Journal of Advances in Microbiology

18(4): 1-10, 2019; Article no.JAMB.52188
ISSN: 2456-7116

Phenotype and Molecular Characterization of Antibiotic Resistance of *Salmonella* spp. from Cattle in Abidjan District, Côte d'Ivoire

Coulibaly Kalpy Julien[1,2*], Yao Kouamé René[1,2], Dagnogo Komissiri[3], Tiékoura Konan Bertin[1], Koffi Kouassi Eugène[1], Ajayi Abraham[4], Djaman Allico Joseph[1,2], Dosso Mireille[1,2] and Yapi Houphouët Félix[2]

[1]Institut Pasteur de Côte d'Ivoire, Cote d`Ivoire.
[2]Université Félix Houphouët-Boigny, Cote d`Ivoire.
[3]Laboratoire National d'Appui au Développement Agricole (LANADA), Cote d`Ivoire.
[4]Université de Lagos, Cote d`Ivoire.

Authors' contributions

This work was carried out in collaboration among all authors. Author CKJ designed the study, wrote a part of the protocol and the first draft of the manuscript. Authors YKR, DK, TKB and AA collected the samples and managed the analyses of the study. Author KKE managed the breeders, the sellers and wrote a part of the protocol. Authors DAJ and DM corrected the protocol and the article. Author YHF supervised the study. All authors read and approved the final manuscript.

Article Information

DOI: 10.9734/JAMB/2019/v18i430176
Editor(s):
(1) Dr. Muhsin Jamal, Assistant Professor, Department of Microbiology, Abdul Wali Khan University Mardan, Garden Campus, Mardan, Pakistan.
Reviewers:
(1) Pinar Sanlibaba, Ankara University, Turkey.
(2) Afroza Parvin, Jahangirnagar University, Bangladesh.
Complete Peer review History: http://www.sdiarticle4.com/review-history/52188

Original Research Article

Received 12 August 2019
Accepted 22 October 2019
Published 28 October 2019

ABSTRACT

Aims: The overall objective of this study was to study antibiotic-resistant strains of *Salmonella* in livestock sales sites in the Abidjan district.
Place and Duration of Study: Researchers team from Institute Pasteur of Ivory Coast and their students collected samples of cattle feces in five townships of the district of Abidjan from April to September 2016.
Methodology: Fresh cow dung has been collected from sales outlets and livestock pens in five municipalities in Abidjan. The prevalence of *Salmonella* carrying has been studied by classical

**Corresponding author: E-mail: jc_kalpy@yahoo.fr;*

microbiological techniques. These included strain isolation by culture on the Hektoen medium, biochemical identification using Leminor's reduced rack and strain confirmation by MALDI-TOF MS. Phenotypic determination of antibiotic resistance and detection their genes were carried out respectively by the method of discs diffusion on the Muller-Hinton agar and using PCR simplex.
Results: In this study, we collected 420 samples.
The results showed that the overall prevalence of *Salmonella* isolated from cattle feceswas 20% (84/420). Twenty-six (26) strains were resistant to at least one antibiotic. The bla_{CTX-M}, bla_{SHV}, bla_{TEM} and *TetA* resistance genes were detected with the respective frequencies of 7.7%, 57.7% and 7.7%.
Conclusion: The isolation of antibiotic-resistant *Salmonella* strains in these healthy cattle poses a significant threat to public health. However, a good use of antibiotics in farms could help limit the phenomenon of resistance of *Salmonella* to antibiotics.

Keywords: Salmonella spp.*; antibiotics; resistance; cattle; Abidjan; Côte d'Ivoire.*

1. INTRODUCTION

The possibility of transmission of antimicrobial resistant bacteria or their determinants of resistance from food animals to humans has been a public health concern for several decades [1]. This situation is generally due to the misuse of antibiotics in human or veterinary medicine. Indeed, the use of antimicrobials in animal production systems has long been suspected of being responsible for the emergence and spread of resistant bacteria [2].

In addition, resistant bacteria can act as a donor of a determinant of resistance to an optional pathogen of the commensal flora, which could be associated with a disease and in turn provide the resistance gene to another one [3]. Among the animals in the production system, cattle have been implicated as a potential source of human infection by antimicrobial-resistant bacteria through direct contact with livestock and by the consumption of food contaminated with these Bacteria.

Antibiotic resistant and multidrug-resistant bacteria are actually increasing on farms because of the use of antibiotics in the treatment of animals, at prophylactic or metaphylactic doses likely to favor the selection of resistant strains on farms. This situation greatly increases the risks to human health through the consumption of contaminated food products [4].

