Scientific Research Publishing

Open Journal of Applied Sciences, 2026, 16(11), 4638-4651
https://www.scirp.org/journal/ojapps
ISSN Online: 2165-3925
ISSN Print: 2165-3917

# Molecular Characterization and Antibiotic Resistance Profile of *Salmonella* spp. and *Escherichia coli* Strains Isolated from Effluents of Two Hospitals in Ouagadougou, Burkina Faso

**Joseph M. Makaya[1*], Hama Cissé[2], Abasse G. Ouédraogo[2,3], Bithia K. Kaboré[1], Wilfried W. Ouédraogo[1], Aly Savadogo[2]**

[1]Laboratory of Sciences and Technologies, New Dawn University, Bobo-Dioulasso, Burkina Faso
[2]Laboratory of Biochemistry and Applied Immunology (LaBIA), Joseph Ki-Zerbo University, Ouagadougou, Burkina Faso
[3]National Center for Scientific and Technological Research, Institute for Research in Applied Sciences and Technologies, Department of Food Technology (CNRST/IRSAT/DTA), Bobo-Dioulasso, Burkina Faso
Email: *makaya.joseph7@gmail.com

**How to cite this paper:** Makaya, J.M., Cissé, H., Ouédraogo, A.G., Kaboré, B.K., Ouédraogo, W.W. and Savadogo, A. (2026) Molecular Characterization and Antibiotic Resistance Profile of *Salmonella* spp. and *Escherichia coli* Strains Isolated from Effluents of Two Hospitals in Ouagadougou, Burkina Faso. *Open Journal of Applied Sciences*, **16**, 4638-4651.
https://doi.org/10.4236/ojapps.2026.1611255

**Received:** September 29, 2026
**Accepted:** November 20, 2026
**Published:** November 23, 2026

Copyright © 2026 by author(s) and Scientific Research Publishing Inc.
This work is licensed under the Creative Commons Attribution International License (CC BY 4.0).
http://creativecommons.org/licenses/by/4.0/

Open Access

## Abstract

Wastewater generated by hospital activities is thought to contain a wide variety of microbial contaminants, including bacteria that are multi-drug resistant. The aim of this study was to determine the antibiotic resistance profile of *Escherichia coli* and *Salmonella* spp. isolates characterized using PCR in liquid effluents from the Bogodogo and Yalgado Ouédraogo University Hospitals. The antibiotic susceptibility of the *Salmonella* spp. and *Escherichia coli* isolates was assessed in accordance with the recommendations of the Antibiogram Committee of the French Society for Microbiology (2024). In total, 17 *Salmonella* isolates and 30 *Escherichia coli* isolates underwent molecular identification using the PCR technique. Isolates of *Escherichia coli* and *Salmonella* spp. were identified using the respective primers GTG5 and UIDA. Following molecular analysis, 14 out of 17 (82 per cent) and 13 out of 30 (43 per cent) of the isolates were identified as *Escherichia coli* and *Salmonella* spp., respectively. The characteristic bands for *Salmonella* had molecular weights of approximately 2000 bp and 500 bp, whilst those for *Escherichia coli* were approximately 500 bp. The rate of antibiotic resistance among the 14 *Salmonella* spp. isolates was 0% for imipenem, gentamicin and meropenem. Aztreonam was the least active against *Salmonella*. Furthermore, the antibiotic resistance rates for the 13 *Escherichia coli* isolates were 23 per cent, 15 per cent, 23 per cent, 30.8 per cent, 53 per cent, 23 per cent, 30 per cent, 46.15 per cent, 38.46

per cent and 7 per cent respectively to imipenem, amoxiclav, cefotaxime, cefepime, aztreonam, meropenem, ampicillin, temocillin, ceftazidime and gentamicin. Consequently, hospital effluents remain, to date, potential sources of environmental contamination by bacterial strains that are often multi-resistant to antibiotics.

## Keywords

Hospital Effluents, *Enterobacteriaceae*, Molecular Characterization, Antibiotic Resistance, Ouagadougou

## 1. Introduction

Wastewater generated by hospital activities can pose a potential hazard to humans and the environment due to the nature and quantity of the chemical and microbial substances it contains [1] [2]. Untreated or partially treated effluents generated by hospital activities can contribute significantly to the spread of pathogenic and often multi-drug-resistant (MDR) bacteria into surface waters and receiving environments [3]. MDRs in effluents originate primarily either from patients' biological materials (blood, urine, pus, etc.) or from the horizontal transfer of resistance genes between multi-resistant and infectious strains and environmental strains [4] [5]. Indeed, hospital effluents constitute a reservoir of potentially pathogenic microorganisms. Among these microorganisms found in wastewater, *Enterobacteriaceae* are the most prevalent, particularly *Escherichia coli* and *Salmonella* [6] [7]. In West Africa, several authors have reported suspicions that hospital effluent is one of the sources of contamination of surface water with antibiotic residues, trace metals and, above all, multidrug-resistant strains. It has even been reported by Ouédraogo and colleagues that some university hospitals discharge their liquid effluents directly into municipal sewers after only minimal pre-treatment [8]. In Burkina Faso, the use of wastewater has become a viable option along sewerage networks for market gardening on the outskirts of major cities, due to a lack of irrigation water during the dry season. These practices in Burkina Faso, as elsewhere in the world, are suspected of being one of the causes of contamination of market garden produce by *Escherichia coli* and *Salmonella*, which are the main pathogens implicated in millions of cases of gastroenteritis and foodborne infections in humans [9] [10]. Thus, as part of ongoing surveillance of antimicrobial multi-resistance in Burkina Faso and of hospital and environmental hygiene, this investigation aims to assess the sanitary quality and antibiotic resistance profile of bacterial isolates from hospital effluent.

