RESEARCH PAPER

Blood Culture Positivity and Antimicrobial Resistance Profile of Salmonella enterica Among Patients with Fever for 3 or More Days in Dhaka, Bangladesh: A Six-Month Retrospective Cross-Sectional Study

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ABSTRACT:

Background: *Enteric fever remains an important cause of prolonged febrile illness in South Asia, while antimicrobial resistance increasingly complicates treatment. This study assessed blood-culture positivity for Salmonella enterica and described the antimicrobial resistance profile of available Salmonella bloodstream isolates from a private diagnostic centre in Dhaka, Bangladesh.* ***Methods:*** *This retrospective cross-sectional study included 5,008 blood culture samples from patients who had fever for 3 or more consecutive days in the last 7 days during a six-month period. Overall blood-culture positivity was 692/5,008 (13.8%). Among culture-positive samples, 227/692 (32.8%) were positive for Salmonella enterica, and 141/227 (62.1%) isolates were classified as resistant. Antimicrobial susceptibility testing was performed by disc diffusion. For the present analysis, both "R" and "M" entries in the laboratory dataset were classified as resistant, as specified by the investigators. Multidrug resistance (MDR) was defined as resistance to at least one agent in three or more antimicrobial classes.* ***Results:*** *Among 692 culture-positive blood cultures, 227 were Salmonella positive, giving a Salmonella positivity of 32.8%. Among the 141 resistant isolates, 122 (86.5%) were S. Typhi and 19 (13.5%) were S. Paratyphi A. Mean age was 22.20 ± 19.10 years; 72 (51.1%) patients were male. Resistance was highest to nalidixic acid (136/141, 96.5%) and azithromycin (85/141, 60.3%), followed by ampicillin (32/141, 22.7%) and chloramphenicol (28/141, 19.9%). Ceftriaxone and cefixime resistance each occurred in 4/141 (2.8%) isolates, all S. Paratyphi A. Azithromycin resistance was higher in S. Paratyphi A than S. Typhi (89.5% vs 55.7%; Fisher's exact p=0.005). MDR was present in 30/141 (21.3%) isolates.* ***Conclusion:*** *Among 5,008 blood cultures obtained from patients with 3 or more consecutive days of fever in the last 7 days, 692 (13.8%) showed bacterial growth and 227 (32.8% of culture-positive samples) were reported positive for Salmonella. Among the 227 Salmonella-positive cultures, 141 (62.1%) isolates were classified as resistant. Nalidixic acid and azithromycin resistance were frequent, whereas resistance to ceftriaxone and cefixime was uncommon overall but concentrated in S. Paratyphi A. Continued local surveillance and verification of resistance phenotypes are warranted*

Keywords: Salmonella enterica, Enteric fever; Blood culture, Antimicrobial resistance, Salmonella Typhi, Salmonella, Paratyphi A, Bangladesh .

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INTRODUCTION:

Salmonella enterica serovars Typhi and Paratyphi A are the primary cause of enteric fever, which includes typhoid and paratyphoid fever and is a clinically significant systemic infection. These human-restricted viruses are spread by food or water tainted by the excrement of infected individuals or long-term carriers; as a result, the incidence of disease is strongly associated with access to timely diagnosis, safe water, sanitation, and food hygiene. Enteric fever typically results in bacteremia and a persistent systemic infection, in contrast to many non-typhoidal Salmonella infections that primarily induce gastroenteritis.

Patients may experience encephalopathy, sepsis, prolonged hospital stays, gastrointestinal bleeding or perforation, or even death if treatment is ineffective. Therefore, the burden extends beyond acute morbidity: delayed detection may result in wasteful or inefficient antibiotic exposure, subsequent transmission, missed work and school days, and increased strain on health systems. These issues are particularly crucial in endemic areas where fever is prevalent and early symptoms are similar to those of dengue, rickettsial illness, and other bacterial infections. For proper treatment, surveillance, and antimicrobial stewardship, microbiological confirmation and reliable antibiotic susceptibility tests are crucial. Clinical evaluation alone may not be sufficient to determine the source of persistent fever [1-3]. The main confirming test for enteric fever is blood culture, although its sensitivity is not ideal. Pooled sensitivity was estimated by a comprehensive review and meta-analysis to be roughly 59%. Blood volume, prior antibiotic exposure, and length of illness all had an impact on sensitivity [2]. Therefore, it is not appropriate to interpret the percentage of positive cultures in a diagnostic laboratory as the population incidence of disease, even though it is clinically valuable.

