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Occurrence and Antimicrobial Resistance of *Shigella* Isolates in Ready-to-Eat Foods Sold near Primary Schools in Burkina Faso: Implications for Food Safety and Public Health*

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Abstract

Ready-to-eat (RTE) foods constitute an important source of affordable meals for schoolchildren in many low-income countries. However, inadequate hygiene practices during preparation, handling, and sale may facilitate contamination by enteric pathogens, including antimicrobial-resistant bacteria. This study investigated the occurrence of *Shigella* spp. in RTE foods sold near primary schools in Tenkodogo, Burkina Faso, and assessed antimicrobial resistance profiles and factors associated with contamination. A cross-sectional study was conducted from December 2024 to January 2025, including 69 food vendors from nine primary schools. A total of 102 RTE food samples were collected aseptically. *Shigella* was identified using culture, biochemical tests, and multiplex PCR targeting *ipaH* and species-specific genes (*wbgZ*, *rfpB*, *rfc*).

*This study assesses the prevalence and antimicrobial resistance of *Shigella* strains isolated from ready-to-eat foods sold near primary schools in Burkina Faso. Given the susceptibility of schoolchildren to foodborne infections, the presence of antimicrobial-resistant *Shigella* in commonly consumed foods represents a significant public health concern. The study aims to generate data that will support food safety interventions and antimicrobial resistance monitoring within a One Health framework.

Antimicrobial susceptibility was determined by disk diffusion (EUCAST). Sociodemographic and hygiene data were collected via structured questionnaire and observation. Associations with contamination were explored using Firth's penalized logistic regression. *Shigella* contamination prevalence was 5.9% (6/102; 95% CI: 2.2% - 12.4%). All isolates were *Shigella sonnei*. Resistance rates were high for azithromycin (100%), ampicillin (66.7%), and cefoxitin (66.7%). All isolates remained susceptible to ciprofloxacin. The multiple antibiotic resistance (MAR) index ranged from 0.1 to 0.9. No wrapped food was contaminated (0/28) versus 14.6% (6/41) of unwrapped foods (aOR = 0.06; 95% CI: 0.00 - 0.62). Foods exposed to flies had a non-significantly higher contamination rate (28.6% vs 6.5%). Although prevalence was low, the presence of azithromycin resistant *S. sonnei* in foods consumed daily by schoolchildren is a public health concern. Simple, low-cost interventions promoting food wrapping and reducing fly exposure through improved waste management could substantially reduce contamination. The high azithromycin resistance challenges empiric uses of this drug for pediatric shigellosis in this setting. Strengthening AMR surveillance along the informal food chain is urgently needed.

Keywords

Shigellosis, Ready-to-Eat Foods, Antimicrobial Resistance, Schoolchildren, Burkina Faso

1. Introduction

Foodborne diseases cause an estimated 600 million illnesses and 420,000 deaths annually worldwide, with children under five accounting for 30% of deaths [1]. Low- and middle-income countries bear the highest burden, where food safety infrastructure is often weak and informal food vending is widespread. In sub-Saharan Africa, ready to eat (RTE) foods sold on the street have become an essential source of affordable nutrition for urban populations, including schoolchildren [2]. However, the informal nature of this sector frequently eludes regulatory oversight, raising persistent food safety concerns.

Shigellosis remains a significant public health challenge in developing countries, with an estimated annual incidence of 163.2 million cases and 1.1 million deaths, primarily among children under five [3]. Transmission occurs via the fecal-oral route, frequently through contaminated food and water [4]. In street food vending environments, poor hygiene practices such as inadequate handwashing, use of contaminated water, and exposure to flies and domestic animals create critical contamination points [5] [6].

Previous studies have established links between vendor hygiene knowledge and food contamination. In Nigeria, lack of formal education among food handlers was a significant predictor of poor microbiological quality of food samples [7]. In India, vendors lacking soap at vending units had significantly higher fecal coli-

form contamination in food samples [8]. Regarding *Shigella*, studies across Africa have documented its presence in various RTE foods, often linked to contaminated water and improper handling [9]-[11]. Environmental factors such as domestic animals and poor waste management also contribute, as animals can act as mechanical vectors and accumulated waste attracts flies that transfer pathogens from feces to food [12] [13].

In Burkina Faso, street foods have been identified as potential sources of enteric pathogens [14] [15]. However, no study has specifically examined *Shigella* contamination in RTE foods sold near primary schools, nor the associated antimicrobial resistance (AMR) profiles, a critical gap given the rising global threat of AMR. Furthermore, the practical differentiation between *Shigella* and enteroinvasive *Escherichia coli* (EIEC) remains challenging, but molecular screening for the *ipaH* gene still provides valuable public health intelligence in resource limited settings.

