Gastroenterology and Hepatology from Bed to Bench

ORIGINAL ARTICLE

Epidemiological patterns and antimicrobial resistance of bacterial diarrhea among children in Nairobi City, Kenya

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ABSTRACT

Aim: Determine the prevalence of enteric bacterial pathogens and their antimicrobial resistance among diarrheic children in Nairobi City, Kenya.

Background: Regardless of enteric bacterial pathogens being a major cause of gastroenteritis in children, their occurrence and antimicrobial resistance patterns reveals regional spatial and temporal variation.

Methods: In a cross-sectional study, a total of 374 children below five years presenting with diarrhea at Mbagathi County Hospital were recruited. Stool microbiology test was used to detect enteric bacterial infection. Antimicrobial resistance was determined using the disk diffusion method.

Results: Diarrheagenic *E. coli* (36.4%) was the leading species followed by *Shigella* (3.2%), *Salmonella* (2.4%), *Campylobacter* (1.6%), *Yersinia* (1.3%) and *Aeromonas* (1.1%) species. *Escherichia coli* pathotyping revealed that 20.9%, 4.0%, 10.2% and 0.5% of the study participants were infected with enteroaggregative *E. coli* (EAEC), enteropathogenic *E. coli* (EPEC), enterotoxigenic *E. coli* (ETEC) and enteroinvasive *E. coli* (EIEC) pure isolates while the prevalence of mixed pathotype infections was 0.3% for EAEC/EPEC/ETEC and 0.5% for EAEC/ETEC. *Shigella* sero-grouping revealed that 0.5%, 0.3%, 1.9%, and 0.5% were infected with *Shigella boydii*, *Shigella dysentriae*, *Shigella flexneri* and *Shigella sonnei* pure isolates. *Shigella* species and *E. coli* co-infection was detected in 2.4% of the children, specifically, 1.1% for EAEC/*Shigella boydii*, 0.5% for EAEC/*Shigella dysentriae* and 0.3% in each case of EAEC/*Shigella sonnei*, EPEC/*Shigella flexneri* and ETEC/*Shigella flexneri* co-infections. Most of the isolates were resistant to commonly prescribed antibiotics.

Conclusion: There was a high prevalence of enteric bacterial pathogens and co-infection alters epidemiological dynamics of bacterial diarrhea in children. Continuous antibiotic resistance surveillance is justified because the pathogens were highly resistant to commonly prescribed antimicrobials.

Keywords: Epidemiology; antimicrobial resistance; bacterial diarrhea.

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Introduction

In the year 2016, diarrhea accounted for more than 1.6 million deaths globally making it the fifth leading cause of mortality among children less than 5 years (1). The majority of these deaths occurred in resource-limited

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continents including Africa (1, 2). In Sub-Saharan Africa, there were more than 1.2 billion cases of diarrhea, of which 371 million, leading to at least 0.2 million deaths, occurred in children younger than five years (1, 2). Besides parasites and viruses, enteric bacteria continue to be a leading cause of gastroenteritis in children (1).

Enteric bacterial pathogens accounts for more than 300 million episodes of diarrhea and one million deaths among children globally, the majority of which are caused by *Escherichia coli* and the remainder being *Campylobacter*, *Shigella*, *Vibrio* and *Salmonella species* (1). Previous studies across Kenya demonstrated that *Shigella*, *E. coli*, and *Salmonella* species were associated with childhood diarrhea (3), while others did not (4), suggesting geographic uniqueness of gut microbiota in immunity towards enteric infection patterns in Kenya (5-8). Also, previous studies across Kenya found an association between *Campylobacter* and *Shigella* species with diarrhea among HIV infected children (9) while others did not (10), signifying that HIV alters the already geographic unique gut microbiota profile which is critical for host immunity to enteric bacterial infections (11, 12). The risk factors of enteric bacterial pathogens, however, appear to be distributed differently (3, 13, 14) and as a result, the incidences of specific pathogens differ across Kenya (4, 14-20). A more recent study in Nairobi city identified *Yersinia enterocolitica* as an etiology of childhood diarrhea (3) while previous studies did not (13, 17), indicating the emergence and spread of new pathogen strains driven by poor water, sanitation and hygiene (WASH) practices in the city (3) qualifying the need for constant epidemiological surveillance in Nairobi city, Kenya. However, there is paucity of information on the prevalence of enteric bacterial pathogens among diarrheic children in Nairobi city, Kenya.

