GSC Biological and Pharmaceutical Sciences
eISSN: 2581-3250 CODEN (USA): GBPSC2
Cross Ref DOI: 10.30574/gscbps
Journal homepage: https://gsconlinepress.com/journals/gscbps/

(RESEARCH ARTICLE)

Check for updates

Identification and characterization of Shiga toxin–producing and enteropathogenic *Escherichia coli* serotypes in chicken scalding tanks in Bobo-Dioulasso, Burkina Faso

Sonagnon H. S. Kouhounde [1, *], T. Cédric A. R. Sanou [2], Emmanuel Gozoua [3], Namwin Siourimè Somda [4], Mamoudou H. Dicko [5] and Michel K. Gomgnimbou [2]

[1] *Laboratory of Applied Biological Sciences, New Dawn University, 01 BP 234 Bobo-Dioulasso 01, Burkina Faso.*
[2] *Higher Institute of Health Sciences (INSSA), Nazi Boni University, Molecular Biology Laboratory, Muraz Center, Bobo Dioulasso, Burkina Faso.*
[3] *Unité de Formation et de Recherche en Sciences de la Mer, Université de San-Pédro, Côte d'Ivoire.*
[4] *Centre National de la Recherche Scientifique et Technologique (CNRST), IRSAT, Département Technologie Alimentaire (DTA), Bobo-Dioulasso, Burkina Faso.*
[5] *Laboratory of Biochemistry, Biotechnology, Food Technology, and Nutrition, Joseph KI-ZERBO University, 03 BP 7021 Ouagadougou, Burkina Faso.*

GSC Biological and Pharmaceutical Sciences, 2026, 35(03), 027-035

Publication history: Received on 21 April 2026; revised on 04 June 2026; accepted on 06 June 2026

Article DOI: https://doi.org/10.30574/gscbps.2026.35.3.0139

Abstract

Pathogenic strains of Escherichia coli, especially Shiga toxin–producing E. coli (STEC) and enteropathogenic E. coli (EPEC), are primary causes of human gastrointestinal infections and linked to serious clinical outcomes, such as bloody diarrhea and hemolytic uremic syndrome. Their presence in food production settings represents a significant public health issue. This study aimed to characterise STEC and EPEC serotypes isolated from scalding tanks in poultry markets in Bobo-Dioulasso, Burkina Faso. A prospective descriptive study was carried out from May to December 2024. Samples were gathered from various poultry markets and enriched in peptone water before being inoculated onto VRBL agar. Bacterial identification followed standard microbiological procedures. Antibiotic susceptibility testing was conducted in accordance with the 2024 CASFM guidelines. PCR targeting the 16S rRNA gene confirmed the isolates' affiliation with the genus Escherichia, and three virulence genes (*eae*A, *stx*1, *stx*2) were screened using conventional PCR. Of the 33 samples collected, 21 (63.63%) were culture positive. Among these, two isolates carried virulence genes characteristic of EPEC and STEC. A high level of antibiotic resistance was observed, especially at the Yéguéré site, where the multiple-antibiotic resistance index was 0.75. These findings highlight the importance of strengthening hygiene practices and surveillance strategies in poultry markets to reduce the risk of foodborne infections.

Keywords: Burkina Faso; STEC; EPEC; Scalding Water; Chicken; Virulence Genes

1. Introduction

Poultry farming plays a significant role in the livelihoods of people in Burkina Faso, especially in rural areas. The sale of eggs and, more importantly, chickens makes a substantial contribution to rural households' financial needs [1], [2]. The income generated by the poultry sector is spent directly or indirectly on school fees and healthcare. About 30% of the income from poultry sales is invested in health, 22% in children's education, and 21% on household food expenses [3]. Furthermore, women play a vital role in this sector, helping to empower rural communities and support poverty alleviation and better household food security [4], [5].

* Corresponding author: Sonagnon H. S. Kouhounde

Apart from its economic significance, chicken meat is a vital source of essential proteins, readily accessible to all social strata. The high daily consumption of chicken estimated at 80,000 and 50,000 birds in the cities of Ouagadougou and Bobo-Dioulasso, respectively demonstrates its crucial role in the daily diet of Burkinabè populations [6].

