Journal of Rare Cardiovascular Diseases
ISSN: 2299-3711 (Print) | e-ISSN: 2300-5505 (Online)
www.jrcd.eu

RESEARCH ARTICLE

# Prevalence, Antimicrobial Resistance Patterns, and Clinical Outcomes of Salmonella Species Isolated from Blood in a Tertiary Care Hospital

**Rithvika vetrivel[1], Aruna[1] and Nabamita bhaumik[2]**
[1]Department of Microbiology, Saveetha Medical College and Hospital, Saveetha Institute of Medical and Technical Sciences, Chennai 602105, Tamil Nadu, India
[2]Department of Microbiology, Saveetha Medical College and Hospital, Saveetha Institute of Medical and Technical Sciences, Chennai 602105, Tamil Nadu, India

*Corresponding Author
Rithvika vetrivel

Article History
**Received:** 09/07/2025
**Revised:** 23/08/2025
**Accepted:** 12/09/2025
**Published:** 30/09/2025

**Abstract:** Salmonella species are a significant cause of bloodstream infections (BSIs), particularly in low- and middle-income countries. The increasing prevalence of antimicrobial resistance (AMR) among Salmonella isolates poses a serious public health challenge, often complicating treatment strategies and influencing clinical outcomes.This study aimed to assess the prevalence, antimicrobial resistance patterns, and clinical outcomes of Salmonella species isolated from blood cultures in a tertiary care hospital. A retrospective analysis was conducted over a defined period on blood culture samples received in the microbiology department of a tertiary care hospital. Isolates identified as Salmonella spp. were subjected to antimicrobial susceptibility testing using standard protocols. Clinical data were collected to evaluate patient demographics, comorbidities, treatment regimens, and outcomes.Among the total blood cultures processed, Salmonella species were isolated in 8% of cases in 2022,9% in 2023 and 10% in 2024. The majority of isolates were identified as S. Typhi and S. Paratyphi A. High levels of resistance were observed to commonly used antibiotics such as fluoroquinolones and ampicillin, while susceptibility to third-generation cephalosporins and carbapenems remained relatively preserved.Clinical outcomes were significantly worse in patients infected with MDR strains, with increased duration of hospital stay, higher incidence of complications, and a trend toward higher mortality.The study highlights a concerning prevalence of antimicrobial-resistant Salmonella spp. in bloodstream infections. Continuous surveillance, prudent antibiotic use, and implementation of effective infection control measures are critical to managing the burden of Salmonella-related BSIs and improving patient outcomes.

**Keywords**: Bloodstream infection, Salmonella typhi, Salmonella paratyphi A & B, Tertiary care hospital.

## INTRODUCTION

*Salmonella* species represent a significant cause of bloodstream infections (BSIs), particularly in low- and middle-income countries where they pose substantial public health challenges. The genus *Salmonella*, named after American veterinary pathologist Daniel Elmer Salmon, encompasses gram-negative, motile, facultatively anaerobic bacteria first isolated from swine intestines in 1885 by Theobald Smith [1]. These rod-shaped organisms are characterized by their acid-labile nature, hydrogen sulfide production, and possession of O, H, and Vi surface antigens that serve as important diagnostic and epidemiological markers.

Current taxonomic classification recognizes two species within the genus: *S. enterica* and *S. bongori*, with *S. subterranea* proposed as a potential third species. *Salmonella enterica* is subdivided into six subspecies, with subspecies I (*enterica*) containing the greatest diversity of serovars and encompassing virtually all strains of clinical significance to human health [1]. The most prevalent serovars include Enteritidis, Typhimurium, Newport, and Javiana, while typhoidal serovars (*S.* Typhi and *S.* Paratyphi A, B, and C) are responsible for enteric fever, a severe systemic illness requiring prompt antibiotic intervention [2].

*Salmonella* infections in humans manifest along a clinical spectrum ranging from self-limiting gastroenteritis to life-threatening systemic disease. Non-typhoidal *Salmonella* typically causes localized gastroenteritis, while typhoidal serovars cause enteric fever, which can progress to septicemia and systemic complications [3]. *S.* Typhi is uniquely adapted to humans as its exclusive reservoir and is transmitted through the fecal-oral route, making it endemic in regions with poor sanitation infrastructure.

