Dispersal of **a**nti**b**iotic **r**esistant bacteria and antibiotics in **w**ater ecosystems and how it **i**nfluences live**s**tock and aquatic wildlif**e**

P. Akoll[1], J. Bonnedahl[2,3], S. Börjesson[4], AJ. Green[5], P. Krzeminski[6], O. Mahjoub[7], Y. Mani[8], W. Mansour[8], V. Martin[5], C. Masembe[1], J. Mayega[1], A. Messaoudi[8], R. Odong[1], A. Olsson[9], J. Omara[1], M. Rincón Gracia[9], T. Rosendal[9], C. Schwermer[6], R. Söderlund[9] and H. Woksepp[3].

[1]Makerere University (MAK) [2]Linköping University (LiU), [3]Region Kalmar County, [4]Karolinska Institute, [5]Estación Biológica de Doñana, Consejo Superiorde Investigaciones Cientificas (EBD-CSIC), [6]Norwegian Institute for Water Research (NIVA), [7]National Research Institute for Rural Engineering Water, and Forestry (INRGREF), [8]Faculty of medicine Ibn Al-Jazzar Sousse (FMS), and [9]National Veterinary Institute (SVA).

1. Background and aim

Antibiotic resistance is one of the greatest threats to human and animal health. As resistant bacteria emerges, the number of treatment alternatives continues to decline. Bacteria are found in all sorts of environments such as soil and water. The natural environment is a possible source of transmission to humans and animals. In addition, it could function as a reservoir for further antibiotic resistance development. Working with a One Health approach is therefore crucial when dealing with infectious diseases and antimicrobial resistance.

The overall aims of PAIRWISE are to gain increased knowledge on:

I. The dispersal of antibiotic resistant bacteria, antibiotic resistance genes and antibiotics in surface waters downstream of WWTPs

II. Carriage of antibiotic resistant bacteria and resistance genes in livestock linked to surface waters influenced by WWTPs

III. The role of aquatic birds in dispersal of antibiotic resistant bacteria and antibiotic resistance genes

2. Funding

PAIRWISE is a part of the Aquatic Pollutants research call created by the three European Joint Programming Initiatives on Water, Oceans and Antimicrobial Resistance.

The project received funding from the European Union's Horizon 2020 research and innovation programme under grant agreement No. 869178-AquaticPollutants.

Read more

ERA-NET cofound AquaticPollutants

The PAIRWISE web page

3. Materials and methods

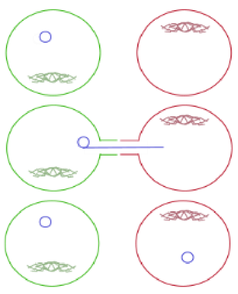
Four sampling periods covering seasonal variability for one year

Study areas	Sites
Norway	2
Spain	1
Sweden	3
Tunisia	2
Uganda	2

Identification of antibiotic residues
High-performance liquid chromatography coupled with tandem mass spectrometry (LC/MS)

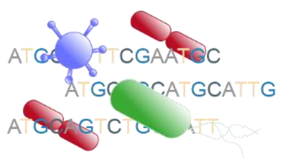
Selection for ESBL & carbapenem resistant *Enterobacterales*

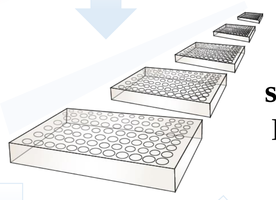
Estimating the level of horizontal gene transfer (HGT)
SOS-response assay



Microbial source tracking (MST)

High-Throughput quantitative PCR (HT-qPCR) screening
including 384 resistance genes and crAssphage





Antimicrobial susceptibility testing (AST)
Broth microdilution (BMD)

Species determination
Maldi-Tof/Vitek

Whole genome sequencing