Additionally, studies conducted in Mexico and Korea have shown that foods of animal origin can act as reservoirs for pathogenic agents [7], [8]. A study by Heredia & García (2018) found that Staphylococcus aureus, Salmonella spp., Campylobacter spp., Listeria monocytogenes, and Escherichia coli were the most common microorganisms involved in foodborne illnesses linked to animal-derived products [7]. According to the World Health Organisation, each year 600 million people fall ill after eating contaminated food, with 420,000 deaths—including 125,000 children under five [9]. Recent studies carried out in markets within the city of Ouagadougou have aimed to determine the prevalence of Salmonella spp. and Escherichia coli in raw meat sold there. The results revealed a 100% presence of E. coli across all types of meat available. [10].

Escherichia coli is a bacterium belonging to the Enterobacteriaceae family and is a common inhabitant of the intestinal microbiota of humans and warmblooded animals [11]. However, Escherichia coli is a bacterium that belongs to the family Enterobacteriaceae and is a common part of the intestinal microbiota in humans and warm-blooded animals. Nevertheless, some strains are linked to serious diseases, such as Shiga toxin–producing E. coli (STEC) and enteropathogenic E. coli (EPEC) [12]. Their detection depends on traditional identification methods, including microbiological, biochemical, and molecular techniques. Strains linked to serious illnesses, like STEC and EPEC, are currently being studied using assays. Several studies have reported the presence of STEC and EPEC strains in chicken carcasses; however, very limited data are available regarding their presence in scalding waters used during poultry processing. This present study was therefore designed with the purpose to "Identify and characterise Shiga toxin–producing and enteropathogenic *Escherichia coli* serotypes isolated from scalding tanks in poultry markets in the city of Bobo-Dioulasso, Burkina Faso."

2. Materials and methods

2.1. Study Type

This was a prospective, descriptive study conducted at Aube Nouvelle University and the MURAZ Research Centre, affiliated with the National Centre of Scientific and Technological Research.

2.2. Sites selection and Sampling

A random sampling strategy was employed to collect samples from eight (08) poultry markets in the city, which were selected as sampling sites because they are known as the principal markets for poultry selling. Additionally, these sites were selected for their high customer traffic, as they are the most frequented locations for chicken sales in Bobo-Dioulasso. During the first sampling round, two samples were collected from each site. Only those samples showing positive microbiological cultures were retained for subsequent analysis. Sites yielding exclusively negative results were excluded from further sampling. Targeted sampling then continued, with additional samples collected solely from the positive sites up to the fourth sampling round. This consisted of hot water collected straight from poultry scalding tanks at markets. Samples were collected in sterile containers to avoid external contamination. Samples were carried out in two sampling rounds at eight (08) sites distributed across various districts of the city (*Yéguéré, Souroukoukin, Sarfalao, Petit-Paris, Belle Ville, Ouezzinville, St. Etienne, and Sector* 25). Two (02) samples were collected per sampling round, for a total of 33 samples collected in sterile containers from different scalding tanks.

2.3. Bacterial medium preparation

Preparation of the different enrichment broths and culture media was performed according to the manufacturer's instructions provided with each product container. For sample preparation prior to culturing, an enrichment broth was prepared according to the manufacturer's instructions. Once prepared, 9 mL of the broth was poured into test tubes, and 1 mL of the sample was added. The tubes were then incubated for 48 hours in an incubator to revive the bacteria. After this incubation, the enriched samples were streaked onto Violet Red Bile Lactose Agar, for isolation [13].

2.4. Isolation and Purification of Presumptive *Escherichia coli* Strains

A volume of 1 mL of the enriched solution (broth + sample) was inoculated onto Violet Red Bile Agar with Lactose (VRBL) using the spread-plate technique. The Petri dishes were incubated in an incubator for 24 hours. After each culture, a single isolated colony was subcultured to obtain pure colonies. This purification step was repeated

approximately three times to ensure the recovery of pure isolates. The purified isolates were then stored in glycerol-containing nutrient broth at –20 °C [14].

