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DETECTION, MICROBIOLOGICAL CHARACTERIZATION, AND ANTIMICROBIAL SUSCEPTIBILITY PROFILE OF SALMONELLA SPP. RECOVERED FROM CHILDREN AT THE UNIVERSITY HOSPITAL FOR MOTHERS AND CHILDREN OF N'DJAMENA, CHAD

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ABSTRACT

Salmonella infections remain an important cause of enteric and invasive disease in children, particularly in sub-Saharan Africa, where diagnostic and therapeutic resources may be limited. However, local data integrating microbiological detection, identification, molecular confirmation, and antimicrobial susceptibility testing of Salmonella in Chad remain scarce. This study aimed to characterize Salmonella isolates recovered from stool and blood specimens collected from hospitalized children at the University Hospital for Mothers and Children of N'Djamena, Chad. A descriptive and analytical study was conducted in 2023. Fifty stool specimens and 50 blood specimens were collected from hospitalized children. Stool specimens were subjected to direct examination, Gram staining, culture, biochemical testing, and identification using the API 20E system and APIweb. Positive blood cultures were subcultured on MacConkey agar, Chapman agar, and 5% sheep blood agar. Presumptive isolates were stored in brain–heart infusion broth supplemented with 15% glycerol. Molecular confirmation was performed following thermal DNA extraction and PCR amplification using the ST11F/ST15R primer pair. Antimicrobial susceptibility testing was performed according to the procedure documented in the source material, with minimum inhibitory concentrations (MICs) interpreted according to the reported susceptible (S) and resistant (R) categories. Salmonella was recovered from 10/50 stool specimens (20.0%) and 8/50 blood specimens (16.0%). Among stool-positive cases, 50% were children aged 0–5 years, whereas blood-

positive cases were equally distributed across the four age categories. The API 20E profile 6704552 predominantly identified *Salmonella spp.* (89.6%), with secondary identifications of *Salmonella enterica subsp. arizonae* (10.3%) and *Citrobacter braakii* (0.1%). PCR amplification produced a band at approximately the expected product size of 421 bp. The characterized isolate exhibited resistance to ampicillin, ticarcillin, piperacillin/tazobactam, cefoxitin, ceftazidime, gentamicin, tobramycin, nalidixic acid, ciprofloxacin, ofloxacin, and trimethoprim/sulfamethoxazole, while susceptibility was reported to ertapenem, imipenem, amikacin, and nitrofurantoin. Overall, Salmonella was recovered from both stool and blood specimens in this pediatric hospital setting, and the characterized isolate displayed resistance to multiple antimicrobial classes. These findings highlight the need to strengthen standardized microbiological surveillance, antimicrobial susceptibility testing, and antimicrobial stewardship in pediatric healthcare settings in N'Djamena.

Keywords: Salmonella; Antimicrobial susceptibility; Antimicrobial resistance; Multidrug resistance; Children; Stool; Blood culture; API 20E; PCR.

