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Chapter

Effects of Antibiotics on Impacted Aquatic Environment Microorganisms

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Abstract

Due to their mass production and intense consumption in human medicine, veterinary, and aquaculture, antibiotics have been widely detected in different ecosystems, leading to a growing worldwide concern. These and their byproducts are being continuously discarded in natural ecosystems via excretion of human and animal urine and feces, also domestic and hospital effluents. Residues of these drugs can persist in natural environments through bioaccumulation due to their difficult biodegradation. Also, they have a gradual deposition in sediments, aquatic surfaces, and groundwater. Studies have shown the presence of these drugs in aquatic environments, which can trigger severe changes in the composition and structure of the bacterial community, such as the ability to develop and propagate genes resistant to these pollutants. In this context, this review aims to address the effects of the antibiotics on microorganisms present in impacted aquatic environments.

Keywords: bacteria, resistance genes, pollutants

1. Introduction

Water, as an essential resource for the maintenance of life, must be ingested in significant amounts daily. However, when this substance does not correspond to levels suitable for human consumption, it can represent a means of transmitting diseases [1]. According to the World Health Organization – WHO (2016) [2],

approximately half of the developing world population will be affected by infections directly related to water outside the quality standards either-or with lack of adequate or even non-existent sanitation.

The inappropriate disposal of residential waste, industrial, and agricultural effluents cause an imbalance in natural aquatic ecosystems. The amount of pollutants interferes with the proper functioning of the fauna and flora of these environments and, consequently, cause damage to the man himself [3]. Among the polluting agents of these ecosystems are pharmaceutical products, which are called emerging contaminants, of which antibiotics have been the subject of studies [4, 5].

Antibiotics are natural, synthetic, or semi-synthetic compounds developed and widely prescribed for therapeutic and prophylactic use against microbial infections in humans and animals [6, 7]. Besides, they have been widely used to stimulate the growth and production of animal [8–10]. The consumption of these drugs has increased considerably in recent decades, which is considered an emerging contaminant increasingly present in several environments, such as water [11, 12].

Despite being found in low concentrations in aquatic environments, data from the literature show that the presence of these contaminants causes negative impacts on several non-target organisms, such as microbial populations [13–15]. Changes in these populations can affect the maintenance of biological processes and change the structure of the entire ecosystem [16].

These drugs are considered the main source of changes in natural environments and influence a diversity of processes, including the development of antibiotic resistance and the spread of genes through horizontal gene transfer (HGT) [12, 17, 18]. Thus, the aquatic environment is considered efficient for the selection of bacterial populations resistant to antimicrobials, through mobile genetic elements [8]. Increased resistance to antimicrobials is often associated with a high adaptive capacity of microorganisms, with bacteria being more susceptible to changes and gene acquisition [19, 20].

Constant monitoring of bacterial communities is a tool that can lead to an understanding of the complexity of this phenomenon and the impact of human activities on natural environments [21]. In this context, this review aims to address the effects of antibiotics on microorganisms present in impacted aquatic environments.

2. Antibiotics

Antibiotics can be either from chemical compositions, derived from natural sources, or synthetic or semi-synthetic formulations. Compounds capable of inhibiting the growth of the invading microorganism, are classified as bacteriostatic. However, those that promote their microbial destruction are bactericidal [22]. The most appropriate antibiotics for the treatment of infections, by any infectious agents, are those that exert their respective mechanisms of action, directly on the pathogen without causing damage to the host, in other words, they present selective toxicity. However, all of these medications can have side effects [23].

They are usually classified according to their respective spectra and mechanisms of action. Through the description and synthesis of new compounds, it was necessary to organize them into the following groups: inhibitors of cell wall synthesis, inhibitors of cytoplasmic membrane synthesis, protein synthesis inhibitors in ribosomes, alteration of nucleic acid synthesis, and alteration of cellular metabolism [24]. The main targets of antibiotic action can be seen in **Figure 1**.