Morphological characterization of *Escherichia coli* Isolates

Macroscopic observations were performed visually. During this examination, the phenotypic characteristics of the bacterial colonies grown on agar were assessed. In this study, the isolates were streaked onto VRBL agar and incubated at 37 °C for 24 hours. The observed characteristics included colony morphology, colour, size, general appearance, and the presence of a surrounding halo. This is followed by microscopic examination. During this step, the shape, size, and staining properties of the bacteria were assessed following Gram staining. Observations were performed under an optical microscope using the ×100 objective (oil immersion) [13].

2.5. Antibiogram susceptibility

Antibiotic susceptibility was determined using the solid-media diffusion method described by Hudzicki, (2009). A total of eight antibiotics were tested (Table 1) amikacin (AK, 30 µg), amoxicillin/clavulanic acid (AMC, 20/10 µg), ampicillin (AMP, 10 µg), cefotaxime (CTX, 30 µg), cefoxitin, and ciprofloxacin (CIP, 5 µg). Interpretation was performed by comparing inhibition zone diameters with tables of critical MIC concentrations and critical inhibition zone diameters [16].

Table 1 Selected Antibiotics by family

Bacterial genius	**Antibiotic**	**Families**	**Code**	**Disk load (µl)**	**Critical diameter (mm)**	
					S ≥	**R ≤**
Escherichia coli	Amoxicillin+Clavulanic Acid	Penicillin	AUG	30	21	18
	Imipenem	Carbapenem	IMP	10	22	19
	Meropenem		MRP	10	32	28
	Cefoxitin	Cephamycin	FOX	30	26	23
	Amikacin	Aminoglycoside	AK	30	23	19

2.6. Microbial DNA extraction

Chelex extraction was performed according to the protocol used by Lubna *et al.*, (2023). Two to three colonies were suspended in an Eppendorf tube containing 200 µl of a 5% Chelex 100 solution. The solution was incubated at 56°C for 30 to 60 minutes, then vortexed at high speed for 10 seconds. It was then boiled at 95°C for approximately 10 minutes. Finally, it was centrifuged at 13,000 rpm for 5 minutes. The solution was stored at -20°C.

2.7. 16S RNA Detection

16S rRNA detection was performed in a reaction mixture containing 4 µl Master Mix, 13.2 µl PCR water, 0.4 µl of forward (F) and reverse (R) primers, and 2 µl of DNA. Amplification was carried out according to the following protocol: initial denaturation at 95 °C for 5 minutes, followed by 35 cycles of denaturation at 95 °C for 15 seconds, hybridisation at 58 °C for 20 seconds, elongation at 70 °C for 40 seconds, and final elongation at 72 °C for 5 minutes.

2.8. Detection of pathogenicity genes

For pathogenicity gene detection, the reaction mixture was prepared using 4 µl of Master Mix, 14 µl of PCR water, 0.5 µl of the forward (F) and reverse (R) primers (Table 2), and 1 µl of DNA. Amplification was performed according to the protocol. Specifically, the samples underwent 35 amplification cycles, each consisting of 1 min of denaturation at 95 °C, 2 min of hybridisation at 65 °C for the first 10 cycles, decreasing to 60 °C in cycle 15, and 1.5 mins of elongation at 72 °C, increasing to 2.5 mins in cycles 25 to 35. PCR products were detected by electrophoresis at 120 V for 30 minutes on a 1.5% agarose gel.

Table 2 Primers used for the touchdown PCR

Sequences (5'⟶3')	Genes	Function	Amplicon size (bp)
AGA GTT TGA TCA TGG CTC AG	16S rRNA	-	1520
ACG GTT ACC TTG TTA CGA CT			
GAC CCG GCA CAA GCA TAA GC	*eaeA*	intimin	384
CCA CCT GCA GCA ACA AGA GG			
ATA AAT CGC CAT TCG TTG ACT AC	*stx-1*	Shiga toxin 1	180
AGA ACG CCC ACT GAG ATC ATC			
GGC ACT GTC TGA AAC TGC TCC	*stx-2*	Shiga toxin 2	255
CGC CAG TTA TCT GAC ATT CTG			