Despite long-term decreases, enteric fever still has a significant global burden. According to the Global Burden of Disease Study 2017, there were 14.3 million typhoid and paratyphoid fever illnesses and roughly 135,900 related deaths globally that year. An estimated 10.3 million cases, or 71.8% of all cases worldwide, occurred in South Asia, and around 75% of cases of enteric fever were caused by Salmonella Typhi [1]. These estimates show how disease is concentrated in areas with inadequate infrastructure for water and sanitation, food safety, prompt diagnosis, and access to healthcare. Because many patients do not seek care at surveillance centers, blood culture is not entirely sensitive, and prior antibiotic usage can decrease organism recovery, enteric fever is especially challenging to measure precisely. As a result, estimates from population-level modeling, hospital-based surveillance, and regular clinical laboratories describe distinct denominators and should be evaluated appropriately [1,2].

The treatment of enteric fever is made more difficult by antimicrobial resistance (AMR). Multidrug-resistant (MDR) bacteria emerged as a result of resistance to conventional first-line treatments including ampicillin, chloramphenicol, and cotrimoxazole. Typhi; decreased sensitivity to fluoroquinolones later extended over South Asia. Because these medications have been used when earlier agents or fluoroquinolones are inappropriate, resistance to later-line treatments, such as azithromycin and third-generation cephalosporins, is particularly problematic [4]. Results from the 2016–2019 Surveillance for Enteric Fever in Asia Project (SEAP) show significant geographical variations: fluoroquinolone non-susceptibility among S. Extensively drug-resistant (XDR) S. Typhi was found in 64% of Pakistani isolates, whereas typhi isolates were found in 98% of isolates in Bangladesh, 87% in Nepal, and 95% in Pakistan. In contrast, azithromycin non-susceptibility was rare in that surveillance's Bangladeshi component [5]. These trends show that resistance is not consistent between nations or between antimicrobial drugs, serovars, and time periods.

Therefore, local, often updated susceptibility data are required to monitor resistance trends, support empirical treatment decisions, and direct antibiotic stewardship. Because variations in testing procedures and classification can restrict direct comparisons between research, reports must additionally specify the laboratory standards and interpretive categories employed [4,5].

Because enteric fever is still widespread and Dhaka has been the subject of both clinical and microbiological study, Bangladesh is a crucial location for this kind of surveillance. According to SEAP, there were 128 incidences of paratyphoid and 913 cases of typhoid per 100,000 person-years in the participating Dhaka pediatric hospital catchments [6]. Although they should not be regarded as nationally representative estimates for all ages, these estimates show a significant burden among the populations under study. The need for ongoing surveillance of circulating lineages and resistance patterns is supported by earlier genomic analysis of S. Typhi isolates collected in urban Dhaka between 2004 and 2016, which revealed a variety of bacterial genotypes, shifting population structure, and decreased fluoroquinolone susceptibility [7]. MDR decreased from 38% in 1999 to 17% in 2022, according to a longer-term laboratory surveillance from Bangladesh that included 12,435 culture-confirmed typhoid cases between 1999 and 2022. However, azithromycin resistance was reported at a significantly lower level, averaging about 2% annually after its initial detection, while ciprofloxacin non-susceptibility remained above 90% [8]. These results indicate that antimicrobial resistance trends ought to be evaluated on a drug-specific basis instead of being consolidated into a singular, unqualified metric of resistance.

