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Evolution of the Incidence of Antibiotic Resistance in *Salmonella* Strains Isolated at the National Laboratory of Clinical Biology and Public Health, Bangui, Central African Republic from 2019 to 2023

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Abstract

In sub-Saharan Africa, foodborne *Salmonella* infections cause around 680,000 deaths per year. The evolutionary aspects of the incidence of antibiotic resistance in Salmonella strains no longer seem to attract much interest in the Central African Republic (CAR), although salmonellosis remains a health problem requiring national and international surveillance. **Methodology**: The study conducted at the National Laboratory of Clinical Biology and Public Health, Bangui, Central African Republic (LNBCSP) was a retrospective descriptive study. The study duration was five years (January 2019 to December 2023). The study sample consisted of patients who underwent bacteriological testing of stool, blood and urine samples for *Salmonella* at the LNBCSP in Bangui during this period. Study variables were age, sex, year and bacteriological test results. Statistical tests were used to compare incidences. Relative risks (RR) were calculated to measure the degree of association. **Results:** From 2019

to 2023, we recorded 353 *Salmonella* strains, of which 5% were found in blood, 37% in urine and 58% in stool. Patient age ranged from 1 to 86 years, with a mean of 27 ± 22.05 years and a mode of 5 years. Children aged 0 to 14 years (34%) and females (55.81%) predominated. The highest rate of contamination by *Salmonella* strains was 1.69% in 2022. The overall incidence of salmonellosis was 6.72 in 2019, 7.05 in 2020, 6.91 in 2021, 16.9 in 2022 and 6.26 in 2023 per 1000 samples. Resistance was 30.47% to β_lactam antibiotics, 24.22% to fluroquinolones and 37.97% to *Salmonella spp.* For *Salmonella arizonae* strains, resistance was 20.25% to aminoglycosides, 43.67% to chloramphenicol and 7.59% to imipenem. **Conclusion:** Laboratory-based surveillance of antibiotic resistance in *Salmonella* strains is needed in both human and veterinary medicine. Another study based on molecular characterization will identify new antibiotic-resistant variants circulating in CAR.

Keywords

Incidence-Resistance-*Salmonella*-Central African Republic

1. Introduction

Salmonellosis is caused by a bacterium of the genus *Salmonella*, a Gram-negative, non-spore-forming, motile, facultative anaerobic bacillus belonging to the Enterobacteriacea family [1] [2]. The *Salmonella* genus comprises two species: *Salmonella enterica* and *Salmonella bongori.* The enterica species is subdivided into six subspecies: *enterica*, *salamae*, *arizonne*, *diarizone*, *houtenae and indica*, which are designated by the Roman numerals I, II, IIIa, IIIb, IV and VI, respectively [3]. *Salmonella enterica* comprises more than 2600 serotypes, over 1500 of which belong to the subspecies Salmonella enterica [2] [4] [5]. One study estimated that they were responsible for 93.8 million human cases of gastroenteritis and 155,000 deaths worldwide each year [6]. In 2021, salmonellosis was the second most reported zoonosis in the European Union (EU), with 60,050 cases recorded, representing a 14.3% increase in the EU notification rate compared with 2020 [7]. According to the Center for Disease Control and Prevention (CDC), Salmonella causes an estimated 1.35 million cases of infection, 26,500 hospitalizations and 420 deaths in the United States each year [8]. In sub-Saharan Africa, foodborne *Salmonella* infections cause around 680,000 cases of death per year [6]. Infections caused by Salmonella in human medicine are classified into two groups: typhoid salmonellosis and non-typical salmonellosis. The first group comprises more invasive serotypes, including Typhi and Paratyphi, which cause typhoid and paratyphoid fever respectively [2]. These two serotypes cause 20 million and non-typical salmonellosis. The first group comprises more invasive serotypes, including Typhi and Paratyphi, which cause typhoid and paratyphoid fever respectively [2]. These two serotypes cause 20 million cases and 220,000 deaths per year worldwide, but are mainly confined to countries in Southeast Asia, South America and

