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3rd IWA Specialized International Conference
Ecotechnologies for Wastewater Treatment 2016 (ecoSTP16)

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Bacterial community and system performance of an aerobic granular sludge reactor treating pharmaceutical wastewater

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Abstract: Pharmaceuticals often reach wastewater treatment systems where low removal rates are observed. In the present study the potential impact of a mixture of such micro-pollutants on an aerobic granular sludge-sequencing batch reactor (AGS-SBR) was investigated using a lab-scale bioreactor. COD and P- removals were affected due to the load of pharmaceuticals resulting in a decrease of the COD uptake and the P-release during the anaerobic feeding phase, but the discharge limits were not exceeded. Nevertheless, both processes returned to its normal operation after resuming the pharmaceuticals feeding. The nitrification process was also affected but the activity of bacteria responsible for both nitrification steps was able to recover. The exposure to the pharmaceuticals induced alterations in the bacterial community structure.

Keywords: Aerobic granular sludge; nutrient removal; bacterial community

Introduction

Pharmaceutical compounds are emerging environmental contaminants that have been detected in various environmental matrices (Santos et al., 2013). Even at low levels, they can affect the composition of the microbial communities, and hence disturbing the metabolic networks. Aerobic granular sludge (AGS) has been successfully applied for the treatment of industrial and domestic wastewaters (Adav et al., 2008) and the implementation of AGS full-scale facilities has been growing worldwide. The possibility to concomitantly remove carbon, nitrogen and phosphorous in a single unