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Molecular Identification, Prevalence and Antimicrobial Susceptibility Profile of *Salmonella enterica* Isolated from Patients Attending Abubakar Tafawa Balewa University Teaching Hospital, Bauchi, Nigeria

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ABSTRACT

Salmonella enterica is a pathogenic bacterium associated with diverse clinical conditions such as gastroenteritis, diarrhea, and enteric fever. Its growing resistance to multiple antibiotics has been linked to numerous fatalities across the globe each year. Despite this public health concern, detailed data on the circulating serovars in Bauchi State remain scarce. This research was designed to explore the molecular identification, prevalence, and antimicrobial susceptibility profiles of *Salmonella enterica* isolated from patients at Abubakar Tafawa Balewa University Teaching Hospital, Bauchi,. In this cross-sectional study, 300 blood and stool samples were collected from patients showing symptoms of fever and gastrointestinal disorder at ATBUTH Bauchi between August 2023 and January 2024. Participants completed a self-administered questionnaire. *Salmonella enterica* was identified through culture, Gram staining, and biochemical tests, with confirmation via 16S rRNA amplification. The antimicrobial resistance pattern analysis was conducted with commercially prepared antibiotics using the Kirby-Bauer disk diffusion method. The prevalence of *Salmonella enterica* in blood and stool samples was found to be 4%. *Salmonella typhi* was the most frequently isolated pathogen, with 9 cases (75%), compared to *Salmonella paratyphi*, which accounted for 3 cases (25%). The highest occurrence was observed in the 0-10 age group at 1.70%, with no isolates detected in the 31-50 age range. Males had a slightly higher infection rate at 2.30% compared to 1.70% in females. The most effective antibiotics against *Salmonella enterica* included Amoxicillin-clavulanic acid, Gentamicin, Imipenem-cilastatin, Levofloxacin, Ceftriaxone-sulbactam, and Ofloxacin. In contrast, the highest resistance was noted with Cefuroxime, Ampiclox, Cefotaxime, Ceftazidime, Cefixime, Nalidixic Acid, and Nitrofurantoin. The results highlight the critical need for continuous monitoring and the implementation of focused antimicrobial interventions to manage *Salmonella* infections effectively.

Keywords: Molecular, Identification, Prevalence, antimicrobial, susceptibility, *Salmonella enterica,* Pathogen

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INTRODUCTION

Salmonella enterica is an intracellular pathogen that affects both people and animals. It is a facultative anaerobe, gram-negative, and not a symbiotic commensal (Crump *et al*., 2015). *Salmonella enterica* is a leading cause of gastroenteritis and bacteremia in humans worldwide (Hindermann *et al.,* 2017). In Africa, regions with high occurrences of both epidemic and endemic typhoid and paratyphoid fever are increasingly recognized as significant contributors to community-acquired bloodstream infections (Crump *et al.,* 2017). Nigeria, like many tropical and subtropical countries, faces a significant burden of *Salmonella enterica* infections, which remain a pressing public health challenge due to their associated rates of illness and death (Ottong *et al.,* 2010). Various animal species—particularly livestock—act as reservoirs for non-typhoidal strains of this bacterium. Although over 2,500 serovars of *Salmonella enterica* have been documented, only a relatively small subset is responsible for the majority of human cases (Bangtrakulnonth *et al.,* 2004). Globally, *Salmonella enterica* serovars Typhimurium and Enteritidis are the leading causes of salmonellosis in humans, although regional variations exist in the dominant serovars (Crump *et al.,* 2015).

The growing occurrence of antibiotic resistance among bacterial pathogens poses a critical challenge to the efficacy of antimicrobial treatment regimens (Nmema, 2013). Ensuring successful clinical outcomes depends heavily on consistent surveillance of resistance patterns, especially among organisms known for drug resistance. The rise of multidrug-resistant (MDR) strains has further complicated treatment protocols, as these organisms often evade first-line antibiotics, leading to longer disease durations, increased mortality rates, and heightened healthcare expenses. This scenario places substantial economic pressure on individuals, communities, and public health systems (Vishal and Trivedi, 2012). According to the World Health Organization (WHO), the United States Centers for Disease Control and Prevention (CDC), and several investigative research institutions, infections linked to MDR bacteria are becoming more frequent, with new resistant pathogens emerging in hospital environments (Kim *et al.,* 2011; Zerfie *et al.,* 2014).

