

Antimicrobial resistance due to the continuous selective pressure from widespread use of antimicrobials in humans and animals, has been a growing problem for decades. Antibiotic resistance is not restricted to pathogenic bacteria. Several studies of drug-resistant environmental strains show that the clinical bacterial strains with increased resistance often come from the natural environment, including soil environment or aquatic ecosystems. These antibiotic resistant environmental bacteria can transfer the resistance genes to human pathogens causing that resistant infections are becoming more difficult or even impossible to treat with current antibiotics, leading to infections causing higher morbidity and mortality. Intrinsic resistance in bacteria of the hospital environment is, in fact, problematic because it limits the therapeutic options. Nowadays, antibiotic resistance represents a significant global health problem, which needs better understanding of the ecology of antibiotic resistance bacteria (ARB) and antibiotic resistant genes (ARGs), including their origins, evolution, selection and dissemination. Antibiotics are constantly released into the environment mainly by treated wastewater discharged from WWTPs. Therefore, this project include the study of the effect of WWTPs' technologies in transmission of the ARBs and ARGs from effluents to the surface water receivers.

Beta-lactam antibiotics, including the sub-groups of penicillins, cephalosporins and carbapenems comprise the largest share of antibiotics for human use in most countries. The second one are tetracyclines, which are the most popular antibiotics for animal use. This accounts for approximately 95% of total antibiotic use in the world. Antibiotics and their transformation products entering the environment can affect the evolution of the bacterial community structure which play a significant role in the ecosystem. Due to this, antibiotics resistant bacteria were selected as indicators of contamination of environmental samples in this project.

In sewage, especially in raw sewage and activated sludge, where the bacterial density is very high, microorganisms have access to a large pool of itinerant genes which move from one bacteria cell to another (horizontal and vertical transfer). The genes may spread through bacterial populations via plasmids and a variety of mobile genetic elements, such as transposons or integrons, carrying genes which encode resistance to other antimicrobial agents. The wastewater treatment plants constitute, therefore, an important reservoir of enteric bacteria which carry potentially transferable resistance genes. Together with purified sewage, they can penetrate the soil, surface water, rural groundwater supplies and drinking water. It creates a potential risk to human and animal health because ARGs and ARB transported to the environment can be transferred back to people and animals. Although wastewater treatment processes reduce bacteria number in the sewage even close to 99%, some antibiotic-resistant bacteria can remain in the sewage outflow and may be emitted from sewage directly into the water bodies, which are receivers of WWTPs effluent. This poses a public health risk, which needs future evaluation and control.

The aim of the project is determining of the relationship between the presence of bacteria resistant to beta-lactam and tetracyclines antibiotics, genes conferring resistance to these antibiotics, the level of antibiotics in wastewater discharged from municipal WWTPs with different capacities and their quantities in surface water reservoirs which are receivers of effluents. This issue is important because of the probable impact of the selective pressure of drugs on the spread of drug resistance genes among both commensals and pathogens, which may have a significant impact on the lives and health of people and animals. Obtained results will help to make the determination of the impact of wastewater treatment plant on the amount of antibiotic-resistant bacteria and genes responsible for drug resistance in waters. It will allow to determine the degree of risk to the environment and people and will allow to identify the most effective wastewater treatment technologies in removing drug-resistant microorganisms. Additionally, by controlling the level of concentration of pollution indicators of organic and inorganic substances in samples of wastewater discharged into surface reservoirs, it will be able to determine the real impact of the sewage treatment plant on the microbiological status of the surrounding environment.