The innovation of antibiotics led to optimism that enteric bacterial infections could be controlled and prevented. However, enteric bacteria resistance to antibiotics is still the leading cause of death globally, including Kenya (21). Many studies have reported that enteropathogenic bacteria isolated from diarrheic children in Kenya including Nairobi city, can develop resistance (3, 13, 14, 22, 23). For instance, a previous study in Nairobi city reported the resistance of *E. coli* and *Shigella* isolates to ampicillin, trimethoprim/sulfamethoxazole, streptomycin, chloramphenicol and tetracycline (3) while a recent study showed changing patterns with increasing resistance (23). This increasing resistance is due to inappropriate antibiotic use increasing selection and transmission of antibiotic resistant strains in the city (3, 13, 22, 24, 25) in this era when there is a serious lack of new antibiotics under development to combat the growing antimicrobial resistance (26, 27), justifying the need for continuous antimicrobial resistance surveillance. However, there is limited information on the prevalence of antimicrobial resistance of enteric bacterial pathogens among children in Nairobi city, Kenya. This study, therefore, aimed at determining the prevalence of enteric bacterial pathogens and their antimicrobial resistance among diarrheic children in Nairobi city, Kenya.

Methods

Study site, design and population

A detailed description of the study site, design and population is presented here (23). Briefly, this was a cross-sectional study targeting diarrheic children <5 years, seeking treatment at Mbagathi hospital, Nairobi city, Kenya. Diarrhea was defined according to World Health Organization (WHO) guidelines as the occurrence of three or more loose, liquid, or watery stools in a 24-hour period (28). Demographic and clinical information of the study participants were collected using a questionnaire. Stool specimens were collected and microbiology laboratory analysis performed within two hours of collection. Stool samples of children who had received antibiotics and who did not provide informed consent were excluded from the study.

Bacteriological procedures

Identification of bacteria species was performed according to WHO recommendations (29). All fecal specimens were cultured in alkaline peptone water, selenite broth and blood agar enrichment media, followed by sub-culture on selective and differential media as described elsewhere (18). Isolates were then subjected to Gram staining and biochemical tests using oxidase test, lysine decarboxylase test, urease test, citrate test, hydrogen sulfide gas production, fermentation test, and motility test to identify the significant characteristic of bacteria according to the standard methods (29). *E. coli*

pathotyping and *Shigella* sero-grouping was performed as previously described (23).

Antimicrobial Resistance

Antibiotic susceptibility was performed using Kirby-Bauer disk diffusion method on Mueller Hinton agar by incubating at 37°C for 18 hours (30). Broth turbidity was made to match with 0.5 McFarland standards. Antibiotics discs of ampicillin, trimethoprim/sulfamethoxazole, ceftriaxone, streptomycin, amoxicillin/clavulanic acid, gentamycin, kanamycin, ciprofloxacin, chloramphenicol, erythromycin, nalidixic acid and tetracycline were tested.

Data analysis

Statistical analyses were performed using SPSS version 19.0 for Windows (IBM SPSS Statistics for Windows, Version 19.0. Armonk, NY: IBM Corp.). Descriptive statistics, namely frequencies and percentages, were used to present demographic and clinical data, frequency of enteric bacteria pathogens and their antimicrobial susceptibility pattern.

Ethical considerations

This study was ethically approved by Kenyatta National Hospital/University of Nairobi (KNH-UoN) Ethics and Research Committee and was conducted according to the Declaration of Helsinki (31). A consent form was read and signed by either parent or guardian of each child. Diarrheic children were treated by clinicians according to World Health Organization (WHO) guidelines for treatment of diarrhea in children (28). All study participants' information and test results were kept confidential. The results of bacterial cultures were used in clinical management of study participants.

Results

Demographic and clinical information of study participants

The demographic and clinical information of study participants is presented in table 1. A total of 374 children were recruited in the study. Age distribution showed that, out of the total study subjects, 242 (70.0%) were between 1 and 36 months and 112 (30.0%) children were between 37 and 60 months. The overall gender distribution was 181 (48%) females and 193 (52%) males. Guardians of 371 (99.2%) and 3 (0.8%) reported using piped and borehole water, respectively. In addition, 220 (58.8%) reported treating drinking water. Occupation distribution showed that 2 (0.5%), 17 (4.5%), 5 (1.3%), 14 (3.7%), and 178 (47.6%) of the guardians were employed in the fields of healthcare, office administrative support, construction/installation/repair, education/ training, and sales, respectively, while 158 (42.2%) were unemployed.

