Original Research Article

Prevalence and antibiotic susceptibility pattern of Escherichia coli isolated from abattoir wastewaters in Abia State, Nigeria

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Wastewaters are considered hotspots for antibiotic resistant bacteria and horizontal gene transfer among related and unrelated bacterial species. This study investigated the prevalence and antibiotic susceptibility pattern of E. coli isolated from abattoir wastewaters in Abia State, Nigeria. Seven hundred wastewater samples from three abattoirs: Aba (300), Ubakala (250) and Lokpa (150) samples were analyzed from 2016 to 2019. Standard microbiological procedures were followed in isolation and identification of the E. coli isolates. The antibiotic susceptibility test was done using the Kirby Bauer disk diffusion method. The results showed high prevalence of E. coli in the three abattoir locations; 202(67.3%) from Aba, 154 (61.6%) from Ubakala and 81 (54%) from Lokpa. The antibiogram showed that the E. coli isolates were highly sensitive to Ofloxacin followed by Gentamicin in Aba (87.1% and 54.5%), Ubakala (95.5% and 60.4%) and Lokpa (92.6% and 64.2%) respectively. The E. coli isolates were highly resistant to Ampicillin and Augumentin with both interchangeably topping the list in the three locations. Most isolates had Multiple Antibiotic Resistance (MAR) index greater than (>0.2). This result shows that the isolates are a public health threat since their contact with the environment might cause the spread of multidrug resistance organisms.

Keywords: Wastewater, antibiotic, resistance, E. coli, abattoir

INTRODUCTION

An abattoir is a facility specially designed and licensed for receiving, holding, slaughtering and inspecting meat, animals and meat products before release to the public (Alonge et al., 2005). In Nigeria, the abattoir industry is an important component of the livestock industry providing domestic meat supply to over 150 million people and employment opportunities for teeming populations (Nafarnda et al., 2012).

During slaughter and meat processing, wastewater is generated consisting of mainly intestinal contents, blood and water. Abattoir wastewater may therefore be defined as water that has been used in the cleaning up of slaughtered cattle, sheep, goat and pig carcasses, the floor of slaughter hall, personnel and slaughter equipment (Coker et al, 2001). It is characterized by presence of high concentration of whole blood of the slaughtered food animals and suspended particles of semi-digested and undigested feeds within the stomach and intestine of slaughtered and dressed food animals.

Abattoir effluents most often enter natural bodies of water like groundwater, streams, lakes, rivers and oceans as a result of natural drainage patterns and sequences (Madigan et al., 1997; Pelczar et al, 2002). Potential health risks from water-borne pathogens can exist in water
contaminated by abattoir effluents (Nafarnda et al., 2012), and this could constitute significant environmental and public health hazards (World Bank, 1998; Coker et al., 2001; Nafarnda et al., 2006; Osibanjo and Adie, 2007). Bacteria from abattoir waste discharged into water columns can be absorbed to sediments, and the bacteria released back into the water columns when the bottom stream is disturbed thus presenting long-term hazards (Shrer et al., 1992).

Several studies have revealed that abattoirs in developing countries have an unhygienic environment (Adeyemo, 2002; Nwanta et al., 2010). The presence of pathogens that are known causes of diarrheal diseases and a possible hazard to human health in the abattoirs’ wastewater and receiving water bodies have been detected in abattoirs (Benka-Coker and Ojior, 1996; Abiade-Paull et al., 2005). This is as a result of meat production activities and failure in adhering to good manufacturing practices (GMP) and good health practices (GHP) (Adesemoye et al., 2006). Pathogens present in animal carcasses or shed in animal wastes may include Bacillus spp, Clostridium perfringes, Pseudomonas aeruginosa, Micrococcus luteus, Vibrio spp, Lactobacillus plantarum, Staphylococcus spp, Streptococcus spp, Escherichia coli, Salmonella spp, Mycobacterium bovis, Mycobacterium tuberculosis Aspergillus niger, Mucor spp, Penicillium spp, Saccharomyces spp and Fusarium spp. (Yakubu et al., 2007; Nafarnda et al., 2012).