Recently, the emergence and spread of antimicrobial-resistant *Salmonella* from animal foods has been recognized as a serious danger in the world, particularly in developing countries [5,6]. According to the Centers for Disease Control and Prevention (CDC), non-typhoid *Salmonella* is one of the leading threats to antibiotic resistance in the United States, associated with about 1.2 million infections, 100,000 antimicrobial-resistant infections and 300 million of dollars in annual medical expenses [7].

In Europe, multi-antibiotic resistant *Salmonella* continues to spread in all health sectors according to the latest available data on the resistance of bacteria in humans, food and animals, provided by ECDC and EFSA [8]. In Côte d'Ivoire, several studies on *Salmonella* have shown an expansion of antibiotic-resistant strains [9,10,11,13,14]. However, data on antibiotic resistance of *Salmonella* in cattle farms are almost nonexistent to our knowledge in Côte d'Ivoire.

The general objective of this study is to characterize by phenotypic and molecular methods, antibiotic resistance in strains of *Salmonella* isolated from cattle feces in the district of Abidjan (Côte d'Ivoire).

2. MATERIALS AND METHODS

2.1 Isolation of *Salmonella* Strains in Cattle Feces

Fresh cattle feces samples were collected in five townships in the Abidjan district of Côte d'Ivoire over a six-month period from April to September 2016.A quantity of about two hundred (200) grams of randomly selected fresh feces was collected from the various sites.

The samples were taken from the surface and inside of feces freshly emitted with wooden spatulas and put in sterile Zip sachets. These in turn, have been placed in coolers containing ice pack and immediately sent to the microbiology laboratory of the Pasteur Institute about to 2

hours after collection. *Salmonella* isolation and identification was performed using the conventional method for the detection of *Salmonella* spp. according to ISO 6579:2002(E)). Briefly, 25 g of fresh feces were pre-enriched in 225 ml of buffered peptone water (EPT) (Bio-Rad) and incubated for 24 hours at 37°C. A suspension of 0.1 ml of the pre-enriched medium was added to 10 ml of Rappaport-Vassiliadis (RV10) enrichment broth (Bio-Rad) and incubated at 44°C for 24 hours. Then, each enrichment broth was streaked onto the Hektoen selective medium (Bio-Rad) and incubated for 24 hours at 37°C. Three to five characteristic *Salmonella* colonies were randomly selected and then identified using the Leminor reduced rack. The *Salmonella* strains identified were subsequently confirmed at MALDI-TOF MS (BioMérieux, France). The strain of *Salmonella* typhimurium (IPCI) was used as a positive control to verify the effectiveness of isolation on Hektoen agar. The strain of *E. coli* ATCC 8739 (Biomérieux, France) was used as a calibration strain of MALDI-TOF.

2.2 The Susceptibility of *Salmonella* Strains to Antibiotics

Antibiotic susceptibility tests were performed on all *Salmonella* strains. A standardized amount was inoculated (standard 0.5 of McFarland) and antimicrobial susceptibility testing was performed by the disk diffusion method on Mueller–Hinton (MH) agar using interpretative criteria of the Antibiogram Committee of the French Society of Microbiology (EUCAST/ CA-SFM, 2016). Quality control was carried out using standard strains of *Escherichia coli* (ATCC 25922). Intermediate susceptibility to each antibiotic was considered to be resistant. The following antibiotic discs (Bio-Rad France) were used: ampicillin (10 µg), amoxicillin + clavulanic acid (30 µg), cefalotin (30 µg), cefepime (30 µg), aztreonam (30 µg), cefoxitin (30 µg), ceftriaxone (30 µg), ceftazidime (30 µg), cefuroxime (30 µg), imipenem (10 µg), tetracyclin (30 µg), minocycline (30 µg), gentamicin (10 µg), tobramycin (10 µg), amikacin (30 µg), nalidixic acid (30 µg), norfloxacin (5 µg), ciprofloxacin (5 µg), chloramphenicol (30 µg), colistine (50 µg) and trimethoprime/ sulfamethoxazole (25 µg).

