



Editorial: Antibiotics and Antibiotic Resistance Genes in Waters: Pollution, Risks, and Control

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Editorial on the Research Topic

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INTRODUCTION

In 1928, British microbiologist Alexander Fleming discovered penicillin from *Penicillium* for the first time. Since then, human society has entered the golden age of antibiotics (Kümmerer, 2009; Zhang et al., 2015). Antibiotics play a great role in preventing and treating the disease, health maintenance, and life extension. However, it is also due to the extensive use and abuse of antibiotics that the continuous residue of antibiotics in the environment has been detected (Wang et al., 2017) resulting in their toxic effects on the ecosystem (Boxall et al., 2003; Sarmah et al., 2006). Moreover, long-term antibiotic exposure could induce the transfer, proliferation and diffusion of microbial antibiotic resistance genes (ARGs), and further, induce “super-resistant bacteria” in the environment or human body (Pruden et al., 2006; Martínez et al., 2015). Once these super-resistant bacteria invade humans, the corresponding diseases typically become incurable. According to the current development trend, it is predicted that “super-resistant bacteria” will cause about 10 million deaths worldwide every year by 2050 (de Kraker et al., 2016). Antibiotic resistance has been listed by the World Health Organization as one of the most urgent public health problems facing the world in the 21st century (WHO, 2014).

Antibiotics are poorly absorbed and metabolized by humans or animals. Studies revealed that up to 70% of antibiotics doses consumed are excreted through urine and faeces including primarily active substances or metabolites (e.g., Jutkina et al., 2018). Conventional sewage or sludge treatment facilities cannot remove antibiotics and resistance genes effectively, and a large number of antibiotics and ARGs eventually enter the natural environment (Berendonk et al., 2015; Cacace et al., 2019). Water is an important sink of antibiotic and resistance gene pollution. Antibiotics and ARGs have been widely detected in surface water, groundwater, and water supply systems (Ma et al., 2017; Wang et al., 2020; Zhang et al., 2022), which pose a great threat to both the ecosystem and human health. Due to the risk of antibiotics and resistance genes, the research on antibiotics and ARGs in the environment has become a hot issue during the past 20 years. Although several investigators have reported the distribution characteristics of antibiotics and ARGs in different environmental media, the understanding of pollution pathways, ecological and health risks, and the degradation and removal mechanisms of

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antibiotics and ARGs remain a challenge for the field of antibiotics and ARG research due to the complexity of the natural and artificial water systems.

CONTENTS OF THIS RESEARCH TOPIC

This topic mainly aims at the challenges in the current basic and technical research of antibiotics and ARGs in water systems. Finally, we selected 10 manuscripts for publishing after peer review. The main authors are from universities and scientific research institutes in China, America, India, Canada, Brazil, Japan, Ukraine, Switzerland, etc. Among ten published articles, one is a mini-review article, one is an opinion, and eight are original research articles. These published articles are all focused on the different aspects of antibiotics and/or antibiotic resistance genes in water.

Peng et al. introduced the method of analyzing antibiotic resistance in the environment by using metagenomic data and bioinformatics tools. They found that although SARG (Structured Antibiotic Resistance Gene database) is a good database, the application of two or more bioinformatics tools and databases could provide comprehensive information and an in-depth understanding of ARG transmission in the environment. In addition, Das et al. introduced HT-ARGfinder (horizontally transferred ARG finder), which is a pipeline for detecting and enumerating horizontally transferred ARGs in metagenomic data and can also estimate the directionality of transfer.