Therefore, this study aimed to: 1) determine the prevalence of *Shigella* contamination in RTE foods sold near primary schools in Tenkodogo, Burkina Faso; 2) characterize the antimicrobial resistance profiles of recovered isolates, with emphasis on antibiotics used in pediatric practice; and 3) identify modifiable vendor level and environmental factors associated with contamination to inform targeted public health interventions.

2. Materials and Methods

2.1. Type and Site of Study

A cross-sectional study was conducted in nine primary schools in the city of Tenkodogo, located in the Nakambé region in Burkina Faso (**Figure 1**), between December 2024 and January 2025.

The selected schools were those where ready-to-eat (RTE) food vending activities were observed during the study period. All food vendors present at the selected schools during the survey visits were approached for participation. Vendors were eligible if they were selling RTE foods to schoolchildren and provided informed consent. Vendors who declined participation or were absent at the time of the visit were not included.

A total of 69 consenting vendors were enrolled in the study. A standardized questionnaire was administered to each participating vendor to collect information on sociodemographic characteristics, hygiene practices, and food-handling conditions. Variables included vendor age, education level, handwashing frequency, food packaging, exposure of food to flies, and the presence of waste at the vending site.

For the purpose of this analysis, the contamination status of RTE food by *Shigella* was considered the primary outcome variable. At the end of the interview, food samples were aseptically collected from the RTE foods sold by each participating vendor. Depending on the diversity of foods available at the time of sampling, one or more food samples could be collected from the same vendor.

Each sample was placed in a sterile bag, immediately transferred to a cooler

containing ice packs, and transported to the microbiology laboratory of the Regional Animal Health Laboratory of Tenkodogo for bacteriological analysis.

Figure 1. Location of the city of Tenkodogo on the map of the Nakambé region, Burkina Faso.

2.2. Microbiology Analysis

Isolation and Preliminary Identification

Approximately 10 g or 10 mL of each food sample was enriched in 90 mL of

selenite broth and incubated at 37˚C for 24 hours. A loopful of the enriched broth was then streaked onto Hektoen enteric agar and MacConkey agar and incubated at 37˚C for 24 hours. Colonies with typical *Shigella* morphology: convex, colourless colonies (2 - 3 mm) on Hektoen agar and smooth, colourless colonies (1 - 2 mm) on MacConkey agar were selected. Presumptive identification was based on biochemical reactions: acid butt (yellow) with alkaline slant (red) on triple sugar iron agar, absence of gas and hydrogen sulfide production, non-motility, and inability to utilize citrate. Suspected colonies were sub cultured on fresh Hektoen or MacConkey agar and incubated at 37˚C for 24 h to confirm purity. All suspected isolates were confirmed using API 20 E test. The performance of both media was verified using reference *Shigella* strains.

2.3. Molecular Characterization of Presumptive *Shigella*

DNA Extraction

Genomic DNA was extracted from pure bacterial cultures using the boiling method. Briefly, 3 to 5 colonies were suspended in 600 µL sterile distilled water and incubated at 100˚C for 30 min, then centrifuged at 12,000 rpm for 10 min at 4˚C. The supernatant containing crude DNA was used directly as PCR template.

Primer design and specificity

Four target genes were used for the molecular identification of *Shigella* species. The *ipaH* gene, which is present in all *Shigella* spp., was selected as a genus level marker [16] [17]. Species-specific identification was achieved using *rfc, wbgZ*, and *rfpB* of *S. flexneri, S. sonnei*, and *S. dysenteriae*, respectively [18]. Primer sequences were obtained from previously published studies [16]-[18] and synthesized commercially. The sequences and expected amplicon sizes are presented in Table 1.

PCR Amplification

All isolates were initially screened using a simplex PCR assay targeting the *ipaH* gene, following the method described by Thong *et al.* [16]. The presence of the expected 423 bp amplicon was considered indicative of *Shigella* spp. PCR amplifications were carried out in a final volume of 25 µL containing 1 µL of genomic DNA template (approximately 50 - 100 ng), 0.5 µL of each primer (10 µM), 4 µL of 5× FirePool PCR Master Mix (Solis BioDyne), and nuclease-free water to complete the volume. Amplifications were performed on an Applied Biosystems™ 2720 GeneAmp™ PCR System thermal cycler, using the following programme: initial denaturation at 95°C for 3 min; 35 cycles of denaturation at 95°C for 30 s, annealing at 58°C for 30 s, and extension at 72°C for 45 s; and a final extension step at 72°C for 5 min.