Table 1. Demographic and clinical information of study participants

Characteristics	Number (%)
Age in months	
1-36	242 (70.0)
37-60	112 (30.0)
Gender	
Female	181 (48)
Male	193 (52)
Source of water	
Piped water	371 (99.2)
Borehole	3 (0.8)
Water treatment	220 (58.8)
Occupation of guardian	
Health care practitioner	2 (0.5)
Office/administrative/support	17 (4.5)
Construction/installation/repair	5 (1.3)
Education/ training	14 (3.7)
Sales	178 (47.6)
Unemployed	158 (42.2)
Body temperature	
<38.0	58 (15.5)
≥ 38.0	316 (84.5)
Duration of diarrhea	
1-3	308 (82.4)
4-6	35 (9.4)
≥7	31 (8.3)
Symptoms	
Vomiting	298 (79.7)
Fever	310 (82.9)
Abdominal cramp	251 (67.1)
Headache	12 (3.2)
Nausea	50 (13.4)
Appetite loss	345 (92.2)
Sunken eyeballs	311 (83.2)
Dry tongue	117 (31.3)
Reduced skin elasticity	192 (51.3)

Data are presented as number and proportions (%) of study participants. ≤, less than or equal to. <, less than. ≥, greater than or equal to. >, greater than.

Temperature of <38.0°C and ≥ 38.0°C was recorded in 58 (15.5%) and 316 (84.5%) children, respectively. In this study, 308 (82.4%), 35 (9.4%) and 31 (8.3%), respectively, reported having diarrhea for 1-3, 4-6 and ≥7 days. Vomiting was reported in 298 (79.7%) patients, fever in 310 (82.9%), abdominal cramp in 251 (67.1%), headache in 12 (3.2%), nausea in 50 (13.4%), and appetite loss in 345 (92.2%) children. Clinical

diagnosis of dehydration revealed that 311 (83.2%) had sunken eyeballs, 117 (31.3%) children had dry tongues and 192 (51.3%) had reduced skin elasticity.

Table 2. Prevalence of enteric bacterial pathogens isolated from study participants

Enteropathogenic bacteria	N (%)
Diarrheagenic *E. coli*	136 (36.4)
EAEC	78 (20.9)
EPEC	15 (4.0)
ETEC	38 (10.2)
EIEC	2 (0.5)
EAEC/EPEC/ETEC	1 (0.3)
EAEC/ETEC	2 (0.5)
Salmonella species	9 (2.4)
Shigella species	12 (3.2)
Shigella boydii	2 (0.5)
Shigella dysentriae	1 (0.3)
Shigella flexneri	7 (1.9)
Shigella sonnei	2 (0.5)
Campylobacter species	6 (1.6)
Yersinia enterocolitica	5 (1.3)
Aeromonas species	4 (1.1)
Shigella species/*E. coli* co-infection	9 (2.4)
EAEC/*Shigella boydii*	4 (1.1)
EAEC/*Shigella dysentriae*	2 (0.5)
EAEC/*Shigella sonnei*	1 (0.3)
EPEC/*Shigella flexneri*	1 (0.3)
ETEC/*Shigella flexneri*	1 (0.3)

Data are presented as number and proportions (%) of study participants. *E. coli*, *Escherichia coli*. EPEC, enteropathogenic *E. coli*. ETEC, enterotoxigenic *E. coli*. EAEC, enteroaggregative *E. coli*. EIEC, enteroinvasive *E. coli*.

