Research Square

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Epidemiology and Antimicrobial Resistance of Salmonella Isolates from Children in China (2017–2024) from a Multicenter ISPED Program

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Abstract

Objective

Salmonella and its increasing antimicrobial resistance (AMR) threaten public health. This study analyzed the epidemiology and AMR profiles of pediatric Salmonella in China to support rational antibiotic use.

Method

A multicenter retrospective study included 17540 Salmonella isolates from ISPED (2017–2024). Antimicrobial susceptibility was tested by disk diffusion and MIC, and analyzed with WHONET.

Results

Most isolates were from feces, peaking in children aged 1–3 years and during June–October. *S. typhimurium* and *S. enteritidis* were predominant. High resistance was observed to ampicillin (77.8%), ampicillin/sulbactam (39.3%), and trimethoprim/sulfamethoxazole (39.3%), while levofloxacin remained highly effective. Resistance differed by serotype, sample type and region, with *S. enteritidis* showing rising resistance to fluoroquinolones and cephalosporins.

Conclusion

Treatment should be individualized according to *Salmonella* serotype, regional epidemiological characteristics and antimicrobial susceptibility. Continuous national antimicrobial resistance surveillance is vital to improve antibiotic stewardship and public health interventions. Based on the multicenter ISPED program, this study clarified the epidemiological features and antimicrobial resistance of *Salmonella* isolates among Chinese children from 2017 to 2024. The findings support targeted public health planning, rational antibiotic use in pediatrics, strengthened *Salmonella* surveillance, and policy development for food safety and childhood infectious disease prevention.

1. Introduction

Salmonella is a genus of non-encapsulated, non-spore-forming, facultative anaerobic Gram-negative bacilli. Most strains within the *Salmonella* genus are unable to ferment lactose, and this distinct biochemical trait is widely employed for the selective isolation, culture, and laboratory identification of this pathogen [1]. *Salmonella* is ubiquitous in the natural environment and commonly colonizes the intestinal tracts of both humans and a wide range of animal hosts. It is transmitted primarily via the fecal-oral route, and represents a clinically significant zoonotic pathogen in both human and veterinary medicine. Additionally, *Salmonella* ranks among the leading causative agents of foodborne illnesses in the United States, with an estimated 1 million cases of infection and 400 associated deaths attributed to this pathogen each year [2]. Globally, approximately 93.8 million cases of gastroenteritis are attributed to *Salmonella* infections [3], with developing countries experiencing over 300,000 deaths annually [3–5]. *Salmonella* species are classified into typhoidal *Salmonella* and non-typhoidal *Salmonella* (NTS) serotypes [6]. In China, NTS is one of the primary bacterial pathogens identified in pediatric patients [7].

Antibiotics are the primary treatment for salmonellosis. However, the unrestrained use of antibiotics in clinical practice and their widespread application in animal husbandry have exacerbated antibiotic resistance in *Salmonella*, leading to increased multidrug resistance (MDR) and expanding resistance profiles, severely compromising the clinical efficacy of conventional antimicrobial treatments. Given its status as a globally predominant foodborne pathogen, the escalating antimicrobial resistance of Salmonella has evolved into a pressing and high-priority public health concern worldwide [8].

To systematically track and monitor the distribution of common bacterial pathogens and dynamic antimicrobial resistance trends among pediatric patients nationwide, the Infectious Disease Surveillance for Pediatrics (ISPED) organization—comprising tertiary teaching children's hospitals across China—annually compiles and analyzes antimicrobial resistance surveillance data from its member institutions. Currently, this project covers 11 provinces and autonomous regions in mainland China, encompassing 13 tertiary pediatric specialty hospitals. This study conducted statistical analysis based on *Salmonella* resistance surveillance data from 2017 to 2024 across twelve ISPED member institutions. Through a retrospective analysis of epidemiological characteristics, antimicrobial resistance profiles, and infection patterns, this study aims to enhance the national understanding of Salmonella infections and further optimize clinical management strategies.

2. Materials and methods

2.1 Strain Isolation and Identification

This retrospective study covered eastern, southern, western, and northern regions of mainland China, encompassing 13 children's hospitals: Children's Hospital of Fudan University, Shanghai; Children's Hospital of Chongqing Medical University, Chongqing; Shenzhen Children's Hospital, Shenzhen, Guangdong; Children's Hospital, Zhejiang University School of Medicine, Hangzhou, Zhejiang; The 2nd Affiliated Hospital and Yuying Children's Hospital of Wenzhou Medical University, Wenzhou, Zhejiang,; Children's Hospital Affiliated to Shandong University, Jinan, Shandong; Shanghai Children's Medical Center Affiliated to Shanghai Jiao Tong University School of Medicine, Shanghai; Xi'an Children's Hospital, Xi'an, Shaanxi; Children's Hospital of Kaifeng City, Kaifeng, Henan; The First Hospital of Jilin University, Changchun, Jilin; Children's Hospital of Wuxi City, Wuxi, Jiangsu; Children's Hospital of Xiamen City, Xiamen, Fujian; Maternal and Child Health Hospital of Inner Mongolia Autonomous Region, Children's Hospital, Hohhot, Inner Mongolia. The research was approved by the

Ethics Committee of the Children's Hospital of Fudan University (Approval No. (2025)191). Clinical Salmonella isolates collected between January 1, 2017, and December 31, 2024, were analyzed, excluding duplicate and contaminated strains.