The emergence of multi-drug resistance in bacterial human pathogens is one of the most serious challenges for healthcare globally. Pathogens that earlier were sensitive to antibiotics are becoming resistant by mutations in their pre-existing DNA or by acquisition of DNA containing resistance genes (Martinez et al., 2009). Most of the antibiotic resistance genes carried by pathogens have their origins in environments other than the clinical world, and the normal bacteria floras of disparate environments are thought to be reservoirs of the resistance genes (Martinez, 2008; Allen et al., 2010; Forsberg et al., 2012; Finley et al., 2013; Wellington et al., 2013). Gene exchange across bacterial species boundaries coupled with mobile genetic elements such as plasmids, transposons, integrons and genomic islands that harbor antibiotic resistance genes are important factors in the spread of acquired antibiotic resistance. (Marathe et al., 2013).

Recent studies have shown that antibiotic resistance genes are ancient and were present in the environment long before the antibiotic era (D’Costa et al., 2011; Bhullar et al., 2012). The abuse of antibiotics has led to increased selection pressures even in the environment. Resistance genes may radically increase in abundance within the populations in bacterial communities exposed to sufficient selection pressure from exposure to antibiotics, (Barbosa and Levy, 2000; Dethlefsen et al., 2008; Kristiansson et al., 2011). Such increases may also be accompanied by increased frequencies in genetic elements facilitating their mobility (Jernberg et al., 2010; Kristiansson et al., 2011). Thus, exposure to antibiotics is expected to increase the risk for the transfer of resistance between bacterial species. This is true not only during antibiotic treatment of humans and animals, but also when a sufficiently high level of antibiotic contamination reaches the external environment. Environments exposed to hospital and agricultural waste typically contain both antibiotic resistance bacteria as well as moderately elevated levels of antibiotics, providing examples of ecosystems wherein antibiotics may exhibit the potential for selecting resistant strains (Segura et al., 2009; Gullberg et al., 2011).

Escherichia coli is a normal inhabitant of the gastrointestinal tract of humans and warm-blooded animals (von Baum and Marre, 2005). Incidentally, it is an important cause of foodborne illnesses and a global public health threat (Awohr et al., 2019). The problem of antibiotic resistance in this widely studied bacterium makes it a double jeopardy in the health sector where it is known to cause a plethora of infections aside food related infections. Certain pathogenic strains such as Shiga-Toxin producing E. coli (STEC), Enterohemorrhagic E. coli (EHEC) and Enterotoxigenic E. coli (ETEC) have been associated with waterborne disease outbreaks and mortality in humans (Ram et al., 2009). ETEC is commonly responsible for infectious diarrhea, vomiting, sunken eyes, massive dehydration and a collapse of the circulatory system due to poor sanitary conditions (Bhunia, 2008). STEC produce Shiga-like toxins (Stx1 and Stx2) after enteric infection that causes massive damage to kidney tubules, bloody urine and Hemorrhagic uremic syndrome (Laing et al., 2011). The gastro-intestinal tract serves as a reservoir for integron-bearing E. coli strains (Vinué et al., 2008).

Studies on farms have also shown an occurrence of multi-antibiotic resistant E. coli after the chronic exposure to antibiotics (von Baum and Marre, 2005). In Abia State, there is no data on the prevalence and resistance of E. coli from the abattoir wastewaters to the current antibiotics used in the treatment of human bacterial infections hence the present study seeks to fill in this research gap with the objective of determining the prevalence and antibiotic susceptibility pattern of Escherichia coli isolated from abattoir wastewaters in Abia State, Nigeria.

MATERIALS AND METHODS
Collection of samples
A total of seven hundred wastewater samples from three abattoirs (300 from Aba, 250 from Ubakala and 150 from Lokpa in the three senatorial zones (Abia South, Abia Central and Abia North respectively) of Abia State, Nigeria were aseptically collected from November, 2016 to February, 2019 with sterile universal screw capped bottles. The samples were immediately transported to the laboratory for analyses.

Isolation and identification
used with slight modification. The abattoir wastewater
samples were isolated in peptone water (Hi media, India) and incubated at 37°C for 18-24h. The aliquots were then inoculated onto Eosin methylene blue Agar (Rapid Labs, UK) and incubated at 37°C for 18-24h. Colonies with green metallic sheen were grown on Nutrient Agar (Rapid Labs, UK) to obtain pure colonies. The pure colonies were identified using Gram reaction, morphological and biochemical tests including motility test, catalase, oxidase, ONPG (Oxoid, UK), methyl red using MR-VP broth (Oxoid, UK) and API 20E (Biomerieux, France).

