

FEMS7-1894

Environmental Microbiology/Microbial Ecology /Microbial Communities - Part III

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

C. Narciso-da-Rocha¹, J. Rocha¹, V.M. Ivone¹, F. Lira², J. Tamames², I. Henriques³, J.L. Martínez², C.M. Manaia¹

¹Universidade Católica Portuguesa - Escola Superior de Biotecnologia,

CBQF - Centro de Biotecnologia e Química Fina – Laboratório Associado, Porto, Portugal

²Consejo Superior de Investigaciones Científicas - CSIC, Centro Nacional de Biotecnología, Cantoblanco- Madrid, Spain

³CESAM - University of Aveiro, Biology Department, Aveiro, Portugal

Backgrounds

It has been proposed that wastewater treatment plant can be reservoirs and reactors of antibiotic resistance. Since wastewater treatment lead to variations on the bacterial community composition, knowing how such variations impact the dynamics of antibiotic resistance genes (ARGs) is critical to improve ARGs removal during wastewater treatment.

Objectives

To study an urban wastewater treatment plant (UWTP) which includes secondary and UV treatment aiming at: i) identifying populations more fitted during the whole process; ii) measure the impact of each treatment step on the abundance of ARGs; iii) infer how population changes may alter the distribution of ARGs.

Methods

Samples were collected at three dates from the raw inflow, secondary (activated sludge) and tertiary (UV disinfection) effluent of a UWTP. The cultivable enterobacteria, bacterial community composition and 8 ARGs were examined in all samples and after three days storage.

Conclusions

Each of the stages of activated sludge and UV disinfection led to ~2 log-units reductions of enterobacteria. Noteworthy it was the secondary treatment, rather than UV, that led to important changes in the bacterial community composition. In addition, quantitative PCR of ARGs, showed 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*.