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Aquatic Antibiotic Pollution and the Environmental Dissemination of Antimicrobial Resistance

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★ Key message

- Antibiotic residues entering aquatic environments create selective pressure that promotes the emergence and spread of antibiotic-resistant bacteria (ARB) and antimicrobial resistance genes (ARGs).
- Rivers, lakes, wastewater systems, agricultural runoff, livestock farms, and hospital effluents serve as important reservoirs and transmission pathways for antimicrobial resistance across humans, animals, and the environment.
- Effective control of antimicrobial resistance requires a One Health approach involving responsible antibiotic use, improved wastewater treatment, environmental surveillance, and public awareness.

Abstract

Antimicrobial resistance (AMR) is one of the greatest public health challenges of the twenty-first century, threatening the effectiveness of medicines used to treat bacterial, viral, fungal, and parasitic infections. Although the misuse and overuse of antibiotics in human and veterinary medicine are well-recognized drivers of AMR, increasing attention is being directed toward antibiotic pollution in the environment, particularly in aquatic ecosystems. A considerable proportion of administered antibiotics is excreted unchanged or as active metabolites, eventually entering wastewater systems, rivers, lakes, and irrigation water. Even at low concentrations, these antibiotic residues exert selective pressure that promotes the survival and spread of antibiotic-resistant bacteria (ARB) and antimicrobial resistance genes (ARGs). These resistant microorganisms can subsequently move through aquatic ecosystems, food chains, livestock, wildlife, and ultimately to humans, highlighting the interconnected nature of environmental, animal, and human health. This article discusses the major sources of antibiotic contamination in water, explains how aquatic environments contribute to the dissemination of antimicrobial resistance, and summarizes current approaches for detecting and tracking resistant bacteria and resistance genes. Reducing antibiotic pollution through responsible antimicrobial use, improved wastewater management, environmental surveillance, and public awareness will be essential to slowing the global spread of antimicrobial resistance.

Keywords: Antimicrobial resistance, antibiotic pollution, aquatic environment, antibiotic-

resistant bacteria, antimicrobial resistance genes, wastewater, One Health

Abbreviations

AMR – Antimicrobial resistance

ARB – Antibiotic-resistant bacteria

ARGs – Antimicrobial resistance genes

AST – Antibiotic susceptibility testing

MDR – Multidrug-resistant

MAR – Multiple Antibiotic Resistance

MST – Microbial source tracking

WGS – Whole-genome sequencing

MGEs – Mobile genetic elements

HGT – Horizontal gene transfer

1. Introduction

Antimicrobial resistance (AMR) has emerged as one of the most serious global public health challenges of the twenty-first century. It occurs when microorganisms—including bacteria, viruses, fungi, and parasites—develop the ability to survive exposure to antimicrobial drugs that were previously effective against them. As a result, common infections become increasingly difficult to treat, leading to prolonged illness, higher healthcare costs, increased mortality, and reduced effectiveness of modern medical procedures such as surgery, organ transplantation, and cancer chemotherapy. Recognizing its growing impact on human health, the World Health Organization (WHO) has identified AMR as one of the top global health threats requiring urgent international action.

The burden of AMR continues to increase worldwide. In 2019 alone, bacterial antimicrobial resistance was directly responsible for an estimated 1.27 million deaths and contributed to nearly 4.95 million deaths globally (Antimicrobial Resistance Collaborators, 2022). Beyond its devastating health consequences, AMR also poses a substantial economic challenge. The World Bank estimates that drug-resistant infections could add nearly US\$1 trillion in healthcare costs by 2050 while reducing global gross domestic product by up to US\$3.4 trillion annually if effective interventions are not implemented (World Bank, 2017). These projections emphasize that AMR is not only a medical problem but also a major socioeconomic challenge affecting sustainable development. The economic consequences of antimicrobial resistance are particularly significant in India, where increasing healthcare costs and long-term productivity losses are expected to place substantial pressure on both the healthcare system and the national economy (Table 1).

Table 1. Estimated Healthcare and Economic Burden of Antimicrobial Resistance (AMR) in India

Category	Key figures (India)	Impact	Source
Direct medical costs	The median cost of treating a resistant infection is US\$199 , compared with US\$109 for a susceptible infection. Similarly, the median daily hospital cost is US\$65 versus US\$35 , respectively.	Resistant infections substantially increase hospitalization, diagnostic investigations, and treatment costs, placing an additional financial burden on patients and healthcare systems.	Shinde <i>et al.</i> , 2026
Macroeconomic impact	AMR is projected to reduce India's GDP by approximately 2–3.8% by 2050 . Globally, cumulative economic losses due to AMR could reach US\$100 trillion by 2050, with India expected to bear a significant share of the burden.	Reduced workforce productivity, increased healthcare expenditure, and losses in livestock production are expected to have major long-term socioeconomic consequences.	Taneja <i>et al.</i> , 2019

The emergence and spread of AMR are primarily driven by the misuse and overuse of antibiotics in human medicine, veterinary practice, agriculture, and aquaculture. However, an equally important but often overlooked contributor is environmental antibiotic pollution. A considerable proportion of antibiotics administered to humans and animals is excreted unchanged or as biologically active metabolites. These compounds eventually enter wastewater treatment systems and are subsequently released into rivers, lakes, groundwater, sediments, and irrigation water (Figure 1). Even at relatively low concentrations, antibiotic residues create selective pressure that favors the survival and proliferation of resistant microorganisms while facilitating the persistence and dissemination of antimicrobial resistance genes (ARGs).