2.3 Detection of Antibiotic Resistance Genes

Detection of antibiotic resistance genes was performed by simplex PCRs on all strains of *Salmonella* phenotypically resistant to at least one antibiotic. Extraction of the bacterial DNA was carried out on 24-hour colonies by heat

Table 1. Specific primer

Gene	Primers	Sequence (5'-3')	Size of fragment (pb)	References
bla_{TEM}	TEM front P1	GCGGAACCCCTATTTG	964	[16]
	TEM-C-R-ny	ACCAATGCTTAATCAGTGAG		[17]
$bla_{CTX\text{-}M}$	CTX-M F	TTTGCGATGTGCAGTACCAGTAA	544	[18]
	CTX-M R	CGATATCGTTGGTGGTGCCATA		
bla_{SHV}	SHV F	TTTATGGCGTTACCTTTGACC	1051	[19]
	SHV R	ATTTGTCGCTTCTTTACTCGC		
tetA	TetA primer1	GTAATTCTGAGCACTGTCGC	956	[20]
	TetA primer2	CTGCCTGGACAACATTGCTT		

Table 2. Reference strains

Strains	Usage	Origin
E. coli ATCC 25922	Quality controls of the antibiogram	DTU Food (Danemark)
Salmonella typhimurium	Quality control of Hektoen agar	IPCI (Côte d'Ivoire)
E. coli ATCC 8739	Souche calibrante du MALDI-TOF	Biomérieux
Salmonella bredeney TEM-104	Positive control for bla_{TEM} gene detection	DTU Food (Denmark)
Salmonella virchou 58.67 Holland	Positive control for $bla_{CTX\text{-}M}$ gene detection	DTU Food (Denmark)
Salmonella keurmassar DAK2	Positive control for bla_{SHV} gene detection	DTU Food (Denmark)
Escherichia coli NCTC50078	Positive control for *tetA* gene detection	DTU Food (Denmark)

DTU: Technical University of Denmark; IPCI: Pasteur Institute of Côte d'Ivoire

Table 3. Amplification program

Amplification step	Temperature C°/Time/cycle	
	CTX-M, TEM, SHV	TetA
Initial denaturation	94°C/5min	95°C/5min
Cyclicaldenaturation	94°C/1min	95°C/30s
Hybridization	60°C/1min	56°C/30s
Cyclicelongation	72°C/1min	72°C/10min
Final elongation	72°C/7min	72°C/10min
Number of cycles	30 cycles	35

shock [14] followed by phenol-chloroform-alcohol-isoamyl (v / v / v) purification [15]. The study of the different resistance genes was carried out by monoplexed PCRs using specific primers recorded in Table 1. The genomic amplification was carried out in a final reaction volume of 50 µl. This reactional mix contained a 5X color buffer (Promega, USA), a 5X non-stained buffer (Promega, USA), MgCl2 concentrated at 25 mM (Promega, USA), dNTPs to 10 mM (Bio-Rad, France), Go taq DNA polymerase to 5U/µl (Promega, USA) and specific primers to 10 µM. The DNA extrated from reference strains provided by the National Food Institute collection (DTU Food) were used as positive controls for PCR (Table 2) and a reaction mixture without DNA extract served as a negative control. The amplification conditions are shown in Table 3. The amplification products were analyzed by electrophoresis on a 1.5% agarose gel prepared from a 10X TAE buffer (Tri-Acetate-EDTA) and 5 µL of a solution of EZ-vision® (Inqababiotec, West Africa) at 120 volts / cm for 1 hour.

3. RESULTS AND DISCUSSION

3.1 Results

3.1.1 Prevalence of *Salmonella* spp. strains

The use of the MALDI-TOF (vitek MS) automated system allowed the effective identification of isolated *Salmonella* strains in cattle feces. Thus, out of a total of 420 samples of bovine feces collected and analysed, 84 (20%) *Salmonella* strains were isolated. Also, the proportion of isolated *Salmonella* strains varied according to the township. Thus, the communes of Port-Bouët (9.8%) and Adjamé (7%) had high proportions. On the other hand, they were 1.2%, 1% and 1% respectively in the communes of Abobo, Yopougon and Bingerville.

3.1.2 Resistance profile of strains of *Salmonella* spp.

The determination of the resistance profile of the strains tested revealed that 26 strains of *Salmonella* spp. were resistant to at least one antibiotic. However, overall, a low level of resistance to beta-lactam antibiotics with resistance rates ranging from 1.2 to 6% was observed. As for quinolones, a low level of resistance was generally observed mainly with nalidixic acid (3.6%), ciprofloxacin (3.6%) and norfloxacin (3.6%). Concerning the level of resistance to cyclins, aminoglycosides and other antibiotics, it appears that the resistance rate was higher at colistin (33.3%) followed by cyclins including tetracycline (20.2%) and minocycline (20.2%). Low levels of resistance were observed with gentamicin (1.2%), tobramycin (3.6%) and trimethoprim/sulfamethoxazole (6%). However, no resistance was observed with cefoxitin, imipenem, amikacin and chloramphenicol Table 4.

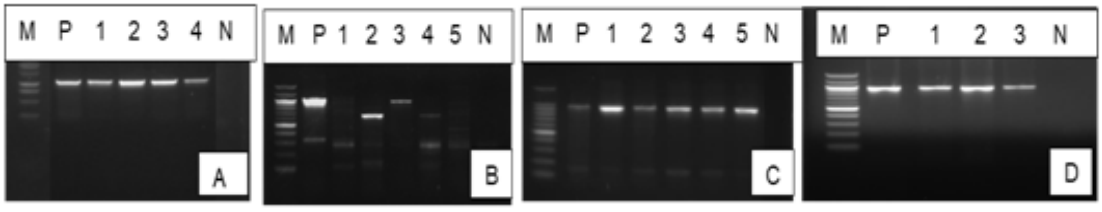

Fig. 1. Electrophoretic profile of antibiotic resistance genes

A: detection of the bla_{CTX-M} gene (544 bp); B: detection of the bla_{SHV} gene (1051bp); C: detection of the bla_{TEM} gene (964bp); D: detection of the TetA gene (956 bp); M: Molecular Weight marker (100 bp DNA Ladder); P: Positive control; Number 1 to 5: Bacterial strain; N: Negative control

Table 4. Antibiotic resistance of *Salmonella* strains

Antibiotic	Resistance rate (%) R (n=84)
Betalactams	
Ampicillin (AMP)	2.4
Amoxicillin/Clavulanicacid (AMC)	1.2
Cefalotine (CEF)	6
Cefuroxine (CXM)	2.4
Cefoxitine (FOX)	0
Ceftriaxone (CRO)	1.2
Ceftazidime (CAZ)	1.2
Cefepime (FEP)	1.2
Aztreonam (ATM)	1.2
Imipem (IMP)	0
Quinolones	
Nalidixicacid (NAL)	3.6
Ciprofloxacin (CIP)	3.6
Norfloxacin (NOR)	3.6
Cyclins	
Tetracycline (TET)	20.2
Minocycline (MNO)	20.2
Aminosides	
Amikacin (AKN)	0
Tobramycin (TMN)	3.6
Gentamycin (GEN)	1.2
Other	
Colistin (CST)	33.3
Chloramphenicol (CHL)	0
Trimethoprim/Sulfamethoxazole (SXT)	6

Table 5. Detection of antibiotic resistance genes

Strains (n=26)	Number of genesdetected (%)			
	bla_{CTX-M}	bla_{SHV}	bla_{TEM}	*TetA*
Salmonella spp.	0	2	15	2
Frequency (%)	0	7.7	57.7	7.7

3.1.3 Molecular detection of antibiotic resistance

In total, the 26 strains of antibiotic-resistant *Salmonella* were selected for antibiotic resistance gene research (Fig. 1). PCR results for bla_{CTX-M} (544pb), bla_{SHV} (1051pb), bla_{TEM} (964bp) and *TetA* (956bp) showed detection rates of 7.7%, 57.7% and 7, respectively. 7% (Table 5). However, no bla_{CTX-M} genes were detected.

3.2 Discussion

The results of this study showed a Prevalence of Salmonella strains isolated from cattle feces was 20%. Also, sectoral prevalence in the five townships have beendetermined and gave relatively high rates in the townships of Port-Bouët (9.8%) and Adjamé (7%), while in other townships (Abobo, Yopougon and Bingerville) a low rate ranging from 1% to 1.2% has been observed. This prevalence of 20% of *Salmonella* strains determined in our study is higher than that determined by Alemayehu et al. [21] who reported a prevalence of 7.1%. Studies in Ethiopia (2.3%) and Nairobi (2.6%) reported lower prevalences than those obtained in this study [22,23]. Significantly lower carriage of *Salmonella* has been reported in cattle in Japan and Great Britain with prevalence of 0.5% and 1.4% respectively [24,25]. The high prevalence observed in this study may be due to the different methods used for isolating strains. However, it is comparable to that obtained by Akoachere et al. [26] in Cameroon. These authors reported a prevalence of 28.7% in cattle during their work. The report of a study by Kagambèga et al. [27] in

Burkina Faso reported a very high prevalence of *Salmonella* (52%) in cattle feces. These fluctuations in results could be explained by the fact that these works were not carried out in the same environments and the difference in the good practice of hygiene during the breeding. Indeed, during the practice of breeding the feces and waste due to livestock feed are not removed regularly. Under these conditions, there may be enough nutrients in moist soils to keep *Salmonella* viable for several years [28].

Isolated *Salmonella* strains showed a low level of resistance to beta-lactam. Also, resistance to beta-lactams mainly to C3G / C4G in animals appears more occasional. Indeed, this bacterium does not seem to constitute a major reservoir of resistance genes [29]. Moreover, the cumulative data from surveillance networks for *Salmonella* strains in France confirm this very small proportion of *Salmonella* strains of animal origin with C3G / C4G. In our study, the low prevalence of the resistance observed with beta-lactam could be explained by the low pressure exerted by beta-lactams on these *Salmonella* strains. Several authors have also reported similar rates of resistance [30,31,32,33]. Variable resistance rates to third generation cephalosporins have been reported in China (1.6%), Romania (11.4%) and the United States (16%) [27,28,29].

