

Full Length Research Paper

***Salmonella* diversity and antimicrobial resistance in Burkina Faso: An investigation of strains from various sources**

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Epidemiologic and traceback evidence of *Salmonella* infection is not much in many developing countries including Burkina Faso. This study investigates the antimicrobial resistance and distribution of *Salmonella* serotypes isolated from diverse sources in Burkina Faso. 615 *Salmonella* serotypes isolated from beef meat, poultry carcasses, poultry, swine, cattle, hedgehog, fish, salad, channel and humans from 2009 to 2011 were analyzed to identify their diversity and distribution among the samples. The *Salmonella* strains were subjected to antimicrobial sensitivity tests using disk diffusion methods, were analyzed and classified into 110 serotypes, with the most prevalent serotype being Derby (91/615) found in beef meat, poultry carcasses, poultry and fish; Muenster (48/615) found in cattle, swine, hedgehog, poultry, human and fish; Chester (38/615) found in poultry carcasses, swine and poultry feces; Hato (32/615) found in beef meat, poultry carcasses, cattle and poultry; Drac (30/615) found in cattle, hedgehog and fish; and Typhimurium (21/615) found in cattle, poultry, human and fish. Among the 615 *Salmonella* strains, 94% (581/615) were resistant to one or more antibiotics; resistance to streptomycin was the most common. The resistance pattern, Str-Sul-Tet, Str-Tet and Str-Sul was dominant and found in 80% of the strains. About 3% of the strains were resistant to 5 or 6 antibiotics; their resistance pattern is amp-str-sul-tet-tmp or amp-chl-str-sul-tet-tmp. One *Salmonella* strain, *S. Kentucky* isolated from human stool was resistant to eight antibiotics; the resistance pattern is amp-str-sul-tet-cip-gen-nal-mec. Findings from this study can help define the guidelines for basic surveillance system of *Salmonella* and other enteropathogenic bacteria circulating among humans, animals, food and environment.

Key words: *Salmonella*, environment, human, risk.

INTRODUCTION

Salmonella spp. especially Non-Typhoid *Salmonella* (NTS) is a common source of foodborne diseases that cause morbidity and mortality worldwide (Smith et al.,

2016). It is estimated that *Salmonella* spp. cause 93.8 million cases of gastroenteritis and 155,000 deaths each year worldwide. Approximately 86% of these cases are

the result of foodborne infections (Majowicz et al., 2010). In Burkina Faso, bacteriological results showed that the rate of *Salmonella* contamination remains quite high (Simpomé et al., 2009). In fact, the infection progresses mostly periodically and rarely in an epidemic mode, and they are not reported due to lack of food borne pathogens surveillance system.

Salmonella spp. can survive for long periods in natural waters, and the persistence of specific and epidemic strains is a great concern in public health. However, information on the diversity and occurrence of *Salmonella* strains is very scarce (Cui et al., 2008), making the ecology of these species remains unknown. Food animals, including poultry, pigs, and cattle are the key reservoirs for human salmonellosis (Hauser et al., 2011). In developing countries, wild and food animals are the sources of *Salmonella* distribution in water, vegetables, salad and the products derived from these animals due to lack of hygiene (Kagambèga et al., 2013). The emergence of antimicrobial resistant *Salmonella* is mostly associated with the non-therapeutic use of various classes of antimicrobials in large quantities in food animals (Marshall and Levy, 2011; Mir et al., 2015).

Researchers have reported a link between the use of antimicrobials in food animals and the emergence of antimicrobial resistance in pathogenic bacteria (Ungemach et al., 2006; Mir et al., 2015). The increasing number of multidrug-resistant NTS strains is a global concern; this has made some countries and international organizations create surveillance systems which include collaboration between human health, veterinary, and food related sectors to monitor the spread of foodborne bacteria.

