

RESEARCH

Open Access



Prevalence and antibiotic resistance characteristics of non-typhoidal *Salmonella enterica* serotypes isolated from food and water consumed by children under five years in Karamoja sub-region of Uganda

Ronald Mpagi¹ , Lawrence Okidi¹ and Duncan Ongeng^{1*}

Abstract

Karamoja, a sub-region in North Eastern Uganda, has consistently experienced a high prevalence of diarrhoea and undernutrition among children under five (CUF) for over a decade. Microbiologically unsafe food is believed to be a key factor for the high prevalence of diarrhoea-associated undernutrition CUF in the sub-region, but specific causative agents have largely remained undelineated. This study investigated the prevalence, serotypes, antibiotic resistance (AMR) characteristics, and association between AMR phenotypes and AMR genes (ARGs) among non-typhoidal *Salmonella* (NTS) *enterica* serotypes isolated from water and food in the sub-region. Isolates (45) confirmed by *invA* PCR amplification were PCR-serotyped targeting various serotype-conserved genes and tested for phenotypic AMR against nine antibiotics and for the presence of ARGs using PCR. Overall prevalence of NTS was at 50%, with *S. Typhimurium* (53%) being the most dominant, followed by *S. Infantis* (16%), *S. Enteritidis* (9%), and *S. Dublin* (4%). Phenotypic resistance was highest for azithromycin (91.1%) followed by ciprofloxacin (31.1%), cefixime (20%), cefotaxime (20%), ceftazidime (15.6%), ceftriaxone (6.7%), cotrimoxazole (6.7%), chloramphenicol (6.7%) and amoxicillin-clavulanic acid (2.2%). The most prevalent ARGs were *mefA* (95.3%), *gyrA* (94.9%), *parC* (92.3%), *blaPSE* (81.3%), *sul1* (66.6%), and *sul2* (66.6%) encoding for macrolides, quinolones, beta-lactams, and sulphonamides, respectively. Phenotypic resistance to beta-lactams, chloramphenicol, cotrimoxazole, and ciprofloxacin was strongly correlated with the presence of *blaPSE*, *floR*, *sul1*, and *parC*, respectively ($p < 0.05$). This study has revealed that foods and water in Karamoja sub-region are contaminated with antibiotic-resistant NTS *enterica* serotypes and therefore need remediation.

Keywords *Salmonella*, Prevalence, Serotypes, Antimicrobial resistance

Introduction

Food safety is a key factor influencing nutrition outcomes through its impact on the utilization dimension of food security. Globally, 22% of children under five years are stunted and 6.7% are wasted with the majority of these concentrated in low-income settings of the world including Uganda (FAO, Ifad, UNICEF WFP and WHO (2022). In Uganda, the Karamoja sub-region is an area that has consistently experienced the highest prevalence of

*Correspondence:

Duncan Ongeng
duncanongeng@hotmail.com

¹ Department of Food Science and Postharvest Technology, Faculty of Agriculture and Environment, Gulu University, P.O. Box 166, Gulu, Uganda



© The Author(s) 2025. **Open Access** This article is licensed under a Creative Commons Attribution-NonCommercial-NoDerivatives 4.0 International License, which permits any non-commercial use, sharing, distribution and reproduction in any medium or format, as long as you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons licence, and indicate if you modified the licensed material. You do not have permission under this licence to share adapted material derived from this article or parts of it. The images or other third party material in this article are included in the article's Creative Commons licence, unless indicated otherwise in a credit line to the material. If material is not included in the article's Creative Commons licence and your intended use is not permitted by statutory regulation or exceeds the permitted use, you will need to obtain permission directly from the copyright holder. To view a copy of this licence, visit <http://creativecommons.org/licenses/by-nc-nd/4.0/>.

undernutrition particularly among children under five over the last decade (Uganda Bureau of Statistics - UBOS and ICF (2018)). Besides other factors such as food insecurity, abject household poverty levels, sanitation factors, feeding practices, and child and caregiver characteristics that have been identified as predictors of childhood undernutrition in Karamoja (Mokori et al. 2023), food safety is a key factor that can influence nutritional outcomes in an individual through its impact on the utilization dimension of food security. Among the food safety elements (physical, chemical, biological, and nutritional), microbial foodborne diseases ostensibly caused by pathogenic protozoa (Chávez-Ruvalcaba et al. 2021), fungi (War et al. (War 2022), viruses (Pexara and Govaris 2020), and bacteria (Ishaq et al. 2021) are a factor that exacerbates malnutrition situation in children under five years mainly through nutrient malabsorption and loss in the form of watery stool.

Among diarrheal/invasive pathogenic agents, *Salmonella* is among the top four prioritized pathogens by the World Health Organization (WHO) with a high capability of causing intestinal or systemic disease in humans (Hasso-Agopsowicz et al. 2021). A study in Uganda revealed that over 40% of hospitalized children diagnosed with diarrhoea had *Salmonella* infections (Appiah et al. 2021). *Salmonella* infections are usually self-limiting, however, in cases of severe gastroenteritis and impaired immunity, the WHO recommends the use of antimicrobial therapy in the clinical management of the disease as well as to eliminate the pathogen (WHO Estimates of the Global Burden of Foodborne Diseases (2015). Several antimicrobial agents, including sulphonamides, beta-lactams, fluoroquinolones, macrolides, and phenicols, have been used to control the disease. However, the excessive and abusive use of antibiotics has exacerbated the development and propagation of antimicrobial resistance (AMR) among previously susceptible human bacterial pathogens such as *Salmonella* (Chokshi et al. 2019). The AMR and AMR genes of *Salmonella* have been reported in previous studies. It has also been reported that *Salmonella* possesses beta-lactam resistance (*bla*_{TEM} *bla*_{PSE} *bla*_{CTX-M}) (Jafari Sales et al. 2021), sulphonamides resistance (*sul1*, *sul2*) (Wang et al. 2021), phenicol resistance (*cat1* and *floR*) (Forgaci et al. 2022), macrolide resistance (*ermB*, *mefA*) (Pereira et al. 2020) and fluoroquinolone resistance (*parC*, *gyrA*) (Zhang et al. 2014).

Besides the reported high levels of poor hygiene and sanitation in the Karamoja sub-region characterized by over 60% of the population practicing open-air defecation (ICF. 61, a recent study by Okidi et al. (2022) revealed a widespread *Salmonella* contamination of the foods and water within the region. Despite this reported massive distribution of the pathogen

within the region, a significant information gap still exists on the prevalence and serotypes of *Salmonella* in the commonly consumed food and water, AMR phenotypes, AMR genes, and the association between the AMR phenotypes and AMR genes. This study investigated the antimicrobial resistance characteristics of *Salmonella* isolated from foods and water commonly consumed by children under five in Karamoja against nine antimicrobial agents and determined the presence of AMR genes in phenotypically resistant isolates. The associations between AMR phenotypes and AMR genes were analyzed. The results of this study provide a glimpse into the epidemiology of AMR in *Salmonella* within the region which is significant in clinical management of the disease and also in informing public health decisions.

Materials and methods

Study area, sample collection, and transportation

Samples for the study were collected from Karamoja sub-region from February to March 2023. The sub-region is located in North East Uganda. It is bordered by Kenya in the East, Lango and Acholi in the West, and Teso in the South. It is composed of nine districts (Kotido, Kaabong, Karenga, Nabilatuk, Abim, Moroto, Napak, Amudat, and Nakapiripirit). A random sampling strategy was used to select locations for sample collection. At the sub-region level, Nakapiripirit and Nabilatuk districts were randomly selected. Subsequently, two sub-counties were randomly chosen from each district. In Nabilatuk district, the selected sub-counties included Lolachat and Lorengedwat, whereas Nakapiripirit Town Council and Namalu were selected from Nakapiripirit district.

As such, fifty samples were collected from each selected sub-county. A total of 200 different food and water samples were aseptically taken from randomly selected households (Table 1). These included cooked cowpea leaves ($n=12$), cooked meat ($n=12$), drinking water from households ($n=30$), water from community water sources ($n=26$), maize flour ($n=12$), raw milk ($n=12$), fermented milk ($n=12$), cooked beans ($n=12$), sorghum bread ($n=12$), maize posho ($n=12$), millet porridge ($n=12$), millet flour ($n=12$), cassava flour ($n=12$) and sorghum flour ($n=12$).

For each food sample, approximately 250 to 400 g were collected using sterile disposable spoons and transferred into sterile disposable bags. For water samples, 200 to 400 ml were collected in properly labelled sterile bottles indicating the location, sampling time, and date. The samples were placed in an ice cool box at 4 °C and transported to the laboratory for analysis within 24 h.

