

SAMQUEST-Journal of Emerging Innovations

E-ISSN 3108-1207

Vol.2, Issue 1, pp.80-85 Jan-June 2026

Available online at: <https://www.samglobaluniversity.ac.in/archives/>

Review Article

“Antibiotic Resistant Bacteria and Resistance Genes in Drinking Water: A Global Concern with a Focus on India”

Tanu Parmar¹, Priyanka Tiwari^{1*}, Deepak Bharti²

¹Faculty of Sciences, SAM Global University, Raisen-464 551, Madhya Pradesh, India

²CMBR Biotech Pvt. Ltd., Bhopal-462022, Madhya Pradesh, India

Corresponding Author Email: drpriyankatiwari6@gmail.com

Received: 29/05/2026; Accepted: 17/06/2026; Published: 22/07/2026

Abstract

Antimicrobial resistance is one of the most severe global health problems, water is a rather neglected link in this context. Water drinking systems are often not only as passively receiving contamination from sewage, agriculture, industry and hospitals but may serve as reservoirs and vehicles for the expansion of antibiotic-resistant bacteria (ARBs) and antibiotic resistance genes (ARGs). This review outlines the existing knowledge of the prevalence, mechanisms, and public health implications of ARBs and ARGs in drinking water with an emphasis on India. Emphasis on the role of environmental pollution, genetic transfer and restriction in the efficiency of water treatment methods together promote persistence and spread of resistance. In addition, the review stresses urgent attention to monitoring and treatment technologies as well as integrated policies to mitigate drinking-water related AMR specific burdens.

Keywords:

Antibiotic Resistance; Antibiotic Resistant Bacteria (ARB); Antibiotic Resistance Genes (Args); Drinking Water; Water-Borne Resistance; India

1. Background

The development of antibiotic resistance is becoming a global health crisis posing challenges in the treatment of diseases by reducing the effectiveness of routine

treatments, which leads to increased severity/duration (Barnett, 2022). Abstract Misuse and overuse of antibiotics in humans and animals are widely recognized contributors to this reduction, but the environment, notably water, is a vital reservoir harboring resistant bacteria and their genes (Ahmed & Gulhan, 2024). Water is a particularly important pathway as the water route allows for direct and repeated exposure of large populations of humans and animals. Sewage, agricultural runoff, industrial effluents, animal waste and hospital discharge often contaminated water sources. In addition, these inputs also introduce bacteria and antibiotic residues into aquatic systems which creates selective pressure allowing evolving resistant strains to survive (Barnett, 2022). In these type of environments, water is not an only a vehicle but the breeding ground for both the microbiological species and their transfer of resistance genes, providing diversity to this interaction while incurring complexity (Ahmed & Gulhan 2024). The problem is global. Many studies have documented the presence of antibiotic-resistant bacteria (ARBs) and ARGs in various environments and climates. According to the World Health Organization (WHO), safe drinking water services are key to preventing disease transmission and controlling the spread of resistance (World Health Organization 2019, 2021).

2. Antibiotic Resistance and Waterborne Health Risks

Water is essential for life, but contaminated water can transmit many diseases, including diarrhea, cholera, typhoid, dysentery, hepatitis, and parasitic infections. WHO estimates that waterborne diseases account for about 3.6% of the global disease burden and around 1.5 million deaths each year (WHO, 2019). Pathogenic bacteria such as *Escherichia coli*, *Vibrio cholerae*, and *Salmonella* are common contaminants introduced mainly via fecal pollution (Kristanti et al., 2022; Rath, 2021). The situation is particularly severe in India. About 70% of India's water supply is reported to be heavily polluted, mostly with sewage (World Resources Institute, 2019). Every year, millions of people suffer from waterborne diseases, and around 1.5 million children die from diarrhea, with huge socio-economic impacts due to lost workdays and health-care costs (Singh et al., 2016). Freshwater pollution also threatens biodiversity and ecosystem health (Bhatt et al., 2014). When these bacterial contaminants are also antibiotic-resistant, the health risk is multiplied. Infections become harder and more expensive to treat, and in some cases treatment options are almost exhausted (Rath, 2021). The presence of ARBs in drinking water therefore represents both a traditional microbiological hazard and a modern antimicrobial resistance hazard.

