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Salmonella enterica isolated from selected poultry farms in Kwara State, Nigeria between 2015 and 2016 showed resistance to critical antimicrobials

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ABSTRACT

Salmonellosis is a major public health hazard globally. This study was designed to determine the antimicrobial resistance among *Salmonella* serovars isolated from selected poultry farms in Kwara State, Nigeria between 2015 and 2016 using a cross sectional approach. A total of 58 *Salmonella* isolates were serotyped, 13 different serovars were identified and subjected to antibiotic susceptibility test using disc diffusion method. All the isolates (100%) exhibited resistance to at least one antimicrobial agent. All of the isolates exhibited 100% resistance to ampicillin, 65.5% of the isolates showed resistance to cefotaxime while 63.8% of the isolates were resistant to either of ciprofloxacin and nalidixic acid. Low level of resistance was observed for neomycin (22.4%) compare to other antimicrobials. *S. enterica* ser. 4, 12, 27: z: - exhibited resistance to all antimicrobial agents. Considering the types of samples that were positive for *Salmonella* across different local government areas, frequencies of resistance were statistically significant only to gentamicin (P =0.016) in Ilorin west local government area, only nalidixic acid (P =0.014) in Irepodun local government area, only compound sulfonamide (P =0.002) in Asa local government area and streptomycin (P =0.025) in Ilorin-South local government area. The results indicated the relatively high resistance to the antimicrobial agents tested and the multi-drug-resistance among the *Salmonella* serovars. These observations pose therapeutic concerns on poultry farms in the study area and may serve as potential sources of multi- drug-resistant *Salmonella* transmission to the humans.

Keywords: Antimicrobials, Local Government, *Salmonella*, Therapeutic, Transmission

INTRODUCTION

Salmonella infection is a well-established malady in poultry industry all over the world, engendering heavy economic losses through reduced production, morbidity and mortality (Adesiyun et al., 2014b, Akter et al., 2007). Salmonellosis in poultry is difficult to control, especially in intensive farming systems (Makaya et al., 2012) because, in addition to vertical transmission from parent stock to chicks, horizontal transmissions on farms often occur (Dawoud et al., 2011, Hannah et al., 2011). Poultry salmonellosis results in acute or chronic infections, but sometimes, may lead to asymptomatic infection, resulting in contamination of poultry meat and poultry products, which subsequently pose a food safety hazard to consumers of poultry meat and poultry products (Adesiyun et al., 2014b, Makaya et al., 2012). *Salmonella* have been isolated from several species

of animals, poultry inclusive and their environments including airborne dust (Iwabuchi et al., 2010, Samanta et al., 2014, Adesiyun et al., 2007, Raufu et al., 2013). Many developed countries have *Salmonella* control programmes which have successfully reduced incidence of the controlled serovars. Such programmes, although not properly implemented, also exist in Africa, including Nigeria (Fagbamila et al., 2018).

Salmonella species is divided into three based on host range, as host restricted, host specific, and generalist serovars (Iwabuchi et al., 2010). Host specific serovars cause pathology in only one type of host, for instance *Salmonella* Gallinarum and *Salmonella* Pullorum are specific for avian species with resultant high morbidity and mortality. Host restricted serovars mainly cause disease in one host but can also affect other species of animals (Iwabuchi et al., 2010, Samanta et al., 2014). The generalist serovars affect a large number of hosts. For instance, *Salmonella* Typhimurium and *Salmonella* Enteritidis have been reported to cause pathology in various host species (Iwabuchi et al., 2010). There are reports of reduced susceptibility to antimicrobial agents among isolates of *Salmonella* in Nigeria and other parts of the world (Fagbamila et al., 2018, Raufu et al., 2013, Fashae et al., 2010, Bischoff et al., 2004). The increase in the use of antimicrobial agents as feed additives and growth promoters in the production of food-animals has aided the resistance of *Salmonella* to antimicrobial agents, and this can be transmitted to humans through the consumption of food products, especially of animal origin (Lu et al., 2010). This spread of antimicrobial resistance through the food chain is a major public health issue.

