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Epidemiology of Antimicrobial-Resistant Diarrheagenic *Escherichia coli* Pathotypes From Children, Livestock and Food in Dagoretti South, Nairobi Kenya

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ABSTRACT

Peri-urban environments, characterized by dense human populations, cohabiting livestock, and complex food systems, serve as hotspots for food contamination and infectious diseases. Children aged 6–24 months are particularly vulnerable, as they often encounter contaminated food and water, increasing their risk of food-borne disease, with diarrhea being a common symptom. We investigated the prevalence of antimicrobial resistance (AMR) in pathogenic *Escherichia coli* from children 6–24 months of age, their food, and cohabiting livestock, in Dagoretti South subcounty in Nairobi, Kenya. Of 540 stools, 296 livestock feces, and 859 food samples collected from 585 randomly enrolled households, 16% harbored diarrheagenic *E. coli* (DEC) pathotypes. The predominant AMR phenotypes observed were trimethoprim–sulfamethoxazole, ampicillin, and tetracycline at 53%, 48% and 41%, respectively. Diarrheagenic *E. coli* from children showed significantly higher resistance to all antibiotics compared to those from livestock and food. Overall, 30% of the 274 DEC isolates from all three sources exhibited multidrug resistance. Network analysis of AMR co-occurrence revealed two clusters: (1) ampicillin, trimethoprim–sulfamethoxazole, tetracycline, amoxicillin/clavulanic acid, and chloramphenicol; and (2) nalidixic acid, ciprofloxacin, gentamicin, and ceftriaxone. The co-resistance backbone of ampicillin–trimethoprim/sulfamethoxazole–tetracycline was significantly higher among isolates from children than from other hosts ($\chi^2 = 29.858$, df = 2, adjusted $P < 0.05$). Logistic regression analysis revealed that on-site disposal of animal manure and garbage, along with a recent history of diarrhea, were significantly associated with AMR carriage in children ($P < 0.05$). These findings emphasize the need for One Health interventions to curb emergence and spread of AMR in these close-contact populations.

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BACKGROUND

Antimicrobial resistance among *Enterobacteriaceae* is an increasing threat to global health. While various studies have linked bacterial AMR in humans to food animals due to the use of antibiotics in food animal production, there is limited evidence of direct exchange of AMR between humans and livestock [1]. Consumption of foods produced and preserved with antibiotics has been linked to the horizontal transmission of antimicrobial resistance (AMR) determinants to humans [2]. However, knowledge on AMR bacteria of community origin isolated from various points of the food continuum, including household livestock, is lacking [3]. Specifically, information is needed on their role in AMR transmission to children aged 6–24 months in resource-constrained community settings. AMR requires interrogation in all of these epidemiological

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compartments to understand its emergence and spread in this vulnerable age group.

Escherichia coli is a significant food-borne pathogen globally, contributing to the 600 million food-borne illnesses and 420,000 deaths annually resulting from consumption of contaminated foods [4]. While diarrheagenic *E. coli* is antigenically distinct from commensal *E. coli* [5], commensal *E. coli* can also act as a reservoir for the spread of multidrug resistance between food and humans [6]. Diarrheagenic *E. coli* is characterized by particular subset of virulence genes that enable its classification into different pathogroups [7]. Young children living in sub-Saharan Africa and South Asia bear the brunt of the disease burden caused by these pathotypes [8], with inadequate access to healthcare, poor sanitation and cohabitation with livestock being major contributing factors. We investigated risk factors associated with the AMR carriage in *E. coli* pathotypes in children aged 6–24 months, household livestock and foods in the resource-limited, peri-urban setting in Dagoretti South subcounty in Nairobi, Kenya. This setting represents a distinct hotspot for environmental AMR transmission due to the dense cohabitation of humans, livestock and vermin, widespread misuse of antibiotics, and inadequate infrastructure for drinking water, drainage and sanitation [9]. Studies from other low- and middle-income countries (LMICs) have similarly highlighted how close human–animal interactions and poor waste management practices create environments that facilitate the exchange of AMR genes across different reservoirs [2,10]. Addressing these challenges requires integrated, multisectoral approaches that address key interfaces within these communities to effectively mitigate the risk of AMR spread.