Prevalence of enteric bacteria pathogens isolated from study participants

The prevalence of enteric bacterial pathogens is presented in table 2. A total of 136 (36.4%) children were infected by diarrheagenic *E. coli*. Of these, 78 (20.9%), 15 (4.0%), 38 (10.2%) and 2 (0.5%) children were infected with enteroaggregative *E. coli* (EAEC), enteropathogenic *E. coli* (EPEC), enterotoxigenic *E. coli* (ETEC) and enteroinvasive *E. coli* (EIEC) pure strains, respectively, while mixed pathotype infections was detected in 1 (0.3%) child for EAEC/EPEC/ETEC and 2 (0.5%) children for EAEC/ETEC. *Salmonella* species was detected in stool samples of 9 (2.4%) children. There were 12 (3.2%) children infected with *Shigella* species, of which 2 (0.5%), 1 (0.3%), 7 (1.9%), and 2 (0.5%) were infected with *Shigella boydii, Shigella dysentriae, Shigella flexneri* and *Shigella sonnei*, respectively. *Campylobacter*, *Yersinia* and *Aeromonas* species were detected in stool samples of 6 (1.6%), 5 (1.3%) and 4 (1.1%) children, respectively. There were 9 (2.4%) children co-infected with *Shigella* species and *E. coli*, of which, 4 (1.1%) were EAEC/*Shigella boydii* co-infections, 2 (0.5%) were EAEC/*Shigella dysentriae* co-infections, while one (0.3%) case was reported for EAEC/*Shigella sonnei*, EPEC/*Shigella flexneri* and ETEC/*Shigella flexneri* co-infection.

Antimicrobial susceptibility patterns of enteric bacterial pathogens isolated from study participants

The antimicrobial susceptibility patterns of the enteric bacterial pathogens isolated from diarrheic children in Nairobi city, Kenya, are presented in table 3. About 80 (55.2%), 89 (61.4%), 18 (12.4%), 91 (76.6%), 38 (26.2%), 69 (47.6%), 91 (62.8%), 41 (28.3%), 90 (62.1%), 12 (8.3%), 16 (11.0%), and 120 (82.8%) of diarrheagenic *E. coli* were resistant to ampicillin, trimethoprim/sulfamethoxazole, ceftriaxone, streptomycin, amoxicillin/clavulanic acid, gentamycin, kanamycin, ciprofloxacin, chloramphenicol, erythromycin, nalidixic acid and tetracycline, respectively. Although none of the *Salmonella* isolate was resistant to trimethoprim/sulfamethoxazole, gentamycin and nalidixic acid, 7 (77.8%), 7 (77.8%), 9 (100.0%), 5 (55.6%), 8 (88.9%), 8 (88.9%), 7 (77.8%), and 6 (66.7%) of *Salmonella* species isolates were resistant to ampicillin, ceftriaxone, streptomycin, amoxicillin/clavulanic acid, kanamycin, ciprofloxacin, chloramphenicol, erythromycin and tetracycline, respectively.

Shigella species resistant to kanamycin was not detected, nevertheless, 13 (28.6%), 10 (47.6%), 10 (47.6%), 12 (57.1%), 4 (19.0%), 2 (9.5%), 4 (19.0%), 12 (57.1%), 2 (9.5%), 4 (19.0%) and 14 (66.7%) of the *Shigella* isolates were resistant to ampicillin, trimethoprim/sulfamethoxazole, ceftriaxone, streptomycin, amoxicillin/clavulanic acid, gentamycin, ciprofloxacin, chloramphenicol, erythromycin, nalidixic acid and tetracycline, respectively. While *Campylobacter* species was not resistant to streptomycin, amoxicillin/clavulanic acid, kanamycin, ciprofloxacin and nalidixic acid, 3 (50.0%), 1 (16.7%), 1 (16.7%), 1 (16.7%), 4 (66.7%), 3 (50.0%), and 5 (83.3%) of the *Campylobacter* isolates were resistant to ampicillin, trimethoprim/sulfamethoxazole, ceftriaxone, gentamycin, chloramphenicol, erythromycin, tetracycline, respectively. *Yersinia* was not resistant to trimethoprim/sulfamethoxazole, ciprofloxacin, and nalidixic acid.

Table 3. Antimicrobial susceptibility patterns of enteric bacterial pathogens isolated from study participants