The unchecked spread of these resistant organisms poses a considerable public health risk and remains a prominent issue for global infection control efforts. In developing countries like Nigeria, this surge has triggered a resurgence of previously controlled illnesses and a rise in opportunistic and chronic infections (Vishal and Trivedi, 2012).In Nigeria, limited access to clean water, effective sanitation, and safe food handling practices contributes to the high burden of typhoid fever (also known as enteric fever), which is primarily caused by *Salmonella Typhi* and *Salmonella Paratyphi* (Sodipo and Wannang, 2015). These infections are endemic across the country and present a considerable public health concern, accounting for numerous cases of unexplained fever along with elevated rates of illness and death (Ramyil *et al.,* 2014). Despite the severity of these infections, comprehensive data on *Salmonella enterica* serovars circulating in Bauchi State remain scarce. This research was conducted to examine the molecular identification, prevalence, and antimicrobial susceptibility profile of *Salmonella enterica* in patients at Abubakar Tafawa Balewa University Teaching Hospital, Bauchi.

MATERIALS AND METHODS

Ethical Approval

Approval for this study was granted by the Ethics Committee of Abubakar Tafawa

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Balewa University Teaching Hospital, Bauchi. Informed consent was obtained from all participants prior to sample collection, including from the guardians of children under six years of age.

Study Area

The research was conducted in the Microbiology Laboratory of Abubakar Tafawa Balewa University Teaching Hospital, located in Bauchi State, Nigeria, in the northeastern region of the country. Bauchi State has a population of 6,537,314 and is situated at geographical coordinates of 10.3060° N and 9.8404° E. This hospital was chosen for the study due to its high patient volume and its pivotal role as a referral centre

Study Design and Subjects

This study adopted a cross-sectional design to determine the prevalence and antimicrobial susceptibility profile of *Salmonella enterica* among patients attending the Abubakar Tafawa Balewa University Teaching Hospital in Bauchi State. A survey was carried out to identify patients exhibiting symptoms of fever and gastroenteritis who were willing to consent to participate in the study. Those without these symptoms and unwilling to give consent were excluded from participation. Informed consent was obtained from all patients or their guardians to ensure their involvement in the study. A multistage sampling technique was utilised to select participants from the eligible patient population.

Sample Size Determination

The sample size of this research was determined using Fisher's formula (Cochrane, 1977)

$$n = \frac{Z^2\, p\,(1-p)}{d^2}$$ Where;

n = sample size

Z = 1.96 (standard error) at 95% confidence interval

p = prevalence from previous studies
d = level of precision at 5% (0.05)
Z= 1.96
p= 0.74
d= 0.05

$$n = \frac{1.96^2 \times 0.74\,(1-0.74)}{0.05^2}$$

$$n = \frac{3.8416 \times 0.1924}{0.0025}$$

$$n = \frac{0.73912384}{0.0025}$$

n= 296 samples

A sample size minimum of 296 was computed. In order to avoid bias in patient selection, the calculated sample size was adjusted to 300 as the study's baseline sample size.

Sample Collection

A total of 300 Stool and blood samples were aseptically collected from patients attending Abubakar Tafawa Balewa University Teaching Hospital. Multistage sampling method was used during the sampling. The sampling was conducted between months of August 2023 to January 2024.

Isolation of *Salmonella enterica*

The blood sample collected in thioglycolate broth was incubated overnight at 37°C for 18 to 24 hours. The tubes that showed turbidity were sub-cultured onto freshly prepared and dried Salmonella Shigella Agar (SSA), MacConkey Agar (MCA), and Chocolate Agar (CA), followed by incubation for 18 to 24 hours at 37°C. The collected stool samples were inoculated into an enrichment medium (selenite F broth) and incubated for 24 hours at 37°C. Each sample was then sub-cultured onto Salmonella Shigella Agar (SSA), Chocolate

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Agar (CA), and MacConkey Agar (MCA). The SSA, CA, and MCA plates were incubated overnight at 37°C. Both the plates inoculated with blood specimens and stool specimens were examined for growth, colony size, shape, and cellular arrangement. Gram staining and biochemical tests were performed according to the method described by Cheesbrough (2010). The biochemical tests included the Catalase test, Coagulase test, Citrate utilization test, Indole test, Oxidase test, and Urease test.

