Prevalence and Antimicrobial Susceptibility Pattern of *Salmonella* in Selected Export Abattoirs, East Shewa, Ethiopia

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Abstract

Background

Salmonella is one of the major causes of zoonotic foodborne pathogens in the world, with increasing concern for the emergence and spread of antimicrobial-resistant strains. In Ethiopia, the burden of *Salmonella* is still scarce in abattoirs.

Objectives

To determine the prevalence and antimicrobial susceptibility pattern of *Salmonella* in selected export abattoirs, East Shewa, Ethiopia.

Methods

A cross-sectional study was conducted from January 2020 to October 2020. A total of 345 samples were systematically included and out of which 150 carcass swabs (100 from goats and 50 from sheep carcass), 60 goat skin swabs, 60 knife swabs, and 75 human stool samples. The isolates were identified and characterized following standard bacteriological procedures and further confirmed by using *Salmonella* genus-specific primer by polymerase chain reaction. The isolates were subjected to antimicrobial susceptibility for 14 antibiotics using the Kirby-Bauer disk diffusion method. Data were entered and analyzed using STATA version 14. Fisher's exact test was used to assess significant differences among the abattoirs and type of samples. P -value < 0.05 was considered as indicative of a statistical significance difference.

Results

Out of 345 total samples, 21(6.08%) were positive for *Salmonella*. The specific prevalence of *Salmonella* in carcass, skin, and knife swabs were 10(6.67%), 7(11.67%), and 4(6.67%) respectively. There were no statistically significant differences in the occurrence of *Salmonella* among export abattoirs, and types of samples ($P > 0.05$). *Salmonella* was not isolated from sheep carcass and human stool samples. Among the 21 molecular confirmed *Salmonella* isolates, 7(33.3%) were resistant to at least one antimicrobial agent and 2(9.04%) of isolates were resistant to two antibiotics, tetracycline, and streptomycin. All the isolates were 100% susceptible to kanamycin, chloramphenicol, cephalothin, gentamycin, and ceftriaxone.

Conclusion

Samples harbored *Salmonella* have significant public health impacts and hinder export performance. Thus, hygienic standards throughout the food chain process, surveillance systems, and one health approach are essential methods to minimize risks associated with the consumption of contaminated carcasses. Surveillance programs of antimicrobial usage in animals and animal products are important to ensure consumer safety.

1. Introduction

Salmonella is a foodborne pathogen that causes morbidity and mortality worldwide [1]. Non-typhoidal *Salmonella enterica* subsp. *enterica* is responsible for causing significant numbers of foodborne diseases in many countries [1]. *Salmonella* is a ubiquitous pathogen disseminated to different animals and environments [2, 3]. Food animals serve as the reservoir of non-typhoidal *Salmonella* (NTS) and pose a serious threat to public health and loss of production [4]. Globally, an estimated 93.8 million illnesses and 155,000 deaths are caused by *Salmonella enterica* annually [5]. Non-typhoidal *Salmonella* (NTS) species is one of the most important causes of foodborne disease and manifested by diarrhea, bacteremia, and focal suppurative infection [6]. The process of removing the gastrointestinal tract during the slaughtering of food animals is regarded as one of the most important sources of carcass and organ contamination with *Salmonella* at abattoirs [7, 8].

Salmonella contamination in the beef chain can occur at several stages along the food supply chain includes production, processing, distribution, retailing, preparing, and handling by consumers [9]. The prevalence of antimicrobial-resistance foodborne pathogen increased during recent decades, and it is a global concern [10]. Antimicrobial-resistance (AMR) is an international one health concern that adversely impacts both animal and human health [11]. The utilization of antimicrobial in agriculture for the growth promotion of animals and for the treatment of diseases caused by bacterial pathogens can lead to select antimicrobial-resistant pathogens [12].

In Ethiopia, different studies have been conducted to analyze the prevalence of *Salmonella* and antibiotics susceptibility profiles both in veterinary and public health setup [13, 14]. However, there was a limited study on the magnitude and antimicrobial susceptibility profile of *Salmonella* in export abattoirs. This study was conducted to determine the magnitude and antimicrobial susceptibility profiles of *Salmonella* in selected export abattoirs in Ethiopia.

