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Prevalence and Antimicrobial Resistance of *Salmonella enterica* Isolated from Chicken and Guinea Fowl in Burkina Faso

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Abstract: Consumption of contaminated poultry and poultry products by Salmonella is a public health problem worldwide. The aim of this study was to determine the prevalence, serotypes and antibiotic susceptibility of *Salmonella* isolated from slaughtered poultry. A total of 563 intestine samples from slaughtered chickens (n= 283) and guinea fowl (n=280) were collected from 7 open markets in 2 urban and 2 rural areas of Burkina Faso. The samples were processed for the isolation and identification of associated *Salmonella* using microbiological standard methods. The suspected colonies were subjected to biochemical tests and serotyped by slide agglutination test according to Kauffman-White scheme. Antibiotic sensitivity patterns of *Salmonella* were also investigated using commonly used antibiotics. Of the 563 intestines samples, 139 (24.69%) isolates were recovered, with 59/283 (20.84%) isolates from chicken and 80/280 (28.57%) isolates from guinea fowl. The successful serotyping of 109/139 isolates revealed 9 serotypes namely Typhimurium, Kentucky, Ouakam, Brancaster, Hato, Kaapstad, Essen, Chester, and Derby. Five strains were untypable and 15 belong to different serogroups such as B, M, E, D, F, and O. The serotypes Brancaster, Chester, Derby, Hato, and Typhimurium were found in chicken and guinea fowl. *S.* Kaapstad was detected only on guinea fowl and *S.* Essen, Kentucky and Ouakam on chicken. Serotype Derby (38.84%), Chester (11.51%) and Hato (10.07%), Typhimurium (8.63%) were the most prevalent. Out of the 139 isolates, 100% show resistance to at least one antibiotic (Erythromycin), while, 50 (35.97%) were multi-resistant. High sensitivity of isolates was recorded for Chloramphenicol, Ciprofloxacin, Nalidixic acid, Cephalexin, Sulfamethoxazole–trimethoprim and Colistin Sulfate. The data confirm that poultry is a potential reservoir of *Salmonella*. This recommends good hygienic practices when producing poultry carcasses.

Keywords: *Salmonella* Serotypes, Antimicrobial Resistance, Chicken, Guinea Fowl, Burkina Faso

1. Introduction

Non-typhoidal *Salmonella* (NTS) is considered one of the most common causes of foodborne human infections worldwide [1]. More than 2610 *Salmonella enterica* serovars have been recognized worldwide, most of them being major causative agents of diseases in humans and animals, producing gastroenteritis and other acute infections [2].

Nontyphoidal *Salmonella* spp. is the primary bacterial pathogen causing foodborne illness and the leading cause of hospitalization among the top five foodborne pathogens in the United States [3]. According to food poisoning statistics from the Infectious Disease Surveillance Center in Japan, there were 93,444 bacterial foodborne illnesses between 1999 and 2002, and 32% of these cases were salmonellosis [4]. Unfortunately, in Sub-Saharan Africa, the foodborne diseases are more frequent with high morbidity and mortality but still underestimated because of the lack of foodborne pathogens surveillance system. However, the World Health Organisation estimated that the African region has the highest burden of foodborne diseases with more than 91 million cases and 137,000 deaths each year [5]. *Salmonella* has been reported to be the second most pathogen affecting foodborne illnesses in Burkina Faso [6, 7]. Poultry is an important reservoir of many zoonotically pathogens, mainly *Salmonella* and *Campylobacter* [8, 9]. Poultry meat can acquire *Salmonella* from intestinal contents, faecal material or from cross-contamination during slaughtering processes [10]. In Sub-Saharan African countries and particularly in Burkina Faso, there is an emergence of poultry farming and it's encouraged by the government for agricultural development, but this activity is dominated by artisanal technologies that lead to human and animal illnesses. In Burkina Faso it's characterized by a system of family farms dispersed in small production units. Traditional livestock farming is characterized by the natural breeding of poultry, rudimentary animal husbandry techniques and equipment, food and water supply, and veterinary health monitoring is virtually absent. Traditional poultry plays a major role in the quest for self-sufficiency and sustainability of food security and contributes to the religious, social and cultural livelihoods of the rural population [11]. In addition, traditional poultry is a source of income for poor farmers in rural areas, especially women, [11].