Serological Identification (Serotyping)

The suspected isolates of *Salmonella enterica* were collected using a sterile wire loop and subcultured onto moist nutrient agar slopes contained in McCartney glass bottles. These bottles were incubated for a minimum of four hours. Subsequently, one to two loopfuls of the agar cultures were combined with normal saline on a clean, grease-free slide to create a paste. A drop of O and H polyvalent sera was added and thoroughly mixed with the organism on the slide. The presence of visible agglutination within 30 seconds indicates a positive result, while its absence denotes a negative result. For cultures that tested positive, the slide tests were repeated using single-factor sera

Genomic DNA Extraction

A glycerol stock of *Salmonella enterica* was streaked onto a Salmonella-Shigella agar plate and incubated at 30 °C for 24 hours. A single colony was then inoculated into 10 mL of nutrient broth and incubated at 30 °C with shaking at 210 rpm for another 24 hours. Genomic DNA was extracted using the Wizard® Genomic DNA Purification Kit (Promega, USA) according to the manufacturer's instructions. The concentration and purity of the genomic DNA were assessed using a NanoDrop spectrophotometer (Thermo Fisher Scientific, USA). The DNA solution was stored at -20 °C until further use.

PCR Amplification of 16srRNA Gene and Sequencing

The amplification of the 16S rRNA gene region was conducted using universal primers: the forward primer E16S-F (5′-CCCCCTGGACGAAGACTGAC-3′) and the reverse primer E16S-R (5′-ACCGCTGGCAACAAAGGATA-3′) (Wang *et al.,* 2002). For the PCR setup, the following components were combined in a PCR tube to achieve a total reaction volume of 50 µL: nuclease-free water, 1 µL of DNA template (300 ng), 25 µL of EconoTaq® PLUS 2X Master Mix (Lucigen, USA), and 1 µL of each primer (both forward and reverse at a concentration of 100 µM). The amplification process was carried out in a thermal cycler for 40 cycles, following these conditions: DNA denaturation at 94ºC for 1 minute, primer annealing at 56ºC for 30 seconds, and primer extension at 72ºC for 1 minute. After amplification, the PCR product was mixed with 5 µL of gel loading buffer. A 1.5% agarose gel was prepared, and the samples were loaded alongside 5 µL of a 1 kb DNA ladder (Thermo Fisher Scientific, USA) as a molecular marker. The gel was then run and visualized under a UV transilluminator (Syngeneic, USA) to observe the bands. Finally, the PCR products were purified using the Wizard® SV Gel and PCR Clean-Up System (Promega, USA), following the manufacturer's instructions, and sequenced with an ABI Prism 3700 DNA Analyzer (Acme Progen Biotech (India) Pvt. Ltd., Salem, Tamil Nadu, India). (Amutha and Kokila, 2014)

Sequence Analysis of 16S rRNA Gene and Construction of Phylogenetic Tree

The sequencing data were validated using BLAST (Basic Local Alignment Search Tool)

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analysis with the NCBI (National Centre for Biotechnology Information) GenBank database, which is available at http://www.ncbi.nlm.nih.gov. Both forward and reverse sequences were analysed using Sequence Scanner Software v1.0 (Applied Biosystems, Thermo Fisher Scientific). For multiple sequence alignment, we utilised the Clustal Omega server provided by the European Molecular Biology Laboratory-European Bioinformatics Institute (EMBL-EBI). A phylogenetic tree was constructed based on the sequence information using the neighbor-joining method in MEGA-X software.

