



Editorial: Environmental Reservoirs of Antibiotic Resistance Determinants: A Ticking Time Bomb for the Future Emergence of Super-Bugs of Environmental and Public Health Importance

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Editorial on the Research Topic

Environmental Reservoirs of Antibiotic Resistance Determinants: A Ticking Time Bomb for the Future Emergence of Super-Bugs of Environmental and Public Health Importance

Access to safe and sufficient water for human consumption is a fundamental human right (United Nations, 2011), spurring increased scientific research, technological development, monitoring, environmental protection, consumer information, and public awareness. However, environmental sources continue to be impacted by various pollutants, including pharmaceuticals and heavy metals (Zhao et al., 2017), resulting in potentially deleterious effects on humans, animals, and the environment. Though a global problem, developing countries are most threatened due to rapid urbanisation and industrialisation, coupled with poor sanitation infrastructure. A major concern of antibiotics in the environment is the evolution and spread of antibiotic resistance genes (ARGs) among environmental microbes, with the likely emergence of antibiotic-resistant super-bugs of public and animal health concerns (Mbanga et al., 2021). To provide an interdisciplinary update, this research topic focused on possible antibiotic interactions with diverse microbial communities in the environment, leading to the emergence of environmental resistome and super-bugs and their potential public health consequences. This special issue has seven articles written by 32 authors from Europe, Asia, North America, and Africa.

Fadare and Okoh investigated the abundance of genes encoding ESBL, pAmpC, and non-lactam resistance in multidrug-resistant *Enterobacteriaceae* in wastewater effluents in the Eastern Cape Province, Republic of South Africa. They observed that 72.4% of the isolates had at least one β -lactamase, while 86.2% had a non-lactam resistance gene determinant, indicating that WWTP effluents are key reservoirs of *Enterobacteriaceae* and their associated antibiotic resistance genes. Hubeny et al. used metagenomics to assess hospital wastewater impact on the occurrence and

diversity of beta-lactamase genes during wastewater treatment in Poland, emphasising carbapenemase genes. Their results showed that bacteria of the *Fusobacteriaceae* family might be involved in antimicrobial resistance (AMR) spread in the environment. Furthermore, they demonstrated that some resistance genes were only found in the wastewater influent, while others like the *bla*_{IMP} showed increased abundance after the WWTP and concluded that the inflow of hospital wastewater contributed to the spread of AMR in the aquatic environment.

Although AMR could occur intrinsically, anthropogenic activities are known to exacerbate the situation. Bong et al. investigated the prevalence and diversity of antibiotic-resistant *Escherichia coli* from anthropogenic-impacted Larut River in Malaysia using culture and a quadruplex PCR. The authors observed a higher prevalence of multiple antibiotic resistance *E. coli* phenotypes and resistance genes in wastewater effluents than in river waters, and they concluded that anthropogenic inputs had an impact on the composition and diversity of multiple antibiotic-resistant (MAR) phenotypes and their resistance genes in the Larut River. Similarly, Kayode et al. used culture and multiplex PCR to explore the presence of multidrug-resistant *Listeria monocytogenes* in South African ambient waters. Their findings revealed 52 resistance patterns against 22 antibiotics, with resistances ranging from 52.63 to 100% in most isolates. More than 80% of the isolates were multidrug-resistant, implying that aquatic environments may serve as a reservoir for antimicrobial-resistant *L. monocytogenes* to other niches such as the food chain. Using culture techniques, Fatoba et al. assessed the impact of chicken litter application on the transfer of antibiotic-resistant *E. coli* to agricultural soils. They found that 61.5% of the multidrug-resistant (MDR) isolates were from litter-amended soil versus only 1.9% from non-amended soil, implying that chicken litter application resulted in the transfer of antibiotic-resistant *E. coli* to the soil, enhancing the soil resistome. This type of resilience could be passed on to farm products. Iwu et al. analysed MDR *E. coli* pathovars levels in preharvest environmental samples, including irrigation water and agricultural soils. About 60% of irrigation

water and 20% of the farm soil pathovars were multidrug-resistant, harbouring different resistance gene combinations and revealing an abundance of highly diverse MDR *E. coli* pathovars in the preharvest environment.

Baquero et al. reviewed the influence of water and soil coalescent microbiotic particles (particles < 2 mm to which bacteria can attach) on AMR evolution and spread. They reported that natural and anthropogenic activities enhance the interaction and merging of these particles in soil and water, creating a favourable environment for the creation of microbial communities and the potential exchange of antimicrobial resistance genes. Therefore, the microbiotic particles could play a significant role in the spread of AMR globally and controlling them could assist in counteracting AMR.

Collectively, these studies reveal how anthropogenic activities like WWTPs and agriculture contribute to the spread of AMR in the environment. They also demonstrate how the environment serves as a reservoir for antibiotic-resistant bacteria and antibiotic resistance genes, which can be transmitted to humans and animals through farm produce, necessitating the adoption of a one health approach to combating antibiotic resistance in the first place.

AUTHOR CONTRIBUTIONS

The editorial was drafted by LA, modified and approved by the topic Co-editors (TS, RS, ME-L, and IK). All authors listed directly, substantially, and intellectually contributed to this Edited Collection and approved this editorial for publication.

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