Epidemiology of salmonella and its serotypes in human, food animals, foods of animal origin, animal feed and environment.

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Abstract

The present review was undertaken to determine the epidemiology of Salmonella serotypes from food animals, food of animal origin, environment, animal feed, water and humans. For this a number of sensitive phenotypic and genotypic detection methods for Salmonella were reviewed. In general, a total of 34,051 samples for quantitative analysis were analyzed. The review result revealed overall 5,738 (16.9%) samples were positive for Salmonella. Of these, 194 serotypes; and 7 Salmonella Enteritidis and 18 Typhimurium phage types were isolated. With regard to examined sample types, of 7027 Poultry, 1888 (26.9%), of 1895 poultry and poultry products, 499 (26.3%), of 170 poultry environment, 100 (58.8%), of 268 chicken meat, 115 (42.9%), of 600 turkey flesh, 62 (10.3%), Of 7744 pig, 1369 (17.7%), of 318 pork meat, 126 (39.6%), of 1923 swine and swine farm environment, 151 (7.9%), of 4709 cattle, 435 (9.2%), of 947 beef, 172 (18.2%), of 50 calf, 35 (70.0%), of 1132 human, 128 (11.3%), of 1536 camel, 238 (15.5%), of 2839 sheep and goat, 56 (2.0%), of 292 mutton, 39 (13.4%), of 200 water, 37 (18.5%), of 2058 animal feeds, 257 (12.5%), of 190 cottage cheese, 4 (2.1%), of 25 Hedgehog, 24 (96.0%) and of 128 fish meat, 3 (2.3%) were infected with Salmonella. These revealed the comparative differential contamination rate among hosts and samples. Salmonella Typhimurium (16.0%), Enteritidis (12.8%) and Derby (9.9%) are dominant serotypes. Large scale production of minimally processed and ready to eat products, trading live infected animals or pets, antimicrobial growth promoters and treatment, unhygienic carcasses evisceration and storage of manure inside of the farm were associated risk factors. In conclusion, Salmonella is widely distributed with diverse hosts, serotype and environmental niche. Therefore, early detection of Salmonella relevant for investigating source of infection and implementing prevention and control measures.

Keywords: Detection tools, Epidemiology, Food animals, Food of animals origin, Human, Salmonella, Serotypes.

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Introduction

Salmonella enterica is a major pathogen in humans as well as in animals [1]. Salmonella comprises greater than 2,500 identified serotypes [2]. They are widely dispersed in nature and are common inhabitants of the intestinal tract of domesticated and wild mammals, reptiles, birds, and even insects. The highly adapted S. enterica Typhi causes typhoid fever only in humans, whereas other serotypes, namely nontyphoid Salmonella serotypes, can cause a wide spectrum of diseases in humans and animals [1].

Foodborne diseases caused by non-typhoid Salmonella represent an important public health problem [3] causing substantial morbidity and mortality, and thus also has significant economic impact worldwide [4] including in industrialized countries [5]. In the 1980s and 1990s, two Salmonella serotypes in particular, S. enteritidis and S. typhimurium, became major causes of food borne illness in Western countries as well as in countries that currently are adopting industrialized food production. By contrast, in most developing countries a more diverse range of Salmonella serotypes are found in humans. Salmonella continues to be the most frequent cause of bacterial food borne disease outbreaks [5].

Non-typhoidal Salmonella spp. are zoonotic agents and foods of animal origin are the main sources for their transmission [3]. Most clinical infections of humans are transmitted from healthy carrier animals to humans through food [5]. Fecal or intestinal contamination of carcasses is the principal source of human food-borne infections. The exception is when Salmonella is directly transmitted into the food product [6].

Salmonella enteritidis has the unique capacity of being able to infect the ovaries of chickens without causing symptoms. Thereby the bacterium may enter the egg internally and thus both spread to the offspring and transmit to consumers. Salmonella may multiply within the egg or in the prepared dish before consumption, thus sometimes growing to high numbers, and increasing the potential for causing disease [5].