Antibiotic Susceptibility Testing

The bacterial isolates were subjected to antibiotic susceptibility testing using the Kirby-Bauer disk diffusion method (Bauer *et al.,* 1966). In this procedure, a lawn culture was created by applying a culture suspension of the bacterial test isolates, adjusted to the 0.5 McFarland standard, onto the surface of Mueller–Hinton agar (MHA) plates (BD DIFCOTM, USA).Standard antibiotics such as Amoxicillin-clavulanic acid (25/5µg, Imipenem-cilastatin 10 µg, Levofloxacin (5µg), Ofloxacin (5 µg), Gentamicin (10 µg), Ceftriaxone-sulbactam (45 µg), Cefuroxime (25 µg) Ampiclox (10 µg), Cefotaxime (30 µg), Ceftazidime (30 µg,), Cefexime (5µg,). Nalidixic Acid (30 µg) and Nitrofurantoin (30 µg) were used to test for the sensitivity of the isolates. The diameters of the zones of inhibition were measured and interpreted according to the standards established by the Clinical and Laboratory Standards Institute (CLSI, 2010). The E. coli strain from the American Type Culture Collection (ATCC) 25922 was sourced from the National Veterinary Research Institute (NVRI), Vom, and served as a control.

RESULTS

Isolation, Identification And Prevalence of *Salmonella enterica*

This study focused on isolating and identifying *Salmonella enterica* from blood and stool samples of gastroenteritis patients at Abubakar Tafawa Balewa University Teaching Hospital, Bauchi, using culture, Gram staining, biochemical analyses, and molecular method. A total of 300 blood and stool samples were collected from the study participants. Of these samples, approximately nine isolates were identified as *Salmonella enterica*, constituting 75% of the total isolates, while three isolates, representing 25%, were classified as *Salmonella paratyphi*. The overall positive rate for *Salmonella enterica* found in the blood and stool samples was 12 out of 300, translating to 4% (see Table 1).

Table 1: Distribution of *S. enterica* isolates in clinical specimens.

Hospitals	**Number of specimens collected**		***Salmonella enterica* species isolated (%)**				
	Specimens		*Salmonella typhi*		*Salmonella paratyphi*		Total (%)
	Blood	Stool	Blood	Stool	Blood	Stool	
ATBUTH	180	120	5	4	1	2	12 (4)
Total	300		9 (75%)		3 (25%)		4

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The *Salmonella enterica* strains initially identified through biochemical methods were subsequently confirmed using a molecular approach based on the homology of their 16S rRNA gene sequences, resulting in the production of a single band, as depicted in Figure 1. The 16S rRNA gene sequence was analyzed using BLAST against the National Center for Biotechnology Information (NCBI) database, and a phylogenetic tree for *Salmonella enterica* was constructed utilizing available reference sequences from the NCBI. The isolated pathogens demonstrated a 97% similarity to other sequences found in the NCBI database, as illustrated in Figure 2.

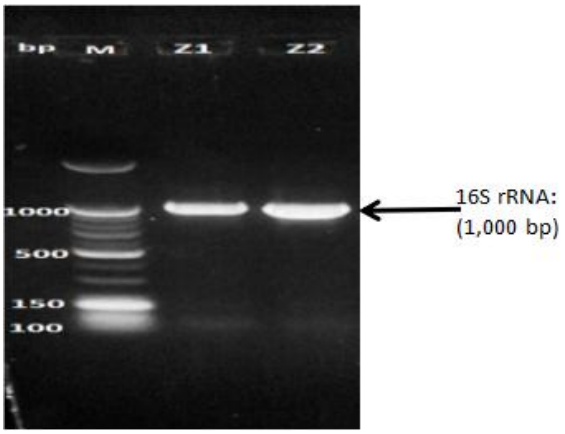

Figure 1: Agarose gel electrophoresis for amplified PCR products using 16s RNA primers of the isolates (lanes Z1-Z2). Lane 1: m-represents marker.