2.9. Data analysis

The collected data were entered into Microsoft Excel 2019, then cleaned and analyzed using RStudio (version 4.5.0). Descriptive statistics were used to determine the percentages of samples positive for *Escherichia coli*, the percentages of strains resistant to the tested antibiotics, the percentages of multiple resistance profiles, and the percentages of strains carrying pathogenicity genes. Subsequently, inferential statistical tests were used to assess associations between variables. Fisher's exact test was used to analyse the relationship between the water source and the presence of *Escherichia coli*, antibiotic susceptibility, and pathogenicity genes. Analysis of variance (ANOVA) was applied to compare the mean multiple resistance indices across the different sample sources. The results were expressed as percentages, and the comparisons were accompanied by their p-values. All statistical analyses were interpreted using a significance threshold set at $p < 0.05$.

3. Results

3.1. Distribution of Isolates According to Collection Sites

A total of eight collection sites were included in this study. Presumptive *Escherichia coli* isolates were recovered from five sites, yielding a contamination rate of 62.5% (Figure 1).

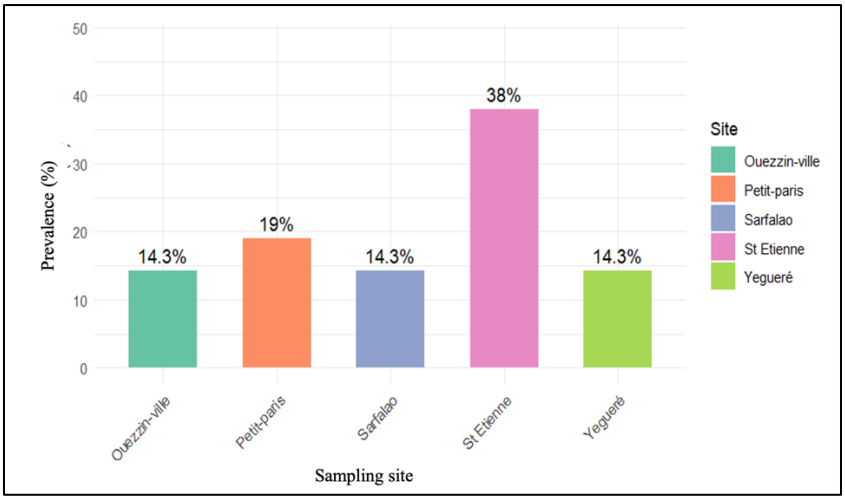

Figure 1 Prevalence of strains according to sampling sites

3.2. Antibiotic Susceptibility Results of the Isolates

Figure 2 presents the results of the susceptibility tests performed on the presumptive *Escherichia coli* strains isolated. Among the antibiotics tested, amikacin proved the most effective, exhibiting strong activity against the *E. coli* strains. In contrast, a significant proportion of these strains displayed resistance to multiple antibiotics: 61.9% to Augmentin

(amoxicillin–clavulanic acid), 66.7% to cefoxitin, and 52.4% to imipenem. These results enabled determination of the antibiotic resistance index by sampling site. The median values were relatively high across all sites. The site-specific indices ranged from 0.45 to 0.75 (Figure 3). The *Yeguéré* market exhibited the highest index and greater dispersion, indicating a high level of antibiotic resistance at this site.

