



Antibiotic Resistance in Aquaculture: Environmental Dissemination, Ecological Consequences, and Sustainable Mitigation Strategies

Mohammad A. A. Al-Najjar^{1*}

¹Department of Pharmaceutical Sciences and Pharmaceutics, Faculty of Pharmacy, Applied Science Private University, Amman, Jordan,

*Corresponding author: Mohammad A. A. Al-Najjar, Email: moh_alnajjar@asu.edu.jo, ORCID: 0000-0003-0001-6902

Abstract

Aquaculture is one of the fastest growing food production sectors globally, and has become an integral force in satisfying the world food requirement and in contributing to economic development. The fast expansion of aquaculture has however, increased the use of antibiotics to prevent, treat and promote growth, which has helped create a potential for the emergence and spread of antimicrobial resistance (AMR). Certain bacteria and genes (antibiotic resistance genes or ARGs) which are resistant to antibiotics have been discharged from aquaculture and become serious environmental contaminants capable of remaining in water, sediment, cultured organisms and ecosystems. They have the potential to spread, impacting aquatic biodiversity, ecosystem functions, animal health and public health via environmental exposures and food chains. New molecular surveillance studies show that there is now a better understanding of resistance dynamics and alternative disease management strategies, like vaccination and probiotics, improved biosecurity and antimicrobial stewardship can be employed to help reduce reliance on antibiotics. There are still major issues due to non-standardized survey techniques, geographical differences in regulation and a lack of long-term ecological studies. The present narrative review aims to bring together the latest available information on the use of antibiotics in aquaculture, the mechanisms underlying the emergence of antimicrobial resistance, the potential for environmental spread, ecological and human health impacts, and new approaches for sustainable antimicrobial resistance mitigation. It also highlights research gaps and priorities for the future that will inform the development of sustainable aquaculture and reduce the global spread of antimicrobial resistance. The antimicrobial resistance is an emerging issue of the day, in relation to aquaculture, antibiotics and antibiotic resistance genes, and the concept of One Health and sustainable aquaculture.

Keywords: antimicrobial resistance, aquaculture, antibiotics, antibiotic resistance genes, One Health, sustainable aquaculture

1. Introduction

Aquaculture has emerged as a vital contributor to the world's fish supply, providing over 50% of all fish consumed globally, and contributing to the livelihoods, nutrition and economic development of many developing and developed countries. Aquaculture has been growing because of a growing demand for aquatic products, a declining capture fisheries sector and improved technologies. The spread of disease outbreaks due to bacterial pathogens, however, has occurred because of the intensification of fish and shellfish production, which also results in the widespread use of antibiotics for therapeutic, prophylactic and, in some areas, growth-promoting purpose (Lulijwa et al., 2020; Bondad-Reantaso et al., 2023).

Although antibiotics have contributed to the reduction of mortality related to disease and to increased production efficiency, the use of antibiotics for a long time and sometimes in an inappropriate manner has led to increased concerns about the development of antimicrobial resistance (AMR). Selective pressure from antibiotic exposure allows antibody resistant bacteria to survive, multiply and transfer resistance on to other bacteria through a number of mechanisms. Aquaculture has therefore become an increasing source of antibiotic-resistant bacteria (ARB) and antibiotic resistance genes (ARGs), which can then be transferred to other aquatic species and contribute to the presence of ARB in animal and human environments and microbial communities that can impact the environment (Cabello, 2006; Cabello et al., 2016).

Aquaculture is an open aquatic production system in which water continuously flows in and out, and its water ecosystems exchange microorganisms, nutrients, antibiotic residues and antibiotic resistance genes. Concentrations of antibiotics fed to cultured organisms and/or introduced directly into the pond water are frequently high in pond water, sediments and neighboring rivers, estuarine and coastal waters due to the fact that the antibiotics are not fully absorbed by the cultured organisms. Antibiotics can cause the growth and spread of resistant bacteria in these environmental reservoirs for long after treatment has concluded (Watts et al., 2017).