The pathogenesis involves sophisticated virulence mechanisms including the Vi capsular polysaccharide exclusive to *S.* Typhi, which confers resistance to phagocytosis, and the typhoid toxin that contributes to neurological manifestations [4]. Following ingestion, *Salmonella* penetrates the intestinal epithelium through microfold cells overlying Peyer's patches, subsequently surviving within macrophages and disseminating throughout the reticuloendothelial system [5]. This process triggers proinflammatory cytokine release, resulting in the characteristic inflammatory response and potential progression to systemic infection [6,7].

Clinical manifestations include gastroenteritis, bacteremia, and enteric fever, with the latter characterized by prolonged fever, headache, myalgia, hepatosplenomegaly, and the pathognomonic rose spots [8]. Complications may include intestinal perforation, neurological involvement, and chronic carrier state with gallbladder persistence, potentially increasing malignancy risk [9]. Enteric fever remains fatal without prompt antibiotic treatment [10,11].

The global burden of typhoid fever is substantial, particularly in South Asia and sub-Saharan Africa, where annual incidence rates exceed 100 cases per 100,000 population [14]. The disease predominantly affects populations in low- and middle-income countries with inadequate sanitation systems [15]. A critical challenge in contemporary management is the emergence of antimicrobial resistance (AMR), which has transformed treatment paradigms and significantly impacts clinical outcomes.

The increasing prevalence of multidrug-resistant (MDR) *Salmonella* strains, defined as resistance to three or more antibiotic classes, has become a global concern. Resistance to fluoroquinolones, traditionally considered first-line therapy for enteric fever, has reached alarming levels in many endemic regions, necessitating reliance on third-generation cephalosporins and alternative agents [12-16]. This resistance pattern has significant implications for treatment duration, hospital stay, complications, and mortality rates.

Given the evolving epidemiological landscape and rising antimicrobial resistance, continuous surveillance of *Salmonella* bloodstream infections is crucial for understanding local resistance patterns and guiding empirical therapy. This study aimed to assess the prevalence, antimicrobial resistance patterns, and clinical outcomes of *Salmonella* species isolated from blood cultures in a tertiary care hospital over a three-year period from 2022 to 2024, providing insights into the current status of *Salmonella* BSIs in our healthcare setting.

## MATERIALS AND METHODS:

### Study design and setting:

This cross-sectional observational study was conducted over a period of three years, from January 2022 to January 2024, at the Central Laboratory, Department of Microbiology, Saveetha Medical College, and Hospital. Blood culture sets were collected from all the patients with fever with chills and rigor associated with vomitting and diarrhoea and processed in the Department of Microbiology. All patient data was handled with strict confidentiality.

### Blood culture collection and processing:

At least two sets of blood samples were collected from different sites, with up to 10 mL for adults before the administration of any antimicrobials. These samples were inoculated into both aerobic and anaerobic culture bottles. These were incubated using the BacT/Alert automated blood culture system (bioMerieux, Marcy l'Etoile, France). A fluorescent-based detector tracking CO2 production was used to track microbial development, and an automated warning signal signaled a positive blood culture.

### Salmonella typhi and paratyphi A and B isolation *and identification:*

In the year 2022, a total of 25 clinical strains of *Salmonella typhi and paratyphi A and B* was isolated from blood cultures and flagged positive by the BacT/ALERT 3D system (bioMérieux, Marcy l'Étoile, France). In the year 2023,a total of 22 clinical strains of *Salmonella typhi and paratyphi A and B* was isolated from blood cultures and flagged positive by the BacT/ALERT 3D system (bioMérieux, Marcy l'Étoile, France). In the year 2024,a total of 32 clinical strains of *Salmonella typhi and paratyphi A and B* was isolated from blood cultures and flagged positive by the BacT/ALERT 3D system (bioMérieux, Marcy l'Étoile, France).when blood cultures flagged positive then it was subcultured blood agar and macconkey agar.Then colonies were picked up from subculture plates and and processed through VITEK2 Automated Bacteriological Identification system.

### Antimicrobial susceptibility testing:

Susceptibility to various classes of antibiotics was determined by the disc diffusion method in accordance with Clinical Laboratory Standard Institute (CLSI 2024) guidelines. The antibiotics tested were *Ceftriaxone* (30µg), *Cefotaxime* (30µg), *Ampicillin* (10µg), *Chloramphenicol* (30µg), *Ciprofloxacin* (5µg), *Tetracycline* (30µg ), *Azithromycin* (15µg) *and Cotrimoxazole* (1.25/23.75 µg). The antimicrobial agents were procured from Himedia Laboratories (Mumbai, Maharashtra, India).