## 2. Materials and Methods

### 2.1. Study Setting and Period

The investigation focused on the liquid effluents from the Bogodogo and Yalgado Ouédraogo university hospitals in the city of Ouagadougou. Each hospital center

has a wastewater pre-treatment plant using a lagooning system before the effluent is discharged into the municipal sewerage system. Effluent samples were collected for analysis between February 2025 and January 2026. The isolation and biochemical characterization of the strains, as well as the preparation of the antibiotic susceptibility profile, were carried out at the Laboratory of Biological and Applied Sciences at "New Dawn" University. The molecular characterization of the strains was carried out at the Laboratory of Biochemistry and Applied Immunology (LABIA) at Joseph Ki-Zerbo University.

## 2.2. Sampling

Sampling was carried out on wastewater from general services and biomedical analysis laboratories in each of the two hospital centers. This wastewater is pre-treated by a lagooning system before being discharged into the municipal sewerage system. As part of our study, wastewater samples were collected from a sewer manhole after the pre-treatment step. Six (06) wastewater samples were collected at each site, at a rate of one sample every two months. A total of twelve (12) liquid effluent samples were collected during the study year. To obtain each sample, wastewater was collected from deep within a sewer manhole and placed in a sterile 500 mL bottle. The samples were stored in a cool box and transported to the laboratory within two hours for the isolation of the bacterial strains of interest.

## 2.3. Isolation and Biochemical Characterization of Bacteria of Interest

➢ **Presumed *Escherichia coli* strains**

The screening for suspected *E. coli* strains was based on the principles of the ISO 16649-2 (2001) standard. Colonies exhibiting a metallic green appearance on EMB medium (Liofilchem®). These strains, suspected of being *E. coli*, were characterized using the API 20E kit (BioMérieux, France). Once the identity of the isolate had been confirmed, it was stored for molecular characterization using the UIDA primer.

➢ **Cases of suspected *Salmonella* spp. strains**

Testing for *Salmonella* was carried out on Xylose Lysine Deoxycholate (XLD) agar in accordance with standard NF ISO 6579: 2002 and consists mainly of four stages:

✓ Pre-enrichment: 100 mL of wastewater was filtered through a 0.45 µm, 50 mm diameter filter and transferred to a flask containing 225 mL of peptone water. The mixture was incubated at 37˚C for 24 hours before being removed for enrichment;

✓ Enrichment: 1 mL of the pre-enriched suspension was added to a test tube containing 9 mL of Rappaport-Vassiliadis broth. This tube was incubated at 37˚C for 48 hours before being removed for isolation on Xylose Lysine Deoxycholate (XLD) agar;

✓ Isolation: 10 µL of enriched Rappaport-Vassiliadis broth was withdrawn using

a micropipette and streaked onto XLD agar using a sterile Pasteur pipette. This culture was incubated at 37˚C for 24 hours and, upon removal, colonies appearing black or red with a black center were identified using biochemical (API 20E kit) and molecular tests;

✓ Identification: a suspect colony was collected using a sterile Pasteur pipette to prepare a suspension equivalent to MacFarlan 0.5 in physiological saline. This suspension was used to inoculate the wells of the API 20E gallery (BioMérieux, France) and then incubated at 37˚C for 24 hours. Molecular confirmation was subsequently carried out using the universal GTG5 primer.

## 2.4. Molecular Characterization of Isolates

➢ **Extraction of bacterial DNA**

Extraction was carried out using the thermal shock method adapted from that of Guessennd *et al*. [5]. To do this, the suspected isolates were streaked onto Muller-Hinton (MH) agar and incubated at 37˚C for 24 hours to obtain young colonies. Using a sterile Pasteur pipette, a few colonies from each bacterial strain were collected and suspended in Eppendorf tubes previously containing 350 microliters (µL) of PCR-grade water, then homogenized using a vortex mixer. The tubes were then placed in the freezer for 10 minutes, before being removed and immediately immersed in a water bath at 95˚C for 10 minutes to induce lysis of the bacterial cells. Following the thermal shock, centrifugation at 10,000 revolutions per minute for 10 minutes was carried out to separate the cell debris from the DNA. The supernatant obtained after centrifugation was collected in a second, pre-sterilized Eppendorf tube, whilst the pellet was discarded.