Specimens were initially inoculated onto appropriate media (e.g., Columbia blood agar, chocolate agar) based on the detection target. For *Salmonella* detection, specimens were inoculated onto selective *Salmonella* agar (Xylose Lysine Deoxycholate, XLD, Komaja)) plates and incubated at 35°C for 18–24 hours. Concurrently, swabs contaminated with specimens were placed in SBG enrichment broth (Komaja) for elution. After 18–24 hours of incubation at 35°C, the enrichment broth is examined for color change. Overnight enrichment broth exhibiting turbidity (≥ 0.5 MacFarland standard) is transferred to XLD agar and incubated at 35°C for 18–24 hours to observe colonies. Subsequently, suspicious colonies (e.g., those exhibiting central black spots on XLD agar plates) were screened and identified using matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS, Bruker Corporation). After identification as *Salmonella*, inoculate onto Krasovitz Bisaccharide Medium and incubate at 35°C for 18–24 hours to observe biochemical reactions. Subsequently, mix the bacterial culture with *Salmonella* diagnostic serum on a microscope slide. The appearance of visible, specific agglutination flocculent patterns indicates the presence of that serotype. *Salmonella* diagnostic serum was purchased from Ningbo Tianrun Biological Pharmaceutical Co., Ltd. The internal quality control (IQC) strain is *Salmonella Typhimurium* ATCC 14028. For EQC, the laboratory participates in the external quality assessment (EQA) program organized by the National Center for Clinical Laboratories (NCCL) of the National Health Commission three times annually.

2.2 Antimicrobial susceptibility testing (AST)

The antibiotic susceptibility testing was performed using the E-test (Taikang Biologicals, China) and disk diffusion methods (Oxoid, UK), in accordance with the reference standards established by the Institute for Clinical and Laboratory Standards M100 and M45, 2024 (Wayne, Pennsylvania, USA). A total of 6 antibiotics were tested: ampicillin, ampicillin/sulbactam, ceftriaxone, azithromycin, levofloxacin and trimethoprim/sulfamethoxazole.

2.3 Statistical analysis

WHONET 2020 was used to analyze antimicrobial susceptibility data. Statistical analysis was performed using SPSS software version 24.0 (IBM, USA), employing the appropriate chi-square test. A *P*-value of less than 0.05 was deemed statistically significant.

3. Results

3.1 Sources of isolates

A total of 17540 *Salmonella* strains were included between 2017 and 2024. Of these, 16630 strains (94.8%) were isolated from fecal specimens, and the remaining 910 strains (5.2%) were from non-fecal sources, including 620 bloodstream isolates, 109 pus specimens, 46 urine samples, and 135 other types of specimens. The age of the included children ranged from 1 day to 17 years, with a median age of 1 year. The largest proportion of isolates (42.6%) was recovered from the 1–3-year age group, followed by the 29 days to 1-year age group (34.2%). *Salmonella* cases showed obvious seasonal variation: 12314 isolates (70.2%) were collected from June to October, with a peak in July (2729 isolates, 15.5%) (Table 1). The geographic distribution of *Salmonella* isolates in mainland China, based on data from institutions participating in the ISPED collaborative group, is presented in Fig. 1.

Table 1
Distribution characteristics of 17540 *Salmonella* strains

Groups	**Number (%)**
Year	**Number (%)**
2017	1633 (9.3)
2018	1469 (8.4)
2019	1847 (10.5)
2020	2188 (12.5)
2021	2821 (16.1)
2022	2188 (12.5)
2023	2548 (14.5)
2024	2846 (16.2)
Month	**Number (%)**
1	318 (1.8)
2	337 (1.9)
3	391 (2.2)
4	769 (4.4)
5	1483 (8.5)
6	2002 (11.4)
7	2729 (15.5)
8	2605 (14.9)
9	2613 (14.9)
10	2365 (13.5)
11	1265 (7.2)
12	663 (3.8)
Age	**Number (%)**
≤ 28d	125 (0.7)
≥ 29d-1y	6001 (34.2)
≥ 1-3y	7470 (42.6)
≥ 3-6y	2447 (14.0)
≥ 6-10y	989 (5.6)
≥ 10y	508 (2.9)
Specimen type	**Number (%)**
Stool	16630 (94.8)
Blood	620 (3.5)
Pus	109 (0.6)
Urine	46(0.3)
Other type	135 (0.8)
Region	**Number (%)**
Eastern region	8926 (50.9)
Southern region	2109(12.0)
Western region	6421(36.6)
Northern region	84(0.5)

