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REVIEW ARTICLE

Systematic review and meta-analyses of the role of drinking water sources in the environmental dissemination of antibiotic-resistant *Escherichia coli* in Africa

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ABSTRACT

Escherichia coli are pathogenic and antibiotic-resistant organisms that can spread to humans through water. However, there is sparse synthesised information on the dissemination of antibiotic-resistant *E. coli* through drinking water in Africa. This review provides an overview of the environmental spread of antimicrobial-resistant *E. coli* through drinking water in Africa. We performed a systematic review based on PRISMA guidelines, and 40 eligible studies from 12 countries were identified until June 2023. Four electronic databases (PubMed, Elsevier, AJOL, and DOAJ) were searched. Studies that employed phenotypic tests ($n = 24/40$) in identifying the bacterium outstripped those that utilised genome-based methods ($n = 13$). Of the 40 studies, nine and five, respectively, assessed the bacterium for antimicrobial resistance (AMR) phenotype and genotype. Multiple antibiotic resistance indices of 0.04–0.1 revealed a low level of antibiotic resistance. The detection of multidrug-resistant *E. coli* carrying resistance genes in certain water sources suggests that AMR-surveillance expansion should include drinking water.

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KEYWORDS
Escherichia coli; drinking water; antibiotic resistance; Africa

Introduction

Escherichia coli is ecologically dichotomous because it occupies the mammalian gastrointestinal tract, and environmental matrices such as water, sediments, and soil, otherwise referred to as secondary habitats of the bacterium (Ishii et al. 2006; Brennan et al. 2010; Lyautey et al. 2010). *Escherichia coli* living outside the gut are classified as naturalised *E. coli* because they are integral members of microbial communities in diverse environmental matrices (Ishii and Sadowsky, 2008). *Escherichia coli* is assorted by phenotypes and genotypes and has been classified into eight phylogroups (A, B1, B2, C, D, E, F, and cryptic Clade-I) based on its genomic context (Clermont et al. 2013). Genome analyses of *E. coli* showed a large open pangenome framework comprising nearly 1,500 core and 22,000 accessory genes (Rasko et al. 2008; Touchon et al. 2009; Robins-Browne et al. 2016).

The genomic diversity of the bacterium comes with adaptive qualities that permit the bacterium to withstand environmental stressors (Ishii and Sadowsky, 2008; Touchon et al. 2009; Berthe et al. 2013). Through phylogenetic associations, *E. coli's* genetic structure is linked to its ecological

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background (Touchon et al. 2020; Zhi et al. 2020; NandaKafle et al. 2021). The ability to withstand the effects of toxic substances such as antibiotics is among the adaptive characteristics developed by the bacterium (Holmes et al. 2016). The rise in antibiotic-resistant bacteria is an existential threat to global public health, especially in *E. coli*, which has the proclivity to acquire resistance features through chromosomal mutations and mobile genetic elements. The possibility of *E. coli* transferring resistance to other bacteria (Petty et al. 2014; Holmes et al. 2016; Poirel et al. 2018) only worsens the situation.

Given its enteric residence and the possibility of disseminating resistance determinants, *E. coli* enjoys the privilege of being an indicator of water fecal contamination. Although the existence of naturalised *E. coli* and the lack of validated water safety procedures cast doubt on the usefulness of *E. coli* as a fecal indicator, the World Health Organisation's drinking water quality recommendations do not exempt naturalised *E. coli* as indicator of fecal contamination (Jang et al. 2017; World Health Organization, 2017). Currently, there is no alternative to the detection of *E. coli* as a touchstone to suggest the presence of feces in the water, notwithstanding the drawbacks of grouping naturalised *E. coli* with fecal coliforms. The use of *E. coli* as a marker for fecal indicators can be beneficial because pathogenic *E. coli* has been found in the water system, as was the case with the enteropathogenic *E. coli* intimin gene, *eaeA*, detected in beach water and sediments [Ishii et al. 2014; Byappanahalli et al. 2015; Zhang et al. 2016). This understanding indicated to the fact that certain *E. coli* lineages can naturalise in the environment, posing a danger to water quality.

Moreover, *E. coli* is one of the leading causes of infection in hospitals and the community (Pitout, 2012; Ludden et al. 2019). In sub-Saharan Africa, the burden of human deaths due to bacterial infections caused by *E. coli* is disproportionately higher than those caused by either the human immunodeficiency virus (HIV) or malaria (Antimicrobial Resistance Collaborators, 2022). The overall role of drinking water sources as potential reservoirs of *E. coli* in the epidemiology of hospital infections caused by the bacterium is obscure. This challenge blurs our understanding of the actual burden of resistance, especially in less-surveilled niches where data are sparse (Ludden et al. 2019), such as drinking water. Moreover, risks associated with the use of contaminated water for drinking as a means for the spread of antibiotic-resistance genes remain to be investigated in greater detail. There are large-scale reviews on the pathogenesis, diagnostics, and clinical dimensions of pathogenic *E. coli* both in Africa and elsewhere (Kaper et al. 2004; Okeke, 2009). We aimed, through this review, to provide a snapshot of the presence of *E. coli* in drinking water sources and its implications for public health and water safety in Africa. We aimed to provide a synopsis of the current level of knowledge on the extent of the presence of *E. coli* in drinking water in several parts of the continent as a basis for further studies. We thus highlighted the need for *E. coli* antimicrobial resistance surveillance in drinking water sources to avert public health emergency in Africa.

Materials and methods

We conducted this review based on the preferred reporting items for systematic reviews and meta-analyses (PRISMA) as previously recommended (Tawfik et al. 2019).

The approach used in performing the literature search

The literature search was performed from 2013 to 2023 to cover the past decade's findings using PubMed, (https://www.nlm.nih.gov/medline/medline_overview.html), Elsevier resources (https://www.elsevier.com/solutions/sciencedirect), the Directory of Open Access Journals (DOAJ) (https://doaj.org/) and African Journals Online (https://www.ajol.info/index.php/ajol). The terms and queries used to perform the literature search are listed in Supplementary file 1S1.

Criteria for selecting research articles for the study

Inclusion criteria

Titles and abstracts were first screened before considering the full-length research articles, and those eligible were included in the study for further analysis. Research articles that reported on *E. coli* isolated from water sources intended for drinking, such as well water, borehole water, river water, streams, and spring water sources, were considered eligible for inclusion in the study. Inclusion criteria also include the use of standard laboratory methods for isolation and identification of the isolates. Studies conducted in Africa and published in English only were considered in this study.

Exclusion criteria

The study excluded articles that reported secondary data such as editorials, opinions, and letters to the editor. Moreover, articles published in journals listed in Beall's list, 2021 (regarded as predatory) were also excluded from this study. Duplicate studies were avoided by analysing the results in the Microsoft Excel 2016 version.

Data analysis and information synthesis

To explore the prospect of integrating the related studies as a single masterpiece and synthesising a comprehensive understanding of the subject, information about the first author, year of publication, country or region, source of bacterial isolates, number of samples the isolates were recovered from, means of identifying isolates, and year of sample collection were profiled and analysed in this study. In the course of the study, we prioritised studies that reported the number of *E. coli* isolates from specific sample source(s) to examine the likelihood of identifying the source(s) that contributed the most to the environmental incidence of the bacterium. To be able to perform this investigation, first, we temporarily eliminated studies that did not report the number of *E. coli* isolates obtained per source. The subsequent data were arranged in Microsoft Excel 2016, where the mean, median, range, and standard deviation (descriptive statistics) of *E. coli* counts were determined. The Kruskal – Wallis test followed by post-hoc Dunn's test that comprised multiple comparisons, effect size, test power, and outliers, with R syntax, was used to determine the test of significance of *E. coli* counts among the various water sources (https://www.statskingdom.com/kruskal-wallis). The post-hoc Dunn's multiple comparison method applied the corrected $\alpha = 0.002381$ using the Bonferroni correction method, where m = the number of tests/pairs, corrected $\alpha = \alpha/m = 0.05/21 = 0.002381$. The normality was checked based on the Shapiro – Wilk test. ($\alpha = 0.05$).