METHODS

Study design, site, and population

A cross-sectional study was conducted in the peri-urban settings of Dagoretti South subcounty in Nairobi, Kenya, between May and October 2021. A total of 585 households, each having at least one child 6–24 months of age, were randomly recruited. With consent from an adult caregiver, a survey questionnaire on ODK Collect was administered, and a stool sample was collected from the child. In addition to stool samples, 585 ready-to-eat foods intended for the child was sampled in a 50-mL Falcon tube. Moreover, food preparation observations were conducted in 109 households and a sample collected. Livestock fecal samples were collected if livestock were present in the households, or from the immediate neighbors where there was observed a possibility of interaction with the enrolled households (n = 296). During traceback, four of the most common foods identified during the household survey were sampled at the retail (n = 98) and supply/production (n = 67) levels. All collected samples were transported at 4ºC for processing at the International Livestock Research Institute (ILRI, Nairobi) laboratories. Details of the participant recruitment and sample collection are provided in the Supplementary Methods (File S1) and are described elsewhere [11].

Isolation, identification and pathotyping of E. coli

Stool samples from children and livestock fecal samples were directly plated on MacConkey agar (BD Difco) and sorbitol MacConkey agar supplemented with cefixime tellurite (CT-SMAC) (Oxoid, UK) to isolate *E. coli* [11]. However, food samples were pre-enriched in buffered peptone water (BPW) (Oxoid, UK) and modified buffered peptone water with pyruvate (mBPWp) (Oxoid, UK), incubated aerobically at 37°C for 18–24 h, followed by plating on MacConkey and CT-SMAC respectively. Presumptive *E. coli* colonies were confirmed using matrix-assisted laser desorption/ionization coupled to time-of-flight mass spectrometry (MALDI-TOF MS). Pathotyping into enterotoxigenic *E. coli* (ETEC), enteropathogenic *E. coli* (EPEC), enteroaggregative *E. coli* (EAEC), enteroinvasive *E. coli* (EIEC), and diffusely adherent *E. coli* (DAEC) was performed using polymerase chain reaction (PCR) targeting pathotype-specific virulence markers [12], provided in the Supplementary Methods (File S1). For non-O157 Shiga-toxin producing *E. coli* (STEC), presumptive red/pink colonies on CT-SMAC were biochemically tested using motility-indole-ornithine (MIO) media and confirmed using MALDI-TOF MS. Sorbitol fermenters were further sero-grouped into non-O157 STEC (O26, O45, O103, O111, O121 and O145) using PCR sero-group-specific virulence markers. Additionally, colorless/transparent colonies with pale brownish appearance on CT-SMAC (non-sorbitol fermenters), typical of *E. coli* O157 were tested for immunochemical reaction with O157:H7 latex reagent. Positive reactions were confirmed by MALDI-TOF MS and further tested for the presence of *stx* 1 and/or 2 and intimin (*eae*) genes by PCR.

Antimicrobial susceptibility testing

Antimicrobial susceptibility testing (AST) against nine antibiotics (Oxoid, UK), namely, ampicillin (10 µg/mL), amoxicillin/clavulanic acid (10/20 µg/mL), ceftriaxone (30 µg/mL), tetracycline (30 µg/mL), gentamicin (10 µg/mL), nalidixic acid (30 µg/mL), ciprofloxacin (5 µg/mL), chloramphenicol (30 µg/mL) and trimethoprim/sulfamethoxazole (1.25/23.75 µg/mL), was performed using the standard Kirby–Bauer disk diffusion method according to the Clinical and Laboratory Standards Institute (CLSI) guidelines [13]. The AST results were interpreted as sensitive (S), intermediate (I) or resistant (R) according to CLSI breakpoints for *Enterobacterales* - Table 2A. *E. coli* ATCC 25922 reference strain was used for quality control. Diarrheagenic *E. coli* isolates exhibiting resistance to at least one antibiotic in three or more antibiotic classes were classified as multidrug resistant (MDR). Pan–drug resistance (PDR) was defined as an isolate being resistant to all the antibiotic classes tested, while extensively drug-resistant (XDR) meant non-susceptibility to at least one agent in all but two or fewer antimicrobial classes [14]. The choice of antimicrobials for this study was determined by antimicrobial prescribing patterns for enteropathogens in the Kenya Essential Medicines List [15–20], and World Health Organisation (WHO)–recommended antimicrobials for clinically recognizable severe gastroenteritis cases [21,22].

Statistical analysis

Descriptive analysis was performed to assess the distribution of resistance phenotypes among populations. To show whether resistance patterns were significantly different across host populations, we used generalized linear models (GLM), implemented by using the “glm” function from the base package in R, with resistance to a particular antibiotic as the outcome variable and pathogen host as the predictor.