2. Materials And Methods

2.1. Study areas and periods

The study was conducted in three selected areas namely, Modjo, Bishoftu, and Dukem which are located in the East Shewa Zone of the Oromia region (Fig. 1). These areas were selected based on the availability of standardized carcass export abattoirs. The study was conducted from January to October 2020.

In Ethiopia, export abattoirs were available in different sites of the country. Export abattoirs created good opportunities for the development of the economy through foreign currency earning. The certified export abattoirs are equipped with livestock reception pens, automatic, and semiautomatic mechanical slaughter processing chilling rooms, packaging equipment, and freezing facilities. The name of these export abattoirs are Luna, Organic, Halal, Abyssinia and Aljunia. Three abattoirs were selected from Modjo and one abattoir was selected from Bishoftu and Dukem.

2.2. Study design

A cross-sectional study design was conducted to determine the prevalence and antibiotic susceptibility pattern of *Salmonella*.

2.3. Population

2.3.1. Source of population

The study animals were apparently healthy young, male goats and sheep that were brought to abattoir for slaughter during the study in the period.

2.3.2 Study population

All apparently healthy young, male goats and sheep that were brought for slaughter, abattoir workers, and knives used for slaughtering were study populations that fulfilled the inclusion criteria.

Eligibility criteria

Inclusion criteria

- Male animals that were normal and ready for slaughtering purpose
- Carcass handlers working in selected export abattoirs and who are willing to participate in the study

Exclusion criteria

- Animals on antibiotic treatment for within two weeks at the time of sampling
- Carcass handlers with clinical symptoms and those are on antibiotic treatment within two weeks before the study

Operational definitions

One health approach

Is an approach that recognizes the health of people is closely connected to the health of animals and our shared environment.

Multidrug-resistance

It is resistant to three or more different classes of antibiotics.

2.4. Sample size determination

The sample size was calculated by using the single population proportion estimation formula given by Thrusfield and Christely [15], with a 95% confidence level and 5% desired precision. The sample size was calculated based on 5.7% and 3.57% expected prevalence of bovine and ovine samples respectively in Addis Ababa Abattoir Enterprise, Ethiopia [2].

$$N = \frac{Z^2 * P_{exp}(1 - P)}{d^2}$$

The sample size was calculated as:

$$d^2$$

Where: N = required sample size, Z = standard normal deviation (1.96) at 95% confidence level

P exp = expected prevalence

d = desired absolute solution (0.05)

Accordingly, the calculated sample size was 150 taking into account a 10% non-response rate. A total of 345 samples (100 from goats and 50 from sheep = 150 carcass swabs, 60 goats skin swabs and 60 knife swabs, and 75 human stool samples) were collected for detection of *Salmonella*. Human stool samples were collected from five export abattoirs and from each export abattoir, 15 stool samples were collected.

2.5. Sampling techniques

To recruit the study participants, a systemic random sampling method was used to enroll eligible study participants. The numbers of study participants to be enrolled from each selected export abattoir were determined by proportionality (based on animal and human study participant load).

2.6. Data collection procedure

Sociodemographic characteristics: For the human sample, after taking written consent from each study participant, a semi-structured questionnaire was used to collect sociodemographic characteristics.

2.7. Sample collection and transportation

Study sites were visited to facilitate research collaboration before sample collection. Subsequently, a support letter requesting cooperation was sent to each study site, and the study was conducted from January 2020 to October 2020. The sampling days were randomly assigned to each abattoir. A minimum of 15 samples that contain carcass, skin, and knives swabs and human stool samples were collected from each abattoir.

Carcass swabs

Samples were collected from the carcass (n = 150, 100 from goats, and 50 from sheep). Each carcass was sampled from four regions; neck, abdomen, thorax, and breast regions. Sampling areas delineated by sterile aluminum foil templates (10×10 cm) resulting from a total area of 400 cm². A sterile cotton-tipped swab (2×3 cm) was first soaked in 9 ml buffered peptone water (BPW) (Oxoid, England) and rubbed over the delineated area horizontally and vertically [2]. Two sterile cotton-tipped swabs were used to collect four consecutive areas.

