

Cross-Species Analysis of Antibiotic Resistance Gene Evolution in Aquatic Environments

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Description

Antibiotic resistance is one of the most pressing global health threats and the emergence of resistant pathogens in aquatic environments has become a significant concern. Antibiotic-Resistant Bacteria (ARB) and their Antibiotic Resistance Genes (ARGs) are selected for and propagated by antibiotic residues, which frequently end up in rivers, lakes and seas due to the extensive use of antibiotics in human health, veterinary care and agriculture. These aquatic environments act as crucial ARB reservoirs, where resistance genes may be transferred across species, resulting in the emergence and spread of populations that are resistant to many drugs. To effectively reduce the negative effects of antibiotic resistance on the environment and human health, it is essential to comprehend how these resistance genes change and spread across species in aquatic habitats.

Freshwater bodies and seas are examples of aquatic habitats, which are complex ecosystems that are home to a variety of microbial species. Bacteria and viruses, as well as fungi and even higher species like plants and mammals, have Antibiotic Resistance Genes (ARGs). High microbial variety, interactions among aquatic animals and the ongoing influx of anthropogenic toxins can all make aquatic ecosystems hotspots for the production and spread of these genes. Horizontal Gene Transfer (HGT), the mechanism by which bacteria transmit genetic material, including ARGs, is made possible by the high density of microorganisms in aquatic settings. HGT may take place in these settings between various bacterial species, genera and even between pathogenic and non-pathogenic strains, which makes it easier for antibiotic resistance to spread widely. Antibiotics in the water also put microbial populations under selective pressure, which promotes the survival of resistant species. Resistance genes and bacteria can spread across great distances thanks to the worldwide movement of water bodies, such as rivers flowing into seas and oceans. Therefore,

antibiotic resistance spreads around the world because ARGs present in aquatic habitats are not limited to their local ecosystems; they can move and perhaps impact distant locations.

The three primary mechanisms of transformation, transduction and conjugation are the main ways that Horizontal Gene Transfer (HGT) spreads Antibiotic Resistance Genes (ARGs) among bacteria in aquatic settings. During transformation, bacteria absorb free DNA from their surroundings and integrate genes resistant to antibiotics into their own genome. Because bacteria may collect resistance DNA from polluted water, this mechanism is frequently seen in aquatic settings with dissolved organic materials. Bacteriophages, or bacterial viruses, are the means by which genetic material is transferred between bacteria. These viruses, which are prevalent in aquatic environments, serve as vectors, dispersing genes that confer resistance to antibiotics and encouraging genetic variety among bacterial populations, both of which can hasten the evolution of resistance. The third method, conjugation, enables bacteria to transmit plasmids circular DNA molecules carrying ARGs, but it necessitates direct cell-to-cell contact. This approach works exceptionally well in aquatic settings, notably in biofilms formed by bacterial populations or when bacteria are stressed by antibiotics. Since it causes quick and extensive resistance across a variety of bacterial species, the transfer of resistance plasmids between species during conjugation is worrisome. The ability of ARGs to transfer across species is a major concern in the context of antibiotic resistance in aquatic environments. Cross-species gene transfer can make previously curable illnesses more difficult to control by transferring a resistance gene from one bacterial species to another, or even from non-pathogenic bacteria to pathogenic bacteria. Bacterial genome plasticity and the previously mentioned HGT mechanisms enable this cross-species interchange. In aquatic environments, cross-species gene transfer has an effect that extends beyond bacterial diseases. Antibiotic resistance genes have been discovered in fungi, viruses and even aquatic plants, which further muddies the dynamics of resistance as a whole. In some situations, human infections can develop resistance through interactions with other species in the ecosystem and aquatic fungus and bacteria can trade resistance genes.

Conclusion

The global health community is seriously threatened by the emergence and dissemination of antibiotic resistance genes in aquatic settings. The fast spread of ARGs across many bacterial populations through cross-species gene transfer can lead to the establishment of resistant diseases. This problem is made worse by anthropogenic activities, which introduce contaminants and antibiotics into water systems, fostering an environment that is conducive to the emergence and spread of resistance. To lessen the negative effects of antibiotic resistance on human and environmental health, it is essential to comprehend the mechanisms underlying gene transfer and track the expansion of ARGs in aquatic habitats.