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Microbiological Quality And Environmental Determinants Of Drinking Water Sources: A Culture-Based And Quantitative Assessment Of Fecal Indicators And Enteric Pathogens

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Abstract
Background: *Microbial contamination of drinking water remains a significant public health challenge in developing regions, contributing to waterborne infections and gastrointestinal diseases. This study assessed the microbiological quality and environmental determinants of drinking water sources in Moradabad district, Uttar Pradesh, India.*
Materials and Methods: *A cross-sectional study was conducted on 246 drinking water samples collected from urban (n=118) and rural (n=128) areas, including well water, municipal tap water, rainwater harvesting systems, and bottled water. Samples were processed using standard culture-based microbiological techniques. Quantitative bacterial load was determined by colony-forming unit (CFU/mL) estimation, and isolates were identified using Gram staining and selective biochemical methods.*
Results: *Overall, 40.7% of samples showed bacterial growth. Rural samples had significantly higher contamination (53.1%) than urban samples (27.1%) ($p<0.001$). Well water showed the highest contamination (64.7%), while bottled water had the lowest (14.8%). Gram-negative bacteria predominated (68%). Moderate bacterial load (10^2–10^3 CFU/mL) was most common. Total coliforms (23.6%) and Escherichia coli (16.7%) indicated fecal contamination. Enteric pathogens identified included Salmonella spp. (7.3%), Shigella spp. (4.9%), and Vibrio spp. (3.7%).*
Conclusion: *Drinking water sources, particularly in rural and groundwater-based settings, show significant microbial contamination, highlighting the need for improved surveillance, source protection, and water treatment interventions.*
Keywords: *Drinking Water; Water Microbiology; Coliform Bacteria; Escherichia coli; Waterborne Diseases*
Highlights
- *40.7% of drinking water samples showed microbial contamination.*
- *Rural and well water sources had significantly higher contamination rates.*
- *Fecal indicators and enteric pathogens pose substantial public health risk.*

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I. Introduction

Safe drinking water is fundamental to public health, yet microbial contamination remains a major concern in developing regions (1). Waterborne diseases continue to contribute significantly to gastrointestinal morbidity and mortality, particularly in rural and environmentally vulnerable settings (2). Fecal contamination of drinking water sources facilitates the transmission of enteric pathogens such as Salmonella, Shigella, and Vibrio species, posing serious health risks (3). Indicator organisms, particularly total coliforms and Escherichia coli, are widely used to assess microbiological safety of drinking water (4). While molecular approaches are increasingly utilized, culture-based microbiological assessment remains the standard reference method in routine surveillance due to its cost-effectiveness and reliability in pathogen detection. Environmental determinants such as rural habitation, industrial exposure, and type of water source may influence contamination levels (5). However, comprehensive analyses integrating culture-based identification, biochemical characterization, quantitative bacterial load estimation, and statistical risk evaluation remain limited (6). The present study was conducted to evaluate the microbiological quality of drinking water sources using culture-based techniques, quantify bacterial load, detect fecal indicators and specific enteric pathogens, and assess the association of contamination with geographical and environmental determinants.

II. Material And Methods

The present cross-sectional study was conducted in Moradabad district, Uttar Pradesh, India. Drinking water samples were collected from various locations across Moradabad and nearby adjoining areas to ensure representative geographical coverage. Sampling was carried out from both urban and rural regions of the district. A total of 246 drinking water samples were collected during the study period. Of these, 118 samples were obtained from urban areas and 128 samples from rural areas. Water samples were collected from multiple sources including well water, municipal tap water, rainwater harvesting systems, and bottled drinking water. Sterile, screw-capped sampling bottles were used for collection. Prior to sampling, taps were allowed to run for 2–3 minutes where applicable. All samples were labeled appropriately with details of location (urban/rural), source type, and date of collection. Samples were transported to the microbiology laboratory within 2–4 hours of collection under aseptic and temperature-controlled conditions to prevent external contamination or microbial overgrowth.

Microbiological analysis was performed in the Department of Microbiology, College of Paramedical Sciences, Teerthanker Mahaveer University (TMU), Moradabad, Uttar Pradesh, India. All samples were processed using standard culture-based microbiological techniques. All microbiological procedures were performed following standard laboratory protocols and quality control measures to ensure reliability and reproducibility of results.

