

The Role of Antibiotics in Environmental Pollution

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ABSTRACT: *Among the most effective medications used for human therapy are antibiotics. As they can challenge microbial communities, however, they must also be treated as essential contaminants. Antibiotics are commonly used for livestock farming and for agricultural uses, in addition to being used for human therapy. Antibiotics and antibiotic resistance genes that can contaminate natural environments can include residues from human environments and from farms. Selection of resistant bacteria is the clearest result of antibiotic release in natural ecosystems. At present, the same resistance genes found in therapeutic environments are spread to sterile environments without any evidence of antibiotic contamination. However, the impact of antibiotics on the biosphere is larger than that, and the composition and function of environmental micro biota may be influenced. Throughout the paper, we discuss the effect that antibiotic pollution or antibiotic resistance genes may have on human health as well as on the development of microbial species in the setting.*

KEYWORDS: *micro-biosphere, antibiotics, pathogens, World Health Organisation (WHO), Horizontal Gene Transfer (HGT).*

INTRODUCTION

Antibiotics are perhaps the most effective drug family that has been created to benefit human health so far. In addition to this basic use, antibiotics have also been used in the prevention and treatment of diseases in animals and plants and in the encouragement of development of animal farming. Both these applications have contributed to the introduction of antibiotics in vast quantity into natural environments[1]. The cumulative impact of antibiotics on the population dynamics of the micro-biosphere is little understood. However, in selecting antibiotic-resistant microorganisms that may harm human health, the impact of antibiotics used to treat diseases or for agricultural purposes has been studied in more depth[2].

The growing development of antibiotic resistance in human pathogens is of particular concern, as reported by the World Health Organisation, not only in the treatment of infectious diseases, but also in other pathologies in which antibiotic prophylaxis is important to prevent related infections. In this respect, "the spread of antibiotic-resistant bacteria." implies that once previously taken for granted, common surgical practices may be conceivably consigned to medical limbo. The effects are almost unthinkable"[3]. It is important to remember that environmental microorganisms develop several antibiotics. In the other hand, antibiotic resistance genes gained by Horizontal Gene Transfer (HGT) pathogenic bacteria have also emerged in environmental bacteria, while they may emerge later during the treatment of infections under

intense antibiotic selective pressure. We would also need to discuss the study of antibiotics and their resistance genes, not only in clinics, but also in normal non-clinical settings, to best understand the evolution of resistance. The condition with antibiotics and their resistance is comparable in certain ways to the toxicity of heavy metals. Heavy metals are natural compounds found in numerous environments, much like antibiotics[4]. Their use by humans, however, has improved their bioavailability, adding to drastic improvements in degraded habitats. Antimicrobials mainly change the micro-biosphere, unlike heavy metals that challenge all aspects of life, and the effects of antibiotic contamination on ecology have undoubtedly attracted less consideration because of this.

The role of antibiotics in ecosystems

It has been generally accepted that their function in nature would be to inhibit microbial competitors, provided that antibiotics are effective inhibitors of bacterial growth created by environmental microorganisms. Antibiotic resistance determinants, on the other hand, should help to prevent antibiotic action in such a way that they are a clear example of the Darwinian battle for survival[5]. While this may also be valid, an alternate theory has been suggested that antibiotics may be signal molecules that shape the structure of microbial communities. According to this view, the hermetic influence of antibiotics is advantageous at low doses that are likely to be present in most natural environments and detrimental at high concentrations used for therapy. Similarly, it has been reported that in their original hosts, certain elements that serve to withstand high antibiotic concentrations have different functional functions. As a result of human activity, the strong rise of antibiotic concentrations in natural environments transfers the original functions of antimicrobials and resistance components to the weapon/shield positions they play in hospitals or farms. These changes may affect not only the selection of microorganisms that are immune to antibiotics, but also the composition of normal microbial communities, and may also alter the morphology of microorganisms.

