



Occurrence of Antibiotic Resistance in *Salmonella* Serotypes Isolated from Environment, Humans, Animals, and Animal Products in Morocco: A Systematic Review

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ABSTRACT

Several studies have been carried out in Morocco on *Salmonella* contamination in humans, domestic and wild animals, food products, and the environment. This bacterial genus is responsible for several infections and foodborne illnesses worldwide. The epidemiological situation of contamination by *Salmonella* is worsened by the development of antibiotic resistance to the main antibiotics used in human and veterinary medicine. The purpose of this study was to review the leading research carried out in this field, emphasizing the antibiotic resistance of this bacterium to antibiotics in humans and animals. Although some studies could not demonstrate the presence of *Salmonella* in the environments studied, the prevalence of contamination remained relatively high in humans, animals, food products, and the environment. The most critical contaminations were observed in poultry farms and poultry meat. *Salmonella* causes 42.8% of food poisoning cases in Morocco. It is the second most common cause of poisoning after pesticide poisoning. Morocco ranks first in the Middle East and North Africa for human salmonellosis, with a prevalence of 17.9% (1997-2012). Its prevalence in food products, especially those of animal origin, is very high and could reach 52.9% in turkey meat. Food products have been studied more for their contamination by *Salmonella* species. Meat products accounted for 17.35% of food poisoning cases. This study revealed that the isolation rate of *Salmonella* from food products of animal origin was dominated by isolations from meat products, with prevalence rates of 41.76 % from red meat and meat products and 25.88% from poultry meat, followed by prevalence rates of 12.44 % from fish products and 11.80 % from eggs. On the coast of Agadir, the incidence rates of *Salmonella* were 6.8% and 4.1% in sediment and seawater, respectively. This occurrence was 2.38% in the surface waters of Oued Khoumane. The development of resistance, particularly multi-resistance to antibiotics of therapeutic interest in both humans and animals, is alarming, especially with the ease of transmission of the bacterium to humans and facilitates its dissemination. Research findings indicated that 93.02% of isolates of *Salmonella* from humans, 79.37% of the strains isolated from poultry, and 46.27% of isolates from food products were resistant to at least one antibiotic.

Keywords: Animals, Environment, Food products, Foodborne disease, *Salmonella*, Resistance

INTRODUCTION

The increasing emergence of salmonellosis threatens the effective control of human foodborne diseases (Ziyate et al., 2016). In European countries, salmonellosis is the second most frequently reported zoonotic infection (Schmid and Baumgartner, 2013). Non-typhoidal *Salmonella enterica* is a leading bacterial that causes acute gastroenteritis in both children and adults (Al-Rifai et al., 2020).

From 2007 to 2011, more than 6960 cases of food poisoning, including 24 deaths, were listed by the Moroccan Poison Control and Pharmacovigilance Center (Rebgui et al., 2013). *Salmonella* would be responsible for 42.8% of food poisoning cases in Morocco, knowing that the incidence of foodborne disease is often underestimated (Cohen et al., 2007). Similarly, a retrospective study conducted by the Moroccan Poison Control and Pharmacovigilance Center covering the period of 2010-2016 revealed 17,076 foodborne diseases, of which 2,963 (17.35%) were linked to the consumption of flesh foods. The majority of cases occurred in urban areas, with a rate of 67.06% (Boukili et al., 2019). The risk assessment of foodborne bacterial pathogens in axis Rabat-Casablanca Morocco revealed that the raw products, particularly poultry meat and red meat, were most contaminated by *Salmonella* with the respective prevalence of 21.05% and 5% (Oba et al., 2014)

On a local scale, the analysis of the epidemiological characteristics of foodborne diseases at the prefecture of Agadir over 3 years (2015-2017) showed 11 foodborne disease outbreaks concerning 163 poisoned individuals with 2 cases of death. *Salmonella* species and *Escherichia coli* (*E. Coli*) were identified in four of six samples subjected to microbiological analysis (Bouchriti et al., 2021). In a similar study in Kenitra, Morocco, 43 foodborne disease outbreaks were reported between 2001 and 2018, affecting 367 poisoned individuals, including 69 hospitalized and 2 death cases. In that study, 25% of the samples revealed the presence of *Salmonella* (Elkhal et al., 2021).

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As part of the salmonellosis epidemiological surveillance in some European countries, salmonellosis cases are often reported in people who have stayed in Morocco. Thus, the European Center for Disease Prevention and Control reported an increase in salmonellosis cases in six European countries due to *Salmonella* Chester in patients who would have traveled to Morocco between 2014 and 2015 (Fonteneau et al., 2017). Other countries have reported isolation in people with digestive disorders who have recently traveled to Morocco, including travelers from France during 2000-2011 (Le Hello et al., 2013), Switzerland during 2011-2012 (Schmid and Baumgartner, 2013), Finland during 1995-2009 (Hinkka, 2011) and in Norway during 2000-2016 (Siira et al., 2019).

The widespread multidrug resistance to antibiotics in human, avian, aquacultural, and environmental *Salmonella* is increasing and has been confirmed by numerous epidemiological studies in Morocco. Thus, En-nassiri et al. (2017) reported the emergence of multiresistant *Salmonella* to fluoroquinolones and third-generation cephalosporins, prescribed in the treatment of severe salmonellosis in adults and children, which is a real public health problem.

The current study aimed to review the leading research and highlight the prevalence, serotypes distribution, profiles, and importance of *Salmonella* isolated from humans, animals, food products, and the environment in Morocco.

METHODOLOGY

The current review covered the studies addressing prevalence, serotype, and antibiotic resistance tests in *Salmonella* isolates in Morocco. The study was performed using the descriptive literature review method. The diagram of the article selection process is inspired by the methodology adopted by Al-Rifaia et al. (2020). The eligibility criteria for studies included the completion of the study on animals, animals' products, the environment, and humans in Morocco in the last 25 years. The studies must be related to the serotyping of the isolated *Salmonella*, and the antibiotic resistance test must be carried out on the isolates. This review study aimed at elucidating the isolation of *Salmonella* from the environment, animals, animal products, and humans.

