

## Tracking and understanding AMR dynamics across European urban water systems

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*Publication date:*  
2017

*Document Version*  
Publisher's PDF, also known as Version of record

[Link back to DTU Orbit](#)

*Citation (APA):*  
Smets, B. F., Dechesne, A., Li, L., Madsen, J. S., Nesme, J., Sørensen, S. J., ... Graham, D. (2017). Tracking and understanding AMR dynamics across European urban water systems. Abstract from International Symposium on Antimicrobial Resistance in the Environment (ISARE 2017), Shenzhen, China.

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# Symposium Program (ISARE 2017)

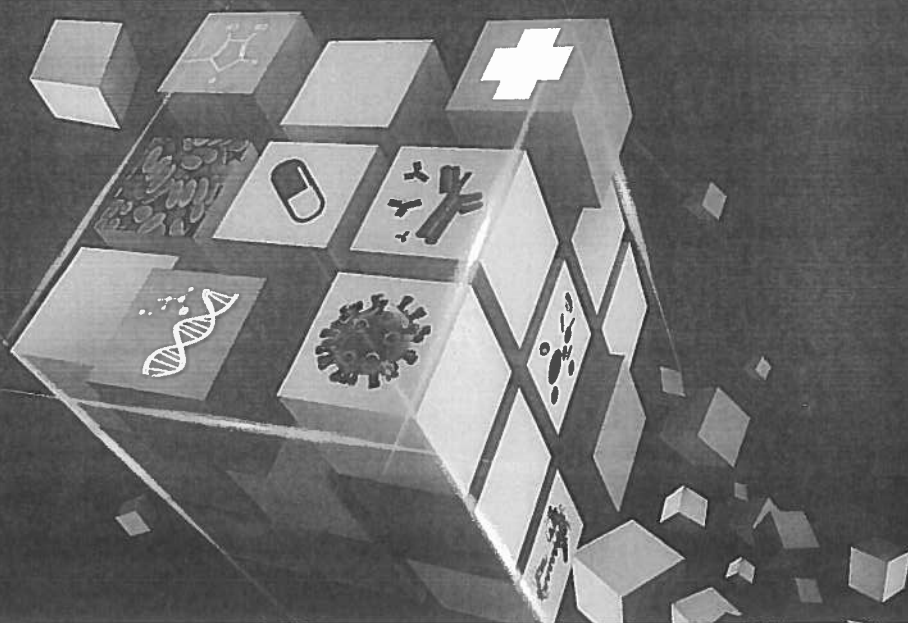
## 2017 | 国际环境耐药基因研讨会

International Symposium on Antimicrobial Resistance in the Environment

November 30 – December 3, 2017

Southern University of Science and Technology

Shenzhen, China



## ARGs as pollutants in waste water and recycled water

**Amy Pruden**

Virginia Polytechnic Institute and State University

Antibiotic resistance is a serious and growing public health challenge in the 21st century. Various national and multi-national action plans for preserving the use of antibiotics as life-saving drugs on into the future are under development, with preventing the spread of resistance as a key aspect of these plans. In particular, there is increasing interest and research on understanding the ecology and evolution of antibiotic resistance and applying this knowledge towards limiting the spread and propagation via environmental pathways. Wastewater treatment plants are a key example, as they receive human sewage, including hospital waste, containing pathogens and antibiotics. The influent stream is subsequently mixed with highly active and concentrated microbial populations responsible for biodegrading and transforming organic carbon and nutrients in the water before reclaiming the purified water and returning it to local lakes, rivers, streams, and groundwater. An important question is the extent to which horizontal gene transfer of antibiotic resistance genes (ARGs) is stimulated amongst the dense bacterial populations inside the WWTP and the overall potential for the effluent to contain pathogens with new antibiotic resistance phenotypes. In this sense, the ARGs themselves can be considered as the pollutants, as they transcend their bacterial hosts. The need to understand the fate of ARGs and the factors at play in horizontal gene transfer becomes particularly acute as communities move towards reuse of the treated wastewater for potable and non-potable purposes, as this results in greater potential for direct exposure to human populations. Here we will apply shot-gun metagenomics in tracking how the resistome shifts through wastewater treatment and through distribution of recycled water at the point of use. We will compare field sampling campaigns, including in the U.S. and internationally, along with lab-scale validation. Major questions that will be addressed include, which ARGs are of concern and which should be targeted for future monitoring? Such questions will be key in moving towards a global strategy for monitoring and containing the spread of antibiotic resistance.

