Prevalence and Antimicrobial Susceptibility Profile of Salmonella Serovars Isolated from Slaughtered Cattle in Addis Ababa, Ethiopia

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Salmonella is one of the top causes of foodborne bacterial illnesses in humans. The primary sources of human Salmonella infection are food producing animals such as cattle, poultry, and swine. A cross-sectional study was undertaken to estimate the prevalence and to determine the serovar distribution and antimicrobial susceptibility profiles of Salmonella spp. isolated from fecal (n=567) and carcass swab (n=159) samples of slaughtered cattle at Addis Ababa Abattoir Enterprise and Kara’alo PLC, Abattoirs, in Addis Ababa, Ethiopia between January 2014 and April 2015. Salmonella isolation was conducted according to Global Foodborne Infections Network Laboratory Protocol and isolates were confirmed by genus specific PCR and serotyped by slide agglutination test. Susceptibility of the isolates to 17 antimicrobials was tested using the Kirby-Bauer disk diffusion method according to the guidelines of the Clinical and Laboratory Standards Institute. Out of the total 726 samples examined, 27 (3.7%) were positive for Salmonella. Salmonella was detected in 4.1% (23/567) fecal and 2.5% (4/159) carcass swab samples. Twelve different serovars were identified and the most predominant serovars were S. Dublin (n=10, 35.7%) and S. Virchow (n=5, 17.9%), followed by S. Braendrerup, S. Haifa, and S. Saintpaul which were isolated from 2 samples each (7.1%). All of the Salmonella isolates investigated were resistant or intermediately resistant to four or more of the 17 drugs tested. High resistance rate was recorded to streptomycin 25 (89.3%), cephalothin 20 (71.4%), ampicillin 19 (67.9%), and amoxicillin+clavulanic acid 19 (67.9%). Resistance to five or more antimicrobials was detected in 20 (71.5%) of the isolates. Multidrug resistance to more than 7 antimicrobials was detected in 5 (17.9%) of the isolates. Isolation of such multidrug resistant strains of Salmonella from slaughtered cattle poses a major public health concern. These findings imply the need for a strict biosecurity and regulation of antimicrobial use across the country.

1. Introduction

Salmonella is one of the most important foodborne bacteria in the world and infection with Salmonella spp. is a major cause of diarrhea in children and adults [1]. Salmonella belongs to the Enterobacteriaceae family which also includes pathogens such as Escherichia coli, Shigella, and Klebsiella [2]. Members of the genus Salmonella are ubiquitous pathogens that infect a wide variety of mammals, birds, fish, and reptiles, as well as humans. There are 2 species of Salmonella: Salmonella enterica and Salmonella bongori. Salmonella enterica is classified into 6 subspecies of which Salmonella enterica subspecies enterica is the dominant subspecies affecting humans and domestic animals [3]. There are currently over 2,700 Salmonella serovars [4], which are serologically identified by antigenic variation in the O (Lipopolysaccharide), H (Flagella), and Vi (Capsular) antigens in accordance with the Kauffmann–White scheme [4, 5].
Salmonellosis represents an important public health problem among the common bacterial foodborne pathogens worldwide. Estimated global burden of 93.8 million gastroenteritis cases and 155,000 deaths are due to Salmonella species annually, of which 85.6% is foodborne [6]. Human salmonellosis has been associated with contaminated food products, mainly those of animal origin such as poultry, beef, pork, and dairy products, as well as direct contact with infected animals [7–9].

The presence of Salmonella in food animals and the consequent cross-contamination of edible carcass present a significant food-safety hazard [10]. Food animals such as cattle may carry Salmonella at slaughter and can serve as sources of contamination and provide an opportunity for entry of the pathogen into the food products. This implies that the presence of Salmonella in slaughter cattle and slaughter house environment and the potential cross-contamination of carcasses and edible organs can pose a significant food-safety hazards [3]. There is little available data on Salmonella presence in cattle feces and carcass swab and such information is important to understand the impact of the bacteria on food producing animals and the subsequent risk to humans which consume cattle products. The aim of the current study was therefore to estimate Salmonella prevalence in feces and carcass swab of cattle slaughtered at Addis Ababa Abattoir Enterprise and Karáalo PLC abattoir. Furthermore, the isolates were serotyped and tested for antimicrobial susceptibility.

2. Materials and Methods

2.1. Study Area and Study Design. The study was conducted in Addis Ababa between January 2014 and April 2015. Addis Ababa is the capital city and administration center for the Federal Democratic Republic of Ethiopia. There are four big abattoirs in Addis Ababa town, of which three of them are government owned and the other one is a private limited company (PLC). Of these four abattoirs, we selected two abattoirs, namely, Addis Ababa Abattoir Enterprise and Karáalo PLC Abattoir.