Since there has been a limited number of studies in Morocco, a general search of several databases was performed to collect the maximum number of studies on *Salmonella* and salmonellosis in Morocco. The search was operated on ProQuest, Cochrane Library, Web of Science, PubMed, CABDirect, Agricultural Documentation Center (CDA-IAV Hassan II), IMIST library, GeoScienceWorld, and EBSCO. The number of bibliographical resources consulted for this study consisted of 114 studies. Several articles, end-of-study dissertations, and research theses in Morocco or having a relationship with *Salmonella* carriage at the national level were derived from the studies abroad on isolates from humans who would have consumed Moroccan food products. Exclusion criteria are shown in Figure 1.

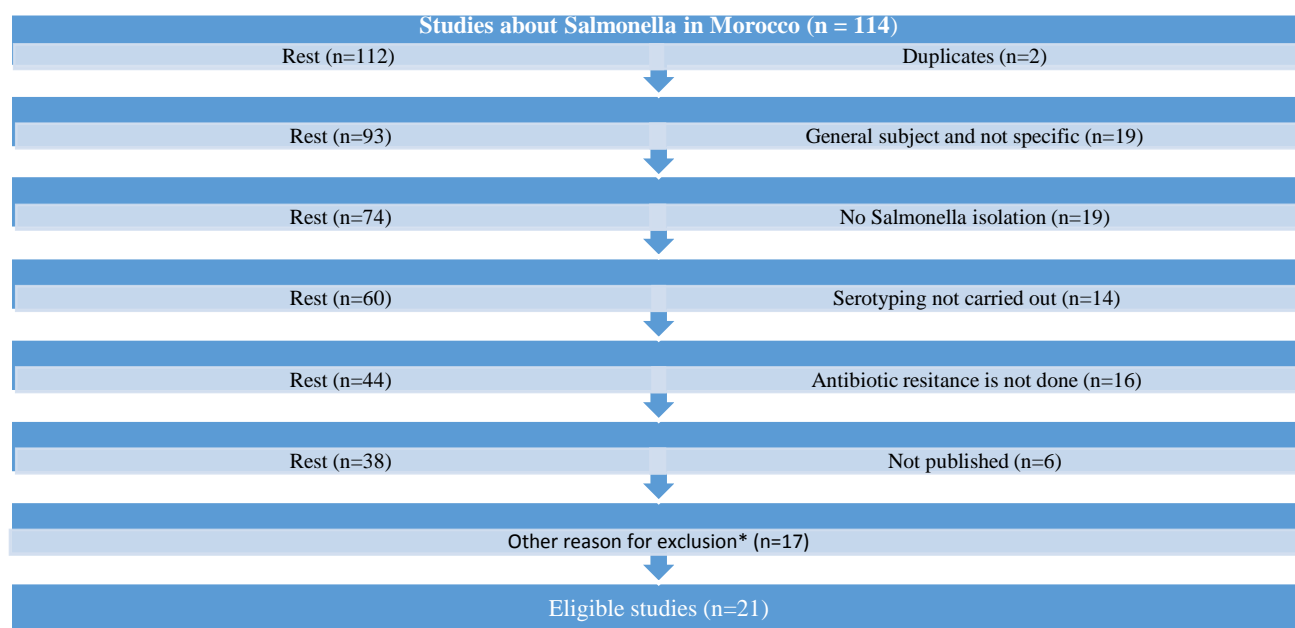


Figure 1. Flowchart of the study eligibility process. * Ancient food of vegetable origin, results not precise, and typhoid (not NTS)

The number of bibliographical resources eligible for this study consists of 21 references from scientific publications. Among these sources, the number of references for serotyping and antibiotic resistance of isolated *Salmonella* was 13 for food products, 6 for humans, 3 for the environment, and 2 for those isolated from animals (poultry). Some source studies have been concerned with more than the studied factors (animal and animal product/environment). The collected data were classified in Excel spreadsheets for their exploitation. Data were classified in terms of food product isolation (animal

species, and food product), serotype, and antibiotic resistance profiles. Table 1 shows the list of studies selected for this study.

Table 1. List of studies eligible for this analysis

Authors	Product/species concerned by the study
Amajoud et al. (2017)	Dairy products, Red meat and meat products, Poultry meat
Ammari et al. (2009)	Food products, Humans
Ben Moussa (2014)	River water
Bouchrif et al. (2009)	Dairy products, Red meat and meat products, Poultry meat, Fish products
Boutaib et al. (2011)	Fish products (bivalve mollusk)
Dejlil et al. (2000)	Food products
Ed-Dra et al. (2018)	Food products
Ed-Dra et al. (2019)	Meat products (Chicken)
El Allaoui et al. (2013)	Turkey meat
El Allaoui et al. (2017)	Turkey
Elared et al. (2001)	Eggs
Fonteneau (2017)	Humans
Karraouan et al. (2010)	Turkey meat
Khallaf M. et al. (2014)	Chicken meat
Le Hello et al. (2013)	Humans
Siira et al. (2019)	Humans
Murgia et al. (2015)	Dairy products, red meat and meat products, Poultry meat, Fish products, Snails
Nassri et al. (2021)	Spring water
Ohmani et al. (2010)	Humans
Zahli et al. (2022)	Chicken meat
Ziyate et al. (2016)	Laying hens

RESULTS

Animals

Most of the studies carried out in Morocco on the *Salmonella* contamination and carriage of animals have addressed the poultry sector since it is the sector most concerned by the presence of *Salmonella*, particularly broiler chickens and turkeys. Several studies on the search for the genus *Salmonella* have been conducted in this sector. The data relating to the analysis of these studies are listed in Table 2, which concerns only two publications on poultry farms.

Studies revealed a highly variable prevalence of *Salmonella* contamination in poultry farms depending on the region and the sub-sector. It was found that 24% of broiler farms were infected with *Salmonella* spp. in Meknes (Chaiba and Rhazi Filali, 2016). In laying hen farms, 76.7% were contaminated by the *Salmonella* genus, with very significant regional variations ranging from 100% in farms in the Greater Casablanca region to 50% of contaminated farms in the Rabat Sale Zemmour Zaer region to 87.5% in the Sous Massa Drâa region (Ziyate et al., 2016).

