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## Abstracts Book



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#### ASSOCIATIONS BETWEEN ANTIMICROBIAL RESIDUES, BACTERIAL COMMUNITIES AND ANTIBIOTIC RESISTANCE IN A HOSPITAL-URBAN WASTEWATER TREATMENT PLANT

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The discharge of untreated hospital effluents has been associated with the dissemination of antibiotic resistant bacteria into the environment. However, studies on the impact of hospital effluents on the receiving urban wastewater treatment plants (UWTP) are scarce. The main goal of this study was to compare the loads of antimicrobials, the antibiotic resistance prevalence and the bacterial community structure of a hospital effluent with those of the receiving UWTP.

These parameters were assessed through successive sampling campaigns of raw hospital effluent (HE) and raw (RWW) and treated (TWW) wastewater of the UWTP. Samples were characterized for amoxicillin and ciprofloxacin resistance prevalence, content of heavy metals and antimicrobial residues and bacterial community structure, based on 16S rRNA gene PCR-DGGE.

The bacterial communities found in HE and RWW of the UWTP were distinct, although with higher similarity between them than with the treated outflow (TWW). While the levels of fluoroquinolones, arsenic and mercury were in general higher in HE than in RWW, the opposite was observed for tetracyclines, sulfonamides and penicillin G. The prevalence of ciprofloxacin, but not of amoxicillin, resistance was significantly higher in HE than in RWW ( $p < 0.05$ ). It was possible to correlate the variations of the bacterial community in wastewater with the concentration of antimicrobials and with antibiotic resistance prevalence. Moreover, the concentration of antimicrobial residues was observed to be significantly correlated with the prevalence of antibiotic resistant bacteria.

Hospital effluent was confirmed as an important, although not the unique, source of antimicrobial residues and antibiotic resistant bacteria to the UWTP. Given the high loads of antibiotic residues and antibiotic resistant bacteria found in hospital effluents, these wastewater habitats serve as models to study and predict the impact of antibiotic residues on bacterial communities.

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