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Impacts of zootechnical factors on *Salmonella* contamination in swab samples using real-time PCR at the Yaounde slaughterhouse

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ABSTRACT

Salmonella contamination of beef carcasses remains a major public health concern, particularly in low- and middle-income countries where abattoir hygiene and traceability systems are often inadequate. This study aimed to generate context-specific data on Salmonella contamination along the cattle slaughter chain at the Yaoundé abattoir using real-time PCR, and to evaluate the influence of zootechnical factors of slaughtered cattle within a One Health framework. A total of 705 swab samples were collected from live cattle ($n = 145$), carcasses ($n = 310$), butchers' hands ($n = 145$), and meat contact surfaces ($n = 105$). *Salmonella* detection was performed using TaqMan probe-based real-time PCR. Overall, 14.9% (95% CI: 12.4%–17.6%) of samples were positive for *Salmonella*, with prevalence rates of 5.20% (95% CI: 2.4%–10.6%) in live cattle, 17.73% (95% CI: 13.89%–22.38%) in carcasses, 1.9% (95% CI: 0.52% – 6.68%) in contact surfaces, and 5.52% (95% CI: 2.8% – 10.5%) in butchers' hand swabs. *Salmonella* occurrence differed significantly among sample categories ($p < 0.05$). However, multivariate logistic regression revealed that none of the assessed zootechnical factors (sex, age, breed, transport, origin, cleanliness, body condition, and production system) were independently associated with contamination ($p > 0.05$). These findings suggest that *Salmonella* contamination in slaughtered cattle is driven by systemic hygiene and biosecurity shortcomings rather than individual animal-related factors. Overall, the moderate prevalence observed reflects gaps in slaughter hygiene and biosecurity. Strengthening sanitation practices, enforcing Hazard Analysis and Critical Control

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Point (HACCP) measures, and adopting molecular surveillance tools such as real-time PCR are essential to reduce contamination risks and protect public health.

Introduction

Salmonella remains a significant foodborne pathogen worldwide, responsible for major outbreaks and sporadic cases of gastroenteritis and posing a persistent challenge to food safety and public health [1–3].

In Cameroon, recurrent *Salmonella* outbreaks linked to contaminated beef and other animal products underscore the ongoing risk of foodborne transmission [4,5]. Beef production plays a central role in the national meat supply; however, slaughterhouses often operate under limited hygiene control and weak surveillance systems. These conditions favor carcass contamination and increase the likelihood of pathogen dissemination along the food chain [6,7].

Cattle are recognized as important reservoirs of *Salmonella*, with contamination occurring at multiple points along the production chain, particularly during transport and slaughter [8–10]. In low- and middle-income countries (LMICs), including Cameroon, limited infrastructure, poor handling practices, and inadequate monitoring systems hinder the identification and control of contamination pathways within abattoirs [11]. Zootechnical factors such as animal origin, transport mode, sex, age, breed, and body condition score have also been reported to influence contamination risk; however, their relative contribution under local production systems remains poorly characterized [12–16].

Detection of *Salmonella* in slaughterhouse settings has traditionally relied on culture-based methods, which, although specific, are laborious and time-consuming, often requiring up to five days for confirmation [17,18]. Such delays may compromise food-safety decisions and allow contaminated carcasses to enter the food chain. Moreover, culture methods may fail to recover injured or stressed cells, potentially leading to an underestimation of contamination levels [19–21].

To overcome these limitations, molecular methods such as real-time PCR have been developed for rapid and sensitive *Salmonella* detection. Targeting the *invA* gene, a conserved single-copy marker specific to *Salmonella* spp., real-time PCR provides high sensitivity, specificity, and shorter turnaround times, and reduced contamination risks associated with post-amplification handling [19,22,23].

This study therefore was aimed to generate context-specific data on Salmonella contamination along the cattle slaughter chain at the Yaoundé abattoir using real-time PCR, and to evaluate the influence of zootechnical factors of slaughtered cattle within a One Health framework. The findings are intended to improve slaughterhouse hygiene practices and strengthen *Salmonella* surveillance across Cameroon's beef production chain.

Methodology

Sample collection and preparation

A total of 705 wet swabs were collected between December 2014 and November 2015 at the Yaoundé abattoir. These include 145 swabs from live cattle (hide and fecal swabs), 310 from beef carcasses, 145 from butchers' hands, and 105 from meat contact surfaces.

Each swab was soaked in 1000 µL of phosphate-buffered saline (PBS) and incubated at room temperature for 28 min to facilitate bacterial elution. The suspension was then vortexed for 30 s, duration consistent within the standard bacterial recovery time reported in similar studies [24]. After vortexing, 200 µL of the supernatant was used for DNA extraction.

Genomic DNA was purified using the QIAGEN (Hilden, Germany) genomic buffer set in combination with Genomic-tip 100/G columns, following the manufacturer's instructions. Briefly, 20 µL of proteinase K was added to the bacterial suspension, followed by 200 µL of buffer AL. The mixture was vortexed thoroughly and incubated at 56 °C for 10 min. Subsequently, 200 µL of ethanol (96–100 %) was added, and the mixture was vortexed again.

The lysate was transferred to a DNA spin column placed in a 2 mL collection tube and centrifuged at 6000 × *g* for 1 min. The column was then washed with 500 µL of buffer AW1 and centrifuged at 6000 × *g* for 1 min, followed by a second wash with 500 µL of buffer AW2 and centrifugation at 20,000 × *g* for 3 min. The spin column was then transferred to a new 1.5 mL Eppendorf tube, and DNA was eluted with 200 µL of buffer AE. After a brief incubation at room temperature, the eluate was centrifuged at 6000 × *g* for 1 min. Extracted DNA was stored at −20 °C until further analysis.

This extraction protocol yielded high-molecular-weight, RNA-free genomic DNA suitable for precise quantification by measuring absorbance at 260 nm.

Real-time PCR amplification

Real-time PCR targeting the *inv*A gene was performed using a Bio-Rad CFX96 Real-Time PCR Detection System (Bio-Rad Laboratories, USA) operated with CFX Manager Software version 2.3 based on fluorescence emission.

The Thermal cycling conditions were as follows: an initial denaturation at 95 °C for 5 min, followed by 45 cycles of denaturation at 94 °C for 20 secondes and combined annealing/extension at 64 °C for 1 min. Data were collected during each elongation step. Each qPCR run included sterile distilled water as a no-template control (NTC) and a *Salmonella typhimurium* DNA as a positive control to confirm assay specificity and amplification efficiency.