However, in a recent study performed in the region of Azemmour (El Jadida-Morocco), the absence of *Salmonella* in breeder farms, broiler farms, and laying hen farms was reported due to size-reduced samples (4 farms per category), and the low quality of health supervision and the establishment of health barriers or vaccination in laying hens (Karib et al. 2021). Furthermore, the reported prevalence in broiler turkey farms in the Khémisset region was 35% (El Allaoui et al., 2014). In local free-range chicken farms, still called traditional or more commonly “Beldi” chicken, the prevalence of *Salmonella* was 6%, 10%, and 5.6% in the locality of Zemamra (El Jadida), Marrakech, and Khénifra, respectively. Seroprevalences of typhosis and pullorosis were 7.6% and 4.4%, respectively (Fagrach, 2021). It is well established that the “Beldi” chicken is a reservoir of *Salmonella* Gallinarum and *Salmonella* that continually threatens the industrial poultry sector (Bouzoubaa et al., 1992; Fagrach et al., 2021).

The serotyping of 126 strains of *Salmonella* isolated from broiler chickens and broiler turkeys is described in Table 2. Ziyate et al. (2016) and El-Allaoui et al. (2017) found that the strains belonged to 12 different serotypes. The predominance of the *S. Kentucky* serotype is notable, with a frequency of 32.54%, of which 51.2% is isolated in turkeys and 48.8% in laying hens, followed by the *S. Enteritidis* serotype representing 22.22% of the isolated serotypes, mainly in laying hens with a percentage of 85.71% of the isolates.

Table 2. Distribution and antibiotic resistance patterns of *salmonella* species isolated from poultry farms in Morocco

Animals	Authors	Serotype	Number of Isolates		Sensitive	Amx	Na	Cip	Caz	Amc	Ctx	C	S	Te	Tmp	Cro	SxT	CEP	Gm	Am	k	SU	Spt
			By animal species	Total																			
Laying hens	Ziyate et al. (2016)	<i>S. Amsterdam</i>	2	2	2																		
Laying hens	Ziyate et al. (2016)	<i>S. Enteritidis</i>	24	28	1		23																
Turkey	El Allaoui et al. (2017)		4		2			1							2						2	2	
Turkey	El Allaoui et al. (2017)	<i>S. Agona</i>	7	10	0				3	2	3		4	4	3	3	3		1	5			
Laying hens	Ziyate et al. (2016)		3		3																		
Laying hens	Ziyate et al. (2016)	<i>S. Thompson</i>	4	4	4																		
Laying hens	Ziyate et al. (2016)	<i>S. Infantis</i>	7	7	7																		
Turkey	El Allaoui et al. (2017)	<i>S. Heidelberg</i>	4	4	1							2	2	3									
Turkey	El Allaoui et al. (2017)	<i>S. Newport</i>	3	3	0							1	2	3	3					1	1		
Turkey	El Allaoui et al. (2017)	<i>S. Parkroyal</i>	10	10	0					2		2	9	10	3		3			2	5		1
Turkey	El Allaoui et al. (2017)	<i>S. Ruzizi</i>	2	2	0								1	2	1								
Turkey	El Allaoui et al. (2017)	<i>S. Saintpaul</i>	6	6	0					1			5	5	3		5			1		3	
Laying hens	Ziyate et al. (2016)	<i>S. Typhimurium</i>	4	9	1	3							1	3									
Turkey	El Allaoui et al. (2017)		5		1		1			2		2	1		3						1		
Laying hens	Ziyate et al. (2016)	<i>S. Kentucky</i>	20	41	4	13	16	16					11	14				13	6			11	
Turkey	El Allaoui et al. (2017)		21		0		21	20		5		1	21	20	3		4	0	12	9	3		18
		Total	126	126	26	16	62	36	3	12	3	8	57	66	19	3	15	13	19	21	11	14	19
			Percentage		20.63	12.7	49.21	28.6	2.38	9.52	2.38	6.35	45.2	52.38	15.08	2.38	11.9	10.3	15.1	16.7	8.73	11	15.1
Am :	Ampicilline		Caz :	Ceftazidime		Ctx :	Cefotaxime		S :	Streptomycin		Te :	Tetracycline										
Amc :	Amoxicilline/acide clavulanique		CEP :	Cephalothin		Gm :	Gentamycine		Spt :	Spectinomycine		Tmp :	Trimethoprim										
Amx :	Amoxicilline		Cip :	Ciprofloxacine		K :	Kanamycine		SU :	Sulfametoaxozal													
C :	Chloramphenicol		Cro :	Ceftriaxone		Na :	Nalidixic acid		Sxt :	Sulfametoaxozal/ trimethoprim													

In the same studies, the antibiotic resistance profile of strains isolated from poultry farms showed that 79.37% of the strains were resistant to at least one antibiotic (Ziyate et al., 2016; El Allaoui et al., 2017). *Salmonella* presents significant antibiotic resistance to tetracyclines, nalidixic acid, and streptomycin at 52.38 %, 49.21%, and 45.20%, respectively. All *S. Newport*, *S. Parkroyal*, *S. Ruzizi*, *S. Saintpaul*, *S. Kentucky*, and *S. Agona* strains isolated from turkey are antibiotic-resistant. However, all isolated strains, including *S. Thompson*, *S. Infantis*, and *S. Amsterdam*, as well as all *S. Agona* isolates from laying hens, indicated sensitivity to all the antibiotics studied (Ziyate et al., 2016; El Allaoui et al., 2017). The studies carried out in Morocco on the carriage of *Salmonella* by other domestic or wild animal species are old, fragmentary, and limited to certain areas of the country. The study by El Jai et al. (2003) on the causes of abortions in sheep allowed the isolation of *Salmonella* Abortusovis from the vaginal swabs of aborting ewes with a prevalence of 4.8% (n = 8820). With the same objective, a similar study on the same species in the regions of Zaer and the Middle Atlas allowed the detection of *Salmonella* antibodies with seropositivity rates in sheep herds of up to 5% (n = 604, El Idrissi et al., 1995).