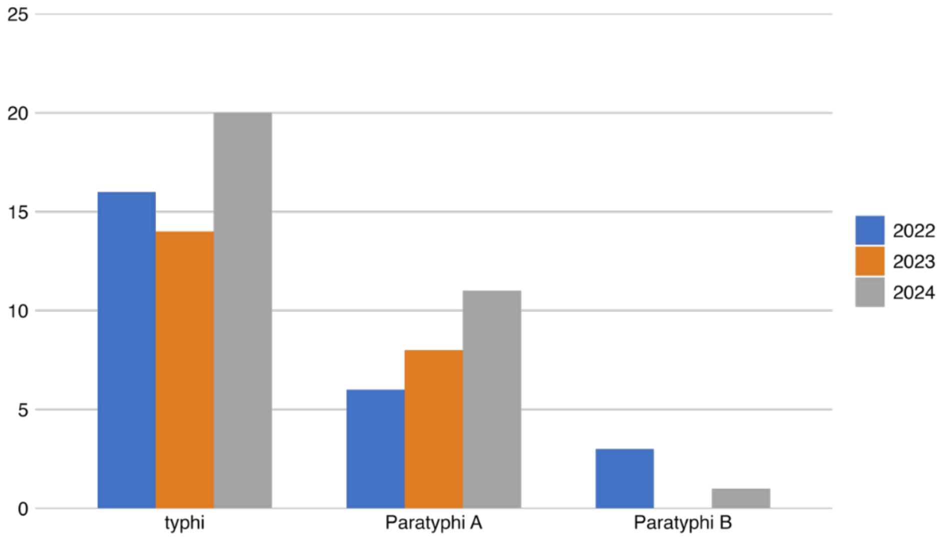
## RESULTS:

- All the positive blood beep subculture plates showed 2-3mm grey moist circular colonies with smooth entire edges on blood whereas it produced 2-3mm non lactose fermenting colonies with smooth entire edges on Macconkey agar.
- In the year 2022, out of (n=25) isolates, 16 (64%) isolates were positive for *Salmonella typhi*, (n=6) (24%) isolates were positive for *Salmonella paratyphi A*, and (n=3) (12%) isolates were positive for *Salmonella paratyphi B.*
- In the year 2023, out of (n=22) isolates, (n=14) (63%) isolates were positive for *Salmonella typhi*, (n=8) (37%) isolates were positive for *Salmonella paratyphi A*, and 0 isolates were positive *Salmonella paratyphi B.*

- In the year 2024, out of (n=32) isolates, (n=20) (62.5%) isolates were positive for *Salmonella typhi*, (n=11) (34%) isolates were positive for *Salmonella paratyphi A*, and (n=1) (3.5%) isolates were positive for *Salmonella paratyphi B.*

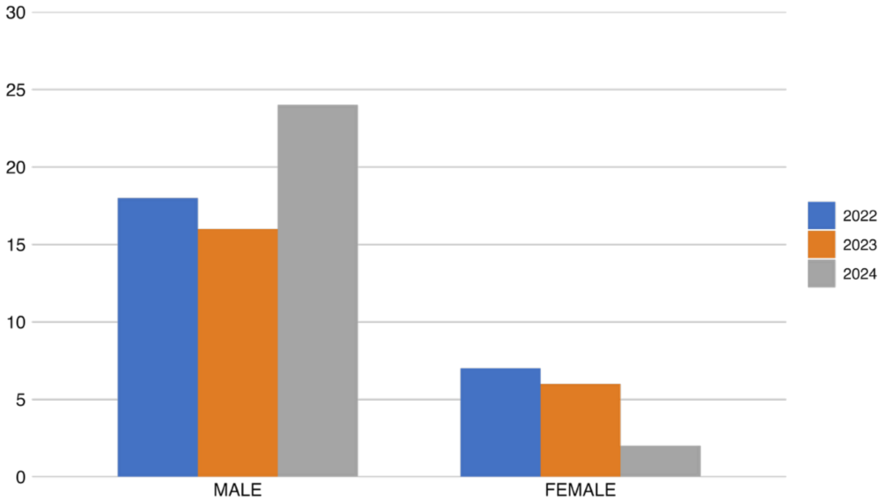
The percentages of *Salmonella typhi*, *Paratyphi A and B* are represented in Figure 1.