Monitoring certain serovars is of equal significance. A 23-year examination of S. Paratyphi A isolates in Bangladesh revealed that over 97% exhibited susceptibility to ampicillin, chloramphenicol, and cotrimoxazole; no resistance to ceftriaxone was identified, and more than 99% were susceptible to azithromycin. Nonetheless, diminished susceptibility

to ciprofloxacin was seen in over 99% of isolates [9]. This contrasts with the resistance profile of S. Typhi and warns against presuming that the two serovars exhibit the same antibiotic susceptibility patterns. Prevention continues to be crucial in conjunction with treatment and laboratory monitoring. In a cluster-randomized trial conducted in metropolitan Dhaka, a Vi-tetanus toxoid typhoid conjugate vaccine demonstrated 85% efficacy in preventing blood-culture-confirmed typhoid in vaccinated children, endorsing vaccination as a key preventive strategy in areas with high disease burden 10. Vaccination, improved water and sanitation, food safety, and judicious use of antimicrobials are to be regarded as interrelated components in the management of enteric fever.

Despite the rich evidence shown by these investigations, a significant disparity persists between specialised surveillance and the microbial profiles observed in standard diagnostic procedures. Significant research in Bangladesh have investigated enduring patterns, specific paediatric hospitals and clinics, delineated surveillance areas, or the genetic traits of certain isolates [6-9]. The recent blood-culture yield and antibiotic susceptibility profile among patients of varying ages sent to a private diagnostic center for fever lasting at least three consecutive days within the last week are not thoroughly detailed. This clinical denominator differs from a community population and cannot yield a national incidence estimate; nonetheless, it can illustrate the role of Salmonella in cultures submitted from patients with ongoing fever and outline local susceptibility trends pertinent to the involved service. Published estimates of azithromycin resistance vary significantly: a limited investigation in Bangladesh including 40 clinical isolates indicated extremely high resistance, while more extensive longitudinal surveillance revealed considerably reduced resistance in S. Typhi and elevated susceptibility in S. Paratyphi A [8,9,11]. This discrepancy may indicate discrepancies in isolate selection, research duration, laboratory techniques, or the interpretation of susceptibility classifications, underscoring the necessity for clear, standardised reporting instead of direct percentage comparisons devoid of context [12]. A modern laboratory assessment can thus enhance, but cannot substitute, population surveillance and molecular research.

Therefore, this study aimed to determine the proportion of blood cultures positive for Salmonella enterica among patients with fever for at least three consecutive days within the preceding seven days at a private diagnostic centre in Dhaka, Bangladesh, during a six-month period, and to describe the serovar distribution and antimicrobial susceptibility patterns, including multidrug resistance, among isolates with available susceptibility data.

MATERIALS AND METHODS:

Study design and setting: A retrospective cross-sectional laboratory-based study was conducted at a private diagnostic centre in Dhaka, Bangladesh over a six-month period from July 2025 to December 2025. The centre receives samples from both outpatient and hospitalized patients.

The study population was defined as patients with fever persisting for 3 or more consecutive days in the last 7 days at the time of blood culture submission. This criterion was selected because it captures the typical timeframe during which enteric fever becomes clinically evident and diagnostic investigations are intensified. Patients presenting with very early fever (1–2 days) may not yet manifest the sustained bacteremia characteristic of enteric fever, while this cutoff enriches the population for suspected enteric fever and other causes of prolonged undifferentiated fever that warrant blood culture evaluation.

Study population and blood cultures: During the study period, blood cultures were obtained from patients with fever for 3 or more consecutive days. Of 5,008 samples, 692 cultures were positive and 227 cultures were reported positive for Salmonella enterica. Among them , 141 isolates were resistant.

Bacterial identification: Blood specimens were processed according to the diagnostic center's routine microbiology protocol. Salmonella identification and serovar assignment were performed using the laboratory methods recorded by the center, including biochemical and automated identification and serologic confirmation where applicable.

Antimicrobial susceptibility testing: In accordance with the investigators' clarification, both "R" and "M" entries were counted as resistant. "S" was counted as susceptible.

Definitions: For descriptive analysis, antimicrobial classes were grouped as follows: β-lactams (ampicillin and cephalosporins), macrolides (azithromycin), folate-pathway inhibitors (cotrimoxazole), quinolones/fluoroquinolones (nalidixic acid, ciprofloxacin, levofloxacin, and moxifloxacin), and phenicols (chloramphenicol). MDR was defined as resistance to at least one tested agent in three or more of these antimicrobial classes, consistent with the general international definition of acquired MDR[13].