The reaction mixture (20 µL final volume) consisted of:

Distilled water 5.9 µL
Master mix 2x 10 µL
*inv*A-*F* + 10 µM 0.8 µL
*inv*A-*R* + 10 µM 0.8 µL
*inv*A Probe +10 µM 0.5 µL
DNA template 2 µL
The primer and probe sequences targeting the invA gene were as follows
*inv*A-F : 5` -GCGTTCTGAACCTTTGGTAATAA-3′
*inv*A-R: 5′-CGTTCGGGCAATTCGTTA-3′
*inv*A-TM (probe) 5′-FAM-TGGCGGTGGGTTTTGTTGTCTTCT-TAMRA-3′

Amplification curves were generated by plotting the normalized reporter signal (ΔRn) against the number of PCR cycles. The cycle threshold (Ct) was defined as the cycle number at which fluorescence exceeded the predetermined threshold. Samples with Ct values < 35 were considered positive, based on assay validation criteria.

Ethical considerations

Approval for this study, including the research design, data collection procedures, and consent forms, was obtained from the Ethics Review and Consultancy Committee of the Cameroon Bioethics Initiative (Ref CBI/406/ERCC/CAMBIN).

Statitical methods

Data were entered and analyzed using STATGRAPHICS PLUS version 5.0 and R software (Comprehensive R Archive Network R 4.3.x). Descriptive statistics were used to summarize categorical variables. The prevalence of *Salmonella* spp. and corresponding 95 % confidence intervals (CI) were calculated using the Wilson score method.

Associations between *Salmonella* contamination and categorical zootechnical factors (sex, age, breed, transport mode, origin, cleanliness, body condition score, and production system) were evaluated using the Chi-square test, or the Fisher's exact test when expected cell frequencies were less than five. Statistical significance was set at $p < 0.05$.

To identify independent predictors of *Salmonella* contamination, a multivariate logistic regression model was fitted, including all zootechnical factors as explanatory variables. Adjusted odds ratios (AOR) and 95 % CIs were calculated, and results were visualized using a Forest Plot generated in R.

Results

Real-time PCR-based detection of salmonella spp

Of the 705 swab samples collected at the Yaounde abattoir, 105 tested positive for *Salmonella* spp., corresponding to an overall prevalence of 14.9 % (95 % CI: 12.4 %–17.6 %) as determined by real-time PCR targeting the *inv*A gene.

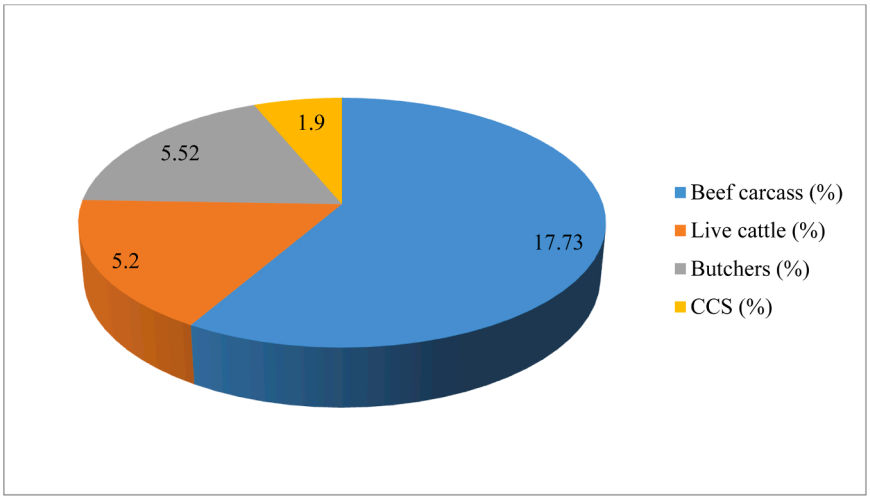

Fig. 1. Salmonella-PCR-based detection by sample category.

Salmonella prevalence by sample categoryCQ1

As shown in Fig. 1, *Salmonella* prevalence differed significantly among sample categories ($p < 0.05$). Beef carcasses exhibited the highest contamination rate (17.73 %; 95 % CI: 13.89 %–22.38 %), followed by butchers' hands (5.52 %; 95 % CI: 2.8 %–10.5 %), live cattle (5.10 %; 95 % CI: 2.4 %–10.6 %), and carcass contact surfaces (1.9 %; 95 % CI: 0.52 % – 6.68 %).

CCS= carcass contact surfaces

Salmonella prevalence by carcass sampling site

As presented in Fig. 2, *Salmonella* prevalence did not differ significantly among the carcass sampling sites ($p > 0.05$). The highest detection rate was recorded in post-eviscerated carcasses (7.38 %; 95 % CI: 5.67–9.54 %), followed by post-skinned carcasses (5.67 %; 95 % CI: 4.19–7.63 %) and carcasses stored in the hall (4.82 %; 95 % CI: 3.47–6.66 %).

PSC= Post-skinned carcass. PEC= Post-evisceration carcass, HSC= Hall stored carcass

Zootechnical characteristics of salmonella-positive cattle

The zootechnical characteristics of 145 slaughtered cattle; including sex, age, breed, geographical origin, mode of transport, cleanliness status, and body condition score (BCS), production system and their influence on *Salmonella* contamination are summarized in Table 1.

Sex

Among the 145 slaughtered cattle, female animals accounted for 110 individuals, of which 33 tested positive for *Salmonella*, yielding a prevalence of 30.0 % (95 % CI: 22.5 – 38.9 %). In contrast, male cattle ($n = 35$) showed a lower prevalence of 17.1 % (95 % CI: 7.8–33.0 %), with 6 positive cases. Despite the apparent difference, sex was not significantly associated with *Salmonella* detection ($p > 0.05$).

Age

Although variation in prevalence was observed across age groups, age-related differences were not statistically significant ($p > 0.05$). The highest prevalence occurred among cattle aged 6–7 years (44.0 %; 95 % CI: 26.67–62.93 %), followed by those aged 4–5 years (25.0 %; 95 % CI: 13.25–42.11 %), 7–8 years (23.53 %; 95 % CI: 9.56–47.26 %), 3–4 years (22.73 %; 95 % CI: 12.84–36.99 %), and 5–6 years (22.22 %; 95 % CI: 10.61–40.76 %).