Prevention of salmonellosis through vaccination has been successfully practiced on poultry farms in several countries (Mughini-Gras et al., 2014, Adesiyun et al., 2014a) but the presence of numerous pathogenic non-host- adapted *Salmonella* serovars makes it difficult to have a successful vaccination especially in developing countries, Nigeria inclusive. The control of salmonellosis in developing countries therefore majorly relies on good sanitary practices and the prophylactic and therapeutic use of antimicrobial drugs in feeds and water because vaccines prepared from local isolates are not commercially available in the market for effective preventive measure (Akter et al., 2007, Adesiyun et al., 2014a). Poultry production in Nigeria relied majorly on antimicrobial therapy for disease control and most poultry farms have been reported to be multi-drug users while all farms used one or more antibiotics for treatment, prophylaxis or for growth promotion (Oluwasile et al., 2014). The routinely used antibiotics in poultry industry in Nigeria includes; penicillin, quinolones, gentamicin, neomycin, tetracycline, streptomycin, tylosin, streptomycin, furaltadone and colistin (Oluwasile et al., 2014). This over-reliance on antimicrobials and its acclaimed successes have resulted in threat to animal and public health through the occurrence of antimicrobial resistance. Therefore, there is reduced therapeutic options for salmonellosis in animals and humans (Elmadiena et al., 2013).

In developing countries like Nigeria, zoonotic bacterial pathogens like *Salmonella* are not routinely investigated, and their resistance pattern to routinely administered antimicrobials both in veterinary and public health practices is rarely determined (Kariuki et al., 2010). Therefore, it is important to institute surveillance programs for detection of antimicrobial resistance in food animals in order to monitor changes in susceptibility trends overtime, this would enhance the establishment of policy that will control the use of antimicrobial drugs in food animals, and to prevent further spread of multidrug-resistant strains. This study was aimed at determining the antimicrobial resistance among *Salmonella* serovars isolated from selected poultry farms in Kwara State, Nigeria between 2015 and 2016.

MATERIALS AND METHODS

Ethics

Ethical approval was obtained from Ethical Review Committee of Faculty of Veterinary Medicine, University of Ilorin, with approval code number, FVER/001/2016.

Study Area

The study was conducted on selected poultry farms in Kwara State, Nigeria during the period of November, 2015 to March, 2016. Kwara state is located between latitudes (8° 30′N) and longitudes (5° 00′E) and it is the transit state that connects southern and northern parts of Nigeria (Ahmed et al., 2017). Local Government areas where poultry farms are concentrated within the state were purposefully selected for the study (Table 1). The farms' selection was based on the poultry farms data records obtained from the state veterinary services and only farms that were consented and agreed to participate in the study were included. All the farms sampled reared layers birds under strict intensive management system.

Sample collection

This is a cross-sectional study and a total of 900 samples were collected from apparently healthy live birds, poultry environment, and dead birds. From live birds, the sample source was cloacal swabs n=315 (35/farm), from poultry environment samples comprising of litters n=45 (5/farm), poultry feed n=90 (10/farm), poultry non-medicated water n=90 (10/farm) were collected, and from dead birds the following samples were collected from a total of 72 birds; liver n=72 (8/farm), spleen n=72 (8/farm), ovarian follicle n=72 (8/farm), caecum n=72 (8/farm) and heart n=72 (8/farm). The dead birds used in the study were those that died overnight in the pen. Litters samples were collected as previously described by Adesiyun et al. (2014b) while cloacal and environmental samples were collected according to method previously described (Ahmed et al., 2017, Enabulele et al., 2010). Samples of organs from dead birds were collected by opening a recently dead bird and aseptically pick approximately 1g of organ, place it in sterile polythene bag. All the samples were labelled properly and kept in a cool box containing ice packs and transported, within three (3) hours, to Veterinary microbiology laboratory, University of Ilorin for analysis.

Isolation and identification of Salmonella

Isolation and identification of *Salmonella* were done according to ISO 6579, as previously described (Fagbamila et al., 2017, Ahmed et al., 2016). All the presumptive *Salmonella* isolates (58) were freeze-dried and shipped to the World Health Organization (WHO) National *Salmonella* and *Shigella* Center, Bangkok, Thailand, for serotyping according to reaction with somatic, flagellar, and capsular hyperimmune sera (S & A Reagents Laboratory, Ltd., Bangkok, Thailand) and serotypes were assigned according to the Kauffmann–White scheme as previously described by Raufu et al. (2013).