## Dynamics of the soil resistome

**Pascal Simonet**

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Most antibiotic resistance genes (ARGs) detected in human pathogens originate from saprophytic environmental microorganisms, especially soil bacteria, which have the highest diversity of ARGs. However, little is known about where saprophytic and pathogen bacteria meet to exchange genes and how gene transfer mechanisms are regulated by bacteria and by the environment. Based on examples drawn from published and unpublished experiments, some soil and plant related ecosystems will be shown to be "hot spots" for gene transfers (i.e where bacteria and/or their DNA are in close contact and where they are sufficiently and physiologically active to exchange genes). While conjugation is thought to be the main mechanism implicated in ARG transfer among pathogens, natural transformation can also occur in situ with extracellular DNA that has moved far from the donor cell and has persisted months in the soil before transforming bacteria.

## Tracking and understanding AMR dynamics across European urban water systems

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Horizontal gene transfer (HGT), especially conjugal plasmid transfer, is one of the key drivers in global antibiotic resistance transmission. To predict the fate of antibiotic resistance gene (ARG) the transfer and host range of ARG carrying plasmids in relevant microbial communities needs to be understood. Urban water systems (UWS) are a potential conduit of ARG transfer between human intestinal and environmental bacteria, and UWS are being examined as potential hot spot of antibiotic resistance dissemination. In this study, a comprehensive assessment of antibiotic resistance transmission is being performed in UWS across three European countries (Denmark, United Kingdom, Spain) with different antibiotic and biocide use and urban sewage management approaches. We are especially keen to examine to what extent community permissiveness varies along different nodes in the sewage catchment area and between countries. Hence, utilizing a well-established bioreporter system, plasmid permissiveness, in distinct microbial communities within an UWS and across different UWSs, is being evaluated. Plasmid transfer frequency is assessed using microscopic image analysis, and host range is identified by combining flow-cytometric sorting and 16S rRNA amplicon sequencing. Using incubations that mimic the environmental conditions at sewage catchment nodes, we challenge different UWS communities with model plasmids that span multiple important incompatibility groups (RP4, IncP-1 $\alpha$ ; pKJK-5, IncP-1e; pB10, IncP1-b; R27, IncHI1; pIP501, Inc18; RSF1010, IncQ), to examine host range variation among the microbial communities and the plasmid groups. Moreover, we will assess transfer using newly isolated antibiotic resistant plasmids and hosts to ensure maximal relevance to ARG transmission potential in real UWS ecosystems. Preliminary results across the sewer-to-wastewater effluent continuum reveal sharp quantitative changes in the permissive fractions, with highest permissiveness observed in residential sewer microbial communities. Taxonomic compositions of the main transconjugal pools have been determined; they are dominated by consistent genera across sample locations.

## U.S. National Science Foundation's cooperation with China

**Nancy Sung**

U.S. National Science Foundation

The U.S. National Science Foundation supports basic science in all fields of science and engineering. This presentation will address how NSF collaborates internationally, how NSF collaborates with China, as well as a new priority area in the Ecology and Evolution of Infectious Diseases.

## Antimicrobial resistance in food production systems

**Ed Topp**

Agriculture and Agri-Food Canada

Large amounts of antibiotics are used in commercial food animal production systems. Medicated animals or poultry excrete antibiotic residues and antibiotic-resistant bacteria. These chemical and biological contaminants are entrained into the environment with the application of manure to crop production systems. This presentation will discuss the relationship between antibiotic use and resistance development, the composition of manure and how it varies with pre-application treatment, and the fate of these contaminants in soil following application. The presentation will emphasize key knowledge gaps.