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Original Article

Molecular typing characteristics and drug resistance of *Salmonella* from food-borne diarrhea patients in Chifeng, China

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Abstract

Introduction: This study aimed to investigate the infection status, serotype distribution, drug resistance, and molecular typing characteristics of *Salmonella* in food-borne diarrhea patients in Chifeng, China, from 2022 to 2024.

Methodology: Fecal samples were collected from diarrhea patients for *Salmonella* isolation and molecular serotype identification. The isolates were tested using the microbroth dilution method and pulsed-field gel electrophoresis (PFGE) to assess drug susceptibility and perform molecular typing. Statistical analysis was conducted using the SPSS 25.0 software.

Results: *Salmonella* was detected in 52 of the 737 fecal samples, yielding a positive detection rate of 7.06% (52/737). A total of 52 *Salmonella* strains were isolated, predominantly *Salmonella Typhimurium* and *Salmonella Enteritidis*, which accounted for 40.38% (21/52) and 21.15% (11/52), respectively. Additionally, 5 other serotypes were identified: *S. Kentucky*, *S. Dublin*, *S. Liverpool*, *S. Vilshaw*, and *S. Paratyphoid A*. Notably, 48 strains (92.31%, 48/52) exhibited resistance to at least one antibiotic, with resistance rates exceeding 50% for ampicillin, streptomycin, tetracycline, and nalidixic acid. The rate of multiple drug resistance reached 86.54% (45/52). Cluster analysis of the 52 *Salmonella* strains revealed 39 band types with similarity indices ranging from 50.1% to 100%. Notably, a higher similarity coefficient indicated greater similarity in drug resistance phenotypes among the strains.

Conclusions: The detection rate of *Salmonella* among food-borne diarrhea patients in Chifeng from 2022 to 2024 was notably high. The predominant serotypes were *S. Typhimurium* and *S. Enteritidis*. The PFGE band types were relatively diverse, and the strains exhibited significant drug resistance, including multiple drug resistance.

Key words: foodborne infections; *Salmonella*; serotype distribution; antimicrobial resistance; PFGE typing.

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Introduction

Salmonella is a significant diarrheal pathogen known for its adaptability to various environments, facilitating its extensive dissemination throughout the food chain, from animal intestines to contaminated food and water sources [1]. The classification system for *Salmonella* is complex, comprising over 2,600 serotypes, primarily divided into two main groups: *Salmonella enterica* and *Salmonella bongori*. Most human infections are attributed to *Salmonella enterica*, which is further classified into 6 subspecies, with *Salmonella enterica* subspecies *enterica* being the most relevant to human health. This subspecies includes more than 1,500 serotypes, among which *S. Typhimurium* and *S. Enteritidis* are particularly notable, as they account for a substantial proportion of salmonellosis cases worldwide [2]. The diversity of serotypes is associated with varying pathogenic potential and drug resistance, making it a crucial factor in the epidemiology of salmonellosis.

Salmonella represents a significant global public health concern and is among the leading causes of foodborne illnesses. Infections caused by *Salmonella* are predominantly associated with gastrointestinal symptoms, which commonly include diarrhea, fever, abdominal cramps, nausea, and vomiting. In severe instances, these infections can lead to sepsis and even death. Annually, *Salmonella* is responsible for an estimated 9.4 million infections and 115,000 fatalities worldwide, with developing countries experiencing a particularly severe impact. There has been a troubling increase in antibiotic resistance among *Salmonella* in recent years, particularly concerning non-typhoid *Salmonella* (NTS) strains that exhibit multidrug resistance (MDR), presenting a substantial public health challenge. Infections caused by these resistant strains are generally more severe than those caused by susceptible strains [3]. The emergence of MDR *Salmonella* strains has exacerbated the clinical management of these infections, as resistance to first-line antibiotics such as ampicillin, tetracycline, and fluoroquinolones continues to rise. For instance, studies

have shown that over 40% of *Salmonella* isolates exhibit resistance to tetracycline, nalidixic acid, and amoxicillin, while resistance to third-generation cephalosporins and carbapenems remains a growing concern [4].

The clinical implications of antimicrobial resistance (AMR) in *Salmonella* are profound, particularly in vulnerable populations such as children, the elderly, and immunocompromised individuals. Invasive salmonellosis, a severe form of infection where *Salmonella* crosses the intestinal mucosa into the bloodstream, is associated with higher mortality rates and prolonged hospital stays, especially when caused by MDR strains. For example, in sub-Saharan Africa, invasive NTS infections in children under 5 years of age have been linked to mortality rates of 20–30%, with resistance to fluoroquinolones and extended-spectrum cephalosporins being a major contributing factor [5]. Furthermore, the presence of virulence genes such as *invA*, *mgtC*, and *sirA* in MDR *Salmonella* isolates underscores their pathogenic potential and ability to cause severe systemic infections [6].

The role of the food chain in the transmission of AMR *Salmonella* cannot be overstated. Contaminated poultry, eggs, dairy products, and fresh vegetables are primary vehicles for *Salmonella* transmission, with poultry being a particularly significant reservoir of MDR strains. Studies have identified *Salmonella* serovars such as Enteritidis, Typhimurium, and Infantis as the most common culprits in foodborne outbreaks, with resistance patterns showing high levels of resistance to trimethoprim/sulfamethoxazole, cefazolin, and tetracycline [7]. The detection of resistance genes such as bla_{TEM}, $bla_{\text{CTX-M}}$, and $bla_{\text{CMY-2}}$ in *Salmonella* isolates from food sources highlights the genetic mechanisms underlying AMR and the potential for these genes to spread across bacterial species [8]. Despite the implementation of control measures in food animal production, the incidence of *Salmonella* infections has not significantly decreased in many regions, indicating that the dynamics of *Salmonella* in food production and processing systems remain poorly understood [9]. The emergence of new serotypes and the evolving patterns of *Salmonella* strains associated with poultry and other foods further complicate the food safety landscape. Therefore, understanding the epidemiology of *Salmonella* is crucial for identifying the sources and transmission routes of infection. Targeted public health initiatives aimed at reducing the incidence of salmonellosis, particularly by focusing on specific serotypes, are essential for developing effective prevention and control strategies [10].

This study systematically investigated the infection status, epidemic characteristics, serotype distribution, drug resistance, and pulsed-field gel electrophoresis (PFGE) typing characteristics of *Salmonella* in foodborne diarrhea patients in Chifeng, China, from 2022 to 2024. The objective was to provide data support for the prevention and control of *Salmonella* foodborne diseases and to inform clinical drug usage.

Methodology

Materials

Fecal samples and clinical data were collected from 737 diarrhea patients at 2 sentinel hospitals in Chifeng City from March to November 2022–2024. Cases defined as infections were characterized by 3 or more daily defecations and abnormal stool characteristics, including watery stool, mucous stool, and stools containing pus or blood. The primary symptom was diarrhea, accompanied by a self-reported history of suspicious food consumption.

Informed consent was obtained from patients for the collection of case information, and key patient information was anonymized and protected. Additionally, the study was reviewed by the Ethical Review Committee of the Chifeng Center for Disease Control and Prevention.

Fecal samples were collected aseptically, stored in Cary-Blair transport medium (Haibo Biotechnology Co., LTD, HBPT004, Qingdao, China) at 4 °C, and sent to the microbiology laboratory for pathogen isolation and culture within 24 hours.