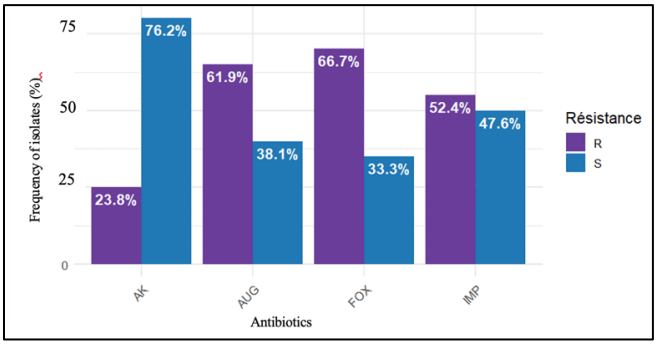

Figure 2 Distribution of isolates based on antibiotic susceptibility testing

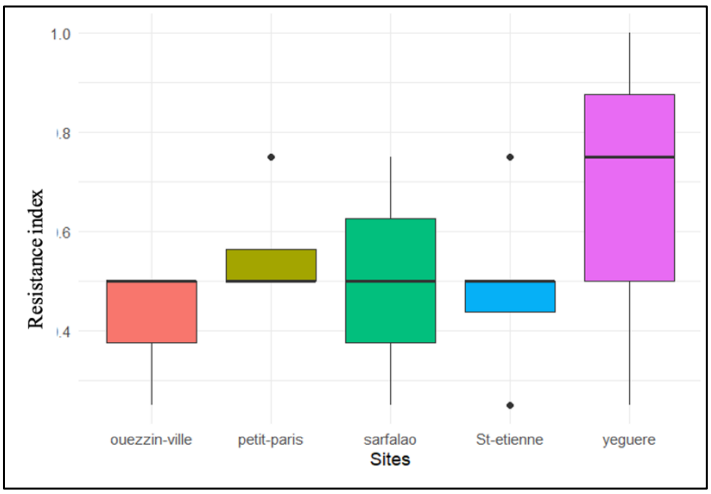

Figure 3 Antibiotic resistance index as a function of sampling sites

3.3. Bacterial Species Confirmation

Figure 4 presents the results of species identity confirmation following 16S rRNA amplification. Among the 21 isolated strains, the DNA of 20 strains was successfully detected, corresponding to an identification rate of 95.23%.

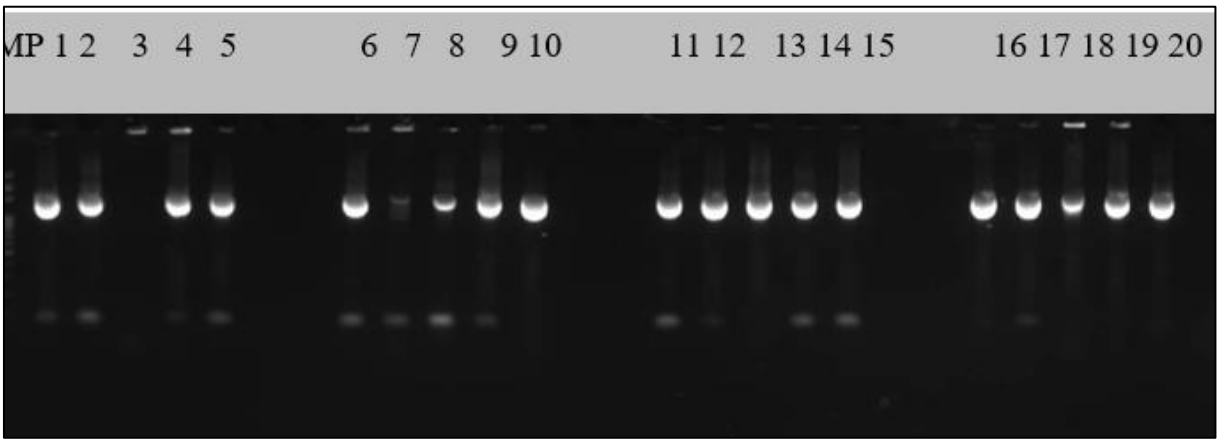

Figure 4 Visualised fragments used to confirm the identity of bacterial species

3.4. Detection of Virulence Genes and Intimin Protein in Presumptive *Escherichia coli* Strains

Table 3 presents the results of virulence gene and intimin protein detection in presumptive *E. coli* strains. Virulence genes and the intimin protein were detected in *E. coli* strains isolated from the Petit Paris district. In contrast, the *stx1* gene was also identified in the same district. These findings indicate that the detected genes originated from Shiga toxin–producing *E. coli*, and no EPEC-associated genes were detected.

