Prevalence and epidemiological distribution of indicators of pathogenic bacteria in households drinking water in Ethiopia: a systematic review and meta-analysis

Ermias Alemayehu Adugna[1*], Abel Weldetinsae[1], Zinabu Assefa Alemu[1], Alemneh Kabeta Daba[1], Daniel Abera Dinssa[1], Tiruneh Tariku[2], Mesaye Getachew Weldegebriel[1], Melaku Gizaw Serte[1], Kirubel Tesfaye Teklu[1], Moa Abate Kenea[1], Gebretsadik Keleb Yehuala[3], Masresha Tessema[1] and Aderajew Mekonnen Girmay[1]

Abstract

Background Ensuring the availability of safe drinking water remains a critical challenge in developing countries, including Ethiopia. Therefore, this paper aimed to investigate the prevalence of fecal coliform and *E. coli* bacteria and, geographical, children availability, and seasonal exposure assessment through a meta-analysis.

Methods Two independent review groups extensively searched internet databases for English-language research articles published between 2013 and 2023. This systematic review and meta-analysis followed PRISMA guidelines. The methodological quality of each included study was evaluated using the STROBE guidelines. Publication bias was assessed by visual inspection of a funnel plot and then tested by the Egger regression test, and meta-analysis was performed using DerSimonian and Laird random-effects models with inverse variance weighting. Subgroup analyses were also conducted to explore heterogeneity.

Results Out of 48 potentially relevant studies, only 21 fulfilled the inclusion criteria and were considered for meta-analysis. The pooled prevalence of fecal coliform and *E. coli* was 64% (95% CI: 56.0–71.0%, $I^2 = 95.8$%) and 54% (95% CI: 45.7–62.3%, $I^2 = 94.2$%), respectively. Subgroup analysis revealed that the prevalence of fecal coliform bacteria increased during the wet season (70%) compared to the dry season (60%), particularly in households with under-five children (74%) compared to all households (61%), in rural (68%) versus urban (66%) areas, and in regions with high prevalence such as Amhara (71%), Gambela (71%), and Oromia (70%). Similarly, the prevalence of *E. coli* was higher in households with under-five children (66%) than in all households (46%).

Conclusions The analysis highlights the higher prevalence of fecal coliform and *E. coli* within households drinking water, indicating that these bacteria are a significant public health concern. Moreover, these findings emphasize the critical need for targeted interventions aimed at improving drinking water quality to reduce the risk of fecal contamination and enhance public health outcomes for susceptible groups, including households with under-five

*Correspondence:
Ermias Alemayehu Adugna
ermi.alex03@gmail.com

Full list of author information is available at the end of the article

children, in particular geographical areas such as the Amhara, Gambela, and Oromia regions, as well as rural areas, at point-of-use, and during the rainy season.

Registration This review was registered on PROSPERO (registration ID - CRD42023448812).

Keywords Prevalence, Fecal coliform, *E. Coli*, Ethiopia, Meta-analysis and systematic review

Introduction

An essential requirement for the health and well-being of people is access to safe drinking water. However, most of the world's population lacks access to adequate, sustainable, and safe water [1, 2]. Considering this, in 2015, the United Nations ratified different developmental goals, including the Sustainable Development Goal (SDG) 6.1, which aspires to achieve universal and equitable access to safe and affordable drinking water for all by 2030 [3]. This goal emphasizes having access to safe drinking water for every household [4]. To monitor this phenomenon, most countries, including Ethiopia, have adopted the World Health Organization's (WHO) guidelines for drinking water quality [1].

Worldwide, water-related diseases account for approximately 80% of all illnesses and diseases and, in turn, cause an estimated 505,000 diarrheal deaths each year [5]. Children are more susceptible to microbiological pollutants and develop an illness due to their immature immune systems [6]. As a result, waterborne diseases continue to be major health problems worldwide. Particularly in most developing nations where access to potable water is scarce, water-borne diseases are a serious public health concern as a result of bacterial contamination of drinking water [7]. Water-borne pathogenic bacteria could infect or harm humans by secreting toxins that could harm human tissue, living as parasites within human cells, or colonizing within the body to interfere with regular bodily processes. Numerous harmful bacteria, such as fecal coliforms, *Escherichia coli*, *Salmonella typhi*, and *Vibrio cholerae*, have been identified in water [8]. These bacteria can lead to various waterborne diseases, including cholera, typhoid, and diarrhea [5].

In developing countries, the main causes of diarrheal diseases are bacteria, protozoa, viruses, and helminths [9]. Specifically, in rural areas of most developing countries, where water sources are communally shared and exposed to several fecal-oral transmission channels within their local boundaries, *fecal* contamination of drinking water is a primary cause of water-borne diseases, including fatal diarrhea [10]. This could be detected by examining the presence of potential indicator organisms such as fecal coliforms [11, 12].

Several pathogenic bacteria can be transmitted via polluted drinking water [13, 14]. Drinking water can be polluted at the source, distribution line, and/or household level, and such polluted water can be a vehicle for several pathogens [2, 15]. In Ethiopia, poor environmental health conditions resulting from subpar water quality and inadequate hygiene and sanitation standards are responsible for more than 60% of infectious diseases [16]. Studies conducted in Ethiopia revealed that the prevalence of fecal contamination in drinking water, including *Escherichia coli* (*E. coli*), total coliforms (TC), and fecal coliforms, have been extremely high [17–22].