Several large outbreaks in humans have been traced back to contaminated animal feed [7]. However, Salmonella is also spread by non-heat-treated animal products [6]. In most industrialized countries, S. enteritidis and S. typhimurium

are the two most frequently occurring serotypes. In Europe, they together constitute more than 80% of all serotypes. S. enteritidis is the most frequent serotype generally responsible for approximately two-thirds of the infections in Europe. In the US, S. typhimurium is generally more frequent than S. enteritidis and their collective share is approximately 35 to 40% of all infections [5].

Animals infected after exposure to infected animals, feed or environmental conditions excrete Salmonella bacteria by fecal shedding [6]. Contamination of animal feed before arrival at and while on the farm contributes to infection and colonization of food producing animals with these pathogens [7]. Salmonella infected food producing animals excrete Salmonella bacteria in large numbers, sometimes intermittently during their entire economic life. Excreted bacteria infect neighboring animals on the farm and contamination of the environment takes place, with infections being transmitted to rodents and other wild fauna. When moved, the Salmonella infected animals are effective at introducing the infection into their new holdings [6].

Salmonella is spread by the trade of live animals within and between countries. Salmonella is additionally spread between countries by humans as a result of food-borne infections acquired abroad. The overall importance of this route of transmission may reflect the prevalence of Salmonella contamination of food (including food of animal origin) in a particular country [6]. Large-scale production of animals and crops and breeding pyramids of specially bred, genetically similar food animals are vulnerable to salmonella infections. Intensified farming may make animals more prone to infections and trade with live animals can, if they become infected, efficiently distribute the infections from one country to another. New types of foods, for instance the increased use of ready-to-eat foods and new production systems may sometimes also be liable to contamination [5].

Salmonella bacteria can survive for long periods in the environment, although in general no significant multiplication occurs. Salmonella infections in wild fauna, such as rodents, are usually secondary to the infection of farm animals, even though infection cycles may continue independently of any continuous input of Salmonella bacteria from farm animals [6].

In Ethiopia, several factors including under and malnutrition, HIV-AIDS, the unhygienic living circumstances and the close relations between humans and animals may substantially contribute to the occurrence of Salmonellosis [8]. The existing scattered efforts of research lack depth, coordination, evaluation, compilation and documentation of the scantly generated information. The depth and width of study on Salmonella varies among countries and among animal species. Research work is utterly wasted unless it is brought to public notice in some form. Therefore, the present review was conducted with the objectives of systematically review the prevalence and distribution of different Salmonella serotypes in different hosts, foods of animal origin and environment by using meta-analytical methods and recognize the major risk factors.

Salmonella Detection Methods for Epidemiological Monitoring

There are over 2,500 identified serotypes of Salmonella. Most of them share a high level of genetic similarity. Because of this genetic similarity the Salmonella genus is now divided into two species, S. enteric and S. bongori. Greater than 99% of the serotypes are grouped into the species *S. enteric* [9].

Phenotypic method

Outbreak investigations and tracing of zoonotic bacteria among livestock and from livestock via food to man can be performed by the use of bacterial typing methods [10].

Serotyping

Salmonella serotyping plays an essential role in determining species and subspecies. It is initial step for routine diagnosis of strains and this can be done with commercially available poly and monovalent antisera. Of the Salmonella, S. enterica and S. bongori, over 99% of serotypes are grouped into species S. enterica, and nearly 60% of them belong to the subspecies enterica (subspecies I) [9]. Serotyping has a wide acceptance as a method to differentiate Salmonella strains, and it is an important tool in public health. This traditional serotyping method has many limitations. It is based on the use of expensive antisera; also the procedure is time consuming, requires well-trained technicians, and some isolates are not typeable [4], but it is highly discriminative [10].