Addis Ababa Abattoir is the largest government owned abattoir in Addis Ababa, established with the objective of providing wholesome and hygienically slaughtered meat to the public. The enterprise gives slaughtering service for average of 1200 cattle, 1000 sheep, and goats and 10 camels per day. Karáalo PLC abattoir is the only private abattoir found in Addis Ababa which is located in Karáalo area, Addis Ababa. The abattoir gives slaughtering services for the average of 350 cattle per day. The animals slaughtered in these abattoirs originate from different parts of the country.

Study Design and Sample Size Determination. A cross-sectional study was conducted on apparently healthy cattle that were slaughtered at both abattoirs. The required sample size of the study was determined by the formula given by Thrusfield [11] with 95% confidence interval and 5% desired precision. Based on the mean prevalence report of 10.6% from previous work [12], we calculated the samples size as follows.

\[
N = \frac{(1.96)^2 \times P \times (1 - P)}{d^2},
\]

where \(N\) is required sample size, \(P\) is expected prevalence, and \(d\) is desired absolute precision of 0.05. Therefore, the calculated sample size was 146, but, to increase the precision of the study and to increase the number of Salmonella isolates, a total of 720 samples (567 fecal and 159 Swab samples) were collected from the two abattoirs.

2.2. Sample Collection. Fresh fecal sample was collected directly from the rectum of each animal during ante-mortem inspection before slaughter using disposable gloves. Fecal samples were collected into sterile zippered plastic bags directly from rectum using disposable gloves and transported to Microbiology Laboratory, Aklilu Lemma Institute of Pathobiology, Addis Ababa University, in ice box. Similarly, carcass swab was sampled by rubbing the entire surface of each carcass (both sides) once from the hind quarter to the forequarter, uniformly using sterile cotton swab. Each swab sample was then placed into screw caped test tubes containing 10 ml of sterilized buffered peptone water (BPW) (Becton Dickinson, Sparks, MD) placed in an ice box with an ice pack and transported to Microbiology Laboratory, Aklilu Lemma Institute of Pathobiology, within 3–4 h of collection.

2.3. Bacterial Isolation and Identification. Isolation and identification of Salmonella were conducted using conventional methods [13]. Briefly, 10 g of feces were preenriched in 90 ml of sterile buffered peptone water (BPW) (Becton Dickinson, Sparks, MD) and incubated overnight at 37°C. Similarly, the carcass swab sample in BPW was placed in incubator overnight at 37°C. A 100μl of each preenriched suspension was added into 9.9 ml of Rappaport-Vassiliadis enrichment Broth (RVB) (Oxoid, USA) and incubated at 42°C for 24 h. At the same time, 1 ml of the suspension was also transferred to 10 ml of Tetrathionate broth (TTB) (Oxoid, USA) and incubated for 24 h at 37°C. It was then streaked from both RVB and TTB to Xylose Lysine Tergitol 4 (XLT-4) (Oxoid, USA) selective media and the plates were incubated at 37°C for 24 to 48 h. Presumptive Salmonella colonies were further investigated biochemically using Triple Sugar Iron agar, Urea, Citrate, and Lysine Iron Agar slants. Those colonies with typical Salmonella biochemical properties were then further confirmed by genus specific PCR [14]. A reference strain of S. Typhimurium (ATCC 14028) was used as a positive control during biochemical analysis and PCR. One confirmed Salmonella isolate from each positive sample was stored at −80°C in 20% glycerol until further testing. When Salmonella was recovered from samples enriched with both RV and TTB, they were considered as different strains until we conduct antimicrobial susceptibility test. Isolates with different antimicrobial susceptibility profile were considered different strains and both of them were submitted for serotyping. However, when isolates exhibited identical antimicrobial susceptibility profile, they were considered as the same strain and only one isolate was randomly selected for further investigation.