**FIGURE 1: Prevalence of *Salmonella typhi, Salmonella paratyphi A & B***



In the year 2022, out of (n=25) positive isolates, (n=7), 28% were female patients whereas (n=18) (72%) isolates were male patients. In the year 2023, out of (n=22) positive isolates, (n=6) 27% were female patients whereas (n=16) 73% isolates were male patients. In the year 2024, out of (n=32) positive isolates, 9(28%) were female patients whereas (n=23) 72% isolates were male patients. The gender distribution of *Salmonella* cases is depicted in Figure 2.

**FIGURE 2: Gender distribution of *Salmonella* cases**



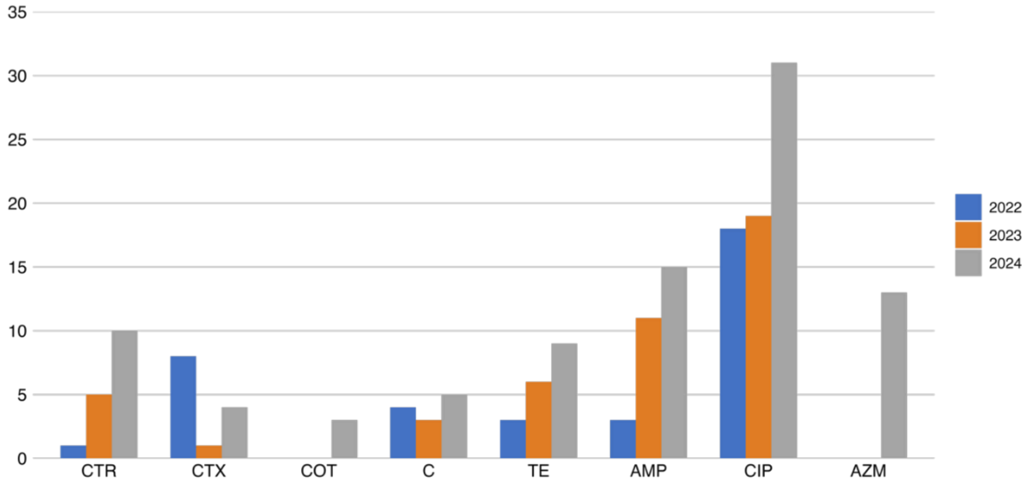
In the year 2022, Out of (n=25) isolates, (n=1) 4% isolates were resistant to ceftriaxone, (n=8) 32% isolates were resistant to Cefotaxime, (n=4), 16% isolates were resistant to Chloramphenicol, (n=3)12% isolates were resistant to Tetracycline (n=3), 12% isolates were resistant to Ampicillin (n=18), 72% isolates were resistant to Ciprofloxacin .

In the year 2023, Out of (n=22) isolates, (n=5)23% isolates was resistant to Ceftriaxone, (n=1) 4.5% isolates was resistant to Cefotaxime , (n=3)14% isolates were resistant to Chloramphenicol, (n=6)7% isolates were resistant to Tetracycline , (n=11) 50% isolates were resistant to Ampicillin , (n=19)86% isolates were resistant to Ciprofloxacin .

In the year 2024,Out of (n=32) isolates,(n=10)31.5% isolates were resistant to Ceftriaxone, (n=4)12.5% isolates were resistant to Cefotaxime, (n=3) 9% isolates were resistant to Cotrimoxazole, (n=5)16% isolates were resistant to Chloramphenicol, (n=9) (28%) isolates were resistant to Tetracycline , (n=18) 56.25% isolates were resistant to Ampicillin , (n=18)56.25% isolates were resistant to Ciprofloxacin and (n=31) 97% isolates were resistant to Azithromycin.

The year-wise resistance pattern of Salmonella cases is depicted in Figure 3.

