Health Sciences Investigations Journal

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ISSN Online 2704-4890 ISSN Print 2720-7609

Online first publication

Perspective/Opinion

HSI Journal (2026) Volume 8 (Issue 2):1437-1441. https://doi.org/10.46829/hsijournal.2026.4.8.2.1437-1441

Potable water systems: an underexplored transmission pathway in antibiotic resistance

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Received January 2026; January 2026; Accepted February 2026

Abstract

Antimicrobial resistance (AMR) remains a critical global health threat despite advances in conventional control measures such as stewardship, surveillance, and infection prevention. Emerging evidence suggests that environmental pathways, particularly potable water systems, may represent significant conduits for AMR transmission, yet the contribution of these pathways to human infection and colonization remains underexplored. In low- and middle-income country settings, vulnerabilities and inequities in drinking water infrastructure may further amplify AMR transmission risk. Rigorous investigations integrating genomic, epidemiological, and infrastructure assessments are essential to determine the role of drinking water in human colonization and infection. Such evidence is urgently needed to inform targeted interventions, particularly for vulnerable urban populations and healthcare settings where water-mediated transmission may significantly contribute to the overall AMR burden

Keywords: Potable water, antibiotic resistance, transmission pathways, health impact, interventions

Cite the publication as Obeng-Nkrumah N, Labi A-K, Opintan JA (2026) Potable water systems: an underexplored transmission pathway in antibiotic resistance. HSI Journal 8 (1):1437-1441. https://doi.org/10.46829/hsijournal.2026.4.8.2.1437-1441

Antibiotic resistance (AMR) is widely recognized as one of the most serious global health threats of the 21st century [1, 2]. Resistance occurs when bacteria evolve mechanisms that allow them to survive exposure to antibiotics that were previously effective, making infections increasingly difficult to treat. Traditional AMR control strategies, including antimicrobial stewardship, strengthened surveillance systems, and improved infection prevention and control (IPC), have formed the foundation of global AMR response efforts [3]. While these interventions remain essential, the prevalence of resistant bacteria — both colonizing and disease-causing strains — continue to rise, particularly in low- and middle-income countries (LMICs). In many settings, interventions focused solely on conventional AMR control do not fully explain the widespread persistence of highly resistant Gram-negative bacteria. One possible explanation receiving growing attention is environmental AMR transmission [4].

Environmental drivers in AMR transmission

In several parts of sub-Saharan Africa, studies have reported a high prevalence of multidrug resistant Gram-negative bacteria among otherwise healthy individuals [5]. Many of these organisms include extended-spectrum beta-lactamase (ESBL)-producing strains, which can inactivate commonly used antibiotics and limit treatment options [6–8]. The magnitude of this carriage, observed even in populations with relatively low healthcare exposure, suggests that transmission is not driven solely by direct antibiotic use. Increasingly, this has led to consideration of environmental pathways through which resistant bacteria may persist and circulate between human populations[9, 10]. Within this environmental perspective, most research has focused on wastewater as reservoirs of AMR bacteria and genes [6, 11–13]. However, this focus has inadvertently overshadowed another potentially important pathway: potable drinking water systems. Unlike wastewater, which serves as a downstream receptor of AMR, potable water systems directly intersect with daily human consumption, hygiene, and healthcare delivery in the exposure pathway [14–16]. Yet its role in AMR transmission remains

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comparatively underexplored [15]. This represents a critical gap in our understanding of AMR human exposure. The gap is especially concerning in LMIC urban settings, where potable water systems are structurally vulnerable [17, 18].