Salmonella isolation

The procedures for the isolation and identification of *Salmonella* were conducted in accordance with the National Foodborne Disease Surveillance Manual [11]. Fresh fecal samples were inoculated into Selenite Brilliant Green (SBG) sulfanilamide solution for pre-incubation and cultured at 36 °C for 18 to 24 hours. Subsequently, the bacterial solution was inoculated onto Xylose Lysine Desoxycholate (XLD) agar plates (Beijing Landbridge Technology Co., LTD., PB030A, Beijing, China) and cultured at 36 °C for an additional 18 to 24 hours, during which 5 suspected colonies were selected. These colonies were then inoculated onto Triple Sugar Iron (TSI; Beijing Landbridge Technology Co., LTD., M150, Beijing, China) and nutrient agar (NA; Beijing Landbridge Technology Co., LTD., PB005A, Beijing, China) and cultured at 36 °C for 18 to 24 hours. Cultures that conformed to the primary biochemical reactions characteristic of *Salmonella* were identified using the VITEK 2 Compact automatic

microbial identification instrument (Biomeerieux, Lyon, France), followed by further identification using a matrix-assisted laser desorption/ionization time of flight mass spectrometry (MALDI-TOF) mass spectrometer (Bruker, Microflex LRF, Munich, Germany).

Serotype identification

A DNA extraction kit (Beijing Zhuochenghui Shengsheng Biotechnology Co., Ltd., Beijing, China) was utilized to isolate the nucleic acids of the *Salmonella* strain, and molecular serotype identification was conducted using the polymerase chain reaction (PCR)-probe method. The procedure was conducted in accordance with the instructions provided with the molecular identification kit (Beijing Meizheng Biotechnology Co., LTD, LR706F2, Beijing, China) for *Salmonella* serotyping. The serotype was initially determined based on the detection results, followed by further verification using diagnostic serum (Ningbo Tianrun Biological Pharmaceutical Co., LTD, TR101, Ningbo, China).

Antibiotic resistance test

Antimicrobial susceptibility testing was performed by the minimal inhibitory concentration (MIC) method using the Gram-negative plate (For details on the concentrations of each antibiotic, please refer to the product manual; Shanghai Fosun Biological Technology Co., Ltd., A-5, Shanghai, China), and the sample was added using the Fully Automatic Drug Susceptibility Sampler (Thermo Fisher Scientific, V3020, Waltham, USA). AMR of *Salmonella* strains was assessed using the microbroth dilution method. The quality control strains employed were ATCC25922 (Nanjing Lecun Biotechnology Company, Nanjing, China). Bacterial colonies were selected from blood agar medium (Beijing Luqiao, Beijing, China) and dissolved in sterile water to create a 0.5 McF bacterial suspension. Subsequently, 60 μL of this bacterial suspension was inoculated into Mueller-Hinton broth and then introduced into each well of the drug sensitivity plate using an automatic sampling apparatus. The cultures were incubated at 36 °C for 18 to 24 hours. The drug sensitivity of 11 classes and 17 types of antibiotics was evaluated according to the guidelines of the Gram-negative aerobic drug sensitivity test board. The antibiotics tested included: ampicillin (AMP), tetracycline (TET), ampicillin/sulbactam (AMS), meropenem (MEM), polymyxin E (CT), ertapenem (ETP), ceftazidime/avibactam (CZA), tigecycline (TIG), cefotaxime (CTX), ceftazidime (CAZ), ciprofloxacin (CIP), azithromycin (AZI), chloramphenicol (CHL), nalidixic acid (NAL), streptomycin (STR), sulfamethoxazole/trimethoprim (SXT), and amikacin (AMK). The results for sensitivity, intermediate resistance, and resistance were determined based on the standards set by the American Clinical Laboratory Standards Institute in 2021 [12]. *Salmonella* isolates were defined as MDR when they exhibited resistance to three or more antimicrobial classes [13].

Molecular typing by PFGE

Pulsed field gel electrophoresis (PFGE) was employed for the molecular typing of *Salmonella* strains. Reagents for the PFGE test were acquired from Solebar Biotechnology Co., Ltd. (Beijing, China), and the restriction endonuclease *Xba* I used for enzyme digestion was sourced from TaKaRa (1093A; Tokyo, Japan). The PFGE instrument uses CHEF MAPPER from Bio-Rad to assess the genetic relationships among the isolates. Following the methodology outlined by Uysal *et al*., PFGE was conducted on pure cultured bacteria in accordance with PulseNet's standardized protocol for *Salmonella* [14].

Bacteria were inoculated on blood agar plates, and colonies were selected and ground in cell suspension buffer (100 mM EDTA, 100 mM Tris, pH 8.0), adjusting the cell concentration to 0.8–1.0 at 610 nm. Subsequently, 20 mL of proteinase K (20 mg/mL) was added to 200 mL of the cell suspension and mixed with 200 mL of 1% SeaKem gold agarose (Lonza, Basel, Switzerland). A total of 300 mL of the agarose mixture was then placed into plug mold of Bio-Rad Laboratories (Hercules, USA) and allowed to solidify. The solidified agarose gel was transferred to a lysis buffer containing 25 mL of protease K (20 mg/mL) (50 mM Tris, 50 mM EDTA, 1% Sarkosyl, pH 8.0) and incubated in a constant temperature water bath at 54 °C (150–175 rpm) for 2 hours. The rubber block was washed with sterile ultrapure water in an oscillating constant temperature incubator 4 times, with each wash lasting 15 minutes. The agarose gel stopper containing DNA was then cut into small pieces (2 mm wide) and digested with *Xba* I (50 U) at 37 °C for 2 hours. The small rubber block was placed on the comb, and electrophoresis was conducted with a 1% SeaKem agarose gel prepared with 0.5 × TBE buffer. The program was set to operate at 14 °C for 18 hours at 6 V/cm, with a duration from 2.12 to 63.8 seconds. The agarose gel was stained with GelRed (1 mg/mL) and visualized using a molecular gel imager (Tanon Mini Space 2000, Beijing, China). BioNumerics 7.6 [15] software was employed to

standardize and cluster the electrophoretic maps. The clustering method utilized was the unweighted group average method, with a tolerance of 1.5% for the difference between the optimal value and strip position. *Salmonella* H9812 was employed as the standard control strain [16].

Statistical analyses

Statistical analyses were conducted using SPSS version 25.0 (IBM Corp, Armonk, NY, USA). χ^2 test or Fisher's exact test was employed for group comparisons, with a significance level set at $p < 0.05$.

Results

Epidemiological characteristics of Salmonella infection

Out of the 737 fecal samples analyzed, 52 tested positive for *Salmonella*, resulting in a prevalence rate of 7.06% (52/737). The majority of these positive cases were observed in infants aged 0–5 years, who accounted for 50.00% (26/52) of the total. The cases were predominantly reported during the summer months, comprising 96.15% (50/52) of the positive samples. Among the suspected sources of infection, food products represented the highest proportion, accounting for 23.08% (12/52). Notably, the prevalence among scattered children across various occupations reached 50.00% (26/52). While the detection rate of *Salmonella* varied among patients with different characteristics, statistical significance was only observed in relation to seasonal differences ($p < 0.05$). The highest detection rate was recorded in the age group ≥ 60 years. The peak detection rate occurred from June to August, with July reporting the highest rate at 13.33% (20/150). In terms of food sources, the detection rates for fruits and vegetables and their products ranked first. Furthermore, a higher detection rate was noted in the catering and food industry, as well as in commercial services, as illustrated in Table 1.

Serotype identification

Of the 52 isolates of *Salmonella*, S. *Typhimurium* (40.38%, 21/52) and *S. Enteritidis* (21.15%, 11/52) were the predominant species, followed by *S. Kentucky* (17.31%, 9/52). *S. Vilshaw*, and *S. Paratyphi A* were the least prevalent, each accounting for 1.92% (1/52) (Supplementary Table 1).