The consequences of antibiotic pollution

Antibiotic application chooses immune microorganisms for medicinal or agricultural purposes. It is also predictable that all forms of toxins would produce contaminants from hospitals or farms: antibiotics and resistance genes. The destiny of these forms of contaminants, though, is probably different. Multiple antibiotics are natural chemicals that have been in interaction with aquatic micro-biota for millions of years and are also biodegradable, even serving many microorganisms as a food resource. Biodegradation can be more refractory to synthetic antibiotics (e.g. quinolones)[6]. They are also degraded, though, in natural habitats at varying amounts. Ciprofloxacin found in river water samples has been shown to be totally degraded after 3 months, although only 20% of the oxolinic acid present in these samples is entirely degraded

after 5 months. Latest study has shown that their biodegradation is hindered by the binding of quinolones to soil and sediments.

Nonetheless, quinolone-polluted water waste water treatment successfully eliminates these antibiotics by methods that require not only biodegradation, but also photo-degradation. It has been shown, consistent with these results that most antibiotics are usually below detectable limits in groundwater samples, although they are more stable after sediment adsorption[7]. Sediment samples from antibiotic-polluted areas therefore have higher concentrations of antibiotics than water samples from the same location.

Effects of antibiotics on ecosystems

The majority of antibiotics used for the prevention or treatment of human or animal diseases, as well as for the development of faster livestock development, are only partly metabolized and then discharged through the excreta, either to sewage treatment plants or directly into the waters or soils. In addition, antimicrobial agents used in extensive fish farming are directly applied to the water, resulting in high local concentrations in both the water and surrounding sediments. In addition, antibiotics are topically applied to contaminated plants' aerial organs, but the amount of antibiotics used in plant farming is limited relative to human and veterinary medicine and the development of livestock[8]. In 1998, in order to mitigate the impact that the release of antibiotics for non-human use may have on the selection of resistance in human pathogens, the European Union prohibited the feeding to livestock of certain antibiotics useful in human medicine for growth promotion. In 2006, all antibiotics and associated medications were extended to include the ban. Similarly, the usage of antibiotics in aquaculture has been limited in many countries, with stringent limits on the use of antibiotic prophylaxis and the ban of the use of antibiotics that are still effective in the treatment of human infections. In many developed nations, for example, the use of quinolones for aquaculture has been prohibited because resistance to one member of the family typically confers resistance to all quinolones at the same time, and because these antibiotics can stay active for long periods in sediments.

Preservation of antibiotic resistance genes

The understanding of their effects on bacterial physiology is a key issue for predicting the fate of antibiotic resistance genes in natural environments. It has been assumed that antibiotic resistance gives the resistant bacteria a metabolic burden in order to be out-competed by their wild-type counterparts in the absence of selective antibiotic pressure. Although this is probably true on some occasions, some examples show that in the absence of antibiotic selection, antibiotic resistance can remain. Some of the various mechanisms involved concern the physiology of bacteria and some others concern the structure of the genetic platforms involved in the transfer of determinants of antibiotic resistance[9]. The price of antibiotic resistance for fitness is not always

the same. Some resistance mechanisms have been described as having no cost to bacteria, in such a way that their wild-type counterparts are not out-competed by resistant microorganisms. In addition, some resistance mechanisms may give the resistant strain a higher fitness compared to the susceptible counterpart. Jejuni shows increased persistence in chickens with a single-point quinolone-resistance mutation in the *gyrA* gene[10]. Therefore, this quinolone resistant mutant is better suited to survival in chicken than the survival of the wild-type counterpart and resistance will be maintained.

CONCLUSION

A recent event in evolutionary terms is the release of high concentrations of antibiotics and resistance genes in natural ecosystems. Nevertheless, the structure and the activity of environmental microbial populations can be affected by both types of pollution. These changes are relevant to the future of human health, given that environmental microorganisms are the original source of resistance genes acquired by human pathogens via HGT. It has been reported that in human pathogens, in pristine environments and in populations (humans and animals) that are isolated and have not been in contact with antibiotics, the same antibiotic resistance genes and the same genetic platforms (plasmids, integrons) currently exist. This indicates that antibiotic resistance genes can persist and spread even in the absence of antibiotics when they are integrated into successful gene-transmission elements. The data available support the notion that the use of antibiotics for other than therapeutic purposes may enrich the population of resistant bacteria capable of infecting humans. There is, however, little reliable quantitative data available on the quantity of antibiotics used for various purposes. The availability of such data by national and international agencies is an urgent need, as recognized by the World Health Organization, to assess the risks associated with the release of antibiotics.

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