1 INTRODUCTION

Salmonella infections remain an important cause of human disease worldwide and may range from self-limited gastroenteritis to invasive bloodstream infection. Nontyphoidal Salmonella (NTS) is a major cause of invasive disease in sub-Saharan Africa, with young children representing an important vulnerable population [1–4]. The burden of invasive NTS disease is disproportionately concentrated in sub-Saharan Africa, where malnutrition, malaria, anemia, HIV infection, environmental exposure, and limitations in access to timely diagnosis and treatment may contribute to severe outcomes [2–7]. Salmonella comprises two recognized species, *Salmonella enterica* and *Salmonella bongori*, with numerous serovars exhibiting distinct epidemiological characteristics, host associations, and virulence properties. NTS is commonly associated with gastroenteritis but can also cause bacteremia and extraintestinal disease, particularly in infants and young children [1–4]. Consequently, both stool culture and blood culture remain important components of microbiological investigation when enteric or invasive salmonellosis is suspected. In resource-constrained settings, reliable laboratory identification is essential for surveillance and clinical management. Conventional bacteriology combines selective enrichment, differential culture, biochemical characterization, and, where available, standardized identification systems such as API 20E. API 20E has demonstrated utility for identification of Enterobacterales, although atypical isolates may yield uncertain or alternative identifications [8]. Serological classification using the Kauffmann–White–Le Minor scheme remains an important reference approach for Salmonella serotyping, while PCR can provide complementary molecular evidence [9–11]. Antimicrobial resistance further complicates the management of invasive Salmonella infections. Resistance may arise through target modification, reduced permeability, enzymatic drug inactivation, and active efflux, while plasmids, transposons, and integrons can facilitate acquisition and dissemination of multiple resistance determinants [12–14]. Resistance patterns vary geographically and according to serovar, antimicrobial exposure, and animal or environmental reservoirs. Recent evidence from sub-Saharan Africa indicates substantial heterogeneity in resistance among Salmonella and other Enterobacterales, reinforcing the value of local susceptibility data [15,16]. The clinical importance of resistance is particularly evident in invasive infection, where effective antimicrobial therapy may be critical. Standardized antimicrobial susceptibility testing (AST) therefore provides information for clinical decision-making and surveillance. Interpretation requires appropriate methodology, quality control, and application of the breakpoint standard documented for the period of testing [17,18].

In Chad, hospital-based microbiological data on Salmonella in children remain limited. The University Hospital for Mothers and Children of N'Djamena provides an appropriate setting in which to document the occurrence and characteristics of Salmonella among hospitalized children. The present study therefore aimed to characterize Salmonella recovered from stool and blood specimens, describe the distribution of positive cases by age, evaluate biochemical and molecular identification, and document the antimicrobial susceptibility profile reported for the recovered isolate.

2 MATERIALS AND METHODS

2.1 Study design, setting, and period

This descriptive observational study was conducted at the University Hospital for Mothers and Children of N'Djamena, Chad in 2023. The study included 50 stool specimens and 50 blood specimens collected from hospitalized children. Sociodemographic information reported in the source material included age, sex, social/educational status, and place of residence.

2.2 Stool specimen processing and bacterial isolation

Stool specimens were collected in sterile containers from freshly passed stool or specimens brought to the laboratory. Macroscopic examination assessed appearance, consistency, and color. A portion of each specimen was suspended in physiological saline. Direct wet-mount examination was performed to assess leukocytes, erythrocytes, epithelial cells, and bacterial motility.

Gram staining was performed using crystal violet for 1 min, Lugol solution for 1 min, alcohol–acetone decolorization, and diluted fuchsin for approximately 30 s. Slides were examined microscopically at ×100 with immersion oil. Selective enrichment was performed in Rappaport–Vassiliadis broth for 18–24 h at 37 °C. Enriched material was inoculated onto Hektoen agar and incubated for 18–24 h at 37 °C. Suspected lactose-negative and/or H2S-positive colonies were selected and subcultured onto Uriselect 4. A second subculture from Rappaport–Vassiliadis broth was performed on Hektoen agar.

2.3 Biochemical identification and API 20E

The oxidase test was performed on fresh isolated colonies using N,N,N′,N′-tetramethyl-p-phenylenediamine. A dark blue/violet reaction within 30 s was considered positive. Identification was subsequently performed using API 20E. A bacterial suspension prepared from an isolated colony was inoculated into the API 20E gallery according to the procedure described in the source material, and reactions were interpreted using API WEB after incubation.

2.4 Blood culture and identification

Blood specimens were cultured directly and incubated at 37 °C. Positive bottles, including those showing turbidity or coagulation, were subcultured onto MacConkey agar, Chapman agar, and 5% sheep-blood agar prepared with tryptic soy agar. Salmonella-oriented isolates were characterized by the reported biochemical reactions: glucose positive, H2S positive, lactose negative, urease negative, ONPG negative, and lysine decarboxylase positive.