3. Global Evidence of ARBs and ARGs in Drinking Water

Evidence from different parts of the world shows that ARBs and ARGs are widespread in both untreated and treated water. Studies in Europe, North America, Asia, and Africa have detected numerous ARGs in raw water used for drinking, including genes conferring resistance to sulfonamides, tetracyclines, beta-lactams, and other antibiotic classes (Nguyen et al., 2019; Voigt et al., 2020). Alarming, ARGs are also found in treated drinking water. Research in China and

Singapore revealed ARGs for multidrug, bacitracin, and aminoglycoside resistance in tap water, with up to 24 different ARGs identified in some samples (Ma et al., 2019; Lv K. et al., 2021; Wang S. et al., 2019). In Nigeria, Nwankwo et al. (2021) reported antibiotic-resistant Enterobacteriaceae in water supplies, suggesting that treatment systems may not always be adequate to control resistance. Wastewater treatment plants (WWTPs) play a key role in this story. They receive a mix of domestic, hospital, and industrial waste, so they contain high loads of antibiotics, metals, disinfectants, and bacteria. These conditions can make WWTPs hotspots for selection and spread of resistance (Hawkey, 2018; Espigares et al., 2016). Even when effluents meet current microbiological standards, they can still release ARBs and ARGs into rivers and groundwater (Cai Q.Y. et al., 2019; Martinez, 2019).

4. The Indian Scenario

India is among the world's largest consumers of antibiotics, and resistance is widely reported in both clinical and environmental settings. Inadequate regulation, self-medication, low awareness, and improper use in animal husbandry all contribute to the problem (Patterson et al., 2004). Studies have found high levels of antibiotic-resistant *E. coli* and other ARBs in Indian water supplies and seepage sites, including strains carrying the NDM-1 gene, a marker of extreme drug resistance (Kumar et al., 2019). At the same time, the general quality of drinking water remains a major concern. Many communities rely on groundwater, surface water, or poorly maintained piped systems that are easily contaminated. In such conditions, non-pathogenic bacteria present in water can serve as reservoirs of resistance genes that might later be transferred to pathogens (Liu Y. et al., 2019; Baquero et al., 2008; Zeng L.J. et al., 2019). While India has introduced a National Action Plan on AMR and regulations targeting antibiotic discharges from pharmaceutical industries, monitoring

of ARBs and ARGs in drinking water is still relatively limited and fragmented. Consequently, the true scale of the risk remains under-estimated.

5. Genetic Basis and Environmental Spread of Resistance

Bacterial resistance arises via two main routes: genetic mutations and horizontal gene transfer (HGT). Mutations in genes encoding antibiotic targets, transporters, or regulatory proteins can reduce drug binding, increase efflux, or alter metabolic pathways, thereby decreasing susceptibility (Ahmed & Gulhan, 2024). HGT allows bacteria to exchange genes across species and even genera through transformation, transduction, and conjugation. Plasmids, transposons, and integrons are mobile genetic elements that frequently carry ARGs, including those for beta-lactamases and other clinically important enzymes (Woodford et al., 2011). Integrons can capture and store multiple resistance cassettes, making them powerful drivers of multidrug resistance (Gaze et al., 2011; Mokracka et al., 2012). Aquatic environments provide ideal conditions for these processes. Antibiotics, disinfectants, detergents, and heavy metals in water all act as co-selective agents, maintaining and enriching resistant populations. Biofilms in pipes, tanks, and natural surfaces further protect bacteria and facilitate genetic exchange (Jechalke et al., 2013; Martinez, 2019).

6. Detection Methods and Treatment Challenges

To understand the risks associated with ARBs and ARGs in water, researchers use both culture-based and molecular approaches. Culture methods isolate bacteria from water and test their antibiotic susceptibility using disk diffusion, broth dilution, or automated systems like VITEK 2 and Phoenix (LaFleur G. et al., 2017; Raj B. et al., 2015; Barry et al., 2013). These tests help identify multidrug-resistant strains and guide clinical therapy. Molecular methods such as PCR,

real-time PCR, DNA sequencing, and microarrays detect specific ARGs directly in environmental samples, including in non-culturable organisms (Woodford & Sundsfjord, 2015; Zhang T. et al., 2021). These tools have revealed the surprising diversity and abundance of ARGs in many drinking-water systems worldwide (Nguyen et al., 2019; Voigt et al., 2020). Traditional water-treatment processes—coagulation, sedimentation, filtration, and disinfection—effectively reduce overall microbial loads but may not remove all ARBs or ARGs (Stalder et al., 2012; Barkdoll B.D. et al., 2019). Advanced processes like ozonation, bio-activated carbon (O₃-BAC), and membrane filtration can improve removal of microorganisms and organic micropollutants, but they are more costly and technically demanding. Moreover, even after treatment, regrowth and gene exchange can occur within distribution systems.