3.2 Serotype Distribution of *Salmonella* Isolates

A total of 17540 Salmonella isolates were collected in this study. After excluding 9844 isolates (56.1%) that were only identified to the genus level, 7696 isolates (43.9%) were further characterized to the serogroup and species level. Forty-two distinct Salmonella serotypes were identified among these isolates. Salmonella Typhimurium was the most predominant serotype, accounting for 59.5% (4575/7696), followed by Salmonella Enteritidis at 18.9% (1454/7696). Notably, 18 isolates (0.2%) of Salmonella Typhi, 44 isolates (0.6%) of Salmonella Paratyphi B, 12 isolates (0.2%) of Salmonella Paratyphi A, and 2 isolates (0.02%) of Salmonella Paratyphi C were recovered. Salmonella London was also commonly detected, with 112 isolates (1.5%). All other serotypes each accounted for less than 1% of the total isolates (Table 2).

Table 2
Serotype distribution of 7696 *Salmonella* Isolates

***Salmonella* serogroup**	**Number (%)**	**specific species**	**Number (%)**
A	**12 (0.2)**	Salmonella Paratyphi A	12 (0.2)
B	**5421 (70.4)**	Salmonella Typhimurium	4575(59.5)
		Salmonella Group B (O:4)	688 (8.9)
		Salmonella Paratyphi B	44(0.6)
		Salmonella Agona	41(0.5)
		Salmonella Saintpaul	37(0.5)
		Salmonella Derby	20(0.3)
		Salmonella Braenderup	9(0.1)
		Salmonella Heidelberg	2(0.0)
		Salmonella Wandsworth	1(0.0)
C	**547 (7.1)**	Salmonella Group C	182 (3.0)
		Salmonella London	112(1.5)
		Salmonella Infantis	62(0.8)
		Salmonella Montevideo	31(0.4)
		Salmonella Newport	28(0.4)
		Salmonella Bovismorbificans	23(0.3)
		Salmonella Kentucky	22(0.3)
		Salmonella Thompson	18(0.2)
		Salmonella Choleraesuis	7(0.1)
		Salmonella Muenster	5(0.1)
		Salmonella Javiana	2(0.0)
		Salmonella Paratyphi C	2(0.0)
		Salmonella Typhisuis	2(0.0)
		Salmonella Rissen	1(0.0)
D	**1685 (21.9)**	Salmonella Enteritidis	1454(18.9)
		Salmonella Group D	64(0.8)
		Salmonella Stanley	53(0.7)
		Salmonella Gallinarum	48(0.6)
		Salmonella Dublin	35(0.5)
		Salmonella Typhi	18(0.2)
		Salmonella Muenchen	6(0.1)
		Salmonella Abortusovis	3(0.0)
		Salmonella Indiana	2(0.0)
		Salmonella Panama	2(0.0)
E	**28 (0.4)**	Salmonella Group E	12(0.2)
		Salmonella Anatum	7 (0.1)
		Salmonella Senftenberg	5(0.1)
		Salmonella Livingstone	2(0.0)
		Salmonella Reading	1(0.0)
		Salmonella Weltevreden	1(0.0)
F	**2(0.0)**		

Salmonella serogroup	Number (%)	specific species	Number (%)
M	1(0.0)		
Total	7696 (100)		

3.3 Antimicrobial susceptibility test

In this study, the resistance rates of Salmonella isolates to ampicillin, ampicillin/sulbactam, trimethoprim/sulfamethoxazole, ceftriaxone, azithromycin, and levofloxacin were 77.8%, 39.3%, 39.1%, 25.0%, 10.5%, and 7.3%, respectively (Table 3).

Table 3
Comparison the antibiotic resistance rates of *Salmonella Typhimurium*, *Salmonella Enteritidis* and other serotype

Antibiotic	Total		*Salmonella Typhimurium*		*Salmonella Enteritidis*		Other serotype		*P*
	N	R (%)	N	R (%)	N	R (%)	N	R (%)	
Ampicillin	16070	77.8	3759	85.5	1346	81.1	1451	65.5	< 0.001
Ampicillin/Sulbactam	11642	39.3	2222	28.3	1200	32.4	1247	39.6	< 0.001
Ceftriaxone	15333	25.0	3920	26.9	1415	16.3	1449	19.4	< 0.001
Azithromycin	4843	10.5	1957	8.3	835	1.9	766	19.6	< 0.001
Levofloxacin	10799	7.3	1913	6.9	881	9.4	977	8.2	0.061
Trimethoprim/Sulfamethoxazole	16813	39.1	4220	44.6	1435	12.2	1582	39.2	< 0.001

Note: The *P*-value is derived from the chi-square test analysis of the number of cases.