Drug sensitivity testing

In addition to exhibiting sensitivity to meropenem (MEM) and ceftazidime/avibactam (CZA), 52 strains of *Salmonella* demonstrated varying degrees of resistance to 15 other antibiotics. The resistance rate to ampicillin (AMP) was the highest at 88.46% (46/52), followed by streptomycin (STR) at 75.00% (39/52), tetracycline (TET) at 55.77% (29/52), and nalidixic acid (NAL) at 53.85% (28/52). Among the *S. Typhimurium* strains, the highest resistance rates were observed for AMP and

Table 1. Analysis of the epidemiological characteristics of diarrhea cases with *Salmonella* infection.

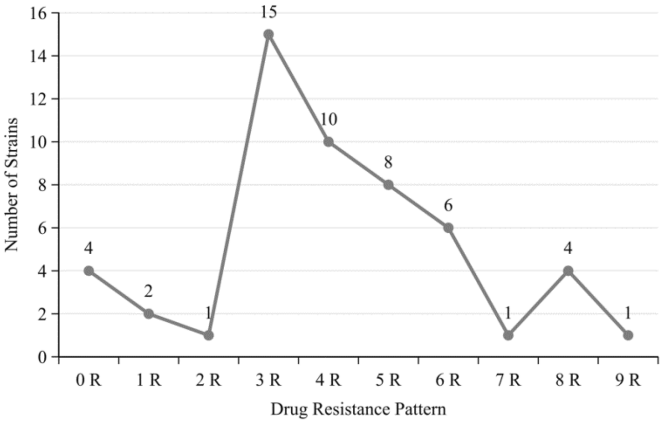
Characteristic	Number of monitoring cases (n = 737)	*Salmonella* infection (n = 52)		Detection rate (%)	χ^2	*p*
		Number of positive	Percentage (%)			
Age group (years)					4.733	0.316
0~5	407	26	50.00	6.39		
6~19	85	5	9.62	5.88		
20~39	79	7	13.46	8.86		
40~59	95	5	9.62	5.26		
≥ 60	71	9	17.31	12.68		
Season (month)					—	0.001[a]
Spring (3~5)	296	2	3.85	0.68		
Summer (6~8)	403	50	96.15	12.41		
Autumn (9~11)	38	0	0.00	0.00		
Suspect food category					8.137	0.149
Fruits and vegetables and products thereof	73	9	17.31	12.33		
Meat and meat products	104	4	7.69	3.85		
Milk and dairy products	163	9	17.31	5.52		
Food and products thereof	112	12	23.08	10.71		
Drinks and frozen drinks	138	8	15.38	5.80		
Mixed/multi-food	147	10	19.23	6.80		
Occupational category					—	0.055[a]
Scattered children	403	26	50.00	6.45		
Commercial service	79	11	21.15	13.92		
Farmers/workers/herdsmen	62	7	13.46	11.29		
Students/nursery children	84	4	7.69	4.76		
Cadres/teachers/medical staff/retirees	46	2	3.85	4.35		
Housework and unemployment/other/unknown	57	1	1.92	3.03		
Catering and food industry	6	1	1.92	16.67		

[a] stands for Fisher's exact test result; — indicates that there is no data.

STR, both at 80.95% (17/21). In the case of *S. Enteritidis*, the resistance rates to AMP and NAL were 100% (11/11), followed by STR at 72.73% (8/11). Additionally, *S. Kentucky*, *S. Dublin*, and *S. Liverpool* exhibited resistance rates of 100% to AMP, as illustrated in Table 2. Three isolates of *S. Typhimurium* were sensitive to all tested antibiotics except for Polypeptide (CT), while one strain of *paratyphoid A* was partially resistant to CT, NAL and STR but sensitive to 14 other antibiotics.

A total of 45 *Salmonella* isolates exhibited MDR to antibiotics classified as class 3 and above, resulting in a MDR rate of 86.54% (45/52). Resistance was primarily to AMP, STR, TET, and NAL; with varying levels of resistance to additional drugs, spanning from 3 to 9 antibiotic classes. Notably, 15 strains (28.85%) demonstrated resistance to 3 antibiotics, followed by 10 strains (19.23%) that were resistant to 4 antibiotics. Additionally, 8 strains (15.38%) showed resistance to 5 antibiotics, while 6 strains (11.54%) were resistant to 6 antibiotics. Furthermore, 4 strains were resistant to 8 classes of antibiotics (7.69%). Notably, one strain of *S. Kentucky* demonstrated resistance to 9 classes of antibiotics (Figure 1). The MDR rates for *S. Typhimurium*, *S. Enteritidis*, *S. Kentucky*, *S. Dublin*, and *S. Liverpool* were 80.95% (17/21), 90.91% (10/11), 100.00% (9/9), 100.00% (6/6), and 100.00% (3/3), respectively. The *Salmonella* strains exhibited no resistance to CZA and MEM (Table 2 and Figure 2). Among the different age groups, the highest MDR rate for *S. Typhimurium* was observed in the 0–5 years' age group, followed by the ≥ 60 years' age group. However, there was no statistically significant difference in the MDR rates of *S. Typhimurium* across the different age groups ($p > 0.05$). In contrast, the MDR rates of *S. Typhimurium* showed significant differences among various age groups ($p < 0.05$), as detailed in Table 3, and the drug sensitivity results of *Salmonella* are displayed in Supplementary Table 2.

Figure 1. Multidrug resistance (MDR) in 52 Salmonella isolates.



The x-axis represents the MDR patterns of Salmonella isolates, specifically their resistance to antibiotic types 0 to 9. The y-axis indicates the number of Salmonella isolates corresponding to various MDR patterns.

Molecular typing

Cluster analysis was used to identify 39 PFGE banding types from 52 strains of *Salmonella*, exhibiting