Skin swabs

Samples were collected from external goats' skin surfaces (n = 60). Four areas were selected to collect the skin swabs. These are the abdomen, thorax, neck, and breast areas. A sterile aluminum foil template (10×10 cm) resulting total area of 400 cm² placed these regions. A sterile cotton-tipped swab with wooden shaft first soaked in 9 ml of sterile buffered peptone water (BPW) (Oxoid, England) and rubbed over delineated area horizontally and vertically [9]. Two sterile cotton-tipped swabs were used to collect four consecutive areas.

Knives swabs

Samples from the knives (n = 60) were collected aseptically using sterile cotton swabs. It was collected by rubbing both sides of the knives using a pre-soaked swab [11].

Stool samples

After proper instruction, each study participant was informed to bring freshly voided stool in a clean, dry, and leak-proof disposable stool cup, and a total of 75 stool specimens were collected

Upon completion of all swabbing processes, the wooden shaft was broken off; and the cotton swab was left inside the test tubes contains 9 ml of sterilized buffer peptone water (BPW) (Oxoid, England). The swab samples within test tubes were shaken for 30 seconds for the uniform distribution of microorganisms before transportation. Then samples were transported to Aklilu Lemma Institute of Pathobiology (ALIPB) medical microbiology laboratory in an icebox within 3–4 hours.

2.8. Microbiological analysis

Isolation and identification of *Salmonella*: Isolation and identification of *Salmonella* were performed at Aklilu Lemma Institute of Pathobiology department of the medical microbiology laboratory. *Salmonella* isolation and identification were carried out in line with guidelines of the International Organization for Standardization (ISO 6579-1: 2017) and World Health Organization (WHO) global foodborne infections network laboratory protocol [8, 16].

Pre-enrichment in non-selective liquid medium

The swab samples were put in 9 ml of buffered peptone water (BPW), (Oxoid, England). This pre-enriched sample incubated for 18–24 hours at 37°C for recovery and proliferation of cell might be injured during

processing or to make a number of the target organism grow to detectable level [4].

Enrichment selective liquid media

Enrichment selective broth namely, Rappaport Vassiliadis soya broth (RVS) (Oxoid, England CM950-500G) for all samples except stool and selenite F broth for a stool sample (Oxoid, England, CM651-500G) were used to inhibit non-targeted microorganisms like gram-positive bacteria and coliforms and permit rapid multiplication of *Salmonella*. After pre-enrichment in buffered peptone water (BPW) 0.1 ml cultures were transferred aseptically into 10 ml of RVs and incubated for 18–24 hours at 41.5°C. For the stool sample, 0.1 ml of culture from BPW was transferred to 10 ml of selenite F broth, homogenized, and incubated for 18–24 hours at 41.5°C and 37°C [4].

Plating out and identification

A loopful of 100 µm was taken from RVs and selenite F broth and streaked into the xylose lysine deoxycholate agar (XLD) (Oxoid, England CM0469-500G) plates and incubated at 37°C for 18–24 hours. Suspected *Salmonella* isolates were subcultured on the nutrient agar (Oxoid, England, CM0003-500G) and incubated at 37°C for 18–24 hours. The isolates from the sub-culture were stored in the refrigerator at 4°C for the biochemical test, molecular testing, and antimicrobial susceptibility test [10].

2.9. Biochemical characterization

Suspected *Salmonella* colonies from nutrient agar (Oxoid, England CM0003-500G) were picked up and determined its biochemical characteristics using triple sugar iron agar (TSI) (Oxoid, England CM277-500G), lysine iron agar (LIA) (Oxoid, England CM0381-500G), Simmon’s citrate agar (Himedia, India CM0129-500G), urea slant (Himedia, India M111A-500G) and sulfide indole motility (SIM) (Oxoid, England S12-500G) agar [12].

10. Molecular techniques

Polymerase chain reaction (PCR) was used to confirm the identification made by phenotypic tests.

DNA extraction: Bacterial colonies confirmed as *Salmonella* by biochemical tests were cultured overnight on xylose lysine deoxycholate agar (XLD agar). Then DNA extraction was performed using the boiling method. The **set of primer targeted conserved regions of *Salmonella* forward and reverse were used** [8].