III. Result

A total of 246 drinking water samples collected from urban and rural areas of Moradabad district and nearby regions were analyzed. The microbiological findings are presented below.

Overall microbiological contamination

Out of 246 samples, 100 (40.7%) showed bacterial growth, while 146 (59.3%) showed no growth (Table 1 and illustrated in Figure 1).

Table 1. Overall culture positivity among drinking water samples (n=246)

Culture result	Number (n)	Percentage (%)
Culture positive	100	40.7
No growth	146	59.3

Values expressed as number and percentage of total samples analyzed.

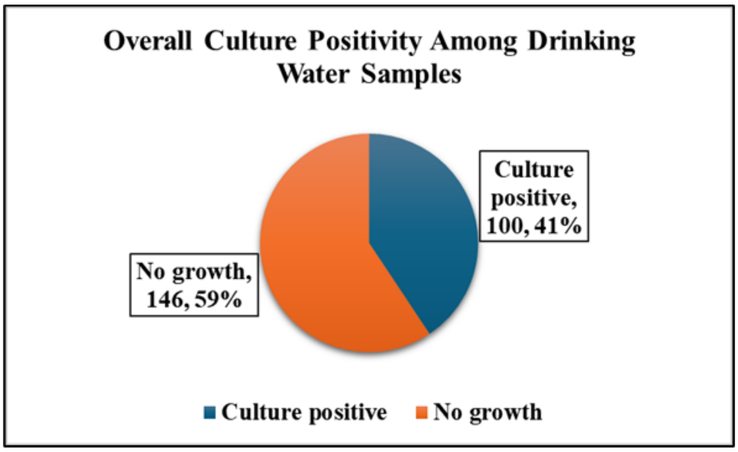

Figure 1. Overall Culture Positivity Among Drinking Water Samples (n = 246)

Distribution according to geographical area

Rural samples demonstrated significantly higher contamination compared to urban samples (Table 2). Among rural samples (n=128), 53.1% were culture positive, whereas only 27.1% of urban samples (n=118) showed contamination.

Table 2. Distribution of culture positivity according to geographical area

Area	Total samples (n)	Culture positive n (%)	Culture negative n (%)
Rural	128	68 (53.1)	60 (46.9)
Urban	118	32 (27.1)	86 (72.9)
Total	**246**	**100 (40.7)**	**146 (59.3)**

Chi-square = 15.84; $p < 0.001$; OR = 3.04 (95% CI: 1.75–5.29). Rural areas showed significantly higher odds of contamination.

Distribution according to water source

Contamination rates varied according to source type (Table 3). Well water demonstrated the highest contamination (64.7%), whereas bottled water showed the lowest (14.8%) as illustrated in Figure 2.

Table 3. Microbial Contamination According to Water Source Type

Water source	Total (n)	Culture positive n (%)
Well water	68	44 (64.7)
Rainwater harvesting	52	28 (53.8)
Municipal tap water	72	20 (27.8)
Bottled water	54	8 (14.8)
Total	**246**	**100 (40.7)**

Percentages calculated within each water source category.

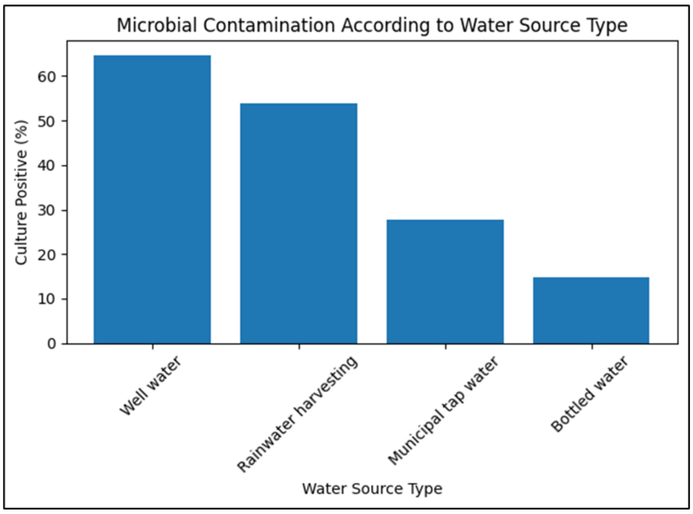

Figure 2. Microbial Contamination According to Water Source Type.

