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Prevalence, Serotypes and Antimicrobial Resistance of *Salmonella* Isolated from Children in Guangzhou, China, 2018–2023

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Purpose: Acute gastroenteritis caused by *Salmonella* spp. among children post a great threat for global public health. The increasing rate of drug-resistant *Salmonella* spp. has also become a challenging problem worldwide. In this study, the prevalence, serotypes, and antimicrobial characteristics of *Salmonella* isolated from children in Guangzhou, China, were investigated to provide supporting information for clinical treatment and prevention.

Methods: Clinical data of children featured with gastroenteritis symptoms from 2018 to 2023 in Guangdong Women and Children Hospital were collected. The difference and fluctuation of antimicrobial resistance between serotypes and years were retrospectively analyzed.

Results: A total of 1304 *Salmonella* isolates were cultural-confirmed. The overall positive rate of *Salmonella* isolated from stool samples was 22.0% (1304/5924). *Salmonella* infections occur mainly from June to September and the majority of infected children aged under 4 years. Serogroup B was the most common serogroup among *Salmonella* isolates (74.6%, 973/1304). The predominant serotypes of *Salmonella* isolates were Typhimurium (63.1%, 823/1304). Higher drug resistance rate of *Salmonella* spp. to ceftriaxone was observed in 2023. The drug resistance rates of *Salmonella* isolates to sulfamethoxazole/trimethoprim and ampicillin are at high level during the past 6 years. Notably, higher multi-drug resistance (MDR) rate was demonstrated in *Salmonella* Typhimurium compared with other serotypes.

Conclusion: *Salmonella* Typhimurium was the most common serotype isolated from children in Guangzhou, China, and it may mainly account for the high drug resistance rate in *Salmonella* spp. to most of the antimicrobial profiles. For controlling the high drug resistance rate of *Salmonella* spp. continuous surveillance of drug resistance and appropriate use of antibiotics based on clinical and laboratory results are of great significance.

Keywords: gastroenteritis, *Salmonella*, antimicrobial resistance, Guangzhou, China

Introduction

Gastroenterology infection caused by enteropathogenic bacteria, viruses and parasites are known to be the major cause of acute diarrhea among children aged under 5 years.[1–3] Frequent isolations of *Salmonella* spp. derived from a wide variety of polluted water, animal feeds, and food animal environment continuously occur worldwide.[4] It was estimated that approximately 93.8 million cases of gastroenteritis were attributed to *Salmonella* infection,[5] which even resulted in more than 300,000 deaths per year in developing countries.[5–7] *Salmonella* is a rod-shaped, gram-negative bacteria with no capsule and spore, commonly transmitted through contaminated food products.[8] *Salmonella* can be classified into typhoidal *Salmonella* and non-typhoidal *Salmonella* (NTS) serovars.[9] NTS that caused bacterial enteritis, especially

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serotypes Typhimurium and Enteritidis, has been recognized as a global burden.[2,5] *Salmonella* comprises 392 species based on more than 2600 serotypes,[10–12] while A-F serogroups are the major serotypes prevalent in China.[13]

A large-scale observation showed that the proportion of *Salmonella* Typhimurium in London, Rissen, American and European countries displayed an increasing tendency during 2006–2019.[14] In China, NTS was one of the leading bacterial pathogens that was identified from pediatric patients.[15] Moreover, the positive rate of NTS in China was reported to be the highest in south regions compared with other areas, which was considered to be related with higher temperature.[16] Currently, increasing resistance to broad range of antibiotics in non-typhoidal *Salmonella* strains has become an emerging threat,[17–19] involving enteric and invasive infection. For the susceptibility to antimicrobial agents, different serotypes of *Salmonella* carrying various virulence genes may exhibit differently. However, the information about the antibiotic-resistance and characteristics of *Salmonella* infection among pediatric patients in the south of China is limited yet.

Therefore, this study analyzed enteric *Salmonella* infection among children in Guangzhou, China, and retrospectively investigated the distribution, characteristics and pattern of drug-resistance from 2018 to 2023 to promote the understanding of *Salmonella* infection and improve the clinical treatment.

Methods and Materials

Population

This retrospective study was conducted in Guangdong Women and Children Hospital, which is one of the largest women's and children's hospitals in Guangdong Province. Clinical information involving date of tests, sex, age, the results of bacterial culture and antimicrobial resistance were included. Children aged under 14 years old who were defined as patients with gastroenteritis symptoms were enrolled in this study.[20] Stool samples (2–5mL liquid stools or 2–5g solid stools) were collected using sterile and dry container for immediate detection (within 2 h). Rectal swab samples should only be collected from infants or severe diarrheal patients without stool for test. The related clinical information in this study was collected from January 2018 to December 2023.