Table 1: Primers used to detect *Salmonella*

Genome	Primers	Sequences (5'-3')
Histidine transport operon gene	Forward	ACTGGCGTTATCCCTTTCTCTGGTA
	Reverse	ATGTTGTCCTGCCCCTGGTAAGAGA

Molecular confirmation by using polymerase chain reaction: All isolates shown specific biochemical characteristics of *Salmonella* was further confirmed by using genus-specific PCR as described by (29). It is based on the amplification of a 496-bp segment of histidine transport operon gene, which is highly conserved among species of *Salmonella*. Reference strain of *S. Typhimurium* (ATCC 14028) was used as a positive control during PCR. Polymerase chain reaction (PCR) amplification was run in reaction mixtures (20µl) with master mix (10µl), forward (0.50µl) and reverse (0.50µl) primer, nuclease-free water (8.0µl) and DNA template (1.0µl). Amplification was performed in a thermocycler with temperature profiles of 2 minutes at 94 °C for initial denaturation followed by 35 cycles of at 94 °C for 1 minute, annealing at 58 °C for 1 minute and extension at 72 °C for 1 minute with final extension step at 72 °C for 5 minutes [7].

Agarose gel electrophoresis and visualization of PCR products: Polymerase chain reaction (PCR) products were electrophoresed using 2 grams agarose powder (Rugby, UK) in 100 ml of 1× TAE buffer (Bio Concept, Switzerland). A volume of 2 µl of ethidium bromide was added to the gel before pouring it into the casting tray. A 100-bp DNA ladder was used as a molecular size marker to estimate the size of the products. A band of 496 base pairs (bp) was considered positive for *Salmonella*. Gel electrophoresis was carried out at 120 volts for 60 minutes, viewed under an ultraviolet (UV) trans-illuminator [5].

2.11. Antimicrobial susceptibility test

The isolates confirmed by polymerase chain reaction (PCR) were subjected to antibiotic susceptibility test using Kirby-Bauer disk diffusion techniques [17], on Mueller-Hinton agar (Oxoid, England) in following Clinical and Laboratory Standard Institute (CLSI, 2018) [18]. From each PCR confirmed isolate, three to four colonies grown on nutrient agar were transferred to a tube containing 3 ml of nutrient broth (Oxoid, England). The broth culture was incubated at 37°C for 18-24 hours and until its turbidity adjusted to 0.5 McFarland standards. The suspension was inoculated onto Mueller-Hinton agar (MHA) plates using sterile cotton swabs. The plates were uniformly inoculated by rubbing against the entire agar surface and rotating the plates at about 90 degrees three times.

The plates were held at room temperature for 15 minutes to allow drying. Antibiotic impregnated disks were applied to the surface of the inoculated plate using sterile forceps and incubated aerobically at 37°C

for 24 hours. *Salmonella* isolates were tested for antibiotics includes kanamycin (30µg, K), ciprofloxacin (5µg, CIP), chloramphenicol (30µg, C), cephalothin (30µg, CEP), tetracycline (30µg, TE), ampicillin (10µg, AMP), nalidixic acid (30µg, NA), streptomycin (10µg, S), gentamicin (10µg, GEN), ceftriaxone (30µg, CRO), amikacin (10µg, AN), neomycin (30µg, N), amoxicillin +clavulanic acid (20/10µg, AMC) and sulfamethoxazole+trimethoprim(1.25/23.75µg, SXT). Following the incubation of the plates at 37°C for 24 hours, a diameter of inhibition zone was measured to the nearest millimeters using a digital caliper and interpreted as sensitive (S), intermediate (I), or resistant (R) accordance with Clinical and Laboratory Standard Institute (CLSI, 2018) [18].

3. Results

Sociodemographic characteristics of human study participants in selected export abattoirs

A total of 75 carcass handlers were enrolled in this study with a response rate of 100%. The sex distributions were 55 males and 20 females with an age range of 22–50 years old with a mean age of 32 years (± 8.61 SD). Educational backgrounds were 3(5%) primary school, 65(86.6%) secondary school and 7(9.33%) have diploma certificate. Most of the respondents were married 50(67%). All participants were trained about food hygiene and wearing personnel protective equipment. Among carcass handlers, 65(86.6%) have a certificate in food safety. All participants undertake periodical medical check-ups and wash their hands with soap and water after the toilet and touching any material (Table 2).