Antimicrobial susceptibility testing

The antimicrobial susceptibility of the 58 *Salmonella* isolates recovered from the selected layer farms was determined by subjecting them to 11 antimicrobial agents by disc diffusion method using Mueller Hinton

Table 1. Farm sources of *Salmonella* isolates from different local Government areas, Kwara State

Local Government	No of registered farms (flock size)	No of farm sampled	No of *Salmonella* isolates
Asa	5 (≥2,000)	2	12
Ilorin West	6 (≥2,500)	2	9
Ilorin South	4 (≥1,900)	1	5
Irepodun	8 (≥2,000)	1	6
Moro	8 (≥8,000)	2	21
Offa	6 (≥8,000)	1	5
Total	37	9	58

agar (Oxoid Ltd, Hampshire, UK) and antibiotic disks (Oxoid Ltd, Hampshire, UK) following the guidelines of the Clinical and Laboratory Standards Institute (CLSI, 2016).

The 11 antimicrobial agents tested were those commonly used in poultry farms in Nigeria (Oluwasile et al., 2014, Fashae et al., 2010). These include; ampicillin (10µg), compound sulfonamide (300 µg), gentamicin (10 µg), ciprofloxacin (5 µg), chloramphenicol (30 µg), ceftazidime (30 µg), cefotaxime (30 µg), neomycin (30 µg), nalidixic acid (30 µg), streptomycin (10 µg) and tetracycline (30 µg). The zones of inhibition were measured and interpreted as recommended by the CLSI (2016). *Escherichia coli* ATCC 25922 (CCM 3954) was used as the control strain.

Data analyses

Data were analyzed using Open Source Epidemiologic Statistics for Public Health (OpenEpi), version 3.03a (http://www.openepi.com/Menu/OE_Menu.htm, accessed on 08/19/2017). Chi-square analysis was performed to determine whether there were statistically significant differences in the frequency of resistance to antimicrobial agents among the isolates and the level of significance was determined at $P< 0.05$.

RESULTS

The most frequently observed serovars among the 58 isolates were 6,7: d: (29.3%), Agama (27.6%) and Typhimurium (13.3%). Although, the serovar distribution was not source dependent, most of the serovars isolated from poultry environment were equally isolated from the other sources (Table 2). All the isolates demonstrated resistance to one or more of the eleven antimicrobial agents used. All the isolates showed total (100% of the strains) resistance to ampicillin. 66% of the isolates showed resistance to cefotaxime while 64% of the isolates were resistant to either of ciprofloxacin and nalidixic acid. *S. enterica* ser. 4, 12, 27: z: - showed resistance to all antimicrobial agents used (Table 3). Of all the eleven antimicrobial agents tested, neomycin showed the least resistance rate (22%). A statistically significant proportion of resistance was obtained to some of the antimicrobials, depending on the samples source. Statistically significant differences were observed in Ilorin-West local government area for gentamicin (P=0.016, from dead birds and live birds) and for streptomycin (P=0.025, from poultry environment and dead birds) in Ilorin-South local government area. Similarly, statistically significant differences were observed in Irepodun local government area for nalidixic acid (P=0.014, from poultry environment and dead birds) and in samples from Asa for compound sulphonamides (P=0.002, from poultry environment, dead birds and live birds) both across and within the local government areas (Table 4).

Generally, the *Salmonella* isolates tested showed 18 different resistance patterns (Table 5). Overall, 41 isolates (70.7%) exhibited multidrug resistance (resistance to 3 or more different antibiotic classes). The predominant patterns detected were ampicillin-ceftazidime-cefotaxime (AMP-CAZ-CTX) (10.3%) and ampicillin-ceftazidime-cefotaxime-nalidixic acid (AMP-CAZ-CTX-NA), cefotaxime-nalidixic (CTX-NA) and ampicillin- ciprofloxacin (AMP-CIP) (8.6% each). One (1.7%) isolate each exhibited ampicillin-chlormphenicol-ceftazidime-ciprofloxacin-gentamicin- cefotaxime-neomycin-nalidicic acid-compound sulfurnamides-streptomycin-tetracycline (AMP-C-CAZ-CIP-CN-CTX-N-NA-S_3-S_{10}-TE), AMP-C-CAZ-CIP-CN-CTX-NA-S_3-S_{10}-TE and AMP-C-CAZ-CN-CTX-NA-N-S_3-S_{10}-TE resistant phenotypes. Specific multidrug resistance phenotypes were not serovar-associated.

