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Motivation

Antibiotics are commonly used to treat bacterial infections, but their overuse leads to rapid development and spread of resistance rendering these drugs ineffective (Fig 1). As a result, the once easy-to-cure infections have become untreatable.

This study focusses on the rise and spread of antimicrobial resistance in water, originating from the clinical environment up to the surface water (Fig 2). Antibiotic resistant bacteria (ARBs), antibiotic resistance genes (ARGs) and medicinal compounds (from clinical settings) end up in the wastewater that leads them to the wastewater treatment plants (WWTPs). WWTPs are not designed to remove either of these compounds, and they are partially released via the WWTP effluent into the surface water. Furthermore, the presence of trace medicine rests and heavy metals plays a role in the spread of resistance as they act as selectors for ARBs. In addition, the environmental reservoir for ARGs might increase the speed of resistance development. Therefore, water is believed to play an important role in the spread of antimicrobial resistance.

Technological challenge

The challenge is to address the impact of water on the rise and spread of antimicrobial resistance. It is proven that the environment is an important reservoir for ARGs and that water acts as a vector which enhances the transport of bacteria and genes. In this research the pathway of antimicrobial resistance in wastewater from different sources (i.e. hospital, nursing homes, community) up to the surface water will be investigated, and the human exposure to this resistance will be determined (Fig 2). Therefore, a reliable sampling campaign is necessary, and DNA extraction methods for genomic, plasmid and phage DNA have to be developed. Wastewater samples will be analyzed for the species and ARGs they contain by molecular methods such as 16S next generation sequencing (NGS) and whole genome sequencing (WGS).

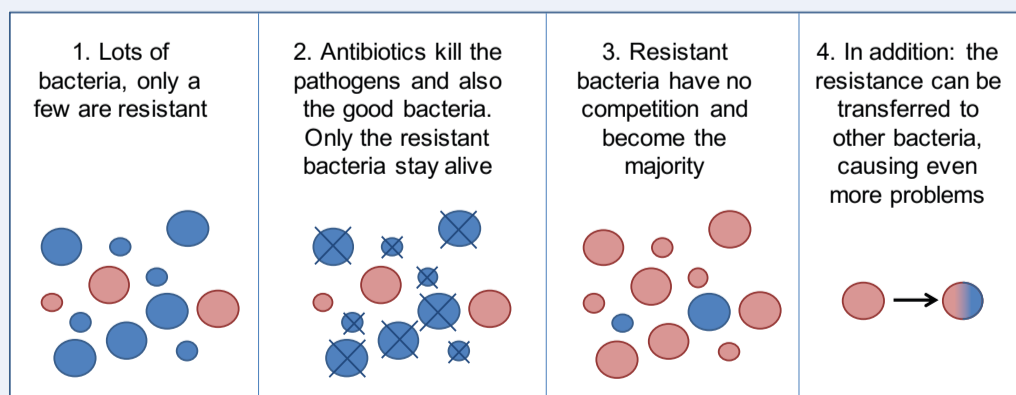


Fig.1 Antibiotic selection pressure

Does antimicrobial resistance in surface water originate from clinical environments?

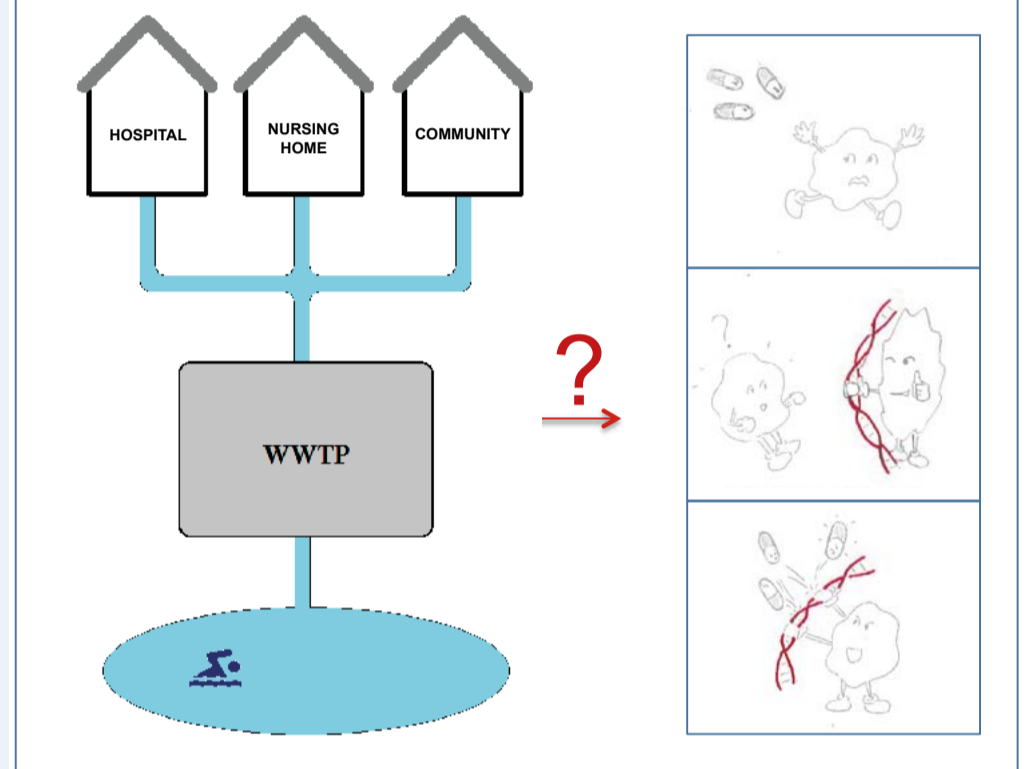


Fig.2 Graphical abstract

Objectives

The goal of this research is to map and monitor antimicrobial resistance in the (waste)water chain from the clinical setting into the environment. This will provide information about important ARBs and ARGs, also on species and genes that are less well documented. The comparison of different sources can lead to specific information about prevention measures. This research pursues the following objectives:

1. Identification of resistance genes on chromosomal DNA, plasmids, mobile genetic elements and/or phages
2. Revealing cross-resistance between heavy metals and antibiotics in water
3. Setting out the transmission of ARB/ARG in the wastewater-chain
4. Mapping the genetic similarity between resistance genes observed in micro-organisms from humans and from water