Our results demonstrated statistically significant differences in antimicrobial resistance rates among different *Salmonella* serotypes. The resistance rates of *Salmonella Typhimurium* to ampicillin, ceftriaxone, and trimethoprim/sulfamethoxazole were significantly higher than those of *Salmonella Enteritidis* and other serotypes. In contrast, the resistance rates of other serotypes to ampicillin/sulbactam and azithromycin were significantly higher than those of *Salmonella Typhimurium* and *Salmonella Enteritidis* (Table 3).

Among *Salmonella Typhimurium* isolates, the resistance rates to ampicillin and ampicillin/sulbactam showed an increasing trend from 2017 to 2024, whereas the rate for trimethoprim/sulfamethoxazole exhibited a decreasing trend. Resistance rates to ceftriaxone, azithromycin, and levofloxacin showed no statistically significant changes over the study period (Fig. 2A, Table S1). For *Salmonella Enteritidis* isolates, the resistance rates to ampicillin, ampicillin/sulbactam, ceftriaxone, levofloxacin, and trimethoprim/sulfamethoxazole all demonstrated statistically significant increasing trends from 2017 to 2024 (Fig. 2B, Table S2). For other *Salmonella* serotypes, the resistance rates to ampicillin, ampicillin/sulbactam, azithromycin, and trimethoprim/sulfamethoxazole showed statistically significant decreasing trends between 2017 and 2024, while the resistance rate to levofloxacin displayed a marked upward trend (Fig. 2C, Table S3).

Significant regional differences in antimicrobial resistance rates were also observed. Among *Salmonella Typhimurium* isolates, the ampicillin resistance rate in the eastern region was significantly lower than those in the southern, western, and northern regions. The southern region exhibited significantly higher resistance rates to ampicillin/sulbactam and trimethoprim/sulfamethoxazole compared with the other three regions. The western region had the highest ceftriaxone resistance rate, while the northern region showed a higher levofloxacin resistance rate than the other three regions (Fig. 3A). Among *Salmonella Enteritidis* isolates, resistance rates to ampicillin/sulbactam, ceftriaxone, and levofloxacin were significantly higher in the northern region than in the other three regions. The highest ampicillin resistance rate was detected in the southern region, whereas the highest trimethoprim/sulfamethoxazole resistance rate was found in the western region (Fig. 3B). Among other *Salmonella* serotypes, resistance rates to ampicillin, ampicillin/sulbactam, and trimethoprim/sulfamethoxazole were significantly higher in the western region than in the other three regions. The eastern region displayed a higher levofloxacin resistance rate compared with the other three regions (Fig. 3C).

Statistically significant differences in antimicrobial resistance rates were also observed among *Salmonella* isolates from different specimen types. Among *Salmonella Typhimurium* isolates, the resistance rate to ampicillin was significantly higher in fecal isolates than in blood isolates (85.8% vs. 59.2%). Conversely, the resistance rate to ceftriaxone was higher in blood isolates than in fecal isolates (16.7% vs. 6.6%). Among *Salmonella Enteritidis* isolates, the resistance rate to ampicillin/sulbactam was significantly higher in blood isolates than in fecal isolates (55.6% vs. 30.1%). For other Salmonella serotypes, the resistance rates to ampicillin and trimethoprim/sulfamethoxazole were significantly higher in fecal isolates than in blood isolates (66.9% vs. 48.0% and 40.5% vs. 20.6%, respectively) (Table 4).

Table 4
Differences in antibiotic resistance ratesamong *Salmonella Typhimurium*, *Salmonella Enteritidis*, and other serotypes isolated from different sample s

