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Antibiogram of *Salmonella* isolates from animal and human sources in Southern Taraba, North-East, Nigeria

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Abstract

Salmonella species are responsible for typhoid and paratyphoid fever in humans, as well as gastroenteritis in humans and other animals. Although infections caused by *Salmonella* are treatable using chemotherapy. Sadly, several antibiotics are now resisted by *Salmonella*. Hence, this research accessed the antibiogram of a total of 120 *Salmonella* isolates from food vendors (18.30%) and animal sources (81.7%) in Donga, Ibi, Takum, and Wukari. Isolates were subjected to an Agar disc diffusion test and the following results were produced. On the one hand, 83(84.6%), 73 (74.4%), 79 (80.6%), and 76 (77.6%) of the total 98 *Salmonella* isolates from animal sources were resistant to Ciprofloxacin, Gentamycin, Tetracycline, and Streptomycin, respectively. Also, all 98 (100%) isolates from this category were resistant to Ampicillin. On the other hand, Chloramphenicol, Gentamycin, Tetracycline, Ampicillin, Ciprofloxacin, and Streptomycin were resisted by 9 (56.3%), 4(25%), 7 (43.8%), 12 (75%) and 5 (31.3%) of the total 16 Non-Typhoidal *Salmonella* isolates from human sources respectively. 16.7% (1) of the 6 Typhoidal *Salmonella* isolates from this study were resisted by Augmentin and Streptomycin. Similarly, Chloramphenicol Tetracycline and Ampicillin were all opposed by 66.7% (4) of TS isolates. All isolates showed considerable susceptibility to, Cefotaxime, and Neomycin. Susceptibility and resistant attributes of antimicrobials are consequences to their limited and long-term usage respectively in chemotherapy and food production. Hence regulations should be intensified for antibiotics usage in both animal production and infection management. Also, opportunities for using plant extracts as alternatives to disease management and animal production should be maximized.

Keywords: Agar Plug diffusion; Antibiogram; Resistance; *Salmonella*; Sensitive

1. Introduction

Salmonella is a member of the *Enterobacteriaceae* family [1]. *Salmonella* which is a Gram-negative rod-shaped bacterium predominantly lives in the intestinal tracts of humans and other warm and cold-blooded animals as their natural habitats [2, 3]. Serovars of medically important *Salmonella* species are divided into Typhoidal Serovars (TS) and Non-Typhoidal Serovars (NTS) according to the spectrum of diseases they cause. TS are responsible for typhoid and paratyphoid fever in humans, while NTS is responsible for *Salmonella* gastroenteritis in humans and other animals [4].

Currently, there is no licensed vaccine globally for NTS infection [5]. However, the oral live-attenuated vaccine, capsular polysaccharide, and the newly licensed Typhoid Conjugate vaccine are the 3 currently recommended vaccines for use globally for protecting against enteric fever caused by TS [6]. Nonetheless, *Salmonella* infections are treatable using antibiotics with a treatment regimen directed towards controlling pain, vomiting, nausea, and replacing lost fluids by oral and intravenous routes [3]. Treating uncomplicated *Salmonella*-inflicted gastroenteritis with antibiotics does not

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limit the symptoms but extensively delays the fecal excretion of the bacteria and reduces the efficacy of the particular antibiotic used by resisting it [3]. Therefore, antibiotic therapy is not encouraged in this instance. However, treatment should be made available for systemic symptoms of typhoid [7]. Ofloxacin, ciprofloxacin, fleroxacin, and pefloxacin collectively known as fluoroquinolones are considered the most efficacious chemotherapy for typhoid fever and other symptoms of invasive NTS in adults and children because of their inexpensive and readily available qualities [8]. Moreover, fluoroquinolones are hardly associated with side effects (WHO 2003). Surprisingly, indiscriminate use of these recommended antibiotics in primary health care settings has prompted antimicrobial resistance of *Salmonella* to conventional drugs of choice [9].