2.4. Salmonella Serotyping and Phage Typing. Salmonella isolates were serotyped and phage-typed at the Public
Table 1: Summary of the prevalence of Salmonella and sample types.

| Abattoir Name | Sample type | Numbers examined | No. positive (%) |
|---------------|-------------|------------------|-----------------|
| Addis Ababa   | Fecal       | 282              | 11 (3.9%)       |
|               | Swab        | 60               | 2 (3.3%)        |
| **Subtotal**  |             | **342**          | **13**          |
| Kara’alo      | Fecal       | 285              | 12 (4.2%)       |
|               | Swab        | 99               | 2 (2.0%)        |
| **Subtotal**  |             | **384**          | **14**          |
| **Total**     |             | **726**          | **27 (3.7%)**   |

Table 2: Salmonella serovars isolated from fecal and swab samples of cattle slaughtered at Addis Ababa, Ethiopia.

| Serovars         | Antigenic formula | No. isolated from each Abattoirs | Total (%) |
|------------------|-------------------|----------------------------------|-----------|
| Dublin           | 9,12:g,p:-         | Addis Ababa 10, Kara’alo 10      | 10 (35.7) |
| Virchow          | 6,7:r:i,1,2        | 2, 3                                      | 5 (17.9) |
| Braendrerup      | 6,7:e,k:e,n,z15    | 2, 0                                      | 2 (71)    |
| Saintpaul        | 4:e,h:1,2          | 2, 0                                      | 2 (71)    |
| Haifa            | 4:z10:i,1,2        | 2, 0                                      | 2 (71)    |
| Kottbus          | 6,8:e,h:1,5        | 1, 0                                      | 1 (3.6)   |
| Kentucky         | 8,20:i,z6          | 1, 0                                      | 1 (3.6)   |
| Mikawasima       | 6,7:y,e,n,z15      | 1, 0                                      | 1 (3.6)   |
| Typhimurium phage type 3 | 4,5:i,1,2 | 1, 0                                     | 1 (3.6)   |
| Typhimurium phage type 193 | 4,5:i,1,2 | 1, 0                                     | 1 (3.6)   |
| Typhimurium phage type 4 | 4,5:i,1,2 | 1, 0                                     | 1 (3.6)   |
| I:ROUGH-O:9:g,p:- | -g,p:-             | 0, 1                                     | 1 (3.6)   |
| **Total**        |                    |                                           | **28 (100)** |

3. Results

3.1. Prevalence of Salmonella. Salmonella was isolated from 27 of the 726 samples examined resulting in an overall Salmonella prevalence of 3.7%. From the total of 567 fecal samples, 23 (4.1%) and from 159 carcass swab samples 4 (2.5%) were found positive for Salmonella. Summary of the prevalence of Salmonella from fecal samples and carcass swab samples in the two abattoirs is presented in Table 1.

3.2. Salmonella Serovar Distribution. A total of 12 different Salmonella serovars were identified and the most predominant serovars identified were S. Dublin 10 (35.7%) and S. Virchow 5 (17.86%). Other serovars like S. Braendrerup, S. Haifa, and S. Saintpaul were also isolated from 2 samples each (7.14%). Two serovars were isolated from single sample, namely, S. Haifa and S. Kottbus: one from fecal sample obtained from a cattle slaughtered in Addis Ababa Abattoir enriched with RV and the other from the same sample enriched with TTB. Table 2 shows the distribution of Salmonella serovars and their antigenic formula.

3.3. Antimicrobial Susceptibility of Salmonella Isolates. The antimicrobial susceptibility profile of Salmonella isolates is shown in Table 3. High resistance rate was recorded among...
Table 3: *Salmonella* serovar distribution and frequency of resistance to various antimicrobials.

| Antimicrobials tested | *Salmonella* serovars and No. (%) of isolates resistant to various antimicrobials (n=28) | No. (%) resistant |
|-----------------------|------------------------------------------------------------------------------------------|------------------|
|                       | Dublin n=10 Virchow n=5 Typhimurium n=3 Saintpaul n=2 Braenderup n=2 Haifa n=2 Kottbus n=1 Kentucky n=1 Mikawasima n=1 I:ROUGH-O:g,p:- |                |
| Amp                   | 10 (100) 3 (60) 2 (66.7) 2 (100) - - - 1 (100) - 1 (100) | 19 (67.9)        |
| Amc                   | 10 (100) 3 (60) 2 (66.7) 2 (100) - - - 1 (100) - 1 (100) | 19 (67.9)        |
| Cf                    | 10 (100) 3 (60) 2 (66.7) 2 (100) - - - 1 (100) | 20 (71.4)        |
| Cro                   | - - - - - - - - - - - - 0                  | 0               |
| Fox                   | 1 (10) - - - - - - 1 (100) | 2 (71)           |
| An                    | - 1 (20) - - 1 (50) 1 (50) - - 1 (100) | 4 (14.3)         |
| Gm                    | 1 (10) - - - - - - 1 (100) | 2 (71)           |
| K                     | 3 (30) 5 (100) 2 (66.7) 1 (50) 1 (50) 2 (100) 1 (100) | 16 (57.1)        |
| S                     | 10 (100) 5 (100) 2 (66.7) 2 (100) 2 (100) 1 (50) 1 (100) | 25 (89.3)        |
| Sxt                   | - - 1 (33.3) - - - - - - - | 1 (3.6)          |
| Cip                   | - 1 (20) 2 (66.7) 2 (100) 2 (100) 1 (50) | 1 (35.7)         |
| Na                    | 1 (10) - - - - - - 1 (100) | 2 (71)           |
| Te                    | - 2 (40) 1 (33.3) 2 (100) 2 (100) 1 (50) 1 (100) 1 (100) | 11 (39.3)        |
| C                     | - - - - - - - - - - - - 0                  | 0               |
| Tmp                   | 1 (10) - - 1 (33.3) - - - - - - | 2 (71)           |
| Su                    | 1 (50) 2 (40) - 2 (100) 2 (100) 2 (100) 1 (100) 1 (100) | 12 (42.9)        |
| Nitro                 | - 2 (40) 2 (66.7) - 1 (50) 2 (100) 1 (100) 1 (100) | 10 (35.7)        |