The prevalence was calculated by dividing the number of positive E. coli isolates with the total number of samples

**Antimicrobial Susceptibility Test of the E. coli isolates**

The Kirby Bauer disc diffusion method was used (Kirby et al., 1966). Commercially impregnated discs containing 30µg Ceftazidime (CAZ), 30µg Cefuroxime (CRO), 10µg Gentamicin (GEN), 5µg Ciprofloxacin (CPR), and 5µg Ofloxacin (OFL), 10µg Ampicillin (AMP), 30µg Augmentin (AUG), 300µg Nitrofurantoin (NIT), 30µg Aztreonam (ATM), 30µg Chloramphenicol (CHL), 10µg Imipenem (IMP) and 25µg Cotrimoxazole (COT) from Rapid Labs and Oxoid, UK were used. Overnight Pure cultures were emulsified in sterile normal saline and adjusted to 0.5 Mc Farland turbidity standard. This is uniformly plated on Mueller Hinton agar using sterile swabstick. The antibiotic discs were placed on the Mueller Hinton agar and allowed to stand faced up for about 30mins for effective diffusion before incubating at 37°C for 18-24h. The diameter zone of inhibition (including the diameter of the disc) was measured to the nearest millimeter and interpreted using Clinical Laboratory Standard Institute guide (CLSI, 2015). Multidrug resistance was defined as resistance to three or more classes of drug (Magiorakos et al., 2012). The multiple antibiotic resistance (MAR) index which is expressed in decimal ranging from 0.1 to 1.0 was determined using the method described by Krumperman (1983) using the formula: a/b, with "a" being the number of tested antibiotics to which an organism is resistant to and "b" being the total number of antibiotics tested

**Statistical analysis**

The data was analyzed using percentage, excel worksheet and bar chart

**RESULTS**

**Prevalence of E. coli isolates**

Table 1 shows the prevalence of E. coli isolates from the three abattoirs sampled. E. coli had a prevalence of 202/300 (67.3%), 154/250 (61.6%) and 81/150 (54%) from Aba, Ubakala and Lokpa abattoirs respectively. The overall prevalence of the E. coli isolates is 437/700 (62.4%).

**Antibiotic susceptibility pattern**

The antibiotic susceptibility pattern of the E. coli isolates from the three abattoirs is presented in Table 2. The results show that the organisms were highly susceptible to Ofloxacin (87.1% in Aba, 95.5% in Ubakala and 92.6% in Lokpa) and highly resistant to Ampicillin (96.5% in Aba, 96.1% in Ubakala and 100% in Lokpa) while the highest intermediate reaction was recorded against Ciprofloxacin ([57.4%, 61.7% and 77.8% ] in Aba, Ubakala and Lokpa abattoirs respectively.

**Multiple Antibiotic Resistance (MAR) Index**

The percentage MAR index of the E. coli isolates was shown in Figure 1. Most of the isolates (30.2% from Aba, 32.5% from Ubakala and 49.4% from Lokpa) were found to have a MAR index of 0.8 with as much as 3.5% of the Aba isolates being resistant to all the antibiotics tested.

**DISCUSSION**

*Escherichia coli* had a high prevalence in this study with an average of 62.4% and a distribution of 67.3%, 61.6% and 54.0% for Aba, Ubakala and Lokpa abattoirs respectively. The presence of *E. coli* indicates possible presence of other pathogenic organisms of public health importance (Atuanya et al., 2018). The variation in the results might be attributed to the impact of human activity in and around the abattoir environments on the bacteria isolates (Abu and Egenonu, 2008).

This result contrasted with the works of Aradhye et al. (2014), who recorded 48% *E. coli* isolates from beef cattle and slaughterhouse premise, Haberecht et al. (2019) who recorded 37% from sewer water, 22% from wastewater treatment plant influent, 14% from surface water and 2.4% from wastewater treatment plant effluent in Colorado and Omererge et al. (2017), who recorded 28.30% and 30.19% respectively for wastewater and sludge samples. Higher prevalence rate was recorded by Abraham et al. (2019) who reported 100%, Gautam et al. (2019) 100% and Tesfaye et al. (2019) 75%. In Wa abattoir, Ghana, *E. coli* from different anatomical sites had a prevalence rate of 98%, 92% and 88% (Adzitey, 2020).

This work was somehow similar to the works of Thanigaivel and Anandhan (2015), who had 70% prevalence. Cabral (2010) suggested that the huge difference between the results might be due to the use of contaminated water during washing, slaughtering and other handling processes and also the fact that *E. coli* is a common inhabitant of the human and animal gut. However since this study did not focus on the quality of the water used in washing and clean up processes in the abattoir, the water quality parameters were not studied.