2.5 Storage and DNA extraction

Bacterial strains were stored in brain–heart infusion broth supplemented with 15% glycerol at −20 °C. For molecular analysis, stored strains were reactivated on nutrient medium and subcultured onto XLD agar to obtain pure cultures. DNA was extracted by thermal lysis. Isolated colonies were suspended in 200 µL Milli-Q water, frozen for 15 min, heated in a boiling-water bath at 100 °C for 10 min, and centrifuged at 4,000 rpm for 10 min.

2.6 PCR amplification

PCR was performed using 5× FIREPol® Master Mix and the ST11F/ST15R primer pair reported in the source material for Salmonella identification (Table 1). Each 20-µL reaction contained 4 µL Master Mix, 1 µL forward primer, 1 µL reverse primer, 11.5 µL Milli-Q water, and 2.5 µL DNA.

Table 1: Primers used for detection of Salmonella

Primer	Sequence (5′–3′)	Expected product
ST11F	GCCAACCATTGCTAAATTGGCGCA	429 bp
ST15R	GGTAGAAATTCCCAGCGGGTACTGG	429 bp

The cycling protocol comprised initial denaturation at 94 °C for 5 min, followed by 30 cycles of 94 °C for 30 s, 63 °C for 60 s, and 72 °C for 60 s, with a final extension at 72 °C for 7 min.

2.7 Agarose gel electrophoresis

Ten microliters of each amplicon were analyzed by electrophoresis on 1.5% agarose gel prepared in 0.5× TAE buffer. Electrophoresis was performed for 60 min at 100 V and 100 mA. A molecular-weight marker was used to estimate fragment size. Gels were visualized under UV illumination using a UVP Transilluminator with a UVP PhotoDoc-it system.

2.8 Antimicrobial susceptibility testing (AST)

Antimicrobial susceptibility testing (AST) was performed using the modified Kirby–Bauer disk diffusion method in accordance with the recommendations of the World Health Organization (WHO). Fifteen antimicrobial agents were tested: ampicillin, ticarcillin, piperacillin/tazobactam, cefoxitin, ceftazidime, ertapenem, imipenem, amikacin, gentamicin, tobramycin, nalidixic acid, ciprofloxacin, ofloxacin, nitrofurantoin, and trimethoprim/sulfamethoxazole. After incubation, the diameters of the inhibition zones were measured in millimeters and interpreted according to the

applicable antimicrobial susceptibility breakpoints. The isolates were classified as susceptible (S), intermediate (I), or resistant (R), according to the interpretation criteria used in the study.

2.9 Data analysis

Data were entered into Microsoft Excel 2019. The source material reports the use of means ± standard deviations and minimum and maximum values for quantitative variables and mentions one-way analysis of variance (ANOVA). Because no inferential results establishing associations between sociodemographic variables and Salmonella positivity or antimicrobial resistance are presented, the present manuscript limits interpretation to descriptive findings.

3 RESULTS

3.1 Recovery of Salmonella from stool and blood

Salmonella was recovered from 10 of 50 stool specimens (20%) and from 8 of 50 blood specimens (16%) (Table 2).

Table 2: Recovery of Salmonella from stool and blood

Specimen type	Total tested	Salmonella-positive	Positivity
Stool	50	10	20%
Blood	50	8	16%

3.2 Age distribution of positive stool specimens

Table 3: Age distribution of positive stool specimens

Age group	Positive cases	Proportion of positive stool cases
0–5 years	5	50%
6–9 years	2	20%
10–12 years	1	10%
13–15 years	2	20%
Total	10	100%

3.3 Age distribution of positive blood specimens

Table 4: Age distribution of positive blood specimens

Age group	Positive cases	Proportion of positive blood cases
0–5 years	2	25%
6–9 years	2	25%
10–12 years	2	25%
13–15 years	2	25%
Total	8	100%

3.4 Microbiological counts

Table 5: Results of microbiological counts

Additional microbiological measurement	Mean ± SD (CFU/g)	Reported criterion
Total aerobic mesophilic flora	$3.7 \times 10^6 \pm 2.3 \times 10^5$	$\leq 10^5$
Coliforms at 37 °C	$1.8 \times 10^5 \pm 2.4 \times 10^4$	$\leq 10^2$
Escherichia coli	$1.5 \times 10^3 \pm 3 \times 10^2$	$\leq 10^2$

Coagulase-positive staphylococci	$1.5 \times 10^4 \pm 9 \times 10^2$	$\leq 10^2$
Salmonella spp.	$1.5 \times 10^3 \pm 3 \times 10^2$	$\leq 10^2$

3.5 Biochemical identification

API 20E profile 6704552 was used to identify Salmonella spp., with a probability of 89.6%. Secondary identifications were *Salmonella enterica* subsp. *arizonae* (10.3%) and *Citrobacter braakii* (0.1%).