Table 1 Distribution of food and water samples collected from Nakapiripirit and Nabilatuk districts ($n=200$)

Product	Nakapiripirit District		Nabilatuk District		Total
	Town Council	Namalu sub-county	Lolachat sub-county	Lorengedwat sub-county	
Cowpea leaves	3	3	3	3	12
Cooked meat	3	3	3	3	12
Water from households	7	8	7	8	30
Water from Community	7	6	7	6	26
Maize four	3	3	3	3	12
Fresh milk	3	3	3	3	12
Fermented milk	3	3	3	3	12
Cooked beans	3	3	3	3	12
Sorghum bread	3	3	3	3	12
Maize posho	3	3	3	3	12
Millet porridge	3	3	3	3	12
Millet bread	3	3	3	3	12
Cassava flour	3	3	3	3	12
Sorghum flour	3	3	3	3	12
Total	50	50	50	50	200

Salmonella isolation

Salmonella isolation was performed following the methods described by the Food and Drug Authority (Andrews 2018). In brief, 25 ml/gram of the food sample was added to 135 ml of 0.1% (w/v) of buffered bacteriological peptone (Cadablab, Madrid, Spain) and incubated at 37 °C for 24 h for pre-enrichment. Further, 0.1 ml of the pre-enriched inoculum was transferred to 10 ml of Rapaport Vassiliadis Soy (RVS) selective enrichment broth (Himedia, Mumbai, India) and incubated at 42 °C for 24 h. In order to ensure thorough mixing, both pre and selective enrichment were done under shaking conditions. Following selective enrichment, a loopful of the inoculum was streaked onto Xylose Lysine Deoxycholate (XLD) Agar (OXOID, Basingstoke, UK) and incubated at 37 °C for 24 h. The presumptive *Salmonella* colonies appearing pink with dark centres were re-streaked on XLD agar to obtain pure cultures which were screened further for confirmation using Colony Polymerase Chain Reaction (PCR).

PCR confirmation of *Salmonella* isolates

Colony PCR assays following a procedure described by Chandra et al. (2013) were performed using a primer targeting the *invA* virulence gene (*InvA* F 5'-GAGGAAAAA GAAGGGTCG-3'), and (*InvAR* 5'-CTCAACTTCAGC AGATACCA-3') (Radhika 2014). *InvA*, a gene particularly involved in host recognition and invasion of the epithelial cells of intestinal mucosa is believed to occur in all *Salmonella* serovars. As such, the *invA* has previously been used in several studies to confirm isolates belonging to the genus *Salmonella* (Alarjani et al. 2021; Zhanabayeva

et al. 2021). The PCR was conducted in a total volume of 25 µL which comprised 12.5 µL of Taq 2X master mix, 0.5 µL of forward primer, 0.5 µL of reverse primer, 9.5 µL of nuclease-free water, and 2 µL of *Salmonella* colony to act as template DNA. The PCR conditions consisted of 1 cycle of initial denaturation at 94 °C for 10 min, this was then followed by 30 cycles of denaturation at 94 °C for 1 min, primer annealing at 54 °C and extension at 72 °C for 1 min followed by a final extension at 72 °C for 5 min. The PCR product was electrophoresed using 1% (w/v) agarose gel stained with ethidium bromide and visualised under the Vilber bio print transilluminator (Vilber smart imaging, CHY, France) set at 230v 50/60 HZ for 45 min. *Salmonella* Typhimurium ATCC 14028 and nuclease-free water were used as PCR-positive and negative controls, respectively (Fig. 1).

PCR serotyping of *Salmonella* isolates

PCR assays targeting conserved genes of the investigated serotypes were performed using genomic DNA. The DNA was extracted using the Quick DNA fungal/bacterial miniprep (Zymo Research, California, United States). The list of targeted genes, primers, annealing temperature, and amplicon sizes is shown in Table 2. PCR was conducted in a total volume of 25 µL with genomic DNA. Amplification reactions were performed using Applied Biosystems thermocycler (SimpliAmp™ thermocycler, Singapore, Singapore) programmed as follows: initial denaturation at 94°C for 2 min followed by 35 cycles of actual denaturation at 94°C for 30 s, annealing for each primer was done at specific temperatures (Table 2) for 1

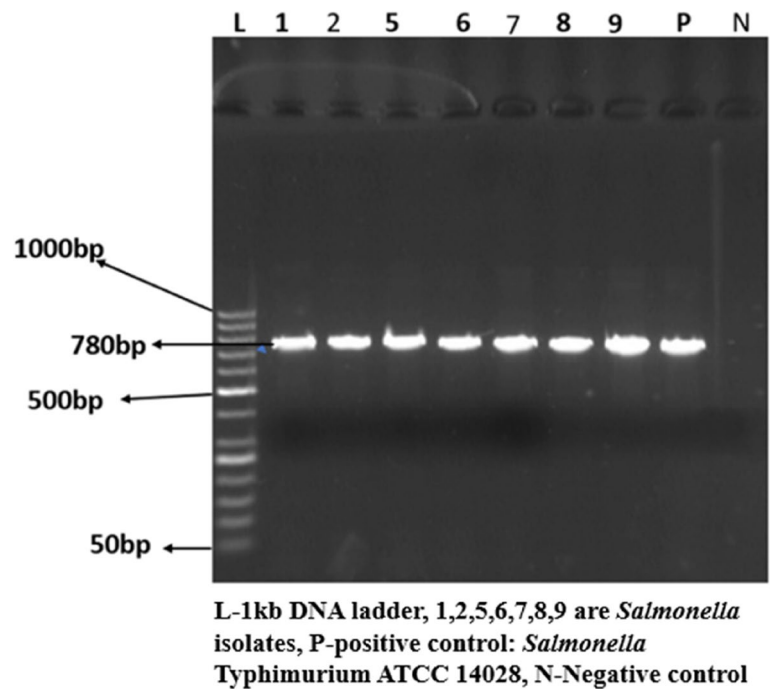


Fig. 1 PCR confirmation of *Salmonella* isolates using the *invA* gene (780 bp). L- 1 kb DNA ladder, PCR products (1,2,5,6,7,8, and 9) are suspected *Salmonella* isolates confirmed as positive, P-positive control; *Salmonella* Typhimurium ATCC 14028, and N-negative control

Table 2 List of primers used in the serotyping of the confirmed *Salmonella* isolates

Targeted serotype	Target gene	Primer sequence (5'–3')	Annealing temp °C	Amplicon size (bp)	Reference
<i>Salmonella</i> Enteritidis	<i>sdf1</i>	F -TGT GTT TTA TCT GAT GCA AGA GG R -TGA ACT ACG TTC GTT CTT CTG G	55	304	Nair et al. (2015)
<i>Salmonella</i> Typhimurium	<i>spy</i>	F- TTG TTC ACT TTT TAC CCC TGA A R -CCC TGA CAG CCG TTA GAT ATT	58	301	Nair et al. (2015)
<i>Salmonella</i> Heildberg	1,067,175 1,068,152 2,541,120– 2,541,716 4,675,756– 4,676,622	F-ACTTCATGCGCAGACTTGCC R'-CAAGAATCGGGAAATTTTGA F-TACCGCCCCATTGTATCT R-CCCTTGCGCAACATAAACT F-GGATCTCAACAAAATGAGGT R-ATGCATCACTGCATCTTCGT	54	105 199 303	Akiba et al. (2011)
<i>Salmonella</i> Choleraesuis	sch_0971 sch_2145 sch_4349	F-AGATATGCGGCTTGCTGACT R-AGCGTGGCTCGAAACAGTAT F-GGCGAAAGAGCTTAACGTGA R-TTACCATCGGACCAAATGT F-TCGGGATCGTCTCTATACG R-GTGGATGTGTGACCGACTG	54	100 198 305	
<i>Salmonella</i> Infantis	3,113,085–3114152 3,711,271–3,711,921 4,621,947–4,622,627	F-GGTCATTGTGCGAAACCTG R-ACATTCCCCCTTCCACTGCC F-CGCGAAGAAGTGCATAAACCC R-CGCCACTTTCGTTATCTGAG F-ACCTACTACTATCCCTGATG R-GCGAATTTTGCTACTTGAAG	54	95 198 304	Akiba et al. (2011)
<i>Salmonella</i> Dublin	sed_A1226 sed_A1104 sed_A2276	F-ATCGGTGCTGGGTAATTTTG R-AGGAACGAGAGAAACTGCTT F-ACGCGAAATCTGATGGTCTT R-GCCCAACAGTTGTGAAAGGC F-ATCACCTCGCAAACCTTGTC R-TCGGGCAATCAGGTCGCCGA	54	105 203 296	Akiba et al. (2011)

min, extension at 72°C for 30 s and final extension at 72°C for 4 min. Nuclease-free water was used as a negative control. The amplified PCR products were analyzed in a horizontal electrophoresis unit (Consort Electrophoresis model E844, Belgium) for 45 min at a voltage of 250. Gel observations were visualized using the Vilber bio print transilluminator projected to a computer screen.