Africa [8]. The second group, non-typhoidal salmonellosis, includes serotypes that generally cause gastroenteritis characterized by clinical signs such as diarrhea, abdominal cramps and vomiting. Every year in the United States, non-typhoidal *Salmonella* causes around 1.2 million illnesses, 23,000 hospitalizations and 450 deaths [9]. Unlike in developed countries, in sub-Saharan Africa, non-typhoidal *Salmonella* (NTS) is identified as the main bacteria isolated from the blood of adults and children, and is associated with 20% - 25% of deaths [10]. It should be noted that most cases of non-typhoidal *Salmonella* isolated in Africa are *Salmonella typhimurium* or *Salmonella enteritidis* [11]. In 2022, the Centre National de Recherche (CNR) in France received 2736 human *Salmonella* strains for typing, representing 2417 unique cases of salmonellosis, an increase of 14.8% in 2021, again approaching pre-pandemic levels. Compared with the previous five years, significantly more *Salmonella* samples were received in the first quarter of 2022 [12]. Antimicrobial resistance (AMR) is the result of evolving inefficiency over time, and occurs when microorganisms no longer respond to drugs, making infections more difficult to treat and increasing the risk of disease spread [13]. The use of antimicrobials in food-producing animals is a major factor in resistance. One example is the use of third-generation cephalosporins in poultry breeding and on agricultural farms [14]-[16]. Third-generation cephalosporins and Fluoroquinolones are used empirically to treat severe non-typhoidal *Salmonella* infections. As Fluoroquinolones are not routinely prescribed for children, third-generation cephalosporins are used in the treatment of non-typhoidal *Salmonella* generation and are particularly important for their use. Ampicillin remains a useful agent for treating infections documented as susceptible [17]-[19]. Resistance to certain antibiotics β_lactams, Tetracyclin, Chloramphenicol, and Trimethoprim is increasingly reported [20]. After a four-year decline resistance to ciprofloxacin has increased again. The proportion of weakly resistant *Salmonella spp* ($0.06 <$ MICCIP < 2 μg/ml) increased from 11.7% in 2021 to 17.3% in 2022 [12]. Estimates of the incidence of resistant *Salmonella* infections are needed to inform policy decisions. The National Antimicrobial Resistance Monitoring System (NARMS) monitors *Salmonella* resistance in testing samples of isolates from sick people and determining the percentage of isolates showing resistance [21] [22]. The emergence of antibiotic resistance, the increase in the rate of resistant strains due to irrational antibiotic use, and the transfer of resistance between different bacteria have all contributed to complicating the problem of antibiotic resistance in strains of pathogenic bacteria [23]-[26]. The "Surveillance de l'AntibioRésistance en Afrique" or SARA project is being carried out by Pasteur Network member or partner institutions in six African countries [27] with CAR not taking part. The evolutionary aspects of the incidence of antibiotic resistance in *Salmonella* strains no longer seem to arouse much interest in the CAR, even though salmonellosis remains a health problem requiring national and international surveillance [1]. It is in this context that this study was carried out, with the aim of assessing the evolution of the incidence of isolated antibiotic-resistant *Salmonella* strains in

biological products analyzed at the National Laboratory of Clinical Biology and Public Health (LNBCSP).

2. Methodology

This was a prospective analytical study over a 5-year period, from January 2019 to December 2023 at LNBCSP. Sampling was exhaustive and included all stool, urine and blood samples from patients who came from the different Sanitary centers in Bangui (the community hospital addressed Center, Pediatric University Hospital Center, Sino Central African Friendship University Hospital Center), for Co-proculture, Cyto-bacteriological examination of urine (ECBU) and Hemoculture analyses at the LNBCSP. A form was used to collect data on sociodemographic characteristics (age, sex, year of study) and trends in the annual incidence of antibiotic resistance in isolated *Salmonella* strains.

3. Diagnosis

Conventional bacteriology was used to isolate *Salmonella* strains from different culture media such as Hecktoen and Mac Konkey. The identification of *Salmonella* strains was based on the description of the macroscopic appearance of colonies on the different culture media, followed by microscopic examination of the bacteria to determine the mode of grouping, and analysis of biochemical characteristics using identification media such as API 20 E gallery (BioMerieux). The latter revealed enzymatic activity and carbohydrate fermentation. For each Salmonella strain isolated, an antibiogram was performed in accordance with the recommendations of the French Society of Microbiology 2022 (CASFM, 2022).