Analysis of isolates' antibiotic resistance profile

The antibiotic resistance profile of the isolates was assessed in the included reports based on the recommendations of the Clinical and Laboratory Standards Institute (CLSI, 2020). Briefly, studies that reported less than 30 *E. coli* isolates were not considered for antimicrobial resistance analysis. The results of the isolates' antibiotic resistance phenotypes were therefore obtained from the qualified studies. As previously described, the multiple antibiotic resistance (MAR) index was determined for *E. coli* isolates per study (Reverter et al. 2020). MAR was computed by dividing the total number of antibiotics tested by the total number of strains tested per antibiotic. Records of antibiotic resistance genes were obtained where available. Data were analysed in Microsoft Excel 2016.

Results

Study description

The search of the four databases produced 1,354 results. Removal of book chapters, conference materials, articles from developed countries, encyclopedic content, and abstract screening resulted

in the exclusion of 1,220 records. The resulting articles ($n = 134$) were first deduplicated; review articles and other reports published outside of Africa were also eliminated. Of the 76 studies assessed for eligibility, 40 were found eligible based on the inclusion criteria because these studies prioritised the isolation of the bacterium from water sources and were published in English (Figure 1). Information on the studies included in this review is provided in supplementary file 1S2.

Demographic and source water analysis

In this review, we observed that the highest number of studies was published in 2022 ($n = 8$), and the lowest number was published in 2013 ($n = 1$). The number of studies from 2020 to 2023 ($n = 22$) is higher than those reported earlier [2013 to 2019; $n = 19$] although the latter period is almost twice the former (Table 1). Country-level analysis revealed that South Africa has the highest number of reports ($n = 11$), followed by Uganda ($n = 6$) and Nigeria ($n = 5$). Sudan and Ethiopia ($n = 1$) had the lowest number of reports that passed the stringent eligibility criteria (Figure 2). The studies that passed the inclusion criteria by country and source of water sampling are listed in Supplementary file 1S3.

Analysis of research articles based on water sampling sources showed that approximately half of the studies ($n = 19$, 47.5%) sampled hand-dug wells compared to borehole ($n = 12$, 30%), river ($n = 9$, 22.5%) and tap ($n = 7$, 17.5%), water sources. The rest of the water sources – [streams/springs ($n = 7$)]; [packaged, stored, lake/ponds ($n = 4$)]; [rain, canals, and unclassified ($n = 3$)] – were less frequent. Analysis of point of sampling by year of sampling indicated that well, river and borehole water sources were frequently sampled and analysed for *E. coli* compared to others – rain, streams, springs, channels, lakes, ponds, tap, standpipes, and cooler water (Figure 3 and Supplementary file 1S4).

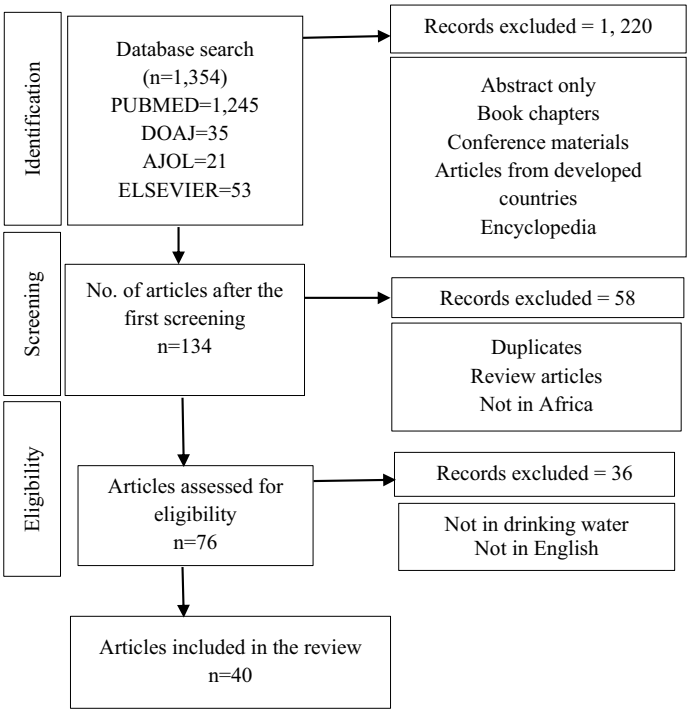

Figure 1. PRISMA diagram of article selection including exclusion and inclusion criteria.

Table 1. Sources, method of isolation, and geographical distribution of *Escherichia coli* in Africa.

Country	Sources of water sampling	No. of samples	Isolated bacterium	Method of Identification	No. of isolates	Performance of AST & Interpretation	List of references
Uganda	well	—	*E. coli*	Phenotypic test	—	NP	(Fuhrimann et al. 2015)
Uganda	sachet water, bottled, spring, and well	122	*E. coli*	PCR	—	NP	(Murphy et al. 2017)
Sierra Leone	packaged and stored	150	*E. coli*	Phenotypic test	—	NP	(Fischer et al. 2015)
Sierra Leone	standpipes and well	48	*E. coli*	Phenotypic test	—	NP	(Kamara et al. 2022)
South Africa	River	18	*E. coli*	MALDI TOF	13	Kirby-Bauer & CLSI	(Fadare et al. 2020)
South Africa	river	6	*E. coli*	VITEK® 2 System	25	Kirby-Bauer & CLSI	(Hoorzook et al. 2021)
South Africa	potable water	100	*E. coli*	16S rRNA	7	NP	(Hoosain et al. 2023)
Nigeria	well	—	*E. coli*	PCR	—	Kirby-Bauer & CLSI	(Adelowo et al. 2014)
Sudan	cooler, stored, and tap	150	*E. coli*	Multiplex PCR	45	Kirby-Bauer & CLSI	(Mahmoud et al. 2020)
South Africa	river	6	*E. coli*	Phenotypic test	—	NP	(Edokpayi et al. 2015)
South Africa	river	20	*E. coli*	API20E and PCR	—	NP	(Potgieter et al. 2020)
Ethiopia	river, rain, and well	90	*E. coli*	Phenotypic test	75	NP	(Amenu et al. 2013)
Tanzania	rivers, lakes, streams, ponds, taps & well	155	*E. coli*	*uidA* PCR	31	Kirby-Bauer & CLSI	(Lyimo et al. 0000)
Tanzania	river	96	*E. coli*	Phenotypic test	12	NP	(Nyambukah and Mihal 2021)
Ghana	boreholes, streams, rivers, canals, & well	122	*E. coli*	Phenotypic test	97	Kirby-Bauer & CLSI	(Odonkor and Addo 0000)
Ghana	boreholes, streams, rivers, canals, & well	464	*E. coli*	Phenotypic test	—	NP	(Odonkor and Mahami 0000)
Cameroon	streams, springs, boreholes, and well	—	*E. coli*	Phenotypic test	3	NP	(Ewang et al. 2021)
Nigeria	tap, borehole, river, and well	53	*E. coli*	Phenotypic test	5	NP	(Adesakin et al. 2020)
Nigeria	well	10	*E. coli*	Phenotypic test	—	NP	(Aboh et al. 2015)
Uganda	spring, channel, lake, and tap	159	*E. coli*	PCR	—	NP	(Sadik et al. 2017)
Egypt	well	216	*E. coli*	Phenotypic test	192	NP	(Salem et al. 2014)
South Africa	Borehole	24	*E. coli*	API 20E assay	—	NP	(Palamuleni and Akoth 2015)
South Africa	Rain	10	*E. coli*	16S rRNA PCR	92	NP	(Dobrowsky et al. 2014)
South Africa	rain	110	*E. coli*	PCR	100	Kirby-Bauer & CLSI	(Malema et al. 2018)
Uganda	NR	344	*E. coli*	Phenotypic test	—	NP	(Agensi et al. 0000)
Uganda	bottle and package	30	*E. coli*	Phenotypic test	—	NP	(Byonanebye et al. 2021)
Uganda	stored water	372	*E. coli*	Phenotypic test	124	NP	(Makoko and Wozei 2021)

(*Continued*)

Table 1. (Continued).