Antibiotic resistance is a natural phenomenon that occurs when microorganisms are exposed for a long term to antibiotics [10]. During the 20th century, antibiotics became a key tool wielded by man in the war against pathogenic microorganisms, however, many years later the microorganisms began to fight back aggressively [11]. Antimicrobials use a specific mechanism of action such as bacterial protein biosynthesis, cell wall biosynthesis, inhibiting nucleic acid synthesis, and destruction of the bacterial membrane in curbing the activities of microorganisms [12]. Antimicrobial resistance (AMR) has persisted as one of the principal public health problems of recent times threatening the effective treatment of the rapidly increasing range of infections caused by microorganisms [13]. Not only the overuse of antibiotics but also the inappropriate use contributes to the increase of antibiotic resistance [10]. Efflux pump, altered target, structural modification of porins, modification and destruction of antibacterial agents are precise ranges of mechanisms of antimicrobial resistance [12].

According to the United States Centre for Disease Control and Prevention [14], over two million people are affected yearly with infections caused by antibiotic-resistant microorganisms with a mortality rate of 23 000. Similarly, in the European area, infections caused by multi-drug resistant antibiotics in 2007 were estimated to be 400,000 from which 25,000 deaths are recorded [15].

Also, the economic impact of antibiotic resistance is difficult to quantify, as several categories of consequences must be considered. Apart from the loss of lives from infections caused by multidrug-resistant microorganisms, they also inflict a huge financial burden on management and treatment [4]. This is because, increased resistance leads to elevated monetary costs associated with more expensive antibiotics especially when infections become resistant to first-line antimicrobials. Sometimes, specialized equipment, longer hospital stay, and isolation procedures may be required for the patients as a direct consequence of AMR [13]. In Europe, at least 1.5 billion Euros is required to combat the AMR menace yearly, while an estimated cost of $55 billion is required yearly in the USA for the same purpose [15]. Unfortunately, the current efforts of novel drug discovery are insufficient to mitigate the severe threat of drug-resistant infections thereby necessitating urgent alternative means of managing health [11]. Hence, this study aims to investigate the antibiogram of *Salmonella* isolates from various poultry farms and food vendors in Ibi, Donga, Takum, and Wukari, North-East, Nigeria.

2. Methods

2.1. Test microorganisms

A total of 22 human and 98 animal *Salmonella* isolates were obtained from pure stock cultures of previous *Salmonella* prevalence studies in Donga, Ibi, Takum, and Wukari towns of Southern Taraba, North-East Nigeria. The isolates were further subjected to culturing using *Salmonella-Shigella* Agar (SSA), microscopy, and biochemical analysis for confirmation.

2.2. Antibiotic Susceptibility Test

Susceptibility patterns of *Salmonella* isolates to selected antibiotics were determined by the agar-disc diffusion method. Two colonies each of plates with observable growth were inoculated into respective tubes containing tryptic soy broth which was incubated at 37 °C for 24 hours. The broth inocula were diluted to meet the 0.5 McFarland standards. A sterile cotton swab was dipped into the suspension, the excess expressed at the side of the tube, and used to swab across the surface of the Mueller-Hinton agar leaving no area un-swabbed. This process was repeated for all plates. Following the inoculation, the plates were air-dried for 5 minutes, and antibiotic discs were carefully placed to ensure contact with the agar using flamed forceps. Zones of inhibition were observed following 24 hours of incubation at 37 °C. The following antibiotic discs were tested for susceptibility against *Salmonella* isolates Chloramphenicol, Cotrimoxazole, Gentamicin, Tetracycline, Ampicillin, Ciprofloxacin, Amoxicillin, Cefotaximee, and Streptomycin.

3. Results

Table 1 presents the prevalence data of *Salmonella* isolated from human and animal sources from Donga, Ibi, Takum, and Wukari towns in Sothern Taraba. Data from the table shows a total of 120 isolates of *Salmonella* was obtained, from which 98 (81.7%) were from poultry farms and domestic chicken coops while the remaining 22 (18.33%) were isolated from mobile and stationed food vendors from which 6 (5%) were of the Typhoidal serovar. Table 2 is a histogram representing the number of *Salmonella* isolates. Morphological and biochemical identification of isolates are shown in Table 3.