Table 2. Serovar distribution of *Salmonella* among different sources in selected poultry farms in Kwara State

Serovar/Source	Poultry environment	Dead bird	Live bird	Total
Agama	4	3	9	16 (27.9)
Albany		1		1 (1.7)
Colindale	1			1 (1.7)
4,5,12: i: -	1			1 (1.7)
4,12,27: z: -	1			1 (1.7)
6,7: d: -	5	5	7	17 (29.3)
45: d: 1,7	1	2	2	5 (8.6)
Istanbul		1		1 (1.7)
Larochelle	1	1		2 (3.4)
Muenster	1	1		2 (3.4)
Nigeria		1		1 (1.7)
Orion	1			1 (1.7)
Typhimurium		4	5	9 (15.5)
Total	16	19	23	58

Table 3. Antimicrobial resistance profile of *Salmonella* serovars from selected poultry farms in Kwara State

Serovar	No of isolates	Number (%) of isolates showing resistance to different antimicrobials									
		AMP10	C30	CAZ30	CIP	CN30	CTX30	N30	NA30	S3	S10	TE30
Agama	16	16(100)	6(38)	8(50)	8(50)	6(38)	11(69)	2(13)	11(69)	6(38)	8(50)	11(69)
Albany	1	1(100)	0(0.0)	1(100)	1(100)	1(100)	1(100)	0(0)	1(100)	0(0)	1(100)	0(0)
Colindale	1	1(100)	0(0.0)	0(0)	1(100)	0(0)	1(100)	1(100)	0(0)	0(0)	0(0)	0(0)
4,5,12: i: -	1	1(100)	1(100)	0(0)	1(100)	1(100)	0(0)	0(0)	1(100)	1(100)	1(100)	1(100)
4,12,27: z: -	1	1(100)	1(100)	1(100)	1(100)	1(100)	1(100)	1(100)	1(100)	1(100)	1(100)	1(100)
6,7: d: -	17	17(100)	5(29)	9(53)	11(65)	9(53)	8(47)	2(12)	11(65)	8(47)	11(65)	9(53)
45: d: 1,7	5	5(100)	1(20)	3(60)	3(60)	2(40)	3(60)	1(20)	1(20)	1(20)	1(20)	2(40)
Istanbul	1	1(100)	0(0)	1(100)	1(100)	1(100)	0(0)	0(0)	1(100)	0(0)	0(0)	0(0)
Larochelle	2	2(100)	1(50)	1(50)	2(100)	1(50)	2(100)	1(50)	2(100)	2(100)	1(50)	2(100)
Muenster	2	2(100)	2(100)	2(100)	0(0)	2(100)	2(100)	2(100)	2(100)	1(50)	2(100)	1(50)
Nigeria	1	1(100)	1(100)	1(100)	1(100)	1(100)	1(100)	0(0)	1(100)	1(100)	1(100)	1(100)
Orion	1	1(100)	0(0)	1(100)	1(100)	0(0)	0(0)	0(0)	1(100)	0(0)	0(0)	1(100)
Typhimuriu m	9	9(100)	5(56)	6(67)	6(67)	5(56)	8(89)	3(33)	4(44)	6(67)	7(78)	7(78)
Total	58	58(100)	23(40)	34(59)	37(64)	30(52)	38(66)	13(22)	37(64)	27(47)	34(59)	36(62)

AMP10, ampicillin (10 µg); C30, chloramphenicol (30 µg); CAZ30, ceftazidime (30 µg); CIP5, ciprofloxacin (5 µg); CN30, gentamicin (30 µg); CTX30, cefotaxime (30 µg); N30, neomycin (30 µg); NA30, nalidixic acid (30 µg); S_3, compound sulfurnamides (300 µg); S_{10}, streptomycin (10 µg); and TE30, tetracycline (30 µg). **4,5,12: i:** - is a monophasic variant of *Salmonella Typhimurium*

Table 4. Proportion of resistance of *Salmonella* isolates by type of samples from different Local Government Areas