Food products with animal origin

Prevalence at the product level

The *Salmonella* prevalence depends on the size of the sample studied; thus, the systematic review and meta-analysis of data on the prevalence of non-typhoid *Salmonella* in food products marketed in the countries of the MENA region (Middle East and North Africa) concluded that the prevalence in studies on less than 100 samples was 13.4%, whereas, it was only 4.1% in studies performed on more than 100 samples (Al-Rifai et al., 2020). As shown in Table 3, contamination of food products with non-typhoid *Salmonella enterica* is relatively common in food products consumed in MENA countries, with a combined global prevalence of 8.8% (Al-Rifai et al., 2020). The variable trend in detection rates between countries could be attributed to the variability of the laboratory methods used, the types of food products analyzed, and their origins (local or imported, Habib et al., 2021). Meat products are the most frequently contaminated by *Salmonella*, predominately in poultry meat and offal. The highest prevalence reported in Morocco is 52.9% in turkey meat (Amajoud et al., 2017) and minced meat and poultry liver, with prevalence rates of 40% and 33.33%, respectively (Bennani et al., 2016). The highest prevalence (30.6%) for red meats and meat products was found in artisanal sausages (Ed-Dra et al., 2018).

Table 3. Meta-analyses of studies reporting non-typhoidal *Salmonella* in Morocco according to the tested food products

Food products	Number of studies	Analyzed samples	<i>Salmonella</i> positive	<i>Salmonella</i> prevalence		
				Range (%) Morocco	Median (%) Morocco	Pooled prevalence MENA
Animal products	18	9622	227	0.0-52.9	5.4	6.8
Fish products	6	893	46	0.0-38.4	8.9	7.7
Plant products	4	2342	6	0.0-2.0	0.1	0.0
Mixed products	4	858	11	1.7-2.0	1.6	1.1
Overall	32	13715	290	0.0-52.9	2.8	4.5

Source: Al-Rifai et al. (2020)

Distribution of isolates by serotype and by food products

Table 4 shows the results of serotypes of *Salmonella* isolated from food products of animal origin in Morocco. The findings indicated that 510 strains of *Salmonella* were isolated from food products distributed on 43 *Salmonella* serotypes, including *Salmonella* isolates that were not typable or on which serotyping was not done.

The most isolated serotypes from food products of animal origin are in descending order as *S. Enteritidis* (n = 74) at 14.51%, *S. Infantis* (n = 71) at 13.92%, *S. Kentucky* (n=54) at 10.59%, *S. Typhimurium* (n = 31) at 6.08%, *S. Bredeney* (n = 30) at 5.88%, *S. Mbandaka* (n = 28) at 5.49%, *S. Blockley* (n=23) at 4.51%, *S. Saintpaul* (n = 18) at 3.53%, *S. Corvallis* (n = 16) at 3.14%, *S. Agona* (n = 15), and *S. Hadar* (n=15) at 2.94%. Non-typable *Salmonella*, or those on which serotyping has not been carried out constituted a significant part of the isolations, including 16 isolates (3.14%).

As shown in figures 2 and 3, the genus *Salmonella* is essentially linked to meat products since 67.65% of isolates were made from these products, particularly from red meats and meat products (41.76% of isolates) and poultry meat (25.88% of isolates). However, some serotypes are much more food products bound than others. Thus, the isolation from red meat and meat products of the following serotypes was in descending order, including *S. Montevideo* (100%), *S. Kiambu* (100%), *S. Mbandaka* (96.43%), *S. Braenderup* (88.89%), *S. Anatum* (87.5%), *S. Indiana* (85.71%) and *S. Infantis* (63.38). The isolation of *S. Saintpaul* (94.44%), *S. Agona* (86.67%), and *S. Muenster* (83.33%) was made mainly from poultry meat. Similarly, the *S. Glostrup* and *S. Newport* serotypes were more closely linked to fishery and aquaculture products, with isolation rates of 100% and 69.23%, respectively. Moreover, 77.03% of *S. Enteritidis* isolations were from eggs.

Table 4. Distribution of *Salmonella* isolates by serotype and by food products in Morocco

Serotype of <i>Salmonella</i>	FOOD PRODUCTS															
	Isolates		Poultry meat		Red meat and meat products		Fish products		Dairy product		Eggs		Food products		Snail	
	No.	(%)**	No.	(%)**	No.	(%)**	No.	(%)**	No.	(%)**	No.	(%)**	No.	(%)**	No.	(%)**
Enteritidis	74	14.51	2	2.70	6	8.11					57	77.03	9	12.16		
Infantis	71	13.92	2	2.82	45	63.38			2	2.817			22	30.99		
Kentucky	54	10.59	18	33.33	8	14.81	26	48.15	2	3.704						
Typhimurium	31	6.08	12	38.71	16	51.61	1	3.226	1	3.226					1	3.23
Bredeney	30	5.88	4	13.33	24	80.00			2	6.667						
Mbandaka	28	5.49	1	3.57	27	96.43										
Blockley	23	4.51	7	30.43	6	26.09	10	43.48								
Saintpaul	18	3.53	17	94.44	1	5.56										
ND*	16	3.14	11	68.75	3	18.75			2	12.5						
Corvallis	16	3.14	4	25.00	12	75.00										
Agona	15	2.94	13	86.67	2	13.33										
Hadar	15	2.94	8	53.33	1	6.67	6	40								
Glostrup	13	2.55					13	100								
Newport	13	2.55	4	30.77			9	69.23								
Montevideo	10	1.96			10	100										
Braenderup	9	1.76	1	11.11	8	88.89										
Anatum	8	1.57			7	87.50			1	12.5						
Indiana	7	1.37	1	14.29	6	85.71										
Muenster	6	1.18	5	83.33	1	16.67										
Kiambu	6	1.18			6	100										
Reading	6	1.18	1	16.67	5	83.33										
Bovismorbificans	4	0.78			4	100										
Chester	4	0.78	4	100												
Give	4	0.78			4	100										
Altona	3	0.59	1	33.33	2	66.67										
Heidelberg	3	0.59	3	100												
Schwarzengrund	3	0.59	3	100												
Berta	2	0.39			2	100										
Labadi	2	0.39			1	50.00	1	50								
Senftenberg	2	0.39			2	100										
Aalbert	1	0.20	1	100												
Bareilley	1	0.20			1	100										
Cerro	1	0.20			1	100										
Derby	1	0.20	1	100												
Djugu	1	0.20	1	100												
Gallinarum	1	0.20	1	100												
Hatford	1	0.20	1	100												
Israel	1	0.20			1	100										
Kiel	1	0.20	1	100												
Livingstone	1	0.20			1	100										
Othmarschen	1	0.20	1	100												
Salamae (type II)	1	0.20	1	100												
Tennessee	1	0.20	1	100												
Zerifin	1	0.20	1	100												
Overall	510	100	132		213		66		10		57		31		1	
Percentage (%)	100		25.88		41.76		12.94		1.96		11.18		6.08		0.2	