In terms of resistance to quinolones and fluoroquinolones, our results showed that *Salmonella* strains are still largely sensitive to quinolones. Similar results have been reported by Gorman and Adley. [34] with nalidixic acid (2.6%) in the Republic of Ireland, ciprofloxacin (5.7%) in India [35]. Lower rates compared to those obtained in our study (less than 1%) were reported by Smith et al. [36]. In addition, high rates of resistance to nalidixic acid have been reported in Kenya (12%) [37], India (17.9% and 24.5%) [38], Romania (65.1%) [39]. However, the low rate observed in our study could be explained by the fact that fluoroquinolones are not widely used in cattle breeding in Côte d'Ivoire. Also, a high rate of resistance to cyclins was observed (20.2% tetracycline, 20.2% minocycline). This increase in cyclin resistance has also been observed by Edrington et al. [40] who reported a resistance rate of 20.9%. High resistance rates compared to the rates obtained in our study were observed in Nigeria [41], Ethiopia [22], the United States [42]. In addition, high resistance rates to tetracycline (62.2%) and minocycline (46.3%) were observed in South Africa [43]. However, low resistance rates have been reported in several studies [38,40]. Tetracycline resistance is usually caused by genes associated with primary resistance mechanisms involving active efflux pumps, ribosomal protection and enzymatic inactivation. Therefore, the high tetracycline resistance observed in this study would probably be due to selection pressure caused by uncontrolled use of cyclins. In terms of resistance to aminoglycosides, there is a general decrease of the *Salmonella* resistance to them. Aminoglycosides generally contained molecules for hospital use like amikacin and gentamicin. According to Ouattara et al. [44] their use in veterinary medicine remains limited.

In addition, the strains showed a fairly high resistance to colistin in this work and involved 33.3% of *Salmonella*. The rate obtained in this work is worrying. Indeed, this rate is much higher than the rates reported in several studies [45,46,47,48]. This high prevalence of colistin resistance may be due to the increasing use of colistin in livestock farming.

Three different beta-lactam resistance genes belonging to Ambler's molecular classes a (*bla*$_{TEM}$, *bla*$_{CTX-M}$ and *bla*$_{SHV}$) were investigated in this study. These genes have recently been reported in cattle, but in varying proportions. In this study, the *bla*$_{SHV}$ and *bla*$_{TEM}$ genes were detected with frequencies of 7.69% and 57.69% respectively. However, no *bla*$_{CTX-M}$ genes were detected. This study showed a high frequency of *bla*$_{TEM}$ genes. Nevertheless, phenotypic tests revealed a low rate of resistance to beta-lactam antibiotics. This result could be explained by the detection of beta-lactamase TEM which has the ability to hydrolyze only early penicillins and/or cephalosporins but not third or fourth generation cephalosporins, which could not be detected phenotypically. As for the beta-lactamase SHV, our results revealed a low frequency of detection. This observed rate is higher than those of Lertworapreecha et al. [49] who reported a negative result for beta-lactamase SHV. This could explain an acquisition of the *bla*$_{SHV}$ gene. About tetracycline resistance, our results revealed the detection of the *tetA* gene with a frequency of 7.6% in *Salmonella* strains. Tetracycline resistance is usually caused by the acquisition of a tetracycline resistance gene (tet). These genes are associated with primary resistance mechanisms, which involve active efflux pumps, ribosomal protection and enzymatic inactivation [50]. The difference between the resistance of *Salmonella* to

tetracycline evaluated by the phenotypic method and the resistance profile obtained by PCR could be due to other tetracycline resistance genes that were not evaluated in this study.

4. CONCLUSION

This study showed a high prevalence of *Salmonella* isolated in cattle feces in the Abidjan district. It has also generally shown a high level of resistance of these strains to antibiotics commonly used in human and veterinary medicine. The isolation of antibiotic-resistant *Salmonella* strains from these healthy cattle is a very significant health threat given *Salmonella*'s place in the causes of diseases with bacterial etiology. In addition, the determination of this resistance by the molecular epidemiology method using resistance markers (PCR) showed the presence of resistance genes such as bla_{SHV}, bla_{TEM} and *TetA*. The emergence and spread of antibiotic-resistant *Salmonella* strains in food-producing animals is a significant public health problem. However, continuous surveillance of antibiotic therapy in farms must be put in place to limit the phenomenon of antibiotic resistance.