Most of the above studies reveal that *E. coli* was the most dominant organism and the public health importance of this organism cannot be over emphasized. *E. coli* O157:H7
Table 1: Prevalence of *E.coli* isolates from the three abattoirs in Abia State

<table>
<thead>
<tr>
<th>Location</th>
<th>Total number of samples (%)</th>
<th>Positive isolates (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Aba</td>
<td>300</td>
<td>202 (67.3)</td>
</tr>
<tr>
<td>Ubakala</td>
<td>250</td>
<td>154 (61.6)</td>
</tr>
<tr>
<td>Lokpa</td>
<td>150</td>
<td>81 (54)</td>
</tr>
<tr>
<td>Total</td>
<td>700</td>
<td>437 (62.4)</td>
</tr>
</tbody>
</table>

Table 2. Antibiotic susceptibility profile of the *E.coli* isolates from the three abattoirs in Abia State

<table>
<thead>
<tr>
<th>Antibiotic</th>
<th>Sensitive (%)</th>
<th>Intermediate (%)</th>
<th>Resistant (%)</th>
<th>Sensitive (%)</th>
<th>Intermediate (%)</th>
<th>Resistant (%)</th>
<th>Sensitive (%)</th>
<th>Intermediate (%)</th>
<th>Resistant (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ceftazidime</td>
<td>19 (9.4)</td>
<td>24 (11.9)</td>
<td>159 (78.7)</td>
<td>24 (15.6)</td>
<td>4 (2.6)</td>
<td>126 (81.8)</td>
<td>5 (6.2)</td>
<td>5 (6.2)</td>
<td>71 (87.7)</td>
</tr>
<tr>
<td>Cefuroxime</td>
<td>15 (7.4)</td>
<td>11 (5.4)</td>
<td>176 (87.1)</td>
<td>14 (9.0)</td>
<td>12 (7.8)</td>
<td>118 (76.6)</td>
<td>0 (0.0)</td>
<td>2 (2.5)</td>
<td>79 (97.5)</td>
</tr>
<tr>
<td>Gentamicin</td>
<td>110 (54.5)</td>
<td>48 (23.8)</td>
<td>44 (21.8)</td>
<td>93 (60.4)</td>
<td>18 (11.7)</td>
<td>43 (27.9)</td>
<td>52 (64.2)</td>
<td>11 (13.6)</td>
<td>18 (22.2)</td>
</tr>
<tr>
<td>Ciprofloxacin</td>
<td>23 (11.4)</td>
<td>116 (57.4)</td>
<td>63 (31.2)</td>
<td>12 (7.8)</td>
<td>95 (61.7)</td>
<td>47 (30.5)</td>
<td>10 (12.4)</td>
<td>63 (77.8)</td>
<td>8 (9.9)</td>
</tr>
<tr>
<td>Ofloxacin</td>
<td>176 (87.1)</td>
<td>9 (4.5)</td>
<td>17 (8.4)</td>
<td>147 (95.5)</td>
<td>0 (0)</td>
<td>7 (4.5)</td>
<td>75 (92.6)</td>
<td>3 (3.7)</td>
<td>3 (3.7)</td>
</tr>
<tr>
<td>Ampicillin</td>
<td>4 (2.0)</td>
<td>3 (1.5)</td>
<td>195 (96.5)</td>
<td>2 (1.3)</td>
<td>4 (2.6)</td>
<td>148 (96.1)</td>
<td>0 (0.0)</td>
<td>0 (0)</td>
<td>81 (100)</td>
</tr>
<tr>
<td>Augmentin</td>
<td>3 (1.5)</td>
<td>8 (4.0)</td>
<td>191 (94.6)</td>
<td>0 (0)</td>
<td>1 (0.6)</td>
<td>153 (99.3)</td>
<td>0 (0.0)</td>
<td>0 (0)</td>
<td>81 (100)</td>
</tr>
<tr>
<td>Nitrofurantoin</td>
<td>61 (30.2)</td>
<td>28 (13.9)</td>
<td>113 (55.9)</td>
<td>73 (47.4)</td>
<td>23 (14.9)</td>
<td>58 (37.9)</td>
<td>10 (12.4)</td>
<td>2 (2.5)</td>
<td>69 (85.2)</td>
</tr>
<tr>
<td>Aztreonam</td>
<td>45 (22.3)</td>
<td>18 (8.9)</td>
<td>139 (68.8)</td>
<td>50 (32.5)</td>
<td>10 (6.5)</td>
<td>94 (61.0)</td>
<td>22 (27.2)</td>
<td>2 (2.5)</td>
<td>57 (70.4)</td>
</tr>
<tr>
<td>Chloramphenicol</td>
<td>22 (10.9)</td>
<td>19 (9.4)</td>
<td>161 (79.7)</td>
<td>8 (5.2)</td>
<td>12 (7.8)</td>
<td>134 (87.0)</td>
<td>9 (1.1)</td>
<td>7 (8.6)</td>
<td>65 (80.2)</td>
</tr>
<tr>
<td>Imipenem</td>
<td>23 (11.4)</td>
<td>8 (4.0)</td>
<td>171 (84.7)</td>
<td>17 (11.0)</td>
<td>10 (6.5)</td>
<td>127 (82.5)</td>
<td>23 (28.4)</td>
<td>2 (2.5)</td>
<td>56 (69.1)</td>
</tr>
<tr>
<td>Cotrimoxazole</td>
<td>24 (11.9)</td>
<td>17 (8.4)</td>
<td>161 (79.7)</td>
<td>6 (3.9)</td>
<td>5 (3.2)</td>
<td>143 (92.9)</td>
<td>5 (6.2)</td>
<td>0 (0)</td>
<td>76 (93.8)</td>
</tr>
</tbody>
</table>