Recent studies have also shown that the emergence of antimicrobial resistance in aquaculture should be considered within the broader context of One Health, as the development of antimicrobial resistance in aquaculture can affect the environment, animal production and human health simultaneously. Humans may also be exposed to resistant bacteria

and ARGs through the consumption of seafood, exposure of water farm workers, recreational water use and contamination of fresh and marine water. Besides, horizontal gene transfer (HGT) also makes it hard to manage infections and restrict the choice of treatment as resistance genes can be transferred from environmental microorganisms to clinically relevant pathogens (Hossain et al., 2022).

Over the last decade, there has been significant research into these interrelated risks. Molecular biology, metagenomics, and whole genome sequencing have made great strides in understanding ARGs in aquaculture systems that has greatly improved the understanding of their diversity, distribution, and evolution. Concurrently, stronger focus is being given to the search for alternative solutions to antibiotics, including vaccination, probiotics and immunostimulants, improved biosecurity and antimicrobial stewardship programs that minimize the use of antibiotics and help maintain animal health and productivity (Nogueira and Botelho, 2021, Zhao et al., 2025).

Despite advances, there are substantial gaps in knowledge pertaining to the relative importance of aquaculture in contributing to AR, persistence of ARGs in the environment, geographic variation of the use of antibiotics and effectiveness of current mitigation interventions. The findings are also inconsistent across regions, although this could be attributed to variation in farming systems, in legislation, in the capacity for surveillance, and in environmental conditions, which makes it difficult to develop management approaches that are applicable across the whole region (Caputo et al., 2023, Xiao et al., 2023).

Therefore, this narrative review aims to critically summarize the current understanding on antibiotic use in aquaculture, the mechanisms of antibiotic resistance, and the environmental dissemination of antibiotics, impact on public health and ecology, and new sustainable methods to reduce antibiotic use. Based on this, the present review provides a summary of current knowledge related to antibiotic use in aquaculture, the mechanisms leading to the development of antimicrobial resistance, the ways in which antibiotics spread in the environment, their ecological and public health effects, and new sustainable solutions to reduce the use of antibiotics. This review integrates the latest scientific knowledge with existing research to identify key research fields and priorities to support environmentally responsible aquaculture and global antimicrobial resistance management.

2. Antibiotic Use in Aquaculture

The intensification of aquaculture has substantially increased the demand for effective disease management, making antibiotics an important component of fish health management in many production systems. Antibiotics are used mainly to treat bacterial infections, to prevent outbreaks in high-yield areas, and, in certain regions, in the past, to encourage growth. But, due to differences in regulatory policies and farming practices, there are significant country-to-country variations in the amount of antibiotics used in aquaculture, with Asia having the highest consumption of antibiotics in aquaculture, accounting for the highest proportion of global aquaculture production (Lulijwa et al., 2020).

Antibiotics are still mainly used in aquaculture for therapeutic purposes. Broad-spectrum antibiotics (oxytetracycline, florfenicol, sulphonamides, quinolones, and β -lactams) are used to control infections caused by bacteria like *Aeromonas spp.*, *Vibrio spp.*, *Edwardsiella spp.*, and *Flavobacterium spp.* can be controlled using broad-spectrum antibiotics (such as oxytetracycline, florfenicol, sulfonamides, quinolones, and β -lactams) (Santos and Ramos, 2018, Deekshit et al., 2023). These antimicrobial agents have played an important role in decreasing disease-related death and enhancing productivity, especially in intensive livestock enterprises where infectious diseases can proliferate quickly.

However, concerns arise because antibiotics administered through medicated feed are often incompletely absorbed by cultured fish. A large portion is excreted as such in the surrounding water and sediments, where it remains and applies selective pressure to the microbial communities in the environment. Residues of antibiotics can thus accumulate in aquaculture systems, and the ARGs can be enriched in aquaculture environmental reservoirs, which can also lead to the emergence of ARGs in the water (Done et al., 2015). Table 1 summarizes the major antibiotic classes used in aquaculture, their therapeutic applications, representative target pathogens, and associated resistance concerns.