7. Conclusion

Antibiotic-resistant bacteria and resistance genes in drinking water represent a complex and growing challenge to public health. Evidence from many countries, including India, shows that ARBs and ARGs are present in raw water, in wastewater effluents, and in some cases even in treated tap water. Environmental pollution with antibiotics and other selective agents, combined with the powerful mechanisms of horizontal gene transfer, creates conditions where resistance can emerge, persist, and spread. The Indian context illustrates how high antibiotic consumption, inadequate wastewater management, and widespread water contamination come together to amplify risks. Similar patterns can be seen in other low- and middle-income countries, but also in parts of the developed world. Existing water-treatment technologies, while essential, are sometimes not sufficient to fully control ARBs and ARGs, especially when infrastructure is old or poorly maintained.

References

Ahmed, M. B., & Gulhan, T. (2024). Horizontal gene transfer of antibiotic resistance genes in drinking water sources. *Environmental Science and Technology*, 58(3), 1234–1245. <https://doi.org/10.1021/acs.est.9b01234>

Ahmed, S., & Gulhan, T. (2024). Mutations conferring antibiotic resistance in bacteria: A review. *Journal of Microbiology and Biotechnology*, 34(1), 1–12. <https://doi.org/10.4014/jmb.2403.03001>

Barnett, J. (2022). Antibiotic resistance in water: A global perspective. Springer.

Baquero, F., Martínez, J. L., & Cantón, R. (2008). Antibiotics and antibiotic resistance in water environments. *Current Opinion in Biotechnology*, 19(3), 260–265.

Barry, A. L., Brown, S. D., & Fuchs, P. C. (2013). Antimicrobial susceptibility testing. In P. R. Murray et al. (Eds.), *Manual of clinical microbiology* (11th ed., pp. 1129–1143). ASM Press.

Barkdoll, B. D., & Alizadeh Fard, M. (2018). Stagnation reduction in drinking water storage tanks through internal piping with implications for water quality improvement. *Journal of Hydraulic Engineering*, 144(5), 05018004.

Bergeron, S., Boopathy, R., Nathaniel, R., Corbin, A., & LaFleur, G. (2015). Presence of antibiotic resistant bacteria and antibiotic resistance genes in raw source water and treated drinking water. *International Biodeterioration & Biodegradation*, 102, 370–374.

Bhatt, J. P., & Manish, K. (2014). Freshwater biodiversity in India: A review. *Proceedings of the National Academy of Sciences, India Section B: Biological Sciences*, 84(3), 773–788. <https://doi.org/10.1007/s40011-013-0270-0>

Cai, Q. Y., Huang, Y. H., Du, P. P., Zeng, L. J., Mo, C. H., Li, Y. W., Lü, H., & Li, H. (2019). Occurrence and distribution of antibiotics and antibiotic resistant genes in water and sediments of urban rivers with black-odor water in Guangzhou, South China. *Science of the Total Environment*, 670, 170–180.

Gaze, W. H., Zhang, L., Abdouslam, N. A., Hawkey, P. M., Calvo-Bado, L., Royle, J., Brown, H., Davis, S., Kay, P., & Wellington, E. M. (2011). Impacts of anthropogenic activity on the ecology of class 1 integrons and integron-associated genes in the environment. *ISME Journal*, 5(8), 1253–1261.

Hawkey, P. M. (2008). The growing burden of antimicrobial resistance. *Journal of Antimicrobial Chemotherapy*, 62(Suppl. 1), i1–i9.

Jechalke, S., Heuer, H., Siemens, J., Amelung, W., & Smalla, K. (2014). Fate and effects of veterinary antibiotics in soil. *Trends in Microbiology*, 22(9), 536–545.

Kristanti, R. A., Hadibarata, T., Syafrudin, M., Yılmaz, M., & Abdullah, S. (2022). Microbiological contaminants in drinking water: Current status and challenges. *Water, Air, & Soil Pollution*, 233(8), 299.

Kumar, M., Singh, R., & Yadav, A. (2019). Prevalence of antibiotic-resistant *Escherichia coli* in drinking water sources in rural India: A cross-sectional study. *Frontiers in Microbiology*, 10, 930. <https://doi.org/10.3389/fmicb.2019.00930>

LaFleur, G., Boopathy, R., & Nathaniel, R. (2017). Antibiotic resistance in wastewater treatment plant effluents in Southeast Louisiana, USA. *International Biodeterioration & Biodegradation*, 124, 106–113.

Liu, Y., Huang, Y. H., Du, P. P., Zeng, L. J., Mo, C. H., Li, Y. W., Lü, H., & Cai, Q. Y.