A total of thirteen antibiotics (Biorad, Marnes-la-coquette, France) from 6 different families were tested. Beta-lactam families: Cefotaxime (CTX: 30 µg), Ceftriaxone (CRO: 30 µg); Amoxicillin + clavulanic acid (AMC: 20 - 10 µg), Ampicillin (AM: 30 µg); Fluroquinolones: Ciprofloxacin (CIP: 5 µg), Ofloxacin (OFX: 5 µg); Aminosides: Amykacin (AK: 30 µg), Kanamycin (K: 30 UI), Tobramycin (TOB: 10 µg); Chloramphenicol (C: 30 µg), Tetracyclin (TE: 30 µg), Imipeneme (IMP: 10 µg). Suspensions equivalent to the Mc Farland 0.5 standard (approx. 108 CFU/mL) were prepared in sterile physiological water from Salmonella strains grown for 18 to 24 hours. One-fifth dilutions of these suspensions were made with distilled water. These fifth-fold dilutions were inoculated into Muller Hinton culture medium. Antibiotic discs were applied using a disc dispenser. The culture medium containing the antibiotic discs was incubated at 37˚C for 24 hours. Inhibition diameters were measured using a calibrated measuring instrument and interpreted as sensitive or resistant, in accordance with the recommendations of the Antibiotic Susceptibility Testing Committee of the French Society 2022 (CASFM, 2022).

4. Statistical Analysis

Data were collected, coded and entered into Microsoft Excel, then exported and

analyzed using Epi Info7.2 software. Study variables were age, sex, year and bacteriological analysis results. Descriptive tests were used to calculate measures of trend (mean, mode, standard deviation and confidence interval) with $p < 0.05$. Fischer Exact and chi 2 tests were used to compare proportions. Relative risks (RR) were calculated to measure the degree of association. Incidence was expressed in sample-years. The incidence rate of antibiotic resistance was calculated as the ratio of the number of antibiotic-resistant Salmonella strains to the total number of samples collected per year.

5. Results

From 2019 to 2023 we recorded a total of 353 *Salmonella* strains, with 5% in blood, 37% in urine and 58% in stool. Patient age ranged from 1 to 86 years, with an average of 27 ± 22.05 years, and the most frequent age (mode) was 5 years. The age range 0 - 14 years (34%) and female gender (55.81%) were predominant. The male/female sex ratio was 0.81. **Figure 1** shows the Frequency of Salmonella strains isolated by sample from 2019-2023.

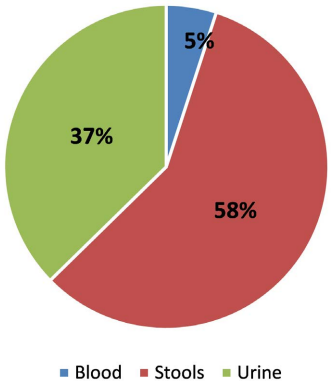

Figure 1. Frequency of *Salmonella* strains isolated by sample from 2019-2023. *Salmonella* strains were found in 58% of stools, 37% of urine and 5% of blood.

The overall contamination rate for *Salmonella* strains was 0.80% over the period 2019 to 2023. The highest *Salmonella* strain contamination rate was 1.69% in 2022. The incidence of Salmonella spp strains was 4.74 per 1000 samples in 2022, followed by a slight increase to 3.37 per 1000 samples in 2020. The change in incidence between 2019, 2021 and 2023 was 1.65, 2.93 and 2.50 per 1000 samples respectively. The incidence of *Salmonella arizonae* strains was 8.76 in 2022 and 3.85 in 2019 per 1000 samples. The incidence of *Salmonella typhi* strains was 1.28 in 2022, followed by a slight decrease to 1.09 in 2020 and then stability between 2019 and 2023, with respective incidences of 0.33 and 0.45 per 1000 samples. *Salmonella enteritidis* strains had a maximum incidence of 1.64 in 2022, with a minimum of 0.099 in 2020. **Table 1** shows the evolution of the incidence of isolated *Salmonella* strains by year.