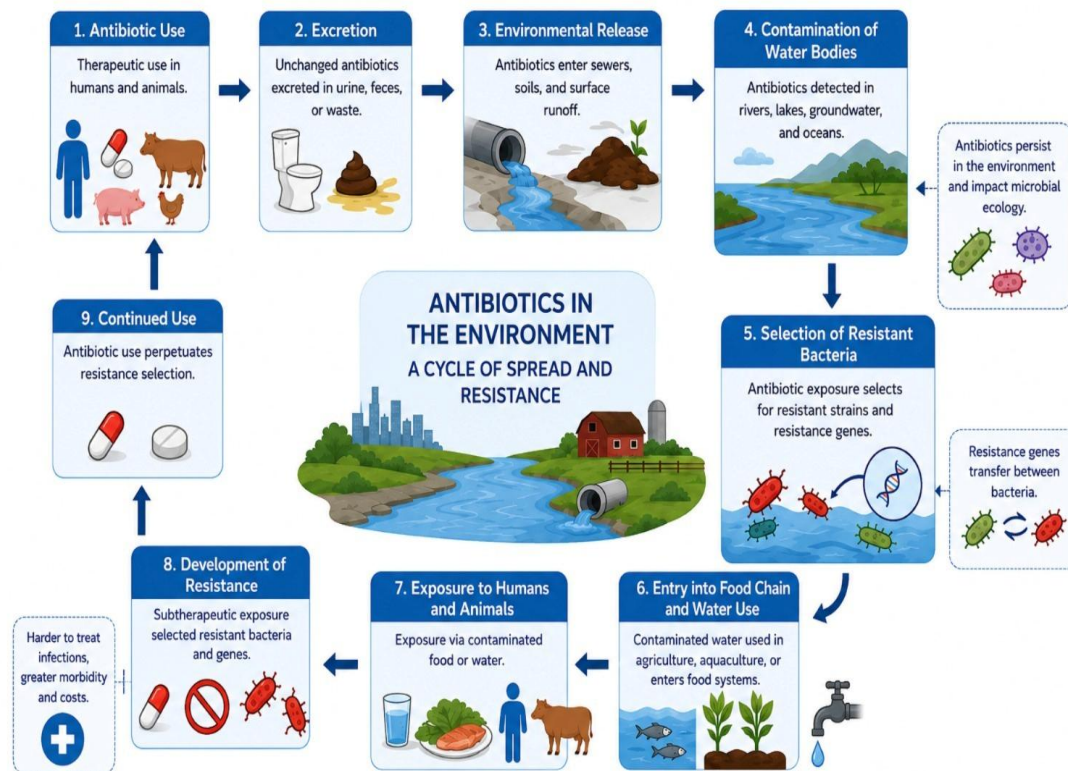


Figure 1: Antibiotics resistance (AMR) spread.

Aquatic environments have therefore become important reservoirs and transmission pathways for antibiotic-resistant bacteria (ARB) and ARGs (Singh et al., 2022). Wastewater treatment plants, hospital effluents, pharmaceutical manufacturing facilities, agricultural runoff, and livestock production systems continuously introduce antibiotics and resistant microorganisms into the environment. Once present, these contaminants interact with diverse microbial communities, promoting horizontal gene transfer and accelerating the evolution and dissemination of antimicrobial resistance. Recent studies have reported antibiotic concentrations of up to 460 ng/L in freshwater and 406 ng/g in sediments, illustrating the widespread occurrence of pharmaceutical contaminants in aquatic ecosystems (Maghsodian et al., 2022).

Compared with clinical and veterinary settings, the environmental dimension of AMR has historically received less attention despite its crucial role in resistance dissemination. Environmental contamination not only exposes native microbial communities to antibiotic residues but also facilitates the exchange of resistance genes among environmental and pathogenic bacteria. Consequently, rivers, lakes, wastewater systems, and agricultural water sources act as interconnected reservoirs that enable resistant bacteria and ARGs to move through aquatic ecosystems, food production systems, livestock, wildlife, and ultimately to human populations. This interconnected movement reflects the principles of the One Health approach, which recognizes that the health of humans, animals, and the environment is closely

linked.

This article highlights how antibiotic pollution in aquatic environments contributes to the spread of antimicrobial resistance. It discusses the major environmental sources of antibiotic contamination, explains the pathways through which resistant bacteria and resistance genes move from water to living hosts, and summarizes the methods currently used to detect and track antimicrobial resistance in aquatic ecosystems. Understanding these environmental pathways is essential for developing effective strategies to reduce antibiotic pollution and preserve the effectiveness of life-saving antimicrobial drugs for future generations.