Next, we assessed the co-occurrence of AMR phenotypes using “cooccur” package (version 1.3) in R. When the probability that two AMR phenotypes would co-occur at frequency more or less than the observed was at <0.05, the AMR phenotype pair was considered to have a statistically significant positive or negative co-occurrence [23]. The co-occurrence networks were visualized using igraph in R.

A Poisson-distributed GLMM model was used to explore household-level risk factors for *E. coli* AMR phenotypes in children with antibiogram length (defined as the number of antibiotics to which an isolate was resistant) as the response variable. A separate logistic regression model was fitted for households where livestock cohabited with people, to investigate the impact of human density (calculated as the number of persons residing in a house)

and presence of animal feces within the premises on AMR carriage among the *E. coli* pathotypes. Additional predictor variables considered included livestock ownership (including ownership by immediate neighbors), presence of garbage within the compound, food type and food handling practices, and recent history of diarrhea. The 'glmer' function of the 'lme4' R package was used to conduct multilevel logistic regression analysis for risk factors of AMR presence, controlling for community health volunteer identity (CHV-ID) as random effects to account for clustering of risk factors associated with AMR in children's stool samples [24]. Univariable logistic regression was performed and all predictors with $P < 0.2$ were included in the multivariable models. A stepwise backward direction model-fitting procedure was used to refine the models. All of the analyses were performed in R version 4.2.2. Generalized variance inflation factors (GVIF) were used to assess for collinearity, and variables with GVIF > 4 were excluded from the final model. The Akaike information criterion (AIC) statistic was used as goodness-of-fit measurement on the final models to assess whether they fitted the observed data adequately using the 'ResourceSelection' package.

RESULTS

Stool samples were collected from 540 of the recruited 585 children. In addition, 859 food samples and 296 livestock fecal samples were collected. Of these, 93% (503/540), 95% (282/296) and 22% (188/859) of children's stool, livestock fecal and food samples respectively were positive for *E. coli* culture. Marker-specific pathotyping revealed a total of 274 DEC (composed of 127 from 540 children, 122 from 296 livestock and 25 from 859 foods) isolates that were subjected to antimicrobial susceptibility testing (Fig. 1). Distribution of *E. coli* pathotypes from different livestock species is provided in Table S1.

Antimicrobial resistance patterns across hosts

The predominant resistance phenotypes among DEC were trimethoprim/sulfamethoxazole, ampicillin and tetracycline at 53%, 48% and 41% respectively (Table 1, Fig. 2a). Overall, low-level resistance (< 5%) was observed against gentamicin, ciprofloxacin and ceftriaxone. Host-wise analysis revealed that DEC resistance in children isolates was higher than in livestock against all antibiotics. Resistance among children's isolates were similarly higher than that of food isolates except against ampicillin, ceftriaxone and ciprofloxacin. Of the 127 children's DEC isolates, 78% were resistant to trimethoprim/sulfamethoxazole, 72% to ampicillin, 46.5% to tetracycline and 26.8% to amoxicillin/clavulanic acid. Resistance against nalidixic acid, chloramphenicol, ceftriaxone, gentamicin and ciprofloxacin was relatively low at ≤ 11.8% (Table 1).

Of the 122 livestock DEC isolates, 41%, 32% and 17% exhibited resistance to tetracycline, trimethoprim/sulfamethoxazole and ampicillin respectively, while resistance to the other antibiotics was < 10% (Table 1). Isolates obtained from pigs and poultry exhibited significantly higher resistance to tetracycline (44-50%) than other livestock species, while trimethoprim/sulfamethoxazole resistance was highest in poultry isolates (47%) (Fig. 2b). Amongst food DEC isolates (n = 25), the common resistance phenotype was ampicillin (80%). Resistance to amoxicillin/clavulanic acid, ceftriaxone, tetracycline and trimethoprim/sulfamethoxazole ranged between 16% and 32%, while chloramphenicol and nalidixic acid resistance was < 10% among food isolates. Of the 274 DEC isolates, 30.6% (n = 84) were susceptible to all nine antibiotics tested. Livestock isolates exhibited a significantly higher proportion of pan-susceptibility (52%, n = 64/122) than human (14%, n = 18/127) and food (8%, n = 2/25) isolates. Overall, 30% (n = 82) of all 274 *E. coli* isolates were multidrug resistant (MDR), that is, resistant to ≥ 3 antibiotic classes (File S2). One food and one human isolate (both originating from the same household) were pan–drug resistant.