L/G	Source of isolates	*N*	No. (%) of isolates resistant to different antimicrobials										
			AMP10	C30	*p*-value	CAZ30	*p*-value	CIP5	*p*-value	CN30	*p*-value	CTX30	*p*-value
Asa	PE	6	6(100)	2(33)	0.135	4(67)	0.513	4(67)	1.0	4(67)	0.598	5(83)	0.549
	DB	3	3(100)	1(33)		2(67)		2(67)		2(67)		3(100)	
	LB	3	3(100)	0(0)		3(100)		2(67)		1(33)		2(67)	
Total		12	12(100)	3(25)		9(75)		8(67)		7(58)		10(83)	
IL-W	DB	5	5(100)	3(60)	0.635	4(80)	0.342	3(60)	0.764	4(80)	0.016	3(60)	0.635
	LB	4	4(100)	3(75)		2(50)		2(50)		0(0)		3(75)	
Total		9	9(100)	6(67)		6(67)		5(56)		4(44)		6(67)	
IL-S	PE	2	2(100)	1(50)	0.709	1(50)	0.171	1(50)	0.171	2(100)	0.361	2(100)	NA
	DB	3	3(100)	1(33)		3(100)		3(100)		2(67)		3(100)	
Total		5	5(100)	2(40)		4(80)		4(80)		4(80)		5(100)	
Irepodun	PE	2	2(100)	0(0)	0.438	0(0)	0.083	1(50)	1.0	0(0)	0.221	1(50)	0.540
	DB	4	4(100)	1(25)		3(75)		2(50)		2(50)		3(75)	
Total		6	6(100)	1(17)		3(50)		3(50)		2(33)		4(67)	
Moro	PE	5	5(100)	2(40)	0.543	3(60)	0.411	3(60)	0.741	3(60)	0.543	3(60)	0.543
	DB	1	1(100)	1(100)		0(0)		1(100)		0(0)		0(0)	
	LB	15	15(100)	7(47)		5(33)		10(67)		7(47)		7(47)	
Total		21	21(100)	10(48)		8(38)		14(67)		10(478)		10(48)	
Offa	PE	1	1(100)	0(0)	0.082	1(100)	0.659	1(100)	0.329	0(0)	0.329	1(100)	0.329
	DB	1	1(100)	1(100)		1(100)		1(100)		1(100)		0(0)	
	LB	3	3(100)	0(0)		2(67)		1(33)		2(67)		2(67)	
Total		5	5(100)	1(20)		4(80)		3(60)		3(60)		3(80)	
All the LG	PE	16	16(100)	5(31)	0.719	9(56)	0.553	10(63)	0.983	9(56)	0.430	12(75)	0.637
	DB	19	19(100)	8(42)		13(68)		12(63)		12(63)		12(63)	
	LB	23	23(100)	10(44)		12(52)		15(65)		9(39)		14(52)	
Total		58	58(100)	23(40)	0.260	34(59)	0.108	37(64)	0.916	30(52)	0.716	38(66)	0.468

L/G = Local Government area, *N* = number of isolates tested, DB = Dead birds, LB = Live birds and PE = Poultry environment

