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Prevalence, Risk Factors and Antimicrobial Resistance Pattern of Salmonella Isolates among Patients Attending Abubakar Tafawa Balewa University Teaching Hospital

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Abstract

Salmonella enterica serovar Typhi (*Salmonella typhi*) remains an important cause of enteric fever, particularly in low-resource settings where poor sanitation and antimicrobial resistance complicate disease control. This study investigated the prevalence, associated risk factors, clinical characteristics and antimicrobial susceptibility pattern of *S. typhi* among patients. A cross-sectional study was conducted on 138 patients whose blood and stool specimens were cultured using standard bacteriological methods. Isolates were identified by conventional microbiological techniques and antimicrobial susceptibility testing was performed using the Kirby–Bauer disk diffusion method. Associations between *S. typhi* isolation and demographic, environmental, behavioural and clinical variables were determined using the Fisher's Exact Test. Five *S. typhi* isolates were recovered, giving an overall prevalence of 3.62%, with stool specimens (4.17%) yielding slightly more isolates than blood specimens (3.03%). *Salmonella typhi* represented 4.0% of all bacterial isolates, while *Escherichia coli* and *Staphylococcus aureus* were the predominant pathogens. Demographic characteristics were not significantly associated with *S. typhi* isolation $P > 0.05$). However, the use of untreated river water, open defecation, overcrowding, poor hand hygiene, failure to wash fruits and vegetables and frequent consumption of roadside foods were significantly associated with infection ($P < 0.05$). All isolates were resistant to nalidixic acid, while high resistance was observed to cefixime and imipenem. Levofloxacin, ofloxacin and nitrofurantoin showed the highest susceptibility (60%). *Salmonella typhi* prevalence was low, but its occurrence was strongly associated with poor

environmental sanitation and hygiene. The detection of multidrug-resistant isolates underscores the need for routine microbiological surveillance, antimicrobial stewardship and improved water sanitation and hygiene interventions to support effective typhoid fever control.

Introduction

Salmonella species are among the leading bacterial pathogens responsible for foodborne and waterborne infections worldwide, posing a significant public health challenge, particularly in low and middle income countries. The genus comprises Gram-negative, facultative intracellular bacilli belonging to the family *Enterobacteriaceae*. Clinically, *Salmonella* infections are broadly classified into typhoidal *Salmonellosis*, caused mainly by *Salmonella enterica* serovars Typhi and Paratyphi and non typhoidal *Salmonellosis* (NTS), which is commonly associated with self-limiting gastroenteritis but can cause invasive bloodstream infections in vulnerable populations such as children, the elderly and immunocompromised individuals (Galán- Relaño et al., 2023; Zhou et al., 2023).

Despite considerable advances in sanitation and disease prevention, *Salmonellosis* remains a major cause of morbidity and mortality globally. The burden of the disease is disproportionately higher in sub-Saharan Africa due to inadequate access to clean water, poor sanitation, unsafe food handling practices, overcrowding and limited healthcare resources. In Nigeria, typhoid fever continues to be one of the most frequently diagnosed bacterial infections, although laboratory confirmation is often limited, resulting in inappropriate treatment and poor disease surveillance (Talukder et al., 2023).

Several epidemiological studies have identified numerous risk factors associated with *Salmonella* infection. These include consumption of contaminated food or drinking water, poor personal hygiene, inadequate hand washing, low socioeconomic status, close contact with infected individuals or animals, indiscriminate use of antibiotics and weakened immunity. In healthcare settings, understanding these risk factors is essential for developing effective preventive strategies and reducing disease transmission among patients (Browne et al., 2020; Galán-Relaño et al., 2023).