Table *3* Molecular identification of different genes (eaeA, stx-1, stx-2)

Samples	***eaeA***	***stx-1***	***stx-2***
Yeg 1-2	-	-	-
P.P 1-1	-	-	-
Ouez 1-2	-	-	-
St E 1-1	-	-	-
St E 1- 2	-	-	-
Sarf 1-1	-	-	-
Yeg 2-2	-	-	-
P.P 2-1	-	-	-
Ouez 2-2	-	-	-
St E 2-2	-	-	-
St E 2-2	-	-	-
Yeg 3-2	-	-	-
P.P 3-1	-	+	-
Ouez 3-2	-	-	-
St E 3-1	-	-	-
St E 3-2	-	-	-
Sarf 3-1	-	-	-
P.P 4-1	+	+	+
St E 4-1	-	-	-
St E 4-2	-	-	-

+, presence ; -, absence

4. Discussion

Pathogenic *Escherichia coli*, particularly STEC and EPEC strains, cause numerous gastrointestinal infections in humans, ranging from bloody diarrhea to hemolytic-uremic syndrome. These strains pose a significant global public health concern due to their frequent presence in both plant- and animal-derived foods, representing a major source of foodborne illness. In a context marked by significant public health challenges and a lack of local data on pathogenic *E. coli* strains, targeted research is essential to better understand the epidemiological situation. This study aimed to assess the microbiological quality of scalding water in poultry markets in Bobo-Dioulasso and to detect virulence genes using molecular methods. A total of 33 samples were collected from eight scalding sites across different poultry markets. Among these, 21 samples were positive for bacterial culture, yielding a positivity rate of 63.6%. This rate is lower than the 74.28% previously reported by [18].

Geographically, bacterial strains were isolated from five of the eight sites yielding a prevalence of 62.5%. These findings indicate significant microbiological contamination of the scalding water, posing a considerable public health risk. Such water, often reused or poorly disposed of, can serve as a reservoir for pathogenic bacteria, facilitating their dissemination into the environment and transmission to humans [19]. Our prevalence results are higher than those

reported by [20], who observed 33%. Although the study matrices differed (chicken and beef), the discrepancies may be explained by inadequate hygiene practices.

Assessment of antibiotic susceptibility of presumptive *E. coli* isolates revealed variable resistance across the antibiotic families tested. High resistance rates were observed for cefoxitin (66.7%), amoxicillin-clavulanic acid (61.9%), and imipenem (52.4%). Regarding cefoxitin, our results show slightly lower resistance than the 73% reported by [21], which may reflect bacterial strain variability. A Canadian study [22] suggested that cefoxitin resistance could be associated with increased AmpC-type cephalosporinase production or acquisition of plasmid-encoded resistance genes. For amoxicillin-clavulanic acid, our resistance rate of 61.9% is lower than the 71.43% reported by [23]. This resistance may be due to excessive use of this combination in poultry, promoting the emergence of resistant strains. The main mechanism involved is the production of β-lactamases, enzymes that hydrolyse the β-lactam ring, rendering these antibiotics ineffective. Imipenem resistance was observed in 52.4% of cases. By comparison to other studies performed in Algeria [24] on avian *E. coli* isolates reported only 6% resistance to imipenem, much lower than in our study. This high level of resistance raises concerns about the current effectiveness of carbapenems. Conversely, some antibiotics showed notable efficacy. Amikacin was the most active, with a susceptibility rate of 71.4%. This is slightly lower than the 75% reported by [25], which may be attributed to geographical variations, different clinical context, or higher antibiotic pressure in our study area. Nevertheless, amikacin remains one of the few antibiotics still largely effective against presumptive *E. coli* isolates. The observed multidrug resistance, particularly to β-lactams and carbapenems, underscores the need to strengthen microbiological surveillance programs and promote more rational antibiotic use.

Following antibiotic susceptibility testing, molecular identification of the presumptive *E. coli* isolates was performed. Preliminary identification using 16S rRNA gene amplification confirmed 20 out of 21 isolates (95.23%) as belonging to the genus *Escherichia*, slightly lower than the 100% reported by [26]. This discrepancy may be due to the specificity of the primers used or genetic variation among strains.

Subsequently, three virulence genes were screened: *eaeA* (intimin), *stx1* (Shiga toxin 1), and *stx2* (Shiga toxin 2). The *eaeA* and *stx2* genes were each detected in 4.76% of isolates, while *stx1* was detected in 9.52%. These findings indicate the presence of Shiga toxin-producing *E. coli* (STEC) strains. Our results differ from those reported in Senegal [27], where *eaeA*, *stx1*, and *stx2* were found in 1.5%, 0%, and 3.7% of isolates, respectively. These differences may be attributed to variations in sample size and type.

