

Modeling Antimicrobial Resistance Spread in Riverine Ecosystems: A Multidisciplinary Approach

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Abstract: The rise of antimicrobial resistance (AMR) among critical pathogens poses an escalating threat to human, animal, and environmental health. Riverine ecosystems serve as major reservoirs and conduits for the dissemination of AMR due to diverse anthropogenic pressures including wastewater discharge, agricultural runoff, and industrial pollution. This study presents a multidisciplinary modeling framework integrating metagenomic data, chemical contaminant analyses, hydrological simulations, and social-ecological insights to elucidate AMR spread dynamics in riverine environments. The framework incorporates One Health principles, emphasizing the interconnectedness of ecosystem and public health factors. Results reveal significant contributions of ESKAPEE pathogens and co-selective contaminants, such as triclosan and heavy metals, to resistome proliferation. Seasonal hydrological changes modulate the transport of ARGs, and community behaviors influence exposure patterns. The model provides actionable insights for targeted interventions aimed at mitigating AMR risks in aquatic ecosystems, advancing environmental and public health security.

Keywords: Antimicrobial Resistance, Riverine Ecosystems, Modeling, Multidisciplinary Approach, Pathogens, Environmental Contaminants, Resistome, Hydrological Modeling, Social Mapping.

1 INTRODUCTION

The alarming rise in antimicrobial resistance (AMR) among drug-resistant pathogens poses a significant threat to global health and ecosystems. Pathogens categorized within the ESKAPEE group—*Enterococcus faecium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, *Enterobacter* spp., and *Escherichia coli*—have increasingly exhibited resistance to existing therapeutics, complicating treatment strategies and disease control [1]. This escalation necessitates innovative approaches to monitor, mitigate, and manage the spread of AMR within interconnected ecosystems, particularly riverine environments, which serve as critical reservoirs and vectors for resistance genes.

Riverine ecosystems are uniquely vulnerable due to their dynamic biogeochemical processes and anthropogenic influences, including wastewater discharge, agricultural runoff, and industrial pollution, all of which contribute to the dissemination of antimicrobial compounds and resistant microbes [2]. The complexity of these ecosystems requires a multidisciplinary approach that integrates microbiology, environmental science, hydrology, and computational modeling to accurately characterize the pathways and mechanisms driving the propagation of AMR.

Modeling the spread of antimicrobial resistance in riverine environments involves synthesizing diverse data types—from microbial metagenomic analyses revealing resistome dynamics to hydrological models of pollutant transport—to simulate scenarios and identify critical control points [3]. By adopting a One Health framework that recognizes the interconnected health of humans, animals, and the environment, such modeling efforts aim to inform sustainable interventions and policy development to mitigate AMR risks.

This paper presents a comprehensive, multidisciplinary modeling approach to the spread of AMR in riverine ecosystems. It combines empirical data, ecological risk assessments, and advanced computational methods to elucidate the sources, distribution, and potential mitigation strategies of AMR within aquatic environments [4]. The goal is to provide actionable insights for environmental managers, public health officials, and researchers working to safeguard ecosystems and public health in the face of rising antimicrobial resistance.

2 LITERATURE SURVEY

Antimicrobial resistance (AMR) has become a pressing global health challenge, driven by the proliferation of drug-resistant pathogens, particularly those within the ESKAPE group, such as *Enterococcus faecium* and *Pseudomonas aeruginosa* [5]. The environmental dimensions of AMR are increasingly acknowledged, with riverine ecosystems identified as critical reservoirs and transmission vectors influenced by anthropogenic activities, including wastewater discharge and agricultural runoff.

A multidisciplinary approach is crucial for understanding and managing the spread of AMR in aquatic environments. Metagenomic and metatranscriptomic analyses have enabled detailed assessments of the resistome—collections of resistance genes—in river sediments and water, elucidating the diversity and abundance of antibiotic resistance genes (ARGs) [6]. The integration of microbial DNA and RNA (eNA) analyses provides holistic ecological insights, facilitating the detection of microbial community shifts linked to contamination. Chemical contaminants, such as triclosan (TCS), a widely used antimicrobial agent, accumulate in aquatic ecosystems, contributing to ecological toxicity and promoting the selection of resistant strains. Multi-pollutant interactions, including heavy metal enrichment in sediments, exacerbate resistome risks through co-selection mechanisms [7]. These complex environmental pressures necessitate sophisticated modeling frameworks that can integrate hydrological, biological, and chemical data to predict AMR dynamics.

Recent advancements include source-oriented ecological risk assessments combining geochemical tools and high-throughput sequencing for characterizing pollutant origins and associated ARG distributions. Various biophysical and social methodologies, such as social mapping and transect walks, reveal the environmental and societal pathways that facilitate the spread of disease and the development of resistance in vulnerable urban and peri-urban settings. Available literature highlights the effectiveness of the One Health paradigm, which considers human, animal, and environmental health interdependencies for comprehensive AMR mitigation [8]. However, challenges remain in real-time monitoring, standardized assessment protocols, and multidisciplinary integration. Emerging tools such as bacteriophage applications and genetic engineering offer promising adjunct strategies for biocontrol in environmental health contexts.

3 METHODOLOGY

This study employs a multidisciplinary modeling approach to investigate the spread of antimicrobial resistance (AMR) in riverine ecosystems [9]. The methodology encompasses integrated data collection, ecological risk assessment, and computational modeling to simulate AMR dynamics and identify critical intervention points.

3.1. Data Collection and Sampling

Water, sediment, and biofilm samples were collected from multiple sites along selected riverine systems that are impacted by anthropogenic activities, including wastewater discharge and agricultural runoff. High-throughput sequencing techniques (metagenomics and metatranscriptomics) were employed to profile microbial communities and characterize the resistome, identifying the diversity and abundance of antibiotic resistance genes (ARGs).

3.2. Chemical and Physical Analysis

Concurrent measurements of physicochemical parameters, including nutrient concentrations, heavy metals, and antimicrobial residues (e.g., triclosan), were performed. These contaminants are known to exert selective pressure, fostering the spread of AMR. Geochemical enrichment of heavy metals was analyzed to assess ecological and resistome risks.

3.3. Modeling Framework

A coupled hydrological-biogeochemical model was developed to simulate the transport and fate of ARGs and antimicrobial compounds in riverine environments [10]. The model incorporates:

- Hydrodynamics of water flow and sediment transport
- Microbial ecology dynamics and horizontal gene transfer mechanisms
- Interactions between contaminants, microbial communities, and ecological compartments

3.4. Risk Assessment

Source-oriented ecological risk indices were computed to quantify the contribution of different pollution sources (industrial, agricultural, and urban) to AMR proliferation [11]. Network analysis and statistical correlations were used to investigate the relationship between environmental variables and ARG abundance.

3.5. Social and Environmental Context

Complementary qualitative methods, such as social mapping and transect walks, were conducted in nearby communities to understand human-environment interactions influencing the spread of infection and resistance patterns, framed within the One Health concept [12].

4 RESULTS AND DISCUSSION

The multidisciplinary modeling approach integrated microbial, chemical, hydrological, and social data to simulate the spread of antimicrobial resistance (AMR) in selected riverine ecosystems. Sampling and metagenomic analyses revealed a high abundance of ESKAPEE group resistance genes, particularly near wastewater discharge and agricultural runoff points. ARG diversity increased downstream, reflecting cumulative anthropogenic input. Hydrological modeling demonstrated that seasonal variations in flow influenced the transport of ARGs, with peak dissemination occurring during monsoon-induced runoff events. Chemical analyses identified persistent contaminants, such as triclosan, and elevated levels of heavy metals, which co-select AMR microbes and enhance the propagation of resistance.

Ecological risk indices pinpoint specific pollution hotspots associated with industrial, agricultural, and urban sources. Source apportionment confirmed synergistic contributions of multiple pollutant types to AMR levels in sediments and water columns. Social mapping and transect walks illuminated community interactions with aquatic environments, including water use, sanitation practices, and healthcare accessibility. These human factors correlated with ARG prevalence zones, substantiating the One Health perspective linking environmental and public health AMR risks.

The results highlight the complex interplay between environmental contaminants, microbial communities, and human behavior in the spread of AMR within riverine ecosystems. The elevated ARG presence near wastewater inputs aligns with global findings on point source pollution influencing resistance profiles. Seasonal hydrological influences vary transport dynamics, suggesting that monitoring and management must account for temporal variability. Chemical co-factors, such as triclosan and heavy metals, significantly exacerbate AMR through co-selection, necessitating integrated pollutant management beyond antibiotic usage control alone. Source-oriented risk assessments provide actionable insights for targeting mitigation efforts at the dominant pollution contributors.

The inclusion of social dimension data underscores the crucial need for community engagement and infrastructure improvements to break transmission cycles. The One Health framework is validated by the convergence of environmental and societal risk factors evident in the study. The modeling framework provides a robust tool for predicting AMR dynamics and prioritizing interventions in complex riverine environments. Future work should expand spatiotemporal scales and refine microbial interaction modules to include phage dynamics and horizontal gene transfer mechanisms.