**FIGURE 3: Resistance pattern of Salmonella cases year from 2022 to 2024**



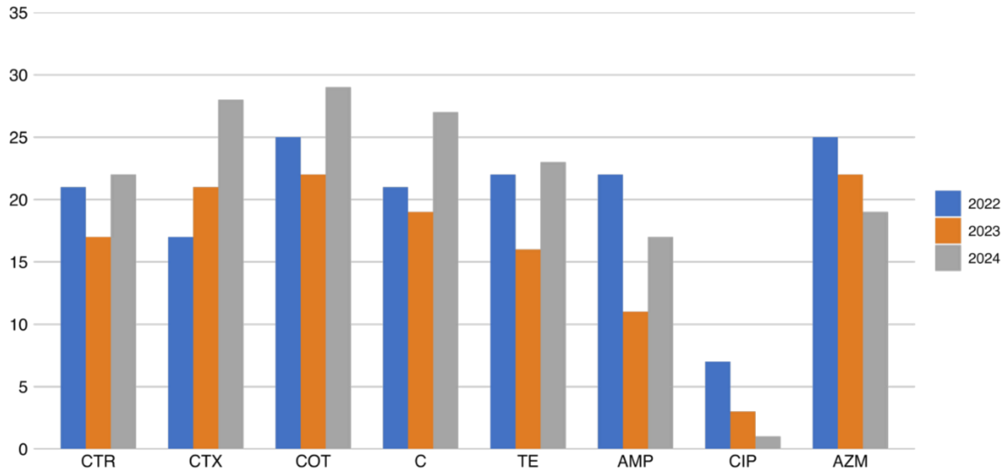
In the year 2022,Out of (n=25) isolates, (n=21)84% isolates were susceptible to Ceftriaxone, (n=17) (68%) isolates were susceptible to Cefotaxime, (n=21) 84% isolates were susceptible to Chloramphenicol, (n=22)88% isolates were susceptible to Tetracycline , (n=22) 88% isolates were susceptible to Ampicillin , (n=7) 28% isolates were susceptible to Ciprofloxacin .

In the year 2023,Out of (n=22) isolates, (n=17) 77% isolates were susceptible to Ceftriaxone, (n=21)95.5% isolates were susceptible to Cefotaxime , (n=19) 86% isolates were susceptible to Chloramphenicol, (n=16)73% isolates were susceptible to Tetracycline , (n=11)50% isolates were susceptible to Ampicillin , (n=3)59.2% isolates were susceptible to Ciprofloxacin .

In the year 2024,Out of (n=32) isolates, (n=22)68.5% isolates were susceptible to Ceftriaxone, 28(87.5%) isolates were susceptible to Cefotaxime, (n=29)91% isolates were susceptible to Cotrimoxazole, (n=27)84% isolates were susceptible to Chloramphenicol, (n=23)62% isolates were susceptible to Tetracycline , (n=14)44.75% isolates were susceptible to Ampicillin , (n=1)44.75% isolates were susceptible to Ciprofloxacin and (n=19)59% isolates were susceptible to Azithromycin.

The year-wise susceptibility pattern of Salmonella cases is depicted year wise in Figure 4.

**FIGURE 4: Susceptibility pattern of Salmonella cases year from 2022 to 2024**



The above figure depicts the geographical distribution of Enteric fever cases isolated from blood culture.
The main hematological derangements included; decreased hemoglobin, thrombocytopenia, leucocytosis and leucopenia .liver enzymes levels were above the reference range which exceeded 3-fold of the upper normal value.
The hematological parameters of these Salmonella cases in the years 2022,2023,2024 are depicted in Tables 1, 2 and 3.

## HEMATOLOGICAL PARAMETERS:

**Table 1: Hematological parameters of Salmonella cases in the year 2022**

| **Parameter** | **No of patients** | **Percentage (%)** |
|---|---|---|
| **WBC count** | | |
| Normal | 20 | 80 |
| Leukocytosis | 3 | 12 |
| Leucopenia | 2 | 8 |
| **Differential count** | | |
| Normal | 21 | 84 |
| Neutropenia | 2 | 8 |
| Neutrophilia | 2 | 8 |
| **Platelet count** | | |
| Normal | 20 | 80 |
| Thrombocytopenia | 5 | 20 |
| **Liver enzymes** | | |
| Normal | 10 | 40 |
| Elevated | 15 | 60 |