- Serotyping by slide agglutination (Kauffmann-White-Le Minor scheme: The genus Salmonella has been identified and classified to have over 2500 serovars by Kaufmann-White scheme. This technique remains as a paramount for differentiating members of the Salmonella genus following biochemical identification. In this method, a series of antisera was used to detect different antigenic determinants such as somatic (O), capsular (Vi) and flagellar (H) antigens on the surface of bacterial cell. The O antigen is the saccharidic component of the lipopolysaccharide (LPS) exposed on the bacterial surface [11]. Its reactivity toward specific antisera forms the basis of the Salmonella serotyping scheme [12].
- False-positive reactions may occur as a result of weak, nonspecific agglutination [13,14] Autoagglutination and loss of antigen expression, such as that observed with rough, non-motile, and mucoid strains, may occasionally lead to strain untypeability, but these strains typically have little epidemiological significance. The method is intended neither to provide a sensitive fingerprint (e.g., for tracing during an outbreak) nor to define phyletic relationships [13]. It requires the use of over 150 specific antisera and carefully trained personnel. It is still defined as the reference method and is commonly used as an initial screening, followed by molecular subtyping to identify outbreak-related strains.
- Serotyping by antibody microarrays: In this assay, the

antibody-antigen reactions are conducted on a micro volume scale on slides following fluorescent labelling of the investigated Salmonella strain. Detection is carried out with a common fluorescence scanner. The main advantages of antibody microarray-based serotyping over traditional serotyping are reduced analysis time, standardized agglutination detection, and simultaneous detection of the O and H antigens [13].

Phage-typing

Phage typing is used to discriminate between Salmonella strains belonging to the same serotype. The advantage of phage typing resides in the simplicity of its implementation, which requires only basic laboratory equipment [13]. This typing method has proven to be epidemiologically valuable in strains differentiation within a particular Salmonella serotype. In this subtyping approach, *Salmonella* strains are separated into different phage types based on their reactivity against a set of serotype specific typing phages. This technique has been developed for some relevant serotypes [10].

Antimicrobial resistance typing

This typing technique determines the profile of resistance of a microbial strain towards a panel of an antimicrobial agent. Antimicrobial susceptibility testing is usually carried out to determine which antibiotic is effective in treating bacterial infection *in vivo*. It has been quite commonly used in the past as subtyping method to determine correlation between isolates. Nowadays, antimicrobial resistance typing is less used frequently for this specific purpose. This technique is cheap and does not require specific equipment and reagents like phage-typing. Antibiogram has poor discriminatory power because antimicrobial resistance is under selective pressure and often is associated with mobile genetic elements and strains which are epidemiologically related may have different antimicrobial susceptibility due to loss of plasmids or the acquisition of new genetic material [11].

Genotypic Methods

Pulsed field gel electrophoresis: Historically, Pulsed field gel electrophoresis [PFGE] is one of the earliest molecular DNA subtyping systems, showing the pattern of fingerprinting for *Salmonella* strains which is suitable as an epidemiological tool for investigating outbreaks. Moreover, it is considered as a gold standard for molecular typing of Salmonella and many other bacterial pathogens. The technique is useful for fingerprinting strains in outbreak situations and is relatively inexpensive to perform [13]. However, PFGE is time-consuming and labor-intensive and does not display equal sensitivity with different serovars [14].

Polymerase Chain Reaction: PCR offers many advantages compared to conventional culture-based detection methods regarding sensitivity, specificity, speed, and possibility of automatization. The PCR-based detection methods in food commonly employ a pre enrichment step combined with subsequent PCR detection. The majority of these PCR assays amplify part of the invA gene, encoding a protein involved in the invasion of epithelial cells, however, it has been shown that invA is lacking in some strains. The major advantage of PCR-based detection of a food borne pathogen like Salmonella is the reduction in time of analysis [5].

Methods used in literature searching and review

Eligibility criteria

Journals are eligible for quantitative syntheses if:

(i) Their objective was not serotype specific.