Country	Sources of water sampling	No. of samples	Isolated bacterium	Method of Identification	No. of isolates	Performance of AST & Interpretation	List of references
South Africa	stored	1867	*E. coli*	API 20E assay	—	NP	(Khabo-Mmekoa et al. 2022)
Tanzania	well, borehole and springs	67	*E. coli*	Phenotypic test	—	NP	(Elisante and Muzuka 2016)
Nigeria	well	143	*E. coli*	16S rRNA PCR	169	NP	(Odetoyin et al. 2022)
Zambia	tap, stagnant, and well	102	*E. coli*	Phenotypic test	68	NP	(Asada et al. 2022)
Ghana	Household water	49	*E. coli*	Phenotypic test	52	Kirby-Bauer & EUCAST	(Kichana et al. 2022)
Kenya	household water	27	*E. coli*	Phenotypic test	2	NP	(Okumu et al. 2022)
Zambia	borehole and well	—	*E. coli*	Phenotypic test	—	NP	(Shimamura et al. 2022)
Cameroon	borehole	46	*E. coli*	Phenotypic test	36	NP	(Ayimele et al. 2021)
South Africa	groundwater and borehole	10	*E. coli*	NR	—	NP	(Odiyo et al. 2020)
Nigeria	borehole and well	283	*E. coli*	PCR and WGS	25	Kirby-Bauer & CLSI	(Rabiu et al. 2022)
Kenya	tap, borehole, and well	9	*E. coli*	PCR and WGS	103	NP	(Nowicki et al. 2021)
Egypt	tap and well	300	*E. coli*	Phenotypic test	16	Agar diffusion & CLSI	(Fakhr et al. 2016)
South Africa	borehole and well	144	*E. coli*	PCR	141	NP	(Abia et al. 2017)

—/NR, Not Reported; NP, Not PerformedPCR, polymerase chain reactionMALDI-TOF, Matrix-assisted laser desorption/ionization time-of flightCLSI, Clinical and Laboratory Standard InstituteEUCAST, European Committee on Antimicrobial Susceptibility TestingAPI, Analytical Profile Index.

Table 2. Analysis of multiple antibiotic resistance indices for *Escherichia coli* isolates.

Country	No. of isolates	No. of antibiotics tested	No. of resistant isolates	No. of strains tested per antibiotic	MAR calculated	References
Sudan	45	6	30	270	0.1	Mahmoud et al. 2020
Tanzania	31	10	31	310	0.1	Lyimo et al. 2016
Ghana	97	14	48	1358	0.04	Odonkor and Addo, 2018
South Africa	100	12	52	1200	0.04	Malema et al. 2018
Ghana	52	8	39	416	0.1	Kichana et al. 2022

Identification and confirmation of the isolates

In this review, we describe standard microbiological methods that utilise general, selective, and differential media to isolate and identify *E. coli* as a phenotypic test, and the term phenotypic test was used in this context throughout the text. We found that more than 50% of the studies ($n = 24$) used phenotypic tests to identify the isolates while 25% ($n = 10$) of the studies used polymerase chain reaction-based identification. In two reports, high-end whole genome sequencing was used to characterise the bacterium. Analytical Profile Index (API 20E) BioMerieux was used in three studies compared to one study each that utilised matrix-assisted laser desorption/ionisation time-of-flight mass spectrometry (MALTIDOF-MS) and VITEK-2 Compact System (Additional information is available in Supplementary file 1S5).

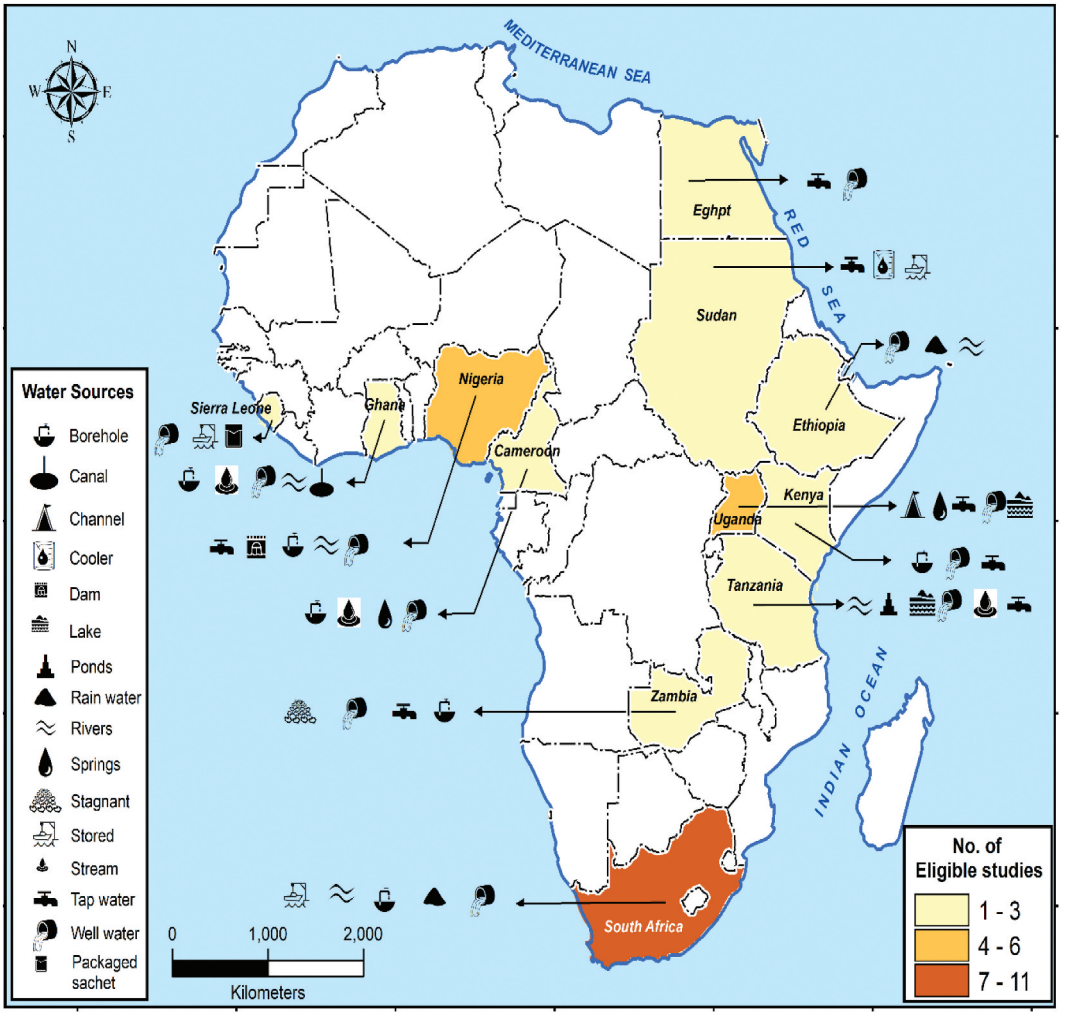

Figure 2. Spatial analysis of studies that reported *Escherichia coli* in different drinking water sources.

