

The objective of this study was to explore the links between hydrology, water chemistry and microbial community structure in a highly impacted Mediterranean river. To this aim, the catchment of the River Tevere (including the main stem, the major tributary Aniene, and the stream Cremera) was sampled at the closing section in differently urbanized areas at two contrasting seasons (winter/summer). The major hydrological, physical and chemical characteristics of river waters were measured directly or retrieved within datasets from monitoring agencies. The microbial community structure was analyzed by NGS Illumina profiles and flow cytometry to identify and quantify the aquatic prokaryotes and picoeukaryotes (i.e., heterotrophs and photoautotrophs).

Our results outlined recurrent patterns and quantitative changes of interacting microbial assemblages across the urbanization gradient at different hydrological settings. *Alphaproteobacteria* largely dominate the microbial community, followed by *Verrucomicrobia* and *Betaproteobacteria*. The total prokaryotic cell abundance increased toward the river mouth, with higher values registered downstream the city of Rome (4×10^6 cells/ml). The per-cell nucleic acid content, intended as a proxy of the cell metabolic activity, increased accordingly, while the ratio between photoautotrophs and heterotrophs decreased downstream the confluence with main tributary.

Given the links between hydrological and microbial community patterns, river microbes could provide valuable indications on the ecological effects of urbanization and altered environmental conditions. Moreover, flow cytometry seems an appropriate tool to rapidly provide multi-parametric data for a better understanding of the biogeochemical processes at the microscale level in river systems.

10-O Fate of antibiotic resistance genes within the microbial communities of three waste water treatment plants. *Andrea Di Cesare, Ester Eckert, Silvia D'Urso, Julia Doppelbauer, Gianluca Corno*

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Although Waste Water Treatment Plant (WWTP) are designed to reduce the biological pollution of urban waters, they lack a specific action against antibiotic resistance bacteria (ARB) or antibiotic resistance genes (ARGs). Nowadays, it is well documented that WWTPs constitute a reservoir of antibiotic resistances and, in some cases, they can be a favorable environment for the selection of ARB. This represents a serious concern for the public health, because the effluents of the WWTPs can be reused for different applications. There is a need for knowledge about the ARGs removal efficiency by different disinfection processes and the potential regrowth of ARB during and after the different wastewater treatments. Moreover, only a few punctual studies determined the role of the antibiotic resistance selection systems in the stabilization of the ARGs within the microbial community of a WWTP. To shed light on these issues, we analyzed three WWTPs with different disinfection treatments (Verbania: chlorination, Cannobio: peracetic acid, and Novara: UV radiation). We performed different sampling strategies: i) integrated samples of three days and of 24h to evaluate the removal of ARGs in each plant and the potential regrowth (each sample was incubated for 96h at 12°C) of ARB and ii) point samples of water at the end of each treatment. The microbial community of each water sample has been counted by flow cytometry to determine the bacterial numbers and their aggregational state. DNA extracts from each sample were analyzed for the abundance of antibiotic resistance genes (ARGs) (*bla*_{TEM}, *bla*_{CTXM}, *tetA*, *qnrS*, *ermB*, *sullI*) the mobile element integron 1 and the heavy metal resistance genes (HMRGs) (*czc*, *arsB*) by qPCR. The prokaryotic cell abundances drastically reduced from the input to the output water, but no significant reduction was observed during the disinfection treatments regardless to the WWTP location. The regrowth experiments showed that the ARGs were significantly reduced in the input water and in the pre-disinfection water (comparing the data pre- and post-incubation) for all three WWTPs, while they were stable in the effluent for the Verbania WWTP, and they decreased in effluents from Cannobio and Novara ones. Altogether, these results demonstrate that WWTPs efficiently remove bacterial cells, however the different disinfection treatments do not impact the bacterial cell numbers and, moreover, in Verbania WWTP, during the disinfection, there is selection towards ARGs. This suggests specific selection pressures within the microbial community of a WWTP, which can co-select for ARGs leading to the not successful functioning of the disinfection treatment. This hypothesis was confirmed by the significant correlation between genes *sullI*, *czc*, *arsB* and *int1*. In conclusion, this study points out the need for knowledge on the mechanisms and the selective pressures that promote the stabilization of ARB within the microbial community of WWTPs.