3.6 Molecular identification

Electrophoresis showed a band reported at approximately 421 bp in some wells, while the reference specifies an expected product of 429 bp (Table 1). Because fragment size estimated from an agarose gel is approximate, the result is described here as a band near the expected size.

3.7 Antimicrobial susceptibility profile

Table 6: Results of antimicrobial susceptibility profile

No.	Antimicrobial agent	Reported MIC	Interpretation
1	Ampicillin	>16	R
2	Ticarcillin	>64	R
3	Piperacillin/tazobactam	>64	R
4	Cefoxitin	>32	R
5	Ceftazidime	>32	R
6	Ertapenem	≤0.5	S
7	Imipenem	≤0.25	S
8	Amikacin	8	S
9	Gentamicin	>8	R
10	Tobramycin	>8	R
11	Nalidixic acid	>16	R
12	Ciprofloxacin	>2	R
13	Ofloxacin	>4	R
14	Nitrofurantoin	64	S
15	Trimethoprim/sulfamethoxazole	>100	R

4 DISCUSSION

The integrated findings demonstrate recovery of Salmonella from both stool and blood specimens among hospitalized children at the University Hospital for Mothers and Children of N'Djamena. Salmonella was detected in 20% of stool specimens and 16% of blood specimens (Table 2). The simultaneous recovery from stool and blood is consistent with the spectrum of Salmonella disease, which includes both enteric infection and invasive bloodstream infection [2–4]. The proportion of stool-positive specimens should be interpreted in relation to hospital-based recruitment, case definition, season, specimen handling, prior antimicrobial exposure, and the microbiological methods used. Pediatric diarrheal disease is etiologically heterogeneous, and the relative contribution of individual pathogens varies substantially between settings [13,19]. Children aged 0–5 years accounted for half (50%) of the stool-positive cases (Table 3), whereas in the case of blood specimens was 25% (Table 4). This descriptive concentration is consistent with the recognized burden of invasive Salmonella disease among young children in sub-Saharan Africa [2–7]. The microbiological identification pathway combined culture, biochemical testing, API 20E/API WEB, and PCR. This layered strategy is useful because culture provides a viable isolate, API 20E provides standardized biochemical orientation, and PCR provides an additional molecular line of evidence. However, the API profile produced alternative identifications at lower probabilities. Therefore, the most defensible taxonomic designation from the available evidence is *Salmonella*