During the period 2019 to 2023, resistance to β_lactams in *Salmonella spp*

strains represented 30.47%. Resistance to Fluroquinolones was 24.22% with $p > 0.05$ and RR > 1. Resistance to β_lactams, Aminosides, Chloramphenicol and Imipenem in *Salmonella arizonae* strains represented 37.97%, 20.25%, 43.67% and 7.59% respectively with RR > 1. Resistance to β_lactams was 44.12%, to Fluroquinolones 29.41%, to Aminosides 23.53% and to Tetracyclin 64.71% of *Salmonella typhi* strains with RR > 1. Low resistance to Fluroquinolones in *Salmonella enteritidis* strains had a significant protective effect ($p < 0.05$ and RR < 1). Table 2 shows the evolution of resistance rates in isolated *Salmonella* strains.

Table 1. Evolution of the incidence of isolated *Salmonella* strains by year.

	Year					
Number of samples	2019 9076	2020 10,068	2021 10,551	2022 5480	2023 8774	Total 43,949
Isolated *Salmonella*	N = 61	N = 71	N = 73	N = 93	N = 55	N = 353
%	0.67	0.70	0.69	1.69	0.62	0.80
Number de *S. spp*	n = 15	n = 34	n = 31	n = 26	n = 22	n = 128
%	24.59	47.88	42.46	27.95	40	36
S. spp-year	0.002	0.003	0.003	0.005	0.003	0.003
Incidence %	0.16	0.33	0.29	0.47	0.25	0.29
Incidence ‰	1.65	3.37	2.93	4.74	2.50	2.91
Number de *S. arizonae*	n = 35	n = 23	n = 27	n = 48	n = 25	n = 158
%	57.37	32.39	39.98	51.61	45.45	44.7
S. arizonae-year	0.004	0.002	0.002	0.009	0.003	0.003
Incidence %	0.38	0.23	0.25	0.87	0.28	0.36
Incidence ‰	3.85	2.28	2.55	8.76	2.85	3.59
Number de *S. typhi*	n = 3	n = 11	n = 9	n = 7	n = 4	n = 34
%	4.92	15.49	12.33	7.52	7.27	9.63
S. typhi	0.0003	0.001	0.0008	0.001	0.0004	0.0008
Incidence %	0.033	0.11	0.085	0.13	0.045	0.077
Incidence ‰	0.33	1.09	0.85	1.28	0.45	0.77
Number de *S. enteritidis*	n = 3	n = 1	n = 4	n = 9	n = 3	n = 20
%	4.92	1.40	5.48	9.67	5.45	5.66
S. enteritidis-year	0.0003	9.10^{-5}	0.0003	0.002	0.0003	0.0004
Incidence %	0.033	0.0010	0.04	0.16	0.034	0.045
Incidence ‰	0.33	0.099	0.38	1.64	0.34	0.45

The 0 - 14 age group represented children with a 34% contamination rate. The 15 to 86 age group had a contamination rate of 66%. We found a significant association between the age range of children 0 to 14 years and the families of antibiotics in occurrence to Fluroquinolones in 2021 and Tetracycline in 2023 with $p < 0.05$. Children aged 0 to 14 showed no resistance to Imipenem in 2019 and 2020, and adults aged 15 to 86 in 2022. On the other hand, in 2022, 60% of Salmonella strains isolated from children showed resistance to Chloramphenicol. Table 3

shows the evolution of the incidence rate of antibiotic resistance in isolated Salmonella strains by age group.

Table 2. Trends in the incidence of antibiotic resistance in isolated *Salmonella* strains.