Salmonella Identification and Serotyping

Isolation of *Salmonella* spp. was conducted according to reported methods.[21,22] A 1 g or 1 mL stool samples were plated and incubated onto XLD (Xylose Lysine Desoxycholate) agars at 36°C for 18–48 h. The suspicious colonies (transparent, round, with or without black centers that reflect H_2S production) were further identified by MALDI-TOF-MS (Matrix-Assisted Laser Desorption Ionization-Time of Flight Mass Spectrometry). Subsequently, O and H antigens of validated *Salmonella* spp. were characterized by commercial anti-serum (Tianrun Bio-Pharmaceutical, China) and the serotypes were classified according to Kauffmann-Le Minor scheme,[23] with PBS (Phosphate Buffered Saline) as negative control and *Salmonella* Typhimurium ATCC 14028 as positive control.

Antimicrobial Susceptibility Testing (AST)

The antimicrobial susceptibility of *Salmonella* isolates was determined according to the guidelines of Clinical and Laboratory Standards Institute (CLSI).[24,25] Antimicrobial susceptibility testing (AST) was carried out on the VITEK 2-Compact system (bioMerieux, Inc., France), using AST-GN09 commercial card (antimicrobial classes and details were displayed in Supplementary Materials and Methods). The MacFarland 0.5 inoculums were prepared and swabbed on the whole surface of Mueller–Hinton agar for dusk diffusion assays. *Escherichia coli* ATCC 25922, *Pseudomonas aeruginosa* ATCC 27853 were used as control strains. Alternative antibiotic susceptibility tests were conducted by Kirby–Bauer disk diffusion method (Oxoid, UK), and classified as resistant (R), intermediate (I) and sensitive (S) according to the CLSI guidelines.

Definitions

Multidrug resistance (MDR) was defined as resistance to three or more antibacterial classes, such as aminopenicillin (ampicillin, amoxicillin), β-lactam combination agents (ampicillin/sulbactam, piperacillin/tazobactam), cephalosporins (ceftriaxone, ceftazidime, cefepime, cefotaxime), monobactams (aztreonam), carbapenems (imipenem), dihydrofolate

reductase inhibitors (trimethoprim/sulfamethoxazole), and fluoroquinolones (ciprofloxacin, levofloxacin).[26,27] First-line agents include the following antimicrobial agents: ampicillin (AMP), ceftriaxone (CRO), ciprofloxacin (CIP), sulfamethoxazole/trimethoprim (SXT).[28]

Statistical Analysis

Information of patients and clinical data in this study were exported from Hospital Information System and categorized in Microsoft Excel. SPSS version 26.0 was utilized to statistical analysis involving *Chi-square* test or *Fisher's* exact probability method in this study. Tables in this study were conducted via Microsoft Excel and Figures were made by R Packages. $P<0.05$ indicates statistically significant differences.

Results

Clinical Information and Prevalence of Salmonella Isolates

A total of 5924 cases were included in this study (Table 1). From 2018 to 2023, the positive rates of *Salmonella* isolation were 20.7%, 20.8%, 21.9%, 21.2%, 25.1%, 24.2%, respectively. The fecal isolation of *Salmonella* was statistically higher in 2022 (χ^2=5.548, P=0.019) than in 2018. *Salmonella* isolation exhibits in season distribution as 9.4% in spring, 26.3% in summer, 30.0% in autumn and 18.8% in winter. Notably, *Salmonella* isolation in summer, autumn and winter were significantly higher than in spring ($P<0.001$). *Salmonella* isolated from in-patients and out-patients were 18.45% and 29.68%, respectively. There were 22.23% male patients and 21.69% female patients were detected as positive in *Salmonella*. Of all the age groups, the positive rates of cultural-confirmed *Salmonella* were 19.7% in <1 age group, 28.2% in 1–3 age group, 15.8% in 4–6 age group and 9.4% in 7–14 age group, respectively. Compared with children under 1 year, children aged 1–3 years old exhibited higher isolation in *Salmonella* (χ^2=52.045, $P<0.001$), while children aged 7–14 years old were statistically lower in positive rate (χ^2=11.570, P=0.001).