Table 4 presents an antibiogram of *Salmonella* isolates from animal sources from which it is evident that 83(84.6%) of isolates were resistant to Ciprofloxacin. Also, Gentamycin, Tetracycline, Streptomycin, and were resisted by 73 (74.4%), 79 (80.6%), and 76 (77.6%) of isolates from farms and chicken coops respectively. Also, all 98 (100%) isolates from this category were resistant to Ampicillin. However, 100% of *Salmonella* isolates were sensitive to Chloramphenicol, Cefotaxime, Augmentin, and Neomycin. Table 5 is an antibiogram of Non-Typhoidal *Salmonella* isolates from Human sources. None of the 16 (100%) isolates from this category were resistant to Neomycin Augmentin and Cefotaxime. Nonetheless, Chloramphenicol, Gentamycin, Tetracycline, Ampicillin, Ciprofloxacin, and Streptomycin were resisted by 9 (56.3%), 4(25%), 7 (43.8%), 12 (75%) and 5 (31.3%) isolates respectively. The antibiotic susceptibility pattern of the Six (6) Typhoidal *Salmonella* isolates from mobile and stationed food vendors are shown in Table 6 below. All TS isolates from this category were sensitive to Neomycin, Ciprofloxacin, and Cefotaxime. Augmentin and Streptomycin were both resisted by 16.7% (1) of isolates. Similarly, Chloramphenicol Tetracycline, and Ampicillin were all resisted by 66.7% (4) of TS isolates.

Table 1 Prevalence of *Salmonella* isolates from animal and human sources in Southern Taraba, North East Nigeria

SN	Location	Positive isolates from animal source	Positive isolates from Food handlers			Total *Salmonella* Isolates
			S. Typhi (A)	*S. spp* (B)	A+B	
1	Wukari	36	2	3	5	41
2	Donga	19	0	5	5	24
3	Takum	16	1	4	5	21
4	Ibi	27	3	4	7	34
		98	6	16	22	120

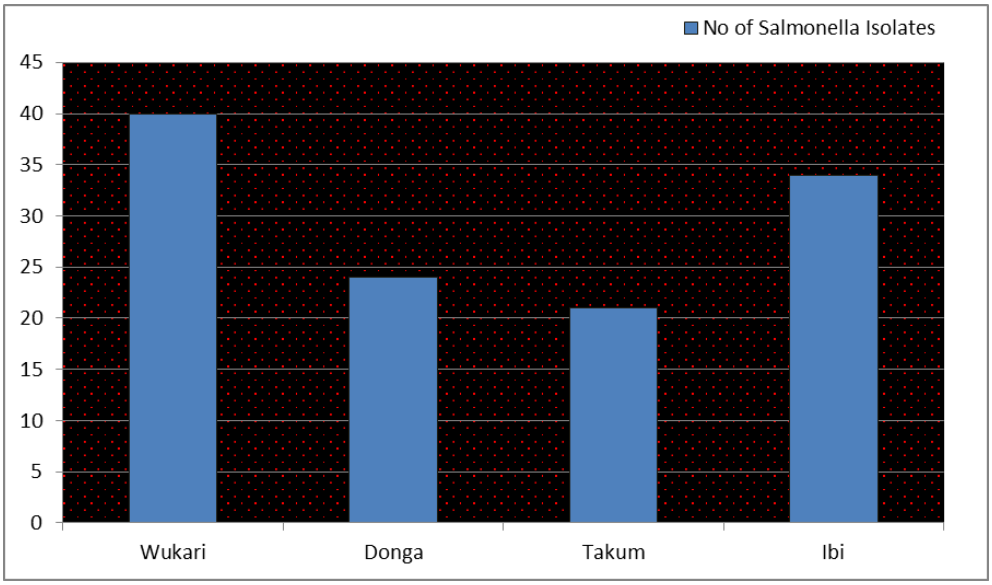


Figure 1 Histogram showing Number of *Salmonella* isolates

Table 2 Morphological and biochemical characteristics of *Salmonella* Isolates

Isolate	Culture media	Morphological Characteristic	Gram stain	Biochemical test						Organism
				CAT	IND	MR	LAC	SUC	GLU	
A	MacConkey Agar	round, flat, shiny and fragile nature with glowing appearance	Negative bacilli	+	-	+	-	-	+	*Salmonella*
	Salmonella-Shigella Agar (SSA)	Colourless colonies with pigment at the middle								

Key: +; Positive, -; Negative. CAT; Catalase, INDO; Indole. MR; Methyl Red, LAC; Lactose, SUC; Sucrose, GLU; Glucose

Table 3 Antibiogram of *Salmonella* isolates from animal source in Southern Taraba