Table 2

Socio-demographic characteristics of human study participants in selected export abattoirs, East Shewa, Ethiopia from January to October 2020

Variables	Category	Frequency (N = 75)	Percentages (%)
Age	22–35	25	33.0
	36–50	50	67.0
Sex	Male	55	73.3
	Female	20	26.6
Marital status	Married	50	67.0
	Single	25	33.0
Education	Primary	3	4.0
	Secondary	65	86.6
	Diploma	7	9.3
Residency	Modjo	45	70.0
	Bishoftu	15	15.0
	Dukem	15	15.0
Having certificate of Food safety	Yes	65	86.6
	No	10	13.4
Periodical medical check-up	Yes	75	100
	No	-	-
Consumption of raw meat	Yes	1	5.0
	No	74	95
Food hygiene training	Yes	75	100
	No	-	-
Using personnel protective equipments	Yes	75	100
	No	-	-
Workexperience years	5–8	62	85.0
	> 9	13	15.0
Hand washing by soap and water after toilet and touching any materials	Yes	75	100
	No	-	-

3.1. Prevalence of *Salmonella*

During the study period, a total of 345 samples were collected from five export abattoirs. Thirty-six of them shown suspected *Salmonella* colonies on xylose lysine deoxycholate agar (XLD) observed and only 21 isolates shown typical biochemical properties of *Salmonella*. These 21(6.08%) isolates were further confirmed by polymerase chain reaction (PCR) amplification and were confirmed as *Salmonella* (Figs. 2 and 3). *Salmonella* was not isolated from all human stool (75) and sheep carcass swabs (50). The highest proportion of positive samples were detected from goat skin swabs 7(11.67%) followed by goat carcass swabs 10(6.67%) and knife swabs 4(6.67%) (Table 3).

Table 3

Prevalence of *Salmonella* on types of study samples in selected export abattoirs, East Shewa, Ethiopia from January to October 2020

Sample types	No. of samples	No. of positives	(95% CI)	Exact test	p-value
Goat carcass swabs	100	10	(3.5, 11.19)		
Knife swabs	60	4	(2.5, 16.64)		
Goat skin swabs	60	7	(5.7, 23)		
Human stool samples	75	0		0.304	0.188
Sheep carcass swabs	50	0			
Total	345	21	(4.9, 11.2)		

PCR result by pi-chart

The 21 of the isolates were confirmed by polymerase chain reaction (PCR) test (Fig. 3).

3.2. Antimicrobial susceptibility test of *Salmonella* isolates

Among the 21 molecular confirmed *Salmonella* isolates, all the isolates were 100% susceptible to kanamycin, chloramphenicol, cephalothin, gentamicin, and ceftriaxone. A total of 21(95.2%) and 1(4.76%) were intermediately resistant to neomycin and streptomycin, respectively (Table 4).

Table 4: Antibiotic susceptibility profiles of *Salmonella* isolates (n=21) in selected export abattoirs, East Shewa, Ethiopia

Antimicrobials Antibiotic susceptibility profiles

		S (%)	I (%)	R (%)
	30µg	21(100%)	0(0%)	0(0)
	5µg	20(95.2%)	0(0%)	1(4.76%)
	30µg	21(100%)	0(0%)	0(0%)
	30µg	21(100%)	0(0%)	0(0%)
	30µg	19(90.47%)	0(0%)	2(9.52%)
	10µg	20(95%)	0(0%)	1(4.76%)
	30µg	20(95%)	0(0%)	1(4.76%)
	10µg	18(85%)	1(4.76%)	2(9.52%)
	10µg	21(100%)	0(0%)	0(0%)
	30µg	21(100%)	0(0%)	0(0%)
	10µg	20(95.2%)	0(0%)	1(4.76%)
	10µg	0(0%)	20(95.2%)	1(4.76%)
acid	20/10µg	20(95.2%)	0(0%)	1(4.76%)
ethoprim	1.25/23.75µg	20(95.2%)	0(0%)	1(4.76%)

S=susceptible I=intermediate R=resistant

Overall, 7(33.33%) of the isolates were resistant to at least one of the tested 14 antimicrobial agents. Among of the 21 isolates, only 2(9.04%) isolates were resistant to tetracycline and streptomycin (Table 5).