Antimicrobial resistance patterns were evaluated across hosts. Resistance to ampicillin, amoxicillin/clavulanic acid, trimethoprim/sulfamethoxazole and nalidixic acid was significantly different between children and livestock isolates (P <0.05), while there was a significant association in resistance to trimethoprim/sulfamethoxazole and tetracycline between children's and food isolates. Ceftriaxone resistance was significantly different between these sources (children's and livestock isolates). Between food and livestock isolates, a significant difference was exhibited for ampicillin and amoxicillin/clavulanic acid resistance, while there was a statistically significant association in tetracycline resistance (Table S2).

Co-occurrence of AMR phenotypes

Network analysis revealed two clusters: the first was ampicillin, trimethoprim/sulfamethoxazole, tetracycline, amoxicillin/clavulanic acid and chloramphenicol with pairwise co-occurrence in 7–108 isolates; the second cluster comprised nalidixic acid, ciprofloxacin, gentamicin and ceftriaxone with pairwise co-occurrence in 1–9 isolates (Fig. S1). A resistance three-way cluster backbone comprising ampicillin, trimethoprim/sulfamethoxazole and tetracycline was present in 24.8% (68/274) of the isolates (Fig. 3), drawn from 54 distinct antibiogram profiles across hosts (children n = 28; livestock n = 16, food n = 10) (Table S3). The proportion of samples exhibiting presence of the backbone antibiogram profile was highest in children (40.2%, 51/127), followed by food (12%, 3/25) and livestock (11.5%, 14/122) ($\chi^2 = 29.858$, df = 2, $P < 0.05$, adjusted for multiple comparisons). Pairwise proportion tests, adjusted for multiple testing, indicated that children had a higher proportion of backbone antibiogram profile (adjusted $P < 0.05$) compared to live-

Table 1
Antimicrobial resistance of *Escherichia coli* isolates from children, livestock and food

	Children (n = 127)	Livestock (n = 122)	Food (n = 25)	Total (N = 274)
Antibiotic	R n (%)	R n (%)	R n (%)	R n (%)
Amoxicillin/clavulanic acid	34 (26.8)	4 (3.3)	4 (16.0)	42 (15.3)
Ampicillin	92 (72.4)	21 (17.2)	20 (80.0)	133 (48.5)
Ceftriaxone	6 (4.7)	0 (0.0)	4 (16.0)	10 (3.6)
Chloramphenicol	11 (8.7)	9 (7.4)	2 (8.0)	22 (8.0)
	99 (78.0)	39 (32.0)	8 (32.0)	146 (53.3)
Trimethoprim/sulfamethoxazole				
Tetracycline	59 (46.5)	50 (41.0)	5 (20.0)	114 (41.6)
Ciprofloxacin	4 (3.1)	1 (0.8)	1 (4.0)	6 (2.2)
Nalidixic acid	15 (11.8)	2 (1.6)	2 (8.0)	19 (6.9)
Gentamicin	5 (3.9)	0 (0.0)	1 (4.0)	6 (2.2)

Abbreviation: R n, number of resistant isolates.