An emerging concern in the management of *Salmonellosis* is the increasing prevalence of antimicrobial-resistant *Salmonella* strains. Over the past decade, resistance to commonly prescribed antibiotics such as ampicillin, tetracycline, chloramphenicol, cotrimoxazole, nalidixic acid and fluoroquinolones has increased considerably. The emergence of multidrug-resistant (MDR) *Salmonella* limits treatment options, prolongs hospital stays, increases healthcare costs and contributes to higher morbidity and mortality. Resistance develops through multiple mechanisms, including acquisition of resistance genes via plasmids, chromosomal mutations, efflux pumps and reduced membrane permeability (Browne et al., 2023; Zhou et al., 2023).

Recent systematic reviews have shown that antimicrobial resistance among *Salmonella* isolates continues to rise globally, particularly in developing countries where inappropriate antibiotic use and weak antimicrobial stewardship remain common. The increasing occurrence of multidrug-resistant isolates highlights the urgent need for continuous surveillance of antimicrobial susceptibility patterns to guide empirical treatment and support antibiotic stewardship programmes (Effah et al., 2022; Talukder et al., 2023).

Therefore, this study seeks to determine the prevalence of *Salmonella* infection, identify associated risk factors and evaluate the antimicrobial resistance patterns of *Salmonella* isolates among patients attending Abubakar Tafawa Balewa University Teaching Hospital, Bauchi. The findings will contribute to the existing knowledge on *Salmonellosis* in Nigeria and provide evidence for clinicians,

microbiologists and public health authorities in developing effective control measures against antimicrobial-resistant *Salmonella* infections.

Materials and methods

Study Area

This study was conducted at the Microbiology Laboratory of Abubakar Tafawa Balewa University Teaching Hospital (ATBUTH), Bauchi, located in Bauchi State, Northeastern Nigeria. Bauchi State lies between latitude 9°30′N and 12°30′N and longitude 8°50′E and 11°00′E, covering a land area of approximately 49,119 km².

Questionnaire Administration and Clinical Specimen Collection

A structured questionnaire was administered to consenting participants to obtain socio-demographic information, including age, sex, marital status, occupation, place of residence and educational attainment. Data on potential risk factors associated with *Salmonella* infection were also collected, including sources of drinking water, sanitation and hygiene practices, toilet facilities, housing conditions and food-handling behaviours. Clinical information such as presenting symptoms, history of recent infections and previous hospital visits was documented.

Isolation and Identification of *Salmonella* Species

A total of 138 clinical specimens comprising blood and stool samples were processed for the isolation and identification of *Salmonella* species using standard aseptic techniques as previously described by Ngogo et al. (2020).

Stool sample processing

Approximately 1g of each stool sample was inoculated into Selenite F enrichment broth and incubated at 37°C for 24h. Following enrichment, cultures were streaked onto *Salmonella–Shigella* (SS) agar and MacConkey agar and incubated at 37°C for an additional 24h. Presumptive *Salmonella* colonies were subjected to Gram staining and microscopic examination for preliminary identification (Cheesbrough, 2018).

Blood sample processing

Venous blood specimens were inoculated into tetrathionate broth and incubated at 37°C for up to 10 days. Broths showing evidence of bacterial growth were subcultured onto SS agar and MacConkey agar and further incubated at 37°C for 24h. Suspected colonies were subsequently examined and identified using standard microbiological procedures (Collee et al., 1996).

Morphological and Biochemical Characterization of Isolates

Pure bacterial isolates were characterized based on colony morphology and Gram-staining reactions. Biochemical identification was performed using conventional tests, including urease, indole production, catalase activity, citrate utilization and Triple Sugar Iron (TSI) agar reactions. Identification of *Salmonella* species was confirmed according to established biochemical characteristics described by Cheesbrough, (2010).

Antimicrobial Susceptibility Testing

The antimicrobial susceptibility profiles of confirmed *Salmonella* isolates were determined using the Kirby–Bauer disk diffusion technique. Bacterial inoculate were standardized to the turbidity of a 0.5 McFarland standard and inoculated onto Mueller–Hinton agar plates. The isolates were tested against commonly prescribed antibiotics, including ceftriaxone, cefuroxime, cefixime, nalidixic acid, ofloxacin, levofloxacin, gentamicin, amoxicillin–clavulanic acid, imipenem, cefotaxime and ampiclox. Following incubation, inhibition zone diameters were measured and interpreted according to the guidelines of the Clinical and Laboratory Standards Institute (CLSI). Isolates exhibiting resistance to three or more classes of antibiotics were classified as multidrug-resistant (MDR).

Data Analysis

Data were analyzed using IBM SPSS Statistics (Version 20.0). Descriptive statistics, including frequencies and percentages, were used to summarize categorical variables. Fisher's Exact Test was used to evaluate associations between *S. typhi* prevalence and demographic, risk factor, and clinical variables. Statistical significance was set at $P < 0.05$.

Results and Discussions

Results

Distribution of *Salmonella typhi* According to Specimen Type

Table 1 presents the distribution of *Salmonella typhi* isolates according to clinical specimen type. Out of 138 samples collected, five isolates of *S. typhi* were recovered, giving an overall prevalence of 3.62%. Blood samples yielded 2 isolates (3.03%), while stool samples yielded 3 isolates (4.17%). Stool samples recorded a higher prevalence compared with blood samples.

Distribution of Bacterial Isolates According to Frequency

Table 2 shows the distribution of bacterial species isolated from clinical specimens. *Escherichia coli* was the most frequently isolated organism, accounting for 25 isolates (20.0%), followed by *Staphylococcus aureus* with 19 isolates (15.2%) and *Klebsiella pneumoniae* with 16 isolates (12.6%). *Salmonella typhi* was isolated five times, representing 4.0% of the total bacterial isolates.

Distribution of *Salmonella typhi* According to Demographic Characteristics

The distribution of *Salmonella typhi* infection in relation to demographic characteristics is presented in Table 3 among the 138 participants; five *S. typhi* isolates were recovered. The highest prevalence was recorded among participants aged 51 years and above (20.0%), followed by those aged 1–10 years (7.41%). No isolates were detected among participants aged 11–20, 21–30, and 31–40 years.

Females recorded a slightly higher prevalence (3.75%) compared with males (3.45%). Regarding marital status, single participants had the highest prevalence (4.76%), followed by married (4.00%) and divorced participants (3.33%).

With respect to occupation, self-employed participants recorded the highest prevalence (7.69%), while employed participants recorded the lowest (1.49%). Rural residents had a higher prevalence (7.50%) compared with urban residents (1.41%) and semi-urban residents (3.70%).

The prevalence of *S. typhi* varied according to educational level, with the highest prevalence observed among participants with none education (22.22%), followed by primary education (8.00%) and secondary education (2.78%). No isolates were recovered among participants with tertiary and non-formal education.

Fisher's exact test revealed no statistically significant association between *S. typhi* infection and most demographic characteristics, including age ($P = 0.076$), gender ($P = 1.000$), marital status ($P = 0.963$), occupation ($P = 0.260$), and place of residence ($P = 0.222$). However, educational attainment was significantly associated with *S. typhi* prevalence ($P = 0.041$).

Distribution of *Salmonella typhi* According to Risk Factors

Table 4 presents the relationship between environmental, hygiene, and socioeconomic factors and *S. typhi* infection. The highest prevalence was recorded among participants who obtained water from rivers (20.0%), followed by well water (4.55%) and borehole water (3.23%). No infection was recorded among participants using tap water.

Participants practicing open defecation recorded the highest prevalence (42.86%) compared with those using pit latrines (1.27%) and water closets (1.92%).

Participants living in crowded areas had a higher prevalence (8.33%) than those living in less crowded environments (1.11%).

Hand hygiene practices showed that participants who never washed their hands recorded the

highest prevalence (50.0%), while no cases were detected among those who consistently washed their hands. Participants who never washed fruits and vegetables recorded a prevalence of 33.33%, compared with lower prevalence among those who washed produce regularly.

Regarding food consumption practices, participants who frequently consumed roadside foods recorded the highest prevalence (37.50%), while those consuming home-prepared meals recorded the lowest prevalence (1.49%).

Fisher's exact test revealed significant associations between *S. typhi* infection and environmental and hygiene risk factors, including source of water (P = 0.003), toilet facilities (P = 0.001), living in crowded areas (P = 0.035), hand washing material (P = 0.022), hand washing frequency (P < 0.001), washing fruits and vegetables (P < 0.001) and eating location (P < 0.001).

Distribution of *Salmonella typhi* According to Clinical Variables

Table 5 presents the association between clinical variables and *S. typhi* infection. Participants with recent infection history recorded a prevalence of 5.00%, compared with 3.39% among those without recent infection. Participants with previous *Salmonellosis* history recorded a prevalence of 5.71%, while those without such history recorded 2.91%.

Participants who had not visited a hospital recorded a prevalence of 5.88%, compared with 3.31% among those who had visited a hospital.

Symptoms presentation showed that participants presenting with typhoid symptoms recorded the highest prevalence (40.0%), followed by gastroenteritis (2.36%). No *S. typhi* isolates were recovered among participants presenting with *Salmonellosis* symptoms.

Fisher's exact test showed that clinical symptom presentation was significantly associated with *S. typhi* infection (P = 0.004). However, recent infection history (P = 0.548), history of Salmonellosis (P = 0.627), and prior hospital visits (P = 0.490) were not significantly associated with infection.

Antimicrobial Susceptibility Profile of *Salmonella typhi*

Table 6 presents the antimicrobial susceptibility profile of *S. typhi* isolates. All isolates showed complete resistance to nalidixic acid (100%). High resistance was observed against cefixime and imipenem (80% each). Moderate sensitivity was observed for levofloxacin, ofloxacin, and nitrofurantoin (60% each). Other antibiotics including ampiclox, amoxicillin, cefotaxime, ceftriaxone, cefuroxime and gentamicin showed 40% sensitivity.

Discussion

The overall prevalence of *Salmonella typhi* observed in this study was low (3.62%), with stool samples showing a slightly higher recovery rate than blood samples. The higher detection rate from stool specimens may be explained by the shedding pattern of *S. typhi*, as infected individuals excrete the organism through feces during infection and carrier states. Stool culture may therefore provide improved detection in endemic settings where blood culture sensitivity is often limited.

The finding agrees with previous reports. Stanaway et al. (2019) documented a 5.6% prevalence of *S. typhi* from stool samples in Nigeria, which is slightly higher than the 4.17% observed in this study. Differences may be attributed to variations in study population, sample size, geographical location and diagnostic methods. Similarly, the blood culture prevalence observed in this study is comparable with the 2.5% reported by Talukder et al. (2023) supporting the generally low yield of blood culture for *S. typhi* detection.

The dominance of *E. coli*, *S. aureus* and *K. pneumoniae* among bacterial isolates suggests that these organisms are more frequently encountered in clinical specimens compared with *S. typhi*. The low frequency of *S. typhi* agrees with findings from Schultz et al. (2021) and Zhou et al. (2023) who reported that *S. typhi* often

occurs at lower prevalence compared with other bacterial pathogens.

Due to the low isolation yield (n = 5) and zero cell counts in certain subgroup categories, Fisher's Exact Test was applied across all variables to prevent asymptotic approximation errors. The higher prevalence among older participants, rural residents, self-employed individuals and those with low educational attainment may be related to differences in exposure patterns, sanitation conditions and health awareness. However, except for educational attainment (P = 0.041), the absence of statistical significance across demographic variables suggests that demographic factors alone may not determine infection risk.

Environmental and behavioral factors demonstrated stronger relationships with *S. typhi* infection. The significant association between unsafe water sources, open defecation, poor hand hygiene, inadequate washing of fruits and vegetables and roadside food consumption highlights the importance of fecal–oral transmission in typhoid epidemiology.

The increased risk among individuals using river water may be due to contamination from human waste and inadequate water treatment. Open defecation remains a major contributor to environmental contamination, allowing *S. typhi* to spread through water and food pathways. Similar observations have been reported by Kahsay et al. (2023) and Galan-Relano et al. (2023) who identified poor sanitation and unsafe water as important risk factors for typhoid fever.

The significant relationship between symptom presentation and *S. typhi* infection indicates that clinical manifestations may assist in identifying suspected cases. However, previous infection history and hospital visits were not associated with infection, suggesting that these factors may have limited predictive value.

The antimicrobial susceptibility results demonstrate an alarming level of resistance among *S. typhi* isolates. Complete resistance to nalidixic acid and high resistance to cefixime and imipenem indicate declining effectiveness of commonly used antibiotics. Reduced susceptibility to β-lactam antibiotics further suggests the emergence of resistant strains.

The moderate activity of fluoroquinolones and nitrofurantoin indicates that these drugs may still retain therapeutic value; however, continuous monitoring is necessary because resistance trends may change over time. Similar antimicrobial resistance patterns have been reported by Marchello et al. (2020) and Browne et al. (2019) who linked increasing resistance among enteric pathogens to antibiotic misuse, self-medication and inadequate antimicrobial stewardship.

Overall, the findings emphasize the need for improved sanitation, safe water supply, proper hygiene practices, food safety measures, routine antimicrobial susceptibility testing and strict antibiotic stewardship programs to control *S. typhi* transmission and reduce antimicrobial resistance.

Table 1: Distribution of Salmonella typhi in relation to specimen's type

Sample Type	No. of Samples Collected (n=138)	No. of *Salmonella typhi* Isolates (n=5)	Prevalence (%)
Blood	66	02	3.03
Stool	72	03	4.17
Total	138	05	3.62

Table 2: Distribution of bacterial species according to frequency of isolate

Isolates	No. of isolates (n = 125)	Percentage (%)
Escherichia coli	25	20.0
Klebsiella pneumoniae	16	12.6
Klebsiella oxytoca	12	9.6
Salmonella typhi	5	4.0
Proteus vulgaris	13	10.4
Proteus mirabilis	8	6.4
Staphylococcus aureus	19	15.2
Streptococcus pneumonia	15	12.0
Citrobacter freundii	8	6.4
Citrobacter diversus	4	3.2

Table 3: Distribution of *Salmonella typhi* in relation to demographic characteristics of the patients

Demographic Characteristics	No. of Samples Collected (n=138)	No. of *Salmonella* Species Isolated (n=5)	Prevalence (%)	*P*-Values (Fisher's Exact Test)
Age (years)				
1-10	27	02	7.41	
11-20	00	00	0.00	
21-30	34	00	0.00	0.076
31-40	37	00	0.00	
41-50	30	01	3.33	
51 & above	10	02	20.0	
Gender				
Male	58	02	3.45	1.000
Female	80	03	3.75	
Marital Status				
Single	42	02	4.76	
Married	50	02	4.00	0.963
Divorced	30	01	3.33	
Widowed	16	00	0.00	
Occupation				
Employed	67	01	1.49	0.260
Unemployed	32	01	3.13	
Self-employed	39	03	7.69	
Residence				
Urban	71	01	1.41	0.222
Rural	40	03	7.50	
Semi-urban	27	01	3.70	
Educational level				
Primary	25	02	8.00	0.041
Secondary	36	01	2.78	
Tertiary	47	00	0.00	

Non-formal	21	00	0.00
None	9	02	22.22

Table 4: Distribution of *Salmonella typhi* in relation to risk factors and socioeconomic variables of the patients