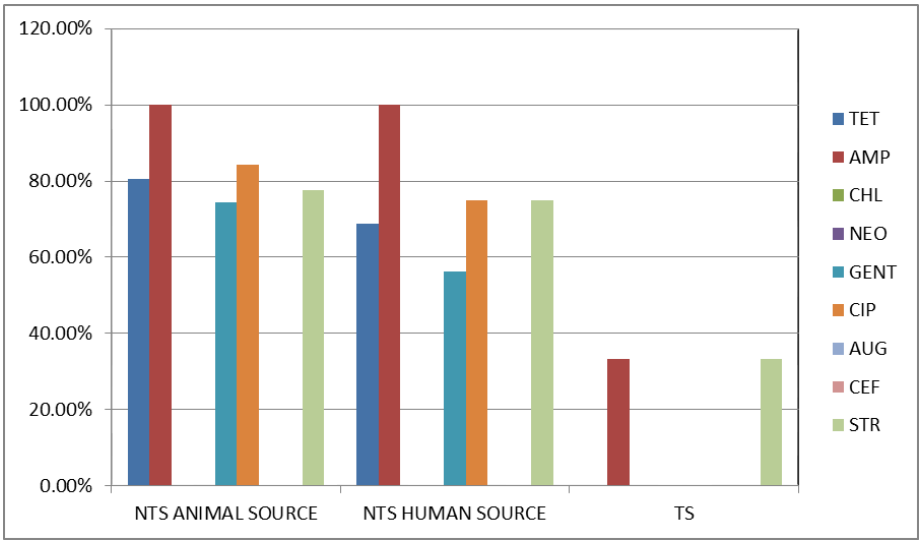
Antimicrobials	Wukari *Salmonella* Spp (Number of Isolate =36)			Donga *Salmonella* Spp (Number of Isolate=16)			Takum *Salmonella* Spp (Number of Isolate =27)			Ibi *Salmonella* Spp (Number of Isolate =19)			*Total* Isolates 98
	R	I	S	R	I	S	R	I	S	R	I	S	% R
CHL	0 (0%)	0 (0%)	36 (100%)	0 (0%)	0 (0%)	16 (100%)	0 (0%)	0 (0%)	27 (100%)	0 (0%)	0 (0%)	19 (100%)	0 (0%)
NEO	0 (0%)	0 (0%)	36 (100%)	0 (0%)	0 (0%)	16 (100%)	0 (0%)	0 (0%)	27 (100%)	0 (0%)	0 (0%)	19 (100%)	0 (0%)
GENT	29 (80.5%)	0 (0%)	9 (25%)	12 (75%)	3 (18.8%)	1 (6.3%)	24 (88.9%)	0 (0%)	3 (11.1%)	8 (42.1%)	3 (15.8%)	8 (42.1%)	73 (74.4%)
TET	30 (83.3.)	2 (5.5%)	4 (11.1%)	12 (75%)	1 (6.3%)	3 (19%)	20 (74.0%)	2 (7.5%)	5 (18.5%)	17 (89.4%)	0 (0%)	2 (10.5%)	79 (80.6%)
AMP	36 (100%)	0 (0%)	0 (0%)	16 (100%)	0 (0%)	0 (0%)	27 (100%)	0 (0%)	0 (0%)	19 (100%)	0 (0%)	0 (0%)	98 (100%)
CIP	29 (80.5%)	2 (6%)	5 (14%)	16 (100%)	0 (0%)	0 (0%)	24 (88.9%)	0 (0%)	3 (11.1%)	14 (73.7%)	0 (0%)	5 (26.3%)	83 (84.6%)
AUG	0 (0%)	0 (0%)	36 (100%)	0 (0%)	0 (0%)	16 (100%)	0 (0%)	0 (0%)	27 (100%)	7 (36.8%)	0 (0%)	12 (63.1%)	0 (0%)
CEF	0 (0%)	0 (0%)	36 (100%)	0 (0%)	0 (0%)	16 (100%)	0 (0%)	0 (0%)	27 (100%)	2 (10.5%)	0 (0%)	17 (89.5%)	0 (0%)
STR	29 (80.5%)	2 (6%)	5 (14%)	8 (50%)	0 (0%)	8 (50%)	24 (88.9%)	1 (3.7%)	2 (7.5%)	15 (78.9%)	1 (5.2%)	3 (15.8%)	76 (77.6%)

Abbreviations: R; Resistance, I; Intermediate, S; Sensitive, CHL; Chloramphenicol, NEO; Neomycin, GENT; Gentamycin, TET; Tetracycline, AMP; Ampicillin, CIP; Ciprofloxacin, AUG; Augmentin, CEF; Cefotaximee, STR; Streptomycin.