Breed

Table 1 illustrates the distribution of *Salmonella*-positive cases among cattle breeds. The highest prevalence was observed in Red Fulani cattle (40.0 %; 95 % CI: 25.7–56.7 %), followed by Mbororo cattle (33.3 %; 95 % CI: 12.1–64.6 %). Although White Fulani cattle constituted the largest proportion of the slaughter population (38.6 %; 95 % CI: 30.9–46.9 %), only 26.5 % (95 % CI: 16.4–39.8 %) tested positive for *Salmonella*. Gudali and crossbred cattle had prevalence rates of 25.0 % (95 % CI: 10.2–49.5 %) and 16.7 % (95 % CI: 7.3–33.6 %), respectively. Breed was not significantly associated with *Salmonella* detection ($p > 0.05$).

Transport mode

Salmonella prevalence varied according to the mode of transport. Cattle transported by truck exhibited the highest contamination rate (30.2 %; 95 % CI: 22.3–39.7 %), followed by those transported by train (22.2 %; 95 % CI: 6.3–54.7 %) and cattle with unknown transport origins (20.0 %; 95 % CI: 8.8–39.3 %). No *Salmonella* was detected in cattle transported on foot. Statistical analysis indicated

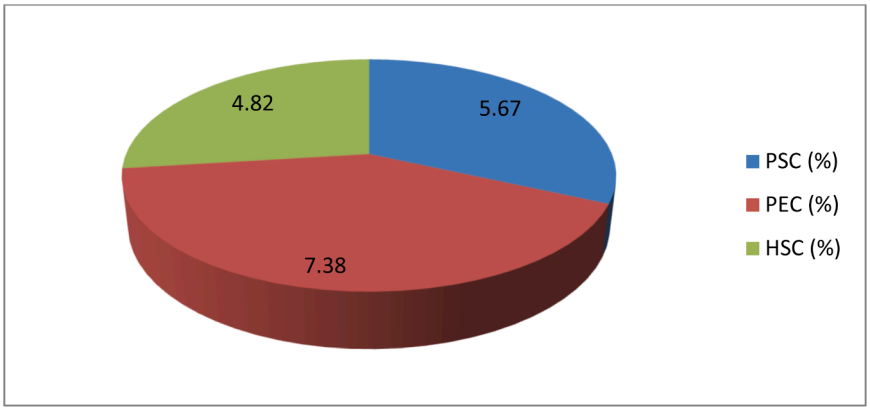

Fig. 2. PCR-based detection of *Salmonella* in beef carcass per sampling site.

Table 1
Summary of *Salmonella* prevalence by zootechnical factors among slaughtered cattle at the Yaoundé abattoir ($n = 145$).

Zootechnical factor	Category	n	Positive (x)	Prevalence (%)	95 % CI	P value
Sex	Female	110	33	30.0	22.1–39.2	**0.15**
	Male	35	6	17.1	8.1–32.2	
Age (years)	3–4	44	10	22.7	12.8–37.0	**0.51**
	4–5	32	8	25.0	13.1–42.1	
	5–6	27	6	22.2	10.6–40.8	
	6–7	25	11	44.0	26.7–62.9	
	7–8	17	4	23.5	9.5–47.7	
Breed	Red Fulani	35	14	40.0	25.7–56.7	**0.66**
	White Fulani	49	13	26.5	16.4–39.8	
	Gudali	16	4	25.0	10.2–49.5	
	Mbororo	9	3	33.3	12.1–64.6	
	Cross-bred	30	5	16.7	7.3–33.6	
Transport mode	Train	9	2	22.2	6.3–54.7	**0.84**
	Truck	106	32	30.2	22.3–39.7	
	Unknown	25	5	20.0	8.8–39.3	
	Foot	0	0	0.0	-	
Origin	Chad	1	0	0.0	0.0–79.3	**0.28**
	West	1	0	0.0	0.0–79.3	
	CAR	5	0	0.0	0.0–43.4	
	East	65	21	32.3	22.3–44.0	
	Adamawa	30	10	33.3	19.7–50.2	
	Unknown	43		16.3	8.2–30.0	
Production system	Transhumance	5	0	0.0	0.0–43.4	**0.74**
	Sedentary	5	0	0.0	0.0–43.4	
	Unknown	135	39	28.9	21.7–37.3	
Body condition score	Medium	11	3	27.3	9.7–56.6	**0.41**
	Fat	82	26	31.7	22.5–42.5	
	Lean	52	10	19.2	10.7–32.1	
Cleanliness	Clean/Dry	139	39	28.1	21.1–36.1	**0.72**
	Slightly dirty	4	0	0.0	0.0–49.0	
	Dirty	2	0	0.0	0.0–65.8	

Key: CAR= Central Africa Republic.

that transport mode was not significantly associated with *Salmonella* prevalence in this population ($p > 0.05$).

Place of origin

Higher contamination rates were observed among cattle originating from the East (32.3 %) and Adamawa (33.3 %) regions, whereas animals of unknown origin showed a moderate prevalence (16.3 %). Despite these apparent differences, statistical analysis revealed no significant association between *Salmonella* contamination and the cattle's place of origin ($p > 0.05$).

Cleanliness scores

Cleanliness status was not significantly associated with *Salmonella* contamination ($p > 0.05$). Cattle classified as clean and dry exhibited the highest prevalence (28.1 %; 95 % CI: 21.1–36.1 %), whereas no *Salmonella* was detected in cattle categorized as slightly dirty (0.0 %; 95 % CI: 0.0–49.0 %) or dirty (0.0 %; 95 % CI: 0.0–65.8 %).

Body condition scores

Although variation in *Salmonella* prevalence was observed across different BCS categories, these differences were not statistically significant ($p > 0.05$). Cattle with a medium BCS exhibited the highest prevalence (79.76 %; 95 % CI: 70.94 %–87.26 %), followed by those with a fat BCS (11.91 %; 95 % CI: 6.69 %–20.68 %). The lowest prevalence was recorded among lean cattle (8.33 %; 95 % CI: 4.09 %–16.22 %).

Production system

Information on the production system was unavailable for the most slaughtered cattle (93.1 %; 95 % CI: 87.5–96.4 %). Only a small fraction (3.45 %; 95 % CI: 1.5–7.7 %) were identified as reared under a sedentary system. *Salmonella* was detected exclusively among cattle of unknown production background, with a prevalence of 28.9 % (95 % CI: 21.7–37.3 %).

Multivariate analysis of zootechnical factors associated with salmonella contamination

Multivariate logistic regression analysis was conducted to evaluate the independent effects of zootechnical factors on *Salmonella* contamination among 145 slaughtered cattle (Fig. 3). The model included sex, age, breed, mode of transport, geographical origin, cleanliness status, body condition score, and production system as explanatory variables. After adjustment, none of these factors showed a statistically significant association with *Salmonella* positivity ($p > 0.05$).