spp. rather than a specific serovar or definitive subspecies. The PCR findings require cautious interpretation. The primer table specifies a 429-bp product (Table 1), whereas the study report describes an approximately 421-bp band. Because gel-based size estimation is approximate, the finding is best described as a band near the expected size. The antimicrobial susceptibility data indicate a broad resistance phenotype. Resistance was reported across several antimicrobial classes, including penicillins, selected cephalosporins, aminoglycosides, quinolones/fluoroquinolones, and trimethoprim/sulfamethoxazole (Table 6). Such multidrug resistance is clinically relevant because antimicrobial options for invasive Salmonella infection may become limited when resistance accumulates across therapeutic classes [4,15,16]. The quinolone/fluoroquinolone findings were notable: nalidixic acid, ciprofloxacin, and ofloxacin were all reported as resistant. Fluoroquinolone resistance in Salmonella may involve mutations affecting DNA gyrase or topoisomerase IV, altered permeability, efflux, and plasmid-mediated determinants [12,14]. Resistance to ampicillin, ticarcillin, piperacillin/tazobactam, cefoxitin, and ceftazidime was also reported. β-lactam resistance may result from β-lactamase production, altered permeability, target changes, or other mechanisms [12,14]. The phenotype should therefore be reported without attributing it to a specific resistance enzyme. The aminoglycoside pattern was heterogeneous: gentamicin and tobramycin were reported as resistant, whereas amikacin remained susceptible. Differences within an antimicrobial class are biologically plausible because resistance determinants can have different substrate spectra. Susceptibility to ertapenem and imipenem was retained under the testing conditions. This finding indicates preserved in vitro activity but does not by itself establish the absence of carbapenem-resistance mechanisms. Nitrofurantoin was also reported as susceptible; however, an in vitro susceptibility result should not be interpreted independently of infection site or pharmacokinetic considerations, particularly for invasive or bloodstream infection. The reported resistance pattern spans multiple antimicrobial categories and is consistent with a phenotypic multidrug-resistant pattern under the reported interpretations. Formal MDR classification should nevertheless be stated together with the verified antimicrobial panel and breakpoint criteria [20]. The findings have implications for hospital microbiology and antimicrobial stewardship in N'Djamena. Repeated standardized AST using documented contemporary or historically appropriate breakpoints would improve comparability over time. At a broader level, Salmonella surveillance should be integrated with human, animal, food, and environmental sources because resistant organisms and resistance determinants can circulate across these interfaces [21,22].

5 CONCLUSION

This study documented Salmonella recovery from 20% of stool specimens and 16% of blood specimens collected from hospitalized children at the University Hospital for Mothers and Children of N'Djamena. Identification combined culture, biochemical characterization, API 20E/API WEB, and PCR, with the API profile predominantly supporting *Salmonella spp*. The antimicrobial susceptibility results showed a broad resistance phenotype involving multiple antimicrobial classes, while activity was retained for ertapenem, imipenem, amikacin, and nitrofurantoin under the reported testing conditions.

The findings support continued local microbiological surveillance, standardized antimicrobial susceptibility testing, and antimicrobial stewardship.

STATEMENTS ON COMPLIANCE WITH ETHICAL STANDARDS

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Disclosure of conflict of interest

Authors have declared that no competing interests exist.

Statement of informed consent

Informed consent was obtained from all individual participants included in the study.

REFERENCES

[1] World Health Organization. Salmonella (non-typhoidal) [Internet]. Geneva: World Health Organization; 2018 [cited 2026 Sep 14].

[2] Stanaway JD, Parisi A, Sarkar K, Blacker BF, Reiner RC Jr, Hay SI, et al. The global burden of non-typhoidal Salmonella invasive disease: a systematic analysis for the Global Burden of Disease Study 2017. Lancet Infect Dis. 2019;19(12):1312-1324. doi:10.1016/S1473-3099(19)30418-9.

[3] Ao TT, Feasey NA, Gordon MA, Keddy KH, Angulo FJ, Crump JA. Global burden of invasive nontyphoidal Salmonella disease, 2010. Emerg Infect Dis. 2015;21(6):941-949. doi:10.3201/eid2106.140999.

[4] Crump JA, Sjölund-Karlsson M, Gordon MA, Parry CM. Epidemiology, clinical presentation, laboratory diagnosis, antimicrobial resistance, and antimicrobial management of invasive Salmonella infections. Clin Microbiol Rev. 2015;28(4):901-937. doi:10.1128/CMR.00002-15.

[5] Graham SM. Nontyphoidal salmonellosis in Africa. Curr Opin Infect Dis. 2010;23(5):409-414. doi:10.1097/QCO.0b013e32833dd25d.

[6] Gilchrist JJ, MacLennan CA. Invasive nontyphoidal Salmonella disease in Africa. EcoSal Plus. 2019;8(2). doi:10.1128/ecosalplus.ESP-0007-2018.

[7] Feasey NA, Dougan G, Kingsley RA, Heyderman RS, Gordon MA. Invasive non-typhoidal salmonella disease: an emerging and neglected tropical disease in Africa. Lancet. 2012;379(9835):2489-2499. doi:10.1016/S0140-6736(11)61752-2.