Table 4 Antibiogram of Non Typhoidal *Salmonella* isolates from Human source in Southern Taraba

Antimicrobials	Wukari *Salmonella* Spp (Number of Isolate =3)			Donga *Salmonella* Spp (Number of Isolate =5)			Takum *Salmonella* Spp (Number of Isolate =4)			Ibi *Salmonella* Spp (Number of Isolate =4)			Total Isolates 16
	R	I	S	R	I	S	R	I	S	R	I	S	% R
CHL	2 (66.7%)	0 (0%)	3 (100%)	1 (20%)	0 (0%)	4 (80%)	3 (80%)	0 (0%)	1 (20%)	3 (75%)	0 (0%)	1 (25%)	9 (56.3%)
NEO	0 (0%)	0 (0%)	3 (100%)	0 (0%)	0 (0%)	5 (100%)	0 (0%)	0 (0%)	4 (100%)	0 (0%)	0 (0%)	4 (100%)	0 (0%)
GENT	1 (33.3%)	1 (33.3%)	1 (33.3%)	1 (20%)	2 (40%)	2 (40%)	0 (0%)	3 (75%)	1 (25.0%)	2 (50%)	2 (50%)	0 (0%)	4 (25%)
TET	3 (100)	0 (0%)	0 (0%)	1 (20%)	1 (20%)	3 (60%)	1 (25.0%)	1 (25.0%)	2 (50%)	2 (50%)	2 (50%)	0 (0%)	7 (43.8%)
AMP	2 (66.7%)	1 (33.3%)	0 (0%)	5 (100%)	0 (0%)	0 (0%)	2 (50%)	2 (50%)	0 (0%)	3 (75%)	1 (25%)	0 (0%)	12 (75%)
CIP	1 (33.3)	0 (0%)	2 (66.7%)	0 (0%)	2 (40%)	3 (60%)	0 (0%)	2 (50%)	2 (50%)	1 (25%)	0 (0%)	3 (75%)	2 (12.5%)
AUG	0 (0%)	0 (0%)	3 (100%)	0 (0%)	0 (0%)	5 (100%)	0 (0%)	0 (0%)	4 (100%)	0 (0%)	0 (0%)	4 (50%)	0 (0%)
CEF	0 (0%)	1 (33.3%)	2 (66.7%)	0 (0%)	0 (0%)	3 (100%)	0 (0%)	0 (0%)	4 (100%)	0 (0%)	1 (25%)	3 (75%)	0 (0%)
STR	1 (33.3%)	2 (66.7%)	0 (0%)	2 (40%)	1 (20%)	2 (40%)	0 (0%)	3 (75%)	1 (25%)	2 (50%)	1 (25.0%)	1 (25%)	5 (31.3%)

Abbreviations: R; Resistance, I; Intermediate, S; Sensitive, CHL; Chloramphenicol, NEO; Neomycin, GENT; Gentamycin, TET; Tetracycline, AMP; Ampicillin, CIP; Ciprofloxacin, AUG; Augmentin, CEF; Cefotaximee, STR; Streptomycin.



Abbreviations: R; Resistance, I; Intermediate, S; Sensitive, TET; Tetracycline, AMP; Ampicillin, CHL; Chloramphenicol, NEO; Neomycin, GENT; Gentamycin, CIP; Ciprofloxacin, AUG; Augmentin, CEF; Cefotaxime, STR; Streptomycin, NTS; Non-Typhoidal *Salmonella*, TS; Typhoidal *Salmonella*

Figure 2 Bar Chart representing summary of Resistant *Salmonella* isolates from Human and Animal sources in Southern Taraba

Table 5 Antibiogram of Typhoidal *Salmonella* isolates from Human source in Southern Taraba