Its prescription, often, considers the symptoms presented by the patients and has no basis in more accurate clinical diagnoses that indicate the need for certain antibiotics or the appropriate dosages for each case [25]. Generally, there are several
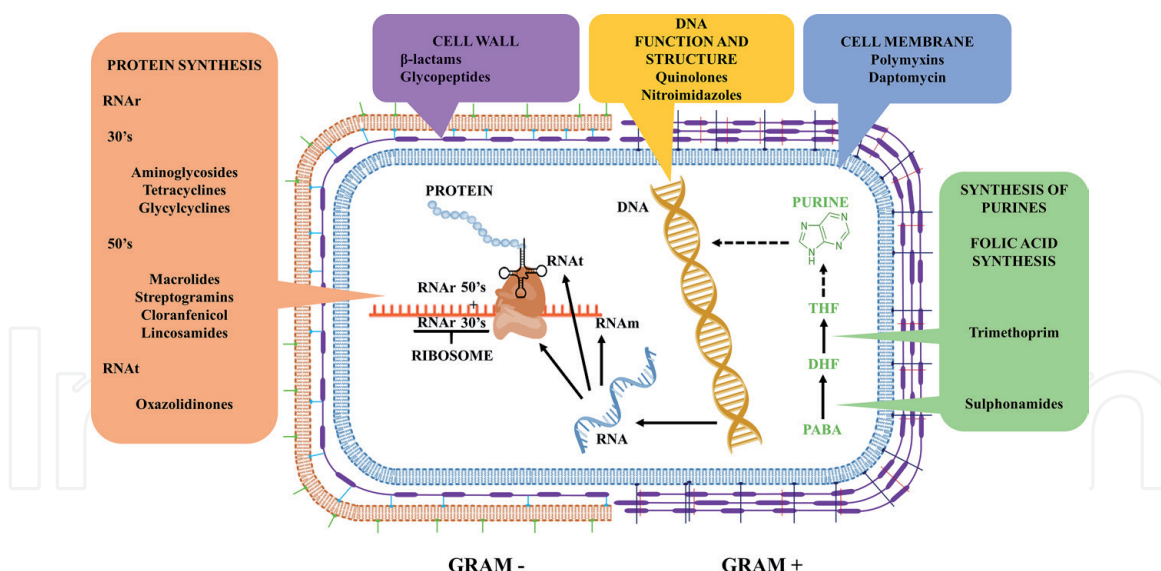
Figure 1.
Classifying scheme of the action mechanisms of antibiotics.

independent factors associated with non-compliance with the guidelines for antimicrobial prophylaxis, such as the lack of well-defined protocols, the lack of knowledge and updating, the lack of communication or disagreement between the prescribing professionals and the absence of tax audits [26]. For this reason, all health institutions and clinical analysis laboratories must use the same procedures and interpretive criteria, especially in the case of bacteria producing carbapenemases [27].

The discovery of antibiotics, initially penicillin by Alexander Fleming in 1928, was a milestone in the history of medicine and represented one of the most important therapeutic interventions for the control of diseases caused by bacteria. Thus, until the early 1960s, more than 20 classes of antibiotics were marketed worldwide. However, since that period, only two new classes were added to this group of drugs [28].

Thus, the obtention of new effective active ingredients capable of reaching different bacterial targets has been significantly reduced, so that new therapeutic approaches are essential to minimize the damage generated to human health [29, 30]. Also, The search for new molecules that have at least one synergistic mechanism in association with drugs already known, thus enhancing their effects, have been highlighted and may help the therapy of infections caused by microorganisms [31, 32].

The diversity of resistance genes identified in pathogenic bacteria, it is pointed out as one of the main causes of the growing increase in antibiotic resistance. However, the prevalence of bacterial resistance both regionally and on a global scale is highly attributed to the mechanisms of dissemination of virulent bacteria, which can colonize and adapt in various environments, including the aquatic [33, 34].

3. Antibiotics in aquatic environments

The extensive and continuous consumption of antibiotics is directly related to their presence in the environment, and for this reason, they have aroused a growing worldwide concern [12, 35]. Also, it estimated that a few thousand tons of these drugs are produced annually, and part of them is introduced into various ecosystems, including aquatic ones [36–38].

It is known that antibiotics can occur naturally in the environment. However, anthropogenic activities are considered the major source of these pollutants. Among these activities, the use in human and veterinary medicine for the treatment and prevention of bacterial infections stands out [7, 39].

After the administration of these drugs, they are not fully metabolized and absorbed by the body of the human or animal, there about 90% of the residues of each dose is excreted in the urine, and 75% of the remainder eliminated in the feces [40, 41]. These non-metabolized compounds are discarded in domestic and hospital effluents, and they can be partially disposed of in water treatment plants, following until they reach natural aquatic environments, such as rivers, lakes, seas, and groundwater [42, 43].

Another important source of environmental contamination by these drugs is through aquaculture, which also contributes to the contamination of the surface, groundwater, and sediment due to the use of antibiotics as fish food additives to promote growth and prevent disease [44, 45]. The pharmaceutical industry can also be considered a relevant source due to the disposal of effluents generated during the synthesis, processing, and filing of these compounds [46–48].

The dynamics of these compounds in the environment is determined by various physical-chemical and biological processes in soil-water systems, being dependent on structural characteristics of antibiotics, properties of soil and water, as well as environmental parameters, such as geographic location, temperature, and pH [10, 49–52]. In aquatic environments, antibiotics are being detected in low concentrations (ng/L e µg/L) [53–55]. However, some of these drugs can persist in the environment due to their low biodegradation. Consequently, they trigger their bioaccumulation and biomagnification [46, 56].

The presence of antibiotics in the natural environment, even in low concentrations, can affect the survival, reproduction, metabolism of populations of organisms, in addition to changing the structure of communities and ecological functions of ecosystems [57–59]. In this context, several studies have shown that these drugs trigger toxic, acute, either-or chronic effects in organisms of different trophic levels, such as bacteria, fungi, algae, invertebrates, and fish [60–62].