Antibiotic	*Salmonella Typhimurium*			*Salmonella Enteritidis*			Other serotype	
	Stool %(N)	Blood %(N)	*P*	Stool %(N)	Blood %(N)	*P*	Stool %(N)	Blood %(N)
Ampicillin	85.8(3155/3677)	59.2(29/49)	< 0.001	82.0(988/1205)	74.5(76/102)	0.062	66.9(888/1328)	48.0(47/
Ampicillin/Sulbactam	28.1(612/2182)	38.5(10/26)	0.243	30.1(330/1093)	55.6(40/72)	< 0.001	40.0(467/1168)	34.4(21/
Ceftriaxone	27.1(1037/3830)	21.3(10/47)	0.371	15.7(197/1259)	20.0(22/110)	0.242	19.7(262/1332)	14.1(13/
Azithromycin	8.3(160/1928)	6.7(1/15)	1.000*	2.0(16/814)	0.0(0/15)	1.000*	19.6(144/733)	5.3(1/19
Levofloxacin	6.6 (122/1846)	16.7(6/36)	0.032*	9.0(66/736)	7.8(8/103)	0.687	7.8(70/895)	5.0(3/60
Trimethoprim/Sulfamethoxazole	44.4(1829/4119)	47.2(25/53)	0.687	11.5(147/1280)	14.6(16/110)	0.338	40.5(586/1448)	20.6(22/

Note: The *P*-value is derived from the chi-square test analysis of the number of cases, *: Fisher's Exact Test.

Discussion

The prevalence and distribution of *Salmonella* present a substantial threat to public health and impose a considerable economic burden [9]. This multicenter study conducted by the ISPED Collaborative Group enrolled more than 15000 *Salmonella* isolates from 13 tertiary pediatric hospitals across mainland China. Owing to the large sample size and the wide geographic distribution of ISPED member hospitals covering eastern, southern, western, and northern China, our findings reliably depict the current antimicrobial resistance profile of pediatric *Salmonella* isolates in mainland China.

This study systematically characterized the epidemiological and etiological features of *Salmonella* infections in mainland China from 2017 to 2024. A total of 17540 cases were enrolled during the study period. The median age of pediatric patients with Salmonella infection was 1 year, with infections occurring predominantly in the 1–3-year age group, followed by the 29 days to 1-year and 3–6-year age groups. This susceptibility may be attributed to the immature immune function and underdeveloped gastrointestinal mucosal barrier in young children, rendering them more vulnerable to foodborne pathogens compared with other age groups [10]. Moreover, caregivers tend to be highly alert to gastrointestinal symptoms in children and seek prompt medical attention for suspected *Salmonella* infection [11].

Our data revealed a marked seasonal pattern, with a significant increase in *Salmonella* infections during warm months, especially in summer. Consistent with previous studies, higher *Salmonella* infection rates have been documented in warmer climates [12, 13]. In hot weather, increased consumption of raw, cold, or undercooked foods — including fresh, frozen, and refrigerated products such as meat and dairy items — has been recognized as an important risk factor for *Salmonella* transmission [14]. In addition, warm and humid environmental conditions favor the proliferation and survival of *Salmonella*, further contributing to the elevated infection rate during summer.

The circulating serotypes of *Salmonella* differ globally, and previous studies have identified distinct serotype distributions between pediatric and adult populations [15]. Nevertheless, *Salmonella Typhimurium* and *Salmonella Enteritidis* remain the most prevalent serotypes worldwide [16] and are widely distributed in developing countries [17]. In China, approximately 70%–80% of foodborne diseases are attributed to salmonellosis, with varying serotype prevalence across different provinces. *Typhimurium* and *Enteritidis* are regarded as dominant and classic serotypes in China, with *Typhimurium* being the most commonly reported serotype in most regions [18–20].

The serotyping results from the present study demonstrated that *Salmonella Typhimurium* and *Salmonella Enteritidis* were the predominant pathogenic serotypes in Chinese children, which is consistent with previous findings [21–23]. A variety of other serotypes were also identified in this study, including *Salmonella Stanleyi*, *Salmonella Derby*, *Salmonella Paratyphi*, and *Salmonella Indiana*, suggesting a highly diverse serotype distribution among pediatric *Salmonella* infections in mainland China.

Antimicrobial resistance represents a major threat in the control and management of *Salmonella* infections [24]. Accumulating evidence has demonstrated that the overuse of antibiotics in clinical settings and animal husbandry has contributed to the rapid emergence and dissemination of drug-resistant strains [24, 25]. In the present study, most of the isolated *Salmonella* strains exhibited high resistance to ampicillin, with a resistance rate exceeding 50%. Since ampicillin is one of the earliest and most widely used antibiotics in China's livestock industry, and meat products serve as the main source of human *Salmonella* infection [26], such high resistance is most likely attributable to the inappropriate use of antibiotics in animal farming. Accordingly, high ampicillin resistance was predominantly detected in *Salmonella Typhimurium* and *Salmonella Enteritidis* [27].

In addition, high resistance rates to cephalosporins and trimethoprim/sulfamethoxazole were also observed, consistent with previous reports [28]. Although the resistance rates to trimethoprim/sulfamethoxazole in *Salmonella Typhimurium* and other serotypes showed a decreasing trend, they still remained at relatively high levels. In contrast, the resistance rate of *Salmonella Enteritidis* to trimethoprim/sulfamethoxazole exhibited a significant upward trend. Zhou et al. [25] reported resistance rates of 75.6% for ampicillin and 45.2% for trimethoprim/sulfamethoxazole, respectively. As these agents are commonly used as first-line treatments for salmonellosis, the reduced efficacy of these antibiotics is of great concern and is closely associated with their extensive application.