Antimicrobials	Wukari *Salmonella* Spp (Number of Isolate=2)			Donga *Salmonella* Spp (Number of Isolate =0)			Takum *Salmonella* Spp (Number of Isolate =1)			Ibi *Salmonella* Spp (Number of Isolate =3)			*Total Isolates* 6
	R	I	S	R	I	S	R	I	S	R	I	S	% R
CHL	0 (0%)	2 (100%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	1 (100%)	0 (0%)	0 (0%)	3 (100%)	0 (0%)	0 (0%)	4 (66.7%)
NEO	0 (0%)	2 (100%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	1 (100%)	0 (0%)	0 (0%)	1 (33.3%)	2 (66.7%)	0 (0%)
GENT	1 (50%)	0 (0%)	1 (50%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	1 (100%)	2 (66.7%)	0 (0%)	1 (33.3%)	3 (50%)
TET	1 (50%)	1 (50%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	1 (100%)	0 (0%)	2 (66.7%)	1 (33.3%)	0 (0%)	4 (66.7%)
AMP	0 (0%)	2 (100%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	1 (100%)	2 (66.7%)	1 (33.3%)	0 (0%)	4 (66.7%)
CIP	0 (0%)	1 (50%)	1 (50%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	1 (100%)	0 (0%)	2 (66.7%)	1 (33.3%)	0 (0%)
AUG	0 (0%)	2 (100%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	1 (100%)	0 (0%)	1 (33.3%)	0 (0%)	2 (66.7%)	1 (16.7%)
CEF	0 (0%)	0 (0%)	2 (100%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	1 (100%)	0 (0%)	0 (0%)	3 (100%)	0 (0%)
STR	0 (0%)	0 (0%)	2 (100%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	1 (100%)	0 (0%)	1 (33.3%)	0 (0%)	2 (66.7%)	1 (16.7%)

Abbreviations: R; Resistance, I; Intermediate, S; Sensitive, CHL; Chloramphenicol, NEO; Neomycin, GENT; Gentamycin, TET; Tetracycline, AMP; Ampicillin, CIP; Ciprofloxacin, AUG; Augmentin, CEF; cefotaxime, STR; Streptomycin

Table 6 Antibiogram summary of Resistant *Salmonella* isolates from Human and Animal sources in Southern Taraba

Antimicrobials	% Resistance NTS Animal Source A (98 Isolates)	% Resistance NTS Human Source B (16 Isolates)	% Resistance TS (6 Isolates)
CHL	0 (0%)	9 (56.3%)	4 (66.7%)
NEO	0 (0%)	0 (0%)	0 (0%)
GENT	73 (74.4%)	4 (25%)	3 (50%)
TET	79 (80.6%)	7 (43.8%)	4 (66.7%)
AMP	98 (100%)	12 (75%)	4 (66.7%)
CIP	83 (84.6%)	2 (12.5%)	1 (16.7%)
AUG	0 (0%)	0 (0%)	1 (16.7%)
CEF	0 (0%)	0 (0%)	0 (0%)
STR	76 (77.6%)	5 (31.3%)	1 (16.7%)

Abbreviations: R; Resistance, I; Intermediate, S; Sensitive, CHL; Chloramphenicol, NEO; Neomycin, GENT; Gentamycin, TET; Tetracycline, AMP; Ampicillin, CIP; Ciprofloxacin, AUG; Augmentin, CEF; Cefotaxime, STR; Streptomycin, NTS; Non Typhoidal *Salmonella*.

4. Discussion

This current study investigated the antimicrobial susceptibility pattern of *Salmonella* species isolated from small-scale poultry farms and domestic chicken coops as well as from mobile and stationed food vendors in Donga, Ibi, Takum, and Wukari towns located in Sothern Taraba, North-East Nigeria. Variations were observed in the susceptibility pattern of tested antibiotics against NTS isolates from animals and humans as well as TS.