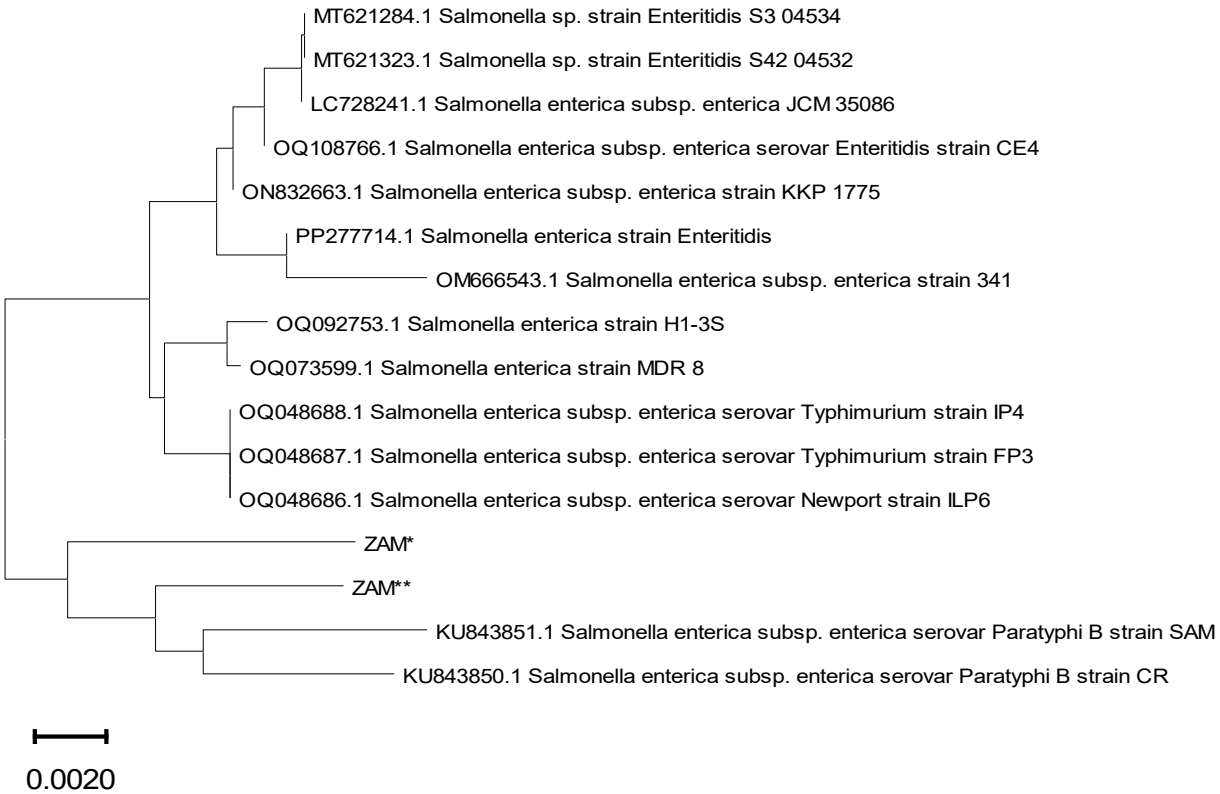

Figure 2: A phylogenetic tree showing relationship between the 16S rRNA gene sequences of Isolated *S. enterica* strains and that of other S. *enterica* species from NCBI. The *S. enterica* isolated were designated as *Salmonella enterica* Strain ZAM1 and *Salmonella enterica* Strain ZAM2, the Evolutionary relationship was inferred using Neighbor-joining method and the horizontal indicate 0.0020.

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Prevalence of *Salmonella enterica* According to Age

Table (2) illustrates the prevalence of *Salmonella enterica* by age, detailing the number of isolates obtained from blood and stool samples across various age groups. The highest prevalence was found in the 0-10 age group, where five (5) isolates were detected, representing 1.70% of the total samples. The second highest prevalence is observed in the 11-20 age group, with three (3) isolates, accounting for 1%. As age increases, the prevalence decreases, with only one (1) isolate found in the 21-30 and 51-60 age groups, corresponding to 0.30%. No *Salmonella enterica* isolates were detected in the 31-40 and 41-50 age groups. In the oldest group, those over 61 years, the isolation rate is 0.70%, with two (2) isolates identified.

Table 2: Prevalence of *Salmonella enterica* according to Age.