Isolates yielding a positive *ipaH* result were further characterised by a multiplex PCR assay targeting species-specific genetic markers, namely *wbgZ, rfpB,* and *rfc* for the identification of *S. sonnei, S. dysenteriae*, and *S. flexneri*, respectively, as described by Ojha *et al.* [18]. The multiplex reaction was performed in the same 25-µL reaction mixture composition described above, with the thermal profile

modified as follows: initial denaturation at 95°C for 3 min; 35 cycles of 95°C for 30 s, 60°C for 30 s, and 72°C for 45 s; and a final extension at 72°C for 5 min.

For each PCR run, DNA extracted from laboratory-confirmed *Shigella* reference strains served as a positive control, while nuclease-free water was included as a negative control. Following amplification, 5 µL of each PCR product were separated by electrophoresis on 1.5% (w/v) agarose gels prepared in 1× TAE buffer, alongside a 100-bp DNA ladder. Electrophoresis was performed at 90 V for 50 min. Gels were then stained with ethidium bromide (0.5 µg/mL) for 15 min, rinsed with distilled water, and visualised under ultraviolet light using a Gel Doc XR+ imaging system (Bio-Rad, Hercules, CA, USA).

Samples displaying the characteristic 423 bp *ipaH* fragment were recorded as positive for *Shigella* spp. Positive isolates were subsequently assigned to species based on the amplification profiles of *wbgZ, rfpB*, and *rfc*, according to the band size interpretation provided by Ojha *et al.* [18]. All positive results were confirmed by repeat amplification from the same DNA extracts.

Table 1. Oligonucleotide primers used in this study.

Target gene		Sequence (5′ → 3′)	Amplicon size (bp)	Annealing temperature (˚C)	Reference
wbgZ	F	TCT GAA TAT GCC CTC TAC	430	55.8	[18]
	R	GAC AGA GCC CGA AGA ACC G			
rfpB	F	TCT CAA TAA TAG GGA ACA CAGC	211	59.3	
	R	CAT AAA TCA CCA GCA AGG TT			
rfc	F	TTT ATG GCT TCT TTG TCG	537	55.8	
	R	CTG CGT GAT CCG ACC ATG			
ipaH	F	GTT CCT TGA CCG CCT TTC CGA TAC CGTC	423	58	[16] [17]
	R	GCC GGT CAG CCA CCC TCT GAG AGT AC			

2.4. Antimicrobial Susceptibility Testing

Antimicrobial susceptibility was determined using Kirby-Bauer disk diffusion method following EUCAST guidelines [19].

The following antibiotics were tested: amoxicillin-clavulanic acid (AMC, 20/10 µg), ceftriaxone (30 µg), cefoxitin (30 µg), ciprofloxacin (CIP, 5 µg), trimethoprim-sulfamethoxazole (1.25/23.75 µg), ampicillin (AMP, 10 µg), azithromycin (15 µg), and nalidixic acid (30 µg), using the disk diffusion method in accordance with established guidelines. Antibiotics were selected based on current literature, local availability, standard treatment protocols, and antimicrobial susceptibility testing (AST) recommendations.

Bacterial suspensions were adjusted to a 0.5 McFarland turbidity using a Densimat device (DEN-1 Biosan). Inoculated Mueller-Hinton agar plates were incubated at 37˚C for 24 hours.

Inhibition zone diameters were measured and interpreted according to the EUCAST Clinical Breakpoint Tables version 13.0 (2023) [19]. The *Enterobacterales* disk diffusion interpretive criteria were applied using as EUCAST version 13.0 does not provide a species-specific azithromycin breakpoint for *Shigella*.

Escherichia coli ATCC 25922 was used as a quality control strain.

2.5. Statistical Analysis

Data were entered into Microsoft Excel and analyzed using R software version 4.5.2. Categorical variables were summarized as frequencies and percentages. Continuous variables were expressed as means ± standard deviations after normality assessment using the Shapiro-Wilk test.

Given the very small number of *Shigella*-positive vendors (6/69), formal statistical testing was applied with caution. Fisher's exact test was used to assess associations between categorical variables and contamination status, including the global association for age categories. Continuous variables were assessed for normality using the Shapiro-Wilk test and compared using the Mann-Whitney U test where applicable. All p-values are exploratory and should be interpreted cautiously.

The multivariable analysis was intentionally restricted to a prespecified set of two predictors considered the most biologically relevant for fecal contamination of ready-to-eat foods: food packaging (wrapped vs. unwrapped foods) and exposure of food to flies, given the very small number of contaminated vendors. These variables also showed the strongest signal in the bivariate analysis and were entered into the Firth penalized logistic regression model.