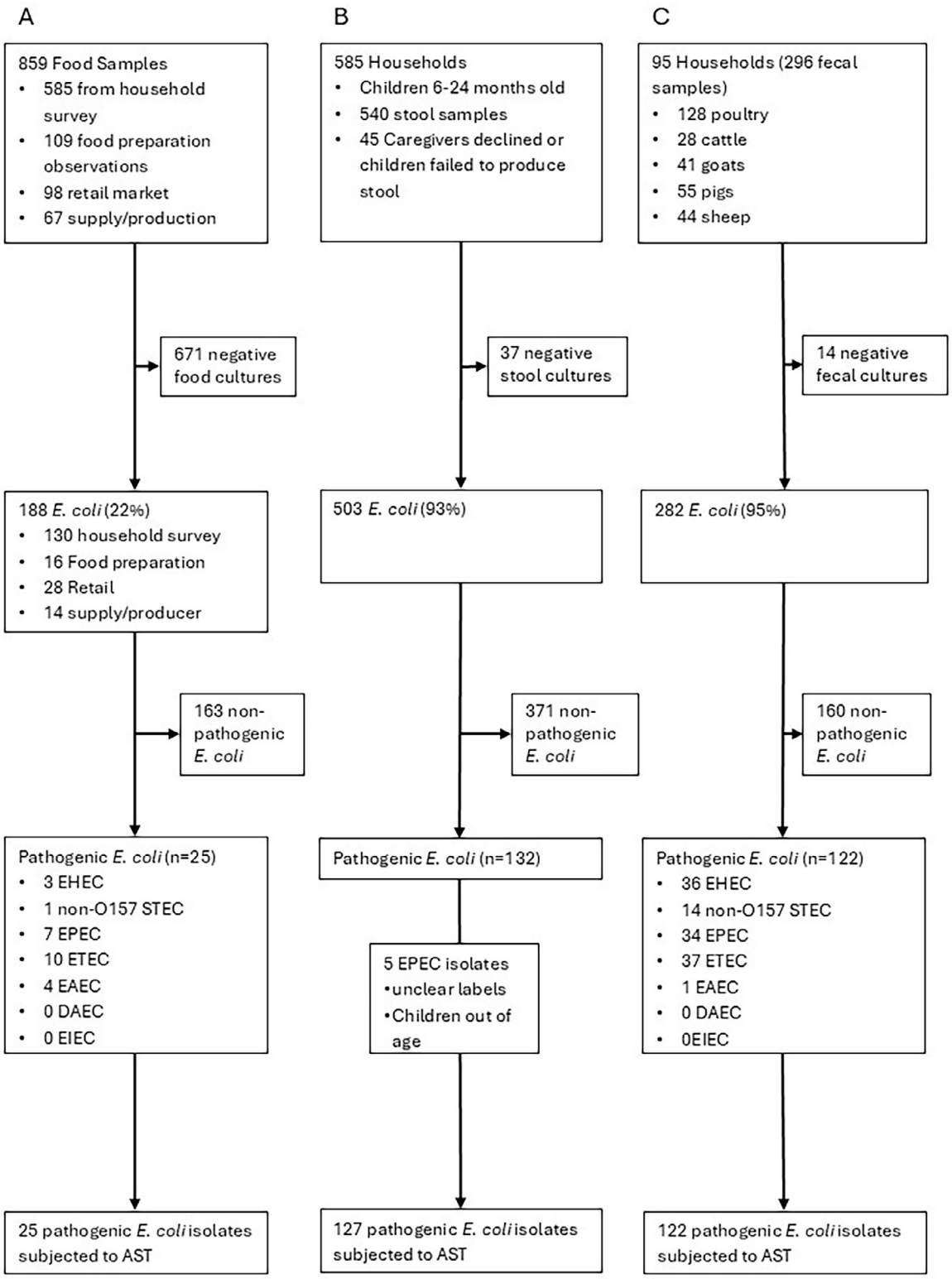

Fig. 1. Flow diagram of the number of diarrheagenic *Escherichia coli* pathotypes isolated from food and stool/fecal samples: (a) food, (b) children and (c) livestock.

stock and food, while there was no significant difference between livestock and food isolates.

Factors influencing AMR carriage in children

We investigated factors associated with AMR carriage in children in the enrolled households with the antibiogram length as the response variable (defined as the number of antibiotics against which an isolate was resistant). While no association was observed between livestock ownership and AMR carriage in children, on-site disposal of livestock manure was significantly associated with AMR carriage in children in those households where livestock co-habited with people (Table 2). On-site garbage disposal (Model 1) and recent history of diarrhea in children were significantly as-

