

MICROBIOTEC 19

December 5th-7th, 2019
University of Coimbra (Pólo II)

CONGRESS OF MICROBIOLOGY
AND BIOTECHNOLOGY 2019

BOOK OF ABSTRACTS



I1. Environmental Microbiology and Biotechnology

P9. Dynamics of carbapenem resistance in urban wastewater treatment plants and receiving water bodies: drivers and opportunities for action

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Urban wastewater treatment plants (UWTPs) are described as reservoirs of antibiotic resistance. It has become increasingly clear that antibiotic resistant bacteria (ARB) and antibiotic resistance genes (ARGs) released by well-functioning UWTPs may have a negative impact on the environment, representing a threat for humans and/or ecosystems. Assessing risks where the environment and humans meet is therefore critical. This study has focused on antibiotic resistance loads and the epidemiological dynamics of resistance in natural water bodies receiving treated urban wastewaters.

Wastewater samples were collected from 4 full-scale UWTPs (PT1-PT4) located in Northern Portugal, at different stages of wastewater treatment, and river water samples were collected upstream and downstream of each treatment plant. All UWTPs have primary and secondary treatments, with PT1- PT3 reporting a tertiary treatment and PT2 an additional step of ozonation. PT4 reported the reception of hospital effluents. Samples collected in early Summer (SC1) and in early Autumn (SC2) were processed for total DNA extraction and isolation of cultivable bacteria resistant to meropenem or cefotaxime. Carbapenem resistance genes (*bla*_{KPC}, *bla*_{OXA-48}, and *bla*_{OXA-58}), class 1 integron- integrase (*intl1*) and 16S rRNA were quantified based on quantitative PCR.

The abundance of ARGs and *intl1* (per mL of sample) in the final effluent of all UWTPs could be ranked as *intl1* > *bla*_{OXA-58} > *bla*_{OXA-48} > *bla*_{KPC}, with a higher abundance of 16S rRNA gene, *intl1*, *bla*_{OXA-48} and *bla*_{OXA-58} observed in PT1. In PT2, *bla*_{KPC} was not detected after secondary treatment and ozonation promoted a reduction of 1.44 to 3.85 log-units in genes abundance. Comparing river water upstream and downstream the UWTPs, the abundance of *bla*_{KPC}, *bla*_{OXA-48} and *bla*_{OXA-58} genes was higher downstream PT4, PT2 and PT3 in SC2, respectively. The genes *bla*_{KPC-2}, *bla*_{CTX-M-15} and *intl1* were detected in isolates (*Klebsiella quasivariicola*) from a secondary effluent of PT3 and downstream the treatment plant (SC1). In addition, *bla*_{KPC-3} and *intl1* were detected in 3 isolates (2 *Klebsiella pneumoniae*, and 1 *Klebsiella variicola*) after secondary and tertiary treatment from PT2, and downstream PT4 (SC1). The results demonstrate that although UWTPs are effective for removal of clinically relevant ARGs, some can persist in the downstream environment and associated with opportunistic pathogens.