For the analysis of factors associated with *Shigella* contamination, the vendor was used as the unit of analysis. Because several ready-to-eat food samples could be collected from the same vendor depending on the diversity of foods sold, a vendor was classified as positive if at least one of her food samples tested positive for *Shigella*. Multiple samples from the same vendor were used to improve microbiological detection but were not treated as independent observations in the regression analysis, as all explanatory variables were measured at the vendor level. The analytical dataset therefore included 69 vendors, among whom 6 were classified as contaminated.

To address the sparse-data problem and reduce small-sample bias, Firth's penalized logistic regression was performed using the *logistf* package in R. Results are presented as adjusted odds ratios (aORs) with 95% profile likelihood confidence intervals. Given the very small number of positive events, the multivariable analysis was strictly exploratory and intended to generate hypotheses rather than provide confirmatory evidence.

Antimicrobial resistance patterns were described using frequencies and percentages. Multi-drug resistance (MDR) was defined as resistance to three or more antibiotic classes. The multiple antibiotic resistance (MAR) index was calculated for each isolate as the proportion of antibiotics to which the isolate was resistant. A heatmap of resistance profiles was generated using the *ggplot2* package.

3. Results

Prevalence and factors associated with *Shigella* contamination (exploratory analysis)

A total of 69 females food vendors participated in the study shown in (Table 2), from whom 102 food samples were collected. At the sample level, the overall prevalence of *Shigella* contamination was 5.9% (6/102; 95% CI: 2.2% - 12.4%). At the vendor level, 8.7% (6/69) of vendors had at least one contaminated food item.

The majority of vendors resided in urban areas (82.6%), and handwashing frequency ≥ 3 times per day was reported by 58.8% of participants.

Table 2. Bivariate analysis of vendor characteristics associated with *Shigella* contamination (n = 69 vendors).

Variable	Category	Overall n (%)	Uncontaminated n (%)	Contaminated n (%)	p-value*
Vendor's Age[a]	≤20 years	7 (10.1)	7 (100.0)	0 (0.0)	0.920
	21 - 35 years	26 (37.7)	24 (92.3)	2 (7.7)	
	36 - 50 years	25 (36.2)	22 (88.0)	3 (12.0)	
	>50 years	11 (15.9)	10 (90.9)	1 (9.1)	
Education Level	No formal education	33 (47.8)	31 (93.9)	2 (6.1)	0.636
	Primary	27 (39.1)	24 (88.9)	3 (11.1)	
	Secondary	7 (10.1)	6 (85.7)	1 (14.3)	
	Higher	2 (2.9)	2 (100.0)	0 (0.0)	
Residence	Unplanned	12 (17.4)	12 (100.0)	0 (0.0)	0.581
	Urban	57 (82.6)	51 (89.5)	6 (10.5)	
Hand-washing Frequency	<3 times/day	28 (41.2)	25 (89.3)	3 (10.7)	0.684
	≥3 times/day	40 (58.8)	37 (92.5)	3 (7.5)	
Wrapped Foods	No	41 (59.4)	35 (85.4)	6 (14.6)	0.074
	Yes	28 (40.6)	28 (100.0)	0 (0.0)	
Food Exposed to Flies	No	62 (89.9)	58 (93.5)	4 (6.5)	0.109
	Yes	7 (10.1)	5 (71.4)	2 (28.6)	
Knowledge of Handling[b]	No	25 (36.2)	24 (96.0)	1 (4.0)	0.406
	Yes	44 (63.8)	39 (88.6)	5 (11.4)	
Domestic Animals	No	45 (65.2)	41 (91.1)	4 (8.9)	1.000
	Yes	24 (34.8)	22 (91.7)	2 (8.3)	
Waste on Site	No	32 (46.4)	29 (90.6)	3 (9.4)	1.000
	Yes	37 (53.6)	34 (91.9)	3 (8.1)	
Total	All vendors	69 (100)	63 (91.3)	6 (8.7)	

[a] for age categories (4 levels), Fisher's exact test was used to assess the global association with contamination status. Due to the small number of contaminated vendors (n = 6), this p-value should be interpreted as exploratory. [b] "Knowledge of handling" refers to awareness of safe food handling and hygiene practices. * p-values were calculated using Fisher's exact test or Chi-square test, as appropriate.

Because only 6 of the 69 vendors (8.7%) were classified as contaminated, the analysis of associated factors was considered exploratory and had limited statistical power for definitive inference. Bivariate associations between vendor characteristics and contamination status are presented in (Table 2). Fisher's exact test was used for categorical variables because of the sparse data.