Antibiotic resistance phenotypes and genotypes

Interestingly, 25% of the studies assessed the isolates for antibiotic resistance phenotypes and reported resistance patterns (Supplementary file 1S6). However, only 12.5% of the studies had 30 or more isolates and were subsequently analysed in this study, with MAR between 0.04 to 0.1 (Table 2). Information on the number of isolates, name/number of antibiotics tested, number of resistant isolates, and number of strains tested per antibiotic are included as supplemental information (please see Supplementary file 1S7). Information on the ARGs was considered irrespective of the number of isolates. We note that β-lactamases, tetracycline, and sulfonamide resistance genes (ARGs) were reported by studies that passed the AST inclusion criteria (number of studies with ARGs = 6) (Supplementary file 1S8).

Determining the water source with the greatest Escherichia coli burden

The test of significance of *E. coli* counts from the various water sources yielded a p value of 0.3691 and test statistic ($H = 6.505$) such that ($P\ (x \leq 6.505) = 0.6309$). The Kruskal – Wallis H test

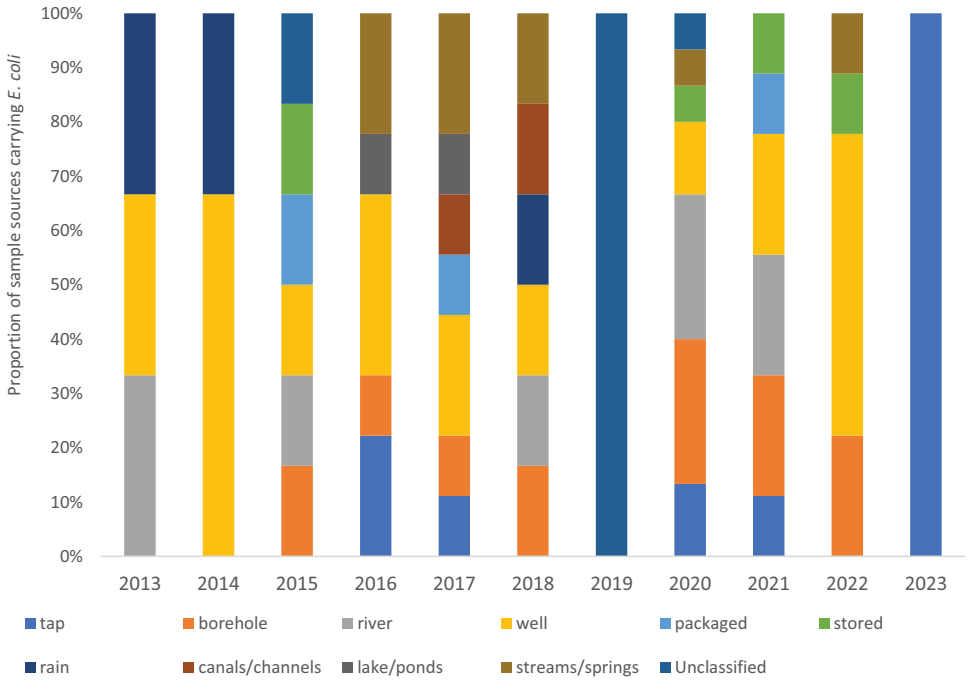

Figure 3. Point by year analysis of source water's carriage of *Escherichia coli*.

indicated an insignificant difference in the *E. coli* counts between the different groups, $\chi 2(6) = 6.5$, $p = .369$, with a mean rank score per sampling source – borehole water (6.33), household water (8.5), rainwater (16.5), river water (11.9), stored water (12.67), tap water (5) and well water (13.63). The observed effect size ($\eta^2 = 0.036$) was small and implied insignificance in the magnitude of the difference between the average values of the isolates per source (Supplementary file 1S9-1S10). The box plot extracted from the Kruskal – Wallis test is shown in Figure 4.

Discussion

In this review, we observed that *E. coli* was recovered from water sources intended for drinking and domestic purposes. Data were available in a few countries: Cameroon, Egypt, Ethiopia, Ghana, Kenya, Nigeria, Sierra Leone, Zambia, South Africa, Sudan, Tanzania, and Uganda. The absence of data in the greater part of the continent showed the lack of attention being paid to understanding the incidence of *E. coli* in drinking water environments. *Escherichia coli* were found in the environment, occurring in the soil, sediments, and water (Ishii and Sadowsky, 2008; Byappanahalli et al. 2015) and described in bacteremia and diarrheagenic and extra-intestinal infections in hospital settings (Sands et al. 2021). Investigating the source(s) that constitute the greatest pool of *E. coli* is analogous to understanding the channel of infection of the bacterium which can be disrupted by means of infection prevention and disease control.

As seen in this review, well water sources constitute the majority of supply sources. This may not be very surprising because the public water infrastructure in several parts of the continent is in a deplorable condition; this applied to Nigeria (Ojelabi et al. 2018), Uganda (Fuhrimann et al. 2015; Murphy et al. 2017), Sierra Leone (Fischer et al. 2015; Kamara et al., 2022), and South Africa (Fadare et al. 2020; Hoorzook et al. 2021; Hoosain et al. 2023). Even though alternative sources of water supply channels such as boreholes, protected springs, rain, bottled and treated tap water were also

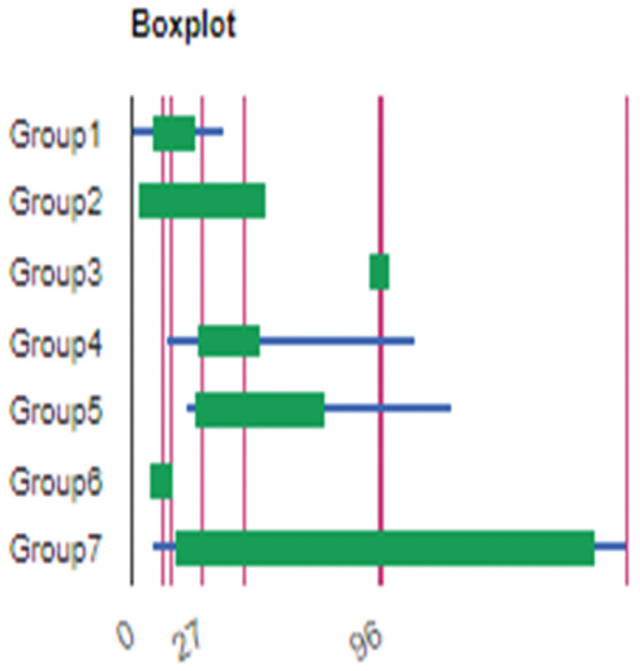

Figure 4. Boxplot analysis of *Escherichia coli* counts from different water sources ($n = 7$) generated using the Kruskal Wallis test. The borehole, household, rain, river, stored, tap, and well water corresponded respectively to Group1, Group2, Group3, Group4, Group5, Group6 and Group7. There were no significant differences in the median values of isolates irrespective of their sampling sources.

available, these sources are not as common as well water sources, most of which are shallow and unprotected (Adelowo et al. 2014; Mahmoud et al. 2020).

