

Antibiotic Resistance Genes in Urban Wastewater: Implications for Public Health

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Abstract: Antibiotic resistance (AR) is a growing global health crisis, and urban wastewater is increasingly recognized as a significant source of antibiotic resistance genes (ARGs). Urban wastewater systems receive contributions from hospitals, industries, and households, making them hotspots for ARGs that can persist even after treatment. Wastewater treatment plants (WWTPs), while effective at reducing organic and pathogenic loads, are not always successful at eliminating ARGs, allowing resistant bacteria and genes to enter natural water bodies. This review explores the sources and mechanisms of ARG spread in urban wastewater, examines the role of WWTPs in mitigating this issue, and discusses the implications for public health. The article also outlines current challenges and future directions for research and policy to reduce ARG dissemination in the environment and safeguard public health.

Keywords: Antibiotic resistance, Urban wastewater, Wastewater treatment plants, Antibiotic resistance genes, Public health, Horizontal gene transfer.

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1.0 Introduction

Antibiotic resistance (AR) has become one of the most pressing global health challenges of the 21st century. The rapid spread of antibiotic-resistant bacteria (ARB) and antibiotic resistance genes (ARGs) poses a significant threat to both human health and the environment. A key contributor to this problem is the release of ARGs into the environment through various channels, one of the most concerning being urban wastewater systems. Wastewater from urban areas, which includes domestic, industrial, and hospital effluents, contains a diverse array of chemical pollutants, including antibiotics, disinfectants, and other antimicrobial agents. These substances create a selective pressure in aquatic environments that fosters the proliferation of resistant bacterial strains and the dissemination of ARGs (1).

Urban wastewater treatment plants (WWTPs) are not fully equipped to eliminate ARGs, allowing them to persist in effluents discharged into rivers, lakes, and oceans. This situation is exacerbated by the fact that WWTPs can act as reservoirs and breeding grounds for ARB. Inside WWTPs, bacteria interact with antibiotics and other pollutants, leading to the horizontal gene transfer (HGT) of ARGs between different bacterial species (2). Consequently, treated wastewater can act as a conduit for ARGs, contributing to the contamination of natural water bodies, agricultural land (through the use of sludge as fertilizer), and even drinking water supplies. This has significant public health implications, as it increases the risk of human exposure to ARB, particularly in communities that rely on contaminated water sources (3).

The widespread presence of ARGs in urban wastewater highlights the urgent need for more effective treatment methods and strategies to mitigate their environmental and public health impacts. A better understanding of the factors driving the spread of ARGs in

wastewater environments is essential for developing targeted interventions. The aim of this article is to explore the mechanisms behind the spread of antibiotic resistance in urban wastewater, assess the public health risks associated with ARGs, and discuss potential strategies for mitigating their dissemination.

2.0 The Global Threat of Antibiotic Resistance

Antibiotic resistance (AR) represents one of the most pressing global health challenges. Due to the widespread and often inappropriate use of antibiotics, resistant bacterial strains have emerged, which are difficult to treat with standard therapies. Infections caused by multidrug-resistant bacteria lead to prolonged hospital stays, higher medical costs, and increased mortality. The World Health Organization (WHO) has recognized AR as a significant threat to global health, food security, and development. Urban wastewater systems have been identified as critical reservoirs for AR, as they collect waste from hospitals, industries, and communities, all of which can contribute antibiotic-resistant bacteria (ARB) and antibiotic resistance genes (ARGs) to the environment (4). This article aims to explore the presence of ARGs in urban wastewater and its implications for public health, while also examining current wastewater treatment methods and future strategies for reducing ARG dissemination.

3.0 Sources of Antibiotic Resistance Genes in Urban Wastewater

Urban wastewater is a confluence of various sources of ARGs. These sources include hospitals, where antibiotic use is high, and pharmaceutical industries, which may discharge antibiotics directly into wastewater systems. Residential areas also contribute ARGs through human waste, as antibiotics taken by people are excreted and enter sewage systems. Agricultural runoff, where antibiotics are used for livestock, also contributes significantly to the ARG

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burden in wastewater (5). Wastewater treatment plants (WWTPs) play a pivotal role in managing this mix, but they are not always equipped to fully eliminate ARGs, allowing these genes to persist and be released into natural water bodies (6).

4.0 Mechanisms of Antibiotic Resistance Spread in Wastewater

In wastewater, ARGs spread primarily through horizontal gene transfer (HGT). This process allows bacteria to exchange genetic material, including ARGs, through plasmids, transposons, and integrons. HGT is facilitated by the complex microbial communities present in wastewater, which include bacteria, viruses, and other microorganisms. Wastewater provides a conducive environment for HGT, as bacteria are often exposed to low concentrations of antibiotics, creating selective pressure that favors the survival of resistant strains (7). Furthermore, biofilms in WWTPs are particularly conducive to HGT, as they foster close contact between different bacterial species, allowing ARGs to spread more easily (8).

