

Located within cities urban recreational reservoirs (URRs), both natural and man-made, are popular resting places and holiday destinations for local residents and tourists. These sites, often accompanied by waterfront infrastructure, also act as places of increased anthropogenic pressure on the reservoir ecosystem. For example, urban lakes and in particular beaches in Masurian District in Poland, are mostly exploited during the summer season when hundreds of thousands of tourists arrive for holidays and seasonally multiply populations of local villages, towns, and cities.

Vacationers affect the environment on many levels. They increase exploitation of local resources (e.g. freshwater) and increase the level of human-originating pollutants, i.e. chemical (e.g. cars and motorboats gasoline and fumes), physical (i.e. trash), and biological (e.g. wastewater). The latter also includes a direct transfer of human-associated microbiota to URRs. Among introduced microbes, there are antibiotic-resistant bacteria (ARB), including pathogens, that may interact with strains from URRs' environment. This may include the exchange of antibiotic resistance genes (ARGs) often carried by mobile genetic elements (MGEs), like plasmids, and result in the accumulation and further dissemination of ARGs in the environment. Potentially it could lead to the origin of novel human pathogens. Therefore, in light of the ongoing increase of the global emergence of antibiotic resistance and its surveillance, it is important to investigate the scale of that process in URRs.

In this project, we plan to determine what is the actual diversity and abundance of ARGs and MGEs carrying ARGs (the resistome) in selected URRs in Poland. We also plan to investigate how anthropogenic pollutants increase the vulnerability of URRs' microbial ecosystems and influence their resistance to biological invasions with antibiotic-resistant bacteria (ARB), as well as the accumulation and horizontal transfer of ARGs. Additionally, we aim to investigate if and to what extent the season change (i.e. temperature change) in the temperate climatic zone (e.g. in Poland) influences the accumulation and dissemination of ARGs and MGEs carrying ARGs in URRs. Accordingly, we plan to determine if the resistome of URRs depends on the seasonal influx of people and the general use of the recreational infrastructure (tourism). All the above-mentioned hypotheses will be verified with an application of metagenomic analyses of samples collected from various URRs in Poland. This allows insight into genetic information of the whole bacterial community which includes the information of bacteria present in the environment and the diversity of their ARGs and ARG-carrying MGEs. This information will be used to design and test a panel of ARGs that could be used for monitoring of URRs. Additionally, analyses will be enriched by an application of a novel microcosm system imitating URR's environment, for exploration of the maintenance and horizontal transfer of ARGs in the laboratory. They will be used to show what happens if pathogenic bacteria carrying ARGs and MGEs are introduced into the URR. This unique experimental approach and newly designed microcosm system may also indicate potential directions of horizontal transfer of ARGs and ARGs-carrying MGEs in URRs, i.e. indicate which bacteria from the natural environment acquire exogenous DNA and what is its fate.