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RESEARCH ARTICLE

Antimicrobial susceptibility and genotypic characterization of *Escherichia coli* isolated from foods controlled by the National Food Safety Agency in Burkina Faso

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Abstract

This study was conducted to determine the antimicrobial resistance profiles of *Escherichia coli* isolated from food samples received at the National Food Safety Agency in Burkina Faso. A total of 155 isolates from dairy foods (29), fish-based dishes (7), mango juices (4), lettuces (35), RTE salads (21), sandwiches (32), and sesames (27) were included for testing with the Kirby-Bauer disk diffusion method. PCR targeting ampicillin (bla_{TEM}, bla_{SHV}, *temA*, and *temB*), tetracyclines [*tet(A)* and *tet(B)*], sulfamethoxazole (*sul1* and *sul2*), aminoglycosides (*StrA* and *aadA*) and quinolones (*GyrA*) resistance genes were performed to elucidate the genotypic resistance mechanism. Of the 155 isolates, 105 (67.7%) were resistant to at least one antimicrobial agent. Resistances to tetracycline (33.5%), ampicillin (32.9%), cefoxitin (18.7%), gentamycin (15.5%), amoxicillin-clavulanate acid (15.5%), nalidixic acid (12.9%), chloramphenicol (11.6%), trimethoprim-sulfamethoxazole (11.6%), and ciprofloxacin (8.4%) were observed. Multidrug resistance was recorded in 26.5% of the isolates. Antimicrobial resistance genes including bla_{TEM} (19/51, 37.3%), bla_{SHV} (19/51, 37.3%), *temB* (17/51, 33.3%), *tet(A)* (24/52, 46.2%), *tet(B)* (9/52, 17.3%), *sul1* (8/18, 44.4%), *sul2* (4/18, 22.2%), *aadA* (11/24, 45.83%) and *GyrA* (31/36, 86.1%) were detected. All *E. coli* isolates resistant to at least 2 antibiotics were positive for the class 1 integron gene (*intI1*). These findings raise concerns about food safety and public health and demonstrate the need for strict government control and continuous monitoring.

Keywords *E. Coli* · Food hygiene · Burkina Faso · Resistance · Antimicrobials

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1 Introduction

Antimicrobial resistance (AMR) is a growing global concern and poses a grave threat to public health (Robinson et al. 2016). The void in the development of new therapeutic substances has exacerbated the problem, and as a result, very few antimicrobials are available to treat infections caused by multidrug-resistant (MDR) pathogens (Robinson et al. 2016). Numerous reports have described the presence of large amounts of antimicrobial resistant bacteria and antimicrobial resistant genes (ARGs) in various food products, such as meat, fish, vegetables, ready-to-eat (RTE) foods, and fruits (Rajaei et al. 2021; Vuthy et al. 2017; Amer et al. 2018). This presence of MDR bacteria in the food chain is a rising public health concern. Indeed, besides contributing to the spread of foodborne pathogens, an additional concern is that food represents a vehicle for the transmission of AMR determinants to humans, which may occur through contact or consumption of contaminated food products (Amer et al. 2018).

Escherichia coli (*E. coli*) is a ubiquitous rod-shaped Gram-negative bacterium abundant in the gastrointestinal tract of humans and animals, where it plays a crucial role in digestion and absorption (Kaushik et al. 2018). However, *E. coli* can infect animals and humans, causing diseases ranging from opportunistic wound infections to severe systemic infections. Furthermore, *E. coli* can easily spread through the food chain and function as ARG carriers/reservoirs, sharing them with other bacteria of the same or other species (Kaushik et al. 2018). As a result, *E. coli* strains are frequently used as an appropriate indicator bacterium in AMR surveillance, as changes in these species can serve as an early warning of the emergence of resistance in similar pathogenic bacteria (Guo et al. 2019). Resistant *E. coli* strains containing various ARGs have been extensively investigated, mainly in industrialized nations (Balbin et al. 2020; Li et al. 2020a). Most of the AMR research in Burkina Faso has focused on clinical samples from humans (Ouedraogo et al. 2016; Dissinviel et al. 2017; Kpoda et al. 2018; Dembélé et al. 2020). There is limited information on the antimicrobial resistance and molecular characteristics of *E. coli* strains isolated from food sources throughout our country. Accordingly, in this study, we performed antimicrobial susceptibility and molecular characterization of resistance genes from *E. coli* strains obtained from various foods controlled by Burkina Faso's National Food Safety Agency. All isolates were tested for antimicrobial susceptibility using the disk diffusion method, followed by a polymerase chain reaction (PCR) assay to screen 11 ARGs and integrons. To our knowledge, this report is the first to investigate the role of *E. coli* in the propagation of AMR in the food chain in Burkina Faso. The results call for strengthening the monitoring of foodborne *E. coli* in the Burkina Faso food chain to protect human health.