5. Conclusion

This study highlighted that the scalding water tanks in poultry markets in Bobo-Dioulasso represent a significant reservoir of microbiological contamination, with a relatively high positivity rate. Biochemical identification, complemented by molecular methods, revealed the circulation of pathogenic strains capable of causing potentially severe infections in humans. Furthermore, antibiotic susceptibility testing indicated alarming resistance to multiple antibiotic classes, particularly β-lactams, reflecting inappropriate antibiotic use in poultry farming. Overall, these findings underscore the urgent need to strengthen hygiene practices and implement rigorous antimicrobial surveillance in Burkina Faso.

Compliance with ethical standards

Acknowledgments

Hereby, I want to acknowledge URBANE for this financial support.

Disclosure of conflict of interest

No conflict of interest to be disclosed.

References

[1] M. Dione *et al.*, "Characteristics of chicken production systems in rural Burkina Faso: A focus on One Health related practices and food security," *PLoS One*, vol. 20, no. 2 February, pp. 1–24, 2025, doi: 10.1371/journal.pone.0317898.

[2] K. Tindano and K. Savadogo, "Local and crossbred chicken production systems in the region of Ouagadougou, Burkina Faso," *Rev. d'Elevage Med. Vet. des Pays Trop.*, vol. 78, 2025, doi: 10.19182/remvt.37435.

[3] P. S. and W. K. A. Anderson AK1*, Nianogo AJ2, Some S3, "Guinea fowl production: the potential for nutrition and income generation in rural households in burkina faso Anderson," *AgEcon Search*, p. 18, 2022, [Online]. Available: file:///F:/Spec 2/Traffic Delay Model.pdf

[4] S. B. Ayssiwede *et al.*, "Elevage des poulets traditionels ou indigènes au Sénégal et en Afrique Subsahariene : État des lieux et contraintes," *Ann. Med. Vet.*, vol. 157, no. 2, pp. 103–119, 2013.

[5] INSD, "Burkina Faso : Enquête démographique et de santé," 2003.

[6] Ministère des Ressources animales et halieutiques, "Consommation de la volaille à Ouagadougou et Bobo-Dioulasso: 130.000 têtes par jour - NetAfrique.net," *L'Economiste du Faso*, Aug. 2021. https://netafrique.net/consommation-de-la-volaille-a-ouagadougou-et-bobo-dioulasso-130-000-tetes-par-jour/ (accessed Jun. 16, 2025).

[7] N. Heredia and S. García, "Animals as sources of food-borne pathogens: A review," *Anim. Nutr.*, vol. 4, no. 3, pp. 250–255, 2018, doi: 10.1016/j.aninu.2018.04.006.

[8] H. Lee and Y. Yoon, "Etiological agents implicated in foodborne illness world wide," *Food Sci. Anim. Resour.*, vol. 41, no. 1, pp. 1–7, 2021, doi: 10.5851/KOSFA.2020.E75.

[9] OMS, "Maladies d'origine alimentaire: près d'un tiers des décès surviennent chez les enfants de moins de 5 ans," *Communiqué de presse - Genève*, Dec. 03, 2015. https://www.who.int/fr/news/item/03-12-2015-who-s-first-ever-global-estimates-of-foodborne-diseases-find-children-under-5-account-for-almost-one-third-of-deaths (accessed Sep. 30, 2025).

[10] A. Kagambèga, K. Haukka, A. Siitonen, A. S. Traoré, and N. Barro, "Prevalence of Salmonella enterica and the hygienic indicator Escherichia coli in raw meat at markets in Ouagadougou, Burkina Faso," *J. Food Prot.*, vol. 74, no. 9, pp. 1547–1551, 2011, doi: 10.4315/0362-028X.JFP-11-124.

[11] Y. Seferoğlu and Ş. Kırkan, "Bovine Escherichia coli Mastitis and Effects on Milk Microbiota," *Anim. Heal. Prod. Hyg.*, vol. 11, no. 2, pp. 56–65, 2022, doi: 10.53913/aduveterinary.1179963.