River water constitutes the most sourced surface water used for drinking in parts of South Africa (Edokpayi et al. 2015; Fadare et al. 2020; Potgieter et al. 2020; Hoorzook et al. 2021), Ethiopia (Amenu et al. 2013), Tanzania (Lyimo et al. 2016; Nyambukah and Mihal, 2021), Ghana (Odonkor and Addo, 2018; Odonkor and Mahami, 2020), Cameroon (Ewang et al. 2021), and Nigeria (Adesakin et al. 2020). Even though seasonal fluctuation is known to account for bacterial abundance in drinking water sources (Jang et al. 2017): well, drainage channels and rivers (Aboh et al. 2015; Sadik et al. 2017) water sources and even groundwater (Salem et al. 2014; Palamuleni and Akoth, 2015) are acquiescent to *E. coli* contamination. Rainwater may not have been frequently used compared to others due to seasonality, the detection of *E. coli* in rainwater (Dobrowsky et al. 2014; Malema et al. 2018) could be attributed to contamination during collection and storage as was the case in Kirundo Subcounty, Kisoro District, Uganda Agensi et al. 2019).

The obvious collapse of municipal water supply infrastructures in Africa became evident as only 25% of the studies ($n = 10$) collected water samples from likely treated sources such as tap, sachet, bottled and "potable" water, even though ≥ 75% of the published studies clearly indicated drinking water in their titles. Nevertheless, evidence of post water treatment recontamination was found in more than a few studies that sampled bottled or treated water (Fischer et al. 2015; Murphy et al. 2017; Mahmoud et al. 2020; Byonanebye et al. 2021) and even stored water (Makoko and Wozei, 2021; Khabo-Mmekoa et al. 2022). Poor water handling, bad water storage conditions, inadequate sanitation and poor hygiene are predictors of water recontamination, even after treatment (Agensi et al. 2019; Makoko and Wozei, 2021). Identified risk factors responsible for perennial contamination of surface water and groundwater sources are their location within a 50 m radius of sanitation facilities, direct inoculation during water abstraction, farmlands and livestock sheds, solid waste

dumps, and grazing animals (Elisante and Muzuka, 2016; Mahmoud et al. 2020; Byonanebye et al. 2021; Odetoyin et al. 2022).

In addition to the detection of *E. coli* in drinking water sources, the situation of poor water microbiological quality is more worrisome in rural communities where *Cryptosporidium* spp., rotavirus, and other microbial pathogens were found in household stored water (Asada et al. 2022; Kichana et al. 2022; Okumu et al. 2022; Shimamura et al. 2022). We observed that borehole water appeared to be safer compared to others and can be cost-effective except that borehole water sources free from fecal contamination need to be further assessed for physicochemical parameters before being certified suitable for drinking (Ayimele et al. 2020; Odiyo et al. 2020; Rabiu et al. 2022).

Twenty-five percent of the eligible studies used a polymerase chain reaction-based assay to identify *E. coli* as against the majority that used phenotypic tests. The identification of *E. coli* based on phenotypes can be confounded and unreliable because atypical *E. coli*, namely, *Enterobacter* spp., *Klebsiella* spp., and *Citrobacter* spp., also exhibit similar growth characteristics on culture media – Eosine Methylene Blue agar (Antony et al. 2016). The PCR-based method is well-suited to rapidly identify *E. coli* from sources that include water (Dobrowsky et al. 2014; Hoosain et al. 2023; Lyimo et al. 2016). Whole-genome sequencing is, however, a game-changer, as it is capable of greatly discriminating *E. coli* from the interfering microbiota. For instance, multi-locus sequence typing (MLST) and WGS data have been used for *E. coli* classification into sequence types and phylogroups (Clermont et al. 2013).

In more than 97% of the studies considered in this review, the distribution of the sequence types, and phylogroups were not available as a result of sparse published genomic data. It was consequently difficult to understand the clonal diversity of *E. coli* in household water sources on the continent, while the clonal relationships between the household water and human-derived strains could not be described. Investigators examining drinking water sources are encouraged to sequence *E. coli* isolates and perform *in silico* analyses to determine the sequence types, serotypes, and phylogroups of the bacterium to have a grasp of *E. coli* epidemiology in Africa. This will go a long way to prepare the ground for serious phylogenomic comparison of isolates' sequences targeted at establishing possible relationships between strains emanating from humans, animals, and the environment.

The fact that less than 25% of the studies included in this review profiled their isolates for antibiotic resistance pointed to the non-prioritisation of the surveillance for drug-resistant *E. coli* in the drinking water environment. Nevertheless, the findings of Malema et al. (2018) in South Africa and Subbiah et al. (2020) in northern Tanzania showed that most of the *E. coli* isolates recovered from drinking water sources were multidrug resistant because they resisted ampicillin, streptomycin, sulfamethoxazole, tetracycline, and trimethoprim. These agents are commonly included in AST (Odonkor and Addo, 2018; Kichana et al. 2022) because they are first line of antibiotics prescribed to patients that present infections to hospitals in these regions due to their affordability and presumed effectiveness. Regrettably, development of resistance to these antibiotics would compel clinicians to administer reserve antibiotics which could amplify the scale of resistance as a result of antibiotic selective pressure. Continuous exposure of susceptible individuals notably children, elderly individuals, and immuno-compromised patients to antibiotic-resistant *E. coli* can be a very serious public health issue (Subbiah et al. 2020).

In addition, few studies reported the detection of antimicrobial resistance genes, notably - bla_{TEM}, $bla_{\text{CTX-M}}$, bla_{KPC}, bla_{VIM}, bla_{IMP}, bla_{NDM}, bla_{SPM}, $bla_{\text{OXA-488 and}}$ $bla_{\text{OXA-48}}$-like genes, in water sources (Lyimo et al. 2016; Fadare et al. 2020; Mahmoud et al. 2020). The presence of these ARGs in *E. coli* from drinking water is worrisome because these genes have global spread and are known to confer resistance to beta-lactam antibiotics. This observation is likely due to the extensive use of these antibiotics in clinical settings for empirical treatment because the resisted antibiotics are commonly used in parts of Africa (Dobrowsky et al. 2014)

Two studies used WGS data to perform MLST for the delineation of *E. coli* into sequence types (Nowicki et al. 2021; Rabiu et al. 2022). Interestingly, we did not find a single study that

cross-sectionally interrogated the incidence of *E. coli* within the framework of human, animal, and plant environments (One Health). Nevertheless, the report of incidence of diarrheagenic *E. coli* in drinking water revealed water contamination either by animal or human feces (Fakhr et al. 2016; Abia et al. 2017; Fadare et al. 2020). The detection of *E. coli* diarrheagenic lineages in water intended for direct human consumption and domestic purposes suggested that these isolates possibly circulate at the human, animal and environmental interface. However, this assertion requires further genomic investigation to examine the possible relationship between *E. coli* isolates from human, animal, and drinking water sources, and to the best of our knowledge, in Africa, there is no well-tailored study focusing on this line of investigation.

We investigated the possibility of determining the water sources with the greatest burden of *E. coli* and reported that all the drinking water sources ($n = 7$) considered for the analysis had equal contribution, $\chi^2(6) = 6.5$, $p = .369$, to the incidence of the bacterium in water. This observation is however not without limitations because many studies did not indicate the sampling period, the number of samples collected, or the number of isolates recovered. The limitations made it difficult to aggregate and systematically stratify the data. Nevertheless, our findings showed that *E. coli* carrying resistance phenotypes and genotypes are embedded in several drinking water sources. As a consequence, the global surveillance for drug-resistant *E. coli* should be up-scaled to include less-surveilled niches such as drinking water in order to avert public health emergency in the continent of Africa.

To afford a comprehensive picture of antibiotic-resistant *E. coli* in drinking water in Africa, future studies prioritising drinking water examination for *E. coli* should assess the bacterium for resistance phenotype and genotype because this would significantly help to fill the knowledge gap identified in this study. We moreover recommend that *E. coli* isolates obtained from drinking water sources should be whole-genome sequenced to understand the genetic structure of the bacterium circulating in drinking water and possibly determine the actual burden of environmental reservoirs of *E. coli* lineages in Africa.