An: amikacin, Amp: ampicillin, Amc: amoxicillin+clavulanic acid, C: chloramphenicol, Cro: ceftriaxone, Cf: cephalothin, Cip: ciprofloxacin, Fox: cefoxitin, Gm: gentamicin, K: kanamycin, Sxt: sulfamethoxazole+trimethoprim, Tmp: trimethoprim, Te: tetracycline, Su: sulfisoxazole, S: streptomycin, Nitro: nitrofurantoin, and Na: nalidixic acid. *Isolates intermediately resistant were also considered resistant.*
Table 4: Antimicrobial resistance pattern of *Salmonella* serovars isolated from slaughtered cattle.

| Serovar                  | No. | Resistance Pattern          | Resistant |
|--------------------------|-----|-----------------------------|-----------|
| Braendrerup              | 1   | Cip, Te, Su, S              | -         |
| Braendrerup              | 1   | An, Cip, K, Te, Su, S       | Nitro     |
| Dublin                   | 2   | K                            | Amp, Amc, Cf, S |
| Dublin                   | 2   | S                            | Amp, Amc, Cf |
| Dublin                   | 1   | S                            | Amp, Amc, Cf, Gm |
| Dublin                   | 1   | S, Su, Tmp                   | Amp, Amc, Cf |
| Dublin                   | 1   | S                            | Amp, Amc, Cf |
| Dublin                   | 1   | -                            | Amp, Amc, Cf, S |
| Dublin                   | 1   | Fox, K                       | Amp, Amc, Cf, S |
| Dublin                   | 1   | Na, S                        | Amp, Amc, Cf |
| Haifa                    | 1   | K, Nitro                     | Te, Su     |
| Haifa                    | 1   | An, Cip, K, Su, S, Nitro     | -         |
| Kottbus                  | 1   | Cf, K                        | Te, Su, Nitro |
| Kentucky                 | 1   | K, Nitro                     | Amp, Amc, Cf, Cip, Gm, Te, Su, S, Na |
| Mikawasima               | 1   | An, Cip, Te                  | Su, S, Nitro |
| Saintpaul                | 1   | Amc, Cip, K, Su, S           | Amp, Cf, Te |
| Saintpaul                | 1   | Amp, Amc, Cf, Cip, Su, S     | Amp, Cf, Te |
| Typhimurium phage type 3 | 1   | Cip, K, Nitro, S             | Amp, Amc, Cf |
| Typhimurium phage type 93| 1   | -                            | Sxt, Tmp, Te, S |
| Typhimurium phage type 4 | 1   | Cip, K, Nitro                | Amp, Amc, Cf |
| Virchow                  | 1   | K, Te, Su, S                 | Nitro     |
| Virchow                  | 1   | Cip, K, Te, Su, S, Nitro     | -         |
| Virchow                  | 1   | An, K                        | Amp, Amc, Cf, S |
| Virchow                  | 2   | K, S                         | Amp, Amc, Cf |
| l:ROUGH-O-g.p:-          | 1   | Fox                          | Amp, Amc, Cf |

An, amikacin; Amp, ampicillin; Amc, amoxicillin and clavulanic acid; Cf, cephalothin; C, chloramphenicol; Cro, ceftriaxone; Cip, ciprofloxacin; Fox, cefoxitin; Gm, gentamicin; K, kanamycin; Tmp, trimethoprim; Sxt, sulfamethoxazole + trimethoprim; Te, tetracycline; Su, sulfisoxazole; S, streptomycin; Nitro, nitrofurantoin; Na, nalidixic acid; N, neomycin.