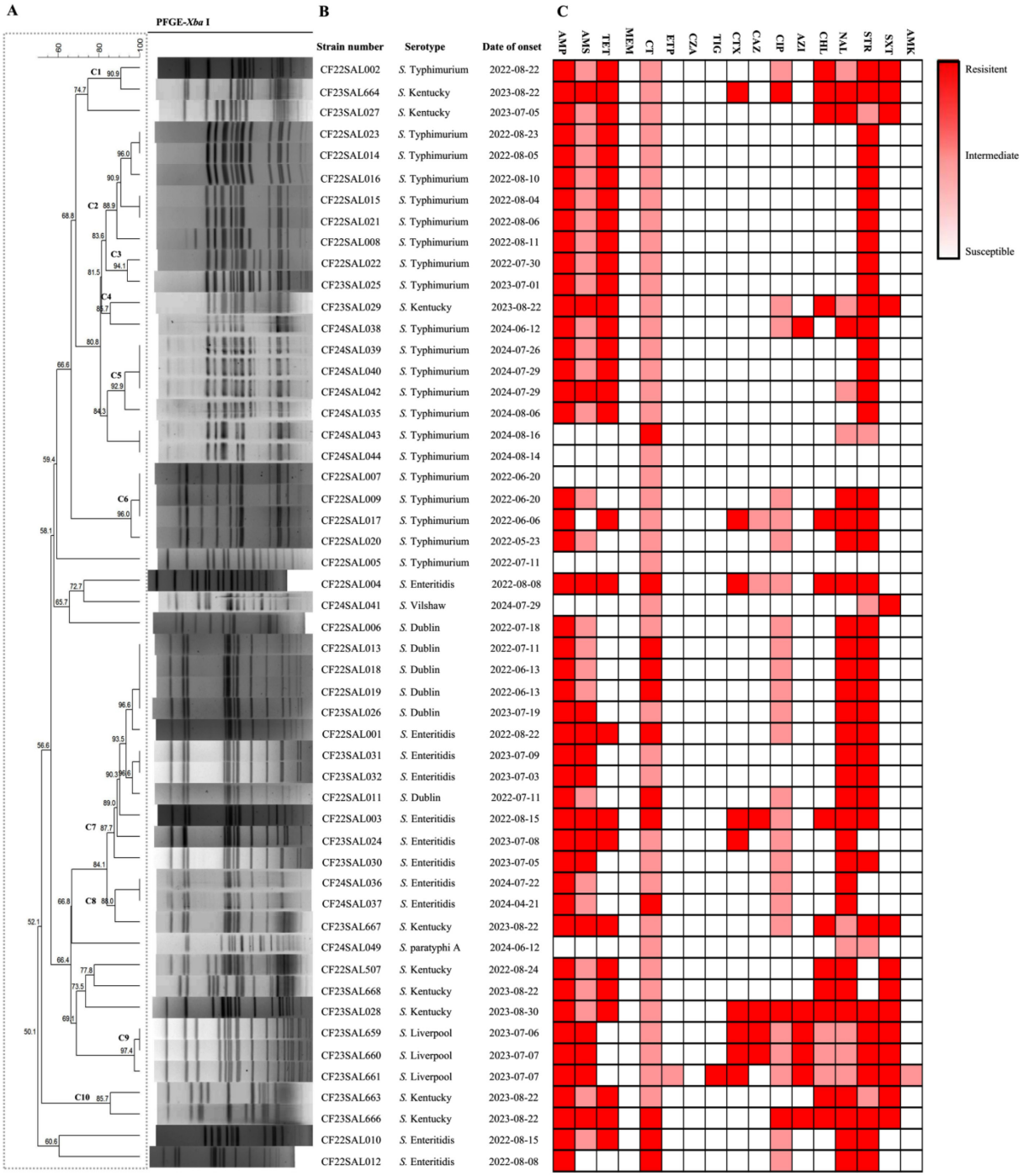
Table 2. Antimicrobial resistance of different *Salmonella* serotypes to 17 antibiotics.

Classification of antibiotics	Antibiotic name	Drug resistance rate/% (Strain number)							
		Salmonella (n = 52)	*Salmonella* Typhimurium (n = 21)	*Salmonella* Enteritidis (n = 11)	*Salmonella* Kentucky (n = 9)	*Salmonella* Dublin (n = 6)	*Salmonella* Liverpool (n = 3)	*Salmonella* Vilshaw (n = 1)	*Salmonella* Paratyphi A (n = 1)
Penicillin	AMP	88.46 (46)	80.95 (17)	100.00 (11)	100.00 (9)	100.00 (6)	100.00 (3)	0.00 (0)	0.00 (0)
Beta-lactam / beta-lactam inhibitor	AMS	30.77 (16)	4.76 (1)	63.64 (7)	44.44 (4)	16.67 (1)	100.00 (3)	0.00 (0)	0.00 (0)
Cephalosporins	CTX	17.31 (9)	4.76 (1)	27.27 (3)	22.22 (2)	0.00 (0)	100.00 (3)	0.00 (0)	0.00 (0)
	CAZ	7.69 (4)	0.00 (0)	9.09 (1)	11.11 (1)	0.00 (0)	100.00 (3)	0.00 (0)	0.00 (0)
	CZA	0.00 (0)	0.00 (0)	0.00 (0)	0.00 (0)	0.00 (0)	0.00 (0)	0.00 (0)	0.00 (0)
Carbapenems	MEM	0.00 (0)	0.00 (0)	0.00 (0)	0.00 (0)	0.00 (0)	0.00 (0)	0.00 (0)	0.00 (0)
	ETP	0.00 (0)	0.00 (0)	0.00 (0)	0.00 (0)	0.00 (0)	0.00 (0)	0.00 (0)	0.00 (0)
Aminoglycosides	STR	75.00 (39)	80.95 (17)	72.73 (8)	55.56 (5)	100.00 (6)	100.00 (3)	0.00 (0)	0.00 (0)
	AMK	0.00 (0)	0.00 (0)	0.00 (0)	0.00 (0)	0.00 (0)	0.00 (0)	0.00 (0)	0.00 (0)
Tetracycline	TET	55.77 (29)	71.43 (15)	45.45 (5)	100.00 (9)	0.00 (0)	0.00 (0)	0.00 (0)	0.00 (0)
	TIG	1.92 (1)	0.00 (0)	0.00 (0)	0.00 (0)	0.00 (0)	33.33 (1)	0.00 (0)	0.00 (0)
Quinolone	NAL	53.85 (28)	19.05 (4)	100.00 (11)	77.78 (7)	100.00 (6)	0.00 (0)	0.00 (0)	0.00 (0)
	CIP	5.77 (3)	0.00 (0)	0.00 (0)	33.33 (3)	0.00 (0)	0.00 (0)	0.00 (0)	0.00 (0)
Chloramphenicol	CHL	25.00 (13)	9.52 (2)	18.18 (2)	100.00 (9)	0.00 (0)	0.00 (0)	0.00 (0)	0.00 (0)
Macrolides	AZI	11.54 (6)	4.76 (1)	0.00 (0)	22.22 (2)	0.00 (0)	100.00 (3)	0.00 (0)	0.00 (0)
Sulfonamides	SXT	26.92 (14)	4.76 (1)	0.00 (0)	100.00 (9)	0.00 (0)	100.00 (3)	100.00 (1)	0.00 (0)
Polypeptide	CT	23.08 (12)	4.76 (1)	54.55 (6)	11.11 (1)	66.67 (4)	0.00 (0)	0.00 (0)	0.00 (0)

AMP: ampicillin; AMS: ampicillin/sulbactam; CTX: cefotaxime; CAZ: ceftazidime; CZA: ceftazidime/avibactam; MEM: meropenem; ETP: ertapenem; STR: streptomycin; AMK: amikacin; TET: tetracycline; TIG: tigecycline; NAL: nalidixic acid; CIP: ciprofloxacin; CHL: chloramphenicol; AZI: azithromycin; SXT: sulfamethoxazole/trimethoprim; CT: polymyxin E.

similarities that ranged from 50.1% to 100%. These strains were categorized into 10 clusters (C1–C10) based on a banding similarity threshold of ≥ 85%, with each cluster comprising between 2 and 11 strains. Cluster C2 contained 6 strains of *S. Typhimurium*, of which 2 groups exhibited identical band types. Similarly, cluster C5 included 4 strains of *S. Typhimurium*, with 3 groups sharing the same band type. Cluster C6 comprised 4 strains of *S. Typhimurium*, which had an onset time span of within 1 month.

Figure 2. Molecular typing and drug sensitivity results of 52 Salmonella isolates.



A: The phylogenetic tree of 52 Salmonella isolates based on the PFGE. Light gray shading shows Clade 1-10. **B:** The serotypes of Salmonella isolates along with their corresponding isolation times. **C:** Antibiotics susceptibility profiles of 52 Salmonella isolates. Different colors represent resistant, intermediate, susceptible (as shown in the inset legend).

Table 3. Comparison of multidrug resistance rates of *Salmonella* in different age groups.