5.0 The Role of Wastewater Treatment Plants (WWTPs)

Wastewater treatment plants (WWTPs) are designed to reduce organic matter, pathogens, and nutrients in sewage, but they are not always capable of removing ARGs and ARB effectively. Traditional treatment methods, including activated sludge and membrane filtration, can reduce the number of bacteria but may not fully eliminate ARGs. Research has shown that WWTPs can act as hotspots for the amplification and dissemination of ARGs, as they often concentrate bacteria in biofilms or sludge, where HGT can occur (9). Effluents from WWTPs, which may still contain ARGs, are often discharged into rivers or lakes, allowing these genes to spread into broader ecosystems. Additionally, treated sludge, used as fertilizer in agriculture, can introduce ARGs into the soil, posing risks for crop contamination and further spread of resistance (10).

6.0 Public Health Implications of ARGs in Wastewater

The spread of ARGs in wastewater has direct implications for public health. Once ARGs enter natural water bodies, they can contaminate drinking water sources, increasing the risk of human exposure to ARB. People can come into contact with these bacteria through recreational activities in contaminated waters, or indirectly through the consumption of crops irrigated with wastewater. Studies have linked the presence of ARGs in the environment to an increase in clinical cases of drug-resistant infections, as environmental ARGs are transferred to human pathogens (11). The widespread dissemination of ARGs also makes it more challenging to control infectious diseases, as treatment options become limited.

7.0 Environmental and Ecological Consequences

Beyond public health, the presence of ARGs in wastewater has significant ecological consequences. Aquatic ecosystems, where treated wastewater is often released, are particularly vulnerable to the spread of ARGs. These genes can be transferred among aquatic microbial communities, potentially leading to the emergence of new resistant strains in the environment. The use of treated sludge as fertilizer can introduce ARGs into the soil, where they persist and accumulate over time, leading to the contamination of crops

and the food chain (12). The long-term ecological impact of ARGs in the environment is still not fully understood, but it poses a serious risk to both wildlife and human populations.

8.0 Strategies for Mitigating ARG Spread in Wastewater

To address the spread of ARGs in wastewater, both technological and regulatory solutions are needed. Advanced wastewater treatment technologies, such as membrane bioreactors, ultraviolet disinfection, and advanced oxidation processes, have shown promise in reducing ARGs in treated effluents. The use of antimicrobial materials in WWTPs may also help limit the spread of resistance. On the regulatory side, stricter controls on the use and disposal of antibiotics, particularly in hospitals and agriculture, are essential to reduce the overall load of antibiotics and ARGs entering wastewater systems (13). Public awareness campaigns about the responsible use of antibiotics can also play a crucial role in mitigating the spread of resistance.

9.0 Future Directions in ARG Research and Public Health Policy

Future research into the role of urban wastewater in ARG dissemination should focus on developing more effective detection and monitoring methods, such as metagenomic approaches that provide a comprehensive view of the resistome in different environments. Studies on the fate and transport of ARGs in different environmental matrices, including water, soil, and air, are also needed to understand the full scope of the problem (14). From a policy perspective, integrating environmental ARG surveillance with clinical data could provide valuable insights into the links between environmental contamination and public health. International cooperation will be crucial in developing a cohesive global strategy to combat the spread of ARGs and ensure the sustainability of antibiotic treatments for future generations (15).

10.0 Conclusion

Urban wastewater serves as a critical reservoir for ARGs, and its role in the spread of antibiotic resistance is undeniable. WWTPs, while essential for managing sewage, are not always effective in removing ARGs and ARB, allowing these genes to persist in treated effluent and sludge. The spread of ARGs in the environment has serious implications for public health, as it increases the risk of resistant infections and limits treatment options. To address this growing problem, technological innovations, regulatory measures, and public awareness are all needed to reduce the spread of ARGs in wastewater and protect both human and environmental health (16).

References

1. Rizzo, L., Manaia, C., Merlin, C., Schwartz, T., Dagot, C., Ploy, M. C., ... & Fatta-Kassinos, D. (2013). Urban wastewater treatment plants as hotspots for antibiotic resistant bacteria and genes spread into the environment: a review. *Science of the total environment*, 447, 345-360. doi:10.1016/j.scitotenv.2013.01.032.
2. Rodríguez-Mozaz S, Chang PH, Jelic A, Gros M, Vineis P, Barcelo D. (2017). Pharmaceuticals and antibiotic resistance spread in urban wastewater treatment plants. *J Hazard Mater*. 15;321:772-791. doi:10.1016/j.jhazmat.2016.09.072.

