

Antibiotics are the most commonly used pharmaceuticals for the treatment of bacterial infectious diseases in humans. However, they are also used in several other fields like veterinary, agriculture and animals farming. Millions of metric tons of antibiotics have been used in the last 60 years. Currently, we have clear evidence for the overuse and misuse of antibiotics in everyday life. Such a great antibiotic usage resulted in the presence of these pharmaceuticals in the environment. Unfortunately, this has led to the accelerated development and spread of antibiotic resistance genes (ARGs) among bacteria. Antibiotic-resistant bacteria, antibiotic resistance genes and antibiotics are now considered a novel class of emerging pollutants that pose a serious risk to both, animal and public health. The problem of arising antibiotic resistance is even more serious taking into account that currently we mostly use synthetically-modified derivatives of known antibiotics and only one really novel antibiotic, i.e. teixobactin, has been discovered in the last 30 years.

Nowadays, antibiotic resistance genes (but also other virulence genes – VGs – found in pathogens) have become highly abundant mainly due to their mobility within bacterial communities as they are frequently associated with mobile genetic elements, such as plasmids, assisting their dissemination. Plasmids can even translocate between taxonomically remote strains of bacteria, and thus horizontal gene transfer is considered the most important factor responsible for the spread of ARGs and VGs in the environment and emerging of multidrug-resistant pathogenic bacteria.

Communal wastewater treatment plants (WWTPs) are recognized as a point sources and bioreactors accumulating antibiotic-resistant bacteria and antibiotic resistance and virulence genes. WWTPs are also important interfaces between the human population and the environment which makes them perfect models for analysis of antimicrobial resistance using One Health approach. One Health concept recognizes that health of people is directly linked to the health of animals and our shared environment.

It was already shown that ARGs and VGs (and even antibiotic-resistant bacteria) can pass WWTPs and then “invade” rivers and subsequently other environments. Recently, it was found that in the WWTPs a huge pool of extracellular DNA (exDNA) is produced. This exDNA mostly derives from disrupted bacterial cells and may contain various fragments of their chromosomes, but also plasmids. Thus, in this project we postulate that this exDNA may also significantly contribute to antibiotic resistance and virulence genes dissemination and emerging of novel antibiotic-resistant bacteria, including multidrug resistant ones. Moreover, we hypothesize that exDNA released from WWTPs may “invade” water ecosystems. ARGs and VGs present in exDNA may be potentially incorporated into genomes of bacteria present in water, sediments and also microbiota of water animals. Showing that not only antibiotic-resistant bacteria but also exDNA containing ARGs and VGs constitute a serious epidemiological threat. This may shed new light on the future trends in wastes treatment and may shape expectations of society in this field. To meet these future expectations, we also planned to develop of a novel technology, based on the use of mineral sorbents, for removal of exDNA (containing ARGs and VGs) from treated communal effluents at the last stage of the waste purification process.

Summarizing, in this project we proposed a complex experimental setup, starting from metagenomic analyses of exDNA generated in WWTPs, throughout analyzing the role of exDNA in dissemination of ARGs and VGs in artificial water ecosystems and finally the development of the sorption technology for exDNA removal from treated effluents.