Growth on different culture media

Growth was observed most frequently on nutrient agar, followed by MacConkey agar as given in Table 4 and illustrated in Figure 3.

Table 4. Growth Distribution on Different Culture Media

Culture medium	Positive samples (n)	Percentage (%)
Nutrient agar	98	39.8
MacConkey agar	64	26.0
XLD agar	34	13.8
TCBS agar	28	11.4

Multiple media growth may occur in the same sample.

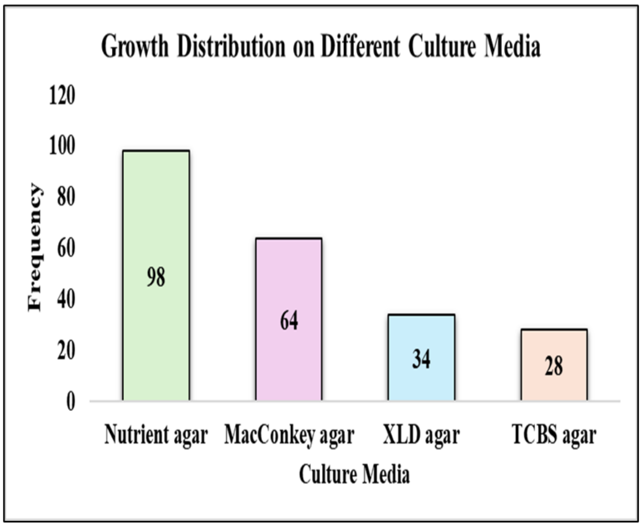

Figure 3. Growth Distribution on Different Culture Media.

Gram staining characteristics

Gram-negative organisms predominated among culture-positive isolates mention in Table 5 and illustrated in Figure 4.

Table 5. Gram staining distribution among culture-positive isolates (n=100)

Gram reaction	Number (n)	Percentage (%)
Gram-negative	**68**	**68**
Gram-positive	**32**	**32**

Percentages calculated among culture-positive isolates only.

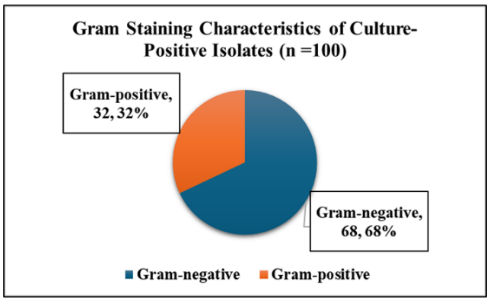

Figure 4. Gram Staining Characteristics of Culture-Positive Isolates (n = 100)

Quantitative bacterial load (CFU/ml distribution)

Quantitative analysis revealed varying degrees of contamination (Table 6). Moderate bacterial load (10^2–10^3 CFU/ml) was the most common among positive samples as illustrated in Figure 5.

Table 6. Quantitative bacterial load distribution (CFU/ml)

Bacterial load (CFU/ml)	Number (n)	Percentage (%)
No growth	146	59.3
$<10^2$	32	13.0
10^2–10^3	38	15.4
10^3–10^4	20	8.1
$>10^4$	10	4.1
Total	**246**	**100**

CFU/ml = Colony, = Colony-forming units per milliliter.

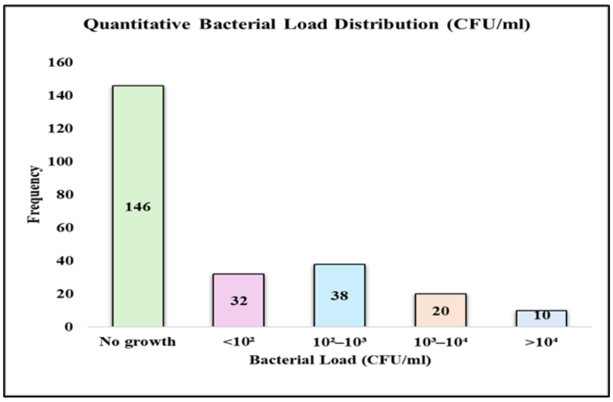

Figure 5. Quantitative Bacterial Load Distribution (CFU/ml).

Detection of fecal indicator organisms

Total coliforms were detected in 23.6% of samples, while Escherichia coli was confirmed in 16.7% (Table 7 and Figure 6).