Age group (years)	Number of multidrug resistant strains (Multiple drug resistance rate/%)							
	Salmonella (n = 52)	*Salmonella* Typhimurium (n = 21)	*Salmonella* Enteritidis (n = 11)	*Salmonella* Kentucky (n = 9)	*Salmonella* Dublin (n = 6)	*Salmonella* Liverpool (n = 3)	*Salmonella* Vilshaw (n = 1)	*Salmonella* Paratyphi A (n = 1)
0~5	24 (46.15)	14 (66.67)	4 (36.36)	1 (11.11)	2 (33.33)	3 (100.00)	0 (0.00)	0 (0.00)
6~19	4 (7.69)	2 (9.52)	1 (9.09)	0 (0.00)	1 (16.67)	0 (0.00)	0 (0.00)	0 (0.00)
20~39	5 (9.62)	0 (0.00)	3 (27.27)	1 (11.11)	1 (16.67)	0 (0.00)	0 (0.00)	0 (0.00)
40~59	5 (9.62)	1 (4.76)	1 (4.76)	3 (33.33)	0 (0.00)	0 (0.00)	0 (0.00)	0 (0.00)
≥ 60	7 (13.46)	0 (0.00)	1 (4.76)	4 (44.44)	2 (33.33)	0 (0.00)	0 (0.00)	0 (0.00)
Total	45 (86.54)	17 (80.95)	10 (90.91)	9 (100.00)	6 (100.00)	3 (100.00)	0 (0.00)	0 (0.00)
p	0.344[a]	0.023[a]	1.000[a]	—	—	—	—	—

[a] stands for Fisher's exact test result; — indicates that there is no data.

Clusters C9 and C10 had 3 strains of *S. Liverpool* and 2 strains of *S. Kentucky* were grouped together, with onset times being closely aligned. Additionally, 5 strains of *S. Dublin* and 6 strains of *S. Enteritidis* were classified into cluster C7, where 4 strains of *S. Dublin* shared identical band types. Furthermore, 2 strains of *S. Enteritidis* in this cluster exhibited a similarity coefficient of 100%, although the time span of the cases associated with these strains was considerably broad. Further details are provided in Figure 2.

Furthermore, a comparative analysis based on drug sensitivity results indicated that strains with higher similarity coefficients also shared similar drug resistance phenotypes. For instance, 6 strains of *S. Typhimurium* belonging to the C2 cluster and 2 strains from the C3 cluster exhibited resistance to AMP, TET, and STR, while showing intermediate susceptibility to AMS and CT, and remaining sensitive to other antibiotics. The 4 strains of *S. Dublin* clustered in C7 cluster were very similar in the drug resistance spectrum; resistant to AMS, NAL, STR, intermediate to CIP. The drug resistance profiles of the 3 strains of *S. Liverpool*, which were clustered in the C9 cluster, exhibited notable similarities. All strains demonstrated resistance to AMP, AMS, CTX, AZI, STR, and SXT; while showing intermediate resistance to CT, CIP, CHL, and NAL. All isolates are susceptible to CZA and MEM, and all isolates except one are also susceptible to ETP and AMK (Figure 2).

Discussion

Salmonella serotype identification, drug susceptibility testing, and PFGE typing were conducted on samples collected from food-borne diarrhea patients in Chifeng City from 2022 to 2024. The aim was to preliminarily assess the epidemic status, drug resistance, and molecular characteristics of these *Salmonella* isolates. The results indicated that the detection rate of *Salmonella* among diarrhea patients in Chifeng City during this period was 7.06%, which is slightly lower than the 8.3% detection rate reported in Shanghai of China. A review of 29,210 diarrhea cases in Shanghai revealed a *Salmonella* detection rate of 8.3%, with a noted increase in detection rates year by year since 2006 [17]. Additionally, a study focusing on stool samples from diarrhea patients in Zhejiang Province collected a total of 308,326 samples from 2012 to 2021, revealing a *Salmonella* positivity rate of 3.65%. This trend aligns with the monitoring results in Shanghai, which demonstrated a significant annual increase in detection rates, rising from 1.69% to 6.61%, particularly noteworthy in 2020 and 2021 [18]. A total of 1,826 strains of *Salmonella* were identified among 40,572 patients with diarrhea in Guangdong Province between September 2009 and December 2012, resulting in an overall detection rate of 4.5%. The highest detection rate was observed in autumn (38.8%), while the lowest was recorded in winter (6.4%). Notably, children under 5 years of age constituted the most affected demographic, representing 73% of the isolates, with *S. Typhimurium* identified as the predominant serotype [19]. Furthermore, national surveillance reports of China from 2009 to 2018 indicate that non-typhoid *Salmonella* is a leading bacterial pathogen in patients with acute diarrhea, with prevalence varying by age and seasonality, peaking in children aged 3–5 years [20]. Consistent with these findings, the current study also revealed the highest detection rate of *Salmonella* in the 0–5 years' age group, suggesting a heightened susceptibility to this pathogen. *S. Typhimurium* was the most frequently isolated serotype, highlighting its dominance among *Salmonella* strains. These observations underscore the significant regional and temporal variations in *Salmonella* detection rates among domestic diarrhea patients, as well as the differences observed across specific age groups and seasons. This variation highlights the significance of context and methodology in understanding the prevalence of *Salmonella* across different settings.

Internationally, *Salmonella* infections are influenced by various factors, including geographic location, food safety measures, and specific serotypes.

A study conducted in the outskirts of Vientiane, Laos, monitored non-typhoid *Salmonella* infection rates over a 9-year period. The findings indicated a decrease in infection rates in one village during the study, highlighting the potential impact of environmental and socioeconomic changes on *Salmonella* prevalence [21]. Additionally, a study in Japan reported a significant increase in *Salmonella paratyphi A* infections among travelers returning from Myanmar in 2015, with the infection rate rising to 13 cases per 100,000 travelers, compared to 2–4 cases per 100,000 previously. This demonstrates that travel and contact with endemic areas can significantly influence infection rates [22]. A study in Ethiopia revealed a 5.5% detection rate of *Salmonella* in foods of animal origin, with higher rates observed in raw meat (12%) and raw eggs (18%), underscoring the importance of food safety measures in reducing *Salmonella* infection rates [23]. Furthermore, a study in Ghana found that the overall detection rate of *Salmonella* in environmental samples from farms was 6.0%, with higher rates detected in dust and soil compared to poultry feces samples. This suggests that the farm environment can serve as a reservoir for *Salmonella*, facilitating its spread [24]. Overall, *Salmonella* infection rates vary widely based on environmental factors, food safety practices, and geographic location. Continuous monitoring and enhanced food safety measures are essential for reducing the risk of *Salmonella* infection.