* ND: isolates not serotypable or serotyping not carried out; **: Percentage isolation of the serotype from the food product; ***: The definition of the nature of the food products was not specified by the authors of the original study; No: Number

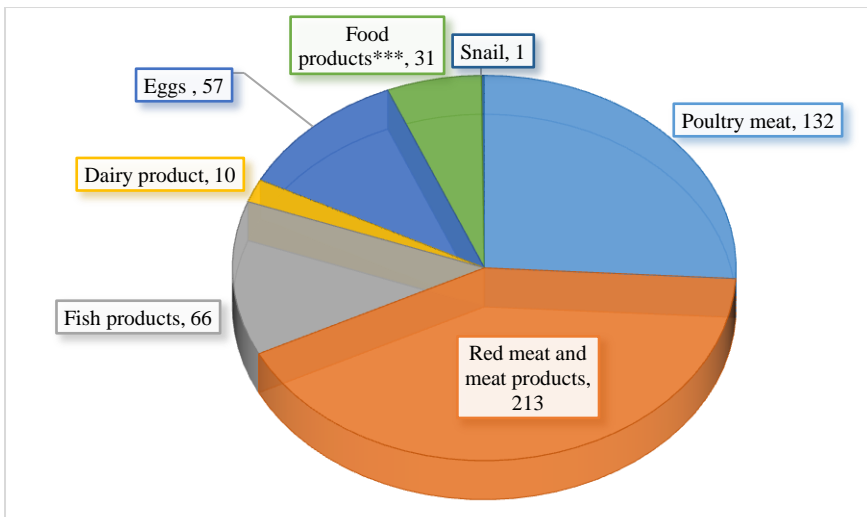


Figure 2. Number of isolates of *Salmonella* spp. from food products

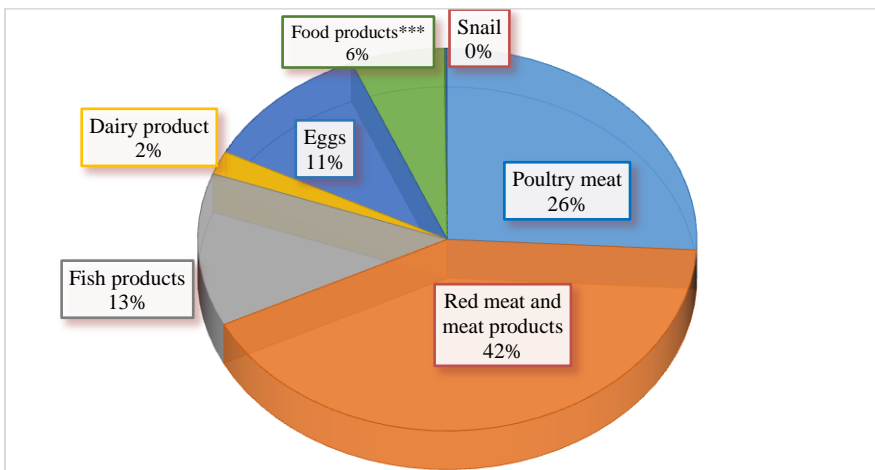


Figure 3. Percentage of isolates of *Salmonella* spp. from food products

Antibiotic resistance of isolates

Although some cases of salmonellosis can come directly from pets or contaminated water, the transmission rate through food was estimated at 95% (Korsak et al., 2004). Table 5 shows the antimicrobial resistance of *Salmonella* strains isolated from animal products in Morocco. Thus, the study of the antibiotic resistance of these isolates showed that 46.27% were resistant to at least one antibiotic. However, 53.73% of isolates were fully susceptible to the antibiotics tested. Including all isolates (n = 510), the antibiotic resistance was highest for *Salmonella* isolated from food products of animal origin against antibiotics with resistance rates of 17.88%, 16.67%, 15.29%, 11.76%, and 10.98% for amoxicillin, ampicillin, tetracyclines, nalidixic acid, and streptomycin, respectively.

The isolates showed a wide range of antibiotic resistance profiles that varied from one serotype to another or even within the same serotype. Some isolated serotypes showed a higher rate of antibiotic resistance. The *S. Glostrup* and *S. Muenster* serotypes are fully antibiotic resistant, followed by resistance rates of 92.59%, 86.67%, 83.33%, 77.42%, and 75% for *S. Kentucky*, *S. Hadar*, *S. Saintpaul*, *S. Typhimurium*, and *S. Corvallis*, respectively. On the other hand, the *S. Bredeney*, *S. Infantis*, and *S. Anatum* serotypes presented the lowest rate of antibiotic resistance at 10% and 11.27%, and 12.50%, respectively. The serotype *S. Typhimurium* isolated from food products of animal origin has antibiotic resistance to a wide range of antibiotics, including 30 different molecules with antibiotic resistance rates varying from 3.23% to 58.06%, depending on the molecules studied. Regarding *S. Typhimurium* isolates from food products, it was found that 58.06% were resistant to amoxicillin, 48.39% to streptomycin, 45.16% to chloramphenicol, and 45.16% to amoxicillin-clavulanic acid. Boutaib et al. (2011) reported *S. Glostrup* serotype from aquaculture products (bivalve mollusks), with 13 isolates presenting the same multiresistant profile to tetracyclines, nalidixic acid, and ampicillin. Another most isolated serotype of the genus *Salmonella* with antibiotic resistance to antibiotics and anti-infectives among the dominant serotypes in food products was *S. Kentucky*, which showed antibiotic resistance to more than 22 molecules of different antibiotics. Furthermore, no resistance to cefquinome and imipenem has been reported; however, this finding should be taken cautiously, knowing that the range of antibiotics tested could vary from one study to another.