This could be due to many reasons, as water safety depends on various factors, from the quality of the source water to its storage and handling practices in the home [23]. Even if the source is clean, the process of collecting, transporting, storing, and drawing water in the household can all lead to fecal contamination [17]. In addition, pollutants in drinking water sources include human excreta, animal waste, effluent agricultural practices, and floods, as well as a lack of knowledge among end-users about hygiene and environmental cleanliness [17, 24]. Due to inadequate access and frequent interruptions in the piped water supply [25], drinking water is commonly stored, often for considerable lengths of time, resulting in gross contamination [26].

Therefore, understanding the extent and epidemiological variation of bacterial contamination in household drinking water is vital for policymakers and public health officials to allocate resources efficiently and target interventions effectively to reduce the burden of waterborne illnesses in Ethiopia. Despite individual studies on contamination levels, there is a notable research gap due to the lack of a national systematic review and meta-analysis. Existing research does not fully examine how contamination varies with factors such as children's availability, geographic regions, water sources, and seasonal changes. This study aims to address this gap by offering a comprehensive review and meta-analysis, providing essential insights for policymakers to effectively allocate resources and target interventions to reduce waterborne illnesses and support vulnerable groups.

Methodology

Data sources and search strategy

The review followed the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) guidelines [S1] and the protocol of this study was registered with the International Prospective Register of Systematic Reviews (PROSPERO), with protocol registration number CRD42023448812. With a focus on English-language

Adugna *et al. BMC Public Health*   (2024) 24:2511

Page 4 of 10

in Epidemiology (STROBE) guidelines [

Results

Search results

A total of 992 articles were identified from the nine databases, and an additional 14 articles were identified through additional manual searching. ree hundred forty-two studies were removed due to being duplicates found both within the same database and across di erent databases. A total of 616 studies were determined to be ineligible during title and abstract screening. At the full-text review stage, 27 articles were excluded because they did not measure microbial indicators of interest. e flow chart of the study selection process is presented in Fig. 1, generated using the PRISMA flow diagram [33].

Characteristics of the included studies

is study included 16 studies with 4,193 samples for fecal coliform [17, 34–48], and eight studies with 2,594 samples for *E. coli* analysis [38, 46, 48–53]. e main characteristics of the selected studies are summarized in the article matrix [S2]. All the articles were cross-sectional studies and followed a random sampling procedure. e articles included in the study were conducted

both fecal coliform (p⌣ 0.10) and *E. coli* (p⌣ 0.18). Moreover, no publication bias was confirmed by the 'Trim and Fill' sensitivity analysis, as we did not find any hypothetical missing studies. A leave-one-out sensitivity analysis found that excluding any single study resulted in an average variation of 1% in the pooled prevalence of fecal coliforms and 1.93% for *E. coli*, indicating no substantial

Adugna *et al. BMC Public Health*   (2024) 24:2511

Page 8 of 10

point (57.8%). Similarly, a study conducted in Bangladesh found a lower contamination rate of 28% in water samples taken from the source compared to a significantly higher contamination rate of 73.96% in samples from stored household sources (point of use) [59].   e higher pooled prevalence of contamination observed in stored household water, compared to source water, is likely due to poor storage conditions, inadequate hygiene practices, and exposure to environmental contaminants. Future research should explore how Ethiopian water management practices and infrastructure impact fecal coliform and *E. coli* prevalence to identify e ective interventions. Longitudinal studies could track changes in water quality over time. Additionally, more research in underrepresented regions is needed to understand water contamination patterns and improve policies for safer drinking water in Ethiopia.

Conclusion

 e findings of this systematic review and meta-analysis point to a higher prevalence of *E. coli*

14. WHO. Guidelines for drinking-water quality: First Addendum to the Fourth Edition. 4th ed. Geneva, Switzerland: World Health Organization; 2017b.

15. Legesse T, Dessie W, Abera F, Gobena W, Girma S, Muzeyin R, Gonfa A, Desta K. Virological and bacteriological quality of drinking water in Ethiopia. Int J Infect Dis. 2018:73. https://doi.org/10.1016/j.ijid.2018.04.3909.

16. WHO. *Water, Sanitation and Hygiene Links to Health, Facts and Figures, World Health Organization, Geneva, 2004.*

17. Amenu D, Gobena. SMT. Assessment of water handling practices among rural communities of dire dawa administrative council, dire dawa, Ethiopia. Sci

58. Bain R, Cronk R, Wright J, Yang H, Slaymaker T, Bartram J. Fecal contamination of drinking-water in low- and middle-income countries: a systematic review and meta-analysis. PLoS Med. 2014;11(5):e1001644.
59. Mahmud ZH, Islam MS, Imran KM, Worth HSAI, Ahmed M. Occurrence of Escherichia coli and faecal coliforms in drinking water at source and household point-of-use in Rohingya camps, Bangladesh. Gut Pathogens. 2019;11(1):52.

Publisher's note

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