(ii) It provided the sample size.

(iii) It described the microbiological and serotyping methods.

(iv) It provided the numbers of isolates.

(iv) It was published in English.

Other studies with relevant information on serotypes, typhoidal and non-typhoid isolates were included in the reviewing.

Literature search strategies: Literature searching is by using lists of references of articles and by using Google scholars. Additional searches were done by using key words like Salmonella prevalence rate, Salmonella incidence, antimicrobial resistance in Salmonella serotypes, Salmonella in different hosts (human, animals, foods of animal origin, contamination in animal feeds) and environment.

Selection of Studies

Initially articles with titles and abstracts that were not relevant to the outcomes of interests (The outcomes of interest is the prevalence and distribution of Salmonella serotypes isolated from different types of human food originated from animals and animal feeds such as swine, poultry, beef, mutton, camel, fish meat, cottage cheese, and water and equine, west and sewages, environment, including samples from Humans etc.,) were excluded. The full texts of all articles screened for eligibility. Of the screened articles, duplicates and articles that did not meet the eligibility criteria were excluded.

Detection methods used by the journals and data extraction

The different types of the journals used different detection methods (Table 1). The majority of the journals used Slide agglutination test (Kauffman White scheme). Regarding the type of data's extracted during the present review, the first author, year of publication, year of study, location, sample size, types and number of samples, microbiological methods, Serotyping methods, number of Salmonella positive samples, serotypes, risk factors and other relevant information from the eligible studies were collected.

Data Analysis

The data were stratified on the basis of feel of relative homogeneity [15] as Salmonella serotypes in different sources. The Salmonella serotype data were further grouped by sample type. Finally Meta-analysis was performed.

Table 1. *Detection methods for epidemiological monitoring used by reviewed journal articles.*

Detection methods	No. of Journal Articles	
	For quantitative Data analysis	For qualitative Data analysis
Microtiter agglutination test according to Kauffmann and White scheme	2	14
Slide agglutination test (Kauffman White scheme)	25	
Microtiter and slide agglutination test according to Kauffmann and White scheme	5	
Pulse field gel electrophoresis	1	
Total	33	14
Grand Total journals	47	

Table 2. *Prevalence of salmonella isolates in different sources.*

Sources	No. of samples	Positive	Prevalence (%)
Animal feed	2058	257	12.5
Beef	947	172	18.2
Calf	50	35	70.0
Camel	1536	238	15.5
Cattle	4709	435	9.2
Chicken meat	268	115	42.9
Cottage cheese	190	4	2.1
Fish meat	128	3	2.3
Goat	600	4	0.7
Hedgehog	25	24	96.0
Human	1132	128	11.3
Mutton	212	23	10.8
Pig	7744	1369	17.7
Pork meat	318	126	39.6
Poultry (Poultry, Broiler, Chicken, Duck)	7027	1888	26.9
Poultry and poultry products	1895	499	26.3
Poultry farm environment	170	100	58.8
Sheep	1677	35	2.1
Sheep and goat	642	33	5.1
Swine and swine farm environment	1923	151	7.9
Turkey flesh	600	62	10.3
Water	200	37	18.5
Over all	34051	5738	16.9

Results

Eligible and excluded studies

A total of 213 studies were found of which 166 were excluded and 47 studies were considered eligible for qualitative and quantitative syntheses based on the stated criteria.

Characteristics of the eligible studies

The studies were conducted between the years 2000 to 2014 (except three which were studied between 1997 to 1999) in different countries. These are Ethiopia, United States, Vietnam, China, Spain, Belgium, India, Japan, Iran, Morocco, Nigeria, Denmark, Great Britain, Egypt, Senegal, Burkina Faso and Brazil. Regarding the samples distribution, different types of food of animal origin and other sources namely, poultry, beef, sheep and goat, camel meat, fish meat, cottage cheese, swine, water, environmental swab, animal feed and human were included in the study.