Table 5
Drug-resistance pattern in selected export abattoirs from January to October 2020

Number of drugs	Antibiotics	No. of resistant Isolates	Isolate origion
One drug	CIP, AM, NA, AN, N, AMP and SXT	7(33.33%)	CS
Two drug	TE (2) and S(2)	2(9.04%)	SW
Key: CIP = Ciprofloxacin, AM = Ampicillin, NA = Nalidic Acid, AN = Amikacin, N = Neomycine, AMP = Amoxacillin + Clavulanic acid, SXT = Sulfamethoxazole + Trimethoprim, TE = Tetracycline, S = Streptomycin, CS = Carcass Swab, S = Skin Swab			

4. Discussion

In this study, the overall prevalence of *Salmonella* was 21(6.08%). This is comparable with finding in dairy cattle in central Ethiopia (7%) [19], Colorado State University veterinary teaching hospital (5.9%) [20], and on pork and goat carcass in the Bahamas (5.9%) [21]. On the contrary, our finding is lower than study reported on exotic chickens in Debre Zeit and Modjo, Ethiopia (14.6%) [22], ground beef at retail store in Jalisco State, Mexico (56.7%) [23], from milk and meat in Bangladesh (60%) [24], Kwata slaughterhouse Awka, Anambra State (33.5%) [16] from abattoir and environment in Nigeria (92.31%) [25] and raw beef in Wolaita Sodo municipal abattoir, Southern Ethiopia (12.5%) [26]. However, the result is higher than study conducted on slaughtered cattle in Addis Ababa, Ethiopia (3.7%) [3], slaughter sheep in Turkey (0.7%) [27], food handlers at the University of Gondar, Ethiopia (3.1%) [28], from animal-origin food items in Gondar, Ethiopia (5.5%) [29] and slaughtered bovine, and ovine in Addis Ababa abattoir enterprise 4.64% [2]. *Salmonella* was not detected from sheep carcass swabs, which is comparable with the study conducted on slaughter sheep carcass swabs in Turkey [30].

The discrepancies in Ethiopia as well as in other countries could be associated with the degree of exposure of animals to stress factors like transportation and starvation, climatic conditions, management practices, age groups, species of animals, hygienic conditions, types of abattoirs and facilities, food handling and geographical difference. In addition, the discrepancies in isolation might be depending on the difference in sampling strategies, study periods, sample size, study population, methodologies, and culture media.

In the present study, the proportion of *Salmonella* in different samples such as skin swabs (11.66%), carcass swabs (6.66%), and knives swabs (6.66%). The findings show that prevalence in this study is lower than the study conducted to the isolation of *Salmonella* in carcass swabs (30%), and skin swabs (59.7%) of cattle slaughtered in South Africa [4] and knives swabs (16.7%) selected dairy farms, abattoir, and humans at Asella Town, Ethiopia [9]. However, it is higher than study conducted (1.8%) on carcass swabs on animal sources in South Africa [31], (2.5%) knife swabs from the abattoir, and environment in Nigeria [32], and (1.6%) skin swabs of dairy cattle slaughter in Northern Italy [33], and (4.5%) Kwata slaughterhouse, Awka, Anambra State [16]. The difference could be associated with hygienic status, management systems, and cross-contamination among materials used in slaughtering procedures.

Animals that entered into abattoirs were particularly dirty, which contributed to the spread and cross-contamination of skin with *Salmonella* pathogen. The proportion of the carcass contamination in this study recorded, and the potential source of contamination is diverse. The carcass could have been contaminated during skin removal or evisceration. In the abattoirs, the same knife was used for the slaughtering of the different animals, and some individuals ignored the adequate sterilization of the knives and this might be contributing to chances of carcass contamination. Occasionally, when moving the carcass from one place to another place; there is close contact between the different carcass and this may result in the carcass-to-carcass transfer of *Salmonella*. All these factors may also contribute to the prevalence of *Salmonella* in selected export abattoirs, East Shewa, Ethiopia.