CONSENT

It is not applicable.

ETHICAL APPROVAL

It is not applicable.

ACKNOWLEDGEMENTS

Authors would like to thank the Governor of Abidjan's district, the head and the staff of the slaughterhouse of Port-Bouët, the staff of Institut Pasteur de Côte d'Ivoire, breeders, salesmen and livestock staff and all persons whom made this work possible.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

1. Moyaert H, De Jong A, Simjee S. Antimicrobial resistance monitoring projects for zoonotic and indicator bacteria of animal origin: Common aspects and differences between EASSA and EFSA. 2014;171:279–283.
2. Alexander KA, Warnick LD, Wiedmann M. Antimicrobial resistant *Salmonella* in dairy cattle in the United States, Vet. Res. Commun. 2009;33(3):191–209.
3. Kemal J. A review on the public health importance of Bovine Salmonellosis. J. Vet. Sci. Technol. 2014;05(2):1-10 .
4. Addis Z, Kebede N, Worku Z, Gezahegn H, Yirsaw A, Kassa T. Prevalence and antimicrobial resistance of *Salmonella* isolated from lactating cows and in contact humans in dairy farms of Addis Ababa: A cross sectional study. BMC Infect. Dis. 2011;11(22):1-7.
5. Yang B, Qu D, Zhang X, Shen J, Cui S, Shi Y, et al. International Journal of Food Microbiology Prevalence and characterization of *Salmonella* serovars in retail meats of marketplace in Shaanxi, China, Int. J. Food Microbiol. 2010;141(1-2):63–72.
6. Pribul BR, Festivo ML, de Souza MMS, dos Rodrigues DP. Characterization of quinolone resistance in *Salmonella* spp. isolates from food products and human samples in Brazil. Braz. J. Microbiol. 2015;47(2016):196–201.
7. CDC, Antibiotic resistance threats in the United States; 2013.
   Available:https://www.cdc.gov/drugresistance/pdf/ar-threats-2013-508.pdf
8. EFSA and ECDC. The European Union summary report on antimicrobial resistance in zoonotic and indicator bacteria from humans, animals and food in 2017. EFSA J. 2019;17(2):5598.
9. Coulibaly KJ, Koffi S, Dou S, Bamba A, N'douba AK, Dosso M. The antibiotic resisting profile of *Salmonella* spp. Isolated from the Sewage of the Campus of the University of Cocody, Abidjan, Côte d' Ivoire. 2014;4(5):608–620.
10. Coulibaly KJ, Stephane K, Serge D, Aboubacar B, N'douba KA, Mireille D. Prevalence of Antibiotics Resistant *Salmonella* in the Abidjan North Wastewater in 2012 and Potential Health Risks to the Population. J. Adv. Microbiol. 2016;1(1):1-9.
11. Bonny A, Karou A, Sanogo M, Atobla Ahonzo-Niamke KS. Prevalence of *Salmonella* and their antibiotic susceptibility patterns in the District of

Abidjan, Côte d'Ivoire. Int. J. Biol. Chem. Sci. 2019;8(2):450-458.