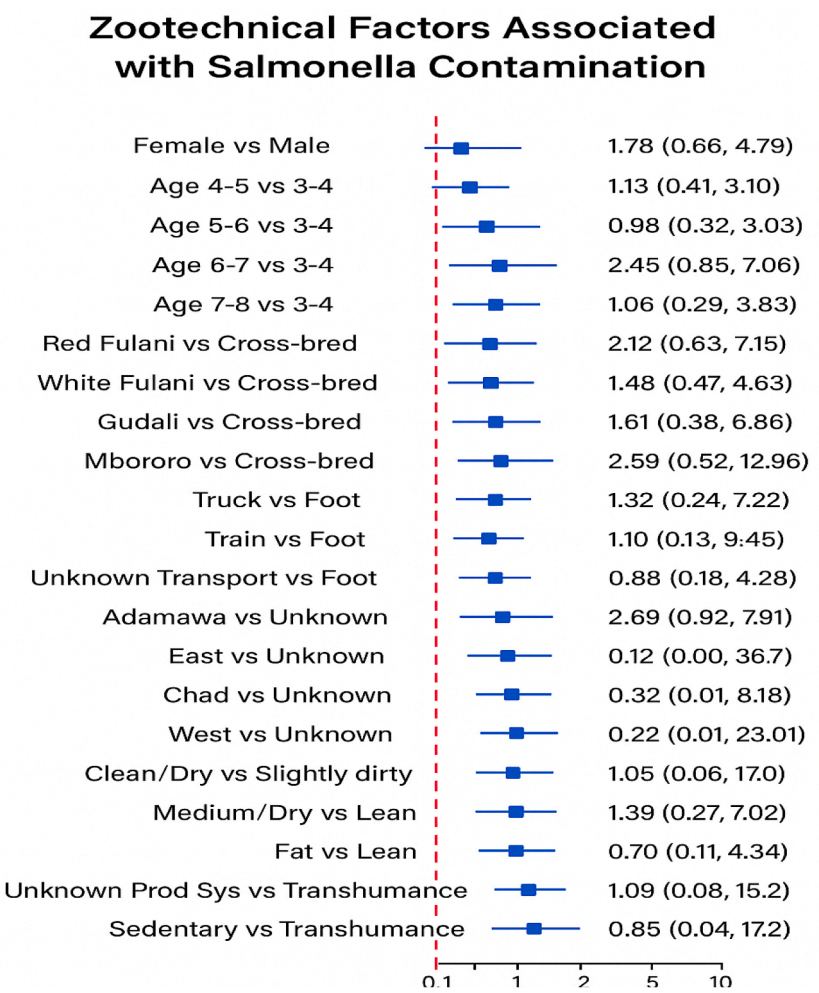

Fig. 3. Multivariate logistic regression analysis of zootechnical factors associated with *Salmonella* contamination in cattle at the Yaoundé Abattoir.

Discussion

General salmonella prevalence and methodological considerations

The overall *Salmonella* prevalence of 14.9 % observed in this study was markedly higher than the 2.3 % previously reported in Cameroon using culture-based methods [25]. Similar discrepancies between PCR-based detection and conventional culture methods have been reported in abattoirs and beef value chains both within Africa and elsewhere [19,26–28]. These differences are likely attributable to the limited sensitivity of culture methods, which often fail to recover stressed or sublethally injured cells, and are affected by loss of viability during storage, or are subject to microbial competition on selective media. In contrast, polymerase chain reaction (PCR) assays detect DNA from both viable and non-viable cells and, when coupled with efficient DNA extraction, can identify *Salmonella* at low bacterial loads [20,21,27]. Consequently, real-time PCR represents a more sensitive and rapid diagnostic tool for *Salmonella* surveillance, including samples that may test negative by culture [27,29].

Distribution of salmonella along the slaughter and processing chain

The carcass contamination rate of 17.73 % observed in this study is consistent with reports from other African abattoirs, where *Salmonella* prevalence varies widely due to differences in hygiene practices, carcass handling procedures, and facility management [10, 30–33]. This finding suggests that sanitary measures at the Yaoundé slaughterhouse are suboptimally implemented.

Detection of *Salmonella* in live cattle (5.2 %) confirms that asymptomatic carriers can introduce the pathogen into the abattoir environment. This prevalence is comparable to reports from Nigerian abattoirs [30] but differs from observations elsewhere [10,14,16, 34,35], likely reflecting variations in study design, seasonality, animal management, and sampling strategies.

Salmonella detection on butchers' hand swabs (5.25 %) was slightly lower than that reported in Ethiopian abattoirs [36,37] but

higher than values found in Nigeria [30]. This finding highlights the critical role of meat handlers in carcass cross-contamination and underscores the need for continuous hygiene training, effective supervision, and consistent use of personal protective equipment.

The significant variation in *Salmonella* prevalence among sample categories ($p < 0.05$) indicates differential contamination risks along the slaughter and processing chain. Beef carcasses exhibited the highest contamination rate (17.73 %; 95 % CI: 13.89–22.38 %) reinforcing their role as the primary vehicle for pathogen transmission to consumers.

Elevated contamination in post-evisceration carcasses (7.38 %) likely reflects intestinal leakage during evisceration [10], while comparable prevalence in the final processing area (4.82 %) suggests ongoing cross-contamination from handlers, tools, and surfaces [38,39]. These findings align with other African abattoirs, where carcass contamination reflects suboptimal hygiene, inadequate post-slaughter interventions, and cross-contamination from equipment or personnel [10,30,33,36].

The absence of significant differences among sampling sites ($p > 0.05$) suggests that contamination occurs throughout the slaughter process, highlighting the need for strict hygiene control, continuous microbiological monitoring and effective implementation of Hazard Analysis and Critical Control Point (HACCP) principles [10,36].

Influence of zootechnical factors

This study evaluated the influence of key zootechnical factors, including sex, age, breed, transport mode, geographical origin, cleanliness, body condition score (BCS), and production system on *Salmonella* contamination. Although they are recognized as important determinants of microbial contamination during slaughter and meat processing, none of these variables showed significant associations with *Salmonella* detection ($p > 0.05$).

A higher proportion of *Salmonella*-positive females (30.0 %) reflected their predominance in the slaughter population (75.9 %), consistent with the national trends in Cameroon [40]. Female-biased slaughter, which is common in sub-Saharan Africa, has implications for herd productivity [41,42]. Few studies directly link higher *Salmonella* contamination to male cattle [10]. This evidence suggests that variations in stress responses, castration status, and management practices may modulate pathogen persistence and dissemination in livestock systems, particularly among male cattle [43,44]. These findings indicate that sex alone is not a significant risk factor ($p > 0.05$), but may interact with physiological and handling factors to influence contamination patterns.