The levofloxacin resistance rate in this study was 7.3%, which was significantly lower than the 23.1% reported in a previous study [28]. This discrepancy may be explained by the predominantly pediatric population enrolled in the present study. Because of potential adverse effects, including central nervous system toxicity and arthropathy, levofloxacin is generally not recommended for the treatment of pediatric patients with Salmonella infections [29]. Furthermore, our results revealed an increasing trend in resistance to third-generation cephalosporins among *Salmonella* isolates, especially ceftriaxone, with a resistance rate of 25.0%, which was higher than the 22.4% reported in a previous study from Zhejiang Province [30]. We also observed a marked upward trend in fluoroquinolone resistance among Salmonella Enteritidis and other serotypes, as well as a significant increase in cephalosporin resistance in Salmonella Enteritidis. Given that these antimicrobial agents are frequently used for the clinical management of foodborne salmonellosis, the rising resistance trends pose a substantial threat to both animal and human health [31, 32].

This study performed a retrospective analysis of the epidemiological characteristics and antimicrobial resistance profiles of *Salmonella* infections among pediatric patients in China from 2017 to 2024. The results showed that the incidence of *Salmonella* infections peaked in summer and autumn. Children under 6 years of age were identified as the primary high-risk population for intestinal *Salmonella* infections. Furthermore, the study revealed distinct differences in antimicrobial resistance patterns among different serotypes and across geographic regions.

Several limitations should be acknowledged: the molecular mechanisms underlying Salmonella antimicrobial resistance were not explored in this study; Antimicrobial susceptibility testing was not conducted for all isolates, which will be a key focus in our future research. Despite these limitations, this retrospective analysis offers the most comprehensive profile to date of epidemiological characteristics and antimicrobial resistance patterns of *Salmonella* infection among children in China. Continuous surveillance of serotype distribution and antimicrobial resistance trends is essential for the prevention and control of pediatric *Salmonella* infection, as well as for guiding rational clinical antimicrobial administration.

This 8-year multicenter investigation systematically delineates the epidemiological landscape and antimicrobial resistance profiles of *Salmonella* isolates from Chinese children, bearing important implications for public health practice and policy formulation. First, the prevailing serotypes and distinct resistance patterns identified in this study underscore the necessity of strengthening surveillance on foodborne *Salmonella* transmission, given that children constitute a high-risk population for *Salmonella* infection. Second, the rising antimicrobial resistance of *Salmonella* isolates highlights an urgent need to promote rational antibiotic use in pediatric clinical practice. Health authorities should reinforce the regulation of antibiotic prescriptions and scale up antimicrobial stewardship programs in primary and secondary healthcare institutions. Third, multicenter data from the ISPED program can provide an evidence-based reference for revising national guidelines on the prevention and control of childhood *Salmonella* infection, and facilitate the optimization of preventive strategies including health education and food safety supervision. Finally, the present findings enrich the global epidemiological database of childhood *Salmonella*, advance international collaboration on curbing the transmission of drug-resistant *Salmonella*, and help safeguard global public health security.

Conclusion

This multicentre ISPED study analysed 17540 *Salmonella* isolates from 13 paediatric hospitals in mainland China. *Salmonella* infections were predominant in children aged 1–3 years and peaked in summer. High resistance rates were detected to ampicillin, ampicillin/sulbactam, and trimethoprim/sulfamethoxazole, while resistance to azithromycin and levofloxacin remained relatively low. Antimicrobial resistance profiles differed significantly by serotype, geographic region, and specimen type. Temporal trends from 2017 to 2024 varied across serotypes, with increasing resistance to multiple agents in *Salmonella Enteritidis* and contrasting trends in *Salmonella Typhimurium* and other serotypes. These findings highlight the substantial regional and serotype-specific variations in paediatric *Salmonella* resistance and support targeted antimicrobial stewardship and surveillance in children.

Declarations

Ethics approval and consent to participate:

The study protocol was approved by the Ethics Committee of the Children's Hospital of Fudan University (No. (2025)191). This study was conducted according to the guidelines laid down in the Declaration of Helsinki. The need for Informed Consent was waived by the Ethics Committee of the Children's Hospital of Fudan University due to the retrospective nature of the study. All authors have approved the final article.

Consent for publication:

Not Applicable. This study did not include any identifying images, personal or clinical details of participants that could compromise anonymity, so no consent for publication from patients is required.

