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Pattern of Blood Culture Isolates in A Tertiary Care Hospital with Emphasis on Salmonella Species and their Antibiotic Susceptibility Pattern- Retrospective Analysis

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ABSTRACT
Background: Bloodstream infections (BSIs) are a major cause of morbidity in tertiary care settings. Salmonella species remain important bloodstream pathogens in endemic regions, with emerging antimicrobial resistance posing therapeutic challenges. This study aimed to evaluate the pattern of blood culture isolates with emphasis on Salmonella species and their antimicrobial susceptibility pattern in a tertiary care hospital.
Methods: This retrospective study was conducted in the Microbiology Department of a tertiary care hospital from June 2024 to July 2025. All blood cultures received during the study period were processed using an automated system. Standard microbiological methods identified organisms. Antimicrobial susceptibility testing was performed by the Kirby–Bauer disc diffusion method and interpreted according to CLSI guidelines.
Results: Of 4058 blood cultures processed, 946 (23.3%) were positive. Gram-positive bacteria accounted for 58.7% of isolates, with methicillin-resistant coagulase-negative staphylococci (28.2%) being the most common. Among Gram-negative organisms, *Pseudomonas* spp (7.1%), *Acinetobacter baumannii* (5.7%), and *Klebsiella pneumoniae* (5.4%) were frequently isolated. *Salmonella* species constituted 53 isolates (5.6% of positives), predominantly *Salmonella typhi* (48 isolates). High susceptibility was observed to azithromycin, carbapenems, cotrimoxazole, and chloramphenicol, whereas 60.4% of isolates were resistant to ciprofloxacin.
Conclusion: The study highlights *S. typhi* as a significant bloodstream pathogen with high fluoroquinolone resistance and better susceptibility to alternative antibiotics. Continuous surveillance of antimicrobial patterns is essential for effective empirical therapy.

Key-words: Blood culture; *Salmonella typhi*; Antimicrobial susceptibility; Enteric fever; Antibiogram

INTRODUCTION

Bloodstream infections (BSIs) remain a major cause of morbidity and mortality worldwide, particularly in low- and middle-income countries where infectious diseases continue to pose a significant health burden [1,2].

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Early diagnosis and prompt initiation of appropriate antimicrobial therapy are critical determinants of clinical outcome in patients with bacteremia [3]. Blood culture remains the gold standard for diagnosing bloodstream infections, as it enables definitive identification of the causative organism and antimicrobial susceptibility testing [4]. The spectrum of pathogens causing BSIs varies by geographical region, patient population, hospital practices, and antimicrobial use patterns [5]. Studies from tertiary care hospitals have consistently demonstrated a diverse range of Gram-positive and Gram-negative organisms responsible for bloodstream infections.

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Common Gram-positive pathogens include *S. aureus*, MRSA, and coagulase-negative staphylococci (CONS).

In contrast, frequently isolated Gram-negative organisms include *Escherichia coli*, *K. pneumoniae*, *Pseudomonas* species, and *Acinetobacter* species [6,7]. The increasing prevalence of multidrug-resistant organisms in hospital settings further complicates the management of BSIs [8]. Among Gram-negative pathogens, *Salmonella* species remain important etiological agents of bloodstream infections in endemic regions. Enteric fever, caused predominantly by *Salmonella enterica* serovar Typhi and *Salmonella Paratyphi A*, remains a significant public health concern in South Asia [9]. India bears a substantial burden of enteric fever, with surveillance studies reporting sustained transmission in both urban and peri-urban settings [10]. Blood culture-confirmed cases from tertiary care centers have demonstrated that *S. typhi* remains the predominant serovar isolated, followed by *S. paratyphi A* [11]. Several Indian studies have highlighted the continued importance of *Salmonella* species as bloodstream pathogens, with variable isolation rates reported across institutions [12,13]. Enteric fever remains a major public health concern in India, particularly in rapidly urbanizing regions. Surveillance data from Navi Mumbai reported culture-confirmed enteric fever cases over five years, highlighting sustained transmission in urban settings [14]. Seasonal variation in isolation rates, particularly an increased incidence during summer and monsoon months, has also been documented in endemic regions [15]. These findings emphasize the need for institution-specific data to understand local epidemiological patterns. Antimicrobial resistance among *Salmonella* species has emerged as a growing concern over recent years [16]. Reduced susceptibility to fluoroquinolones, particularly ciprofloxacin, has been widely reported across different regions [17,18]. Resistance to conventional first-line agents such as ampicillin, chloramphenicol, and cotrimoxazole was historically common; however, recent studies have noted a possible re-emergence of susceptibility to these drugs in certain settings [19]. Most contemporary reports indicate retained susceptibility to third-generation cephalosporins and azithromycin, which continue to form the backbone of therapy for enteric fever [20].