Monthly distribution of *Salmonella* isolates was analyzed. As is shown in Figure 1, the fluctuation of the positive rate from January to December in the past 6 years was similar in total. Higher trend was demonstrated from June to September than other months and the positive rate of *salmonellosis* always reached peak in June or July.

Table 1 Clinical Information of Samples for Suspected *Salmonella* Infection

Category	Subcategory	*Salmonella* cultural tests					OR (95% CI)[#]	χ^2	P
		n	Negative	Proportion (%)	Positive	Proportion (%)			
Years	2018	1400	1110	79.3	290	20.7	–	–	–
	2019	1238	981	79.2	257	20.8	1.00 (0.83–1.21)	0.001	0.977
	2020	636	497	78.1	139	21.9	1.07 (0.85–1.35)	0.342	0.558
	2021	996	785	78.8	211	21.2	1.03 (0.84–1.26)	0.078	0.780
	2022	798	598	74.9	200	25.1	1.28 (1.04–1.57)	5.548	0.019
	2023	856	649	75.8	207	24.2	1.22 (1.00–1.50)	3.719	0.054
Seasons	Spring	1293	1171	90.6	122	9.4	–	–	–
	Summer	1401	1033	73.7	368	26.3	3.42 (2.74–4.27)	128.019	<0.001
	Autumn	1854	1298	70.0	556	30.0	4.11 (3.33–5.08)	190.387	<0.001
	Winter	1376	1118	81.3	258	18.8	2.22 (1.76–2.79)	47.366	<0.001
Sources	In	4027	3284	81.5	743	18.5	–	–	–
	Out	1890	1329	70.3	561	29.7	1.87 (1.64–2.12)	94.451	<0.001
Gender	Male	3562	2770	77.8	792	22.2	–	–	–
	Female	2360	1848	78.3	512	21.7	0.97 (0.85–1.10)	0.241	0.624
Age groups (years)	<1	3496	2808	80.3	688	19.7	–	–	–
	1–3	1964	1410	71.8	554	28.2	1.60 (1.41–1.82)	52.045	<0.001
	4–6	284	239	84.2	45	15.8	0.77 (0.55–1.69)	2.471	0.116
	7–14	180	163	90.6	17	9.4	0.43 (0.26–0.71)	11.570	0.001

Notes: [#]OR, odd ratio. CI, confidence interval.

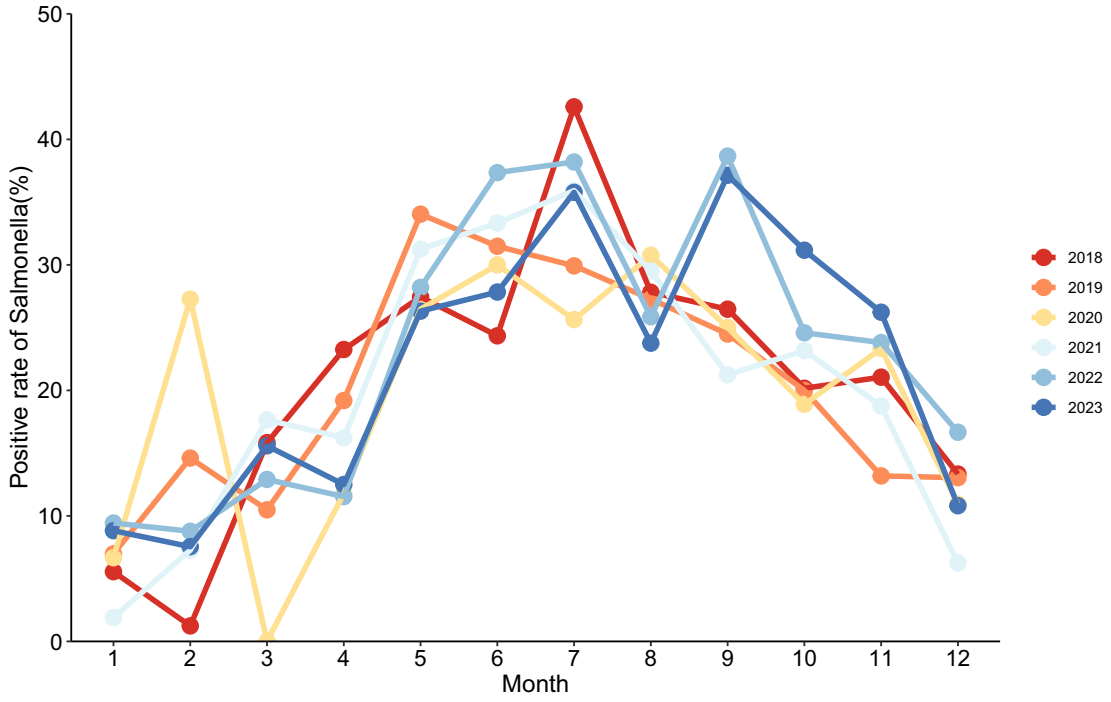

Figure 1 Monthly distribution of *Salmonella* isolates.