Table 1: Common Antibiotics Used in Aquaculture and Associated Resistance Concerns

Antibiotic Class	Common Antibiotics	Major Target Pathogens	Common Resistant Bacteria	Major Environmental Concern	Key References
Tetracyclines	Oxytetracycline	<i>Aeromonas spp.</i> , <i>Vibrio spp.</i>	<i>Aeromonas</i> , <i>Vibrio</i> , <i>Edwardsiella</i>	Sediment accumulation and ARG selection	Cabello (2006); Lulijwa <i>et al.</i> (2020); Santos & Ramos (2018)
Amphenicols	Florfenicol	<i>Flavobacterium</i> , <i>Piscirickettsia</i>	<i>Aeromonas</i> , <i>Flavobacterium</i>	Resistance development during repeated treatments	Miranda <i>et al.</i> (2018); Bondad-Reantaso <i>et al.</i> (2023)

Antibiotic Class	Common Antibiotics	Major Target Pathogens	Common Resistant Bacteria	Major Environmental Concern	Key References
Sulfonamides	Sulfamethoxazole combinations	Gram-negative bacteria	<i>Aeromonas</i> , <i>Vibrio</i>	Dissemination through wastewater	Done <i>et al.</i> (2015); Hossain <i>et al.</i> (2022)
Quinolones	Oxolinic acid, Enrofloxacin	<i>Vibrio spp.</i> , <i>Edwardsiella spp.</i>	Multiple aquatic bacteria	Persistence in aquatic environments	Watts <i>et al.</i> (2017); Yuan <i>et al.</i> (2023)
β -lactams	Amoxicillin	Various bacterial infections	Diverse Gram-negative bacteria	Selection of β -lactamase-producing bacteria	Deekshit <i>et al.</i> (2023); Xiao <i>et al.</i> (2023)

While antibiotics are vital in the control of bacterial diseases, more and more evidence is emerging that their use as prophylaxes and indiscriminately in aquaculture systems has triggered the emergence of antimicrobial resistance. In the past, antibiotics were used before a bacterial infection was identified by laboratory testing, and in some production systems, they were used as a component of routine management rather than as a treatment for bacterial infection. These practices leave pathogenic and non-pathogenic microorganisms under constant antimicrobial stress and enliven the chances of resistant bacterial populations becoming established (Cabello, 2006, Cabello et al., 2016).

The amount of antibiotics used differs widely from country to country, depending on the regulations in place, the level of farming, disease incidence, and veterinary supervision. AmsPs have led to significant decreases in antimicrobial use in countries with well-established programs, including good vaccine strategies, while countries with less regulatory capacity have reported higher antimicrobial use (Caputo et al., 2023). In addition to antibiotic availability, this geographical variation shows that governance, farm management, and biosecurity practices have an impact on antimicrobial resistance.

New evidence, therefore, suggests moving beyond management of the disease by antimicrobials to integrated disease control strategies that involve better husbandry, vaccines, probiotics, and improved biosecurity. Minimizing the need to use antibiotics is one of the best ways to reduce selection pressure, prevent the spread of antimicrobial resistance, and sustain aquaculture production (Mohammed et al., 2025).

3. Drivers and Mechanisms of Antibiotic Resistance

Antimicrobial resistance develops through a combination of biological adaptation and environmental selection, enabling bacteria to survive exposure to antimicrobial agents that would otherwise inhibit growth or cause cell death. Repeated use of antibiotics in aquaculture systems places a high selective pressure on resistant organisms, depleting the susceptible populations. Resistant bacteria can multiply and thus spread the resistance determinants within the aquatic microbial flora, leading to the long-term presence of antimicrobial resistance (Watts et al., 2017).