3. Rizzo, L., Manaia, C., Merlin, C., Schwartz, T., Dagot, C., Ploy, M. C., ... & Fatta-Kassinos, D. (2013). Urban wastewater treatment plants as hotspots for antibiotic resistant bacteria and genes spread into the environment: a review. *Science of the total environment*, *447*, 345-360. doi:10.1016/j.scitotenv.2013.01.032.
4. Karkman, A., Do, T. T., Walsh, F., & Virta, M. P. (2018). Antibiotic-resistance genes in waste water. *Trends in microbiology*, *26*(3), 220-228. doi: 10.1016/j.tim.2017.09.005.
5. Rizzo, L., Manaia, C., Merlin, C., Schwartz, T., Dagot, C., Ploy, M. C., ... & Fatta-Kassinos, D. (2013). Urban wastewater treatment plants as hotspots for antibiotic resistant bacteria and genes spread into the environment: a review. *Science of the total environment*, *447*, 345-360. doi: 10.1016/j.scitotenv.2013.01.032.
6. Rizzo, L., Manaia, C., Merlin, C., Schwartz, T., Dagot, C., Ploy, M. C., ... & Fatta-Kassinos, D. (2013). Urban wastewater treatment plants as hotspots for antibiotic resistant bacteria and genes spread into the environment: a review. *Science of the total environment*, *447*, 345-360. doi: 10.1016/j.scitotenv.2013.01.032.
7. Rodriguez-Mozaz S, Chang PH, Jelic A, Gros M, Vineis P, Barcelo D. (2017). Pharmaceuticals and antibiotic resistance spread in urban wastewater treatment plants. *J Hazard Mater*. *15*;321:772-791. doi: 10.1016/j.jhazmat.2016.09.072.
8. Zhang, T., Zhang, X. X., & Ye, L. (2011). Plasmid metagenome reveals high levels of antibiotic resistance genes and mobile genetic elements in activated sludge. *PLoS one*, *6*(10), e26041. doi: 10.1371/journal.pone.0026041.
9. Su, J. Q., An, X. L., Li, B., Chen, Q. L., Gillings, M. R., Chen, H., ... & Zhu, Y. G. (2017). Metagenomics of urban sewage identifies an extensively shared antibiotic resistome in China. *Microbiome*, *5*, 1-15. doi: 10.1038/ismej.2016.152.
10. Verlicchi, P., Al Aukidy, M., & Zambello, E. (2012). Occurrence of pharmaceutical compounds in urban wastewater: removal, mass load and environmental risk after a secondary treatment—a review. *Science of the total environment*, *429*, 123-155. doi: 10.1016/j.scitotenv.2012.04.028.
11. Marti, E., Variatza, E., & Balcazar, J. L. (2014). The role of aquatic ecosystems as reservoirs of antibiotic resistance. *Trends in microbiology*, *22*(1), 36-41. doi: 10.1016/j.tim.2013.11.001.
12. Gatica, J., & Cytryn, E. (2013). Impact of treated wastewater irrigation on antibiotic resistance in the soil microbiome. *Environmental Science and Pollution Research*, *20*, 3529-3538. doi: 10.1007/s11356-013-1505-4.
13. Manaia, C. M., Rocha, J., Scaccia, N., Marano, R., Radu, E., Biancullo, F., ... & Nunes, O. C. (2018). Antibiotic resistance in wastewater treatment plants: Tackling the black box. *Environment international*, *115*, 312-324. doi: 10.1016/j.envint.2018.03.044.
14. Berendonk, T. U., Manaia, C. M., Merlin, C., Fatta-Kassinos, D., Cytryn, E., Walsh, F., ... & Martinez, J. L. (2015). Tackling antibiotic resistance: the environmental framework. *Nature reviews microbiology*, *13*(5), 310-317. doi: 10.1038/nrmicro3439.
15. Manaia, C. M., Macedo, G., Fatta-Kassinos, D., & Nunes, O. C. (2016). Antibiotic resistance in urban aquatic environments: can it be controlled?. *Applied microbiology and biotechnology*, *100*, 1543-1557. doi: 10.1007/s00253-015-7254-8.
16. Rizzo, L., Manaia, C., Merlin, C., Schwartz, T., Dagot, C., Ploy, M. C., ... & Fatta-Kassinos, D. (2013). Urban wastewater treatment plants as hotspots for antibiotic resistant bacteria and genes spread into the environment: a review. *Science of the total environment*, *447*, 345-360. doi: 10.1016/j.scitotenv.2013.01.032.