Risk Factors	No. of Samples Collected (n=138)	No. of *S. typhi* Isolated (n=5)	Prevalence (%)	*P*-Value (Fisher's Exact Test)
Source of Water				0.003
Tap	70	00	0.00	
Well	22	01	4.55	
Boreholes	31	01	3.23	
Rivers	15	03	20.00	
Toilet Facilities				0.001
Pit Latrine	79	01	1.27	
Water Closet	52	01	1.92	
Open Defecation	07	03	42.86	
Living in Crowded Area				0.035
Yes	48	04	8.33	
No	90	01	1.11	
Washing Hands With				0.022
Soap/Detergent	53	00	0.00	
Ash	33	01	3.03	
Sand/Mud	20	01	5.00	
Water Only	32	03	9.38	
Washing Hands Frequency				< 0.001
Always	84	00	0.00	
Sometimes	50	03	6.00	
Never	04	02	50.00	
Washing Vegetables/Fruits				< 0.001
Always	69	00	0.00	
Sometimes	60	02	3.33	
Never	09	03	33.33	
Home Cooking Practice				0.354
Reheating	28	02	7.14	
Refrigerating	43	02	4.65	
Everyday Cooking	67	01	1.49	
Eating Meals at				< 0.001
Restaurant	29	01	3.45	
Home	71	00	0.00	
Home/Restaurant	30	01	3.33	
Roadside	08	03	37.50	

Table 5: Distribution of *Salmonella typhi* in relation to clinical variables

Clinical Variables	No. of Samples Collected (n=138)	No. of *S. typhi* Isolated (n=5)	Prevalence (%)	*p*-value (Fisher's Exact Test)
Recent Infection				0.548
Yes	20	01	5.00	
No	118	04	3.39	
Historyof *Salmonellosis*				0.627
Yes	35	02	5.71	
No	103	03	2.91	
Hospital Visits				0.490
Yes	121	04	3.31	
No	17	01	5.88	
Symptoms Presentation				0.004
Typhoid	05	02	40.00	
Salmonellosis	06	00	0.00	
Gastroenteritis	127	03	2.36	

Table 6: Sensitivity of *Salmonella typhi* to different antibiotic

	No. (%) of *S. typhi* Isolated and Susceptibility Pattern (n=5)	
Antibiotics (µg)	**Sensitive**	**Resistant**
Ampiclox (10)	2 (40.0)	3 (60.0)
Amoxicillin(30)	2 (40.0)	3 (60.0)
Cefixime (5)	1 (20.0)	4 (80.0)
Cefotaxime(25)	2 (40.0)	3 (60.0)
Ceftriaxone(45)	2 (40.0)	3 (60.0)
Cefuroxime(30)	2 (40.0)	3 (60.0)
Gentamycin(10)	2 (40.0)	3 (60.0)
Imipenem(10/10)	1 (20.0)	4 (80.0)
Levofloxacin (5)	3 (60.0)	2 (40.0)
Nalidixic Acid(10)	0 (0.0)	5 (100.0)
Nitrofurantoin(300)	3 (60.0)	2 (40.0)
Ofloxacin (5)	3 (60.0)	2 (40.0)

Conclusion

The study demonstrated a relatively low prevalence of *S. typhi* but identified poor sanitation, unsafe water sources, inadequate hygiene practices and unsafe food consumption as major drivers of infection. The detection of multidrug-resistant *S. typhi* highlights the need for strengthened antimicrobial stewardship, routine resistance surveillance and laboratory-based diagnosis. Public health interventions aimed at improving water quality, sanitation, food hygiene and community health education are essential for reducing typhoid fever

transmission and limiting the spread of resistant strains.

Ethical Approval

The study was approved by the institutional research ethics committee of Abubakar Tafawa Balewa university teaching hospital (approval no [0065/2023]). Informed consent was obtained from all participants before enrolment

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Conflict of Interest

The authors declare that there is no conflict of interest regarding the publication of the paper.

Author Contribution

All authors read and approved the final manuscript.

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