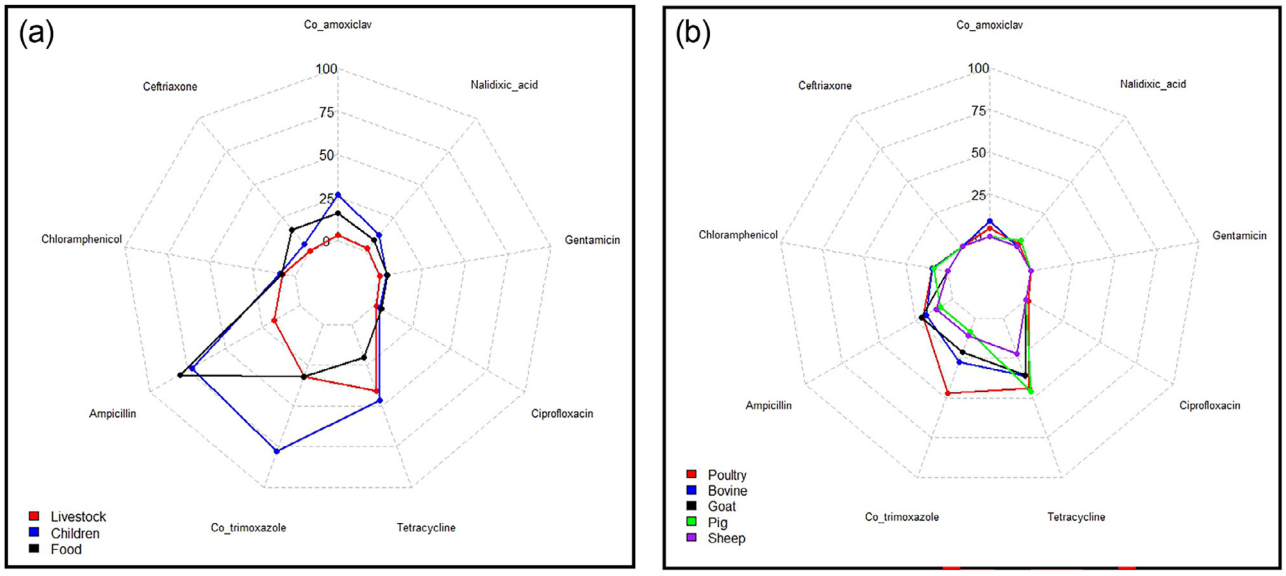

Fig. 2. Radar chart of proportions of diarrheagenic *Escherichia coli* pathotypes resistant to nine antibiotics. (a) Livestock (n = 122), children (n = 127) and food (n = 25); (b) different livestock species (n = 122).

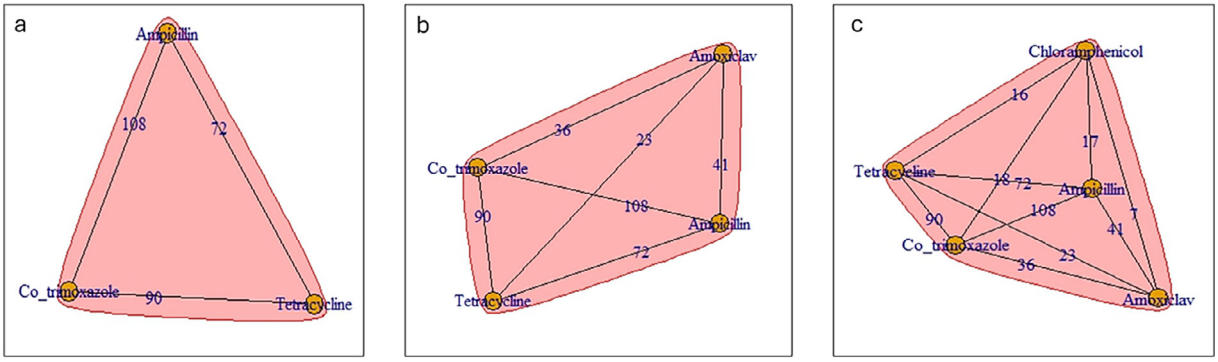

Fig. 3. Network analysis showing statistically significant antimicrobial resistance (AMR) phenotypes co-occurrence patterns amongst *E. coli* isolates (children n = 127, livestock n = 122, food n = 25). (a) Resistance backbone of tetracycline, ampicillin and co-trimoxazole; (b) threshold set at 8% to include amoxiclav; (c) threshold set at 2.5% to include chloramphenicol. The numbers between antibiotic pairs indicate the frequency of co-occurrence of AMR within isolates

Table 2
Results of two generalized Poisson mixed models investigating risk factors for carriage of antimicrobial resistance in children at the household level

Model 1 (all households)	Estimate	SE	*P* value
Garbage visible within premises	0.303	0.14	0.031*
Diarrhea in the past week	0.327	0.158	0.038*
Using utensils (spoon and fork to feed child)	0.876	0.465	0.06
Model 2 (livestock-owning households)			
Animal feces within premises	1.10	0.524	0.036*
Garbage visible within premises	−0.241	0.181	0.181
Diarrhea in the past week	0.415	0.176	0.019*

Abbreviation: SE, standard error.
* Represents statistically significant association of this variable with carriage of antimicrobial resistance in children.

sociated with AMR carriage in these children ($P < 0.05$, GLMM) (Table 2).

DISCUSSION

AMR is a substantial challenge to global health, and its impact on community-acquired infections, especially among asymptomatic children, remains a critical area of investigation [25]. The 16% prevalence of diarrheagenic *E. coli* pathotypes reported in this study is consistent with prevalence rates reported in samples collected using a One Health approach in other regions [26]. In this study, we conducted phenotypic AMR testing on diarrheagenic *E. coli* pathotypes from a diverse set of community samples, including presumptive healthy children 6–24 months old, household livestock and foods along the value chain. Third-generation cephalosporin and carbapenem-resistant *E. coli* is one of the WHO priority pathogens with public health significance [27]. Drug–pathogen combinations monitored through GLASS surveillance include penicillins, carbapenems, third- and fourth-generation cephalosporins, aminoglycosides, fluoroquinolones, tetracyclines, macrolides, polymyxins and trimethoprim/sulfamethoxazole, most of which were considered in this study. Resistance to ampicillin, trimethoprim/sulfamethoxazole and tetracycline in children was significantly higher than in livestock isolates. This may be attributed to their widespread unrestricted use in such resource-limited settings to treat diarrheal disease, much as increased resistance has been reported in the treatment of shigellosis [21]. These results are consistent with recent research findings that have underscored the increasing prevalence of AMR in community settings