Age-related trends were consistent with previous reports showing increased infection risk in older animals [29,45,46]. Cattle aged 6–7 years exhibited the highest prevalence (44.0 %), likely due to cumulative exposure to contaminated environments, repeated handling, transport stress, and age-related immune decline. Younger cattle (3–4 years) displayed moderate prevalence (22.7 %), possibly reflecting incomplete immune maturation. However, overlapping confidence intervals indicate that age alone does not significantly determine *Salmonella* contamination, underscoring the importance of multivariate approaches.

Breed-related variations were not significant, although Red Fulani cattle exhibited the highest prevalence (40.0 %), potentially reflecting breed-specific variation in stress tolerance or immune response [47]. Although limited sample size restricts generalization, these findings provide baseline data for future breed-specific risk assessments in Cameroonian abattoirs and suggest that control measures should be applied universally rather than targeting specific breeds.

Cattle transported by trucks showed the highest prevalence (30.2 %), likely due to stressors such as overcrowding, fasting, dehydration, and inadequate ventilation, which can impair immune function and increase pathogen shedding [48,49]. Although transport mode was not statistically significant in our analysis, minimizing transport-related stressors is crucial for improving animal welfare and health outcomes, irrespective of transport classification [49,50].

Cattle originating from Adamawa, the principal cattle-producing region supplying Yaounde, exhibited the highest contamination rate (33.3 %). The region's high livestock density and frequent animal movements may facilitate *Salmonella* persistence and dissemination, as observed in other sub-Saharan African studies [51–53]. Although no Salmonella was detected in cattle from neighboring countries (Chad and the Central African Republic), cattle from these countries may contribute to cross-border pathogen introduction, particularly where informal trade and shared grazing routes lack veterinary oversight [54,55]. These findings reinforce the need for traceability, biosecurity, and regional collaboration in livestock health management.

Visual cleanliness at slaughter was not predictive of *Salmonella* contamination, as all positive animals were classified as clean and dry. This finding corroborates reports of poor agreement between visual cleanliness scores and microbial contamination [56,57], and suggests that abattoir hygiene and handling practices exert a greater influence than pre-slaughter hide condition [10,36]. Consequently, visual inspection alone is insufficient for predicting *Salmonella* contamination during slaughter operations.

Although not statistically significant, lean cattle exhibited relatively higher *Salmonella* prevalence, consistent with evidence linking poor nutritional status and compromised immunity to increased infection susceptibility [58,59]. Conversely, fat cattle appeared less affected, reflecting better body reserves and immune competence. These findings highlight the complex interactions between nutritional status, immunity, and hygiene in influencing contamination risk [7,43].

Information on production systems was limited, restricting interpretation. Nevertheless, production systems influence exposure risk through differences in grazing behavior, stocking density, and veterinary management [60,61]. The lack of traceable production data underscores systemic gaps in animal identification and record-keeping, which impede evidence-based risk management.

Multivariate analysis of zootechnical factors associated with salmonella contamination

The multivariate logistic regression analysis showed that none of the examined zootechnical factors (including sex, age, breed, transport mode, origin, cleanliness, body condition score, or production system) were independently associated with *Salmonella* contamination ($p > 0.05$). This finding reinforces that *Salmonella* contamination in slaughtered cattle is multifactorial, shaped by the

combined influence of biological, environmental, and management-related factors rather than any single determinant. Similar patterns have been reported in other African contexts, where farm practices, abattoir hygiene, and carcass handling collectively explains contamination dynamics [10,29,36,62]. Nevertheless, these results should be interpreted with caution due to the limited sample size and incomplete production data, which may have constrained statistical power.

Conclusion

This study provides the first integrated assessment of *Salmonella* contamination and associated zootechnical risk factors among slaughtered cattle at the Yaoundé abattoir using real-time PCR. The overall prevalence of 14.9 % indicates a moderate but epidemiologically significant level of contamination, reflecting persistent deficiencies in slaughter hygiene and biosecurity practices. The higher sensitivity of real-time PCR compared with conventional culture methods underscores its suitability for routine surveillance in abattoir settings.

The higher prevalence observed in carcasses (17.7 %) and the detection of *Salmonella* on butchers' hands (5.52 %) highlight not only substantial exposure risks within the slaughter environment but point to cross-contamination during processing.

Although no zootechnical factor showed a statistically significant association with *Salmonella* contamination, the relatively higher detection rates among older, female, and truck-transported cattle suggest that cumulative exposure and handling-related stress may contribute to infection risk. Furthermore, the elevated *Salmonella* prevalence in cattle from the Adamawa region underscores the role of regional livestock movement and cross-border trade in pathogen dissemination.

Overall, *Salmonella* contamination at the Yaoundé abattoir derives from multifactorial interactions involving animal handling practices, environmental contamination, and deficiencies in hygiene and process control, rather than from single animal-level determinants.

To effectively mitigate the aforementioned risks, it is recommended that:

1. Strict hygiene and sanitation protocols be enforced at all slaughter stages, particularly during evisceration and carcass handling.
2. HACCP-based monitoring and staff hygiene training be implemented to strengthen food safety management and minimize cross-contamination.
3. Routine molecular surveillance and traceability systems be established to enable early detection, track contamination sources, and enhance regional biosecurity coordination.

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Declaration of competing interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.this paper.