Phenotypic antimicrobial susceptibility evaluation of *Salmonella* isolates

Disc diffusion method according to the Clinical Laboratory and Standards Institute (CLSI) was used to screen the isolates for antimicrobial resistance. A total of 9 antimicrobial agents including beta-lactams (amoxicillin clavulanic acid or AMC (20/10 µg), Cephems (cefotaxime or CXT (30 µg); ceftriaxone or CRO (30 µg); ceftazidime or CAZ (30 µg); cefixime or CFM (5 µg), Sulphonamides (cotrimoxazole or SXT (25 µg), macrolides (azithromycin or AZI (15 µg), Phenicol (chloramphenicol or C (30 µg) and Fluoroquinolone (ciprofloxacin or CIP (5 µg) were used. Prior to the spreading of the isolates on already prepared Mueller–Hinton Agar (MHA) (OXOID, Basingstoke, UK) plates, the inoculum was standardized using normal saline to a turbidity equivalent to 0.5 McFarland standard. This turbidity is estimated to be equivalent to $1\text{--}2 \times 10^8$ cfu/ml of *Escherichia coli* (*E. coli*) cells. The inoculated plates were incubated at 37°C for 24 h. After incubation,

the inhibition zone diameters were then measured, and the results were interpreted according to the CLSI guidelines (Clinical and Laboratory Standards Institute (2022)). Isolates were scored as either susceptible, intermediate, or resistant. Resistance to ≥ 3 antimicrobial classes were classified as multidrug resistant (MDR).

Genotypic characterization of antibiotic resistance of *Salmonella* isolates

PCR assays were performed to detect the presence of ARGs known to confer resistance to beta-lactams (*bla*_{TEM}, *bla*_{PSE}, *bla*_{CTX}) chloramphenicol (*cat*_I, *flo*_R), quinolones (*par*_C, *gyr*_A), macrolides (*erm*_B, *mef*_A), and sulphonamides (*sul*₁, *sul*₂). The ARGs, primers, annealing temperatures, and expected band size of each amplified PCR product are listed in Table 3. The PCR was conducted in a total volume of 25 µL, which included 12.5 µL of Taq 2X master mix, 0.5 µL of forward primer, 0.5 µL of reverse primer, 9.5 µL of nuclease-free water, and 2 µL of template DNA. Amplification reactions were performed using Applied Biosystems thermocycler (SimpliAmp™ thermocycler, Singapore, Singapore) using PCR conditions described under Sect. 2.4, making use of the annealing temperatures provided in Table 3. Gel maps for the AMR genes are presented in additional file 1, Figs. 2–11.

Table 3 List of primers used to detect the genetic resistance of the different antibiotics

Antibiotic	Targeted gene	Primer Sequence (5'–3')	Annealing Temperature	Amplicon size	References
Chloramphenicol	<i>cat</i> _I	F- GGCATTTTCAGTCAGTTG	50	551	Kikuvu et al. (2010)
	<i>flo</i> _R	R-CATTAAGCATTCTGCCG F-AACCCGCGCTCTGGATCAAGTCAA R CAAATCACGGGCCACGCTGTATC	60	548	
Beta-lactams	<i>bla</i> _{TEM}	F-CCGTGTCGCCCTTATCCCC R-GCCTGACTCCCCGTCGTGT	71	780	Kikuvu et al. (2010)
	<i>bla</i> _{PSE}	F-CGCTTCCCGTTAACAAGTAC R-CTGGTTCATTTCAGATAGCG	58	465	Kikuvu et al. (2010)
	<i>bla</i> _{CTX-M}	F-ATGTGCAGYACCAGTAARGTKATGGC R: GGGTRAARTARGTSACCAGAAYSAGCGG	58	592	Mulvey et al. (2003)
Quinolone	<i>par</i> _C	F- CTATGCGATGTCAGAGCTGG R- TAACAGCAGCTCGGCGTATT	62	270	Elbadawi et al. (2017)
	<i>gyr</i> _A	F-AAATCTGCCCGTGTCTGGT R-GCCATA CCTACGGCGATACC	55	343	Elbadawi et al. (2017)
Macrolides	<i>erm</i> _B	F-CGTACCTTGGATATTCACCG	60	224	Skittrall et al. (2021)
	<i>mef</i> _A	R-GTAAACAGTTGACGATATTC F-CTGTATGGAGCTACCTGTCTGG R-CCCAGCTTAGGTATACGTAC	60	294	
Sulphonamides	<i>sul</i> ₁	F-GCGCTCAAGGCAGATGGCATT R- GCGTTTGATACCGGCACCCGT	70	420	Xu et al. (2020)
	<i>sul</i> ₂	FGCGCTCAAGGCAGATGGCATT R GCGTTTGATACCGGCACCCGT	70	284	Goni et al. (2018)

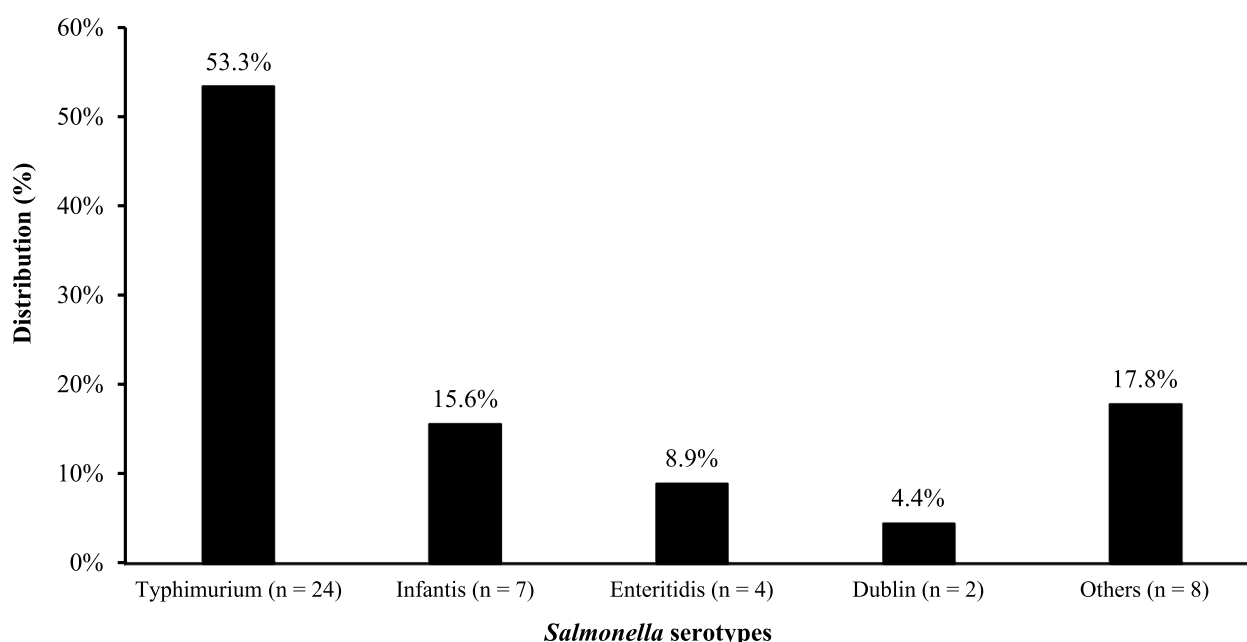


Fig. 2 Distribution of *Salmonella* serotypes among the isolates confirmed ($n=45$)

Data analysis

Descriptive statistics in form of percentages were used to report the resistance patterns of the observed phenotypes of the isolates. The same was used to characterize the prevalence of ARGs among the *Salmonella* isolates. A chi-square analysis was performed to determine the association between specific ARGs and AMR phenotypes. Statistically significant associations were shown as odd ratios (ORs) with 95% confidence intervals. An odd ratio of >1 (positive association) indicated an increased probability of co-concurrence of the genotype or phenotype being studied with the measured phenotype or genotype. An OR <1 (negative association) indicated a decreased probability of co-occurrence of the genotype or phenotype studied with the measured phenotype or genotype. Statistical analysis was performed using SPSS (version 20.0), while a $p < 0.05$ was considered significant.

Results

Isolation and molecular identification of *Salmonella* strains from food and water

Out of 200 food and water samples, 90 (45%) yielded *Salmonella* suspect colonies that were characterized by pink colonies with a black centre on XLD agar. No *Salmonella* suspect colonies were detected from dry and processed flours such as maize flour, sorghum flour, cassava flour, and millet flour in this study.

Following the application of PCR targeting the *invA* gene (Fig. 1), 45 (50%) isolates were confirmed as

Salmonella. Of these, 13 (28.9%) isolates were from cooked cowpea leaves, 6 (13.3%) isolates were from millet bread, 5 (11.1%) isolates were from cooked meat, 4 (8.9%) isolates were from community water samples, fresh milk, and millet porridge. A total of 3 (6.7%) isolates each were obtained from household drinking water, fermented milk and maize posho, respectively.

Characterization of *Salmonella* serotypes from food and water by PCR

Serotyping of the PCR confirmed isolates revealed that *S. typhimurium* was the most dominant (24/45, 53.3%), followed by *S. infantis* (7/45, 15.6%), *S. enteritidis* (4/45, 8.9%), and *S. dublin* (2/45, 4.4%). However, 8 (17.8%) isolates were non-typable (Fig. 2).