4. Effects of antibiotics on microorganisms in aquatic environments

Antibiotics were strategically developed to act against pathogenic microorganisms, and their advantages for the control and treatment of infectious diseases are indisputable [62]. However, its bioactive properties, the increase in its presence in the environment, and its toxicity on non-target organisms have aroused growing concern worldwide [15, 63].

Among the different groups of organisms, microorganisms are considered the most sensitive and most affected by the action of these drugs [61, 64]. Their bactericidal and bacteriostatic effects can trigger changes in the structure of microbial populations and their ecological functions in the environment. Microbial biodiversity is essential for the maintenance of biological processes in aquatic and terrestrial environments, including biogeochemical cycles [16].

Studies have shown that the presence of antibiotics, even at low concentrations, can cause changes in essential microbial processes for the ecosystems, such as nitrogen transformation, methanogenesis, sulfate reduction, nutrient cycle, and degradation of organic matter [16, 59, 65].

Another widely discussed effect of this class of drugs on the environment, it is the contribution to the emergence of antibiotic-resistant bacteria (ARB), and genes of resistance to antibiotics (GRA) [66]. Antibiotic resistance may occur naturally in the environment, but the increase has been reported due to the overuse and inappropriate disposal of these drugs. According to WHO, the occurrence of BRA and GRA is recognized as one of the most worrying public health problems of the century, with GRA being considered an emerging environmental pollutant [12, 67].

Among the different ecological niches, the aquatic environment is considered the most efficient for the selection of resistant bacterial populations. This environment is prone to constant changes that can apply selective pressure, favoring the evolution of these microorganisms regarding the adaptation process to various antimicrobial agents [68].

Literature data have been reporting the presence of antibiotic-resistant opportunistic pathogens such as *Escherichia coli*, *Klebsiella pneumoniae*, *Acinetobacter* spp., *Pseudomonas* spp., *Shigella* spp. [69–71], in several urban rivers, lakes, and streams, which receive an untreated effluent discharge domestic, hospital, and industrial, or inefficient water treatment plants [72–74].

Studies have shown that ARBs are introduced in these environments mainly by contamination by enteric bacteria that are exposed to high concentrations of antibiotics in the gastrointestinal tract of humans and animals [75]. Among various sources of these bacteria, urban water treatment stations stand out due to their high microbial density and the high presence of contaminants such as antibiotic residues, pharmaceuticals, heavy metals, among others. The combination of these substances puts selective pressure on these microorganisms, amplifying the development of resistance and its dissemination [76–78].

These bacteria act as a source of resistance in natural environments and can spread GRAs present in the environment [79]. Literature data suggest that the increase in the frequency of resistant bacteria in the water is influenced by the spread of GRAs among bacterial populations through vertical gene transfer (VGT) and horizontal gene transfer (HGT). VGT is parental genetic transmission via reproduction, and mutations in bacterial DNA can occur. On the other hand, HGT consists of the exchange of genes between microorganisms, intra or inter-specific, through mobile genetic elements, such as plasmids and transposons encoding antimicrobial resistance [80–82].

As mentioned above, microorganisms present in these impacted aquatic environments can develop different resistance mechanisms to adapt to the stress caused by various contaminants, such as heavy metals. Studies suggest that contamination by metals in the natural environment may play an important role in maintaining and proliferating resistance to antimicrobials [83–85]. In these environments, the selective pressure exerted by metals can select resistant isolates in a similar way to antibiotics, since both resistance genes are often located in the same moving elements [86, 87].

Martins et al. [88] observed that *P. aeruginosa* isolate, obtained from a contaminated river in southeastern Brazil, presented a conjugative plasmid with co-resistance to tetracycline and copper, reinforcing that resistance to antibiotics can be induced by the selective pressure of heavy metals in the environment. Rasmussen and Sorensen [89] demonstrated an increase in the occurrence of conjugative plasmids in contaminated sites. They observed that the mercury and tetracycline resistance genes were located on the same plasmid. This data that corroborates with the study carried out by Araújo et al. [90], who verified genes for resistance to mercury and tetracycline in isolates of *K. pneumoniae* obtained from an impacted urban stream in Pernambuco, Brazil.

In this way, not only the indiscriminate use of antibiotics but also environmental contamination by other substances can pose risks and damage to the environment and human health, since resistance genes can be transferred horizontally from environmental microorganisms to human commensals [91, 92]. Given this problem, there is a clear need to develop research and technologies for monitoring and removing these substances in the aquatic environment, in order to reduce their impact on the environment and public health.

5. Conclusion

The presence of antibiotics in aquatic ecosystems, although considered less than other contaminants, can alter the microbiota of these environments and favor the emergence of multi-resistant bacterial populations. Considering the importance of water bodies for human subsistence and due to the risk of bacterial spread, strategies for controlling the disposal of these contaminants must be evaluated, as well as the other agents that impact aquatic environments.

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