The AMR of *Salmonella* exhibits significant regional variations influenced by antibiotic usage patterns, local epidemiology, and specific resistance genes. A study conducted in Guangdong Province, China, revealed that 72% of the 1,826 isolated *Salmonella* strains were resistant to at least 1 antibiotic, with 46% classified as MDR. The resistance rates to quinolones, such as NAL and CIP, were notably high at 61.9% and 8.05%, respectively [19]. Additionally, a study involving 87 *Salmonella* isolates from Shaoxing City, China, tested against 28 different antibiotics found high resistance rates to cefazolin (86.21%), STR (81.61%), and AMP (77.01%). Furthermore, 83.91% of these isolates were identified as MDR [25]. A comprehensive survey of *S. Typhimurium* across 11 Southeast Asian countries, including China, has demonstrated that this serotype represents a substantial public health threat due to its resistance to multiple antibiotics [26]. A study investigating clinical and food-derived *Salmonella Enteritidis* in Huzhou, Zhejiang Province, revealed that all strains exhibited resistance to NAL, with 90.70% resistant to AMP, and 81.40% classified as MDR, thereby underscoring the concerning trend of MDR [27]. Furthermore, the emergence of *Salmonella* strains producing extended-spectrum β-lactamases (ESBLs) has been reported, particularly among isolates from patients experiencing diarrhea. A study involving 2,283 *Salmonella* strains from various sources, including patients and food, indicated that 56.4% were MDR, with a significant proportion harboring the ESBL gene, complicating treatment options [28]. A report from Saudi Arabia indicated that the resistance of *Salmonella* to various antibiotics increased significantly from 2011 to 2018. By 2018, all isolates exhibited varying degrees of resistance to certain cephalosporins, and the prevalence of fluoroquinolone-resistant *Salmonella* in the region was notably high [29]. In Europe, the prevalence of *Salmonella* infections and the associated patterns of resistance also vary, with serotypes such as *S. Enteritidis* and *S. Typhimurium* being predominant. Resistance to critically important antibiotics, such as fluoroquinolones, is regarded as a major public health concern [30]. In conjunction with the findings of this study, the resistance rates of *Salmonella* to AMP, STR and NAL were found to be high, indicating a serious issue of MDR. Thus, the drug resistance of *Salmonella* isolates is on the rise across different regions. Resistance patterns are influenced by several factors, including *Salmonella* serotype, patient age, and regional differences in antibiotic use and surveillance practices. Ongoing regional studies are essential for understanding resistance patterns in *Salmonella* and for guiding clinical usage.

The cluster analysis revealed that the PFGE band types of 52 *Salmonella* strains exhibited significant diversity in their distribution. Notably, the clustering rate for *S. Typhimurium* was high. Specifically, 6 strains of *S. Typhimurium* were grouped in cluster C2, comprising 2 groups with identical band types. Additionally, 4 strains of *S. Typhimurium* were found in cluster C5, categorized into 3 groups of identical band types, while 2 strains with identical band types were located in cluster C6, with cases originating from the same region and an onset time span of 1 month. This clustering may indicate an infection caused by the same strain [31]. Three strains of *S. Liverpool* and 2 strains of *S. Kentucky* were identified in clusters C9 and C10, with closely timed onset, suggesting a potential common origin. Furthermore, the 5 strains of *S. Dublin* and 6 strains of *S. Enteritidis* in cluster C7 were closely related, with 4 strains of *S. Dublin* sharing the same band type and 2 strains of *S. Enteritidis* exhibiting a similarity coefficient of 100%. However, it is noteworthy that the onset time span for the clustered

strains exceeded 1 month, which may be indicative of clonal transmission. The PFGE spectrum analysis of the 52 *Salmonella* strains demonstrated a diverse and relatively dispersed range of band types. In conjunction with a previous study analyzing 243 strains of *S. Enteritidis* via PFGE, a total of 34 distinct PFGE spectra were identified. The classification of these characteristics by serotype and origin underscores the considerable genetic diversity among isolates collected from various sites and sample types [32].

This study represents the first systematic investigation into the epidemic status, drug resistance, and molecular typing of *Salmonella* in patients with food-borne diarrhea in Chifeng City. It serves as a valuable reference for the scientific prevention and control of *Salmonella*, molecular traceability, and the rational use of clinical drugs. However, certain limitations must be acknowledged. This research exclusively examined *Salmonella* strains isolated from stool samples of food-borne diarrhea patients and did not systematically type *Salmonella* isolates from food sources. Consequently, this may hinder the accurate tracing of the strains. Therefore, it is imperative to enhance the monitoring of the etiology, molecular typing, and drug resistance of food-borne *Salmonella* in Chifeng City, China. This should be conducted in conjunction with a systematic analysis of food-derived *Salmonella* to facilitate effective prevention and control measures in the future.

Conclusions

This study underscores the significant public health challenge posed by *Salmonella* in Chifeng, China, particularly due to its high incidence, extensive antibiotic resistance spectrum, and genetic diversity. The findings indicate that *S. Typhimurium* is the most prevalent serotype among patients with foodborne diarrhea, followed by *S. Enteritidis* and *S. Kentucky*. Alarmingly, resistance to commonly used antibiotics such as AMP, STR, and TET was notably high, with over 80% of strains exhibiting MDR. Additionally, PFGE analysis revealed genetic polymorphism among *Salmonella* strains, with a relatively wide range of similarity coefficients, indicating a diverse and evolving bacterial population. These results highlight the urgent need for enhanced surveillance, prudent antibiotic use, and targeted public health interventions to mitigate the spread of *Salmonella* infections and address the escalating threat of antimicrobial resistance in Chifeng.

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Ethics approval

This study was performed in line with the principles of the Declaration of Helsinki. Approval was granted by the Ethical Committee of the Chifeng Center for Disease Control and Prevention (2024-zr-006).

Authors' contributions

CW, investigation and formal analysis, writing-initial draft; FY, YB, conceptualization, data curation, funding, resources, writing-editing final draft; HY, HL, conceptualization, data curation, writing-editing; PP, formal analysis; YZ, conceptualization, writing-editing. All the authors approved the final draft and submission of the manuscript.

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Conflict of interest

No conflict of interest is declared.

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Annex – Supplementary Items

Supplementary Table 1. Distribution of the serotypes among 52 *Salmonella* isolates.

Strain type	Colony characteristics on XLD plate	Phenomena on TSI	Results of serum agglutination	Strain number	Percentage (%)
Salmonella Typhimurium	Pink, black in center or all black	K/A, H_2S+	1,4,[5],12:i:1,2	21	40.38
Salmonella Enteritidis	Pink, black in center or all black	K/A, H_2S+	1,9,12:g,m:[1,7]	11	21.15
Salmonella Kentucky	Pink, black in center or all black	K/A, H_2S+	8,20:i:z6	9	17.31
Salmonella Dublin	Pink, black in center or all black	K/A, H_2S+	1,9,12[Vi]:g,p:-	6	11.54
Salmonella Liverpool	Pink, black in center or all black	K/A, H_2S+	1,3,19:d:e,n,z15	3	5.77
Salmonella Vilshaw	Pink, black in center or all black	K/A, H_2S+	6,7,14:r:1,2	1	1.92
Salmonella Paratyphi A	Pink, black in center or all black	K/A, H_2S+	1,2,12:a:[1, 5]	1	1.92

XLD: xylose lysine desoxycholate agar plates: TSI: triple sugar iron culture medium.

Supplementary Table 2. Drug sensitivity MIC values of 52 *Salmonella* isolates.

