

ANTIBIOTIC RESISTANCE AS AN EMERGING ENVIRONMENTAL CONTAMINANT

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There is mounting evidence that antibiotic resistant bacteria are released in large quantities from all sites of antibiotics application, e.g. hospitals, private households, animal husbandry, and most recently, orchards treated against firebrand. Many of these bacteria enter the wastewater stream and wastewater treatment facilities where high concentrations of contaminants, high cell densities, and mixing with environmental bacteria provide a potential evolutionary hotspot for the selection, mobilization, and horizontal transfer of antibiotic resistance between potential pathogens and environmental bacteria. Eventually resistant bacteria can enter natural aquatic ecosystems and resistance can potentially spread to natural populations, possibly increasing the natural resistance background over time, with unknown consequences for the likelihood of a transfer back into clinically relevant bacterial strains.

Antibiotics resistant (AR) bacteria, their resistance genes and their mobile genetic elements represent a complex emerging contaminant requiring new approaches to risk assessment, monitoring, and new approaches for risk reduction and management. This represents a complex task that will require a multidisciplinary effort. A COST Action (TD0803 DARE - Detecting evolutionary hot spots of antibiotic resistances in Europe) has to date identified that there are considerable quantities of resistant, often multiresistant bacteria in water, WWTP and soils. WWTPs and animal production settings, where extensive human-animal contact takes place, are hot spots for the transfer of AR genes. Studies from a number of other groups in Europe and worldwide show that this is a global problem. We aim to outline strategies for assessing, monitoring, and mitigating risks associated with releasing antibiotic resistant bacteria.