	Year					Total	p-value	RR
	2019	2020	2021	2022	2023			
Isolated Salmonella	N = 61	N = 71	N = 73	N = 93	N = 55	N = 353		
Salmonella spp	n = 15	n = 34	n = 31	n = 26	n = 22	n = 128		
	%	%	%	%	%	%		
	24.59	47.89	42.47	27.96	40	36.58		
*β*_lactams	40	27.21	29.04	27.89	39.77	30.47	0.09	0.81
Fluroquinolones	20	33.83	17.74	13.46	31.82	24.22	0.23	1.15
Aminosides	26.67	2.94	16.13	20.51	28.79	16.41	0.23	0.53
Chloramphénicol	60	38.24	41.94	30.77	36.36	39.84	0.25	0.91
Tétracyclin	40	55.88	48.39	61.54	31.82	49.22	0.12	0.88
Imipenèm	13.33	5.88	6.45	3.85	13.64	7.81	0.18	1.46
Salmonella arizonae	n = 35	n = 23	n = 27	n = 48	n = 25	n = 158		
%	57.38	32.39	36.99	51.61	45.45	44.76		
*β*_lactams	48.57	33.7	32.41	36.46	37.00	37.97	0.13	1.17
Fluroquinolones	18.57	32.61	20.37	15.63	24.00	22.15	0.49	1.00
Aminosides	23.81	1.45	16.05	19.67	25.33	20.25	0.21	1.19
Chloramphénicol	45.71	52.17	40.74	43.75	36.00	43.67	0.30	1.06
Tétracyclin	48,57	56.52	55.56	56.25	44.00	52.53	0.40	0.97
Imipenèm	0	4.35	11.11	8.33	16.00	7.59	0.17	1.48
Salmonella typhi	n = 3	n = 11	n = 9	n = 7	n = 4	n = 34		
%	4.92	15.49	12.33	7.53	7.27	9.51		
*β*_lactams	66.67	50	38.39	35.72	31.25	44.12	0.12	1.30
Fluroquinolones	0	50	22.22	21.43	25.00	29.41	0.14	1.37
Aminosides	55.56	12.12	18.52	4.76	16.67	23.53	0.21	1.31
Chloramphénicol	33.33	27.27	22.22	14.29	75.00	29.41	0.25	0.67
Tétracyclin	100	63.64	33.33	85.71	75.00	64.71	0.12	1.24
Imipenèm	0	0	0	0	0,00	0		
Salmonella enteritidis	n = 3	n = 1	n = 4	n = 9	n = 3	n = 20		
%	4.92	1.41	5.48	9.68	5.45	5.39		
*β*_lactams	50	25	18.75	11.11	66.67	30	0.33	0.33
Fluroquinolones	0	0	0	22.22	33.33	0	0.002	10^{-4}
Aminosides	0	0	16.67	3.7	0.00	5	0.05	0.26
Chloramphénicol	33.33	0	50	77.78	66.67	60	0.05	1.45
Tétracyclin	33.33	100	50	77.78	0.00	55	0.43	1.03
Imipenèm	0	0	0	0	0.00	0	0.13	10^{-4}

Table 3. Trends in the incidence of antibiotic resistance in isolated *Salmonella* strains by age group.

	Year									
	2019		2020		2021		2022		2023	
Population at risk	9076		10,068		10,551		5480		8774	
Isolated Salmonella	N = 61		N = 71		N = 73		N = 93		N = 55	
Number	n = 19	n = 42	n = 27	n = 44	n = 31	n = 42	n = 28	n = 65	n = 15	n = 40
Age group	<14	>14	<14	>14	<14	>14	<14	>14	<14	>14
Antibiotic	%	%	%	%	%	%	%	%	%	%
*β*_lactams	48.68	44.64	25.93	14.66	38.71	23.81	34.82	29.23	33.33	40.63
Fluroquinolones	26.32	13.10	29.63	37.50	16.13	19.05	12.50	16.92	30.00	26.25
Aminosides	31.57	19.05	7.41	15.15	15.05	19.05	22.62	18.97	24.44	24.17
Chloramphénicol	47.37	50.00	44.44	38.64	41.94	38.10	32.14	44.62	60.00	35.00
Tétracyclin	47.37	50.00	74.07	50.00	51.61	47.62	60.71	63.08	60.00	32.50
Imipenèm	0,00	4.76	3.70	4.55	0.00	11.90	17.86	0.00	13.33	12.50

The highest rate of Chloramphenicol resistance in *Salmonella* strains was 58.33% in 2019, followed by 47.06% in 2023 for females and a minimum of 36.00% in 2019 for males. We found a significant difference between the Chloramphenicol resistance of *Salmonella* strains and gender (p = 0.04). However, we found no significant association between gender and the other families of antibiotics used (p > 0.05). Table 4 shows the evolution of the incidence of antibiotic resistance in isolated Salmonella strains by gender.

Table 4. Trends in the incidence of antibiotic resistance in isolated *Salmonella* strains by gender.