Resistance can develop either by spontaneous genetic mutation or from the acquisition of resistance genes from other bacteria. The horizontal gene transfer, by transferring antibiotic resistance genes (ARGs) via plasmids, transposons and integrons between various species of bacteria, is one of the most important mechanisms involved in the spread of resistance in aquatic ecosystems. This implies that non-pathogenic environmental microorganisms can serve as reservoirs for genes of resistance that are transferred to clinically important fish and human pathogens (Taylor et al., 2011).

Bacterial resistance is due to multiple molecular mechanisms. Antimicrobials are not active against the bacteria until they have reached the target inside the cell, whereas target-site modification can reduce binding efficiency of antibiotics if mutations occur in the essential bacterial proteins. Bacterial cells have efflux pumps which actively expel antibiotics from the cell, thus decreasing the amount of antibiotic found inside the bacterial cells and that is what multidrug resistance is. Other bacteria make membranes less permeable, thus limiting the uptake of antibiotics and decreasing the effectiveness of treatment. The complementary mechanism often work together in the same bacterial population leading to difficulty in controlling the disease and consequently difficulty in treating the disease (Deekshit et al., 2023, Preena et al., 2020).

Resistance evolution is further enhanced by environmental conditions in aquaculture. High stocking densities cause the accumulation of organic material, bacteria proliferation and the presence of antibiotic residues; conditions are optimal for the interaction of the microorganisms and the exchange of genes. Sediments, biofilms, and wastewater treatment systems are ecological reservoirs in which resistant bacteria and ARGs can survive for long periods after the use of antibiotics has stopped. Environmental reservoirs are sources of continuous resistance circulation and provide more opportunities for resistance to be passed on from aquatic organisms to their environment and in the environment (Buschmann et al., 2012).

However, recent developments in metagenomics have significantly enhanced the knowledge of resistance mechanisms, as the potential for comprehensive analysis of microbial communities without cultivation is greatly increased. Unlike the traditional microbiological approach, the metagenomic sequencing approach can reveal the diversity of bacteria, the genes for resistance, the mobile genetic elements in bacteria, and the ecological connections

among them. These technologies have been used to identify that the aquatic resistome is much more diversified than was previously thought and that many resistance determinants are missing from culture-based surveillance (Hemamalini et al., 2022). The principal biological mechanisms responsible for antimicrobial resistance in aquaculture are summarized in Table 2.

Table 2: Major Mechanisms of Antimicrobial Resistance in Aquaculture

Resistance Mechanism	Description	Representative Genes	Consequences	Key References
Enzymatic degradation	Enzymes deactivate antibiotics	bla , tetX	Loss of antibiotic efficacy	Watts <i>et al.</i> (2017); Deekshit <i>et al.</i> (2023)
Target modification	Mutation alters the antibiotic binding site	gyrA , parC	Reduced drug susceptibility	Preena <i>et al.</i> (2020); Yuan <i>et al.</i> (2023)
Efflux pumps	Active removal of antibiotics	tetA , tetB	Multidrug resistance	Santos & Ramos (2018); Hossain <i>et al.</i> (2022)
Reduced permeability	Decreased antibiotic uptake	Porin modifications	Lower intracellular antibiotic concentration	Deekshit <i>et al.</i> (2023)
Horizontal gene transfer	ARG transfer via plasmids, transposons, integrons	int11 , plasmids	Rapid spread among bacterial species	Taylor <i>et al.</i> (2011); Nogueira & Botelho (2021)

Environmental Dissemination of Antibiotic Resistance

Aquaculture environments are significant reservoirs of the presence and spread of antibiotic resistant genes (ARGs) and antibiotic resistant bacteria (ARB). In contrast to terrestrial livestock production, aquaculture is directly linked to the aquatic ecosystem, with the continuous exchange of water, which allows the transmission of microorganisms, antibiotic residues, and resistance determinants between the systems. This can cause resistance to spread beyond the farm, affecting the environmental resistome at a larger scale (Taylor et al., 2011). After antibiotic treatment, there is a significant amount of antimicrobials excreted in pond water and sediments that are not metabolized. Residual antibiotics exert long-term selection pressure, which favours the presence of ARGs in the population of environmental microorganisms and selects for increased microbially resistant strains. Sediments are especially significant, since they can include organic matter, bacterial biofilms, and antimicrobial residues, and are able to harbor resistant bacteria for an extended period after the application of an antibiotic has been ended (Done et al., 2015).