Serotype Distribution of Salmonella Isolates

Serogroup B (74.6%) was the predominant *Salmonella* serogroup (Table 2), followed by serogroup C (10.20), D (7.0%), E (4.4%) and ungrouped (2.6%). Notably, *Salmonella* Typhimurium accounted for the major composition of *Salmonella* isolates (63.1%, 823/1304). The classified *Salmonella* Enteritidis and *Salmonella* Stanley was both 2.1% (28/1304),

Table 2 Distribution of 1304 *Salmonella* Isolates in Serogroups and Serotypes

Serogroups and Serotypes	*Salmonella* isolates	
	Number	Proportion (%)
Typhoidal	14	1.1
Salmonella Typhi	1	0.1
Salmonella Paratyphi A	2	0.2
Salmonella Paratyphi B	11	0.8
Non-typhoidal (NTS)	1290	98.9
NTS Serogroup B	973	74.6
Salmonella Typhimurium	823	63.1
Salmonella Agona	5	0.4
Salmonella Stanley	28	2.1
Salmonella Derby	11	0.8
Salmonella Saintpaul	2	0.2
Untyped B	104	8.0
NTS Serogroup C	133	10.2
Untyped C1	90	6.9
Untyped C2	41	3.1
Untyped C	2	0.2

(*Continued*)

Table 2 (Continued).

Serogroups and Serotypes	*Salmonella* isolates	
	Number	Proportion (%)
NTS Serogroup D	91	7.0
Salmonella Enteritidis	28	2.1
Salmonella Dublin	5	0.4
Salmonella Blegdam	16	1.2
Untyped D	42	3.2
NTS Serogroup E	57	4.4
Salmonella London	15	1.2
Salmonella anatum	1	0.1
Salmonella Weltevreden	6	0.5
Untyped E1	30	2.3
Untyped E2	5	0.4
NTS Serogroup F	2	0.2
Untyped F	2	0.2
Ungrouped	34	2.6

respectively. Other serotypes of classified isolates included *Salmonella* Paratyphi B (0.8%, 11/1304), *Salmonella* Derby (0.8%, 11/1304), *Salmonella* London (1.2%, 15/1304) and *Salmonella* Blegdam (1.2%, 16/1304). During the past 6 years, *Salmonella* Typhimurium was always the predominant serotype, and the proportion of *Salmonella* Enteritidis in 2021 was significantly higher than others. The lowest frequency of positive cases was observed in 2020 (Figure 2).

Antibiotic Susceptibility Tests

The antibiotic resistance profiles of *Salmonella* isolates were analyzed followed by dividing *Salmonella* isolates into serotypes of Typhimurium, Enteritidis, Stanley and Other (Table 3, Supplementary Table 1). Statistical difference was