Unfortunately, these surveillance systems are missing in many developing countries like Burkina Faso. The absence of controlled reporting of *Salmonella* serotypes through the WHO-GFN program in Burkina Faso inspired the compilation of data on the sporadic reporting of *Salmonella* serotypes isolated from various sources. Therefore, the purpose of the present study is to provide information on the diversity and antimicrobial resistance of *Salmonella* strains isolated from environment, animals, food and humans. These data will allow one to follow the trends in *Salmonella enterica* serotypes that provide information about sources of infection and the efficacy of prevention and control measures.

MATERIALS AND METHODS

Salmonella strains (n= 615) isolated from meat, poultry carcasses, poultry, cattle, pigs, hedgehog, water, salad and humans were collected in Burkina Faso from 2009 to 2011. Sampling was done based on the microbiological conditions. The strains were isolated

using standard bacteriological methods and serotyped according to Kauffman White scheme (Kagambèga et al., 2013; Bonkougou et al., 2013; Traoré et al., 2015).

Antimicrobial susceptibility of the isolates was tested by a standard disk diffusion method, and *Escherichia coli* RHE 6715 (ATCC 25922) was used for validating the antimicrobial test results (CLSI, 2015). The antimicrobial agents used were ampicillin (10 µg), chloramphenicol (30 µg), streptomycin (10 µg), sulphonamides (3 µg), trimethoprim (5 µg), tetracycline (30 µg), gentamicin (10 µg), nalidixic acid (30 µg), ciprofloxacin (5 µg), cefotaxime (30 µg), mecillinam (10 µg) and imipenem (10 µg). Minimal inhibitory concentration (MIC) for ciprofloxacin (0.002 to 32 µg/ml) was determined by E-test (AB Biodisk, Solna Sweden) of the isolates resistant to nalidixic acid. MIC breakpoint ≤ 1 µg/ml was interpreted as susceptible (CLSI, 2009).

Ethics approval and consent to participate

Permission to conduct this study was obtained from the slaughterhouse authorities and the study protocol was approved by the Ethical Committee of Burkina Faso.

RESULTS AND DISCUSSION

A total of 615 strains of *Salmonella* isolated from meat, poultry carcasses, poultry, cattle, pigs, hedgehog, water, salad and humans were distributed into 110 different serotypes (Table 1). The six most prevalent serotypes were Derby, Muenster, Chester, Drac, Hato and Typhimurium. *Salmonella* Derby (91/615) was found in beef meat (n=2), poultry carcasses (n= 34), poultry (n= 52) and fish (n = 3). Our findings show that *S. Derby* is the most often isolated serotypes in poultry. This is in contrast with results reported by some authors, showing that this serotype is most common in pig and also the 4 most frequently isolated serotype in humans in Europe (Kerouanton et al., 2013; Hauser et al., 2011).

Salmonella Muenster was the second most common serotype and was found in cattle, swine, hedgehog, poultry, human and fish. This finding shows that this serotype is not restricted to one host but can be found in animals, foods, water or humans. A documented food poisoning outbreak caused by *S. Muenster* occurred in Canada in 1982; it infected cheddar cheese made from unpasteurized milk (Wood et al., 1984). *Salmonella* Chester was found in poultry carcasses, swine and poultry feces; this serotype has been reported in many countries: in Canada, *S. Chester* was responsible for an outbreak associated to frozen meals in 2010 (Taylor et al., 2012); in 2014, six European countries (Belgium, France, Spain, Germany, Sweden and the UK) reported *S. Chester* cases to the European Centre for Disease Prevention and Control (ECDC) associated with travel in Morocco (Whitworth, 2016). *Salmonella* Hato was found

Table 1. *Salmonella* serotypes and antimicrobials profile.