[8] Holmes B, Willcox WR, Lapage SP. Identification of Enterobacteriaceae by the API 20E system. J Clin Pathol. 1978;31(1):22-30. doi:10.1136/jcp.31.1.22.

[9] Grimont PAD, Weill FX. Antigenic formulae of the Salmonella serovars. 9th ed. Paris: WHO Collaborating Centre for Reference and Research on Salmonella, Institut Pasteur; 2007.

[10] 10. Aabo S, Rasmussen OF, Rossen L, Sørensen PD, Olsen JE. Salmonella identification by the polymerase chain reaction. Mol Cell Probes. 1993;7(3):171-178. doi:10.1006/mcpr.1993.1026.

[11] Malorny B, Hoorfar J, Bunge C, Helmuth R. Multicenter validation of the analytical accuracy of Salmonella PCR: towards an international standard. Appl Environ Microbiol. 2003;69(1):290-296. doi:10.1128/AEM.69.1.290-296.2003.

[12] Davies J, Davies D. Origins and evolution of antibiotic resistance. Microbiol Mol Biol Rev. 2010;74(3):417-433. doi:10.1128/MMBR.00016-10.

[13] Chaudhari R, Singh K, Kodgire P. Biochemical and molecular mechanisms of antibiotic resistance in Salmonella spp. Res Microbiol. 2023;174(1-2):103985. doi:10.1016/j.resmic.2022.103985.

[14] Punchihewage-Don AJ, Ranaweera PN, Parveen S. Defense mechanisms of Salmonella against antibiotics: a review. Front Antibiot. 2024;3:1448796. doi:10.3389/frabi.2024.1448796.

[15] Amir Y, Omar M, Adler A, Abu-Moch S, Donkor ES, Cohen D, et al. The prevalence of antimicrobial drug resistance of non-typhoidal Salmonella in human infections in sub-Saharan Africa: a systematic review and meta-analysis. Expert Rev Anti Infect Ther. 2024;22(9):761-774. doi:10.1080/14787210.2024.2368989.

[16] Kowalski M, Obama BM, Catho G, Dewez JE, Merglen A, Ruef M, et al. Antimicrobial resistance in Enterobacterales infections among children in sub-Saharan Africa: a systematic review and meta-analysis. EClinicalMedicine. 2024;70:102512. doi:10.1016/j.eclinm.2024.102512.

[17] Jorgensen JH, Ferraro MJ. Antimicrobial susceptibility testing: a review of general principles and contemporary practices. Clin Infect Dis. 2009;49(11):1749-1755. doi:10.1086/647952.

[18] Humphries RM, Miller L, Zimmer B, Matuschek E, Hindler JA. Contemporary considerations for establishing reference methods for antibacterial susceptibility testing. J Clin Microbiol. 2023;61(6):e01886-22. doi:10.1128/jcm.01886-22.

[19] Kotloff KL, Nataro JP, Blackwelder WC, Nasrin D, Farag TH, Panchalingam S, et al. Burden and aetiology of diarrhoeal disease in infants and young children in developing countries (GEMS): a prospective, case-control study. Lancet. 2013;382(9888):209-222. doi:10.1016/S0140-6736(13)60844-2.

[20] Magiorakos AP, Srinivasan A, Carey RB, Carmeli Y, Falagas ME, Giske CG, et al. Multidrug-resistant, extensively drug-resistant and pandrug-resistant bacteria: an international expert proposal for interim standard definitions for acquired resistance. Clin Microbiol Infect. 2012;18(3):268-281. doi:10.1111/j.1469-0691.2011.03570.x.

[21] Chainier D, Barraud O, Masson G, Couve-Deacon E, François B, Couquet CY, et al. Integron digestive carriage in human and cattle: a One Health cultivation-independent approach. Front Microbiol. 2017;8:1891. doi:10.3389/fmicb.2017.01891.

[22] Larsson DGJ, Flach CF. Antibiotic resistance in the environment. Nat Rev Microbiol. 2022;20(5):257-269. doi:10.1038/s41579-021-00649-x.