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References

[1] ECDC, Salmonellosis. In: ECDC. Annual Epidemiological Report for 2023. Stockholm, 2025.
[2] M. Pal, T. Ragasa, T. Rebuma, R. Zende, Salmonellosis remains the hidden menace in our global food supply: a comprehensive review, Am J. Med Biol. Res. 12 (1) (2024) 1–12, https://doi.org/10.12691/ajmbr-12-1-1.
[3] A.D. Teklemariam, R.R. Al-Hindi, R.S. Albiheyri, M.G. Alharbi, M.A. Alghamdi, A.A.R. Filimban, A.S. Al Mutiri, A.M. Al-Alyani, M.S. Alseghayer, A. M. Almaneea, et al., Human salmonellosis: a continuous global threat in the farm-to-fork food safety continuum, Foods 12 (2023) 1756, https://doi.org/10.3390/foods12091756.
[4] S.M. Soto, L. Castellsagués, V. Ballén, Y. Gabasa, P. Mayor, G.R. Brull, S.M. Funk, E. Julia, J.E. Fa, Prevalence of bacterial contamination on wild meat processing and cooking surfaces in rural Cameroon, One Health 20 (2025), https://doi.org/10.1016/j.onehlt.2025.101028.
[5] M.N. Tanyitiku, W. Agwanande, E.A. Teh, R.M. Laison, I.C.N. Petcheu, antimicrobial susceptibility pattern, and associated health risks of foodborne pathogens in street foods sold in elementary schools, Yaounde, Cameroon, Advances Infect. Dis. 15 (2025) 171–183, https://doi.org/10.4236/aid.2025.151014.
[6] MINEPIA, Situation of Production and Imports in the Livestock, Fisheries & Animal Industries Sub-sector, Year 2023, Division of Studies, Planning, Cooperation, and Statistics, Yaoundé, Cameroon, 2024.
[7] C. Matchawe, E.M. Machuka, M. Kyallo, P. Bonny, G. Nkeunen, I. Njaci, S.N. Esemu, D. Githae, J. Juma, B.M. Nfor, Detection of antimicrobial resistance, pathogenicity, and virulence potentials of non-typhoidal Salmonella isolates at the Yaoundé abattoir using whole-genome sequencing, Pathogens 11 (2022) 502, https://doi.org/10.3390/pathogens11050502.
[8] K.E. Bentum, E. Kuufire, R. Nyarku, V. Osei, S. Price, D. Bourassa, T. Samuel, C.R. Jackson, W. Abebe, Salmonellosis in cattle: sources and risk of infection, control, and prevention, Zoonotic Dis 5 (2025) 4, https://doi.org/10.3390/zoonoticdis5010004.

[9] Y.L. Pereira, A.D. da Cunha, E.H. Ossugui, I.S. Kroning, L.M. Fonseca, A.M. Fiorentini, W.P. da Silva, G.V. Lopes, Salmonella enterica isolated from a Brazilian beef production chain: prevalence, virulence genotypes, sanitizer and antimicrobial susceptibility, and biofilm formation ability, The Microbe 8 (2025) 100527, https://doi.org/10.1016/j.microb.2025.100527.

[10] F.A. Tafere, M.D. Fenta, M.B. Atanaw, E.M. Tsehay, Y.H. Mengstu, A.S. Mebiratu, Prevalence and antimicrobial susceptibility patterns of Salmonella from apparently healthy slaughtered cattle and abattoir workers at Gondar Elfora abattoir, Central Gondar Zone, Ethiopia, BMC Microbiol 25 (2025) 504, https://doi.org/10.1186/s12866-025-04262-3.

[11] M-Y.I. Mohamed, H.O. Khalifa, I. Habib, Food pathways of Salmonella and its ability to cause gastroenteritis in North Africa, Foods 14 (2025) 253, https://doi.org/10.3390/foods14020253.

[12] F. Duarte, A. Allepuz, J. Casal, R. Armengol, E. Mateu, J. Castella, J. Heras, G. Ciaravino, Characterization of biosecurity practices among cattle transport drivers in Spain, Preventive vet, Medicine 224 (2023) 106138, https://doi.org/10.1016/j.prevetmed.2024.106138.

[13] J. Wang, X. Zhu, Y. Zhao, Y. Xue, Z. Zhang, L. Yan, Y. Chen, I.D. Robertson, A. Guo, J.W. Aleri, Risk factors associated with Salmonella in dairy cattle farms in Henan and Hubei provinces, China, Animal Dis 3 (2023) 20, https://doi.org/10.1186/s44149-023-00085-9.

[14] D.L. Hanson, G.H. Loneragan, T.R. Brown, T.S. Edrington, Salmonella prevalence varies over time and space in three large, adjacent cattle operations in the southwestern United States, Front. Anim. Sci 3 (2022) 878408, https://doi.org/10.3389/fanim.2022.878408.

[15] N. Bhatt, N.P. Singh, A.K. Mishra, D. Kandpal, S.Jamwal Rajneesh, A detailed review of transportation stress in livestock and its management techniques, Int. J. Livestock Res. 11 (1) (2021) 30–41, https://doi.org/10.5455/ijlr.20201109102902.

[16] L. Bonifait, A. Thépault, L. Baugé, S. Rouxel, F.Le Gall, M. Chemaly, Occurrence of Salmonella in cattle production in France, Microorganisms 9 (2021) 872, https://doi.org/10.3390/microorganisms9040872.

[17] L.A. Neyaz, H.S. Alghamdi, R.M. Alghashmari, S.S. Alswat, R.O. Almaghrabi, F.S. Bazaid, F.M. Albarakaty, K. Elbanna, A comprehensive review on the current status of culture media for routine standardized isolation of Salmonella and Shigella spp. From contaminated food, J. Umm Al-Qura Univer. Appl. Sci. (2024), https://doi.org/10.1007/s43994-024-00205-2.

[18] ISO, Microbiology of the Food Chain — Horizontal method For the detection, Enumeration and Serotyping of Salmonella — Part 1: Detection of Salmonella spp, ISO, International Organization for Standardization, Geneva, 2022, p. 2020, 2022 ISO 6579-1:2017 + Amd 1.

[19] S. Selim, M. Harun-Ur-Rashid, I. Jahan, E.M. Mostafa, Culture-independent molecular techniques for bacterial detection in bivalves, Egypt J. Aq. Res. 50 (2024) (2024) 585–600, https://doi.org/10.1016/j.ejar.2024.11.002.

[20] M. Aladhadh, A review of modern methods of foodborne pathogens, Microorganisms 2023 (11) (2023) 1111, https://doi.org/10.3390/microorganisms11051111.

[21] H.R. Shehata, B. Hassane, S.G. Newmaster, Real-time PCR methods for strain-specific identification and enumeration of lacticaseibacillus paracasei 8700:2, Front. Microbiol. 13 (2023) 1076631, https://doi.org/10.3389/fmicb.2022.1076631.

[22] M. Dmitric, D. Vidanovic1, K. Matovic, B. Tesovic, S. Sekler, I. Vicic, N. Karabasil, Development of a novel invA gene-based real-time PCR assay for the detection of Salmonella in food, Czech J. Food Sci. 41 (4) (2023) 287–294, https://doi.org/10.17221/114/2022-CJFS.

[23] S.J. Bloomfield, A.L. Zomer, J. O'Grady, G.L. Kay, J. Wain, N. Janecko, R. Palau, A.E. Mather, Determination and quantification of microbial communities and antimicrobial resistance on food through host DNA-depleted metagenomics, Food Microbiol 110 (2023) 104162, https://doi.org/10.1016/j.fm.2022.104162.