2 Material and methods

2.1 Bacterial isolates and storage

This study included 155 *E. coli* isolates from food samples obtained from the Burkina Faso National Food Safety Agency surveillance activities between 2018 and 2021. All samples received were processed for isolation and identification of *E. coli* on MacConkey agar (HiMedia, Mumbai, India) and Eosin methylene blue (EMB) agar (HiMedia, Mumbai, India) followed by biochemical characterization by standard procedures. Isolated strains were stored at -80 °C in brain heart infusion (BHI), (HiMedia, Mumbai, India) medium containing 15% (v/v) glycerol (HiMedia, Mumbai, India). For the purpose of this study, all frozen *E. coli* isolates were reactivated from cryovials on Nutrient Agar (HiMedia, Mumbai, India) at 37 °C for 18–24 h. The identification of *E. coli* was confirmed by Gram staining and biochemical characterization using API 20E kits (BioMérieux, Marcy l'Etoile, France). The isolates were recovered from 7 types of food samples, including dairy foods (29), fish-based dishes (7), mango juices (4), lettuces (35), RTE salads (21), sandwiches (32) and sesame (27) (Table 1).

2.2 Antimicrobial susceptibility tests

The disk diffusion method on Mueller-Hinton (MH) agar (HiMedia, Mumbai, India) was used for antimicrobial susceptibility testing, as recommended by the Clinical and Laboratory Standards Institute (CLSI, 2017). In brief, a single bacterial colony from nutrient agar was randomly selected and suspended in 0.85% sterile saline (HiMedia, Mumbai, India) to achieve an inoculum equivalent to 0.5 McFarland (HiMedia, Mumbai, India). A sterile cotton swab (HiMedia, Mumbai, India) was immersed in the 0.5 McFarland suspension and spread on MH plate. The plate was then allowed to dry completely at room temperature (no more than 15 min). Antimicrobial disks (Condalab, Madrid, Spain) were then applied to the MH (HiMedia, Mumbai, India) agar surface with sterile fine curved stainless-steel splinter forceps at a distance to avoid overlapping of the inhibition zones. The following antibiotics were used: cefotaxime (CTX, 30 µg), ceftazidime (CAZ, 30 µg), cefepime (FEP, 30 µg), aztreonam (ATM, 30 µg), amoxicillin/clavulanic acid (AMC, 30 µg), ampicillin (AMP, 10 µg), cefoxitin (FOX, 30 µg), chloramphenicol (C, 30 µg), trimethoprim-sulfamethoxazole (STX, 1.25/23.75 µg), nalidixic acid (NA, 30 µg), tetracycline (TE, 30 µg), imipenem (IMP, 10 µg), meropenem

Table 1 Percentages of *E. coli* isolates resistant to antimicrobials from various food sources

Antimicrobials	Dairy food (gapal) n (29) resistant (%)	Fish n (7) resistant (%)	Mango juice n (4) resistant (%)	Lettuce n (35) resistant (%)	RTE Salad n (21) resistant (%)	Sandwich n (32) resistant (%)	Sesame n (27) resistant (%)	Total n (155) resistant (%)
Ampicillin	11 (37.9)	2 (28.6)	1 (25)	11 (31.4)	10 (47.6)	7 (21.9)	9 (33.3)	51 (32.9)
Amoxicillin–clavulanate acid	3 (10.3)	1 (14.3)	0 (0)	11 (31.4)	5 (23.8)	1(3.1)	4 (14.8)	24 (15.5)
Cefoxitin	5 (17.2)		0 (0)	5 (14.3)	6 (28.6)	5(15.6)	7 (25.9)	29 (18.7)
Cefepime	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)
Cefotaxime	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)
Ceftazidime	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)
Aztreonam	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0(0)
Imipenem	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)
Meropenem	0 (0)	0 (0)	0 (0)	0(0)	0 (0)	0 (0)	0 (0)	0 (0)
Tetracycline	13 (44.8)	5 (71.4)	1 (25)	14 (40)	7 (33.3)	7 (21.9)	5 (18.5)	52 (33.5)
Gentamicin	6 (20.7)	2 (28.6)	0	3 (8.6)	4 (19.0)	4 (12.5)	5 (18.5)	24 (15.5)
Amikacin	1 (3.4)	2 (28.6)	0	0	0	0	0	3 (1.9)
Chloramphenicol	4 (13.8)	1 (14.3)	1 (25)	3 (8.6)	2 (9.5)	7 (21.9)	0 (0)	18 (11.6)
Trimethoprim–sulphamethoxazole	3 (10.3)	3 (42.9)	0 (0)	5 (14.3)	0 (0)	4 (12.5)	3 (11.1)	18 (11.6)
Nalidixic acid	2 (6.9)	1 (14.3)	0 (0)	3 (8.6)	3 (14.3)	1 (3.1)	10 (37.0)	20 (12.9)
Ciprofloxacin	3 (10.3)	0	0	0	2 (9.5)	8 (25)	3 (11.1)	13 (8.4)
Resistance to 1 Antimicrobial	21 (72.4)	7 (100.0)	2 (50.0)	19 (54.3)	17 (81.8)	18 (56.3)	21 (77.8)	105 (25.0)
Resistance to 2 Antimicrobials	7 (24.1)	3 (42.6)	0 (0.0)	2 (5.7)	3 (14.3)	2 (6.3)	5 (18.5)	23 (14.8)
Resistance to ≥ 3 Antimicrobials	7 (24.1)	3 (42.6)	0	11(31.4)	7 (33.3)	8 (25.0)	6 (22.2)	42 (27.1)