No variable reached the conventional statistical significance threshold of $\alpha = 0.05$ in the bivariate analysis. However, wrapped foods and exposure of food to flies showed the strongest signals of association and were considered the most biologically relevant factors for fecal contamination of ready-to-eat foods. No contaminated vendor was observed among those selling wrapped foods (0/28; 0%), whereas contamination was detected in 6 of 41 vendors (14.6%) selling unwrapped foods (p = 0.074). Vendors whose foods were exposed to flies had a contamination rate of 28.6% (2/7) compared with 6.5% (4/62) among those whose foods were not exposed to flies (p = 0.109). Given the very small number of contaminated vendors, the multivariable analysis was intentionally restricted to these two prespecified predictors to reduce the risk of model overfitting. Firth's penalized logistic regression was applied to address sparse-data bias and quasi-complete separation.

The results of this exploratory model are presented in (Table 3). In the multivariable analysis, selling wrapped foods was associated with substantially lower odds of *Shigella* contamination (aOR = 0.06; 95% CI: 0.00 - 0.62).

Exposure of food to flies was associated with higher odds of contamination (aOR = 2.70; 95% CI: 0.40 - 16.20), although the confidence interval was wide and the association was not statistically significant. Given the limited number of positive events, these findings should be interpreted with considerable caution and regarded as hypothesis-generating rather than confirmatory evidence.

Table 3. Exploratory multivariable analysis using Firth's penalized logistic regression (vendor-level analysis, n = 69).

Variable	aOR (95% CI)[a]	p-value*
Wrapped foods (Yes vs No)	0.06 (0.00 - 0.62)	<0.05
Food exposed to flies (Yes vs No)	2.7 (0.4 - 16.2)	0.2881

[a] Estimates were obtained using Firth's penalized logistic regression, adjusted for all variables listed in the table; aOR: adjusted odds ratio; CI: confidence interval; * p-values correspond to the significance of regression coefficients.

Characteristics of contaminated food items

The most common food category sold near primary schools presented in (Table 4) was cereals/dry snacks (38.2%), followed by traditional dishes (26.4%) and beverages/sweets (21.5%). Among the six contaminated food samples, cereals/dry snacks were the most frequent contaminated items (3/6, 50.0%), followed by beverages/sweets (2/6, 33.3%) and traditional dishes (1/6, 16.7%). Due to the small number of contaminated samples, these differences between food types have been not tested statistically. The observed distribution should be interpreted as descriptive only.

Table 4. Distribution of contaminated food by food categories.

Food Category	Food type	Number of collected sample	Contaminated food[b]	Prevalence of contaminated food (%)[c]
Cereals/Dry snacks[a]	Cake; Bread, Soy, Gari, Peanuts, "Bassi", Coconut; Croquette; Sesame	39(38.2%)	3 (2 cakes, 01 bread)	7.69
Traditional dishes	"Atiéké"; "Babenda"; "Donkounou"	27(26.4%)	1 ("babenda")	3.70
Beverages/Sweets	Juice; Milk Yoghurt, Candy	22(21.5%)	2 (01 caramel; 01 juice)	9.09
Animal proteins	Fish	2(1.9%)	0	0.0
Other	Cabbage; Doughnut; Melon; Sweet ball	12(11.7%)	0	0.0
	Total	**102**	**6**	**5.88**

[a] "Bassi", "Attiéké", "Babenda", and "Donkounou" are local dishes. Bassi is a sweet semolina made from millet mixed with peanut paste and spices; Attiéké is a fermented cassava product; Babenda is a leafy vegetable-based dish mixed with cereals; Donkounou is a steamed cereal-based food. [b] Prevalence was calculated as the number of contaminated samples divided by the number of collected samples in each food category; [c] Values in parentheses indicate de prevalence of contaminated food.

Antimicrobial resistance profiles

Antimicrobial susceptibility testing presented in (Figure 2), revealed high resistance rates to azithromycin (100%), ampicillin (66.7%), and cefoxitin (66.7%).

All isolates remained susceptible to ciprofloxacin. Resistance to nalidixic acid and trimethoprim-sulfamethoxazole was low (16.7% each), and ceftriaxone retained good activity with 16.7% of resistance rates.