Table 7. Detection of fecal indicator organisms

Organism detected	Number (n)	Percentage (%)
Total coliforms	58	23.6
Escherichia coli	41	16.7

Presence of *E. coli* indicates fecal contamination.

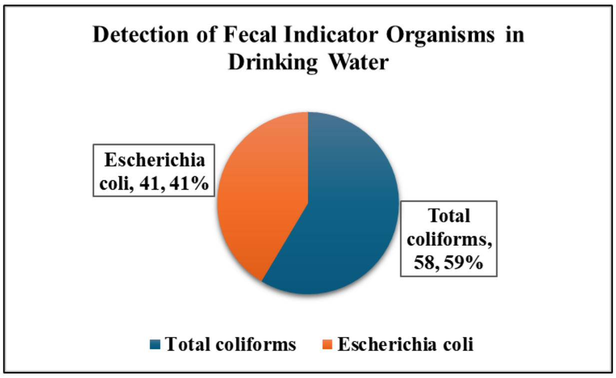

Figure 6. Detection of Fecal Indicator Organisms in Drinking Water.

Isolation of enteric pathogens

Selective culture identified enteric pathogens in a subset of samples (Table 8 and Figure 8).

Table 8. Isolation of enteric pathogens

Pathogen	Number (n)	Percentage (%)
Salmonella spp.	18	7.3
Shigella spp.	12	4.9
Vibrio spp.	9	3.7

Identification based on selective culture and biochemical characterization.

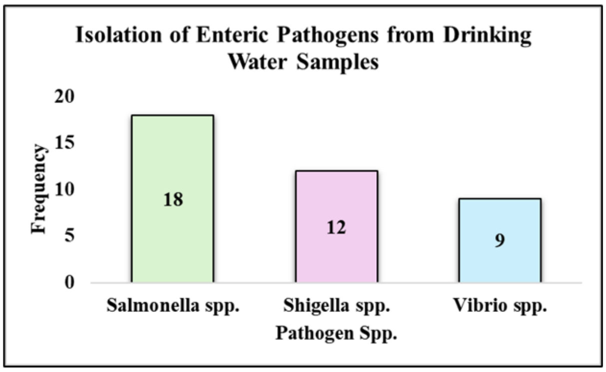

Figure 7. Isolation of Enteric Pathogens from Drinking Water Samples

IV. Discussion

The present study demonstrates substantial microbiological contamination of drinking water sources in Moradabad district, with an overall culture positivity rate of 40.7%. This finding exceeds the permissible microbiological limits recommended by the **WHO (2017)**, which stipulate zero detectable Escherichia coli per 100 mL in safe drinking water (WHO Guidelines for Drinking-water Quality, 2017; 2022 update). The observed contamination burden indicates compromised water safety and inadequate treatment or post-treatment handling practices in the study region (7). The significantly higher contamination in rural areas (53.1%) compared to urban areas (27.1%) ($p < 0.001$; OR = 3.04) aligns with previous Indian and international studies reporting increased vulnerability of rural water systems due to poor infrastructure, shallow wells, open defecation, agricultural runoff, and lack of routine chlorination. **Bain et al. (2014)** reported that rural water sources in low- and middle-income countries are disproportionately affected by fecal contamination, particularly at the point of use. (8) Similarly, a national assessment by **Mukherjee et al, (2019)** highlighted higher coliform contamination rates in rural groundwater compared to piped municipal supplies (9). Our findings are also consistent with a recent systematic review by **Li et al. (2026),** which demonstrated a significantly greater likelihood of microbial contamination in non-piped rural sources (10). Analysis by water source revealed the highest contamination in well water (64.7%), followed by rainwater harvesting (53.8%), municipal tap water (27.8%), and bottled water (14.8%). This pattern agrees with global evidence showing that unimproved groundwater and surface water sources are more susceptible to microbial contamination than treated or packaged water **Li et al., (2021)** (11)**. Kostyla et al. (2015)** found that shallow wells without secure linings frequently harbor fecal bacteria (12). Source-wise analysis revealed the highest contamination in well water (64.7%), followed by rainwater harvesting systems (53.8%), municipal tap water (27.8%), and bottled water (14.8%). These results corroborate findings by **Wright et al.**