(MEM, 10 µg), gentamicin (CN, 10 µg), amikacin (AK, 30 µg), and ciprofloxacin (CIP, 10 µg). The inoculated plates were incubated at 37 °C for 24 h and the inhibition zones were measured in millimeters across the diameters. The standard strain of *E. coli* ATCC 35218 was used as a quality check. Isolates exhibiting resistance to 3 or more classes were considered multidrug-resistant (MDR) (Magiorakos et al. 2012). Multiple antimicrobial resistance (MAR) indexes were calculated using Krumperman's approach (Krumperman 1983).

2.3 DNA extraction

The heat lysis method (Yang et al. 2019) was used to extract genomic DNA from resistant bacteria, which was then used as a PCR template for all assays. Briefly, a single pure bacterial colony from a Nutrient agar (HiMedia, Mumbai, India) plate was subcultured in 1 ml of BHI (HiMedia, Mumbai, India) overnight. The next day, each culture broth was centrifuged at 13,000 rpm for 5 min at 4 °C, and the cell pellets were resuspended in 500 µl of sterile distilled water and heated at 100 °C in a water bath for 10 min. The cell suspension was immediately frozen at -20 °C for 10 min and then centrifuged at 13,000 rpm for 5 min at 4 °C. The supernatant was transferred to a new Eppendorf tube and conserved at -20 °C until use.

2.4 Identification of resistance genes and integrons

The presence of antimicrobial resistance genes among the resistant isolates was determined using the uniplex PCR tests to amplify ARGs. 11 pairs of oligonucleotide primers (Genecust, Paris, France) were used to target antimicrobial resistance genes that confer resistance to antimicrobial agents, including ampicillin ($bla_{TEM}$$bla_{SHV}$, *temA*, *temB*), tetracycline, [*tet(A), tet(B)*], aminoglycosides (*StrA*, *aadA*), quinolone (*GyrA*) and trimethoprim-sulfamethoxazole (*sul1*, *sul2*). The PCR cycling conditions for reactions were set at 94 °C for 3 min, followed by 30 cycles of 1 min at 94 °C, 30 s at annealing temperature and 1 min at 72 °C and final step for 7 min at 72 °C. Furthermore, uniplex PCR was conducted to detect the presence of *intI1* integrase genes in the 65 isolates resistant to at least 2 antimicrobials, to detect the presence of Class 1 integrons. The thermal cycling conditions included preincubation at 94 °C for 1 min, followed by 35 cycles of denaturation at 98 °C for 30 s, annealing at 60 °C for 30 s, and polymerization at 72 °C for 30 s, and final extension at 72 °C for 10 min. Subsequently, the variable regions (VRs) of the strains that were positive for the *intI1* gene were evaluated by uniplex PCR using the primers hep58 and hep59 with the following cycling conditions: preincubation at 94 °C for 1 min, followed by 35 cycles of denaturation at 98 °C for 30 s, annealing at 55 °C for 30 s, and polymerization at 72 °C for 4 min and final extension at 72 °C for 10 min. The primer (Genecust, Paris, France) sequences, the annealing temperatures, expected product

sizes, and references are presented in Table 2. The PCR was done using a TECHNE Prime Elite thermal cycler (Bibby scientific, Staffordshire, United Kingdom). Appropriate positive and negative controls for amplifications were used in each PCR procedure. All PCR amplifications were performed in a reaction mixture comprising of 4 µl FIREPol® Master Mix (Solis BioDyne, Tartu, Estonia), 0.4 µl of each primer, 3 µl of DNA template and nuclease-free water to make volume up to 20 µl. Amplified PCR products were run on a 1.5% agarose gel containing 0.5 µg/ml of ethidium bromide (ThermoFisher, Waltham, United States) for 60 min at 100 V, then visualized using the gel documentation system E-BOX VX5 (VILBER, Marne-la-Vallée, France).