Age	Blood	Stool	Total	No. of *Salmonella enterica* isolated	Percentage (%) of *Salmonella enterica* Isolated
0-10	60	40	100	5	1.70
11-20	30	20	50	3	1
21-30	25	16	35	1	0,30
31-40	22	14	32	0	0
41-50	17	12	25	0	0
51-60	15	11	25	1	0.30
>61	11	7	15	2	0.70
Total	180	120	300	12	4

Prevalence of *Salmonella enterica* According to Sex

Among the total participants in the study, there were 150 males and an equal number of 150 females, resulting in a balanced gender distribution of 50% for each group. When examining the prevalence of *Salmonella enterica*, the results indicated that males experienced a marginally higher infection rate, measuring at 2.30%. In contrast, the prevalence among females was recorded at 1.70%. (Table 3).

Table 3: Prevalence of *Salmonella enterica* according to Sex

Sex	Blood	Stool	Total	No. of *Salmonella enterica* isolated	Percentage (%) of *Salmonella enterica* Isolated
Male	90	60	150	7	2.30
Female	90	60	150	5	1.70
Total	180	120	300	12	4

Antibiotic Susceptibility Pattern of *Salmonella enterica*

The results of the antibiotic susceptibility study revealed that the most effective antibiotics against the *Salmonella enterica* isolates included Amoxicillin-clavulanic acid 12(100%) Gentamicin 12(100%), Imipenem-cilastatin 12(100%), Levofloxacin 12(100%), Ceftriaxone-sulbactam 12(67%) and Ofloxacin 12(100%) (Table 4). On the other hand, the highest rates of resistance were observed with Cefuroxime 12(100%), Ampiclox 12(100%), Cefotaxime 12(100%), Ceftazidime 12(100%), Cefexime 9(75%), Nalidixic Acid 8(67%), and Nitrofurantoin 8(67%).

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Table 4: Antibiotic susceptibility test result of *Salmonella enterica species* isolated.

	Codes	Concentration	Diameter of zone of inhibition in mm		
			≥ Sensitive%	Intermediate%	≤ Resistant%
Amoxi-clav	AUG	25/5µg	12(100%)	0(0%)	0(0%)
Ceftazidime	CAZ	30 µg	(0%)	0(0%)	12(100%)
Ceftriaxone-sulbactarm	CTR	45 µg	8 (67%)	0(0%)	4(33%)
Cefotaxime	CTX	25 µg	0(0%)	0(0%)	12(100%)
Ofloxacin	OFX	5 µg	12(100%)	0(0%)	0(0%)
Gentamycin	GN	10 µg	12(100%)	0(0%)	0(0%)
Ampiclox	ACX	10 µg	0(0%)	0(0%)	12(0%)
Imipenem-cilastatin	IPM	10 µg	12(100%)	0(0%)	0(0%)
Nalidixic Acid	NA	30 µg	4(0%)	0(0%)	8(67%)
Levofloxacin	LBC	5µg	12(100%)	0(0%)	0(0%)
Cefexime	ZEM	5µg	3(100%)	0(0%)	9(75%)
Cefuroxime	CXM	30 µg	0(0%)	0(0%)	12(100%)
Nitrofurantoin	NF	300 µg	4(100%)	0(0%)	8(67%)

DISCUSSION

The prevalence of *Salmonella enterica* in blood and stool samples varies across different studies, with several reporting specific figures. In our study, we found a general prevalence of 4% for *Salmonella enterica* in blood and stool samples. This finding aligns with several other studies. For example, a study conducted in Bangladesh reported a 4% positivity rate for Salmonella spp. among 350 stool samples from diarrheal patients (Uddin *et al.,* 2018). Additionally, research from the Democratic Republic of Congo indicated a cumulative prevalence of 4.4% for *Salmonella* in stool samples from healthy individuals (Mbuyi-Kalonji *et al.,* 2023). A study in Ghana revealed a prevalence of 3.4% for *Salmonella enterica* among diarrheal patients (Nkansah, 2016). In a multi-country study, the prevalence of Salmonella spp. among children with moderate-to-severe diarrhea was also reported to be 4.0% (Kasumba *et al.,* 2023). In The Gambia, *Salmonella* was isolated from the stool samples of healthy individuals at a rate of 3.5% to 4%, suggesting possible asymptomatic carriage (Dione *et al.,* 2010).