**Table 2: Hematological parameters of Salmonella cases in the year 2023**

| **Parameter** | **No of patients** | **Percentage (%)** |
|---|---|---|
| **WBC count** | | |
| Normal | 10 | 45 |
| Leukocytosis | 7 | 32 |
| leucopenia | 5 | 23 |
| **Differential count** | | |
| Normal | 17 | 77 |
| Neutropenia | 3 | 13 |
| Neutrophilia | 2 | 10 |
| **Platelet count** | | |
| Normal | 15 | 68 |
| Thrombocytopenia | 7 | 32 |
| **Liver enzymes** | | |
| Normal | 4 | 18 |
| Elevated | 18 | 82 |

**Table 3: Hematological parameters of Salmonella cases in the year 2024**

| Parameter | No of patients | Percentage (%) |
|---|---|---|
| **WBC count** | | |
| Normal | 12 | 37.5 |
| Leukocytosis | 14 | 44.75 |
| leucopenia | 6 | 18.75 |
| **Differential count** | | |
| Normal | 15 | 47 |
| Neutropenia | 10 | 31 |
| Neutrophilia | 7 | 22 |
| **Platelet count** | | |
| Normal | 25 | 78 |
| Thrombocytopenia | 7 | 22 |
| **Liver enzymes** | | |
| Normal | 2 | 6 |
| Elevated | 30 | 94 |

# DISCUSSION:

Among the total blood cultures processed, *Salmonella* species were isolated in 8% of cases in 2022,9% in 2023 and 10% in 2024. Our findings highlight a notable prevalence of *Salmonella* species isolated from bloodstream infections in our tertiary care center, echoing similar reports from South India, where isolation rates ranged from ~0.5–0.6% in pediatric blood cultures[17]. As in other Indian studies, *S. Typhi* predominated over *S. Paratyphi*[18].

The resistance percentage of ceftriaxone in our study was 4%,25% and 31.5% in the year 2022,2023 and 2025. The resistance percentage of ciprofloxacin in our study was 72%,86% and 97% in the year 2022,2023 and 2025. A central concern is the high level of resistance to fluoroquinolones (e.g., ciprofloxacin), observed in up to 90–100% of typhoidal strains since about 2011[19]. This trend was confirmed in our isolates, where non-susceptibility to ciprofloxacin and nalidixic acid was marked, mirroring findings from Northern India showing 100% resistance to pefloxacin and >80% to nalidixic acid[18]. The combination of plasmid-mediated quinolone resistance genes (e.g., *qnrS1*) and chromosomal mutations (e.g., *gyrA*, *parC*) are likely contributors, and will require molecular analysis[20].

Encouragingly, susceptibility to third-generation cephalosporins (*e.g.*, ceftriaxone) and older antibiotics like chloramphenicol remained high, consistent with reports from Kolkata and Hangzhou[20]. Our detection of multi-drug resistant (*MDR*, i.e. resistance to ≥3 classes) *Salmonella* parallels rates noted in Karachi (~57% for *S. Typhi*)[19]. Worldwide surveillance indicates growing MDR clone emergence, particularly in low–middle income regions .

In our study,in the year 2022,out of (n=25) all patients were treated with appropriate antibiotic treatment and there was no significant mortality and morbidity. In our study,in the year 2023,out of (n=22) all patients were treated with appropriate treatment and there are no significant mortality and morbidity except two patients who had prolonged hospital stay and one patient has peritonitis as complication. In our study,in the year 2024,out of (n=32) all patients were treated with appropriate treatment despite which five patients had complications of peritonitis andrelative bradycardia .Patients infected with MDR strains exhibited longer hospital stays, more ICU admissions, and higher complication rates—aligning with South American data where bloodstream infections had ~4% mortality and ~12% complication rates . In British Columbia, although typhoidal *Salmonella*-linked mortality was rare (<1%), cases with sepsis or non-typhoidal strains had serious outcomes, reinforcing the importance of prompt, appropriate therapy[19].

