



Received: 27 July 2026
Revised: 29 Aug 2026
Accepted: 06 Sep 2026
Published: 18 Sep 2026

Volume 12 Issue 09, 2026
Page No - 63-69
DOI - 10.55640/ijmsdh-12-09-09

Article Citation: Al-Mamouri, H. F. A. (2026). Health Risk Indicators Resulting from The Spread of Antibiotic Resistance Genes in Rural Aquatic Environments in Babylon Governorate. International Journal of Medical Science and Dental Health, 12(09), 63-69. <https://doi.org/10.55640/ijmsdh-12-09-09>

Copyright: © 2026 The Authors. Published by IJMSDH under the Creative Commons CC BY License

Health Risk Indicators Resulting from The Spread of Antibiotic Resistance Genes in Rural Aquatic Environments in Babylon Governorate

Haider Farhan Abdullah Al-Mamouri

Department of Community Health/Babylon Polytechnic College/Al-Furat Al-Awsat

Abstract

The main objective of this review was to examine the health risk indicators related to the dissemination of antibiotic resistance genes in the rural aquatic environment, focusing on the Babylon Governorate. The significance of this topic is derived from the fact that the problem of antibiotic resistance exists not only in the treatment pathway in healthcare but in an environment that is interconnected to humans, animals, and water because of the growing presence of wastewater, animal waste, agricultural runoff, and disposal of pharmaceuticals in water systems. A descriptive-analytical method was used to review the scientific literature that has explored the occurrence of resistant bacteria, resistance genes, and antibiotic residues in freshwater, wastewater, and water sources impacted by human activities. The analysis was conducted to identify the sources of the resistance factor that enters water, the genetic classes most linked to the most frequently used antibiotics, the mechanisms for gene survival and transfer, and factors that enhance the risk of human and animal exposure. There are indications that the aquatic environment can serve as a reservoir and a facilitator for the dissemination of resistance, notably in case of organic contamination, selection pressure, and transposable genetic elements. However, the presence of a resistance gene does not necessarily mean that pathogenic bacteria or that humans have been infected are present. Must be used in conjunction with water quality indicators, bacterial isolation, susceptibility testing and the nature of use of the source. The review recommends that risk assessment in Babylon Governorate needs to be done regularly and in a standardized manner, through local field studies, better management of waste water and sewage, rational use of antibiotics and institutional cooperation with One Health approach into consideration, and implementation of preventive measures taking into account the safety and living conditions of the population.



Keywords: Health risk, Resistance genes, Aquatic environments, Rural water, Babylon Governorate

1 Introduction

Antibiotic resistance is one of the most complex health problems of our time, affecting not only how well we can treat bacteria, but also our environment, food systems and communities. The large scale and/or irrational use of antibiotics in human and animal care and in agricultural production has raised the risk of emergence of resistant bacteria in the environment and spread of resistance genes between microorganisms. In this context, water is no longer a mere source of life but can also be a recipient of antibiotic residues, resistant bacteria, or any kind of transmissible genetic material, especially when it comes in contact with animal manure, agricultural runoff, unregulated drainage and wastewater. Rural aquatic ecosystem is of special significance because of its multi-purpose and interface with the life of the rural folk. Water sources may be used for irrigation, livestock husbandry and/or domestic purposes and water quality may be influenced by the proximity of fields, livestock areas and drainage sources. This interaction could lead to opportunities for the movement of resistant bacteria or even resistance genes via water, soil, crop and animals. But the risk of exposure does not always mean that infection and health damage will follow. Finding a resistance gene in a sample of water does not, by itself, indicate pathogenic bacteria in the water or transfer of the gene to humans. Instead it should be considered in relation to the organism in which the gene is located, its biological condition, genetic transmission factors, pollution levels, and water usage type [2]. The challenge of this review is the limited systematic presentation of evidence related to antibiotic resistance genes in rural aquatic environments in Babylon Governorate, and all the difficulties to generalize the results of the international or regional studies without having the data from field work. Thus, this article focuses on the sources of resistance in water, the most common gene classes found in the literature and the mechanisms by which they survive and are transmitted, and indicators of health risk from water use or exposure. It also aims to emphasize the disparity between environmental markers and clinical findings, as well as gaps in research that need to be addressed in the future in the governorat [3]. The review takes a One Health approach, in which human, animal and environmental health are interlinked. With this vision, AMR is not only reduced through antimicrobial prescription control, but also by making improvements to water and sanitation, waste management, monitoring pollution sources, and sharing information among the sectors of health, environment, agriculture and animal health, with consideration about the needs of the population and their right to safe water [4].