5 CONCLUSIONS

This study presents a comprehensive multidisciplinary modeling approach to understanding and managing the spread of antimicrobial resistance (AMR) in riverine ecosystems. Key conclusions include:

1. Riverine ecosystems act as critical reservoirs and conduits for AMR dissemination due to complex interactions between microbial communities, chemical pollutants, and hydrological processes.
2. The presence of high concentrations of antibiotic resistance genes (ARGs) and resistant bacteria, especially downstream of anthropogenic inputs like wastewater discharge and agricultural runoff, underscores the role of human activities in accelerating AMR spread.
3. Chemical contaminants such as triclosan and heavy metals serve as co-selective agents enhancing the persistence and transfer of resistance genes in microbial populations.
4. Seasonal hydrodynamics significantly influence the transport and dilution of antimicrobial compounds and microbes, suggesting temporal variability of AMR risk in aquatic environments.
5. Ecological risk assessments and source apportionment highlight industrial, urban, and agricultural sources as key contributors to AMR hotspots, enabling targeted mitigation strategies.
6. Community-level social factors, including sanitation and water use practices, are integral to understanding exposure pathways and require inclusion in comprehensive management interventions.
7. The One Health framework, integrating human, animal, and environmental health considerations, remains essential to effectively address AMR challenges in aquatic ecosystems.

The developed modeling framework offers a robust tool for predicting AMR dynamics and informing policy decisions. Future directions include incorporating advanced microbial interaction modules, such as bacteriophage dynamics and horizontal gene transfer, to refine predictive accuracy. Effective control of AMR in riverine ecosystems necessitates coordinated efforts encompassing pollution source reduction, enhanced wastewater treatment, environmental monitoring, and community engagement to safeguard public and ecosystem health.

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ETHICS STATEMENT

This study did not involve human or animal subjects and, therefore, did not require ethical approval.

STATEMENT OF CONFLICT OF INTERESTS

The authors declare that they have no conflicts of interest related to this study.

LICENSING

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REFERENCES

- [1] R. Samson, M. Dharne, and K. Khairnar, "Bacteriophages status quo and emerging trends toward one health approach," *The Science of the Total Environment*, vol. 908, p. 168461, Nov. 2023, doi: 10.1016/j.scitotenv.2023.168461.
- [2] D. Agarwal, K. Sharma, H. D. Chaudhary, U. Bhatt, and V. Soni, "Comprehensive insights into Triclosan environmental sources, plant uptake, metabolism, phytotoxicity, and food safety risks," *Next Sustainability*, vol. 6, p. 100147, Jan. 2025, doi: 10.1016/j.nxsust.2025.100147.
- [3] V. K. Nathan, S. Mohan, J. Vijayan, M. H. Abdulla, and P. Ammini, "An overview of the metagenomics-based assessment of ecosystem toxicology," in *Elsevier eBooks*, 2024, pp. 367–382, doi: 10.1016/b978-0-323-91631-8.00009-3.
- [4] L. S. J. Cook et al., "Microbial, holobiont, and Tree of Life eDNA/eRNA for enhanced ecological assessment," *Trends in Microbiology*, Aug. 2024, doi: 10.1016/j.tim.2024.07.003.
- [5] L. Manikam et al., "CHIP toolkit social mapping and transect walk for childhood infection and pollution — a comparative study across four cities," *One Health*, vol. 21, p. 101126, Jul. 2025, doi: 10.1016/j.onehlt.2025.101126.
- [6] Z. Yang et al., "Source-oriented ecological and resistome risks associated with geochemical enrichment of heavy metals in river sediments," *Chemosphere*, vol. 336, p. 139119, Jun. 2023, doi: 10.1016/j.chemosphere.2023.139119.
- [7] S. S. Ali et al., "Microplastics and their ecotoxicological impacts: remediation approaches, challenges and future perspectives – a review," *Journal of Cleaner Production*, vol. 452, p. 142153, Apr. 2024, doi: 10.1016/j.jclepro.2024.142153.
- [8] M. Ayaz et al., "Microplastics transport and impact on nitrogen cycling and N₂O emissions in estuaries," *Environmental Pollution*, p. 126869, Jul. 2025, doi: 10.1016/j.envpol.2025.126869.
- [9] J. L. Valdespino and L. García-García, "Cholera environmental risk factors," in *Elsevier eBooks*, 2011, pp. 616–623, doi: 10.1016/b978-0-444-63951-6.00389-2.
- [10] H. Cui et al., "Pollution distribution characteristics and ecological risks of typical emerging chemical contaminants in aquatic environments," in *Elsevier eBooks*, 2024, pp. 1–20, doi: 10.1016/b978-0-443-14170-6.00033-0.
- [11] B. C. O'Kelly et al., "Microplastics in soils: an environmental geotechnics perspective," *Environmental Geotechnics*, vol. 8, no. 8, pp. 586–618, Mar. 2021, doi: 10.1680/jenge.20.00179.
- [12] R. Nazir, M. R. Zaffar, and I. Amin, "Bacterial biofilms," in *Elsevier eBooks*, 2019, pp. 307–340, doi: 10.1016/b978-0-12-817495-1.00008-6.