Statistical analysis: Categorical variables are presented as number and percentage. Continuous age data are summarized as mean ± standard deviation, median and interquartile range, and range. Resistance proportions were calculated using available results for each antimicrobial. Comparisons between S. Typhi and S. Paratyphi A were performed using Fisher's exact test because several cells contained small or zero

counts. Two-sided $p<0.05$ was considered statistically significant.

Ethical considerations

This study used retrospectively collected routine laboratory data. Patient identifiers were not used in the analysis.

STROBE Participant Flow Diagram

Blood culture specimens received during the six-month study period of patients having fever ≥3 days (N=5008)

↓

Salmonella enterica isolates included in the study
n = 227 (32.8% of positive isolates)

↓

Resistant isolates identified (n=141; 62.1% of all Salmonella isolates)

↓

S. Typhi n = 122 (86.5%)	**S. Paratyphi A** n = 19 (13.5%)

↓

Antimicrobial resistance and multidrug-resistance (MDR)analysis
Final analysis of the included isolates

RESULTS:

Blood-culture positivity and isolate characteristics

Patients with 3 or more consecutive days of fever in the last 7 days underwent blood culture. Among 5,008 samples, 692 patients were reported to be culture positive (13.8%). Salmonella was isolated from 227 cultures, corresponding to a positivity of 32.8% (227/692). Among the 227 Salmonella-positive cultures, 141 isolates were found resistant (62.1%). Among the resistant isolates, 122 (86.5%) isolates were S. Typhi and 19 (13.5%) were S. Paratyphi A. The mean age was 22.20 ± 19.10 years, the median age was 18 years (IQR 9–29 years), and the range was 0.5–93 years. There were 72 (51.1%) male and 69 (48.9%) female patients (Table 1).

Table 1. Demographic and microbiological characteristics resistant Salmonella isolates (n=141)

Characteristic	n (%)
S. Typhi	122 (86.5%)
S. Paratyphi A	19 (13.5%)
Age, mean ± SD	22.20 ± 19.10 years
Age, median (IQR)	18 (9–29) years
Age, range	0.5–93 years
0–5 years	24 (17.0%)
6–10 years	19 (13.5%)
11–20 years	36 (25.5%)
21–30 years	29 (20.6%)
31–40 years	13 (9.2%)
41–50 years	8 (5.7%)
>50 years	12 (8.5%)
Male	72 (51.1%)
Female	69 (48.9%)

Overall antimicrobial resistance

Nalidixic acid showed the highest resistance rate (136/141, 96.5%), followed by azithromycin (85/141, 60.3%). Resistance to ampicillin, chloramphenicol and cotrimoxazole was 22.7%, 19.9% and 16.3% respectively. Ceftriaxone and cefixime resistance were each 2.8%, while no resistance was recorded to ceftazidime or cefepime. Ciprofloxacin, levofloxacin, and moxifloxacin resistance were each 2.8% after "M" was classified as resistant (Table 2).

Table 2. Antimicrobial susceptibility profile of detailed Salmonella isolates (N=141)

Antimicrobial	Susceptible n (%)	Resistant n (%)
Ampicillin	109 (77.3)	32 (22.7)
Ceftriaxone	137 (97.2)	4 (2.8)
Cefixime	137 (97.2)	4 (2.8)
Ceftazidime	141 (100.0)	0 (0.0)
Cefepime	141 (100.0)	0 (0.0)
Azithromycin	56 (39.7)	85 (60.3)
Cotrimoxazole	118 (83.7)	23 (16.3)
Nalidixic acid	5 (3.5)	136 (96.5)
Ciprofloxacin	137 (97.2)	4 (2.8)
Levofloxacin	137 (97.2)	4 (2.8)
Chloramphenicol	113 (80.1)	28 (19.9)
Moxifloxacin	137 (97.2)	4 (2.8)

†Both R and M were classified as resistant.

Resistance by serovar

S. Paratyphi A had significantly higher azithromycin resistance than S. Typhi (17/19, 89.5% vs 68/122, 55.7%; Fisher's exact p=0.005). Ceftriaxone and cefixime resistance occurred in 4/19 (21.1%) S. Paratyphi A isolates and in no S. Typhi isolates ($p<0.001$ for each comparison). Cotrimoxazole resistance was detected in 23/122 (18.9%) interpretable S. Typhi results but in no Paratyphi A isolates (p=0.043). Differences for the other tested agents were not statistically significant (Table 3).

