The impact of urban contamination on antibioresistance in microbial communities from periphyton and sediments

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Abstract

Since the early 20's antibiotics have been massively produced and consumed for the benefit of both human and animal health. Nevertheless, antibiotics have also reached the aquatic environment through diffuse sources (*e.g.* veterinary treatment, contaminated manure application...) and through wastewater. Consequently, antibiotics concentrations between the ng/L and μ g/L range are regularly detected in surface water and those molecules have also been found in sediments and aquatic biota. The ubiquitous presence of antibiotics exerts a selective pressure on microbial communities leading to the acquisition and dissemination of antibioresistance in the environment. While both antibiotics and antibioresistance have been found in different aquatic compartments, more investigation is required to better understand their distribution and to identify hot spots of accumulation.

In this context, we investigated the repartition of antibiotics and antibioresistance in different aquatic compartments on 4 stations belonging to regional observatories and presenting contrasting levels of pharmaceuticals: 2 on the Arve river belonging to Sipibel observatory and 2 on Lake Geneva belonging to the Observatory on Lakes. On the Arve river, the 2 stations were located up- and down- stream the discharge place of a wastewater treatment plant (WWTP) collecting both urban and hospital wastewaters. On Lake Geneva, one station was located in a relatively pristine area while the second was close to the discharge of an urban WWTP. To better identify a potential temporal dynamic of antibiotics and antibioresistances over seasons, 6 samplings were conducted during 1.5 year. On each sampling campaign, the following parameters were determined: (i) antibiotics levels in water, sediments and periphyton; (ii) antibioresistance in periphyton and sediments using various techniques: detection of resistance genes, integrons quantification, detection of tolerance acquisition *via* a PICT (Pollution Induced Community Tolerance) approach; (iii) antibiotics biodegradation potential of

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microbial community from sediments (by radiorespirometric measurement); (iv) diversity of bacteria and diatoms in periphyton and sediments; (v) physico-chemical parameters and (vi) metallic contamination in sediments.

While microbial resistance to antibiotics is commonly assessed by quantifying resistance genes or isolating antibiotic resistant bacteria, antibiotic resistance can also be estimated by measuring the acquisition of antibiotics tolerance at community level, following a PICT approach. In our study, periphytic microbial communities from the Arve river were found to have a higher tolerance to the tested antibiotics (ciprofloxacin, ofloxacin, sulfamethazine and erythromycin) than communities from Lake Geneva, in agreement with the expected levels of contamination. In addition, in some cases, a higher tolerance was also found at stations close to WWTP effluents than in upstream/protected stations. For example, periphytic microbial communities collected downstream the WWTP on the Arve river were generally found to have a higher tolerance to ciprofloxacin than the upstream communities. Comparing whole community tolerance to other classical indicators of antibioresistance and to antibiotics levels in the aquatic ecosystems allows us to better understand the interconnection between pharmaceutical exposure, *in situ* tolerance and genetic potential for antibioresistance.

Keywords: pharmaceutical residue, antibiotic, PICT, passive sampling, antibiotrophy, biofilm