Nevertheless, emerging reports of cephalosporin resistance and extensively drug-resistant (XDR) strains underline the importance of regular antimicrobial surveillance [21]. Institutional antibiograms derived from periodic evaluation of blood culture isolates provide critical guidance for empirical therapy and antimicrobial stewardship practices [22]. Given the dynamic nature of pathogen distribution and resistance trends, periodic local assessments are essential. In this context, the present study was undertaken in the Department of Microbiology of D.Y. Patil Medical College and Hospital, Navi Mumbai, to analyze the pattern of blood culture isolates in a tertiary care setting, with special emphasis on *Salmonella* species and their antimicrobial susceptibility pattern. The study aims to contribute institution-specific data to guide empirical treatment and strengthen antimicrobial stewardship strategies.

MATERIALS AND METHODS

Study Design and Setting- This retrospective, cross-sectional, laboratory-based study was conducted in the Department of Microbiology at a tertiary care hospital. All blood culture samples from patients with suspected bloodstream infections between June 2024 and July 2025 were included. Duplicate isolates from the same patient were excluded.

Sample Processing and Identification- Blood cultures were processed using an automated system (BD Bactec Fx40) as per manufacturer's instructions. Positive samples were subjected to Gram staining and sub-cultured onto appropriate media. Organisms were identified using colony morphology, Gram staining, and standard biochemical tests.

Antimicrobial Susceptibility Testing- Antimicrobial susceptibility testing was done using Kirby–Bauer disc diffusion on Mueller–Hinton agar, interpreted per CLSI guidelines [23,24].

Data Collection- Data on total blood cultures, culture positivity, organism distribution, and antimicrobial susceptibility patterns were obtained from laboratory records.

Statistical Analysis- Descriptive statistics were used. Categorical variables were expressed as frequencies and percentages. Blood culture positivity rate and percentage distribution of isolates (n=946) were calculated. The temporal distribution of *Salmonella* isolates was analyzed month-by-month.

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Ethical Considerations- As this was a retrospective study without patient identifiers, informed consent was not required. Institutional ethical approval was obtained as per hospital policy.

RESULTS

During the study period, a total of 4058 blood culture samples were processed. Of these, 946 samples yielded positive growth, resulting in an overall blood culture positivity rate of 23.3%. Gram-positive bacteria constituted most isolates (555; 58.7%), while Gram-negative bacteria accounted for 391 isolates (41.3%). Among Gram-positive organisms, methicillin-resistant coagulase-negative staphylococci (MRCONS) were the predominant isolates (267; 28.2%), followed by CONS (69; 7.3%), *Staphylococcus haemolyticus* (46; 4.9%), *Staphylococcus epidermidis* (42; 4.4%), and *S. aureus* (41; 4.3%). MRSA constituted 11 isolates (1.2%). Among Gram-negative organisms, *Pseudomonas* spp (67; 7.1%), *A. baumannii* (54; 5.7%), *K. pneumoniae* (51; 5.4%), *E. coli* (49; 5.2%), and *Burkholderia cepacia* complex (43; 4.5%), *Salmonella* spp. (53; 5.6%) were frequently isolated (Table 1).