Phenotypic antimicrobial resistance profile of *Salmonella* isolates

In general, all 45 (100%) of the PCR-confirmed *Salmonella* isolates were resistant to at least one antimicrobial agent, with 17 (37.8%) isolates displaying MDR. The highest resistance was recorded against azithromycin (91.1%), followed by ciprofloxacin (31.1%), cefixime or cefotaxime (20%), ceftazidime (15.6%), chloramphenicol, ceftriaxone and cotrimoxazole with each (6.7%) respectively, and amoxicillin-clavulanic acid (2.2%) in decreasing order of magnitude (Table 4).

Table 4 Proportion of *Salmonella* isolates exhibiting various antimicrobial resistance profiles aggregated by antibiotic group ($n = 45$)

S/N	Antibiotics types	Antibiotic gents	Susceptible	Intermediate	Resistant
01	Beta-lactams	Ceftriaxone (CAX)	41(91.1%)	1(2.2%)	3(6.7%)
		Ceftazidime (CAZ)	37(82.2%)	1(2.2%)	7(15.6%)
		Cefixime (CFM)	36(80.0%)	0	9(20.0%)
		Amoxiclav (AMC)	43(95.6%)	1(2.2%)	1(2.2%)
		Cefotaxime (CTX)	35(77.8%)	1(2.2%)	9(20.0%)
02	Quinolones	Ciprofloxacin (Cip)	6(13.3%)	25(55.6%)	14(31.1%)
03	Macrolides	Azithromycin (Azi)	4(8.9%)	0	41(91.1%)
04	Sulphonamides	Cotrimoxazole (SXT)	42(93.3%)	0	3(6.7%)
05	Phenicol	Chloramphenicol (C-20)	38(84.4%)	4(8.9%)	3(6.7%)

Genotypic antibiotic resistance profiles of *Salmonella* isolates

Results of PCR analysis conducted to determine genetic markers of antibiotic resistance to the antibiotics investigated are presented in Table 5. Most of the isolates carried multiple resistance genes.

In the case of beta-lactams, 13 (81.25%) beta-lactam resistant isolates carried one of the genes conferring resistance to beta-lactam antibiotics. The most prevalent beta-lactam resistance gene among the screened isolates was a penicillinase encoding *bla_{PSE}* (Table 5). The extended-spectrum beta-lactamase (ESBLs) *bla_{TEM}* and *bla_{CTX-M}* types were not detected in any isolates (Table 5). Worth noting is that three isolates which displayed resistance to beta-lactam antibiotics phenotypically, did not carry any of the beta-lactam ARGs that were investigated. Multiple mutations in the quinolone resistance-determining regions (QRDR) of the DNA gyrase sub-unit gene

gyrA, combined with mutations in the DNA topoisomerase gene *parC*, are expected to result in full resistance to ciprofloxacin. Among the isolates, 35(89.7%) carried both *gyrA* and *parC* genes. Two isolates carried only *gyrA*, and one isolate harboured only the *parC* gene (Table 5). Notably, one isolate showed phenotypic resistance to ciprofloxacin despite carrying neither the *gyrA* nor the *parC* gene. With regard to macrolides, 41(95.3%) isolates had the macrolide efflux gene *mefA*. The *ermB* gene was not detected in any of the isolates that displayed resistance to azithromycin phenotypically. Two isolates that displayed phenotypic resistance to azithromycin did not carry any of the associated ARGs tested for in this study. In the case of phenicol, genes linked to their resistance were present in all isolates that displayed phenotypic resistance to chloramphenicol. The efflux pump gene *floR* ($n=7$) was the most common among all isolates. However, chloramphenicol acetyltransferase gene *catI* was not detected in

Table 5 Distribution of antibiotic-resistance genes in *Salmonella* strains isolated from food and water

Resistance genes	Number of <i>Salmonella</i> strains resistant to antibiotics				
	Beta-lactams (16)	Macrolides (43)	Phenicol (7)	Quinolones (39)	Sulphonamide (3)
<i>bla_{TEM}</i>	-	-	-	-	-
<i>bla_{PSE}</i>	13	-	-	-	-
<i>bla_{CTX}</i>	-	-	-	-	-
<i>CatI</i>	-	-	-	-	-
<i>floR</i>	-	-	7	-	-
<i>parC</i>	-	-	-	36	-
<i>gyrA</i>	-	-	-	37	-
<i>ermB</i>	-	-	-	-	-
<i>mefA</i>	-	41	-	-	-
<i>sul1</i>	-	-	-	-	2
<i>sul2</i>	-	-	-	-	2

Key: *bla_{TEM}*-resistance gene of beta-lactams, *bla_{PSE}*-resistance gene of beta-lactam, *bla_{CTX-M}*-resistance gene of beta-lactams, *sul1*- resistance gene of sulphonamides *sul2*- resistance gene of sulphonamides, *gyrA*- resistance gene of quinolones, *parC*- resistance gene of quinolones, *ermB*- resistance gene of macrolides, *mefA*- resistance gene of macrolides, *catI*- resistance gene of phenicol, *floR*- resistance gene of Phenicol

any of the isolates. For the case of sulphonamides, genes that encode their resistance were detected in all three isolates that displayed phenotypic resistance to cotrimoxazole, with one isolate found to carry both *sul1* and *sul2* genes whereas each of the other two isolates carried either *sul1* or *sul2* gene (Table 5).

Association between genotypic and phenotypic antibiotic resistance profiles of *Salmonella* isolates

Results of the chi-square analysis performed to determine the association between specific ARGs and AMR phenotypes are presented in Table 6.

Significant associations were found between AMR phenotypes and genotypes of the *Salmonella* isolates. For beta-lactams, the phenotype was strongly associated with the presence *bla_{PSE}* (OR=24.7, $p=0.001$). For phenicols, resistance was strongly associated with the presence of *floR* (OR=12.545, $p=0.031$). There was no significant association between macrolide resistance with any of the tested responsible macrolide ARGs (*mefA* and *ermB*). Resistance to quinolones in this study was strongly associated with the presence of *parC* (OR=13.284, $p=0.015$). Lastly sulphonamide resistance among isolates in this study was strongly associated with *sul1* (OR=11.9, $p=0.000$).

Discussion

Prevalence and serotypes of *Salmonella* associated with foods and water in Karamoja sub region

At a general scale, the occurrence of *Salmonella* at 45% demonstrates that food and water in Karamoja sub region are potential reservoirs for pathogens of public health concern such as *Salmonella*. As such, the human population and in particular those that are immune compromised such as children under five years are still at risk

of being exposed to *Salmonella* infections. This also suggests that there is a higher degree of unhygienic practices within the region. These high levels of poor food sanitary practices have earlier been reported to be predominant in pastoral communities (Wanjala et al. 2016). Therefore, there is need to educate the community of Karamoja on food safety and sanitary practices. The *Salmonella* prevalence in foods reported in this study though is higher than 5.8% and 20% reported by Peruzy et al. (2022) and Miao et al. (2022), respectively, it is lower than 60 and 70% reported by Al-Rifai et al. (2020) in food products. These variations in *Salmonella* prevalence in food across studies among others can be attributed to several factors including differences in sample collection, study design, sample size, and geographical locations (Sanchez et al. 2007). Additionally, for Karamoja, this can also be attributed to the high level of human-livestock interaction in the Karamoja sub-region. The livestock gut is known to be a potential reservoir for zoonotic pathogens such as *Salmonella* as such aiding their spread in the environment through livestock excreta (Demirbilek 2018).

Among the investigated food samples, the highest *Salmonella* occurrence (28.9%) was found in cowpea leaves. The findings in this study are comparable with those of Okidi et al. (2022), who also reported a high *Salmonella* prevalence in green leafy vegetables in the Karamoja sub-region (66.7% -cowpea leaves, 87.5%—pumpkin leaves). This suggests that green leafy vegetables in Karamoja, such as cowpea leaves, are some of those foods with high levels of poor food sanitary conditions, which could be as a result of contaminated water sources and unhygienic food handling practices. As such, cowpea leaves may be classified as high-risk foods for children under five years. There was no *Salmonella* detected in cooked beans and dry processed cereal flours such as cassava flour, maize flour, and sorghum flour in this study. Comparable findings with respect to dry processed cereal flours were reported by Xu et al. (2019) who reported a low *Salmonella* prevalence of 2% in dry processed wheat. The absence of *Salmonella* in dry processed cereal flours in this study may be attributed to low moisture content inhibiting bacterial growth and very high shear stress during milling which could have disrupted the *Salmonella* cells. Low moisture content in foods and high shear stress during milling (Chitrakar et al. 2019) have been reported to greatly hinder microbial growth in foods. On the other hand, legumes such as beans contain high levels of lectins and phytates (Zhou et al. 2019). These compounds have been reported to possess significant antimicrobial properties against both gram-negative and positive bacterial pathogens (Zhou et al. 2019). However, the observed presence of *Salmonella* in cooked foods and its absence in corresponding dry uncooked foods may

Table 6 Associations between phenotypes and genotypes of AMR of *Salmonella* isolates

Antibiotic type (Outcome)	Resistance genes (Predictor)	Outcome predictor association		
		OR	95% CI	P-VALUE
β- lactam	<i>bla_{TEM}</i>	-	-	-
	<i>bla_{PSE}</i>	24.7	0.000—0.064	0.001
	<i>bla_{CTX-M}</i>	-	-	-
Macrolides	<i>ermB</i>	-	-	-
	<i>mefA</i>	2.3	0.936—1.000	0.958
Phenicols	<i>cat1</i>	-	-	-
	<i>floR</i>	12.5	0.000—0.065	0.031
Sulphonamides	<i>sul1</i>	11.9	0.000—0.065	0.000
	<i>sul2</i>	3.4	0.343—0.635	0.583
Fluoroquinolones	<i>parC</i>	13.3	0.000—0.064	0.015
	<i>gyrA</i>	8.4	0.066—0.289	0.144

contamination to have originated from other sources such as food handlers or water used during food preparation. This suggestion draws evidence from results which show that 4.4% of the overall *Salmonella* prevalence came from household drinking water (Table 1). Nonetheless, there is a need for further investigation to identify other likely sources of *Salmonella* food contamination. This is necessary for a comprehensive understanding of *Salmonella* food contamination scenarios in the Karamoja sub-region.