Antibiotic-resistant bacterial infections caused an estimated 1.2 million deaths in 2019, more than AIDS or malaria. Antimicrobial resistance (AMR) is a global health concern affecting significantly low- and middle-income countries, though high-income countries are also facing the threat of AMR at an alarming level[21]. Among diarrheal illnesses, salmonella is one of the most common causes of death worldwide. Salmonella is regarded as a universal disease due to its wide host range. Therefore, it is essential to comprehend Salmonella's epidemiological condition in order to control this pathogen[22]. There are regional variations in the incidence of salmonella infections. This change could be caused by variations in feeding habits [23], availability of migrating birds [24], temperature, humidity, and other weather-related events [23,24]. The capacity of each serovar to generate pathogenicity and adapt to the host environment varies. While some Salmonella serovars have a wide host spectrum, others are limited to a single host [25]. From the above study,it is evident majority of the isolates were positive for salmonella typhi,followed by paratyphi A and paratyphi B. We analyzed the resistance percentage of *Salmonella* against different antibiotics for three years .

Between 2022 to 2024, there was a rise in the prevalence of all Salmonella strains resistant to antibiotics. The increased prevalence of AMR bacteria is a result of the indiscriminate use of antibiotics in food production, human and animal health, and subsequent environmental leaching of the antibiotics [26]. It has been observed that S. typhi and S. Paratyphi are endemic in South Asia. Several antibiotics were used to treat enteric fever, which led to the development of antibiotic resistance [27].Due to the resistance of most *Salmonella* species to first-line antibiotics in clinical cases, critically important antibiotics such as fluoroquinolones, third and fourth generation cephalosporins, macrolide, etc. have become a choice for the treatment of invasive *Salmonella* infections [28, 29]. As a consequence of increasing resistance, WHO enlisted fluoroquinolone-resistant *Salmonella* spp. in the list of priority pathogens describing the urgent need for antibiotics against these bacteria [30].

# CONCLUSION:

Between 2022 and 2023 to 2024, there was an increase in the prevalence of Salmonella with general antibiotic resistance. According to this study, there are several possible explanations for the rising prevalence of AMR Salmonella throughout time. Therefore, preventing the development of antibiotic-resistant bacteria requires the appropriate use of antibiotics, routine AMR surveillance, the application of antibiotic stewardship, and the creation and execution of policies.

## ACKNOWLEDGEMENT

The authors would like to acknowledge all the study patients.