3 Results and discussion

In this study, we characterized the antimicrobial resistance profiles and ARGs of a collection of 155 *E. coli* isolates recovered from sandwich, dairy food, fish, sesame, lettuce and RTE salad at the Burkina Faso National Food Safety Agency. To our knowledge, this is the first time a study was conducted with many *E. coli* isolates from various food sources in our country.

3.1 Antimicrobial susceptibility of *E. coli* isolates

Among the *E. coli* isolates used in the present study, 105 (67.7%) were resistant to at least 1 of the 16 antimicrobials used (Table 1). A similarly high level of resistance (74.2%) was reported in isolates collected from RTE foods in 2017 in Shaanxi Province, Republic of China (Baloch et al. 2017). In our study, resistances to tetracycline, ampicillin, gentamycin, amoxicillin-clavulanate acid, nalidixic acid, chloramphenicol, and trimethoprim-sulfamethoxazole were generally observed. These findings are consistent with previously published studies showing that *E. coli* isolates from foods were resistant to several older antimicrobials, including tetracycline, streptomycin, sulfonamides, ampicillin, gentamicin, and nalidixic acid. Vuthy et al. (2017), reported high resistances to tetracycline, amoxicillin, and sulfamethoxazole (63.1–76.1%) of *E. coli* isolated from chicken food chains in Phnom Penh (China). In addition, *E. coli* isolated from RTE foods (Singapore) during a study of Guo et al. (2019) showed resistances to tetracycline (17.2%), ampicillin (15.2%) and chloramphenicol (10.1%). In a study conducted by Ayamah et al. (2021) in Ghana, all isolates obtained from kebabs (beef, chevon, and gizzard) were resistant to ampicillin, tetracycline, and

Table 2 Primer sequences, annealing temperature, product size and source of primers used during this study

Target gene		Primers sequence (5'to3')	Annealing temperature (° C)	Product Size (bp)	Reference
bla_{TEM}	F	ACCAATGCTTAATCAGTGAG	50	857	Abatcha et al. 2018
	R	ACCAATGCTTAATCAGTGAG			
bla_{SHV}		TCGCCTGTGTATTATCTCCC	52	768	Abatcha et al. 2018
		CGCAGATAAATCACCACAATG			
temA	F	ATGAGTATTCAACATTTCCG	62	867	Abatcha et al. 2018
	R	CTGACAGTTACCAATGCTTA			
temB	F	TTTTCGTGTCGCCCTTATTCC	62	798	Abatcha et al. 2018
	R	CGTTCATCCATAGTTGCCTGACTC			
tet(A)	F	GTGAAACCCAACATACCCC	60	888	Sivakumar et al. 2021
	R	GAAGGCAAGCAGGATGTAG			
tet(B)	F	CCTTATCATGCCAGTCTTGC	60	774	Sivakumar et al. 2021
	R	ACTGCCGTTTTTTCGCC			
sul1	F	TCA CCG AGG ACT CCT TCT TC	53	435	Sivakumar et al. 2021
	R	CAG TCC GCC TCA GCA ATA TC			
sul2	F	GCGCTCAAGGCAGATGGCAT	53	293	Sivakumar et al. 2021
	R	GCGTTTGATACCGGCACCCT			
StrA	F	CCAATCGCAGATAGAAGGC	58	548	Vuthy et al. 2017
	R	CTTGGTGATAACGGCAATTC			
aadA	F	GTGGATGGCGGCCTGAAGCC	58	528	Vuthy et al. 2017
	R	AATGCCCAGTCGGCAGCG			
GyrA	F	ATGAGCGACCTTGCGAGAGAAATTACACCG	58	659	Vuthy et al. 2017
	R	TTCCATCAGCCCTTCAATGCTGATGTCTTC			
intI1	F	GGCTTCGTGATGCCTGCTT	60	146	Fang et al. 2019
	R	CATTCCTGGCCGTGGTTCT			
Class-1 integron VRs	hep58	TCATGGCTTGTTATGACTGT	55	variable	Fang et al. 2019
	hep59	GTAGGGCTTATTATGCACGC			

gentamicin. Furthermore, Somda et al. (2018) found that *E. coli* isolated from RTE chickens in Burkina Faso were resistant to tetracycline (64.3%), ampicillin (42.8%), amoxicillin + clavulanic acid (46.3%), and trimethoprim-sulphamethoxazole (32.14%). These traditional antimicrobials have been overused and abused throughout the years by consumers, veterinarians, farmers, physicians, and patients due to their low prices and easy availability over the counter, rendering them empirically ineffective (Guo et al. 2019). Interestingly, our study did not find an *E. coli* isolate resistant to cefotaxime, ceftazidime, cefepime, and aztreonam (ESBL-producing strain). On the contrary, resistance to