Conclusion

As a result of the deplorable water supply infrastructure in several parts of Africa, the use of surface and groundwater for drinking and domestic chores is commonplace. This development comes with an increased possibility of human acquisition of *E. coli* infections and is further exacerbated by risk factors such as poor water handling, location of pit latrines, and other poor water sanitary issues. The incidence of MDR *E. coli* isolates carrying resistance determinants in drinking water worsen the circumstance of the environmental spread of the bacterium. To prevent public health emergencies that could arise from consuming water contaminated by MDR isolates, priority attention should be given to regulations guiding the construction of wells and boreholes. We recommend that subsequent studies focusing on *E. coli* in drinking water in Africa should profile the bacterium for antibiotic resistance and use high-end techniques that can sufficiently provide a fine resolution of the bacterium. There is the need to know the genetic structure of the antibiotic-resistant *E. coli* lineages circulating in drinking water sources to predict the infection risk of the bacterium.

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Author contributions

AGR and OIF contributed to the conceptualisation and design of the systematic review, performed literature searches, data extraction and synthesis, and data interpretation, and wrote the first draft of the manuscript. AJM and MOO performed literature searches, data extraction, and synthesis, contributed to the design of the systematic review, and provided critical feedback on the manuscript. All authors contributed to the article and approved the final draft of the manuscript.

Data availability statement

The authors confirm that the data supporting the findings of this study are available within the article [and/or] its supplementary materials.

References

Abia AL, Schaefer L, Ubomba-Jaswa E, Le Roux W. 2017. Abundance of pathogenic *Escherichia coli* virulence-associated genes in well and borehole water used for domestic purposes in a peri-urban community of South Africa. Int J Environ Res Public Health. 14(3):320. doi: 10.3390/ijerph14030320.

Aboh EA, Giwa FJ, Giwa A. 2015. Microbiological assessment of well waters in Samaru, Zaria, Kaduna State, Nigeria. Annals Afr Med. 14(1):32. doi: 10.4103/1596-3519.148732.

Adelowo OO, Fagade OE, Agersø Y. 2014. Antibiotic resistance and resistance genes in *Escherichia coli* from poultry farms, southwest Nigeria. J Infect Dev Ctries. 8(9):1103–1112. doi: 10.3855/jidc.4222.

Adesakin TA, Oyewale AT, Bayero U, Mohammed AN, Aduwo IA, Ahmed PZ, Abubakar ND, Barje IB. 2020. Assessment of bacteriological quality and physico-chemical parameters of domestic water sources in Samaru community, Zaria, Northwest Nigeria. Heliyon. 6(8):e04773. doi: 10.1016/j.heliyon.2020.e04773.

Agensi A, Tibyangye J, Tamale A, Agwu E, Amongi C. Contamination potentials of household water handling and storage practices in Kirundo Sub-county, Kisoro District, Uganda. J Environ Public Health. 2019:1–8. 7932193. 10.1155/2019/7932193.

Amenu D, Menkir S, Gobena T. 2013. Assessing the bacteriological quality of drinking water from sources to household water samples of the rural communities of Dire Dawa administrative council, Eastern Ethiopia. Star. 2 (3):126–133. doi: 10.4314/star.v2i3.98750.

Antimicrobial Resistance Collaborators. 2022. Global burden of bacterial antimicrobial resistance in 2019: a systematic analysis. Lancet 12. 399(10325):629–655. doi: 10.1016/S0140-6736(21)02724-0.

Antony AC, Paul MK, Silvester R, Aneesa PA, Suresh K, Divya PS, Paul S, Fathima PA, Abdulla MH. 2016. Comparative evaluation of EMB agar and hicrome *E. coli* agar for differentiation of green metallic sheen producing non-*E. coli* and typical *E. coli* colonies from food and environmental samples. J Pure And Appl Microbiol. 10(4):1–9. doi: 10.22207/JPAM.10.4.48.

Asada Y, Chua ML, Tsurumi M, Yamauchi T, Nyambe I, Harada H. 2022. Detection of *Escherichia coli*, rotavirus, and *Cryptosporidium* spp. From drinking water, kitchenware, and flies in a peri-urban community of Lusaka, Zambia. J Water Health. 20(7):1027–1037. doi: 10.2166/wh.2022.276.

Ayimele HE, Bijingisi M, Ayonghe S. 2020. An assessment of the potability of groundwater from boreholes based on microbial quality and physical properties: case of Buea and tiko subdivisions, south west region of Cameroon. J Cam Acad Sci. 16(2):147–163. doi: 10.4314/jcas.v16i2.6.

Beall J. 2021. Beall's list of potential predatory journals and publishers. Available online at https://beallslist.net/.

Berthe T, Ratajczak M, Clermont O, Denamur E, Petit F. 2013. Evidence for the coexistence of distinct *Escherichia coli* populations in various aquatic environments and their survival in estuary water. Appl Environ Microbiol. 79 (15):4684–4693. doi: 10.1128/AEM.00698-13.

Brennan FP, Abram F, Chinalia FA, Richards KG, O'Flaherty V. 2010. Characterization of environmentally persistent *Escherichia coli* isolates leached from an Irish soil. Appl Environ Microbiol. 76(7):2175–2180. doi: 10.1128/aem.01944-09.

Byappanahalli MN, Nevers MB, Whitman RL, Ishii S. 2015. Application of a microfluidic quantitative polymerase chain reaction technique to monitor bacterial pathogens in beach water and complex environmental matrices. Environ Sci Technol Lett. 2(12):347–351. doi: 10.1021/acs.estlett.5b00251.

Byonanebye M, Kizza E, Serunjogi D. 2021. Occurrence of *Escherichia coli* in packaged drinking water distributed in Katabi sub county Uganda. A cross-sectional study. SJHR-Africa [Internet]. 2(12):6.

Clermont O, Christenson JK, Denamur E, Gordon DM. 2013. The Clermont *Escherichia coli* phyllo-typing method revisited: improvement of specificity and detection of new phylogroups. Environ Microbiol Rep. 5(1):58–65. doi: 10.1111/1758-2229.12019.

CLSI. 2020. CLSI M100-ED29: 2021 performance standards for antimicrobial susceptibility testing. 30th. Clinical and Laboratory Standards Institute, Pittsburgh. pp. 50–51.

Dobrowsky PH, van Deventer A, De Kwaadsteniet M, Ndlovu T, Khan S, Cloete TE, Khan W. 2014. Prevalence of virulence genes associated with pathogenic *Escherichia coli* strains isolated from domestically harvested rainwater during low- and high-rainfall periods. Appl Environ Microbiol. 80(5):1633–8. doi: 10.1128/AEM.03061-13.

Edokpayi JN, Odiyo JO, Msagati TA, Potgieter N. 2015. Temporal variations in physicochemical and microbiological characteristics of Mvudi river, South Africa. Int J Environ Res Public Health. 12(4):4128–4140. doi: 10.3390/ijerph120404128.

Elisante E, Muzuka ANN. 2016. Sources and seasonal variation of coliform bacteria abundance in groundwater around the slopes of Mount Meru, Arusha, Tanzania. Environ Monit Assess. 188(7):395. doi: 10.1007/s10661-016-5384-2.

Ewang ABA, Chelea M, Bonglaisin JN, Baomog BAM, Jorelle JBA, Hippolyte TM, Mbanga MRB, Ebeng SR, Marie-Chantal N, Lantum DN. 2021. The use of alternative water sources as a means of adaptation to water shortages in Nsimeyong, Yaounde city: a quality assessment. Sci Afr. ISSN 2468-2276. 13:e00861. doi: 10.1016/j.sciaf.2021.e00861.