in people, particularly among enteric pathogens. Noteworthy is the work by Bumbangi et al. [28], which highlighted the rising trend of multidrug resistance in community-acquired infections. Additionally, studies by Higginson et al. [29] emphasized the need for a nuanced understanding of AMR in asymptomatic carriers, shedding light on potential reservoirs for resistant strains within communities.

Nearly all of the *E. coli* isolates from food were resistant to at least one antibiotic within the panel (92%), a possible origin for the AMR reported in children. 85.8% of children isolates and 47.5% of livestock isolates were resistant to at least one antibiotic. The results of this study reveal a concerning prevalence of β-lactam combinations (AMC), penicillins and folate pathway antagonist resistance in presumptive healthy children. These results are consistent with the review by Tadesse et al. [30], which identified similar AMR phenotypes for *E. coli* from diverse settings, emphasizing the vulnerability of asymptomatic carriers to antibiotic-resistant strains. Since tetracycline is contraindicated in children [31], the observed resistance in this study could be as a result of zoonotic transfer, co-selection or cross-resistance through efflux pump [10]. The emergence of extreme multidrug-resistant strains among presumptive healthy children raises questions about the community-level factors contributing to the development and transmission of such resistant strains. Findings by Bumbangi et al. [28] on the persistence of multidrug-resistant strains in community environments provide valuable context to the results of this study, highlighting 30% multidrug resistance among *E. coli* strains in the population of children 6–24 months of age.

This study reveals variations in resistance patterns among children, livestock and food isolates in the community. Overall, isolates from children had higher AMR rates than the other hosts. This variation in AMR patterns could be due to differences in antimicrobial use in these three compartments. Although there is extensive antimicrobial use both in veterinary and human clinical medicine, previous findings have indicated a higher use in humans than veterinary practice, particularly in areas with limited resources [32]. Further, over-the-counter access and purchase of antibiotics and empiric treatment is a common practice in resource-limited community settings [33,34]. The 7.4% chloramphenicol resistance observed in livestock isolates in this study could be due to cross-resistance with chloramphenicol derivatives (florfenicol), which are widely used in livestock following the 2011 ban of chloramphenicol use in Kenya [35]. Similarly, the 0.8% ciprofloxacin resistance observed in livestock could be attributed to cross-resistance with other quinolones used in treatment of livestock (e.g., norfloxacin and enrofloxacin), considering that ciprofloxacin is not used in livestock treatment. Further, the observed fluoroquinolone resistance in children may not be associated with use, since quinolones are not prescribed in children. This ciprofloxacin and nalidixic acid resistance in children could therefore be spreading from older people or from foods [36,37].

These patterns of AMR are consistent with other studies that have demonstrated the impact of human practices and environmental factors on AMR patterns in community settings [38]. One such local practice that has been attributed to AMR in the community is unnecessary antibiotic use, further complicated by lack of published data on the amount of antibiotics consumed at the community level [39]. The high prevalence of multidrug-resistant strains among presumptive healthy children has direct clinical implications for community health. The study by Balachandra et al. [40] emphasizes the importance of considering community-specific resistance patterns in the development of targeted treatment strategies. This study, focusing on community samples, aligns with the principles of One Health approach. The significant possibility of co-carriage of AMR phenotypes between the epidemiological compartments considered in this study, as explained by the GLM models, underscores the interconnectedness of human, animal and environmental health in the context of AMR in community settings. Further, the lack of significant difference in AMR profiles between isolates originating from the two host populations (human and livestock) could be indicative of overlapping trends in use of antibiotics and their derivatives (e.g., chloramphenicol and ciprofloxacin) and of AMR acquisition from a common source or through clonal expansion. There was a significant association observed in trimethoprim/sulfamethoxazole and tetracycline resistance between human and food isolates. Trimethoprim/sulfamethoxazole resistance could be associated with use in humans, since it is largely used to treat acute gastroenteritis in children [21]. With up to 50% excreted unchanged in urine, this may end up in foods, including those of animal origin [41]. Use of tetracycline in animal production systems may explain the observed resistance in pig- and poultry-derived isolates. Animal-derived foods may therefore spread tetracycline-resistant DEC in food and human hosts through co-selection or cross-resistance, since tetracycline is contraindicated in children [10,31].