2 Methodology

In the present article, the published evidence on the prevalence of antibiotic resistance genes in aquatic environments is compiled and analyzed, the sources and potential transmission pathways of these genes are discussed, and the potential health implications are presented, with focus on the relevance to understanding the reality of aquatic environments in rural areas in the Babylon Governorate. No samples were taken, new results in the field were obtained, and no local ratios or measurements were found and documented. The scientific literature was compiled from the available databases and Academic sources (PubMed, Google Scholar) and reports and guidelines issued by international health and environmental organizations. The following English Keywords were used:

Antimicrobial resistance.

Antibiotic resistance genes.

Aquatic environment.

Freshwater.

Rural water.

Wastewater.

One Health.

Human health risk.

The corresponding Arabic terms were used when searching Arabic sources. Reference Selection Criteria

Studies addressing one or more of the following themes were included:

1. Presence of antibiotic resistance genes in water.
2. Prevalence of resistant bacteria in aquatic environments.
3. Sources of pollution related to wastewater, agriculture, or animal husbandry.
4. Mechanisms of resistance gene transmission and persistence in the environment.
5. The relationship between water pollution and health risk indicators.
6. Environmental monitoring of antibiotic resistance within the One Health framework.

Sources not related to aquatic environments or lacking clear methodological information were excluded, as were non-



academic materials lacking verifiable author, journal, or publisher information.

3 Methodology for Analyzing Evidence

Information gathered from studies was categorized into thematic areas, including sources of resistance genes, circulating gene classes, modes of transmission, factors affecting survival, health exposure indicators, and methods for reducing their spread. Overall results were then compared, taking into account differences in water type, study location, sample size, laboratory detection methods, treatment level, and the nature of human or agricultural water use. Evidence interpretation relied on distinguishing between the detection of genetic material and the confirmation of the presence of live or pathogenic bacteria. Furthermore, the results of external studies were not to be directly generalized to Babylon Governorate, but rather used to identify general scientific trends and gaps requiring local field research.

3.1 Methodological Limitations

This review has some main limitations: limited number of sources directly addressing Babylon Governorate, variations in sample

collection methods, variations in sample analysis methods and lack of standardized field data for estimating the prevalence of the genes in field. The results shown are thus based on published evidence and are not a replacement for laboratory and epidemiology investigations.

3.2 Presentation and Analysis of Scientific Evidence

Aquatic environments are known to be important receptacles for ARGs and ARG bacteria, particularly if they are impacted by wastewater, livestock or farmland runoff [6]. Resistance can spread via multiple routes and is a function of human, animal and environmental factors, depending on the region, health and agricultural services and water use [7]. Water has also been found to be a potential vehicle or short-term reservoir of resistance genes, but the occurrence of resistance genes in water does not automatically mean that there are clinical risks associated with it [8]. Table 1 is a summary of the most notable previous studies which dealt with aquatic environments and their association with resistance.