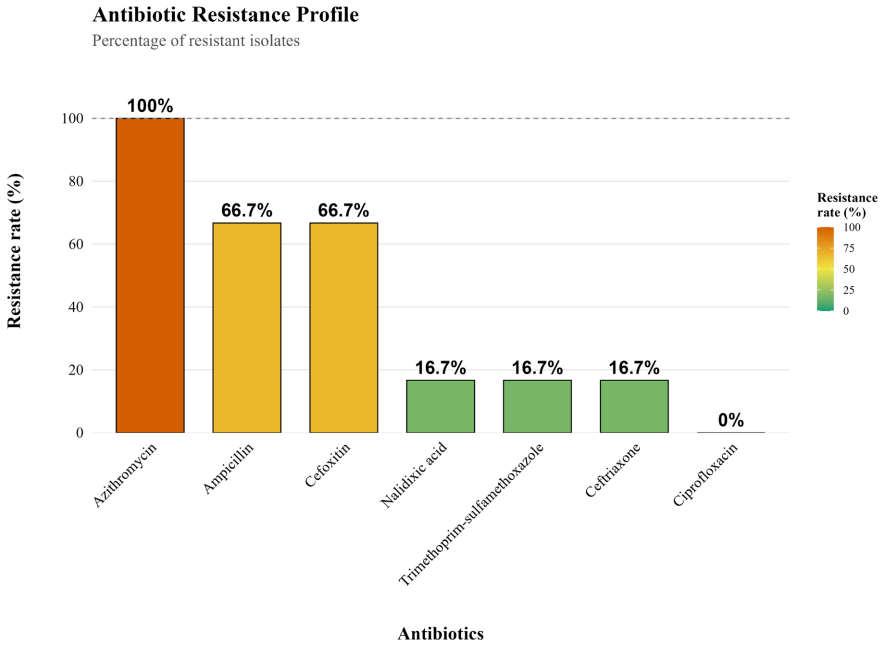

Figure 2. Resistance rates among 6 *Shigella sonnei* isolates.

Multidrug resistance patterns

The multiple antibiotic resistance (MAR) index presented in (Figure 3) ranged

from 0.1 to 0.9, with the majority of isolates showing MAR indices between 0.4 and 0.6, indicating resistance to multiple antibiotic classes. One isolate exhibited a MAR index of 0.9, reflecting near-complete resistance to the antibiotics tested.

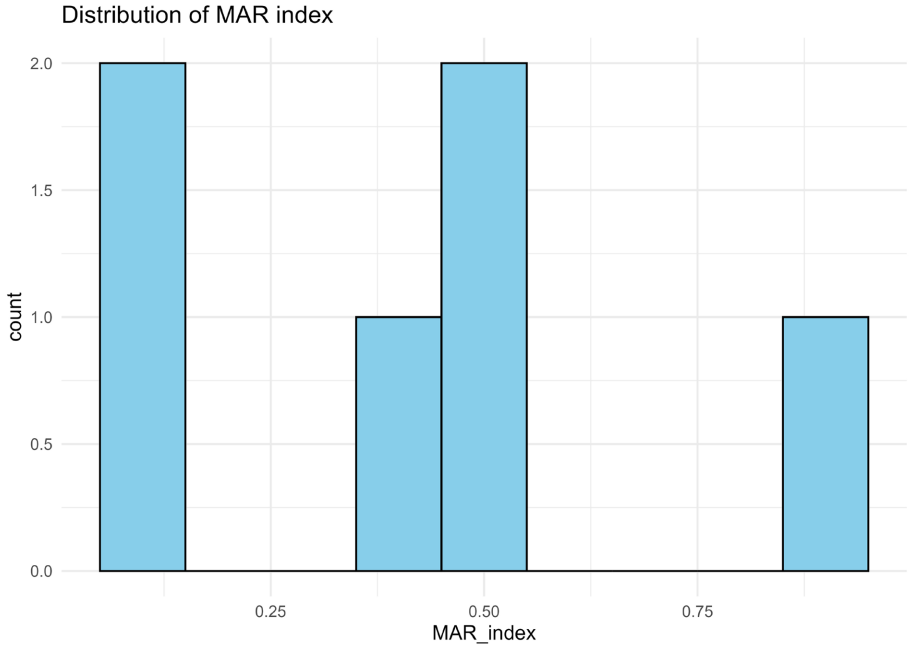

Figure 3. Distribution of multiple antibiotic resistance (MAR) indices among *Shigella sonnei* isolates.

Hierarchical clustering of resistance profiles (**Figure 4**) revealed two main resistance phenotypes: 1) one characterized by isolated resistance to azithromycin, and 2) another by multidrug resistance involving β lactams (ampicillin, cefoxitin, amoxicillin-clavulanic acid). Isolates recovered from bread, juice, and cake displayed broader resistance spectra compared to those from caramel.