Network analysis of co-occurrence detected clusters of antibiotics that tend to have co-occurring resistance. The backbone cluster comprising of ampicillin, trimethoprim/sulfamethoxazole and tetracycline had the strongest edge between ampicillin and trimethoprim/sulfamethoxazole highlighting frequent co-resistance. This pattern likely reflects usage trends, since these antibiotics are common in treating diarrheal diseases in children [21]. Further, the ease of over-the-counter access and empirical treatment practices in LMICs could be driving these co-occurrences [33,34]. In this peri-urban setting where livestock and humans cohabit within complex food systems, the co-occurrence of resistance particularly between ampicillin and tetracycline, indicates potential transmission of resistant bacteria across sources, emphasizing the need for a One Health approach to address AMR. This co-occurrence reduces treatment options by compromising the efficacy of first-line antibiotics commonly prescribed for diarrheal diseases. Additionally, resistance to amoxicillin/clavulanic acid and ampicillin limits the use of β-lactam–based therapies, restricting options for effective empirical treatment. The increased reliance on broader-spectrum or combination therapies for infections exacerbates AMR challenges and highlights the critical importance of implementing robust antimicrobial stewardship in such settings. Co-resistance to multiple antibiotics suggests underlying genetic linkages such as plasmids or integrons carrying multiple resistance genes, facilitating co-selection and co-acquisition. Further molecular studies are required to identify these genetic elements and to understand their role in resistance dissemination. Comparing these results with the broader literature on AMR in community samples, especially asymptomatic carriers, reinforces the need for tailored interventions to break these networks. The work of Knight et al. [42] highlights how the community dynamics affect the control of AMR pathogens, emphasizing the importance of community-wide strategies to curb the spread of resistant strains.

Risk factors associated with phenotypic AMR patterns were investigated. The results paint an interesting picture of the complex interplay between environmental factors, health indicators, and antibiotic resistance in both children and livestock at the household level. The significant association between the presence of animal feces within premises and AMR carriage in children suggests a potential route of transmission. This finding underscores the importance of maintaining hygienic conditions to mitigate the risk of antibiotic resistance [43]. Further, the association between garbage disposal within premises and AMR carriage in children highlights the role of proper waste management in reducing the spread of antibiotic resistance. This could be linked to the potential for environmental contamination contributing to resistance patterns. The increased risk of AMR carriage in children who recently had di-

arrhea is intriguing. A possible explanation for this is that over-the-counter antibiotics access through self-medication or improper prescriptions is common in LMICs, and recent diarrheal episodes would most likely have attracted antibiotics use [33,34]. Similarly, in such low-resource settings, infections are empirically treated without performing any laboratory microbiological confirmation. This antibiotic use would alter the gut microbiota and select for resistant strains that would act as reservoirs of AMR. This consistency strengthens the argument for exploring the relationship between recent illness, alterations in gut microbiota, and the acquisition or proliferation of resistance determinants. However, the lack of significant association between livestock ownership and AMR carriage challenges common assumptions. It is crucial to emphasize that the mere presence of livestock might not be the primary driver; instead, specific practices or exposures related to livestock need consideration.

In conclusion, while finding that pan-susceptible *E. coli* is increasingly uncommon in resource-limited settings where antibiotic use is largely unregulated, the observed prevalence of MDR at 30% presents a serious public health concern in this community. Although no evidence linked livestock ownership to AMR carriage in these children, indirect association could be on-site disposal of livestock feces and garbage. Healthcare professionals should examine recent diarrheal illnesses in children, as these may drive AMR. Promoting antibiotic stewardship in Kenya is particularly crucial, including implementing stricter regulations on the use of antibiotics in both human and veterinary medicine, promoting the rational use of antibiotics in clinical settings and addressing over-the-counter sales of antibiotics without prescriptions. Integrating these insights into designing a context-specific intervention within a One Health framework is crucial for breaking co-resistance networks and supporting preventive efforts to mitigate AMR in peri-urban environments. One Health interventions should include separating livestock from human dwellings, implementing or reinforcing policies for safe manure and garbage disposal to minimize environmental contamination, and strengthening diagnostic capacity at local health centers to ensure appropriate treatment of diarrhea, thereby reducing unnecessary use of broad-spectrum antibiotics.

Declarations

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Supplementary materials

Supplementary material associated with this article can be found, in the online version, at doi:10.1016/j.ijantimicag.2024.107419.

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