Table 1: Summary of previous studies related to the topic of the review

Researchers and Sunnah	Subject of study	Type of work	The most important points discussed in the study	Its relevance to the current review
Danner et al. (2019)	Freshwater contamination with antibiotics and its effects	Scientific review	Sources of surface water pollution with pollutants, particularly wastewater and runoff from wild areas, were discussed, as well as the potential effects of these pollutants on aquatic organisms.	It supports the analysis of water pollution sources and environmental risk indicators.
Felis et al(2020) .	The presence of antimicrobial preparations in the aquatic environment and their effects	Scientific review	The presentation reviewed the presence of antibiotics in the aquatic environment, the role of wastewater treatment plants in their reaching water sources, and the potential environmental impacts.	The discussion supports the preservation of antimicrobial residues and their sources of water.
Kraemer et al. (2019)	Environmental pollution with antibiotics from an ecology and public policy perspective	Analytical review	Environmental pollution from antibiotics has been linked to microbial changes, the spread of resistance, and the need for multi-sectoral interventions and policies.	It supports the adoption of a One Health perspective and institutional collaboration.



Nnadozie and Odume (2019)	Fresh water as a reservoir for resistant bacteria and resistance genes	Scientific review	The discussion covered freshwater pollution from agricultural runoff and wastewater discharge, methods for detecting resistant bacteria and resistance genes, and their potential persistence in the environment.	The analysis supports the role of freshwater in the survival and transmission of resistance factors.
Nappier et al. (2020)	Antibiotic resistance in recreational waters	Scientific review	The study examined the presence of resistant bacteria and resistance genes in recreational waters, and the possibility of human exposure to them during swimming and water activities.	The discussion supports human exposure, with water types varying across rural environments.
Sánchez-Baena et al (2021) .	Composition of resistant bacterial communities in aquatic environments	Systematic review	Studies on resistant bacteria and resistance genes in natural and artificial aquatic systems have been reviewed.	The analysis of bacterial and genetic diversity supports the need to compare detection methods.
Zheng et al. (2021)	Antibiotics and resistance genes in coastal and estuarine environments	Systematic review	Evidence regarding the presence of antibodies and resistance genes in coastal environments, estuaries, and transmission sources has been gathered	It supports understanding the transfer of resistance factors across water systems, with the environment differing from that of Babylonian waters.

Source: Prepared by the researcher based on previous studies.

Prior works suggest that antibiotic resistance in aquatic ecosystems may be related to the interaction of human, animal and agricultural origins, and that the presence of antibiotic residues, resistant bacteria and resistance genes can be often found in wastewater, agricultural runoff and animal wastes. Published evidence also shows variability in aquatic environment type, sampling techniques and molecular isolation and detection

methods, which restricts the potential for direct quantitative comparisons. Although none of the above studies give results for the localities of Babylon Governorate, it gives a scientific basis for determining the indicators of risks in the design of future field studies taking into account the nature of water sources and their applications in Babylon Governorate, according to the diversity and overlap of water sources as shown in (Table 2).

Table 2: Sources of resistance genes in aquatic environments

Source	How to achieve water resistance	Possible meaning
Domestic Wastewater	Excretion of resistant bacteria and drug residues with feces	Continued presence of resistance factors in the aqueous medium
Animal Waste	Animal waste	Increased selective pressure and resistance transfer
Agricultural Runoff	Carrying waste from the soil and farms to waterways	Water pollution and the spread of resistance to other areas
Improper Disposal of Medications	The arrival of antibiotics or their containers at water sources	Providing conditions that help the survival and selection of resistance



One point of agreement in the various studies has been that wastewater and agricultural and animal run-off are most important routes for the entry of antibiotic-resistant bacteria into aquatic systems. These, however, are not mutually exclusive and the importance of each source will depend on site conditions; the extent of contamination will be influenced by the quality of treatment, quantity of discharge, water motion, soil

characteristics and whether there are any other farming or stocking operations in the surrounding area. If molecular detection is complemented by bacterial isolation, susceptibility testing and identification of genetic transmission factors, the strength of the conclusion would be enhanced and a broadened approach to indicators for assessing health risk should be adopted (Table 3).

