

Environmental Microbiology and Biotechnology

O-16 - MICROBIOLOGICAL QUALITY OF TREATED WATER BY SOLAR-DRIVEN OXIDATION PROCESSES

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Background

The commonly implemented wastewater treatments have a limited capacity to remove organic micropollutants, including pharmaceuticals, and human pathogens, as well as antibiotic resistant bacteria (ARB) and related genes (ARG). As a consequence, the continuous disposal of antibiotics and related products into the environment can lead to the development and proliferation of ARB, a problem that needs urgent solutions. The present study aimed at comparing the efficiency of different solar-driven oxidation processes on the removal of undesirable microorganisms, with the simultaneous elimination of organic micropollutants, in the secondary effluent of an urban wastewater treatment plant, using a solar compound parabolic collector at pilot-scale.

Method

Wastewater samples were spiked with 100 µg L⁻¹ of each selected model organic micropollutant: carbamazepine, sulfamethoxazole and diclofenac. Quantitative analysis of the organics was made by HPLC. The abundance of total and tetracycline and ciprofloxacin resistant cultivable faecal indicator bacteria and of the genes 16S rRNA, *int11*, *bla_{TEM}*, *qnrS*, *sul1*, *bla_{CTX-M}* and *vanA* was followed by using the membrane filtration method and qPCR, respectively. Bacterial community was analysed based on the hypervariable V3/V4 region of 16S rRNA gene Illumina sequencing. Samples were analysed before treatment, immediately after treatment, and after 3-days of storage of treated wastewater at room temperature.

Results & Conclusions

The highest efficiency on the removal of the parent model organic compounds to concentrations below the limit of detection (LOD) was observed for H₂O₂-assisted photocatalysis using TiO₂ as photocatalyst. Tetracycline and ciprofloxacin resistant enterococci and faecal coliforms were removed to levels below the LOD (1 CFU 100 mL⁻¹), irrespective of the treatment applied with H₂O₂, even upon storage of the treated wastewater for 3-days. However, reactivation assessed based on 16S rRNA and *sul1* quantification was observed in all the treatments. Regardless of the type of process, wastewater treatment and storage caused notorious bacterial communities disturbances, characterized by an increase in the relative abundance of *Proteobacteria* (classes *Beta*- and *Gammaproteobacteria*), namely of the genera *Pseudomonas*, *Rheinheimera*, *Methylothera*.

References & Acknowledgments

This work was supported by Project nº P1404290052 (SFERA Program, EC/FP7-Integrating Activities), and by NORTE 2020 (AIProcMat@N2020 NORTE-01-0145-FEDER-000006; LEPABE-2-ECO-INNOVATION NORTE-01-0145-FEDER-000005), under the Portugal 2020 Partnership Agreement, through ERDF, Projects POCI-01-0145-FEDER-006984 (UID/EQU/50020/2013) and POCI-01-0145-FEDER-006939 (UID/EQU/00511/2013), and COMPETE2020 – and by national funds (FCT, UID/Multi/50016/2013-CBQF and Water JPI/0001/2013 STARE). NFFM, LMPM and AMTS acknowledge PD/BD/114318/2016, IF/01248/2014 and IF/01501/2013, respectively. The authors acknowledge also the COST-European Cooperation in Science and Technology, to the COST Action ES1403: New and emerging challenges and opportunities in wastewater reuse (NEREUS). Microbiological quality of treated water by solar-driven oxidation processes

Keywords: Solar-driven oxidation treatment, Organic micropollutants, Human pathogens, Antibiotic resistance, Bacterial communities