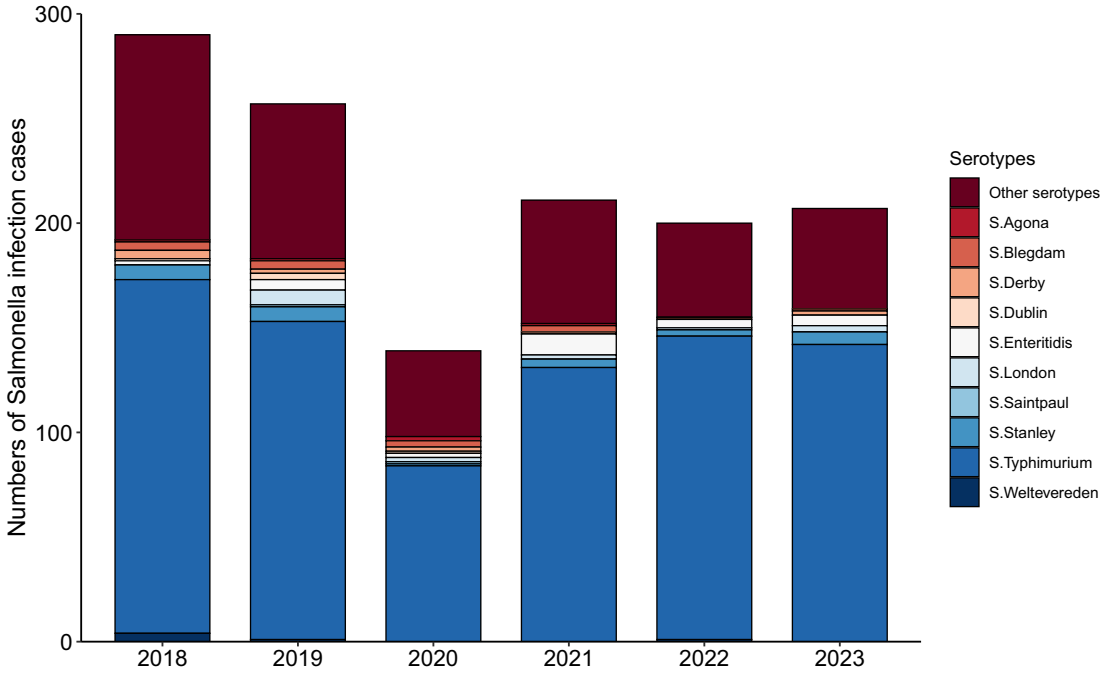

Figure 2 Distribution of *Salmonella* serotypes by years.

Table 3 Resistance of *Salmonella* Isolates to Antimicrobials

Antimicrobials	Typhimurium		Enteritidis		Stanley		Other Serotypes		χ^2	*P*
	R (%)	R/n	R (%)	R/n	R (%)	R/n	R (%)	R/n		
AMP	90.73	(587/647)	86.96	(20/23)	8.33	(2/24)	69.62	(236/339)	131.563[#]	<0.001
AMO	89.47	(221/247)	100.00	(6/6)	8.33	(1/12)	68.10	(111/163)	29.125	<0.001[a]
SAM	79.28	(199/251)	100.00	(6/6)	8.33	(1/12)	60.74	(99/163)	16.855	<0.001[a]
TZP	2.21	(6/271)	0.00	(0/6)	0.00	(0/13)	2.98	(5/168)	–	–
IPM	0.62	(4/641)	0.00	(0/22)	0.00	(0/24)	0.00	(0/327)	–	–
ATM	21.20	(53/250)	0.00	(0/6)	0.00	(0/12)	11.52	(19/165)	6.502	0.011[a]
FEP	10.70	(29/271)	0.00	(0/6)	0.00	(0/13)	4.79	(8/167)	4.668	0.031[a]
CAZ	17.46	(110/630)	4.35	(1/23)	0.00	(0/23)	11.64	(39/335)	5.671	0.017[a]
CTX	34.72	(25/72)	0.00	(0/1)	0.00	(0/2)	22.22	(6/27)	1.427	0.232[a]
CRO	27.11	(177/653)	4.55	(1/22)	0.00	(0/23)	15.32	(51/333)	17.246	<0.001[a]
LEV	0.74	(2/271)	0.00	(0/6)	0.00	(0/12)	0.60	(1/166)	–	–
CIP	6.58	(42/638)	0.00	(0/22)	0.00	(0/22)	8.92	(29/325)	1.726	0.189[a]
SXT	79.28	(199/251)	100.00	(6/6)	8.33	(1/12)	60.74	(99/163)	16.855	<0.001[a]
First-line agents										
0 agent (no resistant)	8.79	(59/671)	13.04	(3/23)	87.50	(21/24)	28.70	(99/345)	123.698[#]	<0.001
1 agent	28.76	(193/671)	69.57	(16/23)	12.50	(3/24)	22.03	(76/345)	29.018	<0.001
2 agents	45.75	(307/671)	17.39	(4/23)	0.00	(0/24)	34.49	(119/345)	17.491	<0.001[b]
3 agents	14.90	(100/671)	0.00	(0/23)	0.00	(0/24)	12.75	(44/345)	0.865	0.393[a]
4 agents	1.79	(12/671)	0.00	(0/23)	0.00	(0/24)	2.03	(7/345)	0.072	0.789[a]
Class Level										
0 class (no resistant)	8.79	(59/671)	13.04	(3/23)	87.50	(21/24)	28.70	(99/345)	123.698[#]	<0.001
1 class	19.82	(133/671)	47.83	(11/23)	8.33	(2/24)	12.46	(43/345)	21.544[#]	<0.001
2 class	36.66	(246/671)	34.78	(8/23)	4.17	(1/24)	27.25	(94/345)	18.326	<0.001
3 class	23.99	(161/671)	4.35	(1/23)	0.00	(0/24)	23.19	(80/345)	0.082	0.815[a]
≥4 class	10.73	(72/671)	0.00	(0/23)	0.00	(0/24)	8.41	(29/345)	1.375	0.269[a]
MDR	34.72	(233/671)	4.35	(1/23)	0.00	(0/24)	31.59	(109/345)	9.749	0.007[b]