Table 3 Antimicrobial patterns and multiple antimicrobial resistance index of *E. coli* isolates

Antimicrobial resistance profile	Source	No. of isolates	MAR index
CIP C	Sandwich, sandwich	2	0.13
AMP TE	RTE salad, RTE salad, dairy food, dairy food	4	0.13
CN CIP	Dairy food	1	0.13
AMP CN	Dairy food	1	0.13
TE SXT	Dairy food, sesame	2	0.13
FOX TE	Fish	1	0.13
CN AK	Fish	1	0.13
TE CN	Fish	1	0.13
AMP FOX	Sesame	1	0.13
FOX NA	Sesame, lettuce	2	0.13
NA CN	Sesame, sesame	2	0.13
AUG AMP	RTE salad, dairy food, lettuce	3	0.13
AMP C	Fruit juice, dairy food	2	0.13
AMP TE CIP	Sandwich	1	0.2
AMP FOX TE	Dairy food	1	0.2
TE NA SXT	Dairy food, fish	2	0.2
AMP TE SXT	Fish, sesame, sandwich	3	0.2
AUG AMP FOX	Sesame	1	0.2
AUG AMP TE	Sandwich, lettuce	2	0.2
AMP FOX C	RTE salad	1	0.2
TE CN C	Lettuce	1	0.2
AUG AMP NA	Lettuce	1	0.2
AMP FOX CIP	Sandwich	1	0.27
AMP TE CIP C	RTE salad	1	0.27
AMP TE CN CIP	RTE salad, sandwich	2	0.27
AUG AMP FOX	RTE salad	1	0.27
AMP TE CIP SXT	Sandwich	1	0.27
AMP TE AK SXT	Fish	1	0.27
AMP TE NA SXT	Sesame	1	0.27
AUG AMP FOX NA	Sesame, RTE salad, RTE salad	3	0.27
AUG AMP FOX CIP	Dairy food	1	0.27
AUG AMP FOX CN	RTE salad	1	0.27
AMP FOX SXT C	Sandwich	1	0.27
AUG AMP FOX TE	Dairy food, lettuce, lettuce	3	0.27
AUG AMP TE SXT	Lettuce	2	0.27
AUG AMP FOX NA	Sesame	1	0.27
AMP FOX TE SXT C	Dairy food	1	0.33
AMP TE NA CN AK	Dairy food	1	0.33
AUG AMP FOX TE NA	Sesame	1	0.33
AUG AMP FOX TE CN	Lettuce	1	0.33
AUG AMP TE SXT C	Lettuce	1	0.33
AUG AMP TE NA SXT	Lettuce	1	0.33
AUG AMP FOX TE SXT	Lettuce	1	0.33
AMP FOX TE CN CIP C	Dairy food	1	0.4
FOX TE NA CN CIP SXT C	Sandwich	1	0.47

TE = Tetracycline, NA = Nalidixic acid, AK = Amikacin, SXT = Sulphamethoxazole-Trimethoprim, AMP = Ampicillin, AUG = Amoxicillin + clavulanic acid, FOX = Cefoxitin, CN = Gentamicin, C = Chloramphenicol

Table 4 Occurrence of resistance genes among *E. coli*

Antimicrobial agents	Number of resistant isolates	Genes detected	Number of positive amplicons (%)
Ampicillin	51	*temB*	17 (33.3)
		bla_{TEM}	19 (37.3)
		bla_{SHV}	19 (37.3)
Tetracycline	52	*tet(A)*	24 (46.2)
		tet(B)	9 (17.3)
		tet(A) + tet(B)	4 (7.7)
Sulfamethoxazole	18	*Sul1*	8 (44.4)
		Sul2	4 (22.2)
		Sul1 + Sul2	1 (5.6)
Nalidixic acid / ciprofloxacin	36	*GyrA*	31(86.1)
Gentamycin	24	*StrA*	0
		aadA	11 (48.3)

Data are expressed as N, RG (%); N: Number of resistant isolates; RG: Number of positive isolates with resistance gene; (%): percentage of resistant

these antimicrobials was observed among *E. coli* isolated from street foods in India (Sivakumar et al. 2021). Additionally, a study of street food in Tamale (Ghana) showed that 55.4% (41/74) of the isolated *E. coli* were ESBL producers (Karikari et al. 2022). This disparity may be attributed to the sample sources, that is, foods of plant origin in our case and street foods in the others. In addition, bacteria found in meat (especially meat poultry origin) can be resistant to a wide range of antibiotics, including quinolones and the third generation of cephalosporins (Guo et al. 2019). It is important to note that none of the isolates in this study were resistant to carbapenems (imipenem and meropenem). Until recently, carbapenems, such as meropenem, imipenem, ertapenem, and doripenem, were the antibi-otics of last choice for treatments of MDR pathogenic bacteria (Osei et al. 2016). As a result, prescribers should not abuse these antibiotics to avoid the emergence and development of resistances. In our study, the *E. coli* isolates also showed low resistance to ciprofloxacin (8.4%). This finding is of public health significance, as they are critically important for the treatment of serious human infections. In developed countries, the use of fluoroquinolones has been banned for use in animal husbandry; therefore, *E. coli* isolated from this source showed very little resistance to these antibiotics (Boerlin et al. 2005).