Antibiotic	Serotype	Ampicillin	Ampicillin/sulbactam	Tetracycline	Meropenem	Polymyxin E	Ertapenem	Ceftazidime/Avibactam	Tigecycline	Cefotaxime	Ceftazidime	Ciprofloxacin	Azithromycin	Chloromycetin	Nalidixic Acid	Streptomycin	Sulfamethoxazole	Amikacin
Number	——	AMP	AMS	TET	MEM	CT	ETP	CZA	TIG	CTX	CAZ	CIP	AZI	CHL	NAL	STR	SXT	AMK
CF22SAL001	*S.* Enteritidis	> 32	> 32/16	> 16	≤ 0.12	4	≤ 0.25	≤ 0.25/4	≤ 0.25	≤ 0.25	0.5	0.25	4	≤ 4	> 32	> 32	≤ 0.5/9.5	≤ 4
CF22SAL002	*S.* Typhimurium	> 32	16/8	> 16	≤ 0.12	0.5	≤ 0.25	≤ 0.25/4	≤ 0.25	≤ 0.25	0.5	0.5	4	> 32	8	32	> 8/152	≤ 4
CF22SAL003	*S.* Enteritidis	> 32	32/16	> 16	≤ 0.12	4	≤ 0.25	≤ 0.25/4	0.5	> 16	> 16	0.5	8	> 32	> 32	> 32	≤ 0.5/9.5	≤ 4
CF22SAL004	*S.* Enteritidis	> 32	32/16	> 16	≤ 0.12	4	≤ 0.25	≤ 0.25/4	≤ 0.25	16	8	0.25	8	> 32	> 32	> 32	≤ 0.5/9.5	≤ 4
CF22SAL005	*S.* Typhimurium	≤ 2	≤ 2/1	≤ 1	≤ 0.12	0.5	≤ 0.25	≤ 0.25/4	≤ 0.25	≤ 0.25	≤ 0.25	≤ 0.015	4	≤ 4	≤ 4	8	≤ 0.5/9.5	≤ 4
CF22SAL006	*S.* Dublin	> 32	16/8	≤ 1	≤ 0.12	2	≤ 0.25	≤ 0.25/4	≤ 0.25	≤ 0.25	≤ 0.25	0.12	≤ 2	≤ 4	> 32	> 32	≤ 0.5/9.5	≤ 4
CF22SAL007	*S.* Typhimurium	≤ 2	≤ 2/1	≤ 1	≤ 0.12	1	≤ 0.25	≤ 0.25/4	≤ 0.25	≤ 0.25	0.5	≤ 0.015	4	≤ 4	≤ 4	8	≤ 0.5/9.5	≤ 4
CF22SAL008	*S.* Typhimurium	> 32	16/8	> 16	≤ 0.12	0.5	≤ 0.25	≤ 0.25/4	≤ 0.25	≤ 0.25	0.5	0.03	4	≤ 4	≤ 4	> 32	≤ 0.5/9.5	≤ 4
CF22SAL009	*S.* Typhimurium	> 32	16/8	4	≤ 0.12	2	≤ 0.25	≤ 0.25/4	≤ 0.25	≤ 0.25	0.5	0.12	4	≤ 4	> 32	> 32	≤ 0.5/9.5	≤ 4
CF22SAL010	*S.* Enteritidis	> 32	16/8	> 16	≤ 0.12	4	≤ 0.25	≤ 0.25/4	≤ 0.25	≤ 0.25	0.5	0.12	4	8	> 32	> 32	≤ 0.5/9.5	≤ 4
CF22SAL011	*S.* Dublin	> 32	16/8	≤ 1	≤ 0.12	4	≤ 0.25	≤ 0.25/4	≤ 0.25	≤ 0.25	0.5	0.25	≤ 2	≤ 4	> 32	> 32	≤ 0.5/9.5	≤ 4
CF22SAL012	*S.* Enteritidis	> 32	4/2	≤ 1	≤ 0.12	4	≤ 0.25	≤ 0.25/4	≤ 0.25	≤ 0.25	≤ 0.25	0.12	4	≤ 4	> 32	> 32	≤ 0.5/9.5	≤ 4
CF22SAL013	*S.* Dublin	> 32	16/8	≤ 1	≤ 0.12	4	≤ 0.25	≤ 0.25/4	≤ 0.25	≤ 0.25	0.5	0.12	≤ 2	≤ 4	> 32	> 32	≤ 0.5/9.5	≤ 4
CF22SAL014	*S.* Typhimurium	> 32	16/8	> 16	≤ 0.12	0.5	≤ 0.25	≤ 0.25/4	≤ 0.25	≤ 0.25	≤ 0.25	0.03	4	≤ 4	≤ 4	> 32	≤ 0.5/9.5	≤ 4
CF22SAL015	*S.* Typhimurium	> 32	16/8	> 16	≤ 0.12	0.5	≤ 0.25	≤ 0.25/4	≤ 0.25	≤ 0.25	≤ 0.25	0.03	4	≤ 4	≤ 4	> 32	≤ 0.5/9.5	≤ 4
CF22SAL016	*S.* Typhimurium	> 32	16/8	> 16	≤ 0.12	0.5	≤ 0.25	≤ 0.25/4	≤ 0.25	≤ 0.25	0.5	0.03	4	≤ 4	≤ 4	> 32	≤ 0.5/9.5	≤ 4
CF22SAL017	*S.* Typhimurium	> 32	8/4	> 16	≤ 0.12	1	≤ 0.25	≤ 0.25/4	≤ 0.25	> 16	8	0.25	4	> 32	> 32	> 32	≤ 0.5/9.5	≤ 4
CF22SAL018	*S.* Dublin	> 32	16/8	≤ 1	≤ 0.12	4	≤ 0.25	≤ 0.25/4	≤ 0.25	≤ 0.25	0.5	0.25	4	≤ 4	> 32	> 32	≤ 0.5/9.5	≤ 4
CF22SAL019	*S.* Dublin	> 32	16/8	≤ 1	≤ 0.12	4	≤ 0.25	≤ 0.25/4	≤ 0.25	≤ 0.25	0.5	0.12	≤ 2	≤ 4	> 32	> 32	≤ 0.5/9.5	≤ 4
CF22SAL020	*S.* Typhimurium	> 32	16/8	≤ 1	≤ 0.12	2	≤ 0.25	≤ 0.25/4	≤ 0.25	≤ 0.25	0.5	0.12	≤ 2	≤ 4	> 32	> 32	≤ 0.5/9.5	≤ 4
CF22SAL021	*S.* Typhimurium	> 32	16/8	> 16	≤ 0.12	0.5	≤ 0.25	≤ 0.25/4	≤ 0.25	≤ 0.25	0.5	0.03	4	≤ 4	≤ 4	> 32	≤ 0.5/9.5	≤ 4
CF22SAL022	*S.* Typhimurium	> 32	16/8	> 16	≤ 0.12	0.5	≤ 0.25	≤ 0.25/4	≤ 0.25	≤ 0.25	≤ 0.25	0.03	4	≤ 4	≤ 4	> 32	≤ 0.5/9.5	≤ 4
CF22SAL023	*S.* Typhimurium	> 32	16/8	> 16	≤ 0.12	0.5	≤ 0.25	≤ 0.25/4	0.5	≤ 0.25	≤ 0.25	0.03	4	≤ 4	≤ 4	> 32	≤ 0.5/9.5	≤ 4
CF23SAL024	*S.* Enteritidis	> 32	32/16	> 16	≤ 0.12	1	≤ 0.25	≤ 0.25/4	≤ 0.25	> 16	2	0.5	≤ 2	8	> 32	≤ 4	≤ 0.5/9.5	≤ 4
CF23SAL025	*S.* Typhimurium	> 32	16/8	> 16	≤ 0.12	0.5	≤ 0.25	≤ 0.25/4	≤ 0.25	≤ 0.25	0.5	≤ 0.015	≤ 2	8	≤ 4	> 32	≤ 0.5/9.5	≤ 4
CF23SAL026	*S.* Dublin	> 32	32/16	2	≤ 0.12	2	≤ 0.25	≤ 0.25/4	≤ 0.25	≤ 0.25	≤ 0.25	0.12	≤ 2	8	> 32	> 32	≤ 0.5/9.5	≤ 4
CF23SAL027	*S.* Kentucky	> 32	16/8	> 16	≤ 0.12	0.5	≤ 0.25	≤ 0.25/4	≤ 0.25	≤ 0.25	1	0.06	≤ 2	> 32	> 32	16	> 8/152	≤ 4
CF23SAL028	*S.* Kentucky	> 32	16/8	> 16	≤ 0.12	≤ 0.25	≤ 0.25	0.5/4	0.5	> 16	> 16	> 2	32	> 32	> 32	> 32	> 8/152	≤ 4
CF23SAL029	*S.* Kentucky	> 32	> 32/16	> 16	≤ 0.12	0.5	≤ 0.25	≤ 0.25/4	≤ 0.25	≤ 0.25	0.5	0.12	≤ 2	> 32	8	> 32	> 8/152	≤ 4
CF23SAL030	*S.* Enteritidis	> 32	32/16	2	≤ 0.12	2	≤ 0.25	≤ 0.25/4	≤ 0.25	≤ 0.25	0.5	0.12	≤ 2	≤ 4	> 32	> 32	≤ 0.5/9.5	≤ 4
CF23SAL031	*S.* Enteritidis	> 32	32/16	≤ 1	≤ 0.12	1	≤ 0.25	≤ 0.25/4	≤ 0.25	≤ 0.25	≤ 0.25	0.06	≤ 2	8	> 32	> 32	≤ 0.5/9.5	≤ 4
CF23SAL032	*S.* Enteritidis	> 32	32/16	≤ 1	≤ 0.12	1	≤ 0.25	≤ 0.25/4	≤ 0.25	≤ 0.25	≤ 0.25	0.06	≤ 2	8	> 32	> 32	≤ 0.5/9.5	≤ 4
CF22SAL507	*S.* Kentucky	> 32	16/8	> 16	≤ 0.12	≤ 0.25	≤ 0.25	≤ 0.25/4	≤ 0.25	≤ 0.25	0.5	0.06	≤ 2	> 32	> 32	8	> 8/152	≤ 4
CF23SAL666	*S.* Kentucky	> 32	32/16	> 16	≤ 0.12	> 8	≤ 0.25	≤ 0.25/4	1	≤ 0.25	0.5	> 2	32	> 32	> 32	> 32	> 8/152	≤ 4
CF23SAL664	*S.* Kentucky	> 32	32/16	> 16	≤ 0.12	≤ 0.25	≤ 0.25	≤ 0.25/4	≤ 0.25	8	1	> 2	8	> 32	> 32	> 32	> 8/152	≤ 4
CF23SAL668	*S.* Kentucky	> 32	16/8	> 16	≤ 0.12	≤ 0.25	≤ 0.25	≤ 0.25/4	≤ 0.25	≤ 0.25	0.5	0.06	≤ 2	> 32	> 32	8	> 8/152	≤ 4
CF23SAL663	*S.* Kentucky	> 32	16/8	> 16	≤ 0.12	≤ 0.25	≤ 0.25	≤ 0.25/4	≤ 0.25	≤ 0.25	0.5	0.06	≤ 2	> 32	> 32	16	> 8/152	≤ 4