Enterpathogenic bacteria	Antibiotic	Susceptibility pattern (%)		
		Sensitive	Intermediate	Resistant
Diarrheagenic *E. coli*	Ampicillin	22 (15.2)	43 (29.7)	80 (55.2)
	Trimethoprim/sulfamethoxazole	25 (17.2)	31 (21.4)	89 (61.4)
	Ceftriaxone	106 (73.1)	21 (14.5)	18 (12.4)
	Streptomycin	34 (23.4)	20 (13.8)	91 (76.6)
	Amoxicillin/clavulanic acid	87 (60.0)	20 (13.8)	38 (26.2)
	Gentamycin	48 (33.1)	28 (19.3)	69 (47.6)
	Kanamycin	10 (6.9)	44 (30.3)	91 (62.8)
	Ciprofloxacin	94 (64.8)	10 (6.9)	41 (28.3)
	Chloramphenicol	14 (9.7)	41 (28.3)	90 (62.1)
	Erythromycin	81 (55.9)	52 (35.9)	12 (8.3)
	Nalidixic acid	99 (68.3)	30 (20.7)	16 (11.0)
	Tetracycline	15 (10.3)	10 (6.9)	120 (82.8)
Salmonella species	Ampicillin	0 (0.0)	2 (22.2)	7 (77.8)
	Trimethoprim/sulfamethoxazole	9 (100.0)	0 (0.0)	0 (0.0)
	Ceftriaxone	2 (22.2)	0 (0.0)	7 (77.8)
	Streptomycin	0 (0.0)	0 (0.0)	9 (100.0)
	Amoxicillin/clavulanic acid	4 (44.4)	0 (0.0)	5 (55.6)
	Gentamycin	9 (100.0)	0 (0.0)	0 (0.0)
	Kanamycin	1 (11.1)	0 (0.0)	8 (88.9)
	Ciprofloxacin	0 (0.0)	1 (11.1)	8 (88.9)
	Chloramphenicol	2 (22.2)	0 (0.0)	7 (77.8)
	Erythromycin	1 (11.1)	2 (22.2)	6 (66.7)
	Nalidixic acid	9 (100.0)	0 (0.0)	0 (0.0)
	Tetracycline	3 (33.3)	1 (11.1)	5 (55.6)
Shigella species	Ampicillin	2 (9.5)	6 (28.6)	13 (28.6)
	Trimethoprim/sulfamethoxazole	8 (38.1)	3 (14.3)	10 (47.6)
	Ceftriaxone	11 (52.4)	0 (0.0)	10 (47.6)
	Streptomycin	2 (9.5)	7 (33.3)	12 (57.1)
	Amoxicillin/clavulanic acid	16 (76.2)	1 (4.8)	4 (19.0)
	Gentamycin	18 (85.7)	1 (4.8)	2 (9.5)
	Kanamycin	4 (19.0)	17 (81.0)	0 (0.0)
	Ciprofloxacin	11 (52.4)	6 (28.6)	4 (19.0)
	Chloramphenicol	5 (23.8)	4 (19.0)	12 (57.1)
	Erythromycin	5 (23.8)	14 (66.7)	2 (9.5)
	Nalidixic acid	13 (62.0)	4 (19.0)	4 (19.0)
	Tetracycline	4 (19.0)	3 (14.3)	14 (66.7)
Campylobacter species	Ampicillin	2 (33.3)	1 (16.7)	3 (50.0)
	Trimethoprim/sulfamethoxazole	5 (83.3)	0 (0.0)	1 (16.7)
	Ceftriaxone	4 (66.7)	1 (16.7)	1 (16.7)
	Streptomycin	5 (83.3)	1 (16.7)	0 (0.0)
	Amoxicillin/clavulanic acid	6 (100.0)	0 (0.0)	0 (0.0)
	Gentamycin	5 (83.3)	0 (0.0)	1 (16.7)
	Kanamycin	4 (66.7)	2 (33.3)	0 (0.0)
	Ciprofloxacin	6 (100.0)	0 (0.0)	0 (0.0)
	Chloramphenicol	0 (0.0)	1 (33.3)	4 (66.7)
	Erythromycin	1 (16.7)	2 (33.3)	3 (50.0)
	Nalidixic acid	4 (66.7)	2 (33.3)	0 (0.0)
	Tetracycline	1 (16.7)	0 (0.0)	5 (83.3)
Yersinia enterocolitica	Ampicillin	0 (0.0)	0 (0.0)	5 (100.0)
	Trimethoprim/sulfamethoxazole	2 (40.0)	2 (40.0)	1 (20.0)
	Ceftriaxone	0 (0.0)	4 (80.0)	1 (20.0)
	Streptomycin	0 (0.0)	0 (0.0)	5 (100.0)
	Amoxicillin/clavulanic acid	3 (60.0)	1 (20.0)	1 (20.0)
	Gentamycin	0 (0.0)	0 (0.0)	5 (100.0)
	Kanamycin	1 (20.0)	4 (80.0)	0 (0.0)
	Ciprofloxacin	5 (100.0)	0 (0.0)	0 (0.0)
	Chloramphenicol	0 (0.0)	1 (20.0)	4 (80.0)
	Erythromycin	0 (0.0)	4 (80.0)	1 (20.0)
	Nalidixic acid	3 (60.0)	2 (40.0)	0 (0.0)
	Tetracycline	1 (20.0)	1 (20.0)	3 (60.0)