Salmonella serotypes	Beef meat	Poultry carcasses	cattle	swine	Hedgehog	Poultry	Human	Salad	Fish	Reservoirs	Channel	Total	Resistance pattern	Number of antibiotic resistered	Number of resistant serotype
S.Abaetetuba	0	0	1	0	0	1	0	0	0	0	0	2	str	1	1
S.Abony	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0
S.Adabraka	0	0	0	0	0	0	0	0	0	1	0	1	str	1	1
S.Adelaide	0	1	0	0	0	1	0	0	0	0	0	2	0	0	0
S.Agona	0	4	0	0	0	3	0	0	3	0	0	10	str	1	5
S.Ahmadi	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0
S.Albany	0	0	2	0	0	2	0	0	0	0	0	4	str	1	2
S.Anatum	0	1	0	0	0	1	0	0	0	0	0	2	str	1	2
S.Angers	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
S.Ank	0	0	0	0	4	1	0	0	0	0	0	5	str	1	5
S.Antwerpen	0	0	1	0	0	0	0	0	0	0	0	1	str	1	1
S.Apeyeme	0	0	2	0	0	3	0	0	0	0	0	5	str	1	5
S.Banana	0	3	1	0	1	2	1	0	0	0	0	8	str	1	5
S.Bareilly	0	0	1	0	0	0	0	0	0	0	0	1	str	1	1
S.Bargny	0	0	1	0	0	0	0	0	0	0	0	1	str	1	1
S.Binningen	0	0	0	0	0	2	0	0	0	0	0	2	0	0	0
S.Bochum	0	0	0	0	0	0	0	0	2	0	0	2	0	0	0
S.Brancaster	0	1	1	0	0	3	0	0	0	0	0	5	str	1	4
S.Bredeney	1	0	5	0	0	2	0	1	6	0	1	16	str	1	4
S.Brive	0	0	1	0	0	0	0	0	1	0	0	2	str	1	1
S.Carmel	0	0	1	0	0	0	0	0	0	1	0	2	0	0	0
S.Carno	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0
S.Chandans	0	0	2	0	0	0	0	0	0	0	0	2	str	1	1
S.Chester	0	5	1	0	0	31	0	0	0	0	1	38	str	1	37
S.Chomedey	0	0	4	0	0	0	0	0	0	0	0	4	str	1	4
S.Colindale	0	0	1	0	0	0	0	4	0	1	2	8	str	1	2
S.Colobane	0	0	2	0	0	0	0	0	0	0	0	2	str	1	2
S.Cubana	0	0	0	0	0	0	5	0	1	0	0	6	str	1	2
S.Dahra	0	0	2	0	0	0	0	0	0	0	0	2	str	1	1
S.Dakar	0	0	1	0	0	0	0	0	0	0	0	1	str	1	1
S.Derby	2	34	0	0	0	52	0	0	3	0	0	91	str,str-sul,str-tet,str-sul-tet,chl-str,str-cip	5	57
S.Drac	0	0	26	0	1	0	0	0	3	0	0	30	str	1	20
S.Dublin	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0

Table 1. Contd.