Gomes et al. investigated the pollution and risk assessment of 10 antibiotics in the river water of the Doce river watershed (Brazil). They found that the detection rate of acyclovir, amoxicillin, azithromycin, ciprofloxacin, enrofloxacin, fluoxetine, erythromycin, sulfadiazine and sulfamethoxazole was 100%; and the highest concentrations of ciprofloxacin and sulfamethoxazole was 4,854.6 ng/L and 9,640 ng/L, respectively. They found most of the investigated antibiotics were above concentrations that pose an ecotoxicological risk to aquatic biota. Guo et al. detected 12 target antibiotics in Dongting Lake in China and found that the antibiotic concentrations in the surface water and sediment were N.D. ~ 943.49 ng/L and N.D. ~ 177.43 ng/g, respectively. The risk assessment shows that ofloxacin, sulfamethoxazole, ciprofloxacin, enrofloxacin, roxithromycin and erythromycin have high ecological risks.

Duygan et al. systematically studied the biodegradation of 15 antibiotics such as ampicillin, chloramphenicol, erythromycin, penicillin and sulfamethoxazole under different sources of microorganisms and their effects on microbial communities. They found that growth linked biodegradation of antibiotics at low concentrations may be present among typical environmental microbes, but for a selected subset only, whereas for the majority of antibiotics negative effects prevail without any sign of productive growth.

The high concentration of antibiotics in wastewater can lead to the widespread of ARGs. Chen et al. studied the ARG distribution in cephalosporin production wastewater treatment plant (X-WWTP), subsequent municipal wastewater treatment plant (Y-WWTP) and receiving stream based on functional gene

microarray technology. They found that the total abundance of ARGs in X-WWTP wastewater samples were significantly higher than that in Y-WWTP wastewater and stream samples, while the relative abundance of ARGs in river sediments did not change significantly with the distance from the Y-WWTP outlet. Kasuga et al. used a high-throughput quantitative polymerase chain reaction to characterize the profiles of ARGs and mobile gene elements (MGEs) in 24 urban rivers in Tokyo in Japan and their surrounding areas. They also found the effluent from the sewage treatment plant will affect the ARGs of the receiving river and *int1* could be used as a proxy for monitoring these ARGs and MGEs in urban rivers.

Yang et al. investigated the occurrence of ARGs and bacterial communities in the water and soil of the Ili River (in Xinjiang Province, China) using bacterial testing and metagenomic sequencing. They found fluoroquinolone, aminoglycoside, sulfonamide, and tetracycline resistances were the most prevailing types in this river and pointed out that proteobacteria, bacteroidetes, and actinobacteria were the main potential hosts of ARGs. Guo et al. found *sul1* and *sul2* were the dominant ARGs in East Dongting Lake Basin; while in the sea ecosystem, Prekrasna et al. found that although the concentration of antibiotics in the Black Sea was below the detection limit, there were relatively high ARG pollution concentrations of *vanB*, *blaSHV*, *blaCMY* and *mcr-1*.

In addition, Singh et al. published an article on the pollution, risk and control of antibiotics and resistance genes in water. They emphasized the pollution sources and health effects of ARGs in water.

FUTURE PROSPECTS

Due to the extensive use and abuse of antibiotics, it is predictable that residues of antibiotics will be present in the environment for the foreseeable future, and that will contribute to the amplification and transmission of ARGs. In the past half-century, the increasing prevalence of microbial antibiotic resistance has far exceeded the discovery and invention of new antibiotics. Antibiotic resistance has become a global health risk problem. The water environment is the main storage and transmission reservoir of antibiotics and ARGs. The pollution potential of antibiotics and ARGs are bound to have impacts on the ecosystems and human health. Although research on antibiotics and ARGs is increasing in many countries, major scientific gaps and questions persist, including: 1) The environmental behaviour and ecological effects of antibiotics in different environmental media. What concentration and how long exposure can bring irreversible risks to the ecological environment and biosphere? 2) What are the influencing factors or limiting factors of ARG transmission and diffusion, what is the specific mechanism, and whether the purpose of ARG control can be achieved by regulating these factors? 3) How to quantify the risk of ARGs to the ecosystem and human health? 4) Can regulatory standards of ARGs in the water environment be established? 5) How should antibiotics and ARG pollution be managed and controlled in the

future, and how to suggest a balance between antibiotic use and control? All these issues warrant further research.

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