3.2 Profile of MDR *E. coli* isolates

Our study revealed a moderate percentage of MDR strains among *E. coli* (26.5%). MDR strains are isolates resistant to 3 or more different classes of antibiotics (Magiorakos et al. 2012). Previous studies have reported that multidrug resistance is common in poultry and other food animals (Li et al. 2020a; Abatcha et al. 2018; Adzitey et al. 2020). The presence of MDR bacteria in foods (meat, vegetables, fruit and RTE foods) is a public health concern since they can be transmitted to humans directly or indirectly by eating contaminated RTE foods. The MDR bacteria identified in the present study may result from environmental contamination or transmission by food handlers due to poor personal hygiene and inadequate sanitation in the processing plant. Therefore, the microbiological quality of food should be monitored to ensure public health safety. As shown in Table 3, this study also revealed that the multiple antibiotic resistance (MAR) index ranged from 0.13 (resistant to 2 antibiotics) to 0.47 (resistant to 7 antibiotics). 19 resistant isolates (18.7%) had a MAR index > 0.2. Bacteria that have a MAR index > 0.2 originate from a high-risk source of contamination where antibiotics or growth promoters are frequently used (Krumperman 1983). Overall, the extensive use by humans and livestock production, particularly in poultry, may have led to the rise of resistance (Rajaei et al. 2021). Therefore, One Health strategies which require multidisciplinary collaborations, adequate surveillance systems, and strong laboratory capacity are needed in order to reduce antibiotic misuse.

3.3 PCR-based detection of antimicrobial resistance genes

The result of PCR screening for the presence of resistance genes among phenotypically resistant *E. coli* isolates is shown in Table 4. Among drug resistant isolates, PCR tests detected 9 genes (bla_{TEM}, bla_{SHV}, *temB, tet(A), tet(B), aadA, GyrA, sul1, and sul2*). In the present study, detection of beta-lactamase genes among ampicillin resistant isolates revealed the predominance of bla_{TEM} and bla_{SHV} genes (37.3% each), followed by the *temB* genes (33.3%). Beta-lactamase, which deactivates beta-lactam antibiotics by hydrolysis of the beta-lactam ring, is one of the most significant enzymes implicated in bacterial resistance to antibiotics (Shaikh et al. 2015). Although numerous beta-lactamases have been identified, TEM and SHV are reported

Table 5 Distribution of antimicrobial resistance, class1 integrons among the 65 isolates resistant to at least 2 antimicrobials