On the one hand, *Salmonella* isolates showed noticeable resistance to Ciprofloxacin Gentamycin, Tetracycline, and Streptomycin. Until recently, Ciprofloxacin which is a Fluoroquinolones was a fine and foremost drug of choice for treating enteric fever and gastroenteritis caused by *Salmonella* in both humans and animals. Unfortunately, indiscriminate and extensive use of Ciprofloxacin and Ofloxacin in enhancing growth and treatment regimens for farm animals not only heightened the acquisition of resistance genes by *Salmonella* [16] but also increases the chances for horizontal transfer of the plasmid-encoded qnr resistant genes to other organisms [17]. Most of the isolates were also resistant to Gentamycin, Tetracycline, and Streptomycin. According to [18] the multidrug-resistant pattern exhibited by isolates to Gentamycin, Tetracycline, and Streptomycin connotes the presence of *Salmonella* Genomic Island (SGI) conferring resistant plasmid genes among isolates. Also, isolates from this current study were resistant to Ampicillin. This finding is supported by that of [18] who discovered resistance to Ampicillin by *Salmonella* isolates in Maiduguri. On the other hand, NTS isolates from poultry sources were sensitive to Chloramphenicol, Cefotaxime, Augmentin, and Neomycin. In a slightly similar order, NTS isolates from food vendors were susceptible to Augmentin, Cefotaxime, and Neomycin but were resistant to Chloramphenicol. TS isolates showed a similar pattern of resistance but were somewhat resistant to Augmentin. The sensitivity of NTS and TS isolates to Cefotaxime which is a third generation Cephalosporin suggests the absence of extended-spectrum cephalosporinases which confers reduced microbial sensitivity to Cephalosporin [18]. NTS susceptibility to Cefotaxime is in line with findings of [7] that observed little or intermediate resistance by *Salmonella* isolates from livestock to third-generation Cephalosporins even when isolates were found to harbor antimicrobial resistance genes. Unlike Tetracycline which is incessantly abused over the counter for cost-effectiveness, Cephalosporin is arguably one of the most expensive antibiotics in the world today making them less available over the counter for use and abuse hence reducing the chance of microorganisms resisting them [19]. Similarly, the excellent resistance pattern shown by NTS from animal sources to Chloramphenicol may be due to its long-term ban for use in animal production [17]. All Isolates in this current study were outstandingly sensitive to Neomycin. This vulnerability pattern of *Salmonella* to Neomycin may be due to its scarce usage in chemotherapy and animal production owing to its burdensome side effects from sustained usage [20]. Antibacterial attributes of Chloramphenicol, Cefotaxime, and Neomycin in this current study are conversant with an existing philosophy adapted from [9] that, an antibiotic that had previously been resistant to a bacterium may become sensitive again if treatment with the antibiotic has been reduced or even suspended for a while. The potential implications of this to public health remain contentious. Hence, further inquiry into this occurrence is proposed.

Several factors have been identified by various studies to be inherent in promoting antimicrobial resistance. An example is the misleading Widal tests and similarity in clinical symptoms of malaria and typhoid [21]. Also, the co-infection of typhoid and malaria complicates diagnosis and chemotherapy more than necessary. The reason is that the extensive iron deposit in the liver to prevent anemia resulting from excess hemolysis during malaria infection aids the intracellular growth and survival of *Salmonella*, especially in the liver [21]. This implies that preventing anemia by treating malaria could be deadly to the patients by making them super susceptible to typhoid. Additionally, poor sanitation, environmental pollution, and other factors other than antibiotic abuse have been identified to influence antimicrobial resistance with the natural environment being an important conduit [22]. When droppings from animals containing resistant genes of *Salmonella* are released into the environment or used as manure for agricultural purposes, human activities lead to eventual infection, transmission, and reinfection making chemotherapy needlessly difficult [23]. The uncontrolled movement of cattle and other livestock across bothering communities of neighboring states and international boundaries facilitates the horizontal transfer of resistant enzymes such as the Extended Spectrum beta-lactamase produced by *Salmonella* [4]. Resistance of *Salmonella* to some antibiotics is also encouraged by poor biosecurity protocols such as disinfecting surfaces, utensils, protective equipment, and hand washing practices [4].

5. Conclusion

This research has presented informed antibiogram pattern of *Salmonella* species isolated in Southern Taraba, North-East Nigeria. Shockingly, isolates from this current study were resistant to several antibiotics including fluoroquinolones, which are known to be efficacious in treating complicated cases of Salmonellosis. Abuse of antimicrobials in animal and food production as well as long-term use in hospitals were identified as potential risk factors associated with trends in antimicrobial resistance. This is so because isolates showed remarkable sensitivity to

antibacterial which have been suspended for use in both animal production and chemotherapy. Nonetheless, environmental factors including poor biosecurity protocols were identified as significant facilitators of the spread of antimicrobial-resistant genes. Unless implementable regulation policies are enacted and strengthened in addressing the indiscriminate use of antibiotics, the spread of antimicrobial-resistant genes will assume a geometric progression pattern. Also, environmental and personal hygiene should be ensured in animal farms and other aspects of food production.

Compliance with ethical standards

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Disclosure of conflict of interest

We declare no conflict of interests in this article.

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