The grouping of samples based on their sources indicated that, 1895 from poultry and poultry products, 170 from poultry farm environment, 7027 from poultry (Poultry, Broiler, Chicken, Duck), 268 from chicken meat, 600 from turkey flesh, 7744 from pig, 318 from pork meat, 1923 from swine and swine farm environment, 4709 from cattle, 947 from beef, 50 from calf, 1132 from human, 1536 from camel, 212 from mutton, 200 from water, 2058 from animal feed, 190 from cottage cheese, 25 from Hedgehog, 128 from fish meat, 600 from goat, 1677 from sheep, 642 from sheep and goat were considered for quantitative syntheses.

Salmonella isolates prevalence and distribution in different sources

Of 34051 samples examined, 5738 (16.9%) Salmonella isolates were collected from different sample sources. Salmonella was isolated from twenty three different types of samples. Thus, the highest Salmonella isolates were recovered from hedgehog (96.0%) followed by calf (70%) and poultry farm environment (58.8%). The isolates obtained from Chicken meat (42.9%), pork meat (39.6%) and poultry (26.9%) were also highest among other sources (Table 2).

Prevalence of dominantly isolated salmonella serotypes and phage types

Out of 5,738 Salmonella positive samples, 194 different serotypes and 25 phage types of Salmonella thyphimurium and enteritidis were isolated. Among the isolated serotypes, Typhimurium (16.0%) was the dominant followed by others like Enteritidis (12.8%), Derby (9.9%), Anatum (5.2%), Saintpaul (3.5%), Braenderup (3.4%), Hadar (3.1%) and Infantis (3.0%). The dominant isolated Salmonella serotypes are indicated in

Table 3. *Prevalence of dominantly isolated salmonella serotypes and phage types.*

Compound	Diagnostic ions (m/z)			Quantification ion (m/z)	Retention time, min
Heptachlor epoxide	353	272	237	353	22.150
Bifenthrin	181	165	166	181	18.010
Cypermethrin	207	77	181	207	20.511
Endosulfan sulfate	272	389	274	272	17.123
Chlorpyrifos	199	97	197	97	13.836
Fenitrothion	125	109	277	109	13.341
Malathion	125	93	173	121	13.621
Methidathion	145	85	125	145	14.648
Methyl parathion	109	263	125	263	12.950
Profenofos	208	97	139	208	12.475
O, P-DDT	235	165	236	235	16.320

Table 4. *Prevalence of dominantly isolated salmonella serotypes and phage types.*

Serotype and Phage type	Nr. of samples	Positive	Prevalence (%)	Serotype and Phage type	Nr. of samples	Positive	Prevalence (%)
Anatum	4737	244	5.2	Infantis	4737	142	3
Braenderup	4737	160	3.4	Kentucky	4737	115	2.4
Derby	4737	470	9.9	Newport	4737	112	2.4
Dublin	4737	81	1.7	Rissen	4737	63	1.3
Eastbourne	4737	50	1.1	Thompson	4737	87	1.8
Emek	4737	53	1.1	Indiana	4737	113	2.4
Enteritidis	4737	606	12.8	Typhimurium	4737	760	16
Hadar	4737	148	3.1	Virchow	4737	61	1.3
Heidelberg	4737	73	1.5	Saintpaul	4737	165	3.5
Weltevreden	4737	52	1.1	--	--	--	--
Enteritidis PT1	197	10	5.1	Typhimurium DT004	197	2	1
Enteritidis PT13a/7	197	7	3.6	Typhimurium UT	197	4	2
Enteritidis PT4	197	10	5.1	Typhimurium DT003	197	7	3.6
Enteritidis PT6a	197	2	1	Typhimurium PT13a/7	197	6	3
Enteritidis PT14b	197	11	5.6	Typhimurium DT120	197	12	6.1
Enteritidis PT35	197	2	1	Typhimurium DT12	197	11	5.6
Typhimurium DT40	197	2	1	Typhimurium DT17	197	5	2.5
Typhimurium DT104	197	13	6.6	Typhimurium DT170	197	4	2
T. var.Copenhagen	197	63	32	Typhimurium DT193	197	16	8.1
Typhimurium DT004	197	4	2	--	--	--	--

(Table 3). The rest of the isolates are not included in the table as they had below 1% prevalence.