In contrast to our study, several other studies reported different prevalence rates of *Salmonella.* For instance, a study in Burkina Faso found that 6.2% of household members were infected, with genetic analysis revealing a strong relatedness between strains from index patients and their household members, which supports the human reservoir hypothesis (Post *et al.,* 2019). Additionally, research in rural Burkina Faso showed that 6% of children under five with diarrhea carried *Salmonella*, with various serotypes identified,

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indicating the presence of multiple human carriers (Demba *et al.,* 2014). One study reported a 24% positivity rate for Salmonella spp. in blood cultures and a 16% positivity rate in stool samples (Yusuf et *al.,* 2018). Another study identified a prevalence rate of 34.6% among Widal-positive individuals, though this was not based on a general population sample (Tula *et al*., 2022). Furthermore, a study conducted in Lagos, Nigeria, found the prevalence of *Salmonella enterica* in human samples to be 0.9% (Akinyemi *et al.,* 2023). The prevalence of *Salmonella enterica* varies considerably among studies due to several factors, including geographic location, environmental conditions, host characteristics, and variations in study methodologies. Additionally, differences in *Salmonella* serotypes, their virulence, and their capacity to persist in diverse environments further contribute to these discrepancies.

The prevalence of *Salmonella enterica* infections exhibits significant differences between genders. Our study found that males have a higher prevalence rate of 2.30%, compared to 1.7% in females. Similar findings have been reported in various studies. For instance, an analysis of data from eight countries indicated that male children up to age 15 experience higher incidence rates of salmonellosis than their female counterparts, with incidence rate ratios (IRRs) ranging from 1.04 to 1.28% (Peer *et al.,* 2021). Another study highlighted that 11 males (42.3%) were infected, as opposed to 7 females (26.9%) (Tula *et al.,* 2022). Conversely, a study conducted in Lafia, Nigeria, reported a higher prevalence of *Salmonella Typhi* in females (7.05%) compared to males (4.17%), although this difference was not statistically significant (Terna *et al.,* 2021). While the majority of studies suggest a higher prevalence of *Salmonella enterica* in males, it is crucial to note that these patterns can vary based on factors such as age, serotype, and geographical location. Further research is required to explore the underlying mechanisms and to develop targeted interventions that address these gender-specific differences in infection rates.

The prevalence of *Salmonella enterica* varies significantly across different age groups, with our study indicating that the highest prevalence is found among younger individuals, particularly those aged 0-10. This finding aligns with numerous other studies. For instance, research conducted in Teresina, Brazil, revealed that children as young as six months had the highest prevalence of *Salmonella enterica*, which correlates with increased rates of gastroenteritis within this age group (Nunes *et al.,* 2012). Likewise, a study conducted in Ghana found that children under 15 years had nearly four times the odds of contracting *Salmonella enterica* subspecies *Typhi* compared to older populations (Owusu *et al.,* 2023). Another investigation reported that the highest incidence of *Salmonella enterica* bacteremia occurred in children aged 0–9, with male gender identified as a significant risk factor (Laupland et al., 2010). In Ontario, Canada, children under 10 exhibited the highest rates of *Salmonella enterica*, although there were minimal gender differences (Varga *et al.,* 2013). Global surveillance data consistently show that the 0–10 age group has the highest incidence of *Salmonella enterica*, with a slight male predominance boys being marginally more affected (Peer et al., 2021). In contrast, a study in Franceville, Gabon, found that the most affected age group for *Salmonella Typhi* was between 14 and 49 years; however, children also demonstrated significant vulnerability (Ndong *Mba et al.,* 2023). The heightened prevalence of *Salmonella enterica* in younger populations is attributed to underdeveloped

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immunity and increased environmental exposure.