2. Environmental Transmission of Antibiotic-Resistant Bacteria and Resistance Genes from Aquatic Systems to Living Hosts

Water plays a central role in the environmental spread of antimicrobial resistance. Once antibiotic-resistant bacteria (ARB) and antimicrobial resistance genes (ARGs) enter rivers, lakes, wastewater systems, or irrigation channels, they can persist for long periods and move freely through interconnected ecosystems. Unlike many other environmental pollutants, resistant bacteria can multiply and exchange genetic material, allowing resistance to spread even when antibiotic concentrations are low.

Antibiotics enter aquatic environments from a variety of sources, including untreated sewage, hospital wastewater, pharmaceutical manufacturing, livestock farms, aquaculture, and agricultural runoff. These waters become reservoirs where resistant bacteria from different origins come into contact with environmental microorganisms. Such interactions promote **horizontal gene transfer (HGT)**, a natural process through which bacteria exchange resistance genes using mobile genetic elements such as plasmids, transposons, and integrons. As a result, bacteria that were previously susceptible to antibiotics can rapidly acquire resistance.

The movement of resistant bacteria does not stop within aquatic ecosystems. Contaminated water used for irrigation can introduce resistant bacteria onto fruits and vegetables, while polluted rivers and ponds can spread resistance to fish and other aquatic organisms. Livestock drinking contaminated water may also acquire resistant bacteria, which can subsequently enter the food chain. Humans are exposed through the consumption of contaminated food, recreational activities, occupational contact, or inadequate drinking water treatment. These interconnected pathways demonstrate that antimicrobial resistance is not confined to hospitals but circulates continuously between the environment, animals, and humans.

This continuous exchange of resistant microorganisms highlights the importance of the

One Health concept, which recognizes that human, animal, and environmental health are closely linked. Reducing antibiotic pollution in water, improving sanitation and wastewater treatment, and promoting responsible antibiotic use across all sectors are therefore essential steps in limiting the environmental spread of antimicrobial resistance.

3. Tracking Antibiotic-Resistant Organisms in Water

Understanding where antibiotic-resistant bacteria originate and how they spread is essential for controlling antimicrobial resistance. Scientists use a combination of conventional microbiological methods and advanced molecular technologies to monitor resistant bacteria and resistance genes in aquatic environments. Together, these approaches help identify contamination sources, assess public health risks, and guide interventions to reduce the environmental spread of resistance.

The first step usually involves collecting water samples from rivers, lakes, wastewater treatment plants, hospital effluents, irrigation systems, or groundwater. Bacteria are then isolated using selective culture media and tested for their susceptibility to different antibiotics through antibiotic susceptibility testing (AST). The Multiple Antibiotic Resistance (MAR) index is often used to estimate the extent of antibiotic exposure at a particular site, with higher values indicating contamination from high-risk sources such as hospitals or intensive livestock production.

While culture-based methods remain valuable, many environmental microorganisms cannot be grown under laboratory conditions. Molecular techniques therefore play an increasingly important role in environmental surveillance. Polymerase chain reaction (PCR) and quantitative PCR (qPCR) enable rapid detection of important resistance genes, whereas whole-genome sequencing (WGS) provides detailed information about bacterial strains and the genetic elements responsible for resistance. More recently, metagenomic approaches have allowed researchers to study the complete collection of microorganisms and resistance genes present in a water sample without the need for culturing, providing a more comprehensive picture of the environmental resistome.

Scientists also use microbial source tracking (MST) to determine whether contamination originates from human sewage, livestock, wildlife, or other environmental sources. When combined with routine environmental monitoring and antibiotic residue analysis, these tools provide valuable information for identifying contamination hotspots, evaluating wastewater treatment efficiency, and supporting evidence-based policies to reduce antibiotic pollution. Continuous surveillance of aquatic environments is therefore essential for detecting emerging resistance trends before they become major public health threats.

4. Conclusion

Antibiotic pollution in aquatic environments has become an important driver of antimicrobial resistance, transforming rivers, lakes, wastewater systems, and other water bodies into reservoirs of antibiotic-resistant bacteria and resistance genes. These resistant microorganisms can spread across environmental, animal, and human populations through interconnected pathways, making antimicrobial resistance a challenge that extends far beyond hospitals and healthcare settings.

Addressing this growing threat requires a comprehensive One Health approach that recognizes the close relationship between environmental, animal, and human health. Responsible antibiotic use, improved wastewater treatment, proper disposal of pharmaceutical waste, continuous environmental surveillance, and greater public awareness are all essential to reducing the spread of resistance. Equally important is continued investment in research and innovative technologies that can improve the detection and monitoring of resistant microorganisms in the environment.

Protecting our water resources is not only an environmental responsibility but also a public health necessity. Every step taken to reduce antibiotic pollution today helps preserve the effectiveness of life-saving antibiotics for future generations.

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