➢ **Preparation of the reaction medium**

The various reaction buffers were prepared to a total volume of 25 µL for both types of bacteria. However, the GTG5 and UIDA primers were used respectively for the amplification of DNA from *Salmonella* spp. and *E. coli* isolates. Thus, for the amplification of *Salmonella* spp. DNA, the reaction mixture was prepared using bacterial DNA, Master Mix, magnesium chloride ($MgCl_2$), PCR water and the universal primer (GTG)5 in volumes of 5 µL, 4 µL, 2 µL, 12 µL and 2 µL. For the amplification of *E. coli* DNA, the reaction mixture was prepared using bacterial DNA, Master Mix, magnesium chloride ($MgCl_2$), PCR water, UIDA-F and UIDA-R in volumes of 5 µL, 4 µL, 2 µL, 12 µL, 1 µL and 1 µL respectively.

➢ **Gene amplification**

The standard PCR technique was used to amplify the target DNA sequences, in accordance with the protocol detailed in **Table 1** and **Table 2** for the GTG5 and UIDA primers respectively.

## 2.5. Agarose Gel Electrophoresis

The amplicons resulting from the amplification were run on an agarose gel (1.5% concentration prepared with 1X TAE buffer and a few drops of SafeView (abm®)) in a tank containing 1X TAE electrolyte. A DNA molecular weight marker (100

bp DNA Ladder N3231L, New England Biolabs® Inc.) combined with loading dye (Gel Loading Dye, Purple (6X), B7025S, New England Biolabs® Inc.) served as a reference scale. An electric potential of 100 volts was applied to the tank for 23 minutes to separate the fragments via electrophoretic migration.

**Table 1.** GTG5 primer amplification program.

| Steps | Temperatures | Time | Number of cycles |
|---|---|---|---|
| Initial denaturation | 94˚C | 4 min | |
| Second denaturation | 95˚C | 30 s | |
| Hybridization | 45˚C | 1 min | 30 cycles |
| Elongation | 65˚C | 8 min | |
| Final elongation | 65˚C | 16 min | |

**Table 2.** Amplification program for the UIDA primer.

| Steps | Temperatures | Time | Number of cycles |
|---|---|---|---|
| Initial denaturation | 94˚C | 4 min | |
| Second denaturation | 95˚C | 30 s | |
| Hybridization | 63˚C | 1 min | 30 cycles |
| Elongation | 72˚C | 1 min | |
| Final elongation | 72˚C | 7 min | |

## 2.6. Visualization of PCR Products

After electrophoresis, the gel was placed on the imaging surface of a UVP transilluminator (Bio-Rad Molecular Imager®) emitting at 254 nm.

## 2.7. Study of Antibiotic Susceptibility

➢ **Preparation of the bacterial inoculum**

Antimicrobial susceptibility testing was performed on MH agar using the disk diffusion method, applying disks impregnated with known doses of antibiotics in accordance with the 2024 recommendations of the French Society for Microbiology (CASFM) committee. The bacterial inoculum is obtained by homogenizing a young, pure colony (18 - 24 hours old) in 10 mL of sterile physiological saline (0.9% NaCl).

➢ **Performance of the antibiogram**

Petri dishes containing MH agar were inoculated by swabbing near a Bunsen burner. A total of ten (10) antibiotics (Table 3) were applied using sterile forceps. Thus, in one of the dishes, the discs were arranged such that the amoxiclav (amoxicillin + clavulanic acid) disc was in the center of the dish, with the other antibiotic discs surrounding it. The *Escherichia coli* ATCC 8739 strain was used as a nega-

tive control for antibiotic activity quality.

➢ **Incubation and assessment of results**

After 24 hours of incubation, the antibiogram was read by measuring the zones of inhibition in accordance with the CASFM 2024 recommendations (Table 3).

Table 3. Antibiotics used and their critical diameters.

| Families | Antibiotics | Acronyms | Expenses (µg) | Critical diameters | | |
|---|---|---|---|---|---|---|
| | | | | S≥ | I | R< |
| Aminoglycoside | Gentamicin | CN | 120 | 17 | | 17 |
| Carbapenem | Meropenem | MRP | 10 | 22 | | 16 |
| | Imipenem | IMI | 10 | 22 | | 19 |
| Cephalosporin | Cefotaxime | CTX | 30 | 20 | | 17 |
| | Ceftazidime | CAZ | 30 | 22 | | 19 |
| | Cefepime | FEP | 30 | 27 | | 24 |
| Monobactams | Aztreonam | ATM | 30 | 26 | | 21 |
| Penicillins | Ampicillin | AMP | 10 | 14 | | 14 |
| | Temocillin | TMO | 30 | 20 | | 17 |
| | Amoxiciclav | AUG | 30 | 19 | | 19 |

Note. IMI: imipenem, AUG: amoxicillin and clavulanic acid, CTX: cefotaxime, FEP: cefepime, ATM: aztreonam, MRP: meropenem, AMP: ampicillin, TMO: temocillin, CAZ: ceftazidime, CN: gentamicin.