12. Koffi AR, Ouassa T, Dadie A, Karou T, Koffi MDJE. Sérotypes et profils d' antibio-résistance de *Salmonella* suspectées d' origine alimentaire et isolées chez des patients diarrhéiques à Abidjan, Côte d' Ivoire. 2012;56:336-342.
13. Koffi AR, Adjehi D, Tago K, Marcelin DK. Original research article serotypes and antibiotic resistance of *Salmonella* spp. isolated from poultry carcass and raw gizzard sold in markets and catering in Abidjan, Côte d' Ivoire. 2014;3(6):764–772.
14. Lee VT, Smith RS, Tümmler B, Lory S. Activities of *Pseudomonas aeruginosa* effectors secreted by the type III secretion system *in vitro* and during infection. Infect. Immun. 2005;73(3):1695–1705.
15. Serghini MA, Ritzenthaler C, Pinck L. A rapid and efficient miniprep for isolation of plasmid DNA. Press Nucleic Acids Res. 1989;17(9):3604.
16. Olesen I, Hasman H, Aarestrup FM. Prevalence of B-lactamases among ampicillin-resistant *Escherichia coli* and *Salmonella* isolated from food animals in Denmark. Microb. Drug Resist. 2004;10(4):334–340.
17. Moodley A, Guardabassi L, Transmission of IncN Plasmids Carrying bla CTX-M-1 between Commensal *Escherichia* coli in Pigs and Farm Workers †," Antimicrob. Agents Chemother. 2009;53(4):1709–1711.
18. Birkett CI, Ludlam HA, Woodford N, Brown DFJ, Brown NM, Roberts MTM, et al. Real-time TaqMan PCR for rapid detection and typing of genes encoding CTX-M extended-spectrum b-lactamases. J. Med. Microbiol. 2007:56:52–55.
19. Yagi T, Kurokawa H, Shibata N, Shibayama K, Arakawa Y. A preliminary survey of extended-spectrum v-lactamases (ESBLs) in clinical isolates of *Klebsiella pneumoniae* and *Escherichia coli* in Japan. FEMS Microbiol. Lett. 2000;184:53–56.
20. Waters SH, Rogowsky P, Grinsted J, Altenbuchner J, Schmitt R. Nucleic acids research the tetracydine resistance determinants of RP1 and Tnl721: nucleotide sequence analysis. Nucleic Acids Res. 1983;11(17):6089–6105.
21. Alemayehu D, Molla B, Muckle A. Prevalence and antimicrobial resistance pattern of *Salmonella* isolates from apparently healthy slaughtered cattle in Ethiopia. Trop. Anim. Health Prod. 2003;35(4):309–319.
22. Eguale T, Engidawork E, Gebreyes WA, Asrat D, Alemayehu H, Medhin G, et al. Fecal prevalence, serotype distribution and antimicrobial resistance of *Salmonella*e in dairy cattle in central Ethiopia. BMC Microbiol. 2016;16(1):20.
23. Nyabundi D, Onkoba N, Kimathi R, Nyachieo A, Juma G, Kinyanjui P, et al. Molecular characterization and antibiotic resistance profiles of *Salmonella* isolated from fecal matter of domestic animals and animal products in Nairobi. Trop. Dis. Travel Med. Vaccines. 2017;3:2.
24. Ishihara K, Takahashi T, Morioka A, Kojima A, Kijima M, Asai T, et al. National surveillance of *Salmonella* enterica in food-producing animals in Japan. Acta Vet. Scand. 2009;51:35.
25. Milnes AS, Sayers AR, Stewart I, Clifton-Hadley FA, Davies RH, Newell DG, et al. Factors related to the carriage of Verocytotoxigenic *E. coli*, *Salmonella*, thermophilic *Campylobacter* and *Yersinia enterocolitica* in cattle, sheep and pigs at slaughter. Epidemiol. Infect. 2009;137(8): 1135–1148.
26. Akoachere JFTK, Tanih NF, Ndip LM, Ndip RN. Phenotypic characterization of *Salmonella* typhimurium isolates from food-animals and abattoir drains in Buea, Cameroon. J. Heal. Popul. Nutr. 2009;27(5):612–618.
27. Kagambèga A, Lienemann T, Aulu L, Traoré AS, Barro N, Siitonen A, et al. Prevalence and characterization of *Salmonella enterica* from the feces of cattle, poultry, swine and hedgehogs in Burkina Faso and their comparison to human *Salmonella* isolates. BMC Microbiol. 2013;13(1):253.
28. Turpin PE, Maycroft KA, Rowlands CL, Wellington EMH. Viable but non-culturable *Salmonella*s in soil. J. Appl. Bacteriol. 1993;74(4):421–427.
29. Madec J, Haenni M, Jouy E, Granier S, Weill F, Le Hello S. Les entérobcatéries résistantes aux céphalosporines de dernières générations générations : de l'animal à l'Homme," Bull. Epidémiologique, Santé Anim. Aliment. 2012;53(1):37–39.