isolates to streptomycin 25 (89.3%), cephalothin 20 (71.4%), ampicillin 19 (67.9%), and amoxicillin+clavulanic acid 19 (67.9%). All isolates were susceptible to ceftriaxone and chloramphenicol. All *S.* Dublin isolates were resistant to ampicillin, amoxicillin+clavulanic acid, cephalothin, and streptomycin. All of the *Salmonella* isolates investigated were resistant or intermediately resistant to 4 or more of the 17 drugs tested. Resistance or intermediate resistance to five or more drugs was detected in 20 (71.5%) of the isolates and resistance to more than 7 antimicrobials was detected in 5 (17.9%) of the isolates. A single *S.* Kentucky isolated from Addis Ababa Abattoir was resistant to 11 of the 17 antimicrobials tested (Table 4).

4. Discussion

Foodborne gastroenteritis caused by non-typhoidal *Salmonella* represents a major public health problem worldwide. As *Salmonella* is transmitted through contaminated food or water, its presence in food animals and food animal products has relevant public health implications. Thus, monitoring food safety is a key point in preventing and controlling the spread of *Salmonella*, as well as in providing healthier food product [17].

In the current study, overall prevalence of *Salmonella* was 3.7% (fecal= 4.1% and carcass swab 2.5%), which is a little bit lower than that reported from Addis Ababa Abattoir [18] and Debrezeit slaughter house [19] which reported pooled prevalence to be 10.6% and 7.1%, respectively. A much higher prevalence of 14% was also reported from beef cattle in Ethiopia [20]. The prevalence from carcass swab (2.5%) in the current study is in line with the 2% prevalence reported earlier [20]. However, higher rate of recovery of *Salmonella* (4.8%) was reported from carcass swab [21] in slaughtered cattle at Bahir Dar town, North Ethiopia. The probable reason for the fecal and carcass swab prevalence disparity from other studies could be due to seasonal variation in *Salmonella* shedding among animals, difference in infection prevention practices by animal owners, and other factors such as variation in hygiene status of the slaughter houses and difference in the *Salmonella* isolation protocol employed in each study.

In our study, we found *S.* Dublin to be the predominant serovar followed by *S.* Virchow. Similarly, previous studies [12, 18, 19] reported *S.* Dublin as the most predominate serovar in slaughtered cattle and beef in Ethiopia. A single *l:ROUGH-O-g.p:-* isolate obtained from fecal sample of cattle is also likely atypical strain of *S.* Dublin as its antimicrobial
susceptibility profile is closely related to most of the S. Dublin strains in this study. Unlike our study, S. Virchow was not the common serovar isolated from cattle and carcass sample in the previous studies. However, recent study reported S. Virchow to be one of the dominant serovars circulating in dairy cattle in Addis Ababa [15].

In the current study, resistance to 4 or more antimicrobials was observed in the isolates which is much higher than the reports by previous studies [20, 22] in Salmonella serovars isolated from beef and other food of animal origin. Other studies in Ethiopia also reported a much lower rate of resistance to common antimicrobials used in both animal and human health [19, 21]. This difference may be due to the increasing rate of inappropriate utilization of antimicrobials in cattle farms which favored selection for resistant bacterial strains.

Higher resistance rate observed to streptomycin could be due to the fact that it is among the most commonly used antimicrobials for treatment of various infectious diseases of livestock. Similarly, the occurrence of high rate of resistance to ampicillin and amoxicillin+clavulanic acid among isolates in this study could partly be due to coselection of resistance phenomenon with penicillin, a drug frequently prescribed alone or in combination with streptomycin in veterinary practice in Ethiopia [23]. All isolates in the current study showed multidrug resistance to more than four drugs which is alarming for both human and animal health sector. This observation indicates the potential importance of cattle as a source of antimicrobial resistant Salmonella serovars to commonly used antimicrobials including ampicillin, amoxicillin+clavulanic acid, streptomycin, and tetracycline. The fact that all isolates in the current study were susceptible to ceftriaxone and chloramphenicol might be due to low use of these two drugs in veterinary medicine in the country.

5. Conclusion

Antimicrobial resistant bacteria of animal origin are considered an important contributor to the overall phenomenon of increased antimicrobial resistance in bacterial pathogen of public health importance. Use of antimicrobials in one or the other way contributes to the emergence and spread of antimicrobial resistance. Therefore, judicious use of antimicrobials in beef cattle and other food animals is recommended to delay the emergence and spread of antimicrobial resistant bacteria and resistance genetic markers.

Data Availability

The data used to support the findings of this study are included within the article.

Conflicts of Interest

The authors declare that there are no conflicts of interest regarding publication of this paper.

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