Table 4. Continued

L/G	Source of isolates	*N*	No. (%) resistant to[a]									
			N30	*p*-value	NA30	*p*-value	S3	*p*-value	S10	*p*-value	TE30	*p*-value
Asa	PE	6	2 (33)	0.513	5(83)	0.549	6(100)	0.002	3(50)	0.717	4(67)	0.513
	DB	3	0(0)		2(67)		3(100)		2(67)		3(100)	
	LB	3	1(33)		3(100)		0(0)		1(33)		2(67)	
Total		12	3(25)		10(83)		9(75)		6(50)		9(75)	
IL-W	DB	5	1(20)	0.858	4(80)	0.343	3(60)	0.764	5(100)	NA	4(80)	0.099
	LB	4	1(25)		2(50)		2(50)		4(100)		1(25)	
Total		9	2(22)		5(56)		5(56)		9(100)		5(56)	
IL-S	PE	2	0(0)	0.361	1(50)	0.709	1(50)	0.171	0(0)	0.025	2(100)	0.136
	DB	3	1(33)		2(67)		0(0)		3(100)		1(33)	
Total		5	1(20)		3(60)		1(20)		3(60)		3(60)	
Irepodun	PE	2	0(0)	0.439	2(100)	0.014	1(50)	1.0	1(50)	0.540	2(100)	0.221
	DB	4	1(25)		0(0)		2(50)		1(25)		2(50)	
Total		6	1(17)		2(50)		3(50)		2(33)		4(67)	
Moro	PE	5	1(20)	0.884	3(60)	0.724	1(20)	0.164	4(80)	0.288	2(40)	0.543
	DB	1	0(0)		1(100)		0(0)		1(100)		1(100)	
	LB	15	3(20)		9(60)		7(47)		7(47)		8(53)	
Total		21	4(19)		13(62)		8(38)		12(57)		11(52)	
Offa	PE	1	0(0)	0.329	1(100)	0.329	1(100)	0.082	0(0)	0.329	1(100)	0.659
	DB	1	1(100)		0(0)		0(0)		1(100)		1(100)	
	LB	3	1(33)		2(67)		0(0)		1(33)		2(67)	
Total		5	2(40)		3(60)		1(20)		2(40)		4(80)	
All the LG	PE	16	3(18)	0.851	12(75)	0.181	10(63)	0.317	8(50)	0.322	11(69)	0.453
	DB	19	4(21)		9(53)		8(42)		13(68)		13(68)	
	LB	23	6(26)		16(61)		9(39)		13(57)		12(52)	
Total		58	13(22)	0.945	37(64)	0.468	27(47)	0.519	34(59)	0.108	36(62)	0.762

L/G = Local Government area, *N* = number of isolates tested, DB = Dead birds, LB = Live birds and PE = Poultry environment

Table 5. Multidrug resistance patterns detected among *Salmonella* isolates from poultry farms in Kwara State

S/N	Resistance Pattern detected	No. (%) of *Salmonella* isolates	Serovars involved (n)
1	AMP-C	4 (6.9)	Typhimurium (1), 6,7: d: - (3)
2	AMP-CIP	5 (8.6)	Agama (3), Typhimurium (1), Orion (1)
3	CAZ-CN	3 (5.2)	6,7:d:- (2), Larochelle (1)
4	CTX-NA	5 (8.6)	Typhimurium (2), Larochelle (1), Muenster (2)
5	AMP-CAZ-CTX	6 (10.3)	Agama (2), 6,7: d: - (3), 45: d: 1,7 (1)
6	TE-C-GN	3 (5.2)	Agama (2), 6,7: d: - (1)
7	TE-C-CIP-CN	2 (3.4)	Agama (1), Typhimurium (1)
8	CIP-CN-N-NA	2 (3.4)	6,7: d: - (1), Agama (1)
9	AMP-CAZ-CTX-TE	3 (5.2)	Agama (1), Typhimurium (2)
10	AMP-CAZ-CTX-S_3	3 (5.2)	6,7: d: - (2), 45: d: 1,7 (1)
11	AMP-CAZ-CTX-NA	5 (8.6)	Agama (3), Typhimurium (1), Albany (1)
12	AMP-CAZ-CTX-N	4 (6.9)	6,7: d: - (3), 45: d: 1,7 (1)
13	AMP-CAZ-CTX-CN	3 (5.2)	Agama (1), 6,7: d: - (2)
14	AMP-CAZ-CTX-CIP	4 (6.9)	Typhimurium (1), 45: d: 1,7 (2), Colindale (1)
15	AMP- C-CAZ-CTX	3 (5.2)	Agama (2), Istanbul (1)
16	AMP-C-CAZ-CIP-CN-CTX-NA-S_3-S_{10}-TE	1(1.7)	Nigeria (1)
17	AMP-C-CAZ-CN-CTX-NA-N-S_3-S_{10}-TE	1(1.7)	4,5,12: i: - (1)
18	AMP-C-CAZ-CIP-CN-CTX-N-NA-S_3-S_{10}- TE	1(1.7)	4,12,27: z: - (1)

AMP, ampicillin; C, chloramphenicol; CAZ, ceftazidime; CIP, ciprofloxacin; CN, gentamicin; CTX, cefotaxime; N, neomycin; NA, nalidixic acid; S_3, compound sulfonamides; S_{10}, streptomycin; and TE, tetracycline. S/N: serial number