30. Dutta S, Scientist G, Sudhanthirakodi S, Jain P, Chattopadhyay UK. Non-typhoidal *Salmonella* isolates from livestock and food samples, Kolkata, India Conclusion: High prevalence of NTS in poultry and meat samples in Kolkata poses a potential risk of foodborne disease in humans. J. Microbiol. Infect. Dis.2016;66(33):113–120.
31. Yu T, Jiang X, Zhou Q, Wu J, Wu Z. Antimicrobial resistance, class 1 integrons, and horizontal transfer in *Salmonella* isolated from retail food in Henan, China. J. Infect. Dev. Ctries. 2014;8(6):705–711.
32. Mihaiu L, Lapusan A, Tanasuica R, Sobolu R, Mihaiu R, Oniga O, et al. First study of *Salmonella* in meat in Romania. J. Infect. Dev. Ctries. 2014;8(1):050-058.
33. White DG, Zhao S, Sudler R, Ayers S, Friedman S, Chen SG, et al. The isolation of antibiotic-resistant *Salmonella* from retail ground meats. New Englang J. Med. 2001;345(16):1147–1154.
34. Gorman R, Adley CC. Nalidixic acid-resistant strains of *Salmonella* showing decreased susceptibility to fluoroquinolones in the mid-west region of the Republic of Ireland. J. Antimicrob. Chemother. 2003;51:1047–1049.
35. Sanjukta R, Dutta JB, Sen A, Shakuntala I, Ghatak S, Puro AK, et al. Characterization of multidrug-resistant *Escherichia* coli and *Salmonella* isolated from food producing animals in Northeastern India. Int. J. Infect. Dis. 2016;45:114–115.
36. Smith AB, Renter DG, Cernicchiaro N, Shi X, Nagaraja TG. Prevalence and quinolone susceptibilities of *Salmonella* isolated from the feces of preharvest cattle within feedlots that used a fluoroquinolone to treat bovine respiratory disease. Foodborne Pathog. Dis. 2016;13(6):303–308.
37. Nyabundi D, Onkoba N, Kimathi R, Nyachieo A, Juma G, Kinyanjui P, et al. Molecular characterization and antibiotic resistance profiles of *Salmonella* isolated from fecal matter of domestic animals and animal products in Nairobi. Trop. Dis. Travel Med. Vaccines. 2017;3(1):2.
38. Murugkar HV, Rahman H, Kumar A, Bhattacharyya D. Isolation, phage typing and antibiogram of *Salmonella* from man and animals in northeastern India. Indian J. Med. Res. 2005;122(3):237–42.
39. Mihaiu L, Lapusan A, Tanasuica R, Sobolu R, Mihaiu R, Oniga O, et al. First study of *Salmonella* in meat in Romania. J. Infect. Dev. Ctries. 2014;8(1):050-058.
40. Edrington TS, Hume ME, Looper ML, Schultz CL, Fitzgerald AC, Callaway TR E, et al. Variation in the faecal shedding of *Salmonella* and *E. coli* O157:H7 in lactating dairy cattle and examination of *Salmonella* genotypes using pulsed-field gel electrophoresis. Lett. Appl. Microbiol. 2004;38(5):366–372.
41. Umeh SI, Paulinus EC. Antimicrobial resistance profile of *Salmonella* isolates from livestock. Open J. Med. Microbiol. 2014;4(4):242–248.
42. Dargatz DA, Fedorka-Cray PJ, Ladely SR, Kopral CA, Ferris KE, Headrick ML. Prevalence and antimicrobial susceptibility of *Salmonella* spp. isolates from US cattle in feedlots in 1999 and 2000. J. Appl. Microbiol. 2003;95(4):753–761.
43. Igbinosa IH. Prevalence and detection of antibiotic-resistant determinant in *Salmonella* isolated from food-producing animals. Trop. Anim. Health Prod. 2014;47 (1):37–43.
44. Ouattara N, Guessennd N, Gbonon V, Toe E, Dadié T, Tiécoura B. Consommation des antibiotiques dans la filière aviaire à Abidjan: Cas de quelques fermes semi-industrielles. Eur. J. Sci. Res. 2013;94:80–85.
45. de Jong A, Thomas V, Simjee S, Godinho K, Schiessl B, Klein U, et al. A pan-European survey of antimicrobial susceptibility towards human-use antimicrobial drugs among zoonotic and commensal enteric bacteria isolated from healthy food-producing animals. J. Antimicrob. Chemother. 2009;63(4);733–744.
46. Huang X, Yu L, Chen X, Zhi C, Yao X, Liu Y, et al. High prevalence of colistin resistance and mcr-1 gene in *Escherichia coli* isolated from food animals in China. Front. Microbiol. 2017;8:1-5.
47. Kempf I, Fleury MA, Drider D, Bruneau M, Sanders P, Chauvin C, et al. What do we know about resistance to colistin in Enterobacteriaceae in avian and pig production in Europe? Int. J. Antimicrob. Agents. 2013;42(5):379–383.

48. Kempf I, Jouy E, Chauvin C. Colistin use and colistin resistance in bacteria from animals. Int. J. Antimicrob. Agents. 2016;48(6):598–606.
49. Lertworapreecha M, Noomee S, Sutthimusik S, Utarapichat B, Tontikapong K. Multidrug resistant and extended spectrum B-lactamase producing *Salmonella* enterica isolated from food animals in phatthalung, Thailand. Southeast Asian J. Trop. Med. Public Health. 2016;47(6):1257–1269.
50. Koo HJ, Woo GJ. Distribution and transferability of tetracycline resistance determinants in *Escherichia coli* isolated from meat and meat products. Int. J. Food Microbiol. 2011;145(2-3):407–413.

Peer-review history:
The peer review history for this paper can be accessed here:
http://www.sdiarticle4.com/review-history/52188