Notes: [#]*Fisher's* exact test. [a]Comparison of Typhimurium, Stanley and Other serotypes. [b]Comparison of Typhimurium versus Other serotypes.
Abbreviations: AMP, ampicillin; AMO, amoxicillin; SAM, ampicillin/sulbactam; TZP, piperacillin/tazobactam; IPM, imipenem; ATM, aztreonam; FEP, cefepime; CAZ, ceftazidime; CTX, cefotaxime; CRO, ceftriaxone; LEV, levofloxacin; CIP, ciprofloxacin; SXT, sulfamethoxazole/trimethoprim. R, resistance to antimicrobial agents.
First-line agents: ampicillin (AMP), ceftriaxone (CRO), ciprofloxacin (CIP), sulfamethoxazole/trimethoprim (SXT).

observed in ampicillin (AMP, χ^2=131.563, *P*<0.001) resistance among the four groups. Moreover, the following antimicrobial resistance between Typhimurium and Other serotypes were also displayed statistical differences: amoxicillin (AMO, χ^2=29.125, *P*<0.001), ampicillin/sulbactam (SAM, χ^2=16.855, *P*<0.001), aztreonam (ATM, χ^2=6.502, *P*=0.011), cefepime (FEP, χ^2=4.668, *P*=0.031), ceftazidime (CAZ, χ^2=5.671, *P*=0.017), ceftriaxone (CRO, χ^2=17.246, *P*<0.001), sulfamethoxazole/trimethoprim (SXT, χ^2=16.855, *P*<0.001). These antimicrobial resistances in Typhimurium were significantly higher than the group of other serotypes. Intermediate resistance to ciprofloxacin in *Salmonella* isolates was remarkable among all the antimicrobials, specifically 26.33% in Typhimurium, 45.45% in Enteritidis, 13.64% in Stanley and 21.23% in other serotypes (Supplementary Table 1).

In comparison of first-line agent resistance among the four groups (Table 3), the proportion of no resistance was demonstrated statistically different (χ^2=123.698, *P*<0.001). As was estimated, the proportions of no resistance were Typhimurium 8.79% (59/671), Enteritidis 13.04% (3/23), Stanley 87.50% (21/24), and other serotypes 28.70% (99/345). For 1 agent resistance, the proportions of the four groups were Typhimurium 28.76% (193/671), Enteritidis 69.57% (16/23), Stanley 12.50% (3/24) and other serotypes 22.03% (76/345), and the difference was statistically significant (χ^2=29.018, *P*<0.001). The resistance of the four groups in different class levels displayed similar tendency to the resistance in first-line agents. Notably, the rate of MDR were Typhimurium 34.72% (233/671), Enteritidis 4.35% (1/23) and other serotypes 31.59% (109/345), with statistical difference (χ^2=9.749, *P*=0.007) among them.