Horizontal gene transfer also promotes spread in the environment by allowing ARGs to be transferred from environmental microorganisms to bacterial pathogens via plasmids, transposons, and integrons. This genetic interchange takes place within aquaculture ponds as well as in rivers, estuaries, and coastal ecosystems that receive aquaculture effluents. Therefore, environmental bacteria can act as long-term reservoirs, even after antibiotic use has dropped.

Advances in metagenomic sequencing methods have greatly enhanced the knowledge of ARG distribution in aquatic ecosystems in recent years. One key advantage of metagenomics over traditional culture-based approaches is its ability to identify all members of the bacterial communities, resistance genes, and mobile genetic elements from environmental samples simultaneously. These studies have identified that aquaculture-related sediments and effluents have a significantly higher diversity of ARGs than previously known, and therefore, environmental monitoring programs are crucial for AMR surveillance (Hemamalini et al., 2022).

The spread of resistance may be further exacerbated by changes in microbial community structure associated with climate change, higher water temperatures, and increased disease outbreaks that are likely to result in more antimicrobial usage. Warming up can promote the growth of resistant bacteria and increase horizontal gene transfer and the resulting accumulation of resistance in aquatic environments. These interactions suggest that antimicrobial resistance should be taken into account in addition to the other environmental issues that influence the sustainability of aquaculture (Reverter et al., 2020, Suyamud et al., 2024). Representative studies investigating environmental dissemination of antimicrobial resistance in aquaculture are summarized in Table 3

Table 3: Literature Matrix of Representative Studies

Authors	Year	Country/Region	Focus	Methodology	Major Findings
Cabello	2006	Global	Antibiotic use	Narrative review	Highlighted excessive prophylactic antibiotic use and associated AMR risks
Done <i>et al.</i>	2015	Global	Environmental AMR	Review	Aquaculture contributes uniquely to the dissemination of aquatic resistance

Authors	Year	Country/Region	Focus	Methodology	Major Findings
Lulijwa <i>et al.</i>	2020	Top 15 aquaculture-producing countries	Antibiotic use and regulation	Systematic review	Large regional differences in antibiotic use and governance
Reverter <i>et al.</i>	2020	Global	Climate change and AMR	Review	Climate change may exacerbate antimicrobial resistance in aquaculture
Hossain <i>et al.</i>	2022	Global	ARGs and ARB	Review	Emphasized the One Health perspective and environmental dissemination
Hemamalini <i>et al.</i>	2022	Freshwater aquaculture	Metagenomics	Review	Molecular tools improve ARG detection but lack standardization
Bondad-Reantaso <i>et al.</i>	2023	Global	Antibiotic alternatives	Review	Vaccination, probiotics, and biosecurity reduce antibiotic dependence
Caputo <i>et al.</i>	2023	Global	AMR policies	Literature review	National AMR action plans vary considerably among countries
Yuan <i>et al.</i>	2023	Global	Antibiotics and ARGs	Review	Environmental reservoirs are central to ARG persistence
Mohammed <i>et al.</i>	2025	Global	Emerging mitigation strategies	Review	Integrated disease management is recommended over antibiotic reliance

5. Ecological and Human Health Implications

The spread of antimicrobial resistance is not confined to aquaculture production, and poses substantial ecological and public health challenges. Changes in microbial community, nutrient cycling and ecosystem resilience in water can be brought about by ARGs and antibiotic resistant bacteria. Furthermore, the antimicrobial residues might remain long after the treatment and affect non-target organisms that play an important role in maintaining the healthy function of the aquatic system and therefore the health of biodiversity and ecological stability of the aquatic system (Yuan et al., 2023).