Salmonella Typhimurium was found to be the most dominant serotype in this study. The dominance of serotype Typhimurium could be due to cross-contamination from a large number of livestock kept within the Karamoja sub-region. Livestock is known to be a principal reservoir of *S. Typhimurium* (Kijima et al. 2019). On the other hand, *S. Typhimurium* is known to possess advanced virulence mechanisms and preadaptation strategies which it can use to tolerate both mild and extreme environmental conditions as well as to adapt to and occupy various niches in the environment (Zarkani and Schikora 2021). This implies that the *S. Typhimurium* isolates detected in food and water samples may also be from other niches. However, eight isolates were not identified and allocated to any other (unidentified) serovar in this study. These isolates probably belong to other serotypes that were not investigated in this study. Therefore, concerted efforts should be exercised to serotype these isolates. This is because considerable differences have been observed among various serotypes in terms of infectiousness, survival in food, and severity of disease conditions they elicit (Schwan and Kopecko 50).

Phenotypic antibiotic resistance profiles of *Salmonella* isolates

Despite the advantages of antibiotic drugs in treating infections such as salmonellosis, their extensive, abusive, and non-judicious use has resulted in AMR. The uncontrolled use of these drugs exerts selective pressure, which in turn results in the development of drug-resistant *Salmonella* strains in the environment. Results in this study revealed that MDR strains can be obtained from commonly consumed food and water. The resistance patterns in this study varied between *Salmonella* serotypes/sources. The most resisted antimicrobial agent was azithromycin, followed by ciprofloxacin (Table 7). Slightly higher resistance was recorded by Ramatla et al. (2022) regarding azithromycin (95%). Ciprofloxacin resistance pattern in this study was contrasting with those of Ngai et al. (2021), where all the *Salmonella* isolates displayed susceptibility to ciprofloxacin. The difference could be due to differences in strains of the same

Table 7 Prevalence of *Salmonella* strains isolated from food and water samples

Samples	Number of samples examined	Number of <i>Salmonella</i> positive isolates	Positive rate (%)
Cooked cowpea leaves	12	13	28.9
Cooked meat	12	5	11.1
Water from households	30	3	6.7
Water from community	26	4	8.9
Maize flour	12		
Fresh milk	12	4	8.9
Fermented milk	12	3	6.7
Cooked beans	12		
Sorghum bread	12		
Maize posho	12	3	6.7
Millet porridge	12	4	8.9
Millet bread	12	6	13.3
Cassava flour	12		
Sorghum flour	12		
Total	200	45	100

serovars but circulating in different geographical localities (Varga et al. 2020).

Cefotaxime and cefixime were the most resisted third-generation cephalosporins, while the least resistance was recorded for ceftriaxone (Table 7). Contrary to the findings of this study, higher *Salmonella* resistance patterns of more than 50% have been recorded with respect to cefotaxime and cefixime from prior studies (Salman et al. 2022; Yasmin et al. 2020). The ceftriaxone resistance pattern in this present study is in agreement with that of Awol et al. (2019), who recorded all *Salmonella* isolates as susceptible to ceftriaxone. The observed resistance towards third-generation cephalosporins at present suggests that *Salmonella* may be acquiring resistance to these treatment-choice antibiotics. The resistance pattern registered towards chloramphenicol (Table 7) in this study was more than the 3.13% resistance to chloramphenicol recorded by Sohail et al. (2021) but lower than the 12.26% and 10.22% recorded by Teng et al. (2022) and Borah et al. (2022), respectively.

The resistance of *Salmonella* to cotrimoxazole in this study was similar to the results of a study done in Nepal (4%) (Niroula et al. 2020) but lower than those of other studies (Abebe et al. 2019; Assoumy et al. 2021; Pilau 2022). The difference may be due to different susceptibility methods and breakpoints used (Sharp and quot, (n.d.)). A total of 2.2% of *Salmonella* isolates exhibited resistance to amoxicillin-clavulanic acid. This was

comparable to findings of Siddiky et al. (2022) and Rush et al. (2020) who recorded resistance towards amoxicillin-clavulanic acid of less than 2%. The low resistance to amoxicillin-clavulanic acid could be associated with the presence of potassium clavulanate, a beta-lactamase inhibitor in the drug combination (Thompson and Ramos 2017). These resistant isolates observed may work as potential reservoirs for the transfer of resistance genes to other highly infectious gram-negative pathogens in the environment. The fact that all the PCR-confirmed isolates displayed antibiotic resistance to recommended antibiotic drugs indicates that food and water consumed by children in the Karamoja sub-region are generally unsafe because they expose children to antibiotic-resistant *Salmonella*.

Genotypic antibiotic resistance profiles of *Salmonella* isolates

Out of 45 *Salmonella* isolates resistant to at least one antibiotic, 7 resistance genes that conferred resistance to five classes of antibiotics were detected. The PCR results were consistent with individual resistance phenotypes. Among beta-lactamase-encoding genes, *bla_{PSE}* a penicillinase-encoding gene, was the most prevalent (Table 5) in isolates that displayed resistance to the tested beta-lactam antibiotics in this study. These findings are comparable to those of Pietsch et al. (2021), who found *bla_{PSE}* to be the most dominant at 95% among *Salmonella* isolates that displayed resistance to beta-lactam antibiotics. The widespread presence of *bla_{PSE}* resistance gene among *Salmonella* isolates is an important public health concern, suggestive of its ability through horizontal transfer to be propagated in either similar or different bacterial species, as such leading to the proliferation of more antibiotic-resistant strains of pathogens in the environment. This could partly explain why resistance against penicillins such as ampicillin and amoxicillin over the years has been reported to be high in many microbial species, including *Salmonella*.

The genes *bla_{TEM}* and *bla_{CTX-M}* were not detected in any of the beta-lactam resistant isolates in the present study. This contrasts with findings from earlier studies (Ramatla et al. 2022; Langata et al. 2019; Souza et al. 2020) that showed a high prevalence of *bla_{TEM}* and *bla_{CTX-M}* in corresponding resistant *Salmonella* isolates. The cephalosporine and cefotaxime resistance in the present study, therefore, may be attributed to the presence of other resistance genes such as *bla_{SHV}* and *bla_{OXA}*, which were not investigated in the present study. Cotrimoxazole-resistant isolates in this study were found to carry either *sul1* or *sul2* resistance genes. This conforms to that of an earlier study by Ferreira et al. (2021) that showed the presence of *sul1* and *sul2* in all cotrimoxazole-resistant

Salmonella isolates. These genes induce the expression of drug-insensitive dihydropteroate synthase and dihydrofolate reductase, which are responsible for the expression of resistance toward sulfonamides and trimethoprim (Chang et al. 2021).

Whereas no chloramphenicol acetyltransferase gene *cat1* was present in any of the chloramphenicol-resistant *Salmonella* isolates in the present study, all isolates that displayed resistance to chloramphenicol carried the efflux pump gene *floR*. Efflux pump systems in *Salmonella* eject the antibiotic from the bacterial cell, thereby maintaining the cellular internal environment (Nishino et al. 2021). Of the 43 azithromycin-resistant isolates, 41 (95.3%) possessed the macrolide efflux gene *mefA*. The gene *mefA*, is responsible for expressing the macrolide efflux pumps that eject the antibiotic from the bacterial cell. Similar findings were recorded by Tunsagool et al. (2021), who recorded a higher prevalence of *mefA* genes among azithromycin-resistant *Salmonella* isolates.