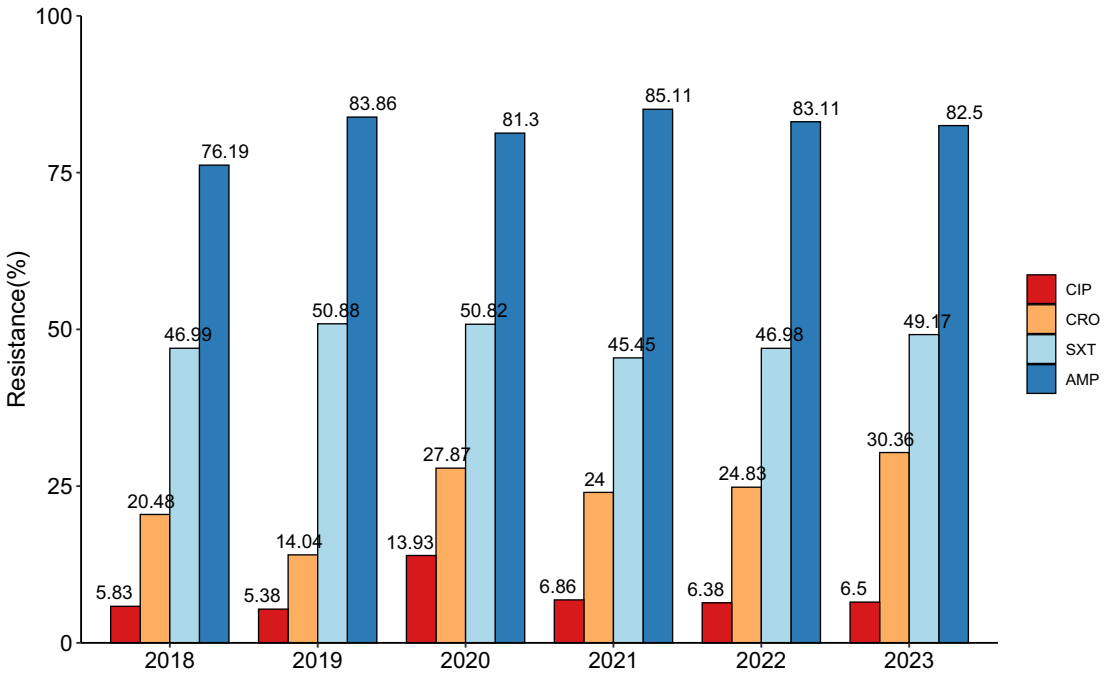

Figure 3 Antimicrobial resistance trends of *Salmonella* isolates to first-line agents from 2018 to 2023.

Among the first-line antimicrobial profiles (Figure 3), the highest resistance rate was AMP. The overall AMP resistance rate from 2018 to 2023 was 76.19%, 83.86%, 81.30%, 85.11%, 83.11% and 82.50%, respectively, with no statistical difference (χ^2=7.127, P=0.211). Also, there was no statistical difference (χ^2=1.832, P=0.872) in SXT resistance among 6 years. However, statistical differences were observed in year distribution of antimicrobial resistance to ceftriaxone (CRO, χ^2=17.026, P=0.004) and ciprofloxacin (CIP, χ^2=182.659, P<0.001). The highest rate of CRO resistance was observed in 2023 (30.36%), while the highest rate of CIP resistance was observed in 2020 (13.93%).

Discussion

Salmonella is one of the leading causes of acute gastroenteritis, with an overall rate of 22.01% from cultural-confirmed tests in this study. From this study, the majority of the cases occurred in children aged under 4 years old, which is consistent with the retrospective studies carried out in other hospitals in Guangzhou, China.[13,29] In a 6-year (2013–2018) surveillance study in Shenzhen,[30] the prevalence of *Salmonella* in children younger than 5 years was 10.1% (137/1361) and in children aged 5–9 years old was 15.1% (11/73), which was lower than the prevalence in this study. Given that Guangzhou and Shenzhen are the two central cities of Guangdong Province that shared with similar economic levels and medical resources, these differences between the studies may be attributed to variation of the number of samples. It was demonstrated in the study of Fujian, China that the proportion of S. Typhimurium and drug-resistance rate was similar to this study.[28] Similar results were also observed in season distributions,[13] and the cases of *Salmonella* (especially NTS) infection were concentrated from June to September.[12,28] Higher environmental temperature was associated with increase of *Salmonella* infections.[31]

The serotype distribution of isolated *Salmonella* varied from regions or countries. In the south of China, S. Typhimurium was the major and dominant serotypes detected from patients,[28,29,32] with the proportion of over 50%, which was also demonstrated in this study. In the southeast of Asia, Vietnam, a relevant study revealed that S. Typhimurium was the most predominant serotype (41.8%) in the NTS isolates.[33] However, in Denmark, the leading non-typhoid *Salmonella* serotypes were S. Enteritidis, monophasic S. Typhimurium and S. Typhimurium.[34] In south America, S. Typhimurium accounted for less than 15% of NTS, although most of the isolates were unclassified.[35] Recently, there were opinions claiming that climate-related foodborne and waterborne diseases have increased and provided possible mitigations against Typhoidal *Salmonella* dissemination.[16] In a nationwide population-based study in Netherlands, the leading serotypes of invasive NTS were

Enteritidis and Typhimurium.[36] An extensive multi-country outbreak of multidrug-resistant monophasic *Salmonella* Typhimurium infection in 10 countries was investigated in 2022, which was linked to chocolate products.[37] The foodborne incidents caused by *Salmonella* are continuous challengeable problems worldwide.