[24] C. Matchawe, L.M. Ndip, A. Zuliani, M.-C. Ngonde, E. Piasentier, Factors influencing Salmonella contamination and microbial load of beef carcass at the Yaoundé slaughterhouse, Cameroon, J. Food Sci. Eng. 9 (2019) 266–275, https://doi.org/10.17265/2159-5828/2019.07.002.

[25] I. Saenkankam, P. Apiwatsiri, N. Supimon, R. Pachanon, D.J. Hampson, N. Prapasarakul, Comparative analysis of Salmonella contamination in pork slaughtering facilities: implications for food safety, Food Control 167 (2025) 110793, https://doi.org/10.1016/j.foodcont.2024.110793.

[26] A.M. Isaac, H.B. Kolla, K.P. Pallavi, S. Bandyadka, C.N. Mhatre, R.M. Urs, J.J. Kingston, Novel TaqMan® real-time PCR targeting invJ gene for 8-h detection of Salmonella from food matrices, Front. Microbiol. 16 (2025) 1517680, https://doi.org/10.3389/fmicb.2025.1517680.

[27] A. Patel, A. Wolfram, T.S. Desin, Advancements in detection methods for Salmonella in food: a comprehensive review, Pathogens 13 (12) (2024) 1075, https://doi.org/10.3390/pathogens13121075.

[28] F.S. Ahmed, J.M. Abdo, N.S.A. Jakhsi, Detection of Salmonella spp. in meat and meat products by culture, biochemical and molecular characterization in Duhok City, Egypt, J. Vet. Sci. 55 (3) (2023) 561–569, https://doi.org/10.21608/EJVS.2023.230031.1569.

[29] L. Alshaerik, I. Buishi, F.A. Almabrouk, Prevalence and risk factors of Salmonella species in cattle presenting at slaughter in Tripoli, Libya, Libyan J. Agricul. 26 (2) (2021) 55–66.

[30] M.K. Aworh, P. Nilsson, B. Egyir, F.A. Owusu, R.S. Hendriksen, Rare serovars of nontyphoidal Salmonella enterica isolated from humans, beef cattle and abattoir environments in Nigeria, PLoS ONE 19 (1) (2024) e0296971, https://doi.org/10.1371/journal.pone.0296971.

[31] M. Seid, W. Negash, A. Nuru, Salmonella prevalence in cattle slaughtered in selected abattoirs of Amhara National Regional State, Ethiopia, Ethiop, Vet J 28 (2) (2024) 103–118, https://doi.org/10.4314/evj.v28i2.7.

[32] A. Alemu, F. Regassa, N. Kebede, R. Ambachew, M. Girma, Z. Asefa, W. Tsegaye, Magnitude and antimicrobial susceptibility profile of Salmonella recovered from export abattoirs located in East Shewa, Ethiopia, Infect. Drug Resist. 15 (2022) 1353–1365, https://doi.org/10.2147/IDR.S313485.

[33] A.O. Shaibu, E.C. Okolocha, B.V. Maikai, O.T. Olufemi, Isolation and antibiogram of Salmonella species from slaughtered cattle and the processing environment in Abuja abattoirs, Nigeria, Food Control 125 (2021) 107972, https://doi.org/10.1016/j.foodcont.2021.107972.

[34] S. Nouichi, L. Mezali, T. Hamdi, Distribution of Salmonella virulence factors originated from sheep and cattle in Algerian slaughterhouses, J. Hellenic Vet. Med. Soci. 73 (4) (2023) 5013–5020, https://doi.org/10.12681/jhvms.29148.

[35] F.D. Gutema, R.D. Abdi, G.E. Agga, S. Firew, G. Rasschaert, W. Mattheus, F. Crombé, L. Duchateau, S. Gabriël, L. De Zutter, Assessment of beef carcass contamination with Salmonella and E. coli O157 in slaughterhouses in Bishoftu, Ethiopia, Int. J. Food Contam. 8 (2021) 3, https://doi.org/10.1186/s40550-021-00082-1.

[36] A. Tadesse, B. Sharew, M. Tilahun, Y. Million, Isolation and antimicrobial susceptibility profile of Salmonella species from slaughtered cattle carcasses and abattoir personnel at Dessie municipal abattoir, Northeast Ethiopia, BMC Microbiol 24 (2024) 357, https://doi.org/10.1186/s12866-024-03507-x.

[37] E.Z. Gebremedhin, G.T. Soboka, B.M. Borana, L.M. Marami, E.L. Sarba, N.D. Tadese, H.A. Ambecha, Prevalence, risk factors, and antibiogram of nontyphoidal Salmonella from beef in Ambo and Holeta towns, Oromia Region, Ethiopia, Int. J. Microbiol. 2021 (2021) 6626373, https://doi.org/10.1155/2021/6626373.

[38] J. Jeong, H. Song, W.-H. Kim, M. Chae, J.-Y. Lee, Y.-K. Kwon, S. Cho, Tracking the contamination sources of microbial population and characterizing Listeria monocytogenes in a chicken slaughterhouse using culture-dependent and -independent methods, Front. Microbiol. 14 (2023) 1282961, https://doi.org/10.3389/fmicb.2023.1282961.

[39] F.D. Gutema, E.A. Getahun, D.A. Reta, J. Alemnesh, L. De Zutter, S. Gabriël, Assessment of hygienic practices in beef slaughterhouses and retail shops in Bishoftu, Ethiopia: implications for public health, Int. J. Environ. Res. Public Health 18 (2021) 2729, https://doi.org/10.3390/ijerph18052729.

[40] Ministry of Finance, 2025. Livestock, hunting, fishing and fish farming in: finance Law Report on the Nation's economic, social and financial Situation and prospects 2024. Financial Year, November 2024. P. 33. www.minfi.gov.cm and www.dgb.cm.

[41] S. Nabasirye, S.A. Baluka, A. Sengooba, Prevalence and economic losses associated with foetal wastage in abattoirs, Vet. Med. Sci. 10 (1) (2021) e1343, https://doi.org/10.1002/vms3.1343.

[42] U.J. Njoga, E.O. Njoga, O.C. Nwobi, F.O. Abonyi, H.O. Edeh, F.E. Ajibo, N. Azor, A. Bello, A.K. Upadhyay, C.O.R. Okpala, Slaughter conditions and slaughtering of pregnant cows in Southeast Nigeria: implications to meat quality, food safety and security, Foods 10 (2021) 1298, https://doi.org/10.3390/foods10061298.