Fadare FT, Adefisoye MA, Okoh AI, Karunasagar I. 2020. Occurrence, identification, and antibiogram signatures of selected Enterobacteriaceae from Tsomo and tyhume rivers in the Eastern Cape Province, Republic of South Africa. PloS One. 15(12):e0238084. doi: 10.1371/journal.pone.0238084.

Fakhr AE, Gohar MK, Atta AH. 2016. Impact of some ecological factors on fecal contamination of drinking water by diarrheagenic antibiotic-resistant *Escherichia coli* in Zagazig City, Egypt. Iran J Pediatr Hematol Oncol. 2016:1–9. doi: 10.1155/2016/6240703.

Fischer MB, Williams AR, Jalloh MF, Saquee G, Bain RES, Bartram JK. 2015. Microbiological and chemical quality of packaged sachet water and household stored drinking water in Freetown, Sierra Leone. PloS One. 10(7):e0131772. doi: 10.1371/journal.pone.0131772.

Fuhrimann S, Stalder M, Winkler MS, Niwagaba CB, Babu M, Masaba G, Kabatereine NB, Halage AA, Schneeberger PH, Utzinger J, et al. 2015. Microbial and chemical contamination of water, sediment, and soil in the Nakivubo wetland area in Kampala, Uganda. Environ Monit Assess. 187(7):475. doi: 10.1007/s10661-015-4689-x.

Holmes AH, Moore LS, Sundsfjord A, Steinbakk M, Regmi S, Karkey A, Guerin PJ, Piddock LJ. 2016. Understanding the mechanisms and drivers of antimicrobial resistance. Lancet 9. 387(10014):176–187. doi: 10.1016/S0140-6736(15)00473-0.

Hoorzook KB, Pieterse A, Heine L, Barnard TG, van Rensburg NJ. 2021. Soul of the Jukskei River: the extent of bacterial contamination in the Jukskei River in Gauteng Province, South Africa. Int J Environ Res Public Health. 18(16):8537. doi: 10.3390/ijerph18168537.

Hoosain N, Korsman J, Kimathi PO, Kachambwa P, Magoba R, Murray SL. 2023. AquaSens: exploring the use of 16S rRNA next-generation sequencing to determine the bacterial composition of various water matrices. Water SA. 49(2):117–125. doi: 10.17159/wsa/2023.v49.i2.3956.

Ishii S, Ksoll WB, Hicks RE, Sadowsky MJ. 2006. Presence and growth of naturalized *Escherichia coli* in temperate soils from Lake Superior watersheds. Appl Environ Microbiol. 72(1):612–621. doi: 10.1128/aem.72.1.612-621.2006.

Ishii S, Nakamura T, Ozawa S, Kobayashi A, Sano D, Okabe S. 2014. Water quality monitoring and risk assessment by simultaneous multi-pathogen quantification. Environ Sci Technol. 48(9):4744–4749. doi: 10.1021/es500578s.

Ishii S, Sadowsky MJ. 2008. *Escherichia coli* in the environment: implications for water quality and human health. Microbes Environ. 23(2):101–8. doi: 10.1264/jsme2.23.101.

Jang J, Hur HG, Sadowsky MJ, Byappanahalli MN, Yan T, Ishii S. 2017. Environmental *Escherichia coli*: ecology and public health implications-a review. J Appl Microbiol. 123(3):570–581. doi: 10.1111/jam.13468.

Kamara D, Bah D, Sesay M, Maruta A, Sesay BP, Fofanah BD, Kamara IF, Kanu JS, Lakoh S, Molleh B, et al. 2022. Evaluation of drinking water quality and bacterial antibiotic sensitivity in wells and standpipes at household water points in Freetown, Sierra Leone. Int J Environ Res Public Health. 19(11):6650. doi:10.3390/ijerph19116650.

Kaper JB, Nataro JP, Mobley HL. 2004. Pathogenic *Escherichia coli*. Nat Rev Microbiol. 2:123–140. doi: 10.1038/nrmicro818.

Khabo-Mmekoa CM, Genthe B, Momba MNB. 2022. Enteric pathogens risk factors associated with household drinking water: a case study in Ugu District Kwa-Zulu Natal Province, South Africa. Int J Environ Res Public Health. 19(8):4431. doi: 10.3390/ijerph19084431.

Kichana E, Opare-Boafoa MS, Bekoe EMO. 2022. Prevalence of multidrug-resistant *Escherichia coli* in household drinking water in rural Ghana. J Water Sanit Hyg Dev. 12(12):862–868. doi: 10.2166/washdev.2022.082.

Ludden C, Raven KE, Jamrozy D, Gouliouris T, Blane B, Coll F, de Goffau M, Naydenova P, Horner C, Hernandez-Garcia J, et al. 2019. One health genomic surveillance of *Escherichia coli* demonstrates distinct lineages and mobile genetic elements in isolates from humans versus livestock. mBio. 10:e02693–18. doi: 10.1128/mBio.02693-18.

Lyautey E, Lu Z, Lapen DR, Wilkes G, Scott A, Berkers T, Edge TA, Topp E. 2010. Distribution and diversity of *Escherichia coli* populations in the South Nation River drainage basin, eastern Ontario, Canada. Appl Environ Microbiol. 76(5):1486–1496. doi: 10.1128/AEM.02288-09.

Lyimo B, Buza J, Subbiah M, Temba S, Kipasika H, Smith W, Call DR. IncF plasmids are commonly carried by antibiotic *Escherichia coli* isolated from drinking water sources in Northern Tanzania. Iran J Pediatr Hematol Oncol. 2016:1–7. 3103672. 10.1155/2016/3103672.

Mahmoud NE, Altayb HN, Gurashi RM. 2020. Detection of carbapenem-resistant genes in *Escherichia coli* isolated from drinking water in Khartoum, Sudan. J Environ Public Health. 2020:1–6. doi: 10.1155/2020/2571293.

Makoko EW, Wozei E. 2021. Assessment of physical conditions and proposed best management practices of domestic storage tanks supplied by a water utility in a rapidly growing city. Int J Biol Chem Sci. 15(7):10–22. doi: 10.4314/ijbcs.v15i7.2S.

Malema MS, Abia ALK, Tandlich R, Zuma B, Mwenge Kahinda JM, Ubomba-Jaswa E. 2018. Antibiotic-resistant pathogenic *Escherichia coli* isolated from rooftop rainwater-harvesting tanks in the Eastern Cape, South Africa. Int J Environ Res Public Health. 15(5):892. doi: 10.3390/ijerph15050892.

Murphy JL, Kahler AM, Nansubuga I, Nanyunja EM, Kaplan B, Jothikumar N, Routh J, Gómez GA, Mintz ED, Hill VR, et al. 2017. Environmental survey of drinking water sources in Kampala, Uganda, during a typhoid fever outbreak. Appl Environ Microbiol. 83(23):e01706–17. doi:10.1128/AEM.01706-17.

NandaKafle G, Huegen T, Potgieter SC, Steenkamp E, Venter SN, Brözel VS. 2021. Niche Prefere Of Escheri Coli In a Peri-Urban Pond Ecosystem Life (Basel, Switzerland). 11(10):1020. doi:10.3390/life11101020.

Nowicki S, deLaurent ZR, de Villiers EP, Githinji G, Charles KJ. 2021. The utility of *Escherichia coli* as a contamination indicator for rural drinking water: evidence from whole genome sequencing. PloS One. 16(1): e0245910. doi: 10.1371/journal.pone.0245910.

Nyambukah R, Mihal MJ. 2021. Seasonal variability of water quality in the Zigi River, northern Tanzania. Huria Journal. 28(1):75–103.

Odetoyin B, Ogundipe O, Onanuga A. 2022. Prevalence, diversity of diarrhoeagenic *Escherichia coli* and associated risk factors in well water in Ile-Ife, Southwestern Nigeria. One Health Outlook. 4(1):3. doi: 10.1186/s42522-021-00057-4.