In recent years, there has been growing public health concern over the worldwide emergence of antibiotic-resistant strains of a number of pathogenic bacteria, including *Salmonella*. Although most cases of human salmonellosis are self-limiting and typically resolved in five to seven days without antimicrobial treatment, antibiotic therapy may be necessary for severe cases, extra-intestinal disease or immune-compromised patients [12]. In this case, resistant *Salmonella* strains are especially threatening because they may compromise the effective treatment of human salmonellosis.

In developing countries, the main factor which contributes to increase the development of antibiotic-resistant bacteria is the use of the same type of antibiotics in veterinary medicine for infection treatment as well as growth promoters and in human medicine for diseases treatment. For all the above, there is an urgent need to prevent human salmonellosis particularly in developing countries and that requires prior monitoring of *Salmonella* from animal origin. The aims of this study were to isolate, identify, serotyped and to determine the antimicrobial susceptibility of *Salmonella* enterica strains isolated from faecal samples of chicken and guinea fowl to obtain data to contribute to the control and to determine the dissemination of *Salmonella* serovars.

2. Material and Methods

2.1. Period and Samples Collection

From February to September 2016, 563 intestine samples from slaughtered chicken (n=283) and guinea fowl (n=280) were collected in seven markets in two cities and two villages. Samples were conditioned into sterile bags and placed at 4°C to the laboratory for microbiological analysis within six hours.

2.2. Samples Processing for Isolation of Salmonella

Samples were processed for *Salmonella* isolation and identification according to the International Organization for Standardization norm 6579-2017 [13]. For pre-enrichment and enrichment step, 10 g of cecal contents were homogenized in 90 mL of sterile buffered peptone water (Liofilchem, France) incubated at 37°C for 24 h and 1 mL was transferred into 10 mL of Muller-Kauffmann broth novobiocin tetrathionate (MKTTn) (OXOID, England) and 0.1 mL on MSRV agar (modified semi-solid agar medium of Rappaport- Vassiliadis) (OXOID, England), then, plates were incubated at 41°C for 24 h.

A loop full of culture from MKTTn enriched broth was also subcultured onto Xylose Lysine tergitol 4 (XLT4) and Xylose Lysine desoxycholate (XLD) agar plates respectively and incubated aerobically at 37°C for 24 h. The suspected *Salmonella* were transferred onto nutrient agar plates and subsequently subjected to pre-identification tests: catalase and peroxidase production, the oxidation/fermentation test, production of indol and H_2S, and fermentation of glucose, lactose and urea [14].

Salmonella strains were confirmed with the API20E Kit (Biomerieux, Marcy l'Etoile, France). The strains were stored in Broth brain heart supplemented with 30% of glycerol at -20°C for further characterization.

2.3. Serotyping and Antimicrobial Susceptibility Testing of Salmonella Isolates

The confirmed strains were serotyped by slide agglutination test according to Kauffman-White scheme [15] in the laboratory (Anses, Hygiene and Quality of Poultry and Pig Products Unit, France).

The antimicrobial susceptibility tests were performed on Mueller Hinton agar using the disk diffusion method [16]. Interpretation of MICs and zone diameters was done according to the European Committee on Antimicrobial Susceptibility Testing [17] and the strains with intermediate resistance to any antibiotic did not count as resistant. The antimicrobials tested were gentamicin (GEN; 10 µg), Streptomycin (STR; 10 µg), Aztreonam (AZT; 30 µg), Ticarcillin (TC; 75 µg), Imipenem (IPM; 10 µg), Amoxicillin–clavulanic-acid (AMC; 30 µg), Cephalexin (CL; 30 µg), Sulfamethoxazole-trimethoprim (SXT; 25 µg),

Erythromycin (E; 15 µg), Colistin Sulfate (10 µg), Chloramphenicol (C; 30 µg), Cefotaxime (CTX; 5 µg), Ceftriaxone (CTR; 30 µg), Ciprofloxacin (CIP; 5 µg), Nalidixic acid (NA; 30 µg), Tetracycline (TE; 30 µg) (Liofilchem, France).

3. Results

3.1. Prevalence and Serotypes Distribution

Salmonella was detected from 139/563 (24.69%), with 59/283 (20.84%) from chicken and 80/280 (28.57%) from guinea fowl (Table 1).