[43] Y. Botero, K. Schneid, K.L. Samuelson, J.T. Richeson, T.E. Lawrence, G. Levent, Investigating the effects of dietary and management modifications on Salmonella enterica population in harvestready beef cattle, Microbiol. Spectrum 13 (8) (2025) 1–14, https://doi.org/10.1128/spectrum.00264-25.

[44] T. Chalalai, P. Srinontong, W. Aengwanich, K. Srisila, S. Promkrathok, M. Sununta, B. Saraphol, Z. Wu, Impact of burdizzo and surgical castration on immune and oxidative stress markers in cattle, Vet. Sci. 12 (2025) 537, https://doi.org/10.3390/vetsci12060537.

[45] F. Parolini, G. Ventura, C. Rosignoli, R.S. Nodari, M. D'Incau, L. Marocchi, G. Santucci, M. Boldini, M. Gradassi, Detection and phenotypic antimicrobial susceptibility of Salmonella enterica serotypes in dairy cattle farms in the Po Valley, Northern Italy, Animals 14 (2024) 2043, https://doi.org/10.3390/ani14142043.
[46] L.R. Wottlin, T.S. Edrington, R.C. Anderson, Salmonella carriage in peripheral lymph nodes and feces of cattle at slaughter is affected by cattle type, region, and season, Front. Animal Sci. 3 (2022) 859800, https://doi.org/10.3389/fanim.2022.859800.
[47] A. Clinquart, M.P. Ellies-Oury, J.F. Hocquette, L. Guillier, V. Santé-Lhoutellier, S. Prache, Review: on-farm and processing factors affecting bovine carcass and meat quality, Animal 16 (1) (2022) 100426, https://doi.org/10.1016/j.animal.2021.100426.
[48] Animal Welfare Institute-AWI, To promulgate regulations under the Animal Health Protection Act to establish fitness for transport standards for animals shipped interstate by land within the United States, AWI (2024) 337–2332, 900 Pennsylvania Avenue, SE, Washington, DC 20003, (202).
[49] K. Buckham-Sporer, B. Earley, S. Marti, Current knowledge on the transportation by road of cattle, including unweaned calves, Animals 13 (2023) 3393, https://doi.org/10.3390/ani13213393.
[50] S.S. Nielsen, J. Alvarez, D.J. Bicout, P. Calistri, E. Canali, J.A. Drewe, B. Garin-Bastuji, J.L.G. Rojas, C.G. Schmidt, V. Michel, M.A.M. Chueca, Welfare of cattle during transport, EFSA J 20 (9) (2022) 7442, https://doi.org/10.2903/j.efsa.2022.7442.
[51] A.S.D. Djibril, F.T.D. Bothon, G.A. Adjibode, et al., Bovine zoonoses in sub-Saharan Africa: epidemiology, impact and control strategies, Adv. Animal Vet. Sci. 13 (6) (2025) 1210–1225, https://doi.org/10.17582/journal.aavs/2025/13.6.1210.1225.
[52] M.A. Geresu, W.Z. Desta, Carriage, risk factors, and antimicrobial resistance patterns of Salmonella isolates from raw beef in Jimma, Southwestern Ethiopia, Infect. Drug Resist. 14 (2021) 2349–2360, https://doi.org/10.2147/IDR.S313485.
[53] D. Ekwem, T.A. Morrison, R. Reeve, J. Enright, J. Buza, G. Shirima, J.K. Mwajombe, T. Lembo, J.G.C. Hopcraft, Livestock movement informs the risk of disease spread in traditional production systems in East Africa, Sci. Rep. 11 (2021) 16375, https://doi.org/10.1038/s41598-021-95706-z.
[54] Food Business, Chad record rise in informal livestock exports to Cameroon. 2025. foodbusinessmea.com/chad-recording-rise-in-informal-livestock-exports-to-cameroon/?utm_source=chatgpt.com.
[55] C. Doras, R. Ozcelik, M.F. Abakar, R. Issa, P. Kimala, S. Youssouf, I. Bolon, S. Dürr, Community-based symptom reporting among agro-pastoralists and their livestock in Chad in a one health approach, Acta Trop 253 (2024) (2024) 107167, https://doi.org/10.1016/j.actatropica.2024.107167.
[56] B. Kallem, P.K. Kizanlik, C. Şahiner, E.Ö. Göksoy, The impact of cattle hide cleanliness scores on microbial contamination of carcasses during slaughtering, Mac Vet, Rev 45 (1) (2022) i–ix.
[57] D.-O. Brătfelan, A. Tăbăran, S.D. Dan, A.-F. Tăbăran, R. Mărgăoan, O.L. Cri¸san-Reget, M. Mihaiu, Assessment of microbiological contamination and prevalence of pathogenic strains in cattle carcasses from Romanian slaughterhouses, Pathogens 14 (2025) 248, https://doi.org/10.3390/pathogens14030248.
[58] M. Ahmed, M. Abdilahi, B. Bashir, Prevalence of Salmonella and E. Coli and Associated Risk Factors in Camel and Bovine Meat Slaughtered At Jigjiga Municipal Abattoir, Somali Regional State, Ethiopia, 2024 Preprint, doi:10.21203/rs.3.rs-4696474/v1.
[59] K.S. Praveen, R.G. Manjula, T. Swetha, B. Deepthipriya, D. Revathi, N.R. Srikanth, M.M. Rao, An update on body condition scoring system in cattle production and reproduction management, Int. J. Vet. Sci. Animal Husb. 9 (5) (2024) 219–220.
[60] C.N. Boiţeanu, F. Neacsu, L. Tudor, N. Ciocîrlie, Surge in foodborne outbreaks and fatalities in the eu, a 2008-2022 overview of zoonotic diseases, emerging threats and ways of mitigation, Scientific papers, Series D, Animal Sci 68 (1) (2025) 194–213.
[61] F.S. Nuvey, G.I. Mensah, J. Zinsstag, J. Hattendorf, G. Fink, B. Bonfoh, K.K. Addo, Management of diseases in a ruminant livestock production system: a participatory appraisal of the performance of veterinary services delivery, and utilization in Ghana, BMC Vet Res 19 (2023) 237, https://doi.org/10.1186/s12917-023-03793-z.
[62] R.O. Adesola, D. Hossain, O.A. Ogundijo, I. Idris, A. Hamzat, B.H. Gulumbe, A.A. Bakre, O.G. Banwo, D.E. Lucero-Prisno III, Challenges, health risks and recommendations on meat handling practices in Africa: a comprehensive review, Environ. Health Insight 18 (2024) 1–11, https://doi.org/10.1177/11786302241301.