Screening for a range of antibiotic resistance genes (ARGs) in the Swedish surface water environment

Foon Yin Lai,[a] Windi Muziasari,[b] Marko Virta,[b] Karin Wiberg,[a] Lutz Ahrens[a]

[a] Dept. of Aquatic Sciences and Assessment (IVM), Swed. Univ. of Agricultural Sciences (SLU), Uppsala, Sweden
[b] Dept. of Food and Environmental Sciences, Univ. of Helsinki, Helsinki, Finland

The occurrence of antibiotic resistance genes (ARGs) in aquatic environments poses a threat to human and environmental health. Water bodies which receive effluent discharge of wastewater treatment plants (WWTPs) are an important media to evaluate ARGs entering the environment. A few European studies have reported ARGs in recipient waters, but such data remains very limited in Sweden. The key objective of this study was to assess the ARG prevalence in the Swedish surface water environments. Specially, it aimed to (a) collect recipient water samples, downstream of the municipal WWTPs, and (b) screen for a wide range of ARGs in the target water environment. Various ARGs and other genes in the samples were identified and quantified using a high-throughput qPCR method with 384 primer sets. A total of 152 ARGs were detected in all the samples, conferring resistance to nine different classes of antiobiotics. Additionally, integrase genes of integrons as well as six other resistance genes were found in the samples. More genes were detected in the downstream than the upstream samples. Our results showed that antibiotic resistance was ubiquitous in the studied water bodies and WWTP effluents were an important impact source for ARGs. Since the recipient water eventually connects to the largest drinking water reservoir in Sweden, there is a potential risk of spreading ARGs to the source of drinking water. Our finding allows to select specific sites for assessing temporal changes of ARGs in the future.