Sample code	Isolate code	Resistance genes	Food Source	Antimicrobial pattern	Presence of Int1	Amplification of Variable regions
O212	238	*GyrA, temB*	Salad	AMP, TE, CIP, C	+	+
O173	239	*GyrA*	Sandwich	CIP, C	+	
SP8	242	*GyrA*	Sandwich	CIP, C	+	
SP16	245	*GyrA,* bla_{TEM}	Sandwich	AMP, FOX, CIP, C	+	+
O206	246	*GyrA* bla_{TEM}	Dairy food	AMP, FOX, TE, SXT, C	+	
O207	248	*aadA, GyrA,* bla_{TEM}*, tetA, temB*	Dairy food	AMP, FOX, TE, CN, CIP, C	+	+
O171	249	*GyrA,* bla_{SHV}*, tetA*	Sandwich	AMP, TE, CIP	+	
O205	250	*aadA, GyrA, tetA*	Dairy food	AMP, TE, NA, CN, AK	+	+
U29EL	251	bla_{TEM}*, tetA*	Salad	AMP, TE	+	
PO5	252	*aadA, GyrA,* bla_{TEM}*,* bla_{SHV}	Salad	AMP, TE, CN, CIP	+	+
U18FP	253		Dairy food	AMP, FOX, TE	+	
YBF	254	*GyrA,* bla_{SHV}*, tetA*	Dairy food	CN, CIP	+	
PK5	256		Salad	AUG, AMP, FOX	+	+
O194	257	*aadA,* bla_{TEM}*, temB*	Dairy food	AMP, CN	+	
O170	261	*aadA, GyrA,* bla_{TEM}*, tetA, temB*	Sandwich	AMP, TE, CN, CIP	+	+
O168	263	*GyrA, tetA, tetB, temB*	Sandwich	AMP, TE, CIP, SXT	+	
O83	266	*tetA*	Salad	AMP, TE	+	
O82/PR10	163	*tetA, sul2*	Dairy food	TE, SXT	+	
O85/U28	270	*GyrA, sul1*	Dairy food	TE, NA, SXT	+	
O59/ PF10	273	bla_{TEM}*, temB*	fish	FOX, TE	+	+
O57/ PF12	274	*aadA,* bla_{SHV}	Fish	AMP, TE, AK, SXT	+	
O58/PF7	275		Fish	CN, AK	+	+
O56PF5	276	*GyrA, tetA, sul1*	Fish	TE, NA, SXT	+	
0055/PF1	277		Fish	TE, CN	+	
O60/PF14	278	bla_{SHV}*, tetA, sul1, sul2, temB*	Fish	AMP, TE, SXT	+	+
M5	279		Sesame	AUG, AMP, FOX	+	
M1	280	*GyrA, tetB*	Sesame	AUG, AMP, FOX, TE, NA	+	
M10	281	*GyrA*	Sesame	AUG, AMP, FOX, NA	+	+
M9	282	*GyrA,* bla_{TEM}*, tetB, temB*	Sesame	AMP, TE, NA, SXT	+	
M4	283	*GyrA,* bla_{SHV}	Sesame	AUG, AMP, FOX, NA	+	+
M3	284		Sesame	AMP, FOX	+	
M6	285	*sul1*	Sesame	AMP, TE, SXT	+	+
ET-42	162	*GyrA*	Sesame	FOX, NA	+	
PK5/O99	128	*GyrA*	Salad	AUG, AMP, FOX, NA	+	+
O85JI	289	*sul1*	Sesame	TE, SXT	+	+
O231	291		Dairy food	AMP, TE	+	
P03(01/6)	292	bla_{SHV}	Dairy food	AUG, AMP, FOX, CIP	+	
PK1/0098	146	*GyrA,* bla_{TEM}	Salad	AUG, AMP, FOX, NA	+	+
U26SM	313	*aadA,* bla_{TEM}*, tetA*	Salad	AUG, AMP, FOX, CN	+	
O87	137	*GyrA*	Sesame	NA, CN	+	
91/2684	294		Sesame	NA, CN	+	
O420	295	*GyrA,* bla_{SHV}*, sul1*	Sandwich	FOX, TE, NA, CN, CIP, SXT, C	+	+
ES13	122		Sandwich	AM, TE, SXT	+	+
O49	296	bla_{TEM}	Salad	AUG, AMP	+	
PB2U21	314	bla_{TEM}*, tetA*	Sandwich	AUG, AMP, TE	+	
EC 018	298		Fruit juice	AMP, C	+	
EC 019	299	*sul, temB*	Sandwich	AMP, FOX, SXT, C	+	
KP6/24	300	bla_{SHV}	Dairy food	AUG, AMP	+	
EC 020/1312	302	bla_{TEM}*, temB*	Salad	AMP, FOX, C	+	
EC MHo2	303		Dairy food	AMP, TE	+	

Table 5 (continued)

Sample code	Isolate code	Resistance genes	Food Source	Antimicrobial pattern	Presence of Int1	Amplification of Variable regions
O1813/1	307		Dairy food	AUG, AMP, FOX, TE	+	+
O20/134	309	*bla_{SHV}*, *bla_{TEM}*, *temB*	Dairy food	AMP, C	+	
ES24	310	*tetA, tetB*	Lettuce	TE, CN, C	+	
ES16	311	*aadA, tetA, temB*	Lettuce	AUG, AMP, FOX, TE, CN	+	
ES37	117	*bla_{SHV}*, *tetA, temB*	Lettuce	AUG, AMP, TE, SXT, C	+	+
ES19	96	*bla_{SHV}*	Lettuce	AUG, AMP, TE	+	
ES41	105		Lettuce	AUG, AMP	+	
ECE	101	*GyrA, bla_{TEM}*	Lettuce	FOX, NA	+	
EP2B1	190	*tetA sul1*	Lettuce	AUG, AMP, TE, SXT	+	+
EPE	114	*GyrA, bla_{SHV}*	Lettuce	AUG, AMP, NA	+	
EB1	204	*GyrA, bla_{TEM}*, *tetA, tetB, sul2 temB*	Lettuce	AUG, AMP, TE, NA, SXT	+	
O122	184	*bla_{SHV}*, *temB*	Lettuce	AUG, AMP, FOX, TE	+	
ES10	174	*tetA*	Lettuce	AUG, AMP, FOX, TE, SXT	+	
ES15	183	*bla_{SHV}*, *bla_{TEM}*, *tetA, temB*	Lettuce	AUG, AMP, FOX, TE	+	
ES17	203	*bla_{TEM}*, *sul2, temB*	Lettuce	AUG, AMP, TE, SXT	+	