The antibiotic resistance profile of isolates is very diverse, ranging from resistance to one antibiotic, the most dominant profile, to multi-resistance to 18 different molecules of antibiotics. Of note, 15 different antibiotic resistance profiles have been identified in isolates from food products of animal origin; resistance to a single antibiotic constitutes was 38.30%, followed by multi-resistance to 3, 2, and 4 molecules of antibiotics at the rates of 18.72%, 17.87%, and 6.38%, respectively. Other profiles are illustrated in Table 6. Most isolates are resistant or multiresistant to less than 6 antibiotics with a rate of 91.91%.

Table 5. Antimicrobial resistance of *Salmonella* strains isolated from animals' products in Morocco

	Isolats	Sensible	Amx	Cs	Na	Cip	Caz	Amc	CtI	B	C	S	Te	Tmp	Cro	SSS	SxT	CEP	Gm	Am	Nor	Cn	Ipm	k	Cef	SU	Cxm	Enr	Oxf	UB	MA	Ak	CQ	F	Tic	FF	Lvx	Mec	Tim	PIP	Cfm	NN	ATM	FEP							
Enteritidis	74	58	2	6	2							4				2		5	5														2	2																	
Infantis	71	63							1			5							2																																
Kentucky	54	4	17		22	36		13			2	10	11			8		6	3	8	2					10		4	4	4	2						1	2	2	2	2										
Typhimurium	31	7	8	3	2			14	2	4	14	15	13	6	5	4	7	2	3	18	1	3		2		9	5			1	2	2								3	3	3	2	3	1						
Bredeney	30	27	1							1										1						1																									
Mbandaka	28	15		2							1	2	5							6				3	0	1																									
Blockley	23	12									1	0	7				7	1	0	0																															
Saintpaul	18	3	8	5	1				10			4		8		3	4			1						1																									
Corvallis	16	4	4	2							1	7	1			1				8						4	1																								
ND*	16	9	1					3			1	4								3						2																									
Agona	15	8	5	1			1	1	1	6	3	2	0	4	1					1																															
Hadar	15	2			13	1		4			1	5	9	1			1			4	1				0	2	1																								
Glostrup	13	0			13								13																																						
Newport	13	7	1		3						1	0	4					1	0	1						1																									
Montevideo	10	6		3								3	0							3				1																											
Braenderup	9	4										0	1							0				3		1																									
Anatum	8	7		1								1	0							1						0																									
Muenster	6	0			1															1						4																									
Reading	6	5														1																																			
Bovismorbifican	4	2										2								2																															
Chester	4	0												2			2																																		
Give	4	0										4								4																															
Heidelberg	3	0								3				1																																					
Schwarzengrund	3	0	1		2	2													1	2	2																														
Aalbert	1	0			1						1	1	1																																						
Derby	1	0	1					1			1																1																								
Gallinarum	1	0									1															1																									
Israel	1	0											1			1	1																																		
Livingstone	1	0																		1																															
Sérotypes sensibles	31	31																																																	
Overall	510	274	49	23	60	39	1	36	3	25	28	56	78	23	6	18	24	10	12	85	10	3	0	9	2	37	6	4	4	5	4	2	0	2	2	3	5	4	8	8	3	2	3	1							
Percentage (n = 510)	100	53.3	17.88	4.51	11.76	7.65	0.20	7.06	0.59	4.90	5.49	10.98	15.29	4.51	1.18	3.53	4.71	1.96	2.35	16.67	1.96	0.59	0.00	1.76	0.39	7.25	1.18	0.78	0.98	0.78	0.39	0.00	0.39	0.39	0.59	0.98	0.78	1.57	1.57	0.59	0.39	0.59	0.39	0.59	0.20						

- Ak: Amikacin
- Am: Ampicilline
- Amc: amoxicillin-clavulanic acid
- Amx: Amoxicilline
- ATM: Aztreonam
- B: Bacitracin
- C: Chloramphenicol
- Caz: Ceftazidime
- Cef: Cefazoline
- CEP: Cephalothin
- Cfm: Cefixime
- Cip: Ciprofloxacine
- Cn: Cefalexine
- CQ: Céfquinome
- Cro: Ceftriaxone
- Cs: Colistine
- Ctx: Cefotaxime
- Cxm: Cefuroxime sodium
- Enr: Enrofloxacin
- F: Furane
- FEP: Cefepime
- FF: Fosfomicin
- Fox: Cefoxitin
- Gm: Gentamycine
- Ipm: Imipénème
- K: Kanamycine
- Lvx: Levofloxacin
- MA: Cefamandole
- Mec: Mecillinam
- Na: Nalidixic Acid
- NN: Tobramycine
- Nor: Norfloxacin
- Oxf: Ofloxacin
- PIP: Piperacillin
- Spt: Spéctinomycine
- SSS: Sulfonamide
- SU: Sulfaméthoxazole
- SxT: Sulfaméthoxazole/ triméthoprim
- Te: Tétracycline
- Tic: Ticarcilline
- Tim: Ticarcilline-Clavulanic acid
- Tmp: Triméthoprim
- UB: Flumequine

Table 6. Resistance profile regarding the number of antibiotics resistant to *Salmonella* isolated from food products in Morocco