DISCUSSION

The detection of *Salmonella* from all the sources indicated high level of *Salmonella* contamination of poultry farms in the study area. This is of veterinary and public health significance as occurrence of a disease in a transit state may predispose the entire country to such disease. High contamination of the poultry farms with *Salmonella* may be attributed to low level of hygiene and biosecurity measures in the poultry industry in the state and the country as a whole as previously reported (Fagbamila et al., 2018). The fact that most of the serovars isolated from the environment were equally isolated from live and dead birds reaffirm the roles of environment in the transmission of *Salmonella* in poultry settings as reported earlier (Davies and Wales, 2010; Raufu et al., 2019). This study reports high rate of resistance to all antimicrobial agents used especially cephalosporin, fluoroquinolones and penicillin. A similarly high level of *Salmonella* resistance to ampicillin (98.4%) was reported in poultry houses in Nigeria (Raufu et al., 2013, Fashae et al., 2010) and Sudan (Elmadiena et al., 2013) and for *Salmonella* isolates from human in Maiduguri, Borno State, Nigeria (Ahmed et al., 2016). The misuse of antibiotics in poultry industry has resulted in increased resistance to antibiotics (Adesiyun et al., 2014b, Cantas et al., 2013), culminating in therapeutic failures and huge economic losses. Similarly, high resistance to fluoroquinolones have been reported from poultry sources in Ibadan,

Nigeria (Fashae et al., 2010) and Ovia North-East Local Government of Edo State, Nigeria (Enabulele et al., 2010). Resistance to quinolones and ceftriaxone in this study give a cause for concern as these drugs are the antibiotics of choice in cases of an outbreak of enteric pathogens including *Salmonella*. Humans relate with animals, especially food producing animals, through food chain and environment which they share (Marshall and Levy, 2011) and high prevalence of multi- resistant *Salmonella* serovars from food producing animals and environment constitute threat to public health. High resistance to these antimicrobials may not be unconnected to abuse these agents as most poultry farmers in the country have been reported to indiscriminately administer antimicrobials to poultry either as therapeutic agents to combat bacterial infections or in subtherapeutic doses in feed (Fagbamila et al., 2018).

The fact that most of the isolates showed low resistance rate (22.4%) to neomycin when compared with other antimicrobial agents used in this study is of therapeutic significance and might be because majority of the farmers in the state developed preference for alternate antimicrobials which they assumed are more potent. The prevalence of resistance to gentamicin in this study (52%) is in agreement with Adesiyun et al. (2014a) which reported a prevalence of (59.5%) among *Salmonella* isolates from poultry farms in three Caribbean countries, however, it is much higher when compared to other results from poultry studies which ranges from 0.0 to 17% (Oluwasile et al., 2014, Snow et al., 2007). The frequency of resistance to streptomycin detected in the current study (60.3%) corroborates with 21.9 to 92.9% previously reported for poultry farms (Adesiyun et al., 2014a, Enabulele et al., 2010). The fact that frequency of resistance was statistically significant to streptomycin, gentamicin, nalidixic acid and compound sulfurnamide in Ilorin south, Ilorin west, Irepodun and Asa Local Government areas respectively suggest possible misuse of the antimicrobials in the areas and therefore, there is need for concern authorities to promulgate policy that will regulate the use of antimicrobials in the areas and the country at large.

This occurrence of a high frequency of multidrug resistance reported in this study, in addition to the occurence of a total of 18 multi-resistance patterns, demonstrate a potential for the likelihood of chemotherapeutic failure that may be connected with the use of these antimicrobials in the area. These findings corroborate the report on *Salmonella* isolates from poultry by other researchers (Ahmed et al., 2017, Adesiyun et al., 2014a, Oluwasile et al., 2014, Elmadiena et al., 2013, Mir et al., 2010).

CONCLUSIONS

The study showed that the isolates exhibited high frequency of resistance to tested antimicrobials especially ampicillin, cefotaxime and ciprofloxacin. There is equally high prevalence of multidrug resistance among the isolates from all sources. There is, therefore, the need for the establishment of active national antimicrobial resistance surveillance programme for foodborne pathogens, (*Salmonella* inclusive). This will help address the public health concerns with respect to spread of multi-drug resistant *Salmonella* between animals and humans and their shared environment. There is, also need for formulation of policies and strengthening of existing ones on judicious use of antimicrobial agents in the poultry industry and other food animal production in the studied area and the country at large.

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