Of the 39 *Salmonella* isolates that displayed resistance to ciprofloxacin, 35 were found to carry both the *gyrA* and the *parC* genes. Multiple mutations present in quinolone resistance-determining regions (QRDR) *gyrA* and topoisomerase gene *parC* are expected to code for full ciprofloxacin resistance. Similar findings have been recorded in previous studies (Shen et al. 2020; Zhan et al. 2019), which showed the occurrence of both the *gyrA* and the *parC* gene among all ciprofloxacin-resistant *Salmonella* isolates. The match between the results of the current study and those recorded earlier with respect to ciprofloxacin shows the widespread occurrence of *Salmonella* resistance to this type of antibiotic. On the other hand, this study's findings show that most of the *Salmonella* isolates carried the genetic markers for resistance to the antibiotics studied. This further confirms that food and water consumed by children in Karamoja sub-region are vehicles for infection with genetically antibiotic-resistant *Salmonella*.

Association between the genotypic and phenotypic antibiotic resistance profiles among *Salmonella* isolates

Strong associations between the phenotypes and genotypes of AMR were found in this present study, such as chloramphenicol with *floR*, sulphonamides with *sul1*, beta-lactams with *bla_{PSE}*, and quinolones with *parC*. This indicates that resistance to the antimicrobial agent was largely caused by the presence of the corresponding ARGs. This finding is similar to the results of previous studies (Gow et al. 2008; Rosengren et al. 2009; Van et al. 2020). However, interestingly, this present study found some isolates that possessed resistance phenotypes but did not carry corresponding ARGs: for example, 3 isolates that displayed resistance to beta-lactams did not

carry any associated ARGs investigated. This could be due to the fact that antibiotic resistance patterns in bacteria are expressed based on the activation of various diverse genetic factors thus, *Salmonella* mechanisms of antibiotic resistance recovered from food and water consumed by children under five years in Karamoja require further investigations.

Limitations of the study

Whereas this study provides vital insights into the prevalence and antibiotic resistance characteristics of non-typhoidal *Salmonella* enterica serotypes isolated from food and water consumed by children under five years, it has some limitations that should be considered. Firstly, the study focused on *Salmonella* isolation from food and water but not clinical specimens, which limits our ability to establish a direct link between *Salmonella* presence and actual infections in children under five years. Furthermore, the study did not link the identified serotypes to specific resistance genes. This calls for future research to link the *Salmonella* serotypes to specific resistance genes. Lastly, considering that environmental and socio-economic conditions vary from one place to another or season and are likely to influence *Salmonella* contamination, the findings of this study are applicable to Karamoja sub-region and other areas with similar environmental and socio-economic conditions.

Conclusion

This study revealed that commonly consumed food and water in Karamoja sub-region are potential reservoirs of MDR *Salmonella* and thus the population particularly children under five years are still at high risk of being exposed to infections. Therefore, a concerted effort is needed to strengthen and implement public health policies to reduce the high prevalence of antibiotic resistance within the region. There is a need to strengthen the epidemiological surveillance of the prevalence and antimicrobial resistance status of microbial foodborne pathogens such as *Salmonella*. This will help to inform public health policy decisions besides the ongoing investments and efforts geared towards curbing the endemic under-nutrition within the Karamoja sub-region.

Supplementary Information

The online version contains supplementary material available at <https://doi.org/10.1186/s40550-025-00117-x>.

Supplementary Material 1.

Acknowledgements

The authors are very thankful to the communities of Nakapiripirit and Nabilatuk districts for their participation and support throughout the study.

The authors are also grateful to the management and staff of Gulu University Multifunctional Research Laboratories for providing adequate laboratory facilities during this study.

Human ethics and consent to participate declaration

Not applicable.

Clinical trial number

Not applicable.

Author's contributions

Mpagi Ronald, MSc: Conceptualization, Data curation, Formal analysis, Investigation, Methodology, Validation, Writing—original draft, and Writing—review and editing. Lawrence Okidi, Ph.D: Conceptualization, Formal analysis, Methodology, Supervision, Validation, and Writing—review and editing. Duncan Ongeng, Ph.D: Conceptualization, Formal analysis, Funding acquisition, Methodology, Project administration, Resources, Supervision, Validation, and Writing—review and editing.

Funding

This work was supported by the Regional Universities Forum for Capacity Building in Agriculture (RUFORUM) and Mastercard Foundation through the “Transforming African Agricultural Universities to meaningfully contribute to Africa’s Growth and Development (TAGDev)” project at Gulu University (Grant number: RU2016MCF002).

Data availability

The datasets supporting the conclusions of this article are included within the article and its additional file.

Declarations

Ethics approval and consent to participate

Ethical approval to conduct this study was sought from and granted by the Gulu University Research Ethics Committee (Approval number: GUREC-2022-456). Consent to collect food and water samples was sought from household members in the selected sub-counties within the respective districts of Karamoja sub-region.

Consent for publication

Not applicable.

Competing interests

The authors declare no competing interests.

Received: 4 May 2025 Accepted: 24 July 2025

Published online: 02 September 2025

References

- Abebe M, Tadesse S, Meseret G, Derbie A (2019) Type of bacterial isolates and antimicrobial resistance profile from different clinical samples at a Referral Hospital, Northwest Ethiopia: five years data analysis. *BMC Res Notes* 12(1):1–6. <https://doi.org/10.1186/s13104-019-4604-6>
- Akiba M, Kusumoto M, Iwata T (2011) Rapid identification of *Salmonella enterica* serovars, typhimurium, choleraesuis, infantis, hadar, enteritidis, dublin and gallinarum, by multiplex PCR. *J Microbiol Methods* 85(1):9–15. <https://doi.org/10.1016/j.mimet.2011.02.002>
- Alarjani KM, Elkhadragey MF, Al-Masoud AH, Yehia HM (2021) Detection of *Campylobacter jejuni* and *Salmonella typhimurium* in chicken using PCR for virulence factor *hipO* and *invA* genes (Saudi Arabia). *Biosci Rep* 41(9):1–17. <https://doi.org/10.1042/BSR20210531>
- Al-Rifai RH, Chaabna K, Denagamage T, Alali WQ (2020) Prevalence of non-typhoidal *Salmonella enterica* in food products in the Middle East and North Africa: a systematic review and meta-analysis. *Food Control* 109:106908. <https://doi.org/10.1016/j.foodcont.2019.106908>
- Andrews WH, Wang H, Jacobson A, Ge B, Zhang G, Hammack T (2018) Bacteriological Analytical Manual (BAM) chapter 5: salmonella. *Bacteriol Anal*