	Year										
	2019		2020		2021		2022		2023		
Pop. at risk	9076		10,068		10,551		5480		8774		
Salmonella	N = 61		N = 71		N = 73		N = 93		N = 55		
Gender	F	M	F	M	F	M	F	M	F	M	
Total	n = 36	n = 25	n = 41	n = 30	n = 37	n = 36	n = 49	n = 44	n = 34	n = 21	p-value
	%	%	%	%	%	%	%	%	%	%	
*β*_lactams	50.00	40.00	34.15	30	32.43	44.40	32.65	29.55	38.24	41.10	
Fluroquinolones	19.44	16.00	31.71	40.00	18.92	19.44	14.29	20.45	26.47	28.57	
Aminosides	19.44	28.00	7.32	20.00	16.22	19.44	20.41	13.64	26.47	19.05	
Chloramphénicol	58.33	36.00	41.46	40.00	40.54	38.89	42.86	38.64	47.06	33.33	0.04
Tétracyclin	52.78	44.00	56.10	63.33	51.35	47.22	61.22	63.64	35.29	47.62	
Imipenèm	5.56	0.00	7.32	0.00	8.11	5.56	8.16	2.27	17.65	4.76	

Gender had a protective effect against resistance in 2019 and 2023 (RR = 0.40 [0.18 - 0.88] and RR = 0.33 [0.14 - 0.77]). This protective effect was statistically

significant (p = 0.01 and p = 0.004 respectively). Age appeared to be associated with resistance in 2021 (RR = 1.10) and 2022 (1.09), but this risk was not significant (p > 0.05). Table 5 shows the association between antibiotic resistance in isolated *Salmonella* strains and socio-demographic characteristics by year.

Table 5. Association between antibiotic resistance in isolated *Salmonella* strains and socio-demographic characteristics by year.

Year	Variable		Number	Résistance	RR	IC (95%)	p-value
2019	Age group (Year)	0 - 14	19	6	0.94	[0.43 - 2.08]	0.45
		15 - 86	42	14			
	Gender	M	36	7	0.40	[0.18 - 0.88]	**0.01**
		F	25	12			
2020	Age group (Year)	0 - 14	27	8	0.93	[0.45 - 1.92]	0.42
		15 - 86	44	14			
	Gender	M	41	10	0.60	[0.30 - 1.22]	0.08
		F	30	12			
2021	Age group (Year)	0 - 14	31	9	1.10	[0.52 - 2.34]	0.39
		15 - 86	42	11			
	Gender	M	37	10	0.97	[0.46 - 2.05]	0.47
		F	36	10			
2022	Age group (Year)	0 - 14	28	9	1.09	[0.56 - 2.12]	0.38
		15 - 86	65	19			
	Gender	M	49	12	0.63	[0.34 - 1.17]	0.07
		F	44	17			
2023	Age group (Year)	0 - 14	15	6	0.19	[0.65 - 3.23]	0.19
		15 - 86	40	11			
	Gender	M	34	6	0.33	[0.14 - 0.77]	**0.004**
		F	21	11			

6. Discussion

The results obtained were based essentially on the isolation, identification and antibiogram of *Salmonella* strains isolated from biological products such as blood, stools and urine on selective media (*Salmonella Shigella* or Hektoen) [28]. This retrospective descriptive study carried out at the LNBCSP enabled us to record 43949 stool, urine and blood samples, from which 353 *Salmonella* strains were isolated, giving a prevalence rate of 0.80%. This result is below that of a study carried out in Europe in 2018 in dairy products, where the *Salmonella* strains isolated represented 8.8% of 44,078 samples. *Salmonella* strains were isolated at a rate of 5% in blood, 37% in urine and 58% in stool [29]. A total of 128 *Salmonella spp* strains were isolated during the study period, representing a rate of 36%. The incidence of *Salmonella spp* strains was 4.74 per 1000 samples in 2022, followed by a slight decrease to 3.37 per 1000 samples in 2020. The change in incidence