Table 3. Antimicrobial resistance by serovar

Antimicrobial	S. Typhi resistant n/N (%)	S. Paratyphi A resistant n/N (%)	p value *
Ampicillin	28/122 (23.0)	4/19 (21.1)	1.000
Ceftriaxone	0/122 (0.0)	4/19 (21.1)	<0.001
Cefixime	0/122 (0.0)	4/19 (21.1)	<0.001

Ceftazidime	0/122 (0.0)	0/19 (0.0)	1.000
Cefepime	0/122 (0.0)	0/19 (0.0)	1.000
Azithromycin	68/122 (55.7)	17/19 (89.5)	0.005
Cotrimoxazole	23/122 (18.9%)	0/19 (0.0)	0.043
Nalidixic acid	117/122 (95.9)	19/19 (100.0)	1.000
Ciprofloxacin	4/122 (3.3)	0/19 (0.0)	1.000
Levofloxacin	4/122 (3.3)	0/19 (0.0)	1.000
Chloramphenicol	24/122 (19.7)	4/19 (21.1)	1.000
Moxifloxacin	4/122 (3.3)	0/19 (0.0)	1.000

***Two-sided Fisher's exact test. Both R and M were classified as resistant.**

Multidrug resistance

Using the prespecified five-class grouping, 30/141 isolates (21.3%) met the MDR definition. Five isolates (3.5%) were susceptible to all tested classes, 49 (34.8%) were resistant to one class, 62 (44.0%) to two classes, 2 (1.4%) to three classes, 10 (7.1%) to four classes, and 18 (12.8%) to all five classes (Table 4).

Table 4. Number of antimicrobial classes with resistance among detailed Salmonella isolates (N=141)

Number of resistant classes	N	%
1	49	34.8
2	62	44.0
3	2	1.4
4	10	7.1
5	18	12.8
MDR (≥3 classes)	30	21.3

DISCUSSION:

In this six-month retrospective laboratory-based study, 692 of 5,008 blood cultures (13.8%) showed bacterial growth, and Salmonella enterica was reported in 227 of the 692 culture-positive samples (32.8%). In the detailed susceptibility tables (n=141), Salmonella Typhi accounted for 122 isolates (86.5%) and Salmonella Paratyphi A for 19 (13.5%). Nalidixic acid resistance was the most frequent finding (136/141, 96.5%), followed by azithromycin resistance (85/141, 60.3%). Resistance to ampicillin, chloramphenicol, and cotrimoxazole was 22.7%, 19.9%, and 16.3%, respectively. Ceftriaxone and cefixime resistance were each reported in four isolates (2.8% overall), all classified as S. Paratyphi A (4/19, 21.1%). The reported multidrug-resistance (MDR) proportion was 30/141 (21.3%) under the study's operational definition. The unusually high azithromycin resistance and the apparent discrepancy between nalidixic acid and ciprofloxacin findings warrant careful interpretation and verification of the original laboratory categories before clinical implications are drawn.

The predominance of S. Typhi in the present susceptibility dataset is consistent with other South Asian reports. In a six-month Nepalese hospital study, Maharjan et al. isolated Salmonella from 40 of 1,298 blood specimens (3.1%); S. Typhi accounted for 72.5% and S. Paratyphi A for 27.5% of the isolates [14]. A more recent tertiary-care study in Nepal reported a similar distribution, with S. Typhi accounting for 77.2% and S. Paratyphi for 22.8% of 114 enteric-fever cases [15]. A Dhaka cohort studied during 2018–2020 also identified more S. Typhi than S. Paratyphi A cases (483 versus 121) [16]. The agreement in serovar predominance supports the epidemiological relevance of the present findings. However, culture yields should not be compared directly across studies because patient selection, referral criteria, blood-culture procedures, and denominators differ. Age distributions also require caution: the present detailed dataset contained the largest age groups among patients aged 11–30 years, whereas the Dhaka cohort reported the highest incidence among children aged 2–4 years in its closed cohort; in its dynamic cohort, the highest overall age-specific incidence was among children aged 5 to less than 16 years [16]. These differences may reflect the contrast between a diagnostic-centre sample and population-based surveillance rather than a true contradiction in age-specific risk.