➢ **Data processing**

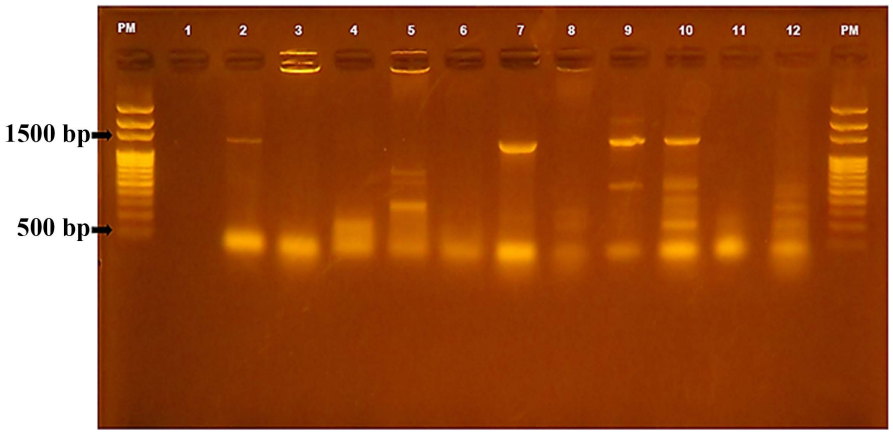
The diagrams, tables and average values for the isolates' antibiotic profiles were generated using Excel 2016. The dendrograms showing the clustering of antibiotic molecule activity against the isolates were generated on the official D-UPGMA website (http://genomes.urv.cat/UPGMA/).

## 3. Results

### 3.1. Molecular Characteristics of the Isolates

➢ **Molecular characteristics of the *E. coli* isolates**

A total of 30 strains were characterized by biochemical tests as suspected *Escherichia coli*. These strains were therefore tested using the PCR technique with the UIDA primer. The *Escherichia coli* strain ATCC 8739 was used as a positive control. The electrophoresis results revealed a characteristic band of approximately 500 bp (Figure 1). Of the 30 isolates analyzed, 13 were positive for this characteristic, representing a prevalence of 43 per cent. In addition to the characteristic band, specific bands were also observed, the predominant one of which was at a molecular weight of approximately 1500 bp and was amplified from the extracts of four (4) isolates (Figure 1).

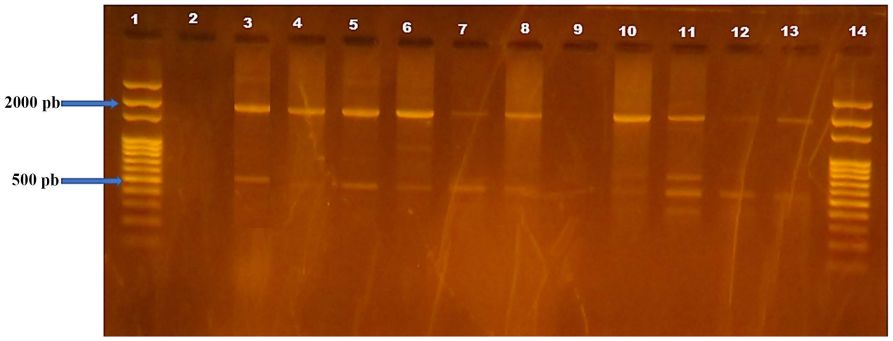



Note. 1: Control well containing water; MW (PM): Molecular Weight; bp: Base Pair; 2: Ec Chr P3; 3: Chr Ec Y4; 4: EMB Ec B1; 5: Ec 556; 6: Ec 8 B6; 7: Chr Ec B2; 8: Ec Chr B1; 9: Ec 579; 10: Chr P3 Ec; 11: Ec EMB P2; 12: Ec 0123/022.

**Figure 1.** Illustration of the synthetic gel showing the electrophoretic profiles of the amplified *Escherichia coli*.

### 3.2. Molecular Characteristics of *Salmonella* spp.

A total of 17 presumptive *Salmonella* spp. isolates were tested using PCR with the (GTG)5 primer, employing a pure *Salmonella* as a reference to identify the other strains. Ten microliters (10 µL) of molecular weight marker were loaded into the first and last wells; the second well served as a negative control; the third well received 10 µL of the amplicon from our reference strain *Salmonella* enteritidis ATCC 13076; and the remaining wells received 10 µL of each *Salmonella* amplicon. Electrophoresis products revealed characteristic bands at 500 bp and 2000 bp for our reference strain. Of the 17 isolates analyzed, 14 tested positives, displaying the characteristic 500 bp and 2000 bp bands. In addition to the characteristic bands, some strains exhibited specific bands at approximately 3000 bp, 1000 bp, 600 bp, and/or 400 bp. **Figure 2** illustrates the electrophoretic profiles of the amplification products from the *Salmonella* isolates.