(2004) and **Kostyla et al. (2015),** who reported that unimproved and groundwater-based sources are more susceptible to fecal contamination due to surface infiltration and inadequate protection (12,13). Although bottled water showed the lowest contamination, the presence of 14.8% positivity indicates potential lapses in storage, handling, or regulatory compliance, echoing concerns raised by **Venieri et al. (2006)** regarding microbiological safety in packaged drinking water in developing regions (14). Gram-negative organisms predominated among isolates in this study (68%), a pattern supported by recent evidence of Gram-negative E. coli and other enteric bacteria dominating drinking water contamination worldwide **(Gaihre et al., 2024; Alawi et al., 2024)** (15,16**).** Contamination with E. coli, coliforms, and other Enterobacteriaceae has been documented in tap and well water, often with antimicrobial resistance profiles indicative of fecal pollution **(Kassa et al., 2026; Nadeem et al., 2025)** (17,18). Multidrug-resistant E. coli and related organisms continue to be isolated from wastewater environments, underscoring the ongoing public health challenge posed by Gram-negative pathogens in water systems **(Abdelgalel et al., 2025)** (19). Additionally, studies on bottled water have found biofilm-forming and resistant Gram-negative bacteria, reinforcing the need for improved handling and regulatory compliance **(Shrestha et al., 2024)** (20). The quantitative bacterial load in this study (10^2–10^3 CFU/mL) aligns with evidence that moderate CFU counts in fecally contaminated drinking water represent intermediate to high risk according to WHO microbial water quality guidelines, highlighting a persistent global public health concern. Detection of total coliforms (23.6%) and Escherichia coli (16.7%) in the present study indicates significant fecal contamination and potential pathogen transmission risk. Similar prevalence has been reported in rural drinking water sources in North India by **Gautam et al. (2025)** (21)**.** A global meta-analysis by **Bain et al. (2014)** further estimated that nearly 25% of improved water sources in low-income settings are contaminated with fecal indicator bacteria (8). More recent studies also report comparable findings, including contamination of drinking and packaged water with E. coli and coliforms **(Shrestha et al., 2024; Alawi et al., 2024; Kassa et al., 2026)** (15,17,20)**.** These studies collectively support the magnitude of fecal contamination observed in the present investigation.

Importantly, selective culture identified enteric pathogens including Salmonella spp. (7.3%), Shigella spp. (4.9%), and Vibrio spp. (3.7%), indicating a direct public health threat from contaminated drinking water. These organisms are recognized as significant waterborne pathogens associated with gastrointestinal illness in unsafe water supplies **WHO, (2025)** (22). The detection of Vibrio species is particularly concerning given its documented prevalence in water environments and association with cholera and other diarrheal outbreaks in endemic regions **Awere-Duodu et al., (2025)** (23). Recent environmental microbiology studies also continue to report the occurrence of Salmonella and Shigella in contaminated water sources, underscoring their ongoing public health relevance (24). Overall, the findings of this study align with national and global evidence demonstrating that rural and groundwater-based sources are at significantly higher risk of fecal contamination. The combined qualitative and quantitative culture-based assessment strengthens the evidence for microbial risk stratification in the study area. Compared with prior studies, the relatively high prevalence of enteric pathogens in our samples underscores the urgent need for improved source protection, routine microbial surveillance, chlorination practices, and community-level hygiene interventions

V. Conclusion

The present study demonstrates a substantial burden of microbiological contamination in drinking water sources of Moradabad district, with an overall culture positivity rate of 40.7%. Rural areas exhibited significantly higher contamination compared to urban regions, and well water and rainwater harvesting systems were identified as high-risk sources. Gram-negative bacteria predominated among isolates, and fecal indicator organisms were detected in nearly one-fourth of samples. The presence of Salmonella, Shigella, and Vibrio species further indicates potential public health risk. These findings highlight the need for strengthened water quality monitoring, improved sanitation infrastructure, and regular microbiological surveillance, particularly in rural and environmentally vulnerable areas. Implementation of preventive strategies and community awareness programs is essential to reduce the risk of waterborne diseases in the region.