Table 1: Organism-wise distribution of blood culture isolates (n = 946)

Organism	Number of isolates n (%)
MRCONS	267 (28.2)
CONS	69 (7.3)
Klebsiella pneumoniae	51 (5.4)
Pseudomonas spp	67 (7.1)
Pseudomonas aeruginosa	40 (4.2)
Acinetobacter baumannii	54 (5.7)
Burkholderia cepacia complex	43 (4.5)
Escherichia coli	49 (5.2)
Staphylococcus aureus	41 (4.3)
MRSA	11 (1.2)
Staphylococcus epidermidis	42 (4.4)
Staphylococcus haemolyticus	46 (4.9)
Staphylococcus hominis	36 (3.8)
Staphylococcus equarium	1 (0.1)
Enterococcus faecalis	26 (2.7)
Streptococcus spp	16 (1.7)
Stenotrophomonas maltophilia	16 (1.7)
Enterobacter cloacae	9 (1.0)
Citrobacter spp	1 (0.1)
Citrobacter freundii	6 (0.6)
Proteus vulgaris	2 (0.2)
Salmonella Typhi	48 (5.1)
Salmonella Paratyphi A	4 (0.4)
Salmonella spp	1 (0.1)

Given the clinical importance of enteric fever, *Salmonella* isolates were analyzed separately. Out of the 946 culture-positive samples, 53 isolates (5.6%) were identified as *Salmonella* species, accounting for 1.31% of all blood cultures processed. The distribution of *Salmonella* species is presented in Table 2. *S. typhi* was the predominant isolate (48; 5.1%), followed by *S. paratyphi* A (4; 0.4%) and Salmonella spp (1; 0.1%).

Table 2: Distribution of *Salmonella* isolates among culture-positive blood samples (n = 946)

***Salmonella* species**	**Number of isolates n (%)**
Salmonella Typhi	48 (5.1)
Salmonella Paratyphi A	4 (0.4)
Salmonella spp	1 (0.1)
Total *Salmonella* isolates	53 (5.6)

The antimicrobial susceptibility pattern of the Salmonella isolates (n=53) is summarized in Table 3. High susceptibility was observed to azithromycin (100%), imipenem (92.5%), meropenem (94.3%), amoxicillin–clavulanate (93.8%), and cotrimoxazole (93.6%). Complete susceptibility was also noted to chloramphenicol and minocycline, although these agents were tested against a limited number of isolates. Moderate susceptibility was observed to ampicillin (75.5%) and ceftriaxone (75.5%). A high level of resistance was observed to ciprofloxacin, with 32 isolates (60.4%) being resistant. Resistance to cefixime was also noted (60%), though the number of isolates tested was small. Complete susceptibility was also observed to chloramphenicol and minocycline; however, these agents were tested against a limited number of isolates. Percentages were calculated based on the number of isolates tested for each antimicrobial agent.

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Table 3: Antimicrobial susceptibility pattern of *Salmonella* isolates (n = 53)

Antibiotic	Number tested (n)	Sensitive n (%)	Resistant n (%)
Ampicillin (AMP)	53	40 (75.5)	13 (24.5)
Amoxicillin–clavulanate (AMC)	32	30 (93.8)	2 (6.2)
Azithromycin (AZ)	21	21 (100)	0 (0)
Ciprofloxacin (CIP)	53	21 (39.6)	32 (60.4)
Cefixime (CFM)	5	2 (40.0)	3 (60.0)
Ceftriaxone (CTR)	49	37 (75.5)	12 (24.5)
Imipenem (IPM)	53	49 (92.5)	4 (7.5)
Meropenem (MRP)	53	50 (94.3)	3 (5.7)
Cotrimoxazole (COT)	47	44 (93.6)	3 (6.4)
Minocycline (MI)	8	8 (100)	0 (0)
Chloramphenicol (C/CH)	15	15 (100)	0 (0)

Month-wise analysis of blood culture isolates demonstrated fluctuating trends over the study period (Table 4). *S. typhi* isolates were observed intermittently throughout the year, with relatively higher isolation during the summer and early monsoon months. No consistent increase or decrease was evident over time. Values represent the number of isolates recovered each month.

