**Environmental Microbiology and Biotechnology**

## P-112 - MICROBIAL COMMUNITY AND ANTIBIOTIC RESISTANCE GENES DISTRIBUTION IN DIFFERENT URBAN WASTEWATER TREATMENT PLANTS EFFLUENTS

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### Background

Urban wastewater treatment plants (UWTPs) are major anthropogenic reservoirs of antibiotic-resistant bacteria (ARB), antibiotic resistance genes (ARG) and antibiotic residues. The information about the occurrence of ARBs and ARGs in UWTPs as well as the mechanisms of their dissemination and how they can represent a public health threat is still scarce. The hypothesis behind this study was that the profiles of ARGs released by different UWTPs can be correlated with the respective bacterial communities. With this aim, the bacterial community composition and ARGs profile were characterized in the effluents of three UWTPs located in the Oporto region.

### Method

A total of 33 treated effluent samples were collected from three UWTPs (PT1, PT2 and PT3), over seven sampling campaigns. All the UWTPs use activated sludge (AS) as secondary treatment, and PT3 is complemented by UV disinfection. The bacterial community composition was analysed based on the 16S rRNA gene amplicon paired-end sequencing using Illumina MiSeq platform and the ARGs (bla$_{TEM}$, bla$_{SHV}$, bla$_{OXA-A}$, bla$_{CTX}$, sul1, sul2 and qnrS) and class 1 integrase (intI1) were measured using quantitative PCR (qPCR).

### Results & Conclusions

Irrespective of the sampling dates, the effluents of the three UWTPs yielded distinct bacterial community compositions independent of sampling dates, albeit with some common traits at the class level. For all the samples *Betaproteobacteria* was the major class. When analysed at the order level it is clear a difference between PT1 and the other two UWTPs, with PT1 presenting a higher abundance of *Burkholderiales* and *Bacteroidales* than PT2 and PT3. Amongst the genes analysed, the same trend was observed for abundance (gene copy number/mL) and prevalence (gene copy number/gene copy number of 16S rRNA), with the ARGs being ranked as *bla$_{CTX}$<bla$_{SHV}$<bla$_{TEM}$<qnrS<sul2<bla$_{OXA}$<intI1<sul1*. Major differences between the three UWTP with regards to ARGs were the higher abundance and prevalence of *bla$_{OXA}$*, and the higher abundance of *qnrS*, and *bla$_{TEM}$* in PT1 than in the other two UWTPs. In general, it was possible to infer that ARGs distribution may be correlated with the bacterial community composition, which in turn may depend on the quality of the inflow and/or the characteristics of the wastewater treatment.

**Keywords: Antibiotic-resistant bacteria, Antibiotic resistance genes, Urban wastewater treatment plants**