	1	2	3	4	5	6	7	8	9	10	11	12	13	16	18	Total
Number of antibiotics	1	2	3	4	5	6	7	8	9	10	11	12	13	16	18	15
Number of isolates	90	44	42	15	13	12	3	3	2	2	1	4	2	1	1	235
Percentage	38.30	18.72	17.87	6.38	5.53	5.11	1.28	1.28	0.85	0.85	0.43	1.70	0.85	0.43	0.43	100

Occurrence of *Salmonella* in the environment

There are a few studies concerning the presence of *Salmonella* in Morocco. When *Salmonella* is isolated from the environment, additional investigations such as serotyping and antibiotic resistance are rarely done. The significant contamination of poultry farms, particularly turkey and laying hen farms, by resistant *Salmonella* promotes the spread and dissemination of this bacterium in other ecosystems, such as the sea coast (Karraouan et al., 2017). Similarly, *Salmonella* contamination can be introduced into the Atlantic coast (between Essaouira and Anza) by sewage or precipitation flows (Mannas et al., 2014). The poultry farming activity developed under the impetus of private investors with sustained growth from the 1960s around the major cities of the Atlantic zone (Sraïri, 2011). The presence of clinically important *Salmonella enterica* in natural waters follows the same trends as infection in humans and wildlife in the same area, suggesting a common origin of this germ (Nassri et al., 2021).

Most of the research work on *Salmonella* in the environment has been carried out in water environments, such as wells (Lotfi et al., 2020, Nassri et al., 2021), running waterways (Ben Moussa et al., 2014), water from dams (Chahboune et al., 2014), wastewaters (Ait Melloul and Hassani, 1999), and seawater (Setti et al., 2009). However, the complete study by serotyping and the study of antibiotic resistance is generally not carried out or not reported. Therefore, a comparative study addressing the contamination of the environment by *Salmonella* cannot be carried out.

Occurrence of *Salmonella* in humans

An increase in international traveling, immigration, and trade accelerates the spread of *Salmonella* pathogens (Hinkka, 2011). *Salmonella* gastroenteritis was the first disease source, with more than 39,983 cases reported in an investigation conducted between the years 1995 and 2015 in Finland on the risk of acquiring foodborne diseases and notifiable sexually transmitted infections among Finnish international travelers (Zöldia et al., 2018). Human movement facilitates the spread of resistant bacteria and antimicrobial resistance genes globally. The enteric species accounted for 65% of the 26 identified bacterial species with drug resistance (Bokhary et al., 2021). The analysis demonstrated an increase in the total number of resistant *Salmonella* spp. associated with travel from 1553 in 1990-1999 (25.75%) to 3549 in 2000-2009 (58.84%). The rates of reporting quinolone-resistant and multidrug resistance *Salmonella* spp. increased from 9.52% and 22.94% in 1990-999 (n = 283 and 329) to 84.40% and 29.08% in 2000-2009 (2510 and 417), respectively (Bokhary et al. 2021).

Morocco comes first among the MENA region countries with the highest *Salmonella* prevalence rate at 17.9%, far exceeding the general average for this region, which is estimated at 6.6% (Al- Rifai et al., 2019). The lack of widespread wastewater treatment and its use in irrigation contributes to the increase in the prevalence of salmonellosis in the exposed population. The prevalence of *Salmonella* carriage is higher in children exposed to wastewater (32.56%) than those who are not exposed with a high risk in male children younger than 10 years and sons of farmers, compared to daughters and children aged over 10 and sons of non-farmers (Ait Melloul and Hassani, 1999).

However, *Salmonella* isolated from wastewater and stool samples from hospitalized children living in the sewage-spreading field of the city of Marrakech showed a different profile from the general finding of antibiotic resistance. The percentage of antibiotic resistance is higher in isolates from children's stools, compared to isolates taken directly from wastewater. In addition, these isolates are rather very sensitive to cefotaxime, gentamicin, trimethoprim-sulfamethoxazole complex, nalidixic acid, kanamycin, trimethoprim, and chloramphenicol with the respective percentages of 100%, 99.88%, 98.04%, 98.04%, 97.30%, 97.07%, and 96.07%, respectively. In comparison, the highest levels of antibiotic resistance were observed for cephalothin, amoxicillin, sulfamethoxazole, and ampicillin, with respective percentages of 29.27%, 26.44%, 26.7%, and 25.21%, respectively (Ait Melloul and Hassani, 1999).

In terms of resistance profile based on the number of antibiotic resistance molecules, the number of isolates resistant to a single antibiotic molecule is dominant, with more than 79.17% of isolates, 90.53% of which are resistant to nalidixic acid. In comparison, resistance profiles to 2 and 4 molecules of antibiotics are 7.5% and 5%, respectively, which are of less importance. The presence of isolates multiresistant to a wide range of antibiotics in humans is worrying, although their percentage is small. Le Hello et al. (2013) reported that some *S. Kentucky* isolates are simultaneously multiresistant to 11, 13, 14, or 15 antibiotics; this broader antibiotic resistance profile is only observed in this serotype (Le Hello et al., 2013).

The *S. Kentucky* serotype is fully multiresistant, while the *S. Enteritidis* and *S. Chester* serotypes showed significant antibiotic resistance of 92.54% and 92.45%, mainly to nalidixic acid with rates of 79.1% and 88.68%, respectively.

However, there is a limited number of publications and an insufficient study of antibiotic resistance to *Salmonella* isolated from humans in Morocco. Nevertheless, the data analysis shows that *S. Enteritidis* and *S. Chester* are the most frequently isolated at the rates of 51.94% and 41.09% of isolates of *Salmonella* in humans in Morocco, respectively. The *S. Kentucky* is occasionally isolated at a rate of 4.65%, occupying the third place or among international travelers (Europeans) who have been infected following their stays in Morocco.

Regarding the conducted studies, the antibiotic resistance of *Salmonella* isolates in humans shows that 93.02% of isolates are resistant to at least one antibiotic. These isolates are resistant to a wide range of antibiotic molecules composed of 23 molecules. The majority of isolated *Salmonella* species are resistant to nalidixic acid, with a percentage of 82.3% of all isolates. In addition, less resistance was noticed to tetracyclines, sulfamethoxazole/trimethoprim, and ampicillin at the rates of 14.6%, 11.5%, and 10%, respectively.