Table 1. *Prevalence of Salmonella in local chicken and Guinea fowl from differents localisations.*

localities		Local chicken	Guinea fowl
Urban	Ouagadougou	31/128 (23.44%)	27/126 (21.43%)
	Bobo Dioulasso	18/130 (13.08%)	28/127 (22.05%)
Rural	Poa	4/13 (30.77%)	4/12 (33.33%)
	Djibasso	6/13 (46.15%)	8/14 (57.14%)
Total per species		59/284(20.07%)	80/279(24.01%)
Total		124/563(57.11%)	

Among the 139 strains isolated, 109 of them could be serotyped and they were found to belong to 9 serotypes namely Typhimurium, Kentucky, Ouakam, Brancaster, Hato, Kaapstad, Essen, Chester, and Derby. Five strains were untypable and 15 belong to different serogroups such as B, M, E, D, F, and O. Serotypes Brancaster, Chester, Derby, Hato, and Typhimurium were present in chicken and guinea fowl. S. Kaapstad was only found on guinea fowl whereas S. Essen, Kentucky and Ouakam were detected on chicken Serotype Derby, Chester, Hato and Typhimurium were the most prevalent.

3.2. Antimicrobial Susceptibility Test

Antimicrobial susceptibility testing of the isolates (chicken and guinea fowl) revealed absolute resistance to Erythromycin (100%), while 50 (35.97%) were multiresistant; More than half of the isolates showed resistance to Amoxicillin-clavulanic acid (63.33% of chicken isolates and 60.97% of guinea fowl isolates) followed by Ticarcillin (60% of chicken isolates and 51.21% of guinea fowl isolates). The high sensitivity of isolates was recorded for Chloramphenicol, Ciprofloxacin, Nalidixic acid, Cephalexin, Sulfamethoxazole–trimethoprim and Colistin sulfate (Tables 2 and 3).

Table 2. *Details of different serotypes of Salmonella enterica obtained from different species of poultry.*

Salmonella serovars	Origin		Total
	guinea fowl	chicken	
S. Brancaster	5 (6.25)	1 (1.70)	6 (4.31)
S. Chester	6 (7.5)	10 (16.95)	16 (11.51)
S. Kaapstad	4 (5.00)	-	4 (2.87)
S. Derby	36 (45.00)	18 (30.50)	54 (38.84)
S. Essen	-	1 (1.70)	1 (0.72)
S. Hato	6 (7.50)	8 (13.55)	14 (10.07)
S. Kentucky	-	1 (1.70)	1 (0.72)
S. Ouakam	-	1 (1.70)	1 (0.72)
S. Typhimurium	11 (13.75)	1 (1.70)	12 (8.63)
S. Group B	2 (2.50)	1 (1.70)	3 (2.15)
S. Group O	-	1 (1.70)	1 (0.72)
S. Group E	2 (2.50)	2 (3.38)	4 (2.87)
S. Group F	1 (1.25)	3 (5.08)	4 (2.87)
S. Group M	-	1 (1.70)	1 (0.72)
S. Group D	2 (2.50)	1 (1.70)	3 (2.15)
Untypable	5 (6.25)	9 (15.25)	14 (10.07)
Total	80 (28.57%)	59 (20.84%)	139 (24.69%)

Table 3. *Antibiogram results of Salmonella isolates from chicken (n= 59).*

Antibiotics	Resistant (n(%))	%intermediate	% sensible
AZT (30µg)	8 (13.33%)	29 (48.33%)	23(38.33%)
AMC(30 µg)	38 (63.33%)	0	22(36.66%)
TC (75µg)	36 (60%)	0	24(40%)
IPM (10µg)	0	16 (26.66%)	44(73.33%)
CL (30µg)	2 (3.33%)	0	58(96.66%)
CTR (30µg)	3 (5%)	14 (23.33%)	43(71.66%)
CTX (5µg)	5 (8.33%)	12 (20%)	43(71.66%)
S (10µg)	6 (10%)	31 (51.66)	23(38.33%)
GEN (10µg)	7 (11.66%)	14 (23.33%)	39(65%)
C (30µg)	1 (1.66%)	0	59(98.33%)
TE (30µg)	19 (31.66)	12 (20%)	29(43.33%)
Na (30µg)	0	1 (1.66)	59(98.33%)
CIP (5µg)	2 (3.33%)	21 (35%)	37 (61.66%)
SXT (25µg)	5 (8.33%)	0	55 (91.66%)
CS (10µg)	14 (23.33%)	0	46(76.66%)

Gentamicin: GEN, Streptomycin: STR, Aztreonam: AZT, Ticarcillin: TC, Imipenem: IPM, Amoxicillin–clavulanic-acid: AMC, Cephalexin: CL, Sulfamethoxazole–trimethoprim: SXT, Colistin Sulfat: Cs, Chloramphenicol: C, Cefotaxim: CTX, Ceftriaxon: CTR, Ciprofloxacin: CIP, Nalidixic acid: NA, Tetracycline: TE

Susceptibility to other antimicrobials was variable 22 strains show resistance to 3 or 4 antibiotics and 17 show resistances to 5 or more antibiotics (Tables 4 and 5).