S.Duisburg	0	0	0	0	0	1	1	0	0	0	0	2	str	1	2
S.Ealing	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0
S.Eastbourne	0	1	2	0	0	2	0	0	1	0	3	9	str	1	5
S.Eastglam	0	0	0	0	0	0	0	0	2	0	0	2	0	0	0
S.Elisabethville	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0
S.Farakan	0	0	3	0	0	0	0	0	0	0	0	3	str	1	2
S.Freetown	0	0	0	0	0	1	0	0	0	0	0	1	str	1	1
S.Fresno	0	0	1	0	0	4	1	0	1	0	0	7	str	1	3
S.Frintrop	0	0	1	0	0	0	0	0	0	0	0	1	str	1	1
S.Fufu	0	0	1	0	0	0	0	0	0	0	0	1	str	1	1
S.Galiema	0	1	0	0	0	2	0	0	0	0	1	4	str	1	4
S.Gaminara	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
S.Gerland	0	0	0	0	0	0	0	1	0	0	0	1	str	1	1
S.Give	0	0	0	0	0	0	0	0	1	0	1	2	0	0	0
S.Gokul	0	0	1	0	0	0	0	0	0	0	0	1	str	1	1
S.Hato	1	4	5	0	0	22	0	0	0	0	0	32	str, tet, str- tet, sul-tet, amp- str, amp-str- sul-tet-tmp	5	15
S.Havana	0	0	0	0	0	0	0	0	2	0	0	2	0	0	0
S.Hermannswerder	0	0	0	0	0	0	0	0	1	0	0	1	str-sul	2	1
S.Hillingdon	0	0	0	0	0	1	0	0	0	0	0	1	str	1	1
S.Hvittingfoss	0	0	0	0	0	0	1	0	0	0	0	1	str	1	1
S.Ikeja	0	0	1	0	0	0	0	0	0	0	0	1	str	1	1
S.Ilala	0	0	2	1	0	0	0	0	0	0	0	3	str	1	1
S.Kaapstad	0	0	0	1	0	4	0	0	0	0	0	5	str	1	2
S.Kalamu	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0
S.Kalina	0	0	2	0	0	0	0	0	0	0	0	2	str	1	1
S.Kentucky	0	0	0	0	0	0	1	0	1	0	0	2	amp-str-sul-tet- cip-gen-nal- mec	8	1
S.Kiambu	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
S.Kingston	0	0	2	0	0	3	0	0	0	0	0	5	str	1	2
S.Kokomlele	0	0	2	0	0	1	0	0	1	0	0	4	str	1	2
S.Korlebu	0	0	2	0	0	0	0	4	1	0	0	7	str	1	5
S.Lagos	0	0	4	0	0	2	0	0	0	0	0	6	str	1	4
S.Llandoff	0	0	0	0	0	0	0	0	1	0	2	3	0	0	0
S.Mbandaka	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0

Table 1. Contd.

S.Minnesota	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0
S.Moero	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0
S.Monschau	2	3	1	0	3	1	0	0	0	0	0	10	str	1	7
S.Montevideo	0	0	0	0	0	0	1	0	1	0	0	2	0	0	0
S.Muenster	0	0	17	3	11	6	4	0	6	0	0	47	str, str-sul, str-tet, str, str-nal, amp-str	5	20
S.Nima	0	1	3	0	0	0	0	0	0	0	0	4	0	0	0
S.Nottingham	0	1	2	0	0	1	0	0	2	0	0	6	str-tet	2	1
S.Offa	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0
S.Oranienburg	0	0	1	0	0	0	0	0	0	0	0	1	str	1	1
S.Othmarschen	0	0	1	0	0	0	0	0	0	0	0	1	str	1	1
S.Ouagadougou	0	0	0	0	0	0	0	0	0	0	1	1	str	1	1
S.Ouakam	0	0	0	1	0	0	2	0	0	0	0	3	str	1	2
S.Poona	0	0	2	0	0	1	3	0	2	1	1	10	str	1	5
S.Rissen	0	0	1	0	0	0	0	0	0	0	1	2	0	0	0
S.Rubislaw	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
S.Ruiru	0	0	8	0	0	0	0	0	0	0	0	8	str, str-tet	2	5
S.Group B	0	1	1	0	0	0	2	0	1	0	0	5	str, str-tet, amp-chl--str-sul-tmp	6	4
S.Group C	0	1	1	0	0	9	0	0	0	0	0	11	str, str-sul	2	11
S.Group ^a D	0	0	0	0	0	1	0	0	0	0	0	1	str	1	1
S.Group ^a E	0	0	1	0	0	5	0	0	0	0	0	6	str, str-sul-tet	3	3
S.Group ^a G	0	0	0	0	1	0	0	0	0	0	0	1	str	1	1
S.Group ^a M	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0
S.Group ^a O:53	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0
S.Saarbruecken	0	1	0	0	0	0	0	0	0	0	0	1	str	1	1
S.Saintpaul	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0
S.Salford	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0
S.Schwarzengrund	0	0	1	0	0	3	0	0	1	1	0	6	str	1	3
S.Senftenberg	1	2	0	0	2	8	0	0	0	0	3	16	str, str-tet, str-sul-tet	3	6
S.Shangani	0	0	0	0	0	1	0	0	0	0	0	1	str-sul	2	1
S.Shubra	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0
S.Soerenga	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
S.Soumbedioune	0	0	4	0	0	0	0	0	0	0	0	4	str	1	3
S.Stanley	0	0	0	0	0	0	1	0	0	0	0	1	str	1	2

Table 1. Contd.

S.Stanleyville	0	0	0	0	0	1	0	0	0	0	0	1	str-tet	2	1
S.Tamberma	0	0	0	0	0	0	1	0	0	0	0	1	str-tet	2	1
S.Tennessee	0	0	3	0	0	0	0	0	0	0	0	3	str	1	1
S.Teshie	0	0	0	0	0	0	0	0	0	0	1	1	str	1	1
S.Tilene	3	2	1	0	0	0	0	0	1	0	1	8	str	1	7
S.Tounouma	0	0	0	0	0	0	1	0	0	0	0	1	str	1	1
S.Trachau	0	0	1	0	0	1	0	0	0	0	0	2	str	1	2
S.Typhi	0	1	0	0	0	0	1	0	0	0	0	2	str,amp-chl-str-sul-tet-tmp	6	2
S.Typhimurium	0	0	3	0	0	4	13	0	1	0	0	21	str,amp-chl-str-sul-tet-tmp,amp-chl-str-sul-tmp	6	21
S.Umbilo	0	0	1	0	0	0	0	0	0	0	0	1	str	1	1
S.Urbana	0	0	13	2	0	1	0	0	0	0	0	16	str, str-tet, chl-str-tmp	4	11
S.Vilvoorde	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
S.Virchow	0	0	1	0	0	0	2	0	0	0	1	4	str	1	1
S.Waedenswil	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0
S.Wagadugu	0	0	0	0	0	0	0	0	0	1	1	2	str	1	2
S.Waycross	0	0	2	0	0	1	0	0	3	0	0	6	str	1	2
S.Yoruba	0	0	1	0	0	0	0	0	0	0	0	1	str	1	1
Salmonella sp.	0	0	1	0	0	0	0	0	0	0	2	3	str	1	2
Total	10	68	161	8	23	193	48	10	56	6	25	608	-	-	359

amp, ampicillin; chl, chloramphenicol; str, streptomycin; sul, sulphonamides; tmp, trimethoprim; tet, tetracycline; nal, nalidixic acid; cip, ciprofloxacin; ftx, cefotaxime; mec, mecillinam.

in beef meat, poultry carcasses, cattle and poultry; *Salmonella* Drac was found in cattle, hedgehog and fish. *Salmonella* Typhimurium was found in cattle, poultry, human and fish. *S. Typhimurium* has been implicated in many outbreaks worldwide (Rayamajhi et al., 2008). This serotype has a well-characterized ability to infect various species (Rabsch et al., 2002) and can survive for a long time in the environment (Baudart et al., 2000); these 2 factors enhance the ability of this serotype to be one of the most common causes of

salmonellosis in many geographically diverse regions and has caused many disease outbreaks (Mather et al., 2013; Cui et al., 2008; Galanis et al., 2006).

Although serotype Typhimurium was associated with several foods of animal origin, the most common was chicken (26% of outbreaks), indicating that chicken is a major route of exposure. This corroborates with our present results, where poultry is identified as the primary source of *S. Typhimurium*. In contrast to the report

of Foley et al. (2008), Typhimurium was the most common serotype among pork associated with outbreaks. This shows that serotype Typhimurium has emerged as the predominant serotype in swine. After the six most prevalent serotypes, the presence of serotype like Typhi (poultry carcasses and human), Senftenberg, Virchow, Kentucky, Stanley and Kingston which have caused many outbreaks in diverse regions were noted. The presence of *S. Typhi* in poultry carcasses shows that there is a cross-contamination during

carcasses handling since humans are the only reservoir of typhoid *Salmonella*. This is also due to the fact that humans can be a chronic carrier of these *Salmonella* (Eng et al., 2015).