Note. 1 and 14: Molecular weights; 2: control well containing distilled water; 3: Xld Y1; 4: Xld B4; 5: SB1; 6: Xld P2; 7: Xld Y-3; 8: SP1B1; 9: Sal E76-1; 10: Xld Y2I; 11: Xld B3 (25/08); 12: Xld P4; 13: Xld B1.

**Figure 2.** Illustration of the synthetic gel showing the electrophoretic profiles of *Salmonella* isolates.

Table 4 below presents a more detailed overview of the electrophoretic profiles of the amplification products from *Salmonella* isolates.

Table 4. Details of the characteristic bands by isolate.

| N° Serial | Isolates codes | Characteristic bands | | Specific bands (pb) |
|---|---|---|---|---|
| | | 2000pb | 500pb | |
| 1 | Reference *Salmonella* | + | + | |
| 2 | Xld B3 (17/08) | + | + | – |
| 3 | Xld Y1 | + | + | 3000 |
| 4 | Xld B4 | + | + | 1000 |
| 5 | SB1 | – | – | – |
| 6 | Xld P2 | + | + | 400 |
| 7 | Xld Y-3 | + | + | – |
| 8 | SP1B1 | – | – | – |
| 9 | Sal E76-1 | + | + | – |
| 10 | Xld Y2I | + | + | – |
| 11 | Xld B3 (25/08) | + | + | – |
| 12 | Xld P4 | + | + | 600 et 400 |
| 13 | Xld B1 | + | + | 400 |
| 14 | Xld B2 | – | – | 400 |
| 15 | Xld P3 | + | + | 400 |
| 16 | Xld-Y3 | + | + | – |
| 17 | Xld B3 (15/09) | + | + | 400 |
| 18 | Xld Y2 | + | + | – |

Note. (+): presence; (–): absence.

## 3.3. Antibiotic Activity against Isolates

➢ **Antibiotic activity against *E. coli* isolates**

The antibiotic susceptibility testing was carried out on the 13 isolates identified as *E. coli* following molecular testing. The activity of the ten (10) different antibiotics showed that all isolates were resistant to at least one antibiotic. The antibiotics that were least active against the strains were aztreonam (53 per cent) and temocillin (46.15 per cent). In contrast, the compounds that exhibited greater activity were gentamicin (93 per cent), amoxiclav (85 per cent), imipenem (77 per cent), cefotaxime (77 per cent), meropenem (77%), ampicillin (70%), cefepime (61.51%) and ceftazidime (53.84%). Table 5 presents the resistance profiles of the

*E. coli* isolates to the antibiotic compounds.

Table 5. Resistance profiles of *E. coli* isolates to antibiotic compounds.

| Isolate codes | Resistance profile of the isolates |
|---|---|
| Chr Y4 | IMI, AUG, CTX, FEP, ATM, MRP, AMP, TMO et CAZ |
| Chr B1 | IMI, ATM, MRP, TMO et CAZ |
| Chr P3 | Nothing |
| EMB P2 | ATM |
| Ec 556 | AMP |
| EMB B2 | CTX, FEP, ATM, AMP et CAZ |
| Ec 579 | TMO |
| 0123\022 | TMO |
| Chr B3 | FEP, ATM, TMO et CAZ |
| Chr B2 | IMI, AUG, CTX, FEP, ATM, MRP, AMP, TMO, CAZ et CN |
| Chr P2 | TMO |
| Chr P3 | FEP, ATM, TMO et CAZ |
| Ec 574 | Nothing |

Note. IMI: imipenem, AUG: amoxicillin and clavulanic acid, CTX: cefotaxime, FEP: cefepime, ATM: aztreonam, MRP: meropenem, AMP: ampicillin, TMO: temocillin, CAZ: ceftazidime, CN: gentamicin.

The resistance rates for the *E. coli* isolates were as follows: 23.00%, 15.00%, 23.00%, 30.80%, 53.00%, 23.00%, 30.00%, 46.15%, 38.46%, and 7.00% for IMI, AUG, CTX, FEP, ATM, MRP, AMP, TMO, CAZ, and CN, respectively.

**Antibiotic activity against *Salmonella* spp. isolates**

A total of fourteen (14) *Salmonella* spp. isolates out of the seventeen (17) suspected cases were confirmed and underwent antibiotic susceptibility testing. The antibiotics tested aztreonam, ceftazidime, temocillin and cefepime were the least effective, with activity rates of 64.28 per cent, 57.14 per cent, 57.14 per cent and 42.85 per cent, respectively, against the strains. Conversely, the *Salmonella* spp. strains showed high susceptibility to imipenem (92.85 per cent), gentamicin (100 per cent), ampicillin (85.72 per cent), Amoxiclav (92.85 per cent), meropenem (100 per cent) and cefotaxime (64.28 per cent), as shown in the supplementary document. Table 6 presents details of the antibiotic activities against *Salmonella* spp. isolates.