DISCUSSION

Salmonella is among the leading causes of collective food poisoning, which can be considered one of the primary causes of infant mortality in developing countries. Control measures are established through control strategies at the level of the different countries in different ways but which remain insufficient (Nacer et al., 2021).

In Morocco, epidemiological studies show the emergence of multi-resistance in *Salmonella* of human, avian, aquaculture, and environmental origins. The main cause is the uncontrolled use of antibiotics in public health and veterinary medicine (En-Nasiri et al., 2017). Thus, the survey was conducted on the use of antibiotics in poultry farms carried out considering the leading private veterinary practices whose main activity is the health supervision of these farms. The findings revealed that 93% of flocks received at least one antibiotic treatment for a minimum of 3 days in Morocco broiler farms (Rahmatallah et al., 2018). In another study, 96.55% of practicing veterinarians surveyed in the eastern region of Morocco considered the abuse of antibiotics in poultry farms by self-medication, 93.11% of them linked it to the purchase of drugs without a prescription, and 89.66% of respondents judged that it was related to the use of contraband antibiotics (El-Youbi et al., 2016).

The emergence of poultry units and the food chain of *Salmonella* strains resistant to antibiotics is considered a cross-sectoral problem. Resistant bacteria and antibiotic-resistance genes can quickly spread through each stage of the food production chain and can cause human infections (Nacer et al., 2021).

Salmonella is ubiquitous in different environments and food products. Their prevalence can reach 52.9%, recorded in turkey meat by Amajoud et al. (2017). All the studies carried out in Morocco agree that the prevalence of *Salmonella* is high in the poultry sector, in particular, in farms intended to produce meat and eggs for consumption. The rate of antibiotic resistance and multi-resistance is alarming. In addition, Morocco comes first among Arab countries in terms of the prevalence of Non-Typhoidal *Salmonella* in humans according to a systematic review and meta-analysis in Arab countries with a prevalence of 17.9%, ranging from 5.7 to 34.8% during 1997-2012 (Habib et al., 2021). In the same geographical area, the predominant serotypes isolated from an environment or food products may not be the same reported in humans (Setti et al., 2009).

Whatever the medium of origin of *Salmonella*, it will eventually be transmitted to humans and therefore constitute a public health problem. However, studies concerning the circulation of *Salmonella* in different environments and *Salmonella* carrier food products are rare. Most studies relating to *Salmonella* are limited to an animal species, a category of products, or a circumscribed region or carried out over a limited period, and even when they exist. The analysis is often not exhaustive since it does not convert the serotyping of the *Salmonella* isolates or not studying their antibiotic resistance profiles.

Thus, the control of the expansion of antibiotic resistance should be considered a public health priority adopting an intersectoral and intermenstrual approach according to the concept “One Health” advocated by the World Health Organization (WHO) and the World Organization for Animal Health (WOAH). This is the case of the USA, which has decided to ban several antibiotics used in humans in poultry farms so that currently, 95% of the chicken produced in the USA is antibiotic-free (Nacer et al., 2021). Similarly, since non-typhoid *Salmonella* are often associated with increased morbidity and mortality, the determination of antibiotic resistance patterns should be considered an essential part of the surveillance of this *Salmonella* in food safety laboratories for public health in Arab countries (Habib et al., 2021).

CONCLUSION

The food products are the most studied in Morocco for the contamination of *Salmonella*. In animals, most studies investigated *Salmonella* contamination in poultry farms. The other animals have been rarely studied especially domestic

animals, such as cattle, sheep, goats, and camels. Isolation of *Salmonella* from humans and the environment are seldom studied. The contamination with non-typhoid *Salmonella* is relatively common in food products consumed in Morocco, with a global prevalence of 4.5%, meat products are the most frequently contaminated by *Salmonella*, with a predominance in red meat and meat products.

The antibiotic resistance of *Salmonella* isolated in Morocco is alarming both from the nature of antibiotics and the number of multidrug resistances. The antibiotic resistance profile of strains isolated from poultry farms shows that 79.37% are resistant to at least one antibiotic; 93.02% of isolates of *Salmonella* from humans are resistant to at least one antibiotic. A rate of 46.27% of the *Salmonella* isolated from food products is resistant to at least one antibiotic. Considering the number of antibiotics to which the isolates are resistant, resistance ranges from resistance to one antibiotic, which is the most dominant profile (38.30% of resistance), to multi-resistance to 18 different molecules of antibiotics.

Although there are many studies on *Salmonella* contamination in Morocco, they remain specific, partial, sectoral, and often incomplete. This shows the importance of setting up a national observatory for surveillance and epidemiological monitoring and coordinating actions between the various departments, particularly those acting in food safety and public health. The national observatory must focus on the evolution of the antibiotic resistance character in the genus *Salmonella*, *Campylobacters*, *E. coli* and all pathogens transmitted by food. The study of all animal species producing food products is necessary, especially *Salmonella* contamination of meat products, while the study of contamination in ruminant breeding is rarely reported. The use of new identification methods, such as Whole Genome Sequencing is essential in the epidemiological investigations of cases of foodborne diseases for tracing the routes of transmission and origin of *Salmonella*.

DECLARATIONS

Authors' contribution

All the authors contributed to the research of the notification data, their analyses, and the writing of the final manuscript. Pr Karib Hakim and Pr Nassik Saadia participated in the collection of scientific articles and the writing of the french version. Pr Bouchriti Nourreddine and Pr Nassik participated in translating the document; Dr Motassim El Hanafi participated in data collection and analysis, and coordination. All authors participated in the advancement of the research, the development of the document, and data analysis.

Competing interests

The authors of the present study declared that there is no financial or unethical conflict related to this work, which can negatively impact its publication.

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Ethical considerations

The authors have checked for ethical issues, such as plagiarism, approval of public misconduct, data fabrication or falsification, duplicate publishing or submission, and redundancy.

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