Potable water in the AMR transmission pathway

Potable water systems function as dynamic conduits through which resistant bacteria and antibiotic resistant genes (ARG) circulate across community and healthcare environments. Within this framework, potable water systems can be conceptualized as continuous pathways of interconnected components[15, 17, 19]. At the source are reservoirs such as pipes, storage containers, and plumbing systems that provide stable habitats, where resistant bacteria persist in distribution networks. Then, within this infrastructure, amplification nodes such as biofilms formation and bacteria growth facilitate persistence and potential genetic exchange, which eventually reach humans through exposure pathways like drinking, food preparation, and clinical use. This cycle is particularly pronounced in hospital settings, where plumbing networks and tap outlets have been directly implicated in outbreaks of multidrug-resistant Gram-negative infections in intensive care and neonatal units, where patients are highly vulnerable [9, 16]. However, to date, no studies have rigorously integrated epidemiological and genomic approaches to quantify the contribution of potable water exposure to human AMR colonization and infection. This evidence gap constrains our ability to establish causal links and fully understand the relevant transmission pathways.

Emerging evidence from population level trials suggest improved access to clean water using methods such as chlorination at the point of collection leads to a reduction in diarrhoea and use of antibiotics [20, 21]. Other interventions such as the use of water filters in critical care and high dependency units of hospitals have been found to be effective in reducing healthcare-associated infections (HAI) [22–26]. Yet in many resource-constrained settings, routine microbiological monitoring of hospital water is limited or absent. As a result, the contribution of contaminated water to HAI remains insufficiently characterized, leaving an important gap in current AMR control strategies.

Inequity, infrastructure, and vulnerability

Potable water-mediated AMR transmission is not merely a microbiological issue; it is also a question of equity and infrastructure. Over 50% of all urban populations in LMICs reside in informal settlements where underlying inequities in housing and access to safe drinking water and sanitation facilities [4]. These structural vulnerabilities disproportionately affect populations already facing overcrowding, poor sanitation, and limited access to healthcare. Similar risks exist within healthcare facilities, where neonatal and intensive care patients, because of compromised immunity, are particularly susceptible to infection from environmental reservoirs. From a technical perspective, intermittent supply and cross-connections with damaged distribution networks may create negative pressure events allowing intrusion of contaminated groundwater into drinking water pipelines. Informal water markets, including tankers and vended water, further complicate quality assurance along the supply chain. At the household level, ageing infrastructure and poorly maintained storage tanks facilitate biofilm formation, providing protected niches where resistant bacteria can persist. Sub-inhibitory concentrations of antibiotic residues, disinfectants, and even heavy metals in potable water systems may also exert selective pressure that favours resistant strains and co-selects ARG. In healthcare settings, sinks, drains, and plumbing traps have been shown to harbour persistent Gram-negative organisms capable of recolonizing tap outlets despite routine cleaning. Together, these conditions can create opportunities for resistant bacteria to persist within potable water systems and circulate between environmental reservoirs and human populations. Where surveillance systems are weak and maintenance budgets constrained, these ecological niches may remain undetected. Consequently, infrastructural fragility and social inequity do not merely increase exposure; they may actively shape the microbial ecology of water systems in ways that sustain and amplify AMR. Emerging evidence supports the plausibility of such transmission pathways.

In Ghana, recent genomic studies have demonstrated overlap between resistant bacteria detected in coastal waters and those carried by humans, suggesting interconnected environmental–human transmission interfaces [6]. Several studies have also reported pathogenic bacteria of public health importance in drinking water systems [27, 28]. Yet the causal role of potable water in sustaining the spread of AMR remains largely overlooked. Addressing this gap requires moving beyond traditional AMR control strategies — focused mainly on antibiotic stewardship and interrupting person-to-person transmission — to examine how potable water systems may function as ecological pathways through which resistant pathogens circulate within human populations [19].