The frequency of multi-drug resistance was common in enteric *Salmonella* isolates. In this study, *Salmonella* Typhimurium attributed to high rate of MDR in 34.72%. The mechanism of MDR occurrence was demonstrated to be related with co-existence of related genes.[38] The transmission of resistance genes may result in great challenge in clinical treatments. Plasmid-mediated quinolone resistance (PMQR) determinants and mutations in quinolone resistance determination regions (QRDRs) were commonly used in assessments of quinolone-resistant genes. High frequency of mutations in *gyr*A, *gyr*B, *par*C, and *par*E genes were found in quinolone-resistant strains,[30] which may be associated with the observed high intermediary resistance to ciprofloxacin in this study. Moreover, high prevalence of intermediate resistance to ciprofloxacin in *Salmonella* isolated from poultry production chain should be paid more attention.[39] Among PMQR determinants, aac(6′)-Ib-cr and oqxA/oqxB were commonly conferred resistance.[40] From this study, the rate of resistance to ceftriaxone in *Salmonella* spp. in 2023 was 30.36%, which was the highest among the past 6 years. The major resistance mechanism of ceftriaxone is the production of AmpC β-lactamases, such as CMY and DHA, and extended-spectrum β-lactamases (ESBL), including TEM, SHV, CTX-M, VEB, and GES.[41] The dissemination of ESBL-producing *Salmonella* spp. aggravates the prevalence of ceftriaxone resistance in children. The evidence above implicated that MDR of *Salmonella* isolates calls for more attention. The prevalence and emergence of MDR isolates suggested that ongoing surveillance of antibiotic resistance are needed.

Indeed, there are also some limits in this study. A larger scale of stool samples, more types of enteric pathogens and clinical information such as syndromes, vaccination and district should be collectively considered. As the gastrointestinal is home to numerous types of microorganisms, the co-infection with multiple pathogens or their communications need to be considered. Accumulating evidence has reported the enteric pathogens co-infection may result in severe outcomes.[42–44] Multiplex polymerase chain reaction assay has been previously used for validation and identification of invasive *Salmonella*.[45] FilmArray Gastrointestinal panel (FAGIP) is a novel multiplex PCR kit used for enteric pathogens detection in infections diarrhea with high sensitivity and efficiency compared to conventional methods.[46,47] Thus, from the evidence above, there would be significant improvement and comprehensive understanding for pediatric enteric infection via updated technology.

Conclusion

In general, prevalence and antimicrobial characteristic enteric *Salmonella* derived from pediatric patients in Guangzhou, China, were retrospectively analyzed. This study showed an overall positive rate of *Salmonella* from 2018 to 2023 in Guangzhou, China, and the infection was most prevalent in summer and autumn. Children under 4 years old were the major infected objects with enteric *Salmonella*. Moreover, this study displayed fluctuation of antimicrobial resistance of overall serotypes of *Salmonella*, specifically *Salmonella* Typhimurium involving ampicillin, ceftriaxone, sulfamethoxazole/trimethoprim and ciprofloxacin during the six years. Differences were observed in antimicrobial resistance between *S.* Typhimurium and other serotypes. This study also implicated potential genotype variants in enteric *Salmonella*, which required larger scale of samples and genotype sequencing for further investigation of mechanism underlying.

There were some limitations in this study: 1) Molecular epidemiological investigation for mechanisms underlying antimicrobial resistance was not conducted in this study. 2) Some of *Salmonella* isolates failed to be typed or grouped and not all isolates were carried out in antimicrobial susceptibility testing. 3) The clinical information and source of samples were limited. To fill these gaps, exploring the molecular mechanisms based on the trends and prevalence of antimicrobial resistance, as well as the distinct features of *Salmonella* isolates in different serotypes would be our future directions. Furthermore, it is crucial to develop large-scale and multi-source investigations for comprehensive understanding in epidemiology and evolution of *Salmonella*.

Data Sharing Statement

The data that support the findings are available from the corresponding author upon non-commercial request.

Ethics Approval

This study was approved by the Medical Ethics Committee of Guangdong Women and Children Hospital, China, and it was conducted according to the ethical guidelines of the Declaration of Helsinki.

Consent to Participants

The informed consent was waived by the Medical Ethics Committee of Guangdong Women and Children Hospital because of the retrospective nature of the study and all data used in this study were strictly anonymous.

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Disclosure

The authors declare that they have no competing interests in publishing this paper.

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