Figure 1: Percentage MAR index of the *E.coli* isolates from the three abattoirs

and 014:H4 both enterohaemorrhagic strains have been associated with many zoonotic outbreaks both in the US and Germany (NYSDH, 2000; Frank et al., 2011). Raw sewage and slaughter house effluent characteristics if untreated may cause dissemination of *E. coli* in the environment (Kabiu et al., 2015). Contamination with *E. coli* in abattoir remains a persistent problem which has negative impact on human health and natural environments (Camizalez-Roman et al., 2016).

The susceptibility pattern of *E. coli* from the various
locations had almost the same pattern with only a slight variation. *E. coli* from Aba was highly susceptible to Ofloxacin (87.1%), Gentamicin (54.5%) and Nitrofurantoin (30.0%). *E. coli* from Ubakala showed similar pattern with only a change in the percentage susceptibility of 95.5%, 60.4% and 47.4% respectively. *E. coli* isolates from Lokpa had a slight deviation with 92.6% susceptibility to Ofloxacin, 64.2% to Gentamicin and 28.4% to Imipenem while Nitrofurantoin and Ciprofloxacin had a sensitivity of 12.4% respectively. This showed that Ofloxacin and Gentamicin might be the only drugs that still have potential in the treatment of infections caused by these *E. coli* isolates.

The *E. coli* isolates were found to have high resistance to most of the antibiotics used in this study. *E. coli* from the three locations (Aba, Ubakala and Lokpa) showed resistance to most of the antibiotics used with the isolates having less resistance (<50%) to only three or four antimicrobials as the case maybe according to the location. High resistance rate in *E. coli* was reported by Igwaran et al. (2019). However, this differs from a study on *E. coli* isolated from Amsterdam meat chickens which showed 63.1% susceptibility to tested antimicrobials (Abraham et al., 2019). The problem of antibiotic resistant bacteria occurring in the environment is the serious threat it poses to public health, the higher disease burden it adds and the fact that the antibiotics effectiveness is reduced leading to increased mortality rate (Amaya et al., 2012; Igwaran et al., 2018).

The high resistance of *E. coli* isolates to Ampicillin (80%), Augmentin (66.7%), Cotrimoxazole (66.7%) is in agreement with Ahmed et al. (2013), Atuanya et al. (2018) and Gautam et al. (2019). Sanjukta et al. (2016) corroborated this work by reporting 74.5% resistance to Cefuroxime although they recorded 68.1% resistance to Gentamicin. Somda et al. (2018) in Burkina Faso reported 100% sensitivity to Ciprofloxacin, Gentamicin and Chloramphenicol with 42.86% resistance in Ampicillin which contrasted with the current work. Partial agreement with this work was observed by Rahman et al. (2017) who recorded 100% sensitivity to Ciprofloxacin and Gentamicin with 71.43% resistance to Azithromycin and Cotrimoxazole respectively. Varied results were obtained by Adzitey, (2020) who recorded 95.56% sensitivity to Ciprofloxacin, 82.22% sensitivity to Cotrimoxazole and 75.56% sensitivity to Gentamicin. Similar results were also reported by Zhao et al. (2012) and Rasmussen et al. (2015) in Ghana and US.