Table 4. *Antibiograms results of Salmonella isolates from guinea fowl (n = 80).*

Antibiotics	Resistant	Intermediate	Sensitive
AZT (30µg)	15 (18.29)	32 (32.02)	33(41.25%)
AMC (30 µg)	50 (60.97)	0	30 (37.5%)
TC (75µg)	42 (51.21%)	0	38 (47.5%)
IPM (10µg)	1 (1.21%)	19 (23.17%)	60(75%)
CL (30µg)	5 (6.09%)	0	75(93.75%)
CTR (30µg)	3 (3.65%)	30 (36.58%)	47(58.75%)
CTX (5µg)	27 (32.92%)	18 (21.95%)	45(56.25%)
S (10µg)	10 (12.19%)	35 (42.68%)	35(43.75%)
GEN (10µg)	6 (7.31%)	12 (14.63%)	62(77.5%)
C (30µg)	2 (2.43%)	0	78(97.5%)
TE (30µg)	29 (35.36%)	15 (18.29%)	36(45%)
Na (30µg)	1 (1.21%)	5 (6.09%)	74(92.5%)
CIP (5µg)	8 (9.75%)	12 (14.63%)	60(75%)
SXT (25µg)	1 (1.2%)	0	79(98.75%)
CS (10µg)	12 (14.63%)	0	68(85%)

Gentamicin: GEN, Streptomycin: STR, Aztreonam: AZT, Ticarcillin: TC, Imipenem: IPM, Amoxicillin–clavulanic-acid: AMC, Cephalexin: CL, Sulfamethoxazole–trimethoprim: SXT, Colistin Sulfat: Cs, Chloramphenicol: C, Cefotaxim: CTX, Ceftriaxon: CTR, Ciprofloxacin: CIP, Nalidixic acid: NA, Tetracycline: TE

Table 5. *Multiple antimicrobial resistance patterns of Salmonella serovars.*

Antimicrobial resistance pattern*	**Number of resistant *Salmonella* serovars**										
	Brancaster (1)	**Chester (10)**	**Derby (18)**	**Essen (1)**	**Hato (5)**	**Kentucky (1)**	**Ouakam (1)**	**Group Z (3)**	**Group B (1)**	**untypable (9)**	**Total (50)**
E- AUG			3							1	4
E- TC		2		1	1						4
E- TE			2								2
E- AUG- TC		1			1		1	1		1	5
E- AUG- TE			4								4
E- TC- CL		1									1
E- TC- CS										1	1
E- AUG- TC- CTX			1					1		1	3
E- AUG- TC- TE			3								3
E- AUG- AZT- TE			1								1
E- AUG- CTR- CTX										1	1
E- AUG- CTX- CS										1	1
E- TC- CTX- CS										1	1
E- S- TE- SXT	1										1
E- AUG- AZT- TC- CRO									1		1
E- AUG- TC- CTX- CS			1								1
E- AUG- TC- SXT- CS		1									1
E- AUG- TC- S- TE					1						1
E- AUG- TC- GEN- CS		1									1
E- AUG- S- TE- SXT								1			1
E- TC- CL- TE- CS			1								1
E- TC- CTX- GEN- CS			1								1
E- AUG- TC- CRO- GEN- CS		1									1
E- AUG- AZT- TC- CTX- C										1	1
E- AUG- TC- S- TE- SXT					1						1
E- TC- S- GEN- TE- SXT						1					1
E- AUG- AZT- TC- CTX- CIP- CS					1						1
E- AUG- AZT- TC- CTX- GEN- CS		2									2
E- AUG- TC- CTR- GEN- TE- CIP		1									1
E- AUG- AZT-TC- CTX- TE- SXT- CS										1	1
E- AUG- AZT- TC- CTX- S- TE- CS			1								1
Resistance to 3 - 4 antibiotics	1	2	9	0	1	0	1	2	0	6	22
Resistance to 5 or more antibiotics	0	6	3	0	3	1	0	1	1	2	17

Gentamicin: GEN, Streptomycin: STR, Aztreonam: AZT, Ticarcillin: TC, Imipenem: IPM, Amoxicillin–clavulanic-acid: AMC, Cephalexin: CL, Sulfamethoxazole–trimethoprim: SXT, Colistin Sulfat: Cs, Chloramphenicol: C, Cefotaxim: CTX, Ceftriaxon: CTR, Ciprofloxacin: CIP, Nalidixic acid: NA, Tetracycline: TE

4. Discussion

Salmonella infections constitute a public health problem in low-income countries because of the weakness of control measures and not following good food safety practices.