to be the main causes of bacterial resistance to beta-lactam antibiotics (Hassani et al. 2022). All beta-lactamase genes detected during our work have been widely documented in the community, clinical isolates, and food-producing animals (Guo et al. 2019). The tetracycline resistance genes *tet(A)* and *tet(B)* were found in 46.2% and 17.3% of the isolates tested in this study, respectively. This finding supports previous research that identified *tet(A)* genes as the most common tetracycline resistance genes (Vuthy et al. 2017; Guo et al. 2019; Dissinviel et al. 2017; Abdelwahab et al. 2022). Currently, 30 different tetracycline resistance genes (*tet* genes) have been identified (Eliopoulos et al. 2003). All *tet* efflux genes encode membrane-associated energy-dependent proteins, which export tetracycline out of the cell. Among our isolates resistant to trimethoprim-sulfamethoxazole, 44.4% carried *sul1* genes, while 22.2% harbored *sul2* genes. These 2 genes that express highly resistant dihydropteroate synthases to sulfamethoxazole are carried by transposons and plasmids (Roberts 1996). However, almost 20 different resistance genes that express drug-insensitive dihydrofolate reductase are spread as cassettes in integrons, transposons, and plasmids (Nelson et al. 2019). In this study, 86% of *E. coli* resistant to quinolones carried the *GyrA* gene. Overexpression of naturally occurring efflux pumps, resistance encoded by the chromosome, mutations in molecular target DNA gyrase and topoisomerase IV, and resistance mediated by plasmids are molecular mechanisms of bacterial resistance to quinolone drugs (Abdelwahab et al. 2022). However, the most common mechanism of resistance to fluoroquinolones are mutations of target genes such as *GyrA*, *parE*, and *parC* that encode type II topoisomerases (Guo et al. 2019; O'Bryan et al. 2018).

In summary, it is worth noting that several genes can be involved in AMR. In this study, we did not evaluate the entire suite of resistance genes. Therefore, some resistant isolates did not carry any of the AMR genes tested, indicating that other AMR genes may be present or there are other novel genetic resistant determinants (Abdelwahab et al. 2022). Therefore, isolates that were phenotypically resistant but negative for PCR should be screened using novel techniques such as metagenomic analysis based on high-throughput sequencing (HTS) to provide more comprehensive information on their antibiotic resistomes (Li et al. 2020b).

3.4 PCR-based detection of class 1 integrons genes

The present study has shown the presence of MDR among *E. coli* isolates, as mentioned above, suggesting the existence of mobile genetic elements such as integrons, plasmids, and transposons (Deng et al. 2015). Of these, integrons play a central role in the spread of ARGs among gram-negative bacteria (Kaushik et al. 2018). Integrons capture gene cassettes using an integron-integrase and then express cassettes using an integron encoded promoter. There are many types of integrons based on the integrase gene (*intI*), but most of the integrons found in clinical isolates belong to Class 1 (Deng et al. 2015). Table 5 shows the distribution of antimicrobial resistance, class-1 integrons in the 65 isolates resistant to at least 2 antimicrobials. All the isolates were positive for class 1 integrons, which is consistent with

previous findings (Zhang et al. 2019; Malek et al. 2015). Particularly in Burkina Faso, class 1 integrons were found in 65% of *Salmonella* isolated from environment and diarrhea stool samples (Somda et al. 2021). Subsequently, strains harboring *intI* genes were elaborated for the amplification of variable regions (VRs). The occurrence of VRs within class 1, integron positive isolates were 32.3% (21/65 strains). The integrons that did not carry gene cassettes are called empty integrons and can have the potential to rapidly convert themselves into MDR strains (Mohamed et al. 2020; Fang et al. 2019).

3.5 Limitations

This study has some limitations due to a lack of financial resources. Firstly, appropriate tests were not done to confirm the PCR product identity. The confirmation tests could be: (i) DNA sequencing of the PCR product; (ii) hybridization of the PCR product with specific DNA probes; (iii) or restriction analysis of the PCR product. Secondly, we have focused exclusively on the antimicrobial resistance in *E. coli* isolates, and the pathogenicity of the collected *E. coli* was not assessed.

4 Conclusion

This study generated preliminary data on the resistance of *E. coli* identified in the food chain of Burkina Faso. Phenotypic characterization revealed resistance to tetracycline, ampicillin, cefoxitin, gentamicin, clavulanic acid, and sulfamethoxazole/trimethoprim. In addition, isolates displayed multidrug resistance characteristics and revealed possible molecular resistance mechanisms. Therefore, a prospective study with a well-designed geographic distribution of the samples is required.

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Declarations

Ethical approval Not required.

Competing interests The authors declare no conflict of interest with this research.

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