Studies have shown a steady increase in the in the occurrence of highly resistant *E. coli* probably because of horizontal gene transfer (Fair and Tor, 2014). *E. coli* resistance is of great public health importance as they are the most common gram-negative bacterial infections in humans. Its resistance to ESBLs has been recorded to be on steady rise in Europe (EMA, 2009). Waterborne *E. coli* have been found to be a major reservoir of antimicrobial resistance including ESBL and *K. pneumonia* carbapenamase mechanism among others (Haberacht et al., 2019). It is worthy to note that ESBL positive strains in bacteremia have also shown increased cross resistance to fluoroquinolones (>80%) and Gentamicin (>40%) (Livermore et al., 2008). Fluoroquinolone resistant *E. coli* have been isolated lately. (Rudolf et al., 2008; Fair and Tor, 2014)

A high intermediate response was observed with Ciprofloxacin. *E. coli* isolates from Aba had 57.4% intermediate sensitivity to Ciprofloxacin, while Ubakala and Lokpa recorded 61.7% and 77.8% intermediate sensitivity respectively. This shows that increased dosage of this drug is needed when in use for the treatment of associated *E. coli* infections. Several studies have established high susceptibility of organisms to fluoroquinolones (Adanaike et al., 2013). However, some researchers associate intermediate response to resistance as the organisms might be in an intermediate process of acquiring resistance, a pointer to abuse or probable misuse of this drug in the treatment of both human and animal bacterial infections.

Most *E. coli* isolates from this study were found to be multdrug resistant (resistance to three or more classes of antimicrobials (Magiorakos et al., 2012)). Alvarez-Fernandez et al. (2013) reported 91.7% multidrug resistant *E. coli* from poultry while Rahman et al. (2017) recorded 76.0 % multidrug resistance from chicken meat and 57.14% from beef in Bangladesh. According to Sharada et al. (2010), the varied antibiogram results indicate variation of antibiotic pattern with isolates time and multidrug resistance development among different *E. coli* isolates found to be related to transmissible R factor/plasmid.

Multiple drug resistance was observed in *E. coli* from the three locations. This finding is supported by Bekele et al. (2014), Adetunji et al. (2014) and Igwaran et al. (2018). The development of drug resistance in *E.coli* and other Gram negative bacteria can be linked to indiscriminate use of antibiotics in humans and food producing animals, selective pressure to extensive use of antibiotics in the animal industry and indiscriminate dumping of antibiotics in the environment.

Most of the *E. coli* (99.8%) isolates in this study had Multiple antibiotic resistance (MAR) index greater than (>0.2, with many of the *E. coli* isolates having MAR index of 0.8 in all the abattoirs investigated. MAR index is a measure of extent of resistance to antibacterial agent and gives an indirect suggestion of the probable source of the organism with MAR values >0.2 indicating isolates recovered from high risk sources where strict rules concerning antibiotic prescription and usage are lacking (Adenaike et al., 2013).

**CONCLUSION**

The result of this study showed high prevalence of *E. coli* in the three abattoir wastewaters investigated. This high prevalence is an indication of the unhygienic nature of the environment and production facilities, the water quality and processes in the abattoirs. The increased resistance of the isolates to the antibiotics used in this study shows that
the discharge of the untreated abattoir wastewater into the
environment (soil, water and vegetation) could not only
increase the spread of antibiotic resistant E. coli but the
spread of other antibiotic resistant bacteria which is
possible through the various mechanisms of transfer of
antibiotic resistance. This study demonstrates that the E.
coli isolates from abattoir wastewaters are multidrug
resistant hence they may pose serious public health threats.
Observation of good hygiene practices in and around the
abattoir environments, treatment of abattoir wastewaters
before discharge into the environment and the active
participation of State Environmental Protection Agency and
Environmental Health officials in monitoring and
enforcement of health and safety protocols are
recommended in order to minimize the spread of
antimicrobial resistance.

Further studies are needed to detect the antibiotic
resistance genes and to determine the genetic evolution
and pathogenicity of the isolates.

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Conflict of Interests

The authors declare that there is no conflict of interests
regarding the publication of this manuscript.

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