Several ways aquaculture-related resistant bacteria can be introduced to humans from a public health point of view, such as from the consumption of seafood that has been contaminated, aquaculture workers coming in contact with each other during their work, recreational activities in contaminated waters, and environmental movement from connected freshwater and marine ecosystems. Although there is currently little direct evidence for people to suffer from clinical infections from aquaculture, ARGs have been found in the environment which implies aquaculture should be viewed from a One Health perspective, recognising that the animal, environmental, and human health sectors are interconnected (Cabello et al., 2016).

In addition, international cooperation is important to promote antimicrobial stewardship as aquaculture expands around the world. Countries with high levels of antibiotic production and low levels of monitoring and regulation may be the largest contributors to environmental dissemination, while countries with high monitoring, responsible antibiotic usage, and vaccination policies have lower levels of antibiotic usage and better results with disease management (Bondad-Reantaso et al., 2023). Therefore, a coordinated and collaborative response between producers, researchers, regulators and public health professionals under the umbrella of One Health is required in order to tackle AMR.

6. Detection, Monitoring, and Sustainable Mitigation Strategies

Effective AMR management in aquaculture relies on the correct surveillance and management of AMR, responsible antibiotic use, and sustainable disease control measures. Resistant bacterial pathogens have been traditionally detected by culture-based methods and antimicrobial susceptibility testing. As described above, these methods are also useful for assessing phenotypic resistance, but do not provide much information about the wider variety of antibiotic resistance genes (ARGs) that might be present in the water, as many environmental microorganisms are not cultured in laboratory conditions (Preena et al., 2020).

In recent years, molecular methods have greatly contributed to the monitoring of resistance. Rapid detection of ARGs directly from water, sediment, and aquaculture organisms can be achieved by the use of polymerase chain reaction (PCR), quantitative PCR (qPCR), whole genome sequencing, and metagenomics analyses without prior culture. The value of metagenomics technologies is that they can characterize microbial communities, resistome genes, and mobile genetic elements all in a single project to understand the aquatic resistome as a whole. However, there are still

methodological biases in sampling, sequencing platforms, and bioinformatic analysis, which should be standardized in surveillance protocols (Nogueira and Botelho, 2021).

Reducing antibiotic dependence is equally important for controlling AMR. Antimicrobial stewardship programmes promote evidence-based antibiotic prescribing, laboratory confirmation of a bacterial infection, respect for withdrawal periods and ongoing surveillance of antimicrobial use. Stewardship programmes with a broader scope are associated with lower antibiotic use and better antibiotic use management outcomes than areas with less oversight (Lulijwa et al., 2020).

Preventive disease management offers additional opportunities to minimize antibiotic use. Several commercial sectors of aquaculture have been successful in lowering the incidence of bacterial diseases through vaccination, and other alternatives such as probiotics, prebiotics, phytochemicals, immunostimulants, and bacteriophages have proven to be effective in improving host immunity, but do not pose a strong selection pressure for the emergence of resistance. Additionally, enhanced farm biosecurity measures, correct stocking rates, water management, and regular health checks on the farm minimise the chance of disease outbreaks and the need for antibiotics (Zhao et al., 2025). Table 4 summarizes the principal sustainable strategies currently recommended to mitigate antimicrobial resistance in aquaculture.

Table 4: Sustainable Strategies for Mitigating Antimicrobial Resistance in Aquaculture

