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Editorial: Antimicrobial resistance in aquatic environments — Bridging surveillance, ecology, and one health action☆

Antimicrobial resistance (AMR) is widely recognised as a major global threat, with health and economic consequences extending across and overlapping with human, animal, and environmental systems [1]. Perhaps the best example of a One Health challenge, the so-called AMR "silent pandemic" is a complex problem driven by anthropogenic activities, which must be tackled across the three realms [2]. Efforts to address AMR have historically focused on clinical and agricultural settings, however, there is increasing recognition that environmental pathways play a critical role in the emergence, persistence, and dissemination of antimicrobial resistant organisms (AROs) and antimicrobial resistance genes (ARGs) [3,4]. Aquatic environments are of particular importance as they receive inputs from diverse anthropogenic sources, including wastewater, agricultural runoff, and industrial discharges, thus creating conditions that support the selection of AROs and horizontal transmission of ARGs [5]. Compounding this, aquatic systems also connect human, animal, and environmental compartments, facilitating the movement of resistant organisms across ecological boundaries [6]. As such, a global strategic priority is understanding the role of aquatic environments, which is central to developing effective and integrated One Health responses to AMR [1]. The objective of this Special Issue of *One Health* is to advance our understanding of AMR in aquatic systems and identify key methodological and conceptual gaps. To this end, the Guest Editors have herein assembled nine contributions of relevance to the One Health audience.

1. Wastewater as a sentinel and source of AMR

Across this Special Issue, wastewater systems emerge as major sources and pathways for environmental AMR transmission. Wastewater treatment plants (WWTPs) receive inputs from domestic, healthcare, industrial and agricultural sources, creating conditions that drive AMR. The global scoping review by Punch et al. [7] included herein documents the rapid expansion of wastewater-based AMR surveillance, while also highlighting substantial variation in analytical methods, target organisms, and reporting approaches. Despite this variability, wastewater surveillance offers a scalable approach to capturing population-level resistance signals and linking environmental and clinical data. However, current treatment processes do not fully irradicate resistant bacteria (re-)entering receiving waters. Indeed, clinically relevant organisms, including antibiotic-resistant *Escherichia coli* (*E. coli*), persist in treated effluents and have been detected in wildlife such as gulls, indicating ongoing environmental dissemination as shown in the original study of Masarikova et al. [8]. Together, these observations position wastewater as both a valuable surveillance matrix and a continuing source of environmental exposure.

2. Expanding environmental reservoirs

Beyond wastewater, this Special Issue highlights a range of environmental reservoirs contributing to AMR persistence. Queiroga et al. [9] examine the role of microplastics, which provide surfaces for biofilm formation, supporting dense and diverse microbial communities that may harbour and facilitate the horizontal transfer of resistance genes. These biofilm-associated communities can enhance microbial survival under environmental stress and may promote genetic exchange, while the persistence and mobility of microplastics suggest a role in the wider dissemination of AMR across aquatic environments. O'Donovan et al. [10] investigate the role of sediments as AMR reservoirs in aquatic systems. Sediment core analysis of microbial and chemical signals deposited over time can reveal faecal inputs and associated resistance determinants, providing insight into historical and ongoing contamination. Sediment-associated microbial communities may also act as long-term sinks for resistance genes, with the potential for subsequent remobilisation under changing environmental conditions. Incorporating sediment analyses alongside water sampling may therefore strengthen environmental monitoring and provide a more temporally resolved understanding of AMR dynamics.

3. Linking environmental and clinical resistance

Several contributions to this Special Issue highlight the links between environmental and clinical AMR. Phylogenomic analyses identify shared lineages of *Acinetobacter baumannii* across urban surface waters and clinical settings in São Paulo, suggesting potential transmission pathways [11]. Complementary evidence comes from the detection across several continents of multi-drug resistant enterotoxigenic *E. coli* in both environmental samples and human cases, including strains carrying extended-spectrum β-lactamase (ESBL) genes, indicating the presence of clinically relevant resistance traits beyond healthcare settings [12]. The occurrence of these analogous strains across environmental and human compartments points to potential bidirectional exchange, highlighting the role of aquatic environments as reservoirs and dissemination

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pathways for pathogenic, resistant bacteria. Taken together, these observations point to ongoing connectivity between environmental reservoirs and clinically relevant pathogens, reinforcing the need for surveillance approaches that integrate environmental and clinical data.

4. Rethinking surveillance and indicators

The presented collection also highlights challenges pertaining to environmental AMR monitoring and interpretation. Methodological advances, including modified detection approaches for extended-spectrum β-lactamase-producing *E. coli*, improve applicability in environmental samples [13]. However, questions remain regarding the suitability of commonly proposed indicators. Fish species, for example, do not consistently reflect resistance patterns in surrounding waters, limiting their value as sentinels [14]. Analyses of fish gut microbiomes further demonstrate complex and context-dependent relationships with anthropogenic pressures, indicating that host-associated resistomes may not reliably represent local environmental conditions [15]. These observations suggest that no single indicator is sufficient and therefore monitoring approaches should be tailored to context and incorporate multiple environmental compartments, including water, sediments, and biota.

5. From detection to action: a one health research approach

The presence of AROs and ARGs in aquatic environments does not directly translate to human health risk; however, the pathways linking environmental reservoirs to clinically relevant resistance remain poorly understood. Addressing this gap will require better integration of environmental microbiology, epidemiology, environmental science, hydrology and risk assessment. Environmental AMR is driven by local conditions, including wastewater infrastructure, antimicrobial use, and regulatory frameworks, with the transboundary nature of aquatic systems underscoring the need for coordinated international responses. Within this context, several priorities emerge. Greater consistency in methods is needed to support comparison across studies, with genomic and metagenomic approaches offering opportunities to strengthen source attribution and clarify transmission pathways. Environmental surveillance should be more fully integrated into broader AMR strategies within a One Health framework, alongside efforts to address upstream drivers such as antimicrobial use and environmental contamination. When viewed in its entirety, the contributions in this Special Issue emphasise the role of aquatic environments in the ecology of antimicrobial resistance. Progress in this area will require coordinated, cross-sectoral approaches that recognise the environment not only as a recipient of antimicrobial pressures, but as an active component in the emergence and spread of resistance.

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