Carriers of *S. Typhi* and *S. Paratyphi* are responsible for the spreading of enteric fever in endemic regions, as the common transmission route is the ingestion of water or food, contaminated with the feces of chronic carriers (Bhan et al., 2005). In this report, *Salmonella* serotypes Drac, Banana, Monschau, Muenster, Seftenberg are found in wild hedgehogs. This animal has been the source of human salmonellosis in many European countries, used as a pet animal (Nauerby et al., 2000). Although little can be done to prevent the spread of *Salmonella* in the environment amongst wild animals, the control should be done in food handling and drinking water.

Our results show that the same serotype of *Salmonella* is found in diverse sources, meaning that this serotype can be transmitted to humans through many sources. In general, food animals such as swine, poultry and cattle are the prime sources of *Salmonella* infections. The major dissemination routes of the pathogens involve trade in animals and uncooked animal food products. The slaughtering process of food animals at abattoirs is considered one of the important sources of organ and carcass contamination with *Salmonella* (Gillespie et al., 2005). In Burkina Faso, all serotypes of *Salmonella* can circulate between animals, foods, fish, water and humans. This happens as animals shed feces in the environment which rain water carries to rivers, barrages and channel; aquatic animals like fish can be contaminated by diverse microorganisms coming from water. In addition, wastewater and/or untreated animal feces are used to grow salad and other vegetable from gardens. Here, we can see how humans can be contaminated in this closed circle, since animals can contaminate meat, water, fish, vegetables and environment; the consumers are exposed to a high risk of contamination by *Salmonella* and other pathogens.

These findings are critical because Burkina Faso is facing serious problems in the area of water and sanitation due to demographic explosion and poor urban planning. This problem is increasing the risk of environmental and human contamination. In Ouagadougou, the capital city of Burkina Faso, wastewater from channel, where we found many *Salmonella* strains, is used to irrigate vegetables from gardens, and animals' feces are also used in vegetable crops, which is a new source of growth for poor people. Vegetables like salad are not nutritive media for microorganisms but can constitute mechanical vectors for transporting microorganisms to humans if hygienic condition in garden is not maintained well.

Based on our findings, as seen in Figure 1, the *Salmonella* transmission routes are based on their diversity and sources. The diversity of possible reservoirs

of infection results in significant challenges for public health authorities to control the infections (Dione et al., 2011). Among the 615 strains, 94% (581/615) were resistant to one or more antibiotics, and resistance to streptomycin was the most common (Table 1). The resistance pattern Str-Sul-Tet, Str-Tet and Str-Sul was dominant and found in 80% of the strains. About 3% of the strains were resistant to 5 or 6 antibiotics; their resistance pattern was amp-str-sul-tet-tmp or amp-chl-str-sul-tet-tmp. One *Salmonella* strain, *S. Kentucky* isolated from human stool was resistant to eight antibiotics with the pattern, amp-str-sul-tet-cip-gen-nal-mec. This serotype was found also in fish in this study. In contrast, Centre for Disease Prevention and Control (CDC) has reported that *S. Kentucky* is typically found in cattle and poultry (CDC, 2011).

In this study, streptomycin resistance was found in 94% of the *Salmonella* serotypes. Majority of aminoglycosides are bactericidal but *Salmonella* use mechanisms to resist their antibiotic families such as expression of plasmid-mediated aminoglycoside modifying enzymes against aminoglycoside (Gebreyes and Altier, 2002). The genes encoding these enzymes have been found in varieties of *Salmonella* subtypes like: Agona, Typhimurium, Newport, Typhimurium var. Copenhagen, Kentucky, Blockley, Bredeney, Anatum, Derby, Give, Enteritidis, Heidelberg, Saint Paul, London, Saintpaul, Hadar, Heidelberg, and 4,5,12:i: (Levings et al., 2005). In this study, resistance to ampicillin was observed in *Salmonella* serotypes: Hato, Kentucky, Muenster, Typhi and Typhimurium. Beta-lactams are generally considered bactericidal; but *Salmonella* strains are now becoming resistant to ampicillin and methicillin due to their wide clinical use (Angulo et al., 2000). In *Salmonella*, the secretion of a beta-lactamase is the common mechanism of resistance to beta-lactamases. Several authors reported beta-lactamases in a variety of *Salmonella* serotypes including Enteritidis, Dublin, Haardt, Anatum, Muenchen, Stanley, Panama, Virchow, and Typhimurium (Gebreyes and Thakur, 2005; Batchelor et al., 2005).