Odiyo JO, Mathoni MM, Makungo R. 2020. Health risks and potential sources of contamination of groundwater used by public schools in Vhuronga 1, Limpopo Province, South Africa. Int J Environ Res Public Health. 17(18):6912. doi: 10.3390/ijerph17186912.

Odonkor ST, Addo KK. Prevalence of multidrug-resistant *Escherichia coli* isolated from drinking water sources. Iran J Pediatr Hematol Oncol. 2018:1–7. 7204013. 10.1155/2018/7204013.

Odonkor ST, Mahami T. *Escherichia coli* as a tool for disease risk assessment of drinking water sources. Iran J Pediatr Hematol Oncol. 2020:1–7. 2534130. 10.1155/2020/2534130.

Ojelabi SA, Agbede OA, Wahab BA, Aiyelokun OA, Ojelabi OA. 2018. Water quality assessment of Eleyele Dam, Ibadan, South-Western, Nigeria. Civil Environ Res. 10(8):52–59.

Okeke IN. 2009. Diarrheagenic *Escherichia coli* in sub-Saharan Africa: status, uncertainties, and necessities. J Infect Dev Ctries 27. 3(11):817–842. doi: 10.3855/jidc.586.

Okumu JO, Gachohi J, Wanjihia V. 2022. Water, sanitation, and hygiene indicator levels eight years post-community-led total sanitation implementation in Kajiado County, Kenya. Afr J Health Sci. 35(2):224–240.

Palamuleni L, Akoth M. 2015. Physico-chemical and microbial analysis of selected borehole water in Mahikeng, South Africa. Int J Environ Res Public Health. 12(8):8619–8630. doi: 10.3390/ijerph120808619.

Petty NK, Ben Zakour NL, Stanton-Cook M, Skippington E, Totsika M, Forde BM, Phan MD, Gomes Moriel D, Peters KM, Davies M, et al. 2014. Global dissemination of a multidrug-resistant *Escherichia coli* clone. Proc Natl Acad Sci U S A. 111(15):5694–5699. doi: 10.1073/pnas.1322678111.

Pitout JDD. 2012. Extraintestinal pathogenic *Escherichia coli*: a combination of virulence with antibiotic resistance. Front Microbiol. 3:9. doi: 10.3389/fmicb.2012.00009.

Poirel L, Madec JY, Lupo A, Schink AK, Kieffer N, Nordmann P, Schwarz S. 2018. Antimicrobial resistance in *Escherichia coli*. Microbiol Spectr. 6(4). doi: 10.1128/microbiolspec.ARBA-0026-2017.

Potgieter N, Karambwe S, Mudau LS, Barnard T, Traore A. 2020. Human enteric pathogens in eight rivers used as rural household drinking water sources in the northern region of South Africa. Int J Environ Res Public Health. 17 (6):2079. doi: 10.3390/ijerph17062079.

Rabiu AG, Falodun OI, Fagade OE, Dada RA, Okeke IN. 2022. Potentially pathogenic *Escherichia coli* from household water in peri-urban Ibadan, Nigeria. J Water Health. 20(7):1137–1149. doi: 10.2166/wh.2022.117.

Rasko DA, Rosovitz MJ, Myers GS, Mongodin EF, Fricke WF, Gajer P, Crabtree J, Sebaihia M, Thomson NR, Chaudhuri R, et al. 2008. The pangenome structure of *Escherichia coli*: comparative genomic analysis of *E. coli* commensal and pathogenic isolates. J Bacteriol. 190(20):6881–6893. doi: 10.1128/JB.00619-08.

Reverter M, Sarter S, Caruso D, Avarre JC, Combe M, Pepey E, Pouyaud L, Vega-Heredía S, de Verdal H, Gozlan RE. 2020. Aquaculture at the crossroads of global warming and antimicrobial resistance. Nat Commun. 11(1):1–8. Internet. https://www.nature.com/articles/s41467-020-15735-6.

Robins-Browne RM, Holt KE, Ingle DJ, Hocking DM, Yang J, Tauschek M. 2016. Are *Escherichia coli* pathotypes still relevant in the era of whole-genome sequencing? Front Cell Infect Microbiol. 18(6):141. doi: 10.3389/fcimb.2016.00141.

Sadik NJ, Uprety S, Nalweyiso A, Kiggundu N, Banadda NE, Shisler JL, Nguyen TH. 2017. Quantification of multiple waterborne pathogens in drinking water, drainage channels, and surface water in Kampala, Uganda, during seasonal variation. Geohealth. 1(6):258–269. doi: 10.1002/2017GH000081.

Salem WM, Sayed WF, Damarany Kh A. 2014. Seasonal physicochemical and microbiological pollutants of potable groundwater in Qena governorate, Egypt: a case study. AJEST. 8(12):730–739.

Sands K, Carvalho MJ, Portal E, Thomson K, Dyer C, Akpulu C, Andrews R, Ferreira A, Gillespie D, Hender T, et al. 2021. Characterization of antimicrobial-resistant Gram-negative bacteria that cause neonatal sepsis in seven low- and middle-income countries. Nat Microbiol. 6(4):512–523. doi: 10.1038/s41564-021-00870-7.

Shimamura Y, Shimizutani S, Taguchi S, Yamada H. 2022. The impact of better access to improved water sources on health, schooling, and water collection of girls and boys in rural Zambia. J Dev Studies. 58(9):1750–1771. doi: 10.1080/00220388.2022.2048650.

Subbiah M, Caudell MA, Mair C, Davis MA, Matthews L, Quinlan RJ, Marsha RJ, Lyimo B, Buza J, Keyyu J, et al. 2020. Antimicrobial-resistant enteric bacteria are widely distributed amongst people, animals, and the environment in Tanzania. Nat Commun. 11(1):228. doi: 10.1038/s41467-019-13995-5.

Tawfik GM, Dila KAS, Mohamed MYF, Tam DNH, Kien ND, Ahmed AM, Huy NT. 2019. A step-by-step guide for conducting a systematic review and meta-analysis with simulation data. Trop Med Health. 1(47):46. doi: 10.1186/s41182-019-0165-6.

Touchon M, Hoede C, Tenaillon O, Barbe V, Baeriswyl S, Bidet P, Bingen E, Bonacorsi S, Bouchier C, Bouvet O, et al. 2009. Organized genome dynamics in the *Escherichia coli* species result in highly diverse adaptive paths. PloS Genet. 5(1). doi: 10.1371/journal.pgen.1000344.

Touchon M, Perrin A, de Sousa JAM, Vangchhia B, Burn S, O'Brien CL, Denamur E, Gordon D, Rocha EP. 2020. Phylogenetic background and habitat drive the genetic diversification of *Escherichia coli*. PloS Genet. 16(6):e1008866. doi: 10.1371/journal.pgen.1008866.

World Health Organization. 2017. WHO guidelines on the use of medically important antimicrobials in food-producing animals. Geneva World Health Organization. https://www.who.int/publications/i/item/9789241550130

Zhang Q, Eichmiller JJ, Staley C, Sadowsky MJ, Ishii S. 2016. Correlations between pathogen concentration and fecal indicator marker genes in beach environments. Sci Total Environ. 573:826–830. doi: 10.1016/j.scitotenv.2016.08.122.

Zhi S, Stothard P, Banting G, Scott C, Huntley K, Ryu K, Otto S, Ashbolt N, Checkley S, Dong T, et al. 2020. Characterization of water treatment-resistant and multidrug-resistant urinary pathogenic *Escherichia coli* in treated wastewater. Water Res. 182:115827. doi: 10.1016/j.watres.2020.115827.