[12] A. R. Rafee *et al.*, "Letters in Animal Biology," vol. 05, no. 2, pp. 107–117, 2025.

[13] Z. Nawel, "Techniques des analyses microbiologiques," pp. 2021–2022, 2022.

[14] M. Manafi, "Culture Media for Detection and Enumeration of 'Total' Enterobacteriaceae, Coliforms and Escherichia coli from Foods," *Handb. Cult. Media Food Water Microbiol. Third Ed.*, pp. 233–260, Dec. 2011, doi: 10.1039/9781847551450-00233.

[15] J. Hudzicki, *Kirby-Bauer Disk Diffusion Susceptibility Test Protocol*. 2009.

[16] Mamadou SIDIBE, "Caracterisation des souches d'Escherichia coli... - Google Scholar," 2020. https://scholar.google.com/scholar?hl=fr&as_sdt=0%2C5&q=Caracterisation+des+souches+d'Escherichia+coli+et+de+Klebsiella+spp+multiresistantes+isolees+chez+les+humains%2C+les+animaux+et+dans+l'environnement+au+lrm+de+Bamako&btnG= (accessed Dec. 02, 2025).

[17] Lubna *et al.*, "Antimicrobial Usage and Detection of Multidrug-Resistant Staphylococcus aureus: Methicillin- and Tetracycline-Resistant Strains in Raw Milk of Lactating Dairy Cattle," *Antibiotics*, vol. 12, no. 673, pp. 1–11, 2023.

[18] N. F. Chaibi , Cherrad, "Recherche et antibiogramme des souches d'Escherichia coli dans les abats de volailles dans un abattoir à Bordj Bou Arreridj. Présenté," 2023.

[19] Sa. T. Sahi L., "Etude du risque de contamination des carcasses et du foie de poulet par les germes (Escherichia coli et Salmonelle spp) et par les résidus d'antibiotiques. Présenté," 2023.

[20] H. I. Bawa, "Caractérisation phénotypique, moléculaire et antibiorésistance des souches de Salmonella spp. et de Escherichia coli isolées d'échantillons de viande vendues dans les marchés et d'échantillons provenant des patients," p. 166, 2016.

[21] L. Zhao *et al.*, "Prevalence of Virulence Factors and Antimicrobial Resistance of Uropathogenic Escherichia coli in Jiangsu Province (China)," *Urology*, vol. 74, no. 3, pp. 702–707, Sep. 2009, doi: 10.1016/J.UROLOGY.2009.01.042.

[22] L. F. Mataseje *et al.*, "Characterization of cefoxitin-resistant Escherichia coli isolates from recreational beaches and private drinking water in Canada between 2004 and 2006," *Antimicrob. Agents Chemother.*, vol. 53, no. 7, pp. 3126–3130, 2009, doi: 10.1128/AAC.01353-08.

[23] D. T. Lemitha Saffa, "Mémoire Phénotypes de résistance aux β -lactamines des souches d ' entérobactéries isolées de la viande du poulet," 2025.

[24] B. F. Hamichine Baya, "Profils d ' antibiorésistance et essais de détection de facteurs de virulence de souches d ' Escherichia coli d ' origine aviaire," 2019.

[25] I. Moş, O. Micle, M. Zdrâncă, M. Mureşan, and L. Vicaş, "Antibiotic sensitivity of the Escherichia coli strains isolated from infected skin wounds," *Farmacia*, vol. 58, no. 5, pp. 637–645, 2010.

[26] A. A. Neamah, K. H. Fahed, J. N. Sadeq, and M. A. Alfatlawi, "Molecular characterization and phylogenetic analysis of Escherichia coli isolated from milk of cattle affected by mastitis," *Iraqi J. Vet. Sci.*, vol. 36, no. 1, pp. 251–254, 2022, doi: 10.33899/ijvs.2021.129934.1702.

[27] Gagara Hama Haladou, "Universite Cheikh Anta Diop De Dakar Ecole Inter-Etats Des Sciences Et Medecine Recherche Des Genes De Virulence Stx1 , Stx2 Et Eae Dans Les Souches De Echerichia . Coli Importee Au Senegal," 2014.