The antibiotic susceptibility of *Salmonella enterica* has been the focus of extensive research, revealing a range of effective and resistant antibiotics. Our study identified Amoxicillin-Clavulanic acid, Gentamicin, Imipenem-Cilastatin, Levofloxacin, and Ceftriaxone-Sulbactam as the most effective treatments for infections caused by *Salmonella enterica*. Similar findings have been reported by various studies. For example, It et al. (2015) noted that Amoxicillin-Clavulanic acid, Gentamicin, Imipenem-Cilastatin, and Ceftriaxone-Sulbactam exhibited susceptibility rates of approximately 86.4%, 98-99%, 100%, and 97.8%, respectively.

In a study conducted by Kim et al. (2013), which investigated antibiotic resistance among *Salmonella* species isolated from the faeces of patients with acute diarrhoea in the Gwangju area of Korea from 2000 to 2009, Levofloxacin was found to be notably effective against *Salmonella*, showing significant susceptibility. In terms of antibiotics resistance, our study found that antibiotics such as Cefuroxime, Ampiclox, Cefotaxime, Ceftazidime, Cefixime, Nalidixic Acid, and Nitrofurantoin exhibited high levels of resistance against *Salmonella enterica*. These results are consistent with those of Kim et al. (2013), which also reported significant resistance of *Salmonella* species to Cefuroxime, Cefotaxime, Ceftazidime, Nalidixic Acid, and Nitrofurantoin, while Ampiclox showed a resistance rate of 73.6% against *Salmonella* spp. (It *et al.,* 2015).

The susceptibility of *Salmonella enterica* to ofloxacin has been a significant focus in recent research, revealing varying resistance patterns across different studies. The highest rates of susceptibility to ofloxacin were observed in several investigations, indicating its potential effectiveness against Salmonella infections, particularly in specific contexts. In a review of 55,853 *Salmonella* isolates, ofloxacin demonstrated a susceptibility rate of 96% (Jombo *et al.,* 2009). A study on 210 clinical isolates of typhoid salmonellae found that all tested strains were highly sensitive to ofloxacin, with MICs ranging from 0.03 mg/l to 0.12 mg/L/ (Hannan, 1985).. The findings suggest that while ofloxacin remains a viable treatment option, continuous monitoring of susceptibility patterns is essential, especially in regions with high rates of resistance (Khadka *et al.,* 2021; Poudel *et al.,* 2014).

In contrast, a study found that *Salmonella enterica* isolates exhibited resistance rates of 66.7%, 100%, and 56.6% to amoxicillin-clavulanate, levofloxacin, and gentamicin, respectively, indicating their ineffectiveness in certain populations (Durrani et al., 2024). In addition, another study indicated a significant resistance rate of 93.3% against quinolones, including ofloxacin, among isolates from febrile pediatric cases (Khadka *et al.,* 2021). Despite the promising susceptibility rates of ofloxacin, the emergence of resistance in certain populations raises concerns about its empirical use. Although these studies emphasise significant antibiotic resistance, it is crucial to recognise that some antibiotics may remain effective in specific contexts or regions. This highlights the need for ongoing surveillance and tailored antibiotic strategies to effectively combat Salmonella infections

CONCLUSION

The study successfully isolated *Salmonella enterica* from blood and stool samples using both culture and molecular methods in patients at the Abubakar Tafawa Balewa University Teaching Hospital in Bauchi. The overall prevalence of *Salmonella enterica* was found to be moderately low, given the number of samples collected in the study area. Notably,

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Salmonella typhi was the most frequently isolated pathogen in both blood and stool samples, surpassing *Salmonella paratyphi*. The highest prevalence was observed in the younger age group, while no isolates were detected in the adult age groups. In terms of gender, males displayed a slightly higher infection rate compared to females. The most effective antibiotics against *Salmonella enterica* included Amoxicillin-clavulanic acid, Gentamicin, Imipenem-cilastatin, Levofloxacin, Ceftriaxone-sulbactam, and Ofloxacin. Conversely, resistance levels were highest with Cefuroxime, Ampiclox, Cefotaxime, Ceftazidime, Cefixime, Nalidixic Acid, and Nitrofurantoin. Continuous surveillance is recommended to monitor epidemiological changes and antibiotic resistance to mitigate the challenges faced in treating this pathogen.

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