CF23SAL667	*S.* Kentucky	> 32	32/16	> 16	≤ 0.12	≤ 0.25	≤ 0.25	≤ 0.25/4	≤ 0.25	0.5	0.5	0.25	≤ 2	> 32	8	> 32	> 8/152	≤ 4
CF23SAL660	*S.* Liverpool	> 32	32/16	≤ 1	≤ 0.12	0.5	≤ 0.25	0.5/4	≤ 0.25	> 16	> 16	0.25	64	16	8	> 32	> 8/152	≤ 4
CF23SAL661	*S.* Liverpool	> 32	> 32/16	≤ 1	≤ 0.12	≤ 0.25	1	≤ 0.25/4	> 8	> 16	2	0.25	64	16	8	> 32	> 8/152	32
CF23SAL659	*S.* Liverpool	> 32	> 32/16	2	≤ 0.12	0.5	≤ 0.25	0.5/4	≤ 0.25	> 16	> 16	0.25	64	16	8	> 32	> 8/152	≤ 4
CF24SAL035	*S.* Typhimurium	> 32	16/8	> 16	≤ 0.12	2	≤ 0.25	≤ 0.25/4	≤ 0.25	≤ 0.25	1	0.03	≤ 2	≤ 4	≤ 4	> 32	≤ 0.5/9.5	≤ 4
CF24SAL036	*S.* Enteritidis	> 32	16/8	2	≤ 0.12	2	≤ 0.25	0.5/4	≤ 0.25	≤ 0.25	0.5	0.12	≤ 2	≤ 4	> 32	≤ 4	≤ 0.5/9.5	≤ 4
CF24SAL037	*S.* Enteritidis	> 32	16/8	2	≤ 0.12	4	≤ 0.25	≤ 0.25/4	≤ 0.25	≤ 0.25	0.5	0.12	≤ 2	≤ 4	> 32	≤ 4	≤ 0.5/9.5	≤ 4
CF24SAL038	*S.* Typhimurium	> 32	16/8	> 16	≤ 0.12	2	≤ 0.25	≤ 0.25/4	≤ 0.25	≤ 0.25	0.5	0.5	> 64	8	> 32	> 32	≤ 0.5/9.5	≤ 4
CF24SAL039	*S.* Typhimurium	> 32	16/8	> 16	≤ 0.12	2	≤ 0.25	≤ 0.25/4	≤ 0.25	≤ 0.25	0.5	0.03	4	≤ 4	≤ 4	> 32	≤ 0.5/9.5	≤ 4
CF24SAL040	*S.* Typhimurium	> 32	16/8	> 16	≤ 0.12	1	≤ 0.25	≤ 0.25/4	≤ 0.25	≤ 0.25	1	0.03	≤ 2	8	≤ 4	> 32	≤ 0.5/9.5	≤ 4
CF24SAL041	*S.* Vilshaw	≤ 2	≤ 2/1	2	≤ 0.12	≤ 0.25	≤ 0.25	≤ 0.25/4	≤ 0.25	≤ 0.25	0.5	0.03	4	≤ 4	≤ 4	16	> 8/152	≤ 4
CF24SAL042	*S.* Typhimurium	> 32	32/16	> 16	≤ 0.12	2	≤ 0.25	≤ 0.25/4	≤ 0.25	≤ 0.25	1	0.03	≤ 2	8	8	> 32	≤ 0.5/9.5	≤ 4
CF24SAL043	*S.* Typhimurium	≤ 2	4/2	2	≤ 0.12	4	≤ 0.25	0.5/4	≤ 0.25	≤ 0.25	1	0.03	4	8	8	16	≤ 0.5/9.5	≤ 4
CF24SAL044	*S.* Typhimurium	≤ 2	≤ 2/1	2	≤ 0.12	2	≤ 0.25	≤ 0.25/4	≤ 0.25	≤ 0.25	0.5	0.03	4	8	≤ 4	8	≤ 0.5/9.5	≤ 4
CF24SAL049	*S.* Paratyphi A	4	4/2	4	≤ 0.12	1	≤ 0.25	0.5/4	≤ 0.25	≤ 0.25	1	0.03	≤ 2	8	8	16	≤ 0.5/9.5	≤ 4

AMP: ampicillin; AMS: ampicillin/sulbactam; TET: tetracycline; MEM: meropenem; CT: polymyxin E; ETP: ertapenem; CZA: ceftazidime/avibactam; TIG: tigecycline; CTX: cefotaxime; CAZ: ceftazidime; CIP: ciprofloxacin; AZI: azithromycin; CHL: chloramphenicol; NAL: nalidixic acid; STR: streptomycin; SXT: sulfamethoxazole/trimethoprim; AMK: amikacin.