Regarding salmonella phage types, Eighteen Out of 25 identified were S. Typhimurium which Typhimurium var. Copenhagen (32.0%) had the highest prevalent and from S. Enteritidis phage types, S. Enteritidis PT14b (5.6%) had the highest prevalence (Table 4). phage types below 1% prevalence of isolation are not included in the table.

Risk factors having contribution for the emergence of salmonella infection in humans and animals

Different risk factors causing different effects on the hosts were identified during the present review. The risk factors for infection in food animals identified were either directly or indirectly had risk of infection in humans by increased the incidence of Salmonella infection, causing outbreaks and by widespread disseminating the contamination. Trading of

Table 5. *Risk factors that have had a major contribution for the emergence of salmonellosis.*

Level of food chain	Factor	Effect	Reference
Consumer level	-Less familiarity with preparation of new risk foods	-Increased incidence of salmonellosis, in particular following emergence of new risk foods	[5]
	-Increasing number of elderly or immuno suppressed consumers		
Retailers and restaurants	-Occasional break down in safety barriers	-Outbreaks, sometimes large	[5]
	-cross-contamination in large kitchens -use of exotic fruits and vegetables		
Food production/ processing	-Large-scale production of minimally processed and ready to eat products	-Amplification of contamination, widespread dissemination of contaminated products	[5]
	-Globalized trade		
Animal production systems	-Trading of live infected animals for food production or pets	-Spread of infection from one country or continent to another. -Infection of large number of animals -Transport induced stress enhances shedding and spread of *Salmonella.*	[5]
	-Increased use of genetically similar animals in breeding pyramids		
	-Large-scale production systems		
	-Long-distance transport of animals		
Feed and antimicrobial drugs for food animals	-Compound feed -international trade with feed	-Changes in intestinal ecology -dissemination of serotypes -selection of resistant bacteria that are passed on to humans	[5]
	-Antimicrobial growth promoters - antimicrobial treatment		
Poultry Meat	-During the evisceration of carcasses	-Mechanical rupturing of crops or intestines can lead to external contamination of edible muscle tissues.	[16]
		-Cross-contamination of carcasses can occur readily in water filled chilling tanks	
Season	-Cold season	29.1% of contaminated batches in Turkey farms	[17]
	-Hot season	72.2% of contaminated batches in Turkey farms	
Duration of crawls pace	>15 days	33.3% of contaminated batches in Turkey farms	[17]
	≤15 days	63.3% of contaminated batches in Turkey farms	
Age of turkeys at levy	>40 days	77.7% of contaminated batches in Turkey farms	[17]
	≤ 40 days	33.3% of contaminated batches in Turkey farms	
Storage of manure	-Inside of the farm	80% of contaminated batches in Turkey farms	[17]
	-Outside of the farm	33.3% of contaminated batches in Turkey farms	
Conservation of sick turkeys in the building	-Yes	62.2% of contaminated batches in Turkey farms	[17]
	-No	28.1% of contaminated batches in Turkey farms	
Use of antibiotics on the first day of Turkey entry in the farm	-Yes	30.5% of contaminated batches in Turkey farms	[17]
	-No	75% of contaminated batches in Turkey farms	
Retail meat	-poor hygiene	-wide spreading of *Salmonella*	[18]
Human infection	-malnutrition, HIV-AIDS, the unhygienic living circumstances	-contribute to the occurrence of Salmonellosis	[18]
	-close relations between humans and animals		

live infected animals for food production or pets, Mechanical rupturing of crops or intestines of poultry meat and poor hygiene of retail meat were among the predisposing factors identified as Salmonella infection in human (Table 5).