In the present study, we have also assessed the antimicrobial susceptibility test of *Salmonella* isolates. The result of the in-vitro antibiotics sensitivity test to *Salmonella* isolates showed different degrees of sensitivity against the tested antibiotics ranging from 0–100%. The highest susceptibility (100%) was observed against kanamycin, chloramphenicol, cephalothin, gentamycin, and ceftriaxone. The isolates were susceptible to ceftriaxone and chloramphenicol, which is in agreement with the previous finding of cattle slaughtered in Addis Abeba [3] and dairy cattle in central Ethiopia [19]. In addition, the isolates in the current study were susceptible to gentamycin and ceftriaxone, which is in line with similar studies from food handlers at the University of Gondar, Ethiopia [28].

Among the 21 molecular confirmed *Salmonella* isolates, 7(33.3%) were resistant to at least one antimicrobial agent and 2(9.04%) of *Salmonella* isolates were resistant to tetracycline and streptomycin. This is in conformity with the study conducted in Ecuador that reported resistance rate for other antibiotics ranged from 11.1% up to 33.3% [34]. Multidrug-resistance has not been recorded in this study. In this study, among tested antibiotics, kanamycin, ceftriaxone, chloramphenicol cephalothin, and gentamicin were found to be the most effective drugs to inhibit the in vitro growth of these isolates. Thus, these drugs could be used for empirical treatment in the area where a culture facility is not available.

Limitation of the study

In this study, isolates were not serotyped and molecularly characterized due to budget constraints.

5. Conclusion And Recommendations

The prevalence of *Salmonella* in selected export abattoirs was found to be 21(6.08%). This may indicate that it has public health impacts and leads to a socio-economic problem. Thus, bacteriological assessment of *Salmonella* pathogen from export abattoirs was essential to improve surveillance system and hygienic standards. Among the tested antimicrobial: kanamycin, ceftriaxone, chloramphenicol, cephalothin, and gentamicin were 100%. Antimicrobial treatment approaches should be based on the bacteriological culture followed by an antimicrobial susceptibility test.

Abbreviations

ALIPB: Akililu Lemma Institute of Pathobiology; AMR: Antimicrobial-Resistance; AST: Antimicrobial Susceptibility Testing; BPW: Buffered Peptone Water; CLSI: Clinical and Laboratory Standards Institute; MoA: Ministry of Agriculture; PCR: Polymerase Chain Reaction; RVS: Rappaport Vassiliadis Soya Broth; SPHMMC: Saint Paul's Hospital Millennium Medical College; WHO: World Health Organization; XLD: Xylose Lysine Deoxycholate

Declarations

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Ethical consideration: Ethical approval was obtained from St. Paul's Hospital Millennium Medical College (SPHMMC) (Pm23/423) Institutional Review Board (IRB). A letter was written from St. Paul's Hospital Millennium Medical College Department of Microbiology, Immunology, and Parasitology to the research study area. In addition, official permission was also obtained from the Ministry of Agriculture (MoA), abattoir inspection, and certification directorate to undertake the study. Study participants were informed about the purpose and procedures of the study. Written informed consent was obtained from each human study participant. To ensure confidentiality, participants' data were linked to the code number.

Availability of data and materials: The data sets used and analyzed in the study are available from the corresponding author on reasonable request.

Consent for publication: Not applicable

Competing interests: The authors declare that they have no competing interests.

Authors' contributions AA, FR, NK, RA, and WTS participated in the conception of the study, drafting, and reviewing the manuscript. AA was involved in sample collection and laboratory investigation. AA and NK have participated in laboratory sample processing. AA and GM were involved in the polymerase chain reaction (PCR). All authors read and approved the final manuscript.

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Figures

Figure 1

Geographical location of the study areas

Figure 2

PCR result by pi-chart

Figure 3

Agarose gel electrophoresis of the 21 *Salmonella* isolates confirmed by PCR test. Mw = Molecular weight marker: (Kb plus DNA ladder): Lane 1-21 positive samples for *Salmonella* NC= negative control, PC= positive control (*S. Typhimurium*: ATCC 14028) Agarose gel electrophoresis of *Salmonella* PCR products at 496 bp (16SrRNA gene) amplification of target region of histidine transport operon.