exposed populations. This is especially concerning in resource-limited settings where access to newer and more expensive antibiotics is often restricted.

Abattoir effluents act as major point sources for the

dissemination of antimicrobial resistance (AMR) into the environment. The discharge of untreated effluents containing resistant bacteria and antibiotic residues promotes the development of environmental reservoirs of AMR (Pruden et al., 2006).

Rivers and groundwater systems contaminated with abattoir effluents can transport resistant bacteria over long distances, thereby exposing communities far from the original contamination source. Such environmental pollution also disrupts aquatic ecosystems and may contaminate fish and other aquatic organisms consumed by humans.

The findings of this study underscore the need for a **One Health approach** that recognizes the interconnectedness of human, animal, and environmental health. Effectively addressing antimicrobial resistance (AMR) in abattoir systems requires coordinated, multisectoral interventions involving public health authorities, veterinary services, environmental agencies, and policymakers.

STUDY LIMITATIONS

This study has several limitations that should be taken into account when interpreting the results. The cross-sectional design provides a snapshot of contamination levels but cannot assess temporal variations in bacterial loads and resistance patterns. The sample size, while representative of the main abattoir and slaughter slabs in the study area, may not capture the full diversity of smaller-scale operations.

The identification methods used, although standard and reliable, could be further enhanced through the application of molecular techniques for more precise species identification and characterization of resistant genes. Additionally, the study did not assess viral contamination or parasitic contamination, which may also pose public health risks.

CONCLUSIONS AND RECOMMENDATIONS

This study demonstrates significant microbial contamination and concerning levels of antimicrobial resistance in water sources and effluents associated with abattoir operations in Jos North and South LGAs. The universal presence of bacterial contamination, high coliform counts, and widespread multidrug resistance poses substantial risks to public health and environmental integrity.

Immediate Interventions Required

1. **Water treatment implementation:** Install appropriate water treatment systems at all abattoir facilities to reduce microbial loads before effluent discharge
2. **Regular monitoring:** Establish routine microbiological surveillance programs to monitor water quality and AMR trends
3. **Regulatory enforcement:** Strengthen enforcement of existing environmental regulations and establish specific standards for abattoir effluent discharge
4. **Alternative water sources:** Provide safe water sources for communities currently relying on contaminated wells and boreholes

Long-term Strategies

1. **Infrastructure development:** Invest in modern abattoir facilities with integrated waste treatment systems
2. **Antimicrobial stewardship:** Implement programs to ensure the responsible use of antibiotics in livestock production
3. **Capacity building:** Train abattoir operators, regulators, and public health officials on best practices for waste management and infection control
4. **Research expansion:** Conduct longitudinal studies to track AMR trends and evaluate intervention effectiveness
5. **Policy development:** Develop comprehensive national policies addressing antimicrobial use in agriculture and mitigating environmental contamination

The findings of this study highlight the urgent need for coordinated action across multiple sectors to address the growing threat of antimicrobial resistance and environmental contamination from abattoir operations. Without immediate intervention, the current situation will likely worsen, posing increasing risks to public health and environmental sustainability.

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REFERENCES

Adelowo, O. O., Fagade, O. E., & Agersø, Y. (2014). Antibiotic resistance and resistance genes in *Escherichia coli* from poultry farms, southwest Nigeria. Journal of Infection in Developing Countries, 8(9), 1103-1112.

APHA (American Public Health Association). (2017). Standard Methods for the Examination of Water and Wastewater (23rd ed.). American Public Health Association, Washington, DC.

Azzopardi, E. A., Azzopardi, E., Camilleri, L., Villapalos, J., Boyce, D. E., Dziewulski, P. & Dickson, W.

A. (2011). Gram negative wound infection in hospitalised adult burn patients—systematic review and metaanalysis. PLoS One, 6(3), e17969.

Bello, M., Lawan, M. K., Aluwong, T., & Sanusi, M. (2019). Management of slaughterhouse waste in Nigeria: A review. Sokoto Journal of Veterinary Sciences, 17(2), 1-12.

Bello, Y. O., & Oyedemi, D. T. A. (2009). The impact of abattoir activities and management in residential neighbourhoods: A case study of Ogbomoso, Nigeria. Journal of Social Sciences, 19(2), 121-127.

Capita, R., & Alonso-Calleja, C. (2013). Antibiotic-resistant bacteria: A challenge for the food industry. Critical Reviews in Food Science and Nutrition, 53(1), 11- 48.

Cheesbrough, M. (2006). District Laboratory Practice in Tropical Countries, Part 2. Cambridge University Press, Cambridge.

Davies, J., & Davies, D. (2010). Origins and evolution of antibiotic resistance. Microbiology and Molecular Biology Reviews, 74(3), 417-433.

Davin-Regli, A. & Pagès, J. M. (2015). Enterobacter aerogenes and Enterobacter cloacae; versatile bacterial pathogens confronting antibiotic treatment. Frontiers in Microbiology, 6, 392.

Dalben, M., Varkulja, G., Basso, M., Krebs, V. L. J., Gibelli, M. A., Van Der Heijden, I. & Rossi, F. (2008). Investigation of an outbreak of Enterobacter cloacae in a neonatal intensive care unit. Brazilian Journal of Infectious Diseases, 12(4), 308-312.

Dong, Y. & Speer, C. P. (2015). Late-onset neonatal sepsis: recent developments. Archives of Disease in Childhood-Fetal and Neonatal Edition, 100(3), F257-F263.

Foxman, B. (2010). The epidemiology of urinary tract infection. Nature Reviews Urology, 7(12), 653-660.