Discussion and Conclusion

Surveillance of Salmonella serotypes and phage types from human and animal sources is relevant for detecting national and global outbreaks, for identifying the source of infection and for implementing prevention and control measures since the distribution may differ between countries. Serotyping plays an essential role in determining species, subspecies and in routine diagnosis of strains [9]. Serotyping uses highly discriminative [10] but expensive antisera that is time consuming, requires well-trained technicians, and some isolates are not typeable [4]. Antimicrobial resistance typing has poor discriminatory power [11]. Pulsed field gel electrophoresis uses for investigating outbreaks and is a gold standard for molecular typing of Salmonella and many other bacterial pathogens but it is time-consuming and labor intensive and does not display equal sensitivity with different serovars [14]. PCR has advantage over conventional culture based detection in sensitivity, specificity, speed and possibility of automatization and have reduction in time of analysis [5].

The present review indicated that, 16.9% prevalence of Salmonella was isolated from human, food animals, food of animal origin, water, food animal farm environment, cottage cheese, fish meat and animal feed.

The risk of Salmonella shedding seems to vary by production system, housing type, general hygiene level, management type and animal age. Salmonella serotypes were isolated from different source but the detection in carcasses was considered as an indicator of carcass surface contamination [16-20]. The most common Salmonella serotypes isolated from humans correlates with common serotypes of animals and food products of animal origin. This implies that the presence of Salmonella in slaughter cattle and slaughter house environment and the potential cross contamination of carcasses and edible organs can pose food safety hazards. Salmonella infections in humans are

often food borne but can also contracted through contact with infected animals. Food containing products from farm animals, especially from poultry, pigs, and cattle, are an important source of human Salmonella infections [3,21]. For example, Pigs can be considered as an important reservoir of *S. Typhimurium* since this serotype was frequently isolated from pig feces and pork [19]. The process of removing the gastrointestinal tract during slaughtering of food animals at abattoirs, contaminated equipment, floors, personnel of the abattoir, Excretion of symptomless animals and during butchering is one of the most source of carcass and organ contamination and Cross-contamination of carcasses and meat products could continue during subsequent handling, processing, preparation and distribution. Poor hygiene in retail meats and Mechanical rupturing of crops or intestines during the evisceration of carcasses in poultry, are risk factors for contamination and spreading the contamination [18,16].

The adaptation of Salmonella to a diversified environments, mammals, non-mammalian hosts as well as non-animated reservoirs makes their eradication by conventional means difficult. Furthermore, the existence of a wide range of Salmonella serotypes (>2500) exacerbates the control efforts although only 194 serotypes were identified in this review. In this line, food animals harbor a wide range of Salmonella serotypes and so act as source of contamination, which is of paramount epidemiological importance in non-typhoid human salmonellosis and remains a significant worldwide public health concern not only in developing countries but also in the industrialized world. Infected animals can present risk factors for transmission to humans. As the movement of people, food animals and food stuffs across national boundaries increases, this in turn expands the risk of salmonellosis. Keeping the food chain free of Salmonella is vital for preventing food infection caused by Salmonella, and the hygiene of retail meat is critical.

Therefore, periodic Surveillance of Salmonella serotypes from human, different food animals, food products and environment is relevant for detecting national and global outbreaks, for identifying the source of infection and for implementing prevention and control measures. The knowledge on the prevalent Salmonella serotypes in a country is important to understand the distribution and means of introduction into a country; Humans working with clinically affected animals should be aware of the risk of acquiring infection; Effective routine cleaning and disinfection of buildings and equipment are essential; Overstocking and overcrowding of food animals for production should be avoided; and finally, Comprehensive study of drug resistance and pattern of resistance profile is essential for treatment of infectious diseases both in animals and humans since multidrug resistance strain is common in Salmonella.

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