The *Salmonella* spp. isolates exhibited the following antibiotic resistance rates: 0.00%, 0.00%, 14.28%, 0.00%, 57.14%, 7.14%, 64.28%, 35.72%, 57.14%, and 42.85% for IMI, CN, AMP, MRP, TMO, AUG, ATM, CTX, CAZ, and FEP, respectively.

**Table 6.** Antibiotic resistance profiles of *Salmonella* spp. Isolates.

| Isolate codes | Resistance profile of the isolates |
|---|---|
| Xld'B3 (17/08) | ATM, CTX, CAZ et FEP |
| Xld Y2 | ATM, CTX, CAZ et FEP |
| Xld Y1 | TMO, ATM et CAZ |
| Sal E76-1 | TMO |
| Xld P3 | TMO, ATM, CAZ et FEP |
| Xld P2 | TMO, ATM, CAZ et FEP |
| Xld-Y3 | TMO |
| XldY-3 | TMO, ATM, CTX, CAZ et FEP |
| Xld P4 | Nothing |
| Xld B3 (15/09) | AMP, TMO, ATM, CTX et CAZ |
| Xld B1 | IMI et TMO |
| Xld B4 | TMO, ATM, CAZ et FEP |
| Xld Y2 (15/09) | AUG, ATM, CTX, CAZ et FEP |
| Xld'B3 (26/08) | AMP, TMO, CAZ et FEP |

Note. IMI: imipenem, AUG: amoxicillin and clavulanic acid, CTX: cefotaxime, FEP: cefepime, ATM: aztreonam, MRP: meropenem, AMP: ampicillin, TMO: temocillin, CAZ: ceftazidime, CN: gentamicin.

### 3.4. Grouping of the Various Isolates According to Patterns of Antibiotic Resistance

Figure 3 is a dendrogram illustrating the patterns of resistance observed in isolates of *E. coli* and *Salmonella* spp. Several patterns of resistance were recorded, which were summarized into five (5) groups or nodes by analysis of the dendrogram (Figure 3).

## 4. Discussion

Our investigation identified isolates of *E. coli* and *Salmonella* spp. in pre-treated hospital effluent discharged directly into the municipal sewerage system of the city of Ouagadougou. These bacterial species, along with many others, have been detected on several occasions in hospital effluent both in Burkina Faso and across much of Africa [11]-[13]. These microbial contaminants may have several sources, the most likely of which is pathological material from sick people. Indeed, the water used to clean technical workstations is subsequently contaminated with a variety of contaminants, including bacteria that may be commensal or pathogenic [14]. Once at the wastewater treatment plants, the treatment of this water is inadequate due to shortcomings in the management systems, as demonstrated by

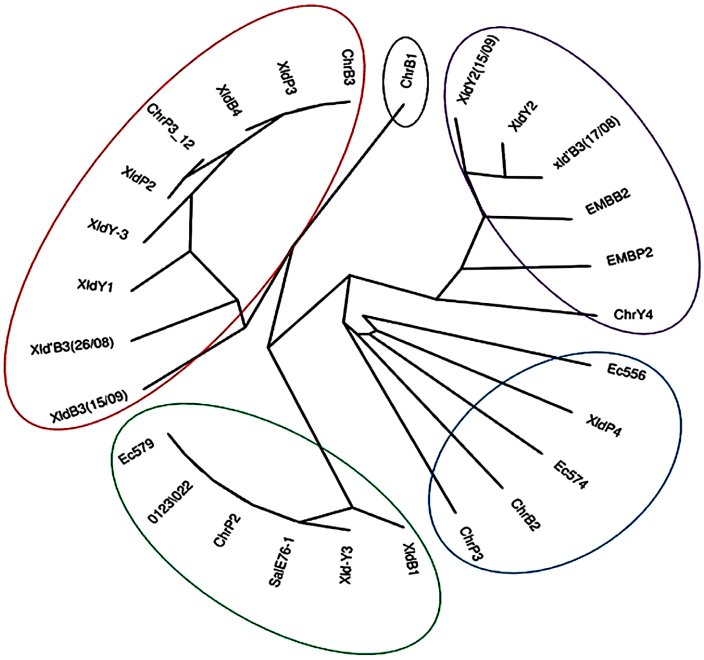



**Figure 3.** Illustration showing the grouping of isolates according to their patterns of resistance to antibiotic molecules.