Table: 3 classes of genes associated with resistance

Resistance category	Examples of genes	associated antibodies
Beta-lactam	blaTEM ‘blaSHV ‘blaCTX-M	Penicillins and Cephalosporins
Tetracycline	tetA ‘tetM	Tetracyclines
Sulfonamides	sul1 ‘sul2	Sulfonamides
quinolones	qnrA ‘qnrB ‘qnrS	Quinolones

These genes are used as indicators of the presence of resistance factors, but their significance varies depending on the bacteria carrying them, the location of their presence, and the possibility of transmission. The gene may be present in non-pathogenic bacteria, and its genetic material may be revealed after cell death, so the molecular finding should not be equated with the presence of a human infection. These genes will serve as indicators of the presence of resistance factors, but their significance varies depending on the bacteria carrying them, the location of their

presence, and the possibility of transmission. The gene may be present in non-pathogenic bacteria, and its genetic material may be revealed after cell death, so the molecular finding should not be equated with the presence of a human infection. The use of molecular detection in addition to bacterial isolation, sensitivity testing, and identification of genetic transfer elements, further strengthens the conclusion. The determination of the indicators and its interpretation is presented as follows in (Table 4).

Table 4: Health Risk Assessment Indicators

Index	What does it measure?	How to interpret it
Water source type	Degree of probability of water being exposed to sources of pollution	It is explained by the nature of the use and proximity to the point of expenditure.
The presence of bacteria indicates contamination.	General microbial status of water	The existence of resistance genes alone does not prove
Gene diversity of resistance	Number of categories or genes discovered	Greater diversity calls for broader monitoring
The presence of genetic transfer elements	Gene transferability between bacteria	The significance of the result increases when combined with pathogenic bacteria
Water usage	The possibility of human or animal exposure	Drinking water and direct irrigation require greater attention.
Quality of scientific evidence	The strength and comparability of the results	It is affected by sample size, methodology, and documentation.



Thus, the data showed that conducting a risk assessment in the rural waters of Babil should be based on the type of water source and the amount of resistance genes, as well as microbial contamination and water use. Moreover, this review paper is not to make a local contribution in itself but to gather published evidence and find scientific gaps for future field studies. This is a more objective method since review studies offer overall trends and methodological variations and should not be used in lieu of actual local measurements.

4 Discussion

Antibiotic resistance genes are not only present in aquatic environments but may be disseminated in these environments in ways that are not exclusively related to human activities, involving rather multiple sources including domestic and sanitary wastewater, animal waste, agricultural runoff, and unregulated disposal of drugs. The risk of this is especially great when the same water supplies are shared for human, animal and agricultural needs in rural environments where resistant bacteria can be spread from humans, animals and the environment. The detection of a resistance gene in a water sample, however, does not necessarily mean pathogenic bacteria and human infection, and the results should be considered with regard to the environmental, microbial and health aspects. Genes related to resistance to beta-lactams, tetracyclines and sulfonamides are significant markers in water pollution research, as suggested by the literature. Their detection rates may, however, differ as a function of the type of source, level of contamination, size of the sample, method of micro-organism concentration and sensitivity of molecular assays. Thus, it is not always correct to compare studies and extrapolate results from other studies to local estimates. In addition, molecular detection is able to detect living or non-living genetic material, enhancing the use of genetic analysis, bacterial isolation and antibiotic sensitivity testing to effectively assess risk in a realistic nature. In the context of rural water environment in Babylon Governorate, a One Health approach is very important because public health is indirectly related to the quality of water and the safety of agricultural production, veterinary practices and drainage and waste management processes. Health risk cannot be assessed from genes alone but needs to be assessed with respect to the type of water use, presence of bacteria indicative of pollution, proximity of source to waste, and probability of exposure of water to food or human use. Hence, the focus shall be on setting up frequent monitoring programme, enhancing treatment of wastewater, avoiding dumping of wastes in water sources, rationalizing antibiotics prescription and usage, and on creating awareness on health, but not saying that it is the fault of the population. Local findings documented remain crucial to ascertain the level of risk and to design interventions in line with reality of environmental and social conditions in the governorate.