Declarations:

- **Ethical Approval:** Not Applicable
- **Informed Consent:** Not Applicable.
- **Conflict of Interest:** The authors declare no conflict of interest.
- **Funding:** The authors received no external funding for this study.
- **Data Availability:** Data supporting the findings of this study are available from the corresponding author upon reasonable request.
- **Author Contributions:** SB, conceptualized the study, conducted laboratory analysis, performed data interpretation, and drafted the manuscript. MF, supervised the research work, contributed to study design, critically revised the manuscript, and approved the final version for publication.

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Bibliography

[1]. Kristanti RA, Hadibarata T, Syafrudin M, Yılmaz M, Abdullah S. Microbiological Contaminants In Drinking Water: Current Status And Challenges. Water Air Soil Pollut. 2022 Jul 22;233(8):299. Doi:10.1007/S11270-022-05698-3

[2]. Yohannes L, Begna BB, Yirdaw AA, Sergindo MT, Bezie AE, Weldegebriel F, Et Al. Bacteriological Quality Of Drinking Water And Associated Factors In Alemwach Refugee Camp In Dabat District, Northwest Ethiopia. Sci Rep. 2025 Apr 18;15(1):13390. Doi:10.1038/S41598-025-96490-W

[3]. Holcomb DA, Stewart JR. Microbial Indicators Of Fecal Pollution: Recent Progress And Challenges In Assessing Water Quality. Curr Environ Health Rep. 2020;7(3):311–24. Doi:10.1007/S40572-020-00278-1 Pubmed PMID: 32542574; Pubmed Central PMCID: PMC7458903.

[4]. Motlagh AM, Yang Z. Detection And Occurrence Of Indicator Organisms And Pathogens. Water Environ Res. 2019 Oct;91(10):1402–8. Doi:10.1002/Wer.1238 Pubmed PMID: 31505073; Pubmed Central PMCID: PMC7169830.

[5]. Khodaparast M, Sharley D, Marshall S, Beddoe T. Advances In Point-Of-Care And Molecular Techniques To Detect Waterborne Pathogens. Npj Clean Water. 2024 Aug 12;7(1):74. Doi:10.1038/S41545-024-00368-9

[6]. Anh NT, Can LD, Nhan NT, Schmalz B, Luu TL. Influences Of Key Factors On River Water Quality In Urban And Rural Areas: A Review. Case Studies In Chemical And Environmental Engineering. 2023 Dec 1;8:100424. Doi:10.1016/J.Cscee.2023.100424

[7]. WHO. Guidelines For Drinking-Water Quality, 4th Edition, Incorporating The 1st Addendum [Internet]. 2017 [Cited 2026 Feb 26]. Available From: Https://Www.Who.Int/Publications/I/Item/9789241549950

[8]. 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 Medicine. 2014 May 6;11(5):E1001644. Doi:10.1371/Journal.Pmed.1001644

[9]. Mukherjee A, Duttagupta S, Chattopadhyay S, Bhanja SN, Bhattacharya A, Chakraborty S, Et Al. Impact Of Sanitation And Socio-Economy On Groundwater Fecal Pollution And Human Health Towards Achieving Sustainable Development Goals Across India From Ground-Observations And Satellite-Derived Nightlight. Sci Rep. 2019 Oct 23;9(1):15193. Doi:10.1038/S41598-019-50875-W

[10]. Li S, Wei Y, Zhou J, Li Y, Qiao L, You D, Et Al. Unsafe Drinking Water And Human Health: A Global Umbrella Review Of Disease Outcomes, Intervention Effectiveness, And Policy Implications. Cell Rep Med. 2026 Feb 4;7(2):102588. Doi:10.1016/J.Xcrm.2026.102588 Pubmed PMID: 41643660; Pubmed Central PMCID: PMC12923958.

[11]. Li P, Karunanidhi D, Subramani T, Srinivasamoorthy K. Sources And Consequences Of Groundwater Contamination. Arch Environ Contam Toxicol. 2021 Jan 1;80(1):1–10. Doi:10.1007/S00244-020-00805-Z

[12]. Kostyla C, Bain R, Cronk R, Bartram J. Seasonal Variation Of Fecal Contamination In Drinking Water Sources In Developing Countries: A Systematic Review. Science Of The Total Environment. 2015 May 1;514:333–43. Doi:10.1016/J.Scitotenv.2015.01.018

[13]. Wright J, Gundry S, Conroy R. Household Drinking Water In Developing Countries: A Systematic Review Of Microbiological Contamination Between Source And Point-Of-Use. Trop Med Int Health. 2004 Jan;9(1):106–17. Doi:10.1046/J.1365-3156.2003.01160.X Pubmed PMID: 14728614.