- Man 1 (December 2015):1–33. <https://doi.org/10.1093/jfp/sfx124>. Available from: <https://www.fda.gov/food/laboratory-methods-food/bacteriological-analytical-manual-bam-chapter-5-salmonella>
- Appiah GD, Mpimbaza A, Lamorde M, Freeman M, Kajumbula H, Salah Z, et al. (2021) Salmonella bloodstream infections in hospitalized children with acute febrile illness — Uganda, 2016 – 2019. 105(1):37–46. <https://doi.org/10.3201/eid2701.203164>
- Assoumy MA, Bedekelabou AP, Teko-Agbo A, Ossebi W, Akoda K, Nimbona F et al (2021) Antibiotic resistance of *Escherichia coli* and *Salmonella* spp. strains isolated from healthy poultry farms in the districts of Abidjan and Agnibilékrou (Côte d'Ivoire). Vet World 14(4):1020–1027. <https://doi.org/10.14202/vetworld.2021.1020-1027>
- Awol N, Nigusse D, Ali M (2019) Prevalence and antimicrobial susceptibility profile of *Salmonella* and *Shigella* among food handlers working in food establishment at Hawassa city. Southern Ethiopia BMC Res Notes 12(1):1–7. <https://doi.org/10.1186/s13104-019-4725-y>
- Borah P, Dutta R, Das L, Hazarika G, Choudhury M, Deka NK et al (2022) Prevalence, antimicrobial resistance and virulence genes of *Salmonella* serovars isolated from humans and animals. Vet Res Commun 46(3):799–810. <https://doi.org/10.1007/s11259-022-09900-z>
- Chandra M, Cheng P, Rondeau G, Porwollik S, McClelland M (2013) A single step multiplex PCR for identification of six diarrheagenic *E. coli* pathotypes and *Salmonella*. Int J Med Microbiol 303(4):210–216. <https://doi.org/10.1016/j.jmm.2013.02.013>
- Chang MX, Zhang JF, Sun YH, Li RS, Lin XL, Yang L et al (2021) Contribution of different mechanisms to ciprofloxacin resistance in *Salmonella* spp. Front Microbiol 12:656141. <https://doi.org/10.3389/fmicb.2021.656141>
- Chávez-Ruvalcaba F, Chávez-Ruvalcaba MI, Moran Santibañez K, Muñoz-Carrillo JL, León Coria A, Reyna MR (2021) Foodborne parasitic diseases in the Neotropics - a review. Helminthol 58(2):119–133. <https://doi.org/10.2478/helm-2021-0013>
- Chitrakar B, Zhang M, Adhikari B (2019) Dehydrated foods: are they microbiologically safe? Crit Rev Food Sci Nutr 59(17):2734–2745. <https://doi.org/10.1080/10408398.2018.1466265>
- Chokshi A, Sifri Z, Cennimo D, Horng H (2019) Global contributors to antibiotic resistance. J Glob Infect Dis 11(1):36–42. https://doi.org/10.4103/jgid.jgid_138_18
- Clinical and Laboratory Standards Institute (2022) M100: performance standards for antimicrobial susceptibility testing, 32nd ed. CLSI. <https://doi.org/10.57447/clsim100/ED32>
- Demirbilek SK (2018) Salmonellosis in animals. *Salmonella - a re-emerging Pathog.* pp. 1–12. <https://doi.org/10.5772/intechopen.76317>
- Elbadawi YB (2017) Prevalence, serotyping and antimicrobials resistance mechanism of *Salmonella enterica* isolated from clinical and environmental samples. Brazilian J Microbiol 1–10. <https://doi.org/10.1016/j.bjm.2016.09.021>
- FAO, IFAD, UNICEF WFP and WHO (2022) The state of food security and nutrition in the world. Repurposing food and agricultural policies to make healthy diets more affordable. Rome, FAO. <https://doi.org/10.4060/cc0639en>
- Fasaei N, Tamai A, Salehi Z (2015) Molecular identification of *Salmonella* Infantis isolated from backyard chickens and detection of their resistance genes by PCR. 293–7. <https://doi.org/10.22059/jvr.2015.54959>
- Ferreira ACADO, Pavelquesi SLS, Monteiro EDS, Rodrigues LFS, Silva CMDS, Silva ICR Da, et al. (2021) Prevalence and antimicrobial resistance of *Salmonella* spp. In aquacultured Nile tilapia (*Oreochromis niloticus*) commercialized in Federal District, Brazil. Foodborne Pathog Dis 18(11):778–83. <https://doi.org/10.1089/fpd.2020.2925>
- Forgaci A, Tabaran A, Colobatiu L, Mihaie R, Dan SD, Mihaie M (2022) Concerning increase in antimicrobial resistance patterns of pathogenic strains of salmonella isolated in poultry meat products. Antibiotics 11(11). <https://doi.org/10.3390/antibiotics11111637>
- Goni AM, Effarizah ME, Rusul G (2018) Prevalence, antimicrobial resistance, resistance genes and class 1 integrons of *Salmonella* serovars in leafy vegetables, chicken carcasses and related processing environments in Malaysian fresh food markets. Food Control 84:437–446. <https://doi.org/10.1016/j.foodcont.2017.08.017>
- Gow SP, Waldner CL, Harel J, Boerlin P (2008) Associations between antimicrobial resistance genes in fecal generic *Escherichia coli* isolates from cow-calf herds in western Canada. Appl Environ Microbiol 74(12):3658–3666. <https://doi.org/10.1128/AEM.02796-07>
- Hasso-Agopsowicz M, Lopman BA, Lanata CF, Rogawski McQuade ET, Kang G, Prudden HJ et al (2021) World Health Organization expert working group: recommendations for assessing morbidity associated with enteric pathogens. Vaccine 39(52):7521–7525. <https://doi.org/10.1016/j.vaccine.2021.11.033>
- Ishaq AR, Manzoor M, Hussain A, Altaf J, Rehman SU, Javed Z et al (2021) Prospect of microbial food borne diseases in Pakistan: a review. Brazilian J Biol 81(4):940–953. <https://doi.org/10.1590/1519-6984.244111>
- Jafari Sales A, Naebi S, Nasiri R, Bannazadeh-Baghi H (2021) The antibiotic resistance pattern and prevalence of blaTEM, blaSHV, blaCTX-M, blaPSE-1, sipB/C, and cmlA/tetR genes in *Salmonella typhimurium* isolated from children with diarrhea in Tabriz. Iran Int J Heal Life Sci 7(4):1–7. <https://doi.org/10.34172/ijhls.2021.07>
- Kijima M, Shirakawa T, Uchiyama M, Kawanishi M, Ozawa M, Koike R (2019) Trends in the serovar and antimicrobial resistance in clinical isolates of *Salmonella enterica* from cattle and pigs between 2002 and 2016 in Japan. J Appl Microbiol 127(6):1869–1875. <https://doi.org/10.1111/jam.14393>
- Kikui GM, Ombui JN, Mitema ES (2010) Serotypes and antimicrobial resistance profiles of *Salmonella* isolates from pigs at slaughter in Kenya. J Infect Dev Ctries 4(9):532–537. <https://doi.org/10.3855/jidc.646>
- Langata LM, Maingi JM, Musonye HA, Kiiru J, Nyamache AK (2019) Antimicrobial resistance genes in *Salmonella* and *Escherichia coli* isolates from chicken droppings in Nairobi, Kenya. BMC Res Notes 12(1):22. <https://doi.org/10.1186/s13104-019-4068-8>
- Miao S, Liu L, Fu Z (2022) Prevalence of *Salmonella* in Chinese food commodities: a meta-analysis. J Food Prot 85(5):859–870. <https://doi.org/10.4315/JFP-21-304>
- Mokori A, Ndungutse AH, Amongin D, Agabiirwe CN, Byabasheija R, Draru J (2023) Use of collaborative learning approach for increased cure rate among children aged 6–59 months with severe wasting in Karamoja, Uganda. BMJ Open Qual. <https://doi.org/10.1136/bmjopen-2022-001941>
- Mulvey MR, Soule G, Boyd D, Demczuk W, Ahmed R (2003) Characterization of the first extended-spectrum beta-lactamase-producing *Salmonella* isolate identified in Canada. 41(1):460–462. <https://doi.org/10.1128/AAC.47.1.460-462.2003>
- Nair A, Balasaravanan T, Malik SVS, Mohan V, Kumar M, Vergis J, et al. (2015) Isolation and identification of *Salmonella* from diarrheagenic infants and young animals, sewage waste and fresh vegetables. 8:669–73. <https://doi.org/10.3844/ojbsci.2021.235.244>
- Ngai DG, Nyamache AK, Ombori O (2021) Prevalence and antimicrobial resistance profiles of *Salmonella* species and *Escherichia coli* isolates from poultry feeds in Ruiru Sub - County, Kenya. BMC Res Notes. 4–9. <https://doi.org/10.1186/s13104-021-05456-4>
- Niroula D, Shrestha J, Sharma S, Singh A (2020) Antibiotic susceptibility pattern of *Salmonella enterica* serovars Typhi and Paratyphi A isolated from patients suspected of enteric fever. Tribhuvan Univ J Microbiol 7:31–36. <https://doi.org/10.3126/tujm.v7i0.33791>
- Nishino K, Yamasaki S, Nakashima R, Zwama M, Hayashi-Nishino M (2021) Function and inhibitory mechanisms of multidrug efflux pumps. Front Microbiol 12:778433. <https://doi.org/10.3389/fmicb.2021.778433>
- Okidi L, Ongeng D, Muliro PS, Matofari JW (2022) Agroecology influences *Salmonella* food contamination with high exposure risk among children in Karamoja sub-region: a high diarrhoea prevalent locality in Uganda. Heliyon 8(11):e11703. <https://doi.org/10.1016/j.heliyon.2022.e11703>
- Pereira JG, Soares VM, Tadielo LE, Ramires T, da Silva WP (2020) Antimicrobial resistance profile of salmonella and listeria monocytogenes isolated from products marketed on the border of Brazil with Argentina and Uruguay. J Food Prot 83(11):1941–1946. <https://doi.org/10.4315/JFP-20-036>
- Peruzy MF, Proroga YTR, Capuano F, Mancusi A, Montone AMI, Cristiano D et al (2022) Occurrence and distribution of *Salmonella* serovars in carcasses and foods in southern Italy: eleven-year monitoring (2011–2021). Front Microbiol 12(13):983171. <https://doi.org/10.3389/fmicb.2022.983171>
- Pexara A, Govaris A (2020) Food-processing technologies. 1–17. <https://doi.org/10.1016/B978-0-12-816514-5.00001-2>
- Pietsch M, Simon S, Meinen A, Trost E, Banerji S, Pfeifer Y, et al. (2021) Third generation cephalosporin resistance in clinical non-typhoidal *Salmonella enterica* in Germany and emergence of blaCTX-M-harboring pESI plasmids. Microb Genomics 7(10). <https://doi.org/10.1099/mgen.0.000625>
- Pilau NN (2022) *Salmonella* infection, isolation and antimicrobial resistance in diarrhoeic dogs presenting to clinics in Northwestern Nigeria. J Adv Biol Biotechnol 25(5):1–10. <https://doi.org/10.9734/jabb/2022/v25i530279>
- Radhika M, Saugata M, Murali HS, Batra HV (2014) A novel multiplex PCR for the simultaneous detection of *Salmonella enterica* and *shigella* species. 676:667–676. <https://doi.org/10.1016/j.mcp.2014.06.004>