the authors' research on hospitals in Burkina Faso and elsewhere in the world [1] [11] [15]. Consequently, the direct discharge of this hospital wastewater into municipal sewers could contribute to the contamination of surface water and market garden produce, and may even pose a threat to the biodiversity of the receiving environments. Consequently, water users downstream of these discharge points for hospital effluent would be exposed to a range of infections, including *E. coli*, which remains the most commonly reported infection in hospitals in Burkina Faso, as in all countries in the sub-region [8] [16]. As for *Salmonella* infection, it remains one of the most common and dangerous forms of food poisoning, particularly through the consumption of raw market garden produce [10]. Hospital effluent could therefore be one of the contributing factors to the poor sanitary quality of surface water and market garden produce, and may even pose a threat to consumers health. As well as generating pathogenic bacterial strains, hospital effluents are also thought to be sources of antibiotic residues and multidrug-resistant bacteria [11]. Indeed, a variety of antibiotics are generally discharged into hospital effluents, which also helps to inhibit susceptible bacteria and provides a selective advantage to resistant bacteria. This study reported on isolates characterized from hospital wastewater in the city of Ouagadougou. *E. coli* strains showed high prevalence of resistance to amoxiclav, temocillin, aztreonam, ceftazidime and ampicillin. Furthermore, *Salmonella* spp. isolates showed high rates of resistance to the same antibiotic compounds. These forms of resistance did not show any significant difference, as shown in **Figure 3**, between the *E. coli* and *Salmonella* spp. strains. Similar findings regarding bacterial multidrug resistance were also reported by Tesfaye and colleagues (2019) in their investigation

into the resistance profile of *E. coli* strains isolated from hospital effluents in Algeria [6]. This may be explained by the presence of residues of these molecules at non-bactericidal concentrations in these hospital effluents, leading to the proliferation of resistance to these molecules in these strains [6] [11]. The present study reported resistance rates of 23 per cent, 30.8 per cent, 38.46 per cent and 53 percent, respectively, for cefotaxime, cefepime, ceftazidime and aztreonam in our strains. Guessennd and colleagues (2013), in Côte d'Ivoire, reported even higher resistance rates of 100 per cent to the aforementioned cephalosporin compounds [5]. These forms of resistance can be explained by selective pressure in effluents and other matrices (food and clinical) and the proliferation of multidrug-resistant strains across various environmental compartments.

## 5. Conclusion

In light of this investigation, hospital effluent discharged into the environment near certain hospitals in the city of Ouagadougou harbours strains of *Salmonella* and *E. coli*. Although this investigation did not examine the pathogenicity of the characterized strains, it demonstrated that these strains exhibit a multi-drug resistance profile against various antibiotic compounds. Thus, penicillins (with the exception of clavulanic acid) and cephalosporins were the least active against *Salmonella* spp. isolates, but were slightly more active against *E. coli* isolates. Statistical analyses showed that there was no significant difference in the patterns of resistance between *Salmonella* and *E. coli* isolates. However, carbapenems and aminoglycosides exhibited a high level of activity against the isolates. These compounds represent the most promising options for the management of Enterobacteriaceae infections. However, one of the isolates carrying the Chr B2 gene in this investigation was resistant to all antibiotic compounds available for this study.

## Acknowledgements

The authors thank the academic staff at New Dawn University for the financial support that made this work possible.

## Author Contributions

J.M.M. and H.C.—contributed to the preparation of original manuscript; J.M.M., C.H., G.A.O. and A.S.—contributed to the conception, development of methods, statistical analyses, and reviewing the manuscript; B.K.K., W.W.O. and J.M.M.—contributed to the methods development and reviewing the manuscript.

## Conflicts of Interest

The authors declare no conflicts of interest regarding the publication of this paper.

## References

[1] Jerie, S., Vurayayi, T., Olivia, M., Tapiwa, C.M. and Takunda, S. (2024) Environmental and Human Health Problems Associated with Hospital Wastewater Management

in Zimbabwe. *Current Environmental Health Reports*, **11**, 380-389.

[2] Luo, J., Zhu, T., Wang, X., Cheng, X., Yuan, Y., Jin, M., *et al*. (2020) Toxicological Mechanism of Excessive Copper Supplementation: Effects on Coloration, Copper Bioaccumulation and Oxidation Resistance in Mud Crab *Scylla paramamosain*. *Journal of Hazardous Materials*, **395**, Article ID: 122600. https://doi.org/10.1016/j.jhazmat.2020.122600

[3] Khan, M.T., Ahmad, R., Liu, G., Zhang, L., Santagata, R., Lega, M., *et al*. (2024) Potential Environmental Impacts of a Hospital Wastewater Treatment Plant in a Developing Country. *Sustainability*, **16**, Article No. 2233. https://doi.org/10.3390/su16062233

[4] Li, M., Zhan, A., Rahman, T.T., Jiang, T. and Hou, L. (2025) From Wastewater to Resistance: Characterization of Multidrug-Resistant Bacteria and Assessment of Natural Antimicrobial Compounds. *Frontiers in Microbiology*, **16**, Article ID: 1612534. https://doi.org/10.3389/fmicb.2025.1612534

[5] Guessennd, N., Ouattara, M., Ouattara, N., Nevry, R., Gbanon, V., Tiekoura, K., *et al*. (2013) Étude des bactéries multirésistantes des effluents hospitaliers d'un centre hospitalier et universitaire (CHU) de la ville d'Abidjan (Côte d'Ivoire). *Journal of Applied Biosciences*, **69**, 5456-5464. https://doi.org/10.4314/jab.v69i0.95071