In the present study, *Salmonella* serotypes Derby, Hato, Muenster, Nottingham, Ruiru, Senftenberg, Stanleyville, Tamberna, Typhi, Urbana and Typhimurium were resistant to tetracycline. Resistance to tetracycline has been reported in several serotypes including Typhimurium, Saintpaul, Enteritidis, Hadar and Choleraesuis, Agona, Anatum, Blockley, Bredeney, Colorado, Derby, Give, Haardt, Heidelberg, Infantis, Orion, Seftenberg, (Frech and Schwarz, 2000; Pezzella et al., 2004). *Salmonella* serotypes Derby, Hato, Hermannswerder, Kentucky, Muenster, Senftenberg, Shangani, Typhi and Typhimurium were resistant to sulfonamide in the present study. Many authors have been reported resistance to sulfonamide in a wide range of *Salmonella* serotypes such as Enteritidis, Hadar, Heidelberg, Orion, Rissen, Agona, Albany, Derby, Djugu, and Typhimurium (Antunes et al., 2005; Doublet et al.,

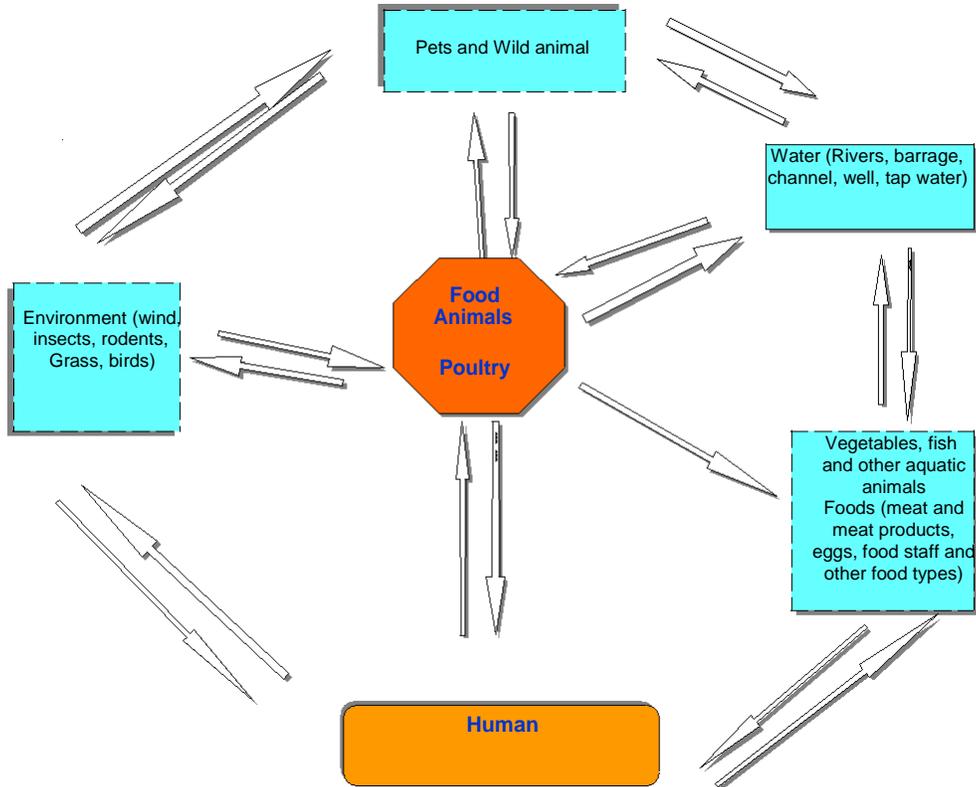


Figure 1. Transmissions routes of Salmonella. Red color = more implicated group in pathogens transmission; Orange color: the second more implicated group.