- Ramatla T, Mileng K, Ndou R, Mphuti N, Syakalima M, Lekota KE, et al. (2022) Molecular detection of integrons, colistin and β -lactamase resistant genes in *Salmonella enterica* Serovars Enteritidis and Typhimurium isolated from chickens and rats inhabiting poultry farms. *Microorganisms*. 10(2). <https://doi.org/10.3390/microorganisms10020341>
- Rosengren LB, Waldner CL, Reid-Smith RJ (2009) Associations between antimicrobial resistance phenotypes, antimicrobial resistance genes, and virulence genes of fecal *Escherichia coli* isolates from healthy grow-finish pigs. *Appl Environ Microbiol* 75(5):1373–1380. <https://doi.org/10.1128/AEM.02171-08>
- Rush EM, Amadi VA, Johnson R, Lonce N, Hariharan H (2020) *Salmonella* serovars associated with Grenadian tree boa (*Corallus grenadensis*) and their antimicrobial susceptibility. *Vet Med Clin* 6(3):565–569. <https://doi.org/10.1002/vms3.257>
- Salman HA, Alhameedawi AK, Alsallameh SMS, Muhamad G, Taha Z (2022) Prevalence of multi-antibiotic resistant bacteria isolated from children with urinary tract infection from Baghdad. *Iraq Microbiol Biotechnol Lett* 50(1):147–156. <https://doi.org/10.48022/mbl.2022.1.147>
- Sanchez J, Dohoo IR, Christensen J, Rajic A (2007) Factors influencing the prevalence of *Salmonella* spp. in swine farms: a meta-analysis approach. *Prev Vet Med* 81(1–3 SPEC. ISS.):148–177. <https://doi.org/10.1016/j.prevetmed.2007.04.005>
- Schwan WR, Kopecko D (1997) Serovar-specific differences in *Salmonella*. In: *Salmonella and Salmonellosis*. p. 277–8. <https://doi.org/10.13181/mji.v7i5u.p01.1118>
- Sharp SE (n.d.) " A practical approach " Available from: <http://www.asmbbranches.org/brcano/meetings/2016SprPpts/5.2SharpRed.pdf>
- Shen H, Chen H, Ou Y, Huang T, Chen S, Zhou L et al (2020) Prevalence, serotypes, and antimicrobial resistance of *Salmonella* isolates from patients with diarrhea in Shenzhen, China. *BMC Microbiol* 20(1):103. <https://doi.org/10.1186/s12866-020-01833-5>
- Siddiky NA, Sarker S, Khan SR, Rahman T, Kafi A, Samad MA (2022) Virulence and antimicrobial resistance profile of non-typhoidal *Salmonella enterica* serovars recovered from poultry processing environments at wet markets in Dhaka. *Bangladesh Plos One* 17:1–22. <https://doi.org/10.1371/journal.pone.0254465>
- Skittrell JP, Levy D, Obichukwu C, Gentle A, Chattaway MA, Hayns D et al (2021) Clinical infection in practice Azithromycin susceptibility testing of *Salmonella enterica* serovar Typhi : impact on management of enteric fever. *Clin Infect Pract* 10:100069. <https://doi.org/10.1016/j.clinpr.2021.100069>
- Sohail MN, Rathnamma D, Priya SC, Isloor S, Naryanaswamy HD, Ruban SW, et al. (2021) *Salmonella* from farm to table: isolation, characterization, and antimicrobial resistance of salmonella from commercial broiler supply chain and its environment. *Biomed Res Int* 2021. <https://doi.org/10.1155/2021/6659496>
- Souza AIS, Saraiva MMS, Casas MRT, Oliveira GM, Cardozo MV, Benevides VP et al (2020) High occurrence of β -lactamase-producing *Salmonella* Heidelberg from poultry origin. *PLoS ONE* 15(3):1–11. <https://doi.org/10.1371/journal.pone.0230676>
- Teng KT yun, Aerts M, Jaspers S, Ugarte-Ruiz M, Moreno MA, Saez JL, et al. (2022) Patterns of antimicrobial resistance in *Salmonella* isolates from fattening pigs in Spain. *BMC Vet Res* 18(1):1–17. <https://doi.org/10.1186/s12917-022-03377-3>
- Thompson DF, Ramos CL (2017) Antibiotic-induced rash in patients with infectious mononucleosis. *Ann Pharmacother* 51(2):154–162. <https://doi.org/10.1177/1060028016677733>
- Tunsagool P, Mhuantong W, Tangphatsornruang S, Am-In N, Chuanchuen R, Luangtongkum T, et al. (2021) Metagenomics of antimicrobial and heavy metal resistance in the cecal microbiome of fattening pigs raised without antibiotics. *Appl Environ Microbiol* 20:87(8):e02944–20. <https://doi.org/10.1128/AEM.02944-20>
- Uganda Bureau of Statistics - UBOS and ICF (2018) Uganda demographic and health survey 2016. Kampala, Uganda and Rockville, Maryland, USA: UBOS and ICF. 2018. Accessed from: https://www.dhsprogram.com/publications/publication-fr333-dhs-final-reports.cfm?csearch=707130_1 on 23 June 2022.
- Van CN, Zhang L, Thanh TVT, Son HPH, Ngoc TT, Huang Q et al (2020) Association between the phenotypes and genotypes of antimicrobial resistance in haemophilus parasuis isolates from swine in Quang Binh and Thua Thien Hue Provinces. *Vietnam Eng* 6(1):40–48. <https://doi.org/10.1016/j.eng.2019.10.014>
- Varga C, John P, Cooke M, Majowicz SE (2020) Spatial and space-time clustering and demographic characteristics of human nontyphoidal *Salmonella* infections with major serotypes in Toronto. *Canada Plos One* 15(7):1–19. <https://doi.org/10.1371/journal.pone.0235291>
- Wang W, Chen J, Shao X, Huang P, Zha J, Ye Y (2021) Occurrence and antimicrobial resistance of *Salmonella* isolated from retail meats in Anhui. *China Food Sci Nutr* 9(9):4701–4710. <https://doi.org/10.1002/fsn3.2446>
- Wanjala NW, Matofari JW, Nduko JM (2016) Antimicrobial effect of smoking milk handling containers' inner surfaces as a preservation method in pastoral systems in Kenya. *Pastoralism* 6(1). <https://doi.org/10.1186/s13570-016-0064-y>
- War JM, Nisa AU, Wani AH, Bhat MY (2022) Microbial food-borne diseases due to climate change. *Climate change and microbes*. 187–234 p. https://doi.org/10.1007/978-3-030-91169-1_9
- World Health Organisation (2015) WHO Estimates of the global burden of food-borne diseases. <https://doi.org/10.1016/B978-0-12-384730-0.00018-7>
- Xu Y, Zhou X, Jiang Z, Qi Y, Ed-dra A, Yue M (2020) Epidemiological investigation and antimicrobial resistance profiles of *Salmonella* isolated from breeder chicken hatcheries in Henan, China. *Front Cell Infect Microbiol* 10:1–13. <https://doi.org/10.3389/fcimb.2020.00393>
- Xu J, Tang J, Jin Y, Song J, Yang R, Sablani SS et al (2019) High temperature water activity as a key factor influencing survival of *Salmonella* Enteritidis PT30 in thermal processing. *Food Control* 98:520–528. <https://doi.org/10.1016/j.foodcont.2018.12.017>
- Yasmin S, Nawaz M, Anjum AA, Ashraf K, Ullah N, Mustafa A et al (2020) Antibiotic susceptibility pattern of *Salmonellae* isolated from poultry from different districts of Punjab. *Pakistan Pak Vet J* 40(1):98–102. <https://doi.org/10.29261/pakvetj/2019.080>
- Zarkani AA, Schikora A (2021) Mechanisms adopted by *Salmonella* to colonize plant hosts. *Food Microbiol* 99:103833. <https://doi.org/10.1016/j.fm.2021.103833>
- Zhan Z, Xu X, Gu Z, Meng J, Wufuer X, Wang M et al (2019) Molecular epidemiology and antimicrobial resistance of invasive non-typhoidal salmonella in China, 2007–2016. *Infect Drug Resist* 12:2885–2897. <https://doi.org/10.2147/IDR.S228115>
- Zhanabayeva DK, Paritova AY, Murzakaeva GK, Zhanabayev AA, Kereev A, Asauova ZS et al (2021) Pcr diagnosis for the identification of the virulent gene of salmonella in poultry meat. *Online J Biol Sci* 21(3):235–244. <https://doi.org/10.3844/ojbsci.2021.235.244>
- Zhang Z, Meng X, Wang Y, Xia X, Wang X, Xi M et al (2014) Presence of qnr, aac(6)-Ib, qepA, oqxAB, and mutations in gyrase and topoisomerase in nalidixic acid-resistant salmonella isolates recovered from retail chicken carcasses. *Foodborne Pathog Dis* 11(9):698–705. <https://doi.org/10.1089/fpd.2013.1704>
- Zhou Q, Zhao Y, Dang H, Tang Y, Zhang B (2019) Antibacterial effects of phytic acid against foodborne pathogens and investigation of its mode of action. *J Food Prot* 82(5):826–833. <https://doi.org/10.4315/0362-028X.JFP-18-418>

Publisher's Note

Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.