In the present study, *Salmonella* was detected in 24.69% of all the poultry intestines samples analyzed with 20.45% in slaughtered chicken intestines and 22.26% in slaughtered guinea fowl intestines. In contrast, a high prevalence of *Salmonella* in slaughtered poultry intestines were detected in the studies conducted by Kagambega *et al*. (2013) (55%) [18] and 2018 (52.42%) [9] in Burkina Faso; Andoh et al. (2016) in Ghana (47%) [19] and Bai *et al*. (2015) in China (45.2%) [20]. This difference could be explained by sampling conditions, isolation method and period of sampling. However, the lowest prevalence of *Salmonella* in poultry was found in Egypt (17%) by Ammar *et al.,* 2016 [21] and in India (6.31%) by Mir *et al*. (2015) [22].

The present study shows a different prevalence of salmonella in chicken (20.45%) and guinea fowl (22.26%). The rate of *Salmonella* contamination in chicken found in our study is high compared to the result found by Parvej *et al.,* 2016 in chicken (7.33%) from Bangladesh [23]. However, a high prevalence (61.1%) of *Salmonella* in chicken was found in Vietnam by Tu *et al.,* 2014 [24]. By contrast, a very low prevalence of *Salmonella* was found in Benin from guinea fowl intestines (6.4%) by Boko *et al*., 2013 [25]. These differences could be explained by the difference in types of poultry species and farming conditions.

The prevalence of *Salmonella* in slaughtered poultry including chicken and guinea fowl intestines in this study is worrying because these *Salmonella* strains can contaminate poultry carcasses if the hygienic practices failed during evisceration. Moreover, most of the poultry carcasses sellers are doing the entire steps of poultry processing in the same place (slaughtering, scalding, plucking, evisceration) and carcasses are stored at ambient temperature for selling without any cooling system, which conditions will increase surely the multiplication of the pathogen in contaminated carcasses [6]. The finding in this study shows a high risk for consumer health if some cross-contamination occurred during carcasses preparation. It is well documented that *Salmonella* infections in humans have been associated with raw chicken [26, 27].

Salmonella serotypes Brancaster, Chester, Derby, Essen, Hato, Kaapstad, Kentucky, Ouakam and Typhimurium were identified in the present study, with Derby being the most prevalent serotype in chicken and Guinea fowl. Similar results were found by Kagambèga *et al*. (2013) [18] in poultry intestines, where *Salmonella* Derby was the most prevalent serotype found in poultry. In contrast, López-Martín *et al*. (2016) [28] reported *Salmonella* Enteritidis as a predominant serotype in chicken and *Salmonella* Typhimurium plus *Salmonella* Derby and *Salmonella* Enteritidis as predominant serotypes in pigs. *Salmonella* Typhimurium was most prevalent in guinea fowl compare to chicken intestines. This finding shows that guinea fowl could be a principal reservoir for *Salmonella* Typhimurium. The nine *Salmonella* serotypes identified in this study have been isolated in patients with diarrhea in Burkina Faso [29, 30]. These findings show that chicken and/or guinea fowl can be considered as the main reservoirs for *Salmonella* and constitutes a potential source for human salmonellosis in Burkina Faso. This hypothesis is true since, there is a lack of a good sanitation and water quality management system in the country, particularly in rural areas, where many people living with poultry running freely in the household. Moreover, there is no abattoir for poultry in Burkina Faso, and poultry meat sellers are slaughtering in open market places without any veterinary control. Therefore, this study shows a serious need for quality checks and surveillance programs in order to reduce the risk of salmonellosis.