5 Conclusions

Although, based on this review, the possibility of antibiotic resistance genes persisting in and being transmitted by rural aquatic environments may be a viable option, especially in the presence of wastewater and animal and agricultural runoff. But the occurrence of these genes does not necessarily mean that a person will be infected with humans, and should only be regarded as an environmental indicator which needs to be confirmed and fully interpreted in the laboratory. Water in Babylon Governorate is significant for various reasons as water is related to people's life, agriculture and animal husbandry. To evaluate the health risk, this necessitates the integration of molecular testing, isolation of the bacteria, sensitivity testing and knowledge of pollution sources and water use. Periodic monitoring, better drainage and waste management, rational use of antibiotics and better cooperation among the sectors of health, environment, agriculture and veterinary services are key in protecting the community and water resources.

Acknowledgments

The researcher thanks and appreciates all those who gave scientific support or academic directions in preparing this article.

Conflict of Interest

The researcher declares that there are no conflicts of interest that may affect the content of this article.

Funding

This article did not receive any funding from any governmental, private, or commercial entity.

References

1. Danner, M.-C., Robertson, A., Behrends, V., & Reiss, J. (2019). Antibiotic pollution in surface fresh waters: Occurrence and effects. *Science of the Total Environment*, 664, 793–804. <https://doi.org/10.1016/j.scitotenv.2019.01.406>
2. Felis, E., Kalka, J., Sochacki, A., Kowalska, K., Bajkacz, S., Harnisz, M., & Korzeniewska, E. (2020). Antimicrobial pharmaceuticals in the aquatic environment—Occurrence and environmental implications. *European Journal of Pharmacology*, 866, 172813. <https://doi.org/10.1016/j.ejphar.2019.172813>
3. Kraemer, S. A., Ramachandran, A., & Perron, G. G. (2019). Antibiotic pollution in the environment: From microbial ecology to public policy. *Microorganisms*, 7(6), 180. <https://doi.org/10.3390/microorganisms7060180>
4. Nappier, S. P., Liguori, K., Ichida, A. M., Stewart, J. R., & Jones, K. R. (2020). Antibiotic resistance in recreational



- waters: State of the science. *International Journal of Environmental Research and Public Health*, 17(21), 8034. <https://doi.org/10.3390/ijerph17218034>
5. Nnadozie, C. F., & Odume, O. N. (2019). Freshwater environments as reservoirs of antibiotic-resistant bacteria and their role in the dissemination of antibiotic resistance genes. *Environmental Pollution*, 254, 113067. <https://doi.org/10.1016/j.envpol.2019.113067>
 6. Sankhla, M. S., Negaa, Sharma, V., Kumar, R., Awasthi, G., Shukla, R., Yadav, B., & Awasthi, K. K. (2026). Antibiotic residues in aquatic environment: Ecological disruption and biotechnological solutions for environmental safety. *Frontiers in Environmental Engineering*, 5, 1872048. <https://doi.org/10.3389/fenve.2026.1872048>
 7. Sánchez-Baena, A. M., Caicedo Bejarano, L. D., & Chávez-Vivas, M. (2021). Structure of bacterial community with resistance to antibiotics in aquatic environments: A systematic review. *International Journal of Environmental Research and Public Health*, 18(5), 2348. <https://doi.org/10.3390/ijerph18052348>
 8. Zheng, D., Yin, G., Liu, M., Chen, C., Jiang, Y., Hou, L., et al. (2021). A systematic review of antibiotics and antibiotic resistance genes in estuarine and coastal environments. *Science of the Total Environment*, 777, 146009. <https://doi.org/10.1016/j.scitotenv.2021.146009>