4. Discussion

The present study investigated the occurrence of *Shigella* in ready-to-eat foods sold near primary schools in Tenkodogo and assessed the antimicrobial susceptibility profiles of the recovered isolates. The overall prevalence of contamination (5.9%) indicates that, while contamination was infrequent in this sample, *Shigella* may occasionally be present in foods intended for direct consumption. This finding is consistent with previous reports from sub-Saharan Africa showing that ready-to-eat foods sold in informal settings can serve as vehicles for enteric pathogens when hygiene conditions are inadequate [9] [20].

The detection of contaminated samples among different food categories, including bread, cakes, beverages, confectionery products, and traditional prepared foods, suggests that contamination was not restricted to a single food matrix in this study. Similar observations have been reported in Burkina Faso and other African countries, where microbial contamination has been identified across a

broad range of ready-to-eat foods [14] [15] [21]. The occurrence of contamination in foods that are consumed without further heat treatment is of potential relevance, as post processing contamination may directly expose consumers to viable pathogens.

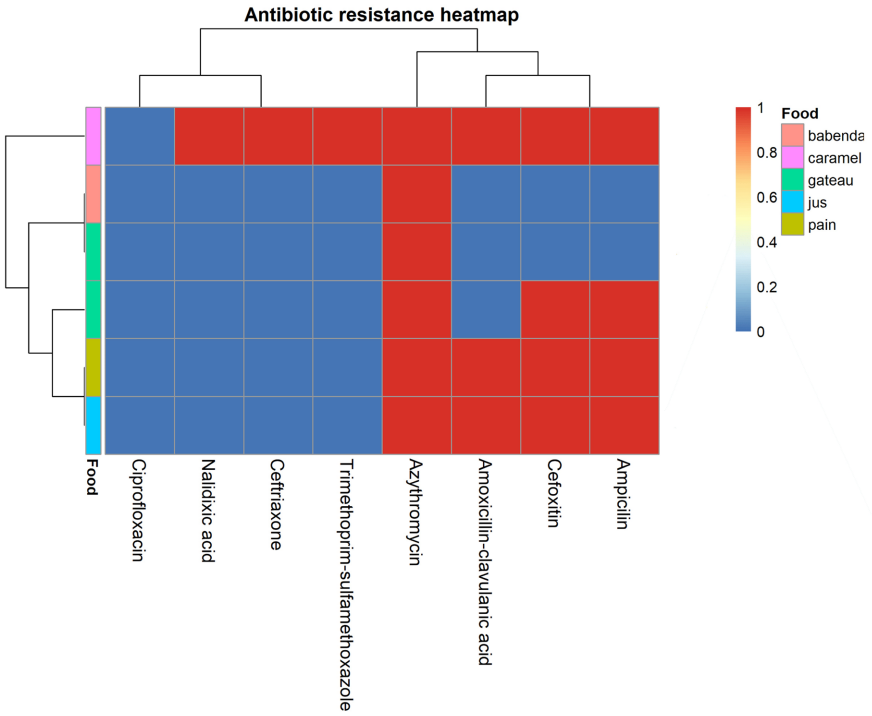

Figure 4. Heatmap of antibiotic resistance profiles among *Shigella* isolates by food source.

Because only six vendors were classified as contaminated, comparisons between exposure factors should be interpreted as exploratory. In the adjusted analysis, food wrapping was the only factor that remained associated with lower odds of *Shigella* contamination. No contaminated vendor was observed among those selling wrapped foods (0/28), whereas contamination was detected among vendors selling unwrapped foods (6/41). Although the confidence interval was wide because of the small number of events, this finding suggests that food protection during storage and sale may reduce exposure to environmental contamination sources such as dust, insects, and repeated handling. Similar observations have been reported in studies identifying inadequate food protection as an important contributor to microbial contamination of street-vended foods [5] [8].

A higher proportion of contamination was descriptively observed among vendors whose foods were exposed to flies (2/7, 28.6%) than among those whose foods were not exposed to flies (4/62, 6.5%). However, this trend was not statistically significant in either the bivariate or the adjusted analysis, and the very small number of contaminated vendors precludes any inference regarding an independent association. Previous studies have described houseflies as potential mechanical vectors of enteric pathogens, including *Shigella* [22] [23], but the present data are

insufficient to confirm such a relationship in this setting.

From a public health perspective, the detection of *Shigella* in foods sold near schools may be of interest because school aged children are an important consumer group for ready to eat foods. *Shigella* remains one of the major bacterial causes of diarrhoeal disease worldwide and is associated with substantial morbidity, particularly in low resource settings where access to safe water and sanitation remains limited [4] [24]. Repeated exposure to enteric pathogens during childhood could contribute to gastrointestinal illness and school absenteeism, although the present study did not directly measure health outcomes.