2004). In our report *Salmonella* serotypes Hato, Urbana, Typhi and Typhimurium were resistant to trimethoprim. Martinez et al. (2005) reported trimethoprim resistance in *Salmonella* serotypes Agona, Djugu, Hadar, Newport, Rissen Albany, Derby, and Typhimurium. Chloramphenicol resistance was found in *Salmonella* serotypes, Derby, Typhi, Typhimurium and Urbana.

This finding corroborates with the report of Alcaine et al. (2005), where *Salmonella* Typhi, Agona, Derby, Kiambo, Albany, Newport, Hardy, Enteritidis and Typhimurium isolates have been found to harbor resistant genes for chloramphenicol. There are two mechanisms in which *Salmonella* resistance to chloramphenicol is conferred: (i) by the plasmid-mediated enzymes called chloramphenicol acetyltransferases (CAT) or nonenzymatic chloramphenicol resistance gene cm1A and (ii) Efflux pump in which the antibiotic is pumped out of the cell. In this study, quinolone resistance was observed in *Salmonella* serotypes Derby, Kentucky, Muenster and Typhimurium. The mechanisms of quinolone resistance for *Salmonella* are all chromosomally mediated, so the numbers of quinolone-resistant *Salmonella* can only increase in two ways: (i) the selection of a quinolone-resistant bacterium after exposure to a fluoroquinolone in humans or animals, or (ii) the spread of a quinolone-resistant bacterium to other

animals or to humans (Pidcock, 2002). According to CDC, outbreaks caused by antimicrobial-resistant *Salmonella* have been associated with an increased rate of hospitalization, and the rate of death was significantly greater in outbreaks caused by resistant strains (CDC, 2011).

Resistance can spread from non-human sources to human by various routes such as animal, water and contaminated foods (Figure 1). Resistance to combinations of many classes of antimicrobial agents in *Salmonella* has led to the re-emergence of multidrug resistance *Salmonella* (MDR) strains (O'Brien, 2002). In this study, *Salmonella* serotypes, Derby, Hato, Hermannswerder, Urbana, Shangani, Tamberma, Kentucky, Muenster, Senftenberg, Shangani, Typhi and Typhimurium were MDR. This is similar to the findings of many authors, who reported that MDR *Salmonella* strains have been found to be of many serotypes such as Agona, Anatum, Pullorum, Schwarzengrund, Choleraesuis, Derby, Dublin, Heidelberg, Kentucky, Newport, Senftenberg, Typhimurium, and Uganda (Chen et al., 2004; Zhao et al., 2008). All *S. Typhimurium* reported in the present study were MDR and most of them were found to display a phenotype of resistance to ampicillin, chloramphenicol, streptomycin, sulfonamides, and tetracycline (ACSSuT). These antibiotics are the

most common drug classes used in veterinary medicine (Mulvey et al., 2006).

Conclusion

The genetic make-up of the *Salmonella* strains permits their adaptation in various environments, including human, animal and non-animal hosts. This increases the difficulty in eliminating the bacteria.

Moreover, the emergence of MDR *Salmonella* strains poses a great challenge in terms of effective treatment of the infections caused by these strains. Several preventive measures have been proposed to stop the spread of antimicrobial resistant *Salmonella* infections, and the restriction of indiscriminate use of antibiotics in food animals is by far one of the most effective measures. This report can help international organization to understand *Salmonella* data and trends and to develop more informed solutions for reducing *Salmonella* contamination along the farm to table chain. The report of sporadic data about *Salmonella* serotype distribution will highlight the importance of the potential source of *Salmonella* infection to humans.

The data obtained in this study can be used by the World Health Organization- Global Foodborne Infections Network (WHO-GFN) and public authority to define the guidelines for basic surveillance system of *Salmonella* and other enteropathogenic bacteria circulating among humans, animals, food and environment.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

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