Availability of data and materials:

The data supporting this study's findings are available from the corresponding author upon reasonable request, and all relevant data on childhood *Salmonella* epidemiology and antimicrobial resistance (2017–2024) are organized and included in the manuscript and supplementary materials.

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Figures



Figure 1

Regional distribution of 17540 *Salmonella* isolates on the map of China

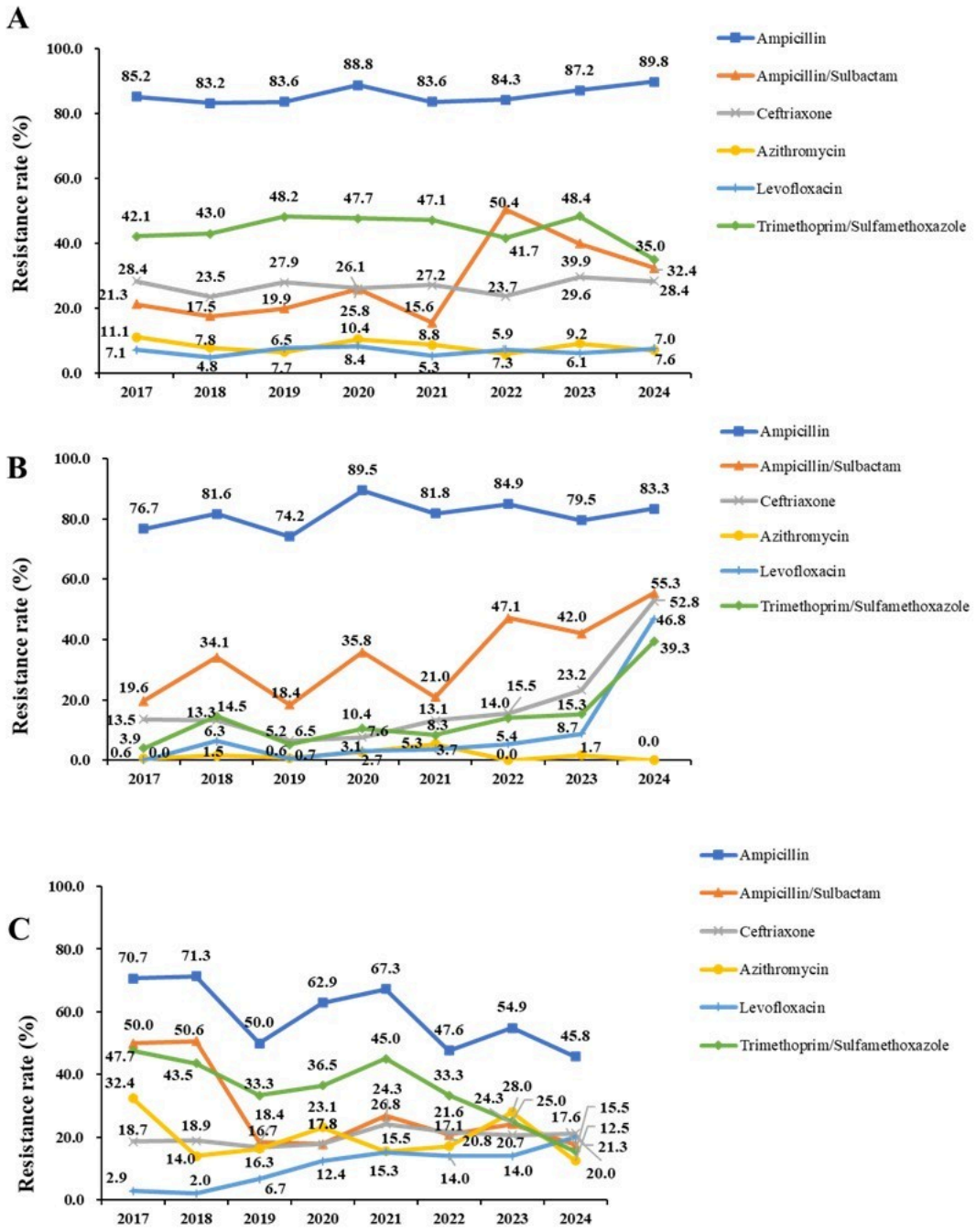


Figure 2

Resistance rates (%) of*Salmonella Typhimurium* (A), *Salmonella Enteritidis*(B), and other serotype (C) to six main antimicrobials, as reported by the ISPED program in 2017 to 2024.Among *Salmonella Typhimurium* isolates, the resistance rates to ampicillin and ampicillin/sulbactam showed an increasing trend from 2017 to 2024, whereas the rate for trimethoprim/sulfamethoxazole exhibited a decreasing trend. For *Salmonella Enteritidis* isolates, the resistance rates to ampicillin, ampicillin/sulbactam, ceftriaxone, levofloxacin, and trimethoprim/sulfamethoxazole all demonstrated statistically significant increasing trends from 2017 to 2024. For other Salmonella serotypes, the resistance rates to ampicillin, ampicillin/sulbactam, azithromycin, and trimethoprim/sulfamethoxazole showed statistically significant decreasing trends between 2017 and 2024, while the resistance rate to levofloxacin displayed a marked upward trend.