Table 4: Month-wise distribution of *Salmonella* isolates during the study period

Month–Year	*Salmonella Typhi*	*Salmonella Paratyphi A*	*Salmonella* spp	Total *Salmonella* isolates
Jun-2024	2	0	0	2
Jul-2024	1	1	0	2
Aug-2024	0	1	0	1
Sep-2024	0	0	1	1
Oct-2024	1	1	0	2
Nov-2024	0	0	0	0
Dec-2024	0	1	0	1
Jan-2025	4	0	0	4
Feb-2025	0	0	0	0
Mar-2025	2	0	0	2
Apr-2025	11	0	0	11
May-2025	4	0	0	4
Jun-2025	13	0	0	13
Jul-2025	10	0	0	10
Total	48	4	1	53

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DISCUSSION

Bloodstream infections remain a major cause of morbidity and mortality, particularly in tertiary care settings [25,26]. Continuous surveillance of blood culture isolates and their antimicrobial susceptibility patterns is essential to guide empirical therapy and antimicrobial stewardship [27]. In the present study, the overall blood culture positivity rate was 23.3%, which is comparable to rates reported in other tertiary care centers in India and in similar healthcare settings [28,29]. Gram-positive organisms accounted for the majority (58.7%) of isolates, with MRCONS as the predominant isolate. The high proportion of coagulase-negative staphylococci may reflect both true bacteremia and possible contamination, findings documented in previous hospital-based studies [30]. Among Gram-negative organisms, *Pseudomonas* spp., *Acinetobacter baumannii, K. pneumoniae*, and *E. coli* were commonly isolated, indicating the continued burden of hospital-associated Gram-negative infections [31,32]. The presence of non-fermenting Gram-negative bacilli underscores the importance of infection control measures in tertiary care settings [33]. *Salmonella* species accounted for 5.6% of culture-positive isolates and 1.31% of total blood cultures processed. *S. typhi* was the predominant species, consistent with the epidemiology of enteric fever in endemic regions [25]. The month-wise distribution demonstrated intermittent isolation throughout the study period, with relatively higher isolation during the summer and early monsoon months, which may correlate with known seasonal patterns of enteric infections [34]. The antimicrobial susceptibility pattern of *Salmonella* isolates revealed high susceptibility to azithromycin, carbapenems, amoxicillin–clavulanate, and cotrimoxazole. Similar susceptibility trends have been reported in recent surveillance studies [26]. Notably, complete susceptibility was observed to chloramphenicol and minocycline, although these agents were tested against a limited number of isolates. These findings suggest a possible re-emergence of susceptibility to older first-line agents, as described in the recent literature [25].

In contrast, a high level of resistance to ciprofloxacin (60.4%) was observed, indicating reduced reliability of fluoroquinolones for empirical therapy in this setting. Increasing fluoroquinolone resistance among *Salmonella* isolates has been widely reported across endemic regions [17,18]. The observed resistance trends underscore the need for periodic local antibiogram monitoring to guide appropriate antibiotic selection. Overall, the findings highlight the importance of continuous microbiological surveillance in tertiary care hospitals to detect changing pathogen profiles and evolving antimicrobial resistance patterns.

CONCLUSIONS

Appropriate antimicrobial therapy remains fundamental to the effective management of bloodstream infections, particularly those caused by Salmonella species. Timely reporting of antimicrobial susceptibility patterns is essential to guide rational treatment decisions and improve patient outcomes. The present study highlights the predominance of S. typhi among Salmonella isolates and demonstrates a concerning level of ciprofloxacin resistance, consistent with recent regional surveillance reports. The observed variability in susceptibility to first-line and second-line agents emphasises the importance of institution-specific antibiograms in formulating empirical therapy protocols based on local epidemiological trends [26]. Continued surveillance of blood culture isolates is necessary to detect emerging resistance patterns and to support evidence-based antimicrobial policies. Implementation of robust antimicrobial stewardship strategies, including rational antibiotic use and periodic review of treatment guidelines, is essential to contain the spread of resistance. Sustained microbiological monitoring and prudent antibiotic practices remain key to preserving therapeutic effectiveness and safeguarding community health.

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