The antibiotics susceptibility results in this study highlighted the higher resistance of the isolates to Erythromycin (100 % of chicken and guinea fowl isolates) followed by Amoxicillin-clavulanic acid (63.33% of chicken isolates and 60.97% of guinea fowl isolates), Ticarcillin (60% of chicken isolates and 51.26% of guinea fowl isolates) and Tetracycline (31.66% of chicken isolates and 35.36% of guinea fowl isolates). These results are similar to those of other studies [31, 32]. This finding confirmed that in poultry, these drugs are used either for disease treatment or as growth promoters without prescription because they are cheap and easily affordable. In addition, the feed is leading to the development of resistance in the enteric bacterial flora of poultry antibiotic *Salmonella* However, lower resistance rates to Chloramphenicol (2.43% for chicken isolates; 1.66% for guinea fowl isolates); Ciprofloxacin (9.75% for chicken isolates, 3.33% for guinea fowl isolates), Imipenem (0% for chicken isolates; 1.21% for guinea fowl isolates); Sulfamethoxazole-trimethoprim (8.33% for chicken isolates; 1.21% for guinea fowl isolates) and nalidixic acid (0% for chicken isolates; 1.21% for guinea fowl isolates) were observed. In contrast, high resistance rates to Chloramphenicol (27.2%), Nalidixic acid (28.8%) was reported from poultry isolates by Tu *et al.,* 2014 in Vietnam [24]; Gharieb *et al.,* 2015 also reported higher resistance rates to chloramphenicol (50%) and ciprofloxacin (30%) from poultry *Salmonella* in Egypt [31]. This finding is worrying because resistance to the third generation antibiotics in a strain isolated in poultry means that these drugs are also used by veterinarians and their effectiveness will decrease in the treatment of human salmonellosis.

In the present study, 35.97% of the *Salmonella* isolates show multiple resistance to the tested antibiotics with 31 different resistances patterns lowest prevalence of MDR *Salmonella* (30.1%) has been reported by Tu *et al.,* 2014 [24]. Many serotypes were resistant to 4 or 8 antibiotics in this study, one Kentucky were resistant to six antibiotics (E-TC- S- GEN- TE- SXT), three Chester resistant to seven antibiotics (E- AUG- TC- CTR- GEN- TE- CIP) one Derby and one *Salmonella* spp were found to be resistant to eight antibiotics (E- AUG- AZT- TC- CTX- S- TE- CS). These results are nearly similar to those of other studies [33, 34], reflecting the use of antibiotics in animal husbandry. Several

studies demonstrated that the increase of antimicrobial resistance among *Salmonella* strains in recent years can be attributed to the selection pressure created by the inappropriate application of antibiotics in veterinary and human medicine [18, 22]. MDR *Salmonella* Kentucky was isolated from chicken in the present study. This finding corroborates with the report of USDA and FDA where *Salmonella* Kentucky has been the most common serotype isolated from chickens and Chicken meat [35, 36]. A highly resistant clone of *Salmonella* Kentucky (MLST type ST198), has been reported to be isolated in Canada and in Europe in travelers returning from Asia and Africa [37]. MDR *Salmonella* has been identified as an emerging pathogen causing invasive bloodstream infections, especially in sub-Saharan Africa [38]. The emergence of multidrug-resistant (MDR) *Salmonella* strains constitutes a public health risk and potentially affects the efficacy of drug treatment in humans. The present study shows the urgent need to control the use of antibiotics in veterinary and human medicine to limit the spreading of MDR *Salmonella* strains. The *Salmonella* Typhimurium isolated in this study was resistant to one antibiotic (erythromycin). This is in contrast to the result found by Kagambega *et al.,* 2013 [18] who found that all *Salmonella* Typhimurium isolated from slaughtered poultry were Penta-resistant with the same sequence type ST313. Highly multidrug-resistant *Salmonella* Typhimurium was also reported in chicken by many authors [39, 33]. The finding in this study could be explained by the fact that there is an emergence of a new *Salmonella* Typhimurium clone among poultry species.

5. Conclusion

In conclusion, the data presented here indicate that chicken and guinea fowl are reservoirs of antibiotic-resistant *Salmonella*. There is potential for these antibiotic-resistant bacteria to be transferred to humans through contaminated poultry and poultry product*s Salmonella* not only poses a serious threat to public health but also causes huge economic losses by generating mortality and morbidity to the poultry industry. Multidrug resistance of *Salmonella* is a public health problem and there is an urgent need to reinforce the surveillance of the use of antibiotics by farmers, veterinarians, and physician*s*. Therefore, the continued development of methods to reduce the risk of foodborne pathogens in poultry is critical.

Ethical Considerations

Permission to conduct this study was obtained from the poultry carcasses sellers and the study protocol was approved by the Ethical Committee of Burkina Faso.

Competing Interests

The authors declare that they have no competing interests.

Authors' Contributions

CB carried out strain isolation and characterization, AK and CB drafted the manuscript, NB and MC supervised and participated in writing the manuscript. All authors read, commented on and approved of the final manuscript.

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