## CONFLICT OF INTEREST

The authors declare no conflict of Interest

# REFERENCES

1. Su, L. H., Chiu, C. H., 2007, Salmonella: clinical importance and evolution of nomenclature. *Chang Gung Med J*, 30(3), 210–219.
2. Andino, A., Hanning, I., 2015, Salmonella enterica: survival, colonization, and virulence differences among serovars. *ScientificWorldJournal*, 2015:520179.
3. Black, P. H., Kunz, L. J., Swartz, M. N., 1960, Salmonellosis—a review of some unusual aspects. *N Engl J Med*, 262, 811, 864, 921.
4. Johnson, R., Mylona, E., Frankel, G., 2018, Typhoidal Salmonella: Distinctive virulence factors and pathogenesis. *Cell Microbiol*, 20(9), e12939.
5. Coburn, B., Grassl, G.A., Finlay, B. B., 2007, Salmonella, the host and disease: a brief review. *Immunol Cell Biol*, 85(2), 112–118.
6. Finlay, B. B., Leung, K. Y., Rosenshine, I., et al., 1992, *Salmonella interactions with the epithelial cell. A model to study the biology of intracellular parasitism. ASM News*, 58, 486.
7. Giannella, R. A., Formal, S. B., Dammin, G. J., et al., 1973, Pathogenesis of salmonellosis. Studies of fluid secretion, mucosal invasion, and morphologic reaction in the rabbit ileum. *J Clin Invest*, 52, 441.
8. Gal-Mor, O., Boyle, E. C., Grassl, G. A., 2014, Same species, different diseases: how and why typhoidal and non-typhoidal Salmonella enterica serovars differ. *Front Microbiol*, 5, 391.
9. Zha, L., Garrett, S., Sun, J., 2019, Salmonella Infection in Chronic Inflammation and Gastrointestinal Cancer. *Diseases*, 7(1).
10. Rubin, R. H., Weinstein, L., 1977, *Salmonellosis: Microbiologic, Pathologic and Clinical Features*. Stratton Intercontinental Medical Book Corp, New York.
11. Stephen, J., Wallis, T. S., Starkey, W. G., et al., 1985, Salmonellosis: in retrospect and prospect. In Evered D, Whelan J (eds): *Microbial Toxins and Diarrhea Disease*, Ciba Foundation Symposium 112. Pitman Press, London, p. 175.
12. Christenson, J. C., 2013, Salmonella infections. *Pediatr Rev*, 34(9), 375–383.
13. Parry, C. M., Hien, T. T., Dougan, G., White, N. J., Farrar, J. J., 2002, Typhoid fever. *N Engl J Med*, 347(22), 1770–1782.
14. Crump, J. A., Sjölund-Karlsson, M., Gordon, M. A., Parry, C. M., 2015, Epidemiology, Clinical Presentation, Laboratory Diagnosis, Antimicrobial Resistance, and Antimicrobial Management of Invasive Salmonella Infections. *Clin Microbiol Rev*, 28(4), 901–937.
15. Ochiai, R. L., Wang, X., von Seidlein, L., et al., 2005, Salmonella paratyphi A rates, Asia. *Emerg Infect Dis*, 11, 1764–1766.
16. Vollaard, A. M., Ali, S., Widjaja, S., et al., 2005, Identification of typhoid fever and paratyphoid fever cases at presentation in outpatient clinics in Jakarta, Indonesia. *Trans R Soc Trop Med Hyg*, 99, 440–450.
17. Iyer, R. N., Jangam, R. R., Jacinth, A., et al., 2017, Prevalence and trends in the antimicrobial susceptibility pattern of Salmonella enterica serovars Typhi and Paratyphi A among children. *Eur J Clin Microbiol Infect Dis*, 36(12), 2399–2404.
18. Varghese, G., Jamwal, A., Deepika, et al., 2024, Trends in antimicrobial susceptibility pattern of Salmonella species isolated from bacteremia patients. *Diagn Microbiol Infect Dis*, 109(4), 116354.
19. Zehra, N. M., Irfan, F., Mirza, I. A., et al., 2017, Current Trends of Antimicrobial Susceptibility of Typhoidal Salmonellae. *J Coll Physicians Surg Pak*, 27(11), 690–692.
20. Yu, L., Fan, J., Lu, S., et al., 2022, Prevalence, antimicrobial resistance, and genomic characterization of Salmonella strains isolated in Hangzhou, China. *Diagn Microbiol Infect Dis*, Two-year study.
21. Murray, C. J., Ikuta, K. S., Sharara, F., et al., 2022, Global burden of bacterial antimicrobial resistance in 2019. *Lancet*, 399, 629–655.

22. Ferrari, R. G., Rosario, D. K. A., Cunha-Neto, A., et al., 2019, Worldwide epidemiology of Salmonella serovars in animal-based foods: a meta-analysis. *Appl Environ Microbiol*, 85, e00591–e619.
23. Edelson, P. J., Harold, R., Ackelsberg, J., et al., 2023, Climate change and the epidemiology of infectious diseases in the United States. *Clin Infect Dis*, 76, 950–956.
24. Ehuwa, O., Jaiswal, A. K., Jaiswal, S., 2021, Salmonella, food safety and food handling practices. *Foods*, 10, 907.
25. Islam, M. S., Paul, A., Talukder, M., et al., 2021, Migratory birds travelling to Bangladesh are potential carriers of multi-drug resistant bacteria. *Saudi J Biol Sci*, 28, 5963–5970.
26. Evangelopoulou, G., Kritas, S., Govaris, A., Burriel, A. R., 2013, Animal salmonelloses: a brief review of "host adaptation and host specificity". *Vet World*, 6, 703–708.
27. Chereau, F., Opatowski, L., Tourdjman, M., Vong, S., 2017, Risk assessment for antibiotic resistance in South East Asia. *BMJ*, 358, j3393.
28. Akhtar, S., Sarker, M. R., Jabeen, K., et al., 2015, Antimicrobial resistance in Salmonella enterica serovar Typhi and Paratyphi in South Asia. *Crit Rev Microbiol*, 41, 536–545
29. Cuypers, W. L., Jacobs, J., Wong, V., et al., 2018, Fluoroquinolone resistance in Salmonella: insights by whole genome sequencing. *Microb Genom*, 4, e000195.
30. Collignon, P. C., Conly, J. M., Andremont, A., et al., 2016, World Health Organization ranking of antimicrobials according to their importance in human medicine: a critical step for developing risk management strategies to control antimicrobial resistance from food animal production. *Clin Infect Dis*, 63, 1087–1093.