[6] Tesfaye, H., Alemayehu, H., Desta, A.F. and Eguale, T. (2019) Antimicrobial Susceptibility Profile of Selected Enterobacteriaceae in Wastewater Samples from Health Facilities, Abattoir, Downstream Rivers and a WWTP in Addis Ababa, Ethiopia. *Antimicrobial Resistance & Infection Control*, **8**, Article No. 134. https://doi.org/10.1186/s13756-019-0588-1

[7] Tilahun, M., Shibabaw, A. and Adane, M. (2025) Prevalence and Multidrug Resistance Patterns of Bacterial Pathogens in Wastewater and Drinking Water Systems from Hospital and Non-Hospital Environments in Ethiopia: A Systematic Review and Meta-Analysis. *BMC Infectious Diseases*, **25**, Article No. 250. https://doi.org/10.1186/s12879-025-10660-9

[8] Ouédraogo, G.A., Cissé, H., Boukaré, K., Sampo, E., Stéphane, K.D., Odetokun, I., Sawadogo, A., Bassolé, I.N. and Savadogo, A. (2022) Spread and Antibiotic Resistance Profile of Pathogens Isolated from Human and Hospital Wastewater in Ouagadougou. *Microbes and Infectious Diseases*, **3**, 318-331.

[9] Zeynudin, A., Degefa, T., Belay, T., Mumicha, J.B., Husen, A., Yasin, J., *et al*. (2025) Detections of Antimicrobial Resistance Phenotypes and Extended-Spectrum Beta-Lactamase (ESBL)-Producing Salmonella Spps and *Escherichia coli* O157:H7 in Raw Vegetables and Fruits from Open Markets in Jimma Town, Ethiopia and Evaluation of Hygiene and Handling Practices of Vendors. *One Health Outlook*, **7**, Article No. 2. https://doi.org/10.1186/s42522-024-00125-5

[10] Somda, N.S., Bonkoungou, I.J.O., Sambe-Ba, B., Drabo, M.S., Wane, A.A., Sawadogo-Lingani, H., *et al*. (2021) Diversity and Antimicrobial Drug Resistance of Non-Typhoid Salmonella Serotypes Isolated in Lettuce, Irrigation Water and Clinical Samples in Burkina Faso. *Journal of Agriculture and Food Research*, **5**, Article ID: 100167. https://doi.org/10.1016/j.jafr.2021.100167

[11] Ouédraogo, G.A., Cissé, H., Ouédraogo, H.S., Kaboré, B., Traoré, R., Traoré, Y., *et al*. (2023) Research of Antibiotic Residues and Bacterial Strain's Antibiotic Resistance Profile in the Liquid Effluents Evacuated in Nature by Two CHUs and a Mixed WWTP of Ouagadougou (Burkina Faso). *Infection and Drug Resistance*, **16**, 2537-2547. https://doi.org/10.2147/idr.s408315

[12] Garba, Z., Bonkoungou, I.O.J., Millogo, N.O., Natama, H.M., Vokouma, P.A.P.,

Bonko, M.d.A., *et al*. (2023) Wastewater from Healthcare Centers in Burkina Faso Is a Source of ESBL, AmpC-*β*-Lactamase and Carbapenemase-Producing *Escherichia coli* and *Klebsiella pneumoniae*. *BMC Microbiology*, **23**, Article No. 351. https://doi.org/10.1186/s12866-023-03108-0

[13] Teferi, G.T., Gebeyehu, A.W., Weldemichael, T.G. and Nure, J.F. (2025) Antibiotic Residues and Multidrug Resistant *Escherichia coli* and *Salmonella* in Wastewater from Tirunesh Beijing Hospital, Ethiopia. *Discover Environment*, **3**, Article No. 240. https://doi.org/10.1007/s44274-025-00423-3

[14] Aguilar-Rangel, E.J., Paredes-Cárcamo, F., Andrade, M.D., Contreras-Sánchez, D., Rain-Medina, V., Campanini-Salinas, J., *et al*. (2025) Hospital Wastewater as a Reservoir of Contaminants of Emerging Concern: A Study Report from South America, Chile. *Antibiotics*, **14**, Article No. 1111. https://doi.org/10.3390/antibiotics14111111

[15] Niman, S., Koledzi, E.K., Batcham, I. and Krou, N.M. (2026) Assessment of Risks Associated with Hospital Effluent from Kara University Hospital (Kara U.H.) in Togo. *International Journal of Environmental Impacts*, **9**, 37-52. https://doi.org/10.56578/ijei090104

[16] Hotor, P., Kotey, F.C.N. and Donkor, E.S. (2025) Antibiotic Resistance in Hospital Wastewater in West Africa: A Systematic Review and Meta-Analysis. *BMC Public Health*, **25**, Article No. 1364. https://doi.org/10.1186/s12889-025-22513-w