An important finding of this study was the observation of antimicrobial resistance among the recovered isolates. Resistance to azithromycin (100%, 6/6), ampicillin (66.7%, 4/6), and cefoxitin (66.7%, 4/6) was noted, while all isolates remained susceptible to ciprofloxacin. Similar trends have been reported in studies investigating antimicrobial resistance among *Shigella* isolates from human and environmental sources [25] [26]. Reduced susceptibility or resistance to azithromycin, interpreted using the EUCAST *Enterobacterales* criteria, observed in all six isolates may have potential clinical implications; however, this finding should be interpreted cautiously. Azithromycin is considered among the therapeutic options for shigellosis in some settings, particularly where resistance to first-line antimicrobials is common [27]. However, because only six isolates were analysed, this finding should be interpreted cautiously and regarded as exploratory and require confirmation through larger surveillance studies before any change in clinical practice can be recommended.

Multidrug resistance profiles (resistance to three or more antibiotic classes) were identified among several isolates. This may indicate exposure to environments where antimicrobial selection pressure exists. Similar concerns have been raised in recent reviews describing the emergence of antimicrobial resistant foodborne bacteria in ready to eat foods across Africa [6] [11].

From a One Health perspective, the occurrence of resistant bacteria in foods could reflect interactions between human, environmental, and animal reservoirs of antimicrobial resistance, emphasising the potential value of integrated surveillance approaches, although the present study was not designed to investigate transmission pathways.

Several limitations should be acknowledged. First, the small number of positive vendors (n = 6) considerably reduced statistical power and limits the precision of all prevalence and resistance estimates. Second, the cross-sectional design does not permit causal inference regarding the factors associated with contamination. In addition, sampling was conducted over a relatively short period and in a single city, which may limit the generalizability of the findings to other settings and may not capture potential seasonal variation in *Shigella* contamination. Third, bacterial characterisation was limited to phenotypic methods and PCR-based identification; serotyping, whole-genome sequencing, and molecular investigation of resistance determinants (e.g., β-lactamase genes and macrolide resistance genes) were not performed. Despite these limitations, the study provides baseline infor-

mation on *Shigella* contamination and antimicrobial resistance in ready-to-eat foods sold near schools in Burkina Faso, where data on this topic remain scarce. Future studies with larger sample sizes and more detailed molecular characterization are needed to confirm and extend these findings.

5. Conclusions

This study provides evidence of *Shigella sonnei* contamination in ready-to-eat foods sold near primary schools in Tenkodogo, Burkina Faso. Although the overall prevalence of contamination was relatively low (5.9%), the detection of antimicrobial-resistant isolates highlights the need for continued surveillance of foodborne enteric pathogens in informal school food vending settings.

In the exploratory adjusted analysis, food wrapping was the only factor associated with lower odds of contamination, whereas exposure to flies was observed only as a non-significant descriptive trend. Given the very small number of contaminated vendors, these findings should be interpreted with considerable caution and regarded as hypothesis-generating rather than confirmatory.

Resistance to azithromycin was observed in all six isolates when interpreted using the EUCAST *Enterobacterales* criteria; however, because only six isolates were analyzed and no species-specific EUCAST breakpoint for *Shigella* was available, the clinical implications of this finding remain uncertain.

Overall, the study provides baseline data for Burkina Faso and supports the need for larger studies with adequate statistical power and molecular characterization of isolates to better understand the epidemiology, transmission pathways, and antimicrobial resistance patterns of *Shigella* in ready-to-eat foods.

Ethics Approval and Consent to Participate

The study was approved by the Burkina Faso Health Research Ethics Committee (Approval No. 2024-09-275). The study was performed in accordance with the ethical standards as laid down in the 1964 Declaration of Helsinki. Written informed consent was obtained from all participating food vendors. Data were anonymized prior to analysis.

Availability of Data and Materials

All data collected and analyses during this study are available in this manuscript and on request from the corresponding author.

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During the preparation of this manuscript/study, the author(s) used Elicit AI for the purposes of bibliography research. The authors have reviewed and edited

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Author Contributions

All authors contributed to the study conception and design. E.B., E.M.M., D.M.A. and A.Z. conceived the study and drafted the initial manuscript. A.Z. and M.Y. collected and processed the surplus Ready-to-eat food samples from the diagnostic laboratory. E.B., E.M.M., D.M.A., H.I.B. and N.B. curated and analysed the data. N.B. supervised the project. E.B. led the manuscript development, supervised all data analysis, and relevantly reviewed the methodology. All authors have read and agreed to the published version of the manuscript.

Conflicts of Interest

The authors declare that they have no competing interests.

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