The significantly elevated resistance to nalidixic acid identified in this research aligns with indications of extensive quinolone resistance or diminished fluoroquinolone susceptibility in South Asia. In the Dhaka cohort from 2018 to 2020, the resistance to nalidixic acid was recorded at 94.4% for S. Typhi and 98.3% for S. Paratyphi A isolates; there was also a prevalent intermediate susceptibility to ciprofloxacin [16]. A genomic epidemiology investigation revealed that almost 99% of sequenced isolates from Dhaka had quinolone-resistance mutations, whereas 89% of isolates from Kathmandu did as well [17]. In Nepal, Maharjan et al. documented that 85% of Salmonella isolates exhibited resistance to nalidixic acid, although 65% shown intermediate susceptibility to ciprofloxacin [14]. A comprehensive analysis of Indian research revealed a reduction in conventional MDR while fluoroquinolone resistance escalated, with the latter increasing from 10% during 2001–2005 to 66% in 2011–2015 [18]. These results generally corroborate the significant resistance to nalidixic acid documented above. The current study's stated

ciprofloxacin resistance rate of 2.8% is significantly inconsistent with regional data indicating a common occurrence of diminished susceptibility or intermediate findings. Nalidixic acid resistance, intermediate susceptibility to ciprofloxacin, and ciprofloxacin resistance are separate laboratory results and therefore not be regarded as equivalent. The initial disk-diffusion documentation, zone measurements, relevant CLSI edition, and the significance of the dataset code "M" must be verified prior to clinical interpretation of these results.

The most notable and ambiguous discovery in the current dataset is azithromycin resistance. The overall reported rate was 60.3%, with S. Paratyphi A exhibiting a greater rate than S. Typhi (89.5% compared to 55.7%). Authentic azithromycin-resistant typhoidal Salmonella has been recorded in Bangladesh. Sajib et al. validated the presence of azithromycin-resistant isolates from both serovars and illustrated that AcrB-R717Q/L mutations may arise in various Typhi and Paratyphi A genotypes [18]. A modest single-centre investigation in Dhaka, published in 2026, indicated that 85% of 60 S. Typhi isolates exhibited resistance to azithromycin, while all isolates were found to be susceptible to ceftriaxone [20]. These reports indicate that significant azithromycin resistance has been detected in certain isolate collections from Bangladesh; however, they do not confirm that these rates are indicative of the broader population. Conversely, the extensive Dhaka cohort from 2018 to 2020 indicated azithromycin resistance in 1.9% of S. Typhi and 11.6% of S. Paratyphi A isolates [16], although the genomic analysis conducted by Dyson et al. identified acrB-related azithromycin-resistance mutations in merely 1% of the sequenced Dhaka isolates [17]. Variations may indicate the temporal context, selective isolation, laboratory techniques, or interpretative standards. The current investigation indicates that the limited size of the S. Paratyphi A subgroup (n=19) constrains accuracy. The laboratory definition of "M" and the organism-specific interpretation standards require validation; if "M" signifies an intermediate classification, its conjunction with resistant outcomes may inflate resistance estimates. When possible, it is advisable to do repeat susceptibility tests and confirm the MIC prior to presenting the high azithromycin-resistance estimate as conclusive.