Water-mediated AMR interventions

Despite mounting microbiological evidence of AMR within water-supply chains, few studies have thoroughly assessed the effectiveness of interventions targeting water-mediated transmission, particularly in LMICs [29]. As Lewnard et al. [30] note in their recent *Lancet* review, there remains a "continuing need for research and innovation to overcome limitations of existing approaches" to AMR control, particularly those targeting water and sanitation. This gap reflects significant methodological and structural barriers. Establishing causal links between AMR water contamination and human infection or colonization requires longitudinal sampling, genomic analysis, and robust epidemiological designs —approaches that are resource-intensive and technically demanding. In many LMIC settings, fragmented surveillance systems, limited laboratory capacity, and weak integration between water and health sectors further constrain the generation of high-quality intervention data. Consequently, major international organizations, including the WHO [31], the World Bank [32, 33], and the Organisation for Economic Co-operation and Development (OECD) [34], have identified the paucity of water-mediated interventions studies as a significant barrier to sustainable AMR control and argue that the current lack of data is an urgent priority that must be addressed to justify the investments required. The United Nations Environment Programme (UNEP) [35] has similarly emphasized that gathering evidence on the health and financial outcomes of water-mediated AMR mitigation is essential for creating a "One Health" investment case. Collectively, these institutional positions reflect a growing consensus that sustainable AMR control must also address transmission pathways embedded in water systems for water, sanitation, and environmental systems. Responding to these calls requires integrating epidemiological, genomic, and economic data to assess whether water-focused interventions can reduce infection incidence, avert healthcare costs, and improve population-level outcomes in a measurable and policy-relevant manner.

Scientific and operational priorities for water safety in AMR control

Integration of water safety into AMR control requires both scientific and operational action. On the scientific front, a key challenge is delineating transmission direction. In some settings, contaminated water may contribute to human colonization and infection; in others, human shedding may contaminate water systems [14, 15] . The direction and magnitude of these pathways are likely context-specific, requiring specific analytical tools to decouple them. Advances in whole-genome sequencing (WGS), plasmid characterization, and metagenomic profiling provide powerful tools for assessing genetic relatedness between isolates from potable water systems and those from human carriage and clinical infections. When combined with longitudinal sampling of both water infrastructure and exposed populations in high-risk environments such as neonatal intensive care units, these approaches can help clarify when and where AMR pathogens emerge within the system, as well as the sequence of contamination events between water and the human host, thereby strengthening inference regarding potential transmission pathways.

Quantitative microbial risk assessment (QMRA) could further bridge the gap between microbiological findings and public health impact [36]. This method combines data on the concentration of resistant bacteria in water with human exposure patterns (e.g., volume of water consumed, frequency of clinical contact), QMRA models can estimate the probability of colonization or infection following exposure This provides a framework for translating laboratory detections into actionable risk estimates, helping prioritise interventions in settings where the burden is likely highest. Translating these scientific insights into policy, however, requires parallel operational action [29]. The findings from genomic and risk assessment studies can inform the design of context-specific interventions tailored to local transmission dynamics and infrastructure constraints. Proposed interventions in the literature include strategies such as improving distribution system integrity[29], enhancing chlorination[21], controlling biofilm formation[20], and deploying point-of-use filtration in high-risk hospital units[22]. Such interventions should be developed in collaboration with institutional stakeholders to guarantee feasibility and sustainability. Economic evaluation of these water-related interventions is essential to guide prioritization. Cost–benefit analyses could be used to estimate the monetary savings associated with reduced antibiotic use, shorter hospital stays, or fewer infections relative to the costs of implementing the interventions. Complementary cost–utility analyses, which express health outcomes in metrics such as disability-adjusted life-years (DALYs) [36] or quality-adjusted life-years (QALYs)[37], can assess the cost per infection averted by water-mediated interventions and support comparisons with other AMR control measures

Conclusion

Currently, the role of potable water systems in AMR transmission remains a nascent field with substantial evidence gaps. Existing evidence suggests possible epidemiological and genomic overlap between resistant bacteria detected in water systems and those found in human populations. Few studies, however, have integrated epidemiology, genomics, infrastructure assessment, and economic modelling within a unified framework. Addressing this gap is essential to strengthen causal inference, inform policy decisions, and embed potable water interventions within national AMR and WASH strategies — without overstating the strength or direction of current evidence.

DECLARATIONS

Ethical consideration

Not applicable

Consent to publish

All authors agreed on the content of the final paper.

Funding

This work received no external funding.

Competing Interest

The authors declare that there is no conflict of interest regarding the publication of this article.

Author contributions

All authors contributed to the conceptualisation, drafting, and critical revision of the manuscript. All authors reviewed and approved the final manuscript.

Acknowledgement

None

Availability of data

Not applicable.

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