Gellatly, S. L. & Hancock, R. E. (2013). Pseudomonas aeruginosa: new insights into pathogenesis and host defenses. Pathogens and Disease, 67(3), 159-173.

Graczyk, T. K., Knight, R., Gilman, R. H. & Cranfield, M. R. (2001). The role of non-biting flies in the epidemiology of human infectious diseases. Microbes and Infection, 3(3), 231-235.

Hooton, T. M., Scholes, D., Hughes, J. P., Winter, C., Roberts, P. L., Stapleton, A. E. & Stamm, W. E. (1996). A prospective study of risk factors for symptomatic urinary tract infection in young women. New England Journal of Medicine, 335(7), 468-474.

Kadariya, J., Smith, T. C. & Thapaliya, D. (2014). *Staphylococcus aureus* and staphylococcal food-borne disease: an ongoing challenge in public health. BioMed Research International, 2014, 827965.

Karmali, M. A., Gannon, V. & Sargeant, J. M. (2010). Verocytotoxin-producing *Escherichia coli* (VTEC). Veterinary Microbiology, 140(3-4), 360-370.

Kerr, K. G. & Snelling, A. M. (2009). Pseudomonas aeruginosa: a formidable and ever-present adversary. Journal of Hospital Infection, 73(4), 338-344.

Kim, K. S. (2003). Pathogenesis of bacterial meningitis: from bacteraemia to neuronal injury. Nature Reviews Neuroscience, 4(5), 376-385.

Le Loir, Y., Baron, F., & Gautier, M. (2003). *Staphylococcus aureus* and food poisoning. Genetics and Molecular Research, 2(1), 63-76.

Marshall, B. M., & Levy, S. B. (2011). Food animals and antimicrobials: impacts on human health. Clinical Microbiology Reviews, 24(4), 718-733.

McCormick, J. K., Yarwood, J. M., & Schlievert, P. M. (2001). Toxic shock syndrome and bacterial superantigens: an update. Annual Review of Microbiology, 55(1), 77-104.

Mezzatesta, M. L., Gona, F., & Stefani, S. (2012). Enterobacter cloacae complex: clinical impact and emerging antibiotic resistance. Future Microbiology, 7(7), 887-902.

Miller, L. G., Perdreau-Remington, F., Rieg, G., Mehdi, S., Perlroth, J., Bayer, A. S., ... & Diep, B. A. (2005). Necrotizing fasciitis caused by community-associated methicillin-resistant *Staphylococcus aureus* in Los Angeles. New England Journal of Medicine, 352(14), 1445-1453.

Ogbonnaya, C. (2008). Analysis of groundwater pollution from abattoir waste in Minna, Nigeria. Research Journal of Dairy Science, 2(4), 74-77.

Oggioni, M. R., Pozzi, G., Valensin, P. E., Galieni, P., & Bigazzi, C. (1998). Recurrent septicemia in an immunocompromised patient due to probiotic strains of Bacillus subtilis. Journal of Clinical Microbiology, 36(1), 325-326.

Omole, D. O., & 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.

Pruden, A., Pei, R., Storteboom, H., & Carlson, K. H. (2006). Antibiotic resistance genes as emerging contaminants: studies in northern Colorado. Environmental Science & Technology, 40(23), 7445-7450.

Qadri, F., Svennerholm, A. M., Faruque, A. S. G., & Sack, R.B. (2005). Enterotoxigenic *Escherichia coli* in developing countries: epidemiology, microbiology, clinical features, treatment, and prevention. Clinical Microbiology Reviews, 18(3), 465-483.

Roland, P. S., & Stroman, D. W. (2002). Microbiology of acute otitis externa. The Laryngoscope, 112(7), 1166-1177.

Salkinoja-Salonen, M. S., Vuorio, R., Andersson, M. A., Kämpfer, P., Andersson, M. C., Honkanen-Buzalski, T., & Scoging, A. C. (1999). Toxigenic strains of Bacillus licheniformis related to food poisoning. Applied and Environmental Microbiology, 65(10), 4637-4645.

Tena, D., Martínez, N. M., Losa, C., & Solís, S. (2007). Skin and soft tissue infection caused by Bacillus pumilus: report of four cases. Scandinavian Journal of Infectious Diseases, 39(10), 881-884.

Tong, S. Y., Davis, J. S., Eichenberger, E., Holland, T. L., & Fowler Jr, V. G. (2015). *Staphylococcus aureus* infections: epidemiology, pathophysiology, clinical manifestations, and management. Clinical Microbiology Reviews, 28(3), 603-661.

Turnbull, P. C. B. (1996). Bacillus. In S. Baron (Ed.), Medical Microbiology (4th ed., Chapter 15). University of Texas Medical Branch, Galveston.

Von Eiff, C., Peters, G., & Heilmann, C. (2002). Pathogenesis of infections due to coagulase-negative staphylococci. The Lancet Infectious Diseases, 2(11), 677-685.

Walker, C. L. F., Rudan, I., Liu, L., Nair, H., Theodoratou, E., Bhutta, Z. A., ... & Black, R. E. (2013). Global burden of childhood pneumonia and diarrhoea. The Lancet, 381(9875), 1405-1416.

WHO (World Health Organization). (2011). Guidelines for Drinking-water Quality (4th ed.). World Health Organization, Geneva.

WHO (World Health Organization). (2019). Ten threats to global health in 2019. Available at: https://www.who.int/news-room/spotlight/ten-threats-to-global-health-in-2019

Woolhouse, M., Ward, M., van Bunnik, B., & Farrar, J. (2015). Antimicrobial resistance in humans, livestock and the wider environment. Philosophical Transactions of the Royal Society B, 370(1670), 20140083.