between 2019, 2021 and 2023 were 1.65, 2.93 and 2.50 per 1000 samples respectively. Several authors have shown that *Salmonella spp* strains are among the mostcommon foodborne pathogens, and are among the four leading causes of diarrheal disease worldwide [30]. From 2019 to 2023, we isolated 158 strains of *Salmonella arizonae*, representing a contamination rate of 45%. The annual incidence of *Salmonella arizonae* strains was 8.76 in 2022 and 3.85 in 2019 per 1000 samples, followed by a slight variation between 2020 and 2021 with respective incidences of 2.28 and 2.55 per 1000 samples. Some authors have shown that *Salmonella arizonae* strains are also regularly isolated from immune compromised humans [31]. The rate of *Salmonella typhi* strains isolated from pathological products was 9.51%. The annual incidence of these strains was 1.28 in 2022, followed by 1.09 in 2020. Between 2019 and 2023, the incidence was 0.33 and 0.45 per 1000 respectively. It should be noted that humans are the sole reservoir of both typhoidal *Salmonella* strains. They are often infected through ingestion of contaminated food and water [32]. *Salmonella enteritidis* strains were isolated at a contamination rate of 5.39%. The annual incidence of these strains was 1.64 in 2022 and 0.099 in 2020. According to the European Food Safety Authority and the European Centre for Disease Control (EFSA) and 2020. According to the European Food Safety Authority and the European Centre for Disease Control (EFSA and ECDC) in 2019, the number of cases of salmonellosis has risen sharply in certain countries, where the incidence has increased 20-fold in recent years. This is partly due to the increase in bacterial resistance to antibiotics [29]. Some authors have shown that the number of annual cases of salmonellosis is difficult to quantify, but it is estimated that significantly higher than the number of reported cases [33]. We observed a variation in the incidence of *Salmonella* strains during the period of our study. This variation could be explained by differences in the source of contamination, sample size, isolation and identification techniques, which could differ from country to country. The lowest contamination rates were for *Salmonella paratyphi*, *choleraesuis* and *typhimirum*, with rates of 1.42%, 0.27% and 2.07% respectively. The incidence of resistance to β_lactams Fluroquinolones, Aminosides, Chloramphenicol, Tetracyclin and Imipenem in *Salmonella spp* strains was 30.47%, 24.22%, 16.41%, 39.84%, 49.22% and 7.81% respectively, statistical tests showed no significant association between the *Salmonella spp* strains isolated and the families of antibiotics used, with $p > 0.05$. However, Fluroquinolones and Imipenem had an $RR > 1$. Our results are contrary to those of a study carried out in West Africa in 2017 by Ouedraogo A et al. which had shown that since the year 2009, a decrease in resistance to ciprofloxacin 36% in 2009 and 21.9% in 2015 [34]. The study showed that 49.22% of *Salmonella spp* strains were resistant to tetracycline. This result is close to that achieved in Bamako between 2021 and 2022, with tetracycline resistance at 80.8%. This antibiotic is the most widely used by livestock farmers [35]. Of 158 *Salmonella arizonae* strains isolated during the period 2019 and 2023, resistance to β_lactams was 37.97% to Fluroquinolones, 22.15% to Aminosides, 20.25% to Chloramphenicol 43.67% and to Tetracyclin 52.53% with

