

P-091 - BACTERIAL COMMUNITY AND ANTIBIOTIC RESISTANCE DYNAMICS IN A FULL-SCALE WASTEWATER TREATMENT PLANT WITH UV DISINFECTION

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Background

The removal of potentially hazardous microorganisms, as bacteria harbouring acquired antibiotic resistance genes (ARB&ARG), from wastewater is one of the major aims of the treatment. In wastewater treatment, dramatic variations on the bacterial community structure may occur and it is expected that these variations may have an important role on ARG selection.

An urban wastewater treatment plant (UWTP) using activated sludge as biological treatment and UV for disinfection was studied aiming at: i) assessing the dynamics of bacterial lineages during the whole process; ii) measuring of the variations on the abundance of ARGs after each treatment step; iii) inferring if population changes might be associated with ARGs distribution.

Method

Samples from the raw influent, secondary (activated sludge) and tertiary (UV disinfection) treated effluent were collected from an urban wastewater treatment plant, in three dates. Tertiary effluent was also analyzed after 3 days of incubation. Samples were analyzed for cultivable enterobacteria counts, 16S rRNA gene-based of microbial community and quantification of 8 ARGs using quantitative PCR.

Results & Conclusions

The stages of activated sludge and UV disinfection led to ~2 log-units reductions of enterobacteria CFUs. The bacterial community composition suffered the most intense rearrangements after secondary treatment, rather than after UV disinfection. In addition, quantitative PCR of ARGs showed a reduction of ~2 log-units after the secondary treatment and a negligible variation after UV disinfection. The effect of treatment was not identical for all ARGs examined, an observation that was consistent with the fact that different genes were most correlated with distinct bacterial populations. For instance, members of *Bacteroidaceae*, *Lachnospiraceae*, *Campylobacteraceae*, *Aeromonadaceae*, *Enterobacteriaceae* and *Moraxellaceae* were correlated with beta-lactamase and *qnrS* genes, while members of *Comamonadaceae*, *Neisseriaceae* and the classes *TM7-1* and *ZB2* were correlated with the gene *sul2*.

Keywords: antibiotic resistance, wastewater treatment, UV disinfection, antibiotic resistance genes, antibiotic resistant bacteria