

Antibiotics

an Open Access Journal by MDPI

CiteScore: 10.2
Indexed in PubMed
Impact Factor: 5.5

Special Issue Reprint

The Spread of Antibiotic Resistance in Natural Environments

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This Special Issue provides insights into the ecological, genomic, and public-health dimensions of antimicrobial resistance (AMR) in natural and human-impacted environments. Collectively, the articles investigate how resistant bacteria, antibiotic resistance genes, virulence determinants, and mobile genetic elements persist and circulate through wastewater-treatment systems, urban rivers, aquatic environments, food-production systems, and human–animal–environment interfaces. The collection combines shotgun metagenomics, whole-genome sequencing, culture-based investigations, resistance phenotyping, plasmid analysis, and critical reviews. The findings demonstrate that environmental AMR is shaped by pollution sources, treatment processes, microbial ecology, horizontal gene transfer, and co-selective pressures such as antibiotics, metals, biocides, and microplastics. They also show that reductions in bacterial abundance do not necessarily correspond to the elimination of viable resistant organisms or transferable resistance determinants. These contributions position the environment as an active component of AMR evolution and transmission rather than merely a recipient of clinical and agricultural waste. The Special Issue emphasizes the need for source-resolved surveillance, integrated genomic and culture-based methods, improved assessment of treatment performance, and risk frameworks that connect environmental detection with mobility, pathogenicity, persistence, and exposure. Such evidence is essential for designing effective interventions across the human, animal, and ecosystem dimensions of One Health.

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