Table 3 cont. Antimicrobial susceptibility patterns of enteric bacterial pathogens isolated from study participants

Enterpathogenic bacteria	Antibiotic	Susceptibility pattern (%)		
		Sensitive	Intermediate	Resistant
Aeromonas species	Ampicillin	0 (0.0)	3 (75.0)	1 (25.0)
	Trimethoprim/sulfamethoxazole	2 (50.0)	1 (25.0)	0 (0.0)
	Ceftriaxone	4 (100.0)	0 (0.0)	0 (0.0)
	Streptomycin	2 (50.0)	2 (50.0)	0 (0.0)
	Amoxicillin/clavulanic acid	4 (100.0)	0 (0.0)	0 (0.0)
	Gentamycin	4 (100.0)	0 (0.0)	0 (0.0)
	Kanamycin	3 (50.0)	1(25.0)	0 (0.0)
	Ciprofloxacin	4 (100.0)	0 (0.0)	0 (0.0)
	Chloramphenicol	0 (0.0)	2 (50.0)	2 (50.0)
	Erythromycin	1 (25.0)	3 (75.0)	0 (0.0)
	Nalidixic acid	4 (100.0)	0 (0.0)	0 (0.0)
	Tetracycline	0 (0.0)	1 (25.0)	3 (75.0)
	Kanamycin	4 (19.0)	17 (81.0)	0 (0.0)
	Nalidixic acid	3 (60.0)	2 (40.0)	0 (0.0)
	Tetracycline	1 (20.0)	1 (20.0)	3 (60.0)
Aeromonas species	Ampicillin	0 (0.0)	3 (75.0)	1 (25.0)
	Trimethoprim/sulfamethoxazole	2 (50.0)	1 (25.0)	0 (0.0)
	Ceftriaxone	4 (100.0)	0 (0.0)	0 (0.0)
	Streptomycin	2 (50.0)	2 (50.0)	0 (0.0)
	Amoxicillin/clavulanic acid	4 (100.0)	0 (0.0)	0 (0.0)
	Gentamycin	4 (100.0)	0 (0.0)	0 (0.0)
	Kanamycin	3 (50.0)	1(25.0)	0 (0.0)
	Ciprofloxacin	4 (100.0)	0 (0.0)	0 (0.0)
	Chloramphenicol	0 (0.0)	2 (50.0)	2 (50.0)
	Erythromycin	1 (25.0)	3 (75.0)	0 (0.0)
	Nalidixic acid	4 (100.0)	0 (0.0)	0 (0.0)
	Tetracycline	0 (0.0)	1 (25.0)	3 (75.0)

However, antimicrobial resistant to ampicillin, trimethoprim/sulfamethoxazole, ceftriaxone, streptomycin, amoxicillin/clavulanic acid, gentamycin, chloramphenicol, erythromycin and tetracycline was reported to be 5 (100.0%), 1 (20.0%), 1 (20.0%), 5 (100.0%), 1 (20.0%), 5 (100.0%), 4 (80.0%), 1 (20.0%), and 3 (60.0%), respectively, among *Yersinia* isolates. Even though none of *Aeromonas* isolates was resistant to trimethoprim/sulfamethoxazole, ceftriaxone, streptomycin, amoxicillin/clavulanic acid, gentamycin, kanamycin, ciprofloxacin, erythromycin and nalidixic acid, 1 (25.0%), 2 (50.0%) and 3 (75.0%) of *Aeromonas* isolates were resistant to ampicillin, chloramphenicol, and tetracycline, respectively.

Discussion

Globally, enteric bacteria associated diarrhea continues to be a major cause of morbidity and mortality among children under 5 years (1). Enteric bacterial pathogens epidemiology shows variations between countries, and even between geographical regions within the same country (32). There has been a dramatic increase in the emergence of antimicrobial resistant enteric bacterial strains, which has made antibiotic choices for enteric infection treatment increasingly limited and more expensive (21). Thus, continuous epidemiological and antimicrobial resistance surveillances are fundamental in planning treatment.