Resistance to conventional first-line medications was less than the documented resistance to nalidixic acid and azithromycin, however nevertheless significant: ampicillin resistance was 22.7%, chloramphenicol resistance was 19.9%, and cotrimoxazole resistance was 16.3%. Historical monitoring in Dhaka identified classical MDR in 32% of 3,928 samples. Typhi isolates gathered from 1989 to 2002 shown significant temporal variation [21]. In the Dhaka cohort from 2018 to 2020, classical multidrug resistance (MDR) was identified in 20.2% of S. Typhi isolates, whereas it was found in merely 0.8% of S. Paratyphi A isolates [16]. The current reported proportion of MDR at 21.3% closely resembles the Typhi estimate within that cohort; however, the definitions differ: this study characterises MDR as resistance to at least one tested agent across three or more antimicrobial classes, while the Dhaka cohort employed the traditional combination of ampicillin, chloramphenicol, and trimethoprim/sulfamethoxazole. The percentages should hence not be regarded as directly comparable. Geographical disparities hold significant importance. A systematic review and meta-analysis from Pakistan calculated the aggregated resistance of S. Typhi at 80% to ampicillin, 64% to ciprofloxacin, and 92% to nalidixic acid, with multidrug-resistant (MDR) and extensively drug-resistant (XDR) rates of 29% and 25%, respectively [22]. The aggregated estimates exhibited substantial variation across studies, thus serving as general overviews of the Pakistani literature instead of direct standards for Bangladesh. A distinct investigation conducted in Pakistan including 96 S. Typhi isolates revealed that 31 (32.3%) exhibited resistance to ceftriaxone, whereas 95 (99%) were resistant to ciprofloxacin; all ceftriaxone-resistant isolates tested positive for blaCTX-M-15 [23]. In contrast, the Nepalese tertiary-care research indicated an absence of MDR and resistance to third- or fourth-generation cephalosporins [15]. Collectively, these investigations reveal significant spatial and temporal discrepancies and underscore the necessity for localised monitoring instead than inferring from foreign data.

The observed resistance to ceftriaxone and cefixime in four S. Paratyphi A isolates warrants scrutiny, as it contrasts with the 2018–2020 Dhaka cohort that found no resistance to the evaluated third-generation cephalosporins in either serovar [16], and the Nepalese study that indicated full susceptibility to ceftriaxone and cefixime [15]. Conversely, the study from Pakistan indicated that around one-third of its S. Typhi isolates exhibited resistance to ceftriaxone, demonstrating that cephalosporin resistance may be present in the area but should not be presumed to have equivalent incidence in Bangladesh [23]. Four resistant isolates within a subgroup of 19 yield an inaccurate estimation and do not independently create a consistent serovar-specific pattern. Conduct susceptibility testing again using a validated approach, ideally incorporating MIC confirmation and molecular analysis when possible, before making definitive assertions regarding cephalosporin resistance in local S. Paratyphi A.

This research possesses practical advantages: it assesses 5,008 blood-culture submissions from a recent six-month timeframe and presents susceptibility findings for several antimicrobial drugs with a serovar-specific analysis. The constraints encompass the retrospective single-centre methodology, potential referral and selection bias, absence of correlated data on previous antibiotic exposure, treatment, and clinical outcomes, lack of MIC or molecular validation, and the diminutive S. Paratyphi A subgroup. The research additionally depends on standard laboratory codes, and the significance of the category "M" requires verification. If "M" signifies intermediate susceptibility, combining it with resistant outcomes may lead to an overestimation of resistance. The results ought to be conveyed as a local laboratory profile instead of a national resistance assessment. The raw laboratory dataset must be reconciled, susceptibility coding verified, and atypical resistance discoveries confirmed before submission.

CONCLUSION:

Among 692 blood-culture-positive patients with fever 3 or more consecutive days of fever in the last 7 days, 227 (32.8%) were reported Salmonella positive. In the 141 isolates with detailed data, S. Typhi predominated and resistance was particularly frequent to nalidixic acid and azithromycin. Ceftriaxone and cefixime resistance were uncommon overall but occurred exclusively in S. Paratyphi A in the available dataset. These findings emphasize the need for complete local surveillance, careful verification of laboratory susceptibility categories, and antimicrobial selection guided by validated susceptibility testing.

Author contributions

Tasnim Nafian: Conceptualization; Investigation; Data curation; Formal analysis; Visualization; Writing – original draft; **Abdullah Al Mahdi:** Investigation; Data curation; Validation; Writing – review & editing.**Shaheen Lipika Quayum:** Conceptualization; Supervision; Validation; Resources; Writing – review & editing; **Md. Abul Kalam Azad:** Supervision; Project administration; Validation; Resources; Writing – review & editing.

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Conflict of interest statement

The authors declare no conflicts of interest.

Data availability statement

The data that support the findings of this study are available from the corresponding author upon reasonable request, subject to institutional approval and applicable confidentiality requirements.

Ethics statement

This retrospective analysis used routine laboratory data.

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