Strategy	Principle	Advantages	Limitations	Representative References
Antimicrobial stewardship	Rational antibiotic use	Reduces selective pressure	Requires regulatory enforcement	Caputo <i>et al.</i> (2023); Lulijwa <i>et al.</i> (2020)
Vaccination	Disease prevention	Significant reduction in antibiotic use	Pathogen-specific; not available for all diseases	Bondad-Reantaso <i>et al.</i> (2023)
Probiotics	Competitive exclusion and immune enhancement	Environmentally friendly	Variable efficacy across species	Mohammed <i>et al.</i> (2025); Zhao <i>et al.</i> (2025)
Improved biosecurity	Prevent disease introduction	Reduces outbreak frequency	Increased management costs	Santos & Ramos (2018); Bondad-Reantaso <i>et al.</i> (2023)
Metagenomic surveillance	Detection of ARGs and microbial communities	Comprehensive monitoring	High cost and need for bioinformatics expertise	Nogueira & Botelho (2021); Hemamalini <i>et al.</i> (2022)
One Health approach	Integrated human–animal–environment management	Supports sustainable policy development	Requires intersectoral collaboration	Reverter <i>et al.</i> (2020); Hossain <i>et al.</i> (2022)

7. Discussion and Synthesis

The antimicrobial resistance literature clearly shows that this resistance in aquaculture is not due to exposure to antibiotics alone but rather due to the combination of antibiotic use, microbial adaptation, environmental reservoirs, and management practices. While the use of therapeutic antibiotics is still critical to control bacterial diseases, the misuse contributes to the development of resistant bacterial strains and/or to the maintenance of ARGs in aquatic ecosystems (Cabello, 2006).

A major theme emerging from recent studies is the increasing recognition of environmental reservoirs as critical components of resistance dissemination. However, even after antibiotic use has decreased, resistance genes can be found in sediments, biofilms, wastewater, and surrounding aquatic environments, which serve as long-term reservoirs for resistance genes to persist and be transmitted horizontally (Yuan et al., 2023). Therefore, a decrease in antibiotic use is not likely to remove existing resistant bacteria from the environment.

Another key finding is the increasing focus on integrated disease prevention. There is evidence that the use of vaccination, better husbandry, molecular surveillance, and antimicrobial stewardship is more sustainable for long-term control than the use of antimicrobials alone. There are, however, inconsistencies in the different ways that surveillance is undertaken in different regions, as well as inconsistent regulatory capacity and implementation of One Health principles (Caputo et al., 2023), which require the harmonization of monitoring frameworks and enhanced application of One Health principles across the globe.

Research gaps and future directions

Despite substantial progress, several important research gaps remain. One, internationally agreed upon standardized protocols to monitor antibiotic-resistant bacteria and ARGs, there are none, which makes comparisons complicated among studies. Second, most of the investigations available are cross-sectional, and long-term investigations into resistance persistence and ecological recovery are limited. Third, much of the research is focused on the major

aquaculture production areas, with a major knowledge gap in many developing countries. Fourth, the combined effects of climate change and antimicrobial resistance are currently not fully understood, as environmental conditions may affect the microbial ecology and disease dynamics, which should be further investigated.

Future studies should combine metagenomics, whole genome sequencing, environmental DNA technologies, and One Health surveillance programs for a more effective detection of emerging threats of resistance. Antimicrobial stewardship and international collaboration on environmental monitoring should also be increased, as well as the assessment of the long-term effectiveness of other antibiotic alternatives (e.g., vaccination, probiotics) under commercial farming conditions.

Conclusion

One of the biggest threats to the sustainability of modern aquaculture is antimicrobial resistance. Antibiotics have been overused giving rise to antibiotic resistant genes and bacteria that are present in aquatic systems and may be shared via interconnected ecological pathways. The evidence so far suggests that effective resistance management will require a transition from resistance-driven disease control to integrated disease prevention strategies that involve the use of antimicrobial stewardship, vaccination, improved biosecurity, molecular surveillance and sustainable farming systems.

The need for a standardized monitoring system should be highlighted and more cooperation between the aquaculture, environmental, veterinary and public health sector should be promoted in order to reduce the emergence of AMR. Future research needs aimed at filling these gaps will continue to help make evidence-based, informed policy decisions for aquaculture to be productive without compromising environmental protection and public health.

Acknowledgement

The authors would like to thank the work of the researchers that is published as the scientific basis of this narrative review. No external funding was received for this study. The authors do not have any declarations of conflict of interest.

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