Diarrheagenic *E. coli* predominates in this study followed by the rest namely *Shigella, Salmonella, Campylobacter, Yersinia* and *Aeromonus* species, in that order, highlighting the prominent role of *diarrhegenic E. coli* in enterobacteria associated diarrhea among children in Nairobi city, Kenya. These findings are consistent with previous studies involving diarrheic children in Kiambu (18) and Homa Bay counties, Kenya (19). As reviewed by (33), diarrhegenic *E. coli* persists longer in environmental reservoirs supporting the hypothesis of increased transmission of *E. coli* to human population (34), reinforcing the observation of this study. However, the findings of the present study are inconsistent with previous studies in the literature that demonstrated the dominancy of *Shigella* species, followed by diarrhegenic *E. coli, Salmonella* and *Yersinia* species among diarrheic children in Nairobi city, Kenya (3). This may be attributed to the fact that

proved diarrhegenic *E. coli*, particularly EAEC, genome heterogeneity (35), using two virulence genes for EAEC detection decreased the rate of isolation in the previous study (3). Above all, this study detected higher prevalence of *Shigella* mono-infection (3.2%) than *Shigella/E. coli* co-infection (2.4%) suggesting that co-infections alter epidemiological dynamics of infectious disease due to pathogen synergism worsening disease severity and consequent mortality (36), and this observation is consistent with previous studies among diarrheic children in Kiambu county, Kenya (19), China (37), Zanzibar and Rwanda (38). Therefore, diarrhegenic *E. coli, Shigella, Salmonella, Campylobacter, Yersinia* and *Aeromonas* species are principal causes of childhood bacteria associated diarrhea justifying access to safe water, sanitation and hygiene among children in Nairobi city, Kenya.

The current study observed high antimicrobial resistance rates indicating rapid and ongoing spread of antimicrobial-resistant organisms. Specifically, more than half of diarrheagenic *E. coli* isolates were resistant to ampicillin, trimethoprim/ sulfamethoxazole, streptomycin, kanamycin, chloramphenicol and tetracycline which is partly in agreement with studies in Nairobi city (17) and Meru county (14) but inconsistent with a previous study among the Maasai community of Narok and Kajiado counties that reported increased susceptibility to these antibiotics (39), possibly due to reduced antimicrobial use among the Maasai community who mostly practice traditional medicine (40). Over half of the *Shigella* isolates were resistant to streptomycin, chloramphenicol and tetracycline while resistance to ampicillin, ceftriaxone, amoxicillin-clavulanic acid, kanamycin, ciprofloxacin, and erythromycin occurred in more than half of *Salmonella* isolates, which partly agrees with a multisite study conducted in Kisii, Homa Bay and Migori counties, Kenya (22) but conflicts with a study in Zambia (41). Over half of *Campylobacter* isolates were resistant to ampicillin, chloramphenicol, and erythromycin which is consistent with the findings in Ethiopia (42) and disagrees with a study in China (43). At least half of *Yersinia* isolates were resistant to ampicillin, streptomycin, gentamycin and tetracycline which mirrors a study in Ethiopia (44) but disagrees with a study in Mexico (45). At least half of *Aeromonas* isolates were resistant to tetracycline and chloramphenicol which is in agreement with a study in Brazil (46) and disagrees with a study in China (43). These variations in resistance profiles between countries, within regions suggest significant differences in antibiotic use (47). Therefore, antimicrobial stewardship programs have to be developed to influence antibiotic use and prescribing behavior to ensure long-term availability of effective treatment for bacterial infections in Kenya.

This study had limitations. Other studies have detected viral, bacterial and parasitic gastroenteritis among Kenyan children (3, 4, 19) thus it is possible that the bacterial pathogens found may not be the sole cause of the diarrhea. Study participants were recruited within the hospital hence the prevalence of enteric bacteria and antimicrobial resistance does not represent community prevalence. We did not assay antimicrobial resistance genes. The presence of DAEC and AIEC pathotypes were not investigated in this study. We acknowledge the small sample size of *Aeromonas, Yersinia* and *Campylobacter* isolates assayed for antimicrobial resistance.

We conclude that diarrhegenic *E. coli, Shigella, Salmonella, Campylobacter, Yersinia* and *Aeromonas* species are important etiologies of diarrhea in children under five years of age, in Kenya. These pathogens are of public health importance since they are highly resistant to commonly prescribed antimicrobials. It is hoped the results of the present study will guide treatment of bacterial diarrheal diseases among children in the country.

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Conflict of interests

The authors declare that they have no conflict of interest.

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