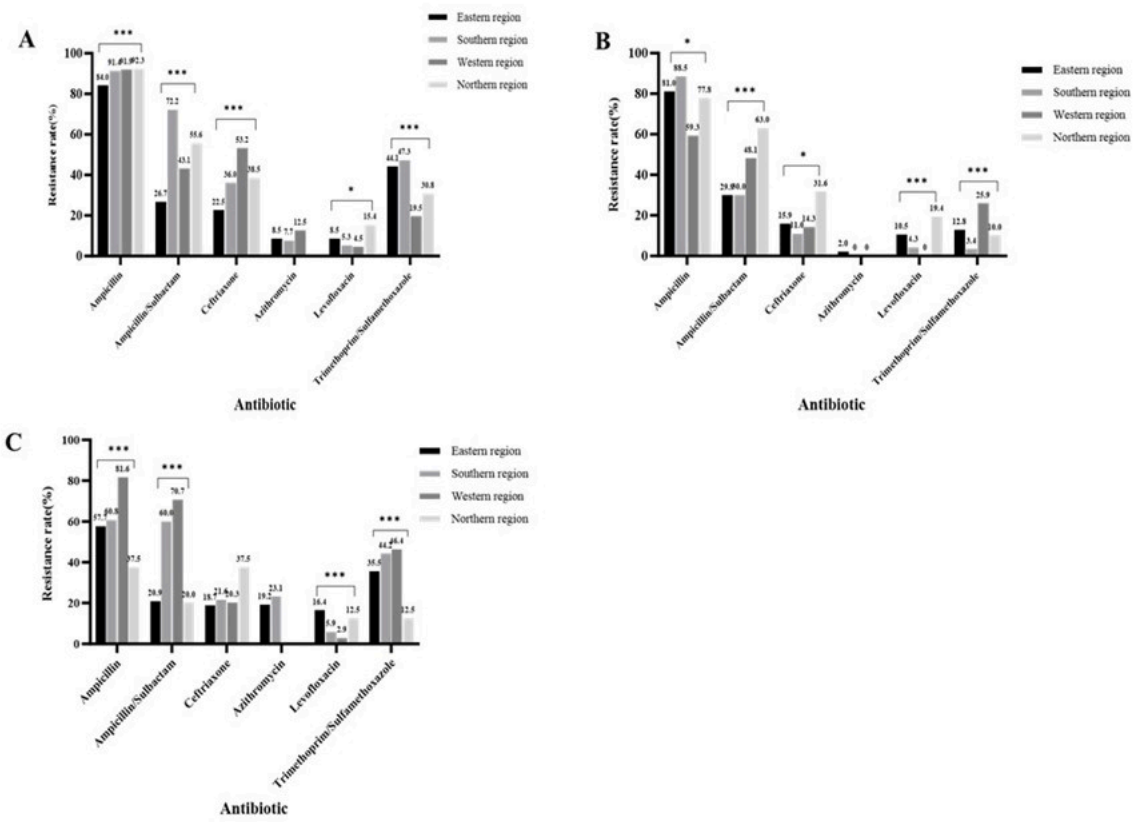


Figure 3

Differences in antibiotic resistance rates among *Salmonella Typhimurium* (A), *Salmonella Enteritidis* (B), and other serotypes (C) across different regions. Among *Salmonella Typhimurium* isolates, the ampicillin resistance rate in the eastern region was significantly lower than those in the southern, western, and northern regions. The southern region exhibited significantly higher resistance rates to ampicillin/sulbactam and trimethoprim/sulfamethoxazole compared with the other three regions. The western region had the highest ceftriaxone resistance rate, while the northern region showed a higher levofloxacin resistance rate than the other three regions. Among *Salmonella Enteritidis* isolates, resistance rates to ampicillin/sulbactam, ceftriaxone, and levofloxacin were significantly higher in the northern region than in the other three regions. The highest ampicillin resistance rate was detected in the southern region, whereas the highest trimethoprim/sulfamethoxazole resistance rate was found in the western regio. Among other *Salmonella* serotypes, resistance rates to ampicillin, ampicillin/sulbactam, and trimethoprim/sulfamethoxazole were significantly higher in the western region than in the other three regions. The eastern region displayed a higher levofloxacin resistance rate compared with the other three region.

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