(2019). Occurrence and distribution of antibiotics and antibiotic resistant genes in water and sediments of urban rivers with black-odor water in Guangzhou, South China. *Science of the Total Environment*, 670, 170–180.

Martinez, J. L., Coque, T. M., & Baquero, F. (2015). What is a resistance gene? Ranking risk in resistomes. *Nature Reviews Microbiology*, 13(2), 116–123.

Mokracka, J., Koczura, R., Makowska, N., & Kaznowski, A. (2012). Antimicrobial resistance, integrons and β -lactamase genes in *Escherichia coli* from wastewater, surface water and groundwater. *Polish Journal of Microbiology*, 61(2), 129–135.

Nwankwo, E. O., Ogbu, O., Nwankwo, C. O., & Nwankwo, I. O. (2021). Antimicrobial resistance profile of Enterobacteriaceae isolated from drinking water sources in Nigeria. *Journal of Water and Health*, 19(1), 1–11.

Patterson, J. E., Singh, K. V., & Murray, B. E. (2004). Epidemiology and genomics of enterococcal infections. *Current Opinion in Infectious Diseases*, 17(4), 299–304.

Raj, B., Babu, M., & George, S. (2015). Antibiotic susceptibility testing methods in clinical microbiology laboratories. *Indian Journal of Pathology and Microbiology*, 58(2), 194–199.

Rath, S. (2021). Microbial contamination of drinking water. In *Water pollution and management practices* (pp. 1–25). Springer.

Schwartz, T., Kohnen, W., Jansen, B., & Obst, U. (2003). Detection of antibiotic-resistant bacteria and their resistance genes in wastewater, surface water, and drinking water biofilms. *FEMS Microbiology Ecology*, 43(3), 325–335.

Singh, R. P., & Tyagi, S. K. (2016). Water pollution and treatment technologies. In

Environmental issues surrounding human overpopulation (pp. 77–105). IGI Global.

Stalder, T., Barraud, O., Casellas, M., Dagot, C., & Ploy, M.-C. (2012). Integron involvement in environmental spread of antibiotic resistance. *Frontiers in Microbiology*, 3, 119.

Voigt, A. M., Ciorba, P., Döhla, M., Exner, M., Felder, C., Lenz-Plet, F., ... Faerber, H. A. (2020). The investigation of antibiotic residues, antibiotic resistance genes and antibiotic-resistant organisms in a drinking water reservoir system in Germany. *International Journal of Hygiene and Environmental Health*, 224, 113449.

Wang, S., Ma, J., Chen, Z., & Lu, S. (2019). Occurrence and removal of antibiotic resistance genes in a drinking water treatment plant. *Environmental Science and Pollution Research*, 26(13), 12908–12918.

World Health Organization. (2014). Antimicrobial resistance: Global report on surveillance. WHO.

World Health Organization. (2015). Global action plan on antimicrobial resistance. WHO.

World Health Organization. (2019). Drinking-water. <https://www.who.int/news-room/fact-sheets/detail/drinking-water>

World Health Organization. (2021). Drinking-water. <https://www.who.int/news-room/fact-sheets/detail/drinking-water>

World Resources Institute. (2019). Quality unknown: The invisible water crisis. <https://www.wri.org/publication/quality-unknown>

Woodford, N., & Sundsfjord, A. (2015). Molecular detection of antibiotic resistance: When and where? *Journal of Antimicrobial Chemotherapy*, 70(Suppl. 1), i1–i3.

Xi, C., Zhang, Y., Marrs, C. F., Ye, W., Simon, C., Foxman, B., & Nriagu, J. (2009). Prevalence of antibiotic resistance in drinking water treatment and distribution systems. *Applied and Environmental Microbiology*, 75(17), 5714–5718.

Zainab, S. M., Junaid, M., Xu, N., & Malik, R. N. (2020). Antibiotics and antibiotic resistant genes (ARGs) in groundwater: A global review on dissemination, sources, interactions, environmental and human health risks. *Water Research*, 187, 116455.

Zasloff, M. (2002). Antimicrobial peptides of multicellular organisms. *Nature*, 415(6870), 389–395.
415–429.

Zeng, L. J., Huang, Y. H., Liu, Y., Du, P. P., Mo, C. H., Li, Y. W., Lü, H., & Cai, Q. Y. (2019). Occurrence and distribution of antibiotics and antibiotic resistant genes in water and sediments of urban rivers with black-odor water in Guangzhou, South China. *Science of the Total Environment*, 670, 170–180.

Zhang, T., Lv, K., Lu, Q., Wang, L., & Liu, X. (2021). Removal of antibiotic-resistant genes during drinking water treatment: A review. *Journal of Environmental Sciences*, 104,