p > 0.05. On the other hand, the β_lactam families, Fluroquinolones and Aminosides had presented an RR > 1 to *Salmonella arizonae* strains. A study carried out in 2019 by Wafa Djellab had shown a β_lactam resistance rate of 28.57% in *Salmonella arizonae* strains. The majority of these strains expressed significant cross-resistance to aminoglycosides, quinolones and sulfonamides [36]. The sources of contamination were not investigated in our study, and the high rate of *Salmonella arizonae* could be explained by the fact that most of our patients were immune compromised. During the study period, *Salmonella typhi* strains were isolated from pathological products at a rate of 10%. Resistance of *Salmonella typhi* strains to β_lactams, Fluroquinolones, Aminosides and Tetracyclin was 44.12%, 29.41%, 23.53% and 64.71% respectively, with no significant association p > 0.05 and an RR > 0.05. Chloramphenicol resistance in *Salmonella typhi* strains was 29.41%. There was no significant association with p > 0.05 and no Relative Risk with RR < 1. The high rate of Tetracyclin resistance was 64.71% of *Salmonella typhi* strains with a p-value ≤ 0.05. Compared to that presented in the Canadian Integrated Program for Antimicrobial Resistance Surveillance (CIPARS), the rate of *Salmonella typhi* strains isolated in Tetracycline-resistant isolates was 13% in 2007 and 6% in 2008 [37]. It should be noted that in CAR, the lack of drinking water for the population and the anarchic opening of gargotes in the city, which are not subject to sanitary controls, could be at the origin of *Salmonella typhi* infections. Tetracyclin remains the most widely and inexpensively used antibiotic for the treatment of abdominal pain in humans, and is also used to treat poultry. In this study, 5.66% of *Salmonella enteritidis* strains were isolated, with resistance to β_lactams at 30%, to aminosides at 5%, to chloramphenicol at 60%, to tetracyclin at 55%, and no strains resistant to imipenem. Our study showed that *Salmonella enteritidis* strains would be resistant to Fluroquinolones by 22.22% in 2022 and 33.33% in 2023. The decline in resistance to Fluroquinolones was According to the WHO, provincial incidence rates of *Salmonella enteritidis* in humans ranged from 4.37 to 10.06 per 100,000 inhabitants per year. A study conducted in 2021 by Foster et al. showed that the percentage of tetracyclin-resistant isolates was significantly lower in 2008 (2%) than in 2007 (6%) [8]. According to the WHO, antibiotic resistance is a natural phenomenon, but misuse of these drugs in humans and animals accelerates the process [38]. In addition, the use of antibiotics in the animal sector for therapeutic or prophylactic purposes, or as feed additives, is a major contributor to the emergence of antibiotic resistance in both animals and humans [34]. The 0 - 14 age group, representing children, had a contamination rate of 34%. The 15 to 86 age group had a contamination rate of 66%. This result is slightly higher than that obtained in Bamako at the Yirimadjo Community Health Center from December 2021 to June 2022, where a rate of 30.19% of *Salmonella* strains was obtained from 308 children aged 0 to 15 years [35]. This result is similar to another study carried out in Côte d'Ivoire in 2012 by KOFFI et al. which found a rate of 62.7% of *Salmonella* strains isolated in adults and 37.3% in children [39]. In this study, the incidence rate of resistance to Fluroquinolones in the pediatric age

group was 16.13% in 2021, to of Salmonella strains isolated in adults and 37.3% in children [39]. In this study, the incidence rate of resistance to Fluroquinolones in the pediatric age group was 16.13% in 2021, to Tetracyclin in 2023 with a $p < 0.05$. The 0 - 14 age group showed no resistance to Imipenem in 2019 and 2020, and adults aged 15 to 86 in 2022. By In 2022, however, the children's age group showed resistance to Chloramphenicol, with a rate of 60%. This result is contrary to that of a study carried out in Bamako, which showed no resistance to chloramphenicol in this age group [35]. Resistance to β_lactam antibiotics in isolated *Salmonella* strains was 50% in females and 40% in males in 2019. In contrast, resistance in males was 44.40% in 2021. During the study period in 2019 and 2023, resistance to Chloramphenicol was 58.33% and 47.06% respectively, and to Tetracyclin 52.78% and 47.62% of *Salmonella* strains isolated from females, with a significant $p < 0.05$ association. Between 2019 and 2022, Chloramphenicol resistance of *Salmonella* strains was respectively 36.00 and 38.64 and Tetracyclin 44.00 and 63.64% in the male sex with a significant association $p < 0.05$. Some authors had shown that any difference in incidence reported according to sex in a given year is simply due in all likelihood to reporting differences linked to chance. This prevalence among women and adults, particularly the elderly, has been reported by several authors [40] [41].

7. Limitation

Data on patient residence and function are not available.

8. Conclusion

Salmonella are enterobacteria that cause gastroenteritis and fever in humans, which can be severe and contagious. Salmonellosis remains a global health problem requiring national and international surveillance. The infection was more common in females than males, and was found in 58% of stools. Children aged 0 - 14 accounted for 34%. Resistance to B_lactams, Fluroquinolones, Aminosides, Chloramphenicol and Tetracyclin in isolated *Salmonella* strains remains a public health problem in the CAR. We have noted a variation in incidence between 2020-2022. We need to set up a laboratory-based system for monitoring antibiotic resistance in *Salmonella* strains in human and veterinary medicine. Laboratory analysis of foodstuffs could also contribute to improving the safety and genotypic characterization of *Salmonella* strains using molecular biology techniques which will help identify new circulating antibiotic-resistant variants in CAR.

Conflicts of Interest

The authors declare no conflicts of interest regarding the publication of this paper.

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