[14]. Venieri D, Vantarakis A, Komninou G, Papapetropoulou M. Microbiological Evaluation Of Bottled Non-Carbonated (“Still”) Water From Domestic Brands In Greece. Int J Food Microbiol. 2006 Mar 1;107(1):68–72. Doi:10.1016/J.Ijfoodmicro.2005.08.013 Pubmed PMID: 16271413.

[15]. Alawi M, Smyth C, Drissner D, Zimmerer A, Leupold D, Müller D, Et Al. Private And Well Drinking Water Are Reservoirs For Antimicrobial Resistant Bacteria. NPJ Antimicrob Resist. 2024 Mar 18;2(1):7. Doi:10.1038/S44259-024-00024-9 Pubmed PMID: 39843970; Pubmed Central PMCID: PMC11721118.

[16]. Gaihre S, Prajapati K, Dhungel S, Dawadi P, Joshi DR, Joshi TP. Occurrence Of Biofilm Forming Escherichia Coli In Drinking Water Supply System In Kathmandu. Water Environ Res. 2024 Aug;96(8):E11096. Doi:10.1002/Wer.11096 Pubmed PMID: 39135331.

[17]. Kassa DF, Bedada TL, Abera D, Getaneh A, Andaga KD, Tesema TF, Et Al. Bacteriological Quality, Antimicrobial Resistance Profile Of Escherichia Coli, And Associated Risk Factors In Tap Water, Addis Ababa, Ethiopia. Sci Rep. 2026 Feb 19. Doi:10.1038/S41598-026-40058-9

[18]. Nadeem N, Nadeem M, Bostan N, Sattar S, Simm R, Javed S. Assessment Of Water Quality And Occurrence Of Multidrug-Resistant Clinically Relevant Bacteria In Drinking Water In The Twin Cities Of Pakistan. Environ Monit Assess. 2025 Apr 12;197(5):543. Doi:10.1007/S10661-025-13989-5 Pubmed PMID: 40220188; Pubmed Central PMCID: PMC11993497.

[19]. Abdelgalel RR, Ibrahem RA, Mohamed DS, Ahmed ABF. Multidrug-Resistant E. Coli In Wastewater Sources: A Comparative Study And Identification Of Resistance Hotspots. BMC Microbiol. 2025 Aug 12;25(1):498. Doi:10.1186/S12866-025-04244-5

[20]. Shrestha S, Bista S, Byanjankar N, Prasai Joshi T. Evaluation Of Bottled Drinking Water And Occurrence Of Multidrug-Resistance And Biofilm Producing Bacteria In Nepal. Environ Pollut. 2024 Jan 15;341:122896. Doi:10.1016/J.Envpol.2023.122896 Pubmed PMID: 37944893.

[21]. Gautam B, Dar SN, Sachan RSK. A Study On Escherichia Coli Contamination In Drinking Water Sources To Combat Waterborne Diseases Effectively In Bist Doab, Punjab, India. J Water Health. 2025 Feb;23(2):155–67. Doi:10.2166/Wh.2025.267 Pubmed PMID: 40018960.

[22]. Top 10 Drinking-Water And Sanitation Related Pathogens [Internet]. [Cited 2026 Feb 27]. Available From: Https://Www.Who.Int/Publications/M/Item/Top-10-Drinking-Water-And-Sanitation-Related-Pathogens

[23]. Awere-Duodu A, Ntim OK, Donkor ES. Vibrio Cholerae In Water Environments: A Systematic Review And Meta-Analysis. Environ Microbiol Rep. 2025 Jun;17(3):E70103. Doi:10.1111/1758-2229.70103 Pubmed PMID: 40437911; Pubmed Central PMCID: PMC12120263.

[24]. Sharif N, Opu RR, Saha T, Khan A, Alzahrani FM, Alsuwat MA, Et Al. Antimicrobial Resistant Enteric Bacteria Are Widely Distributed Among Environmental Water Sources In Dhaka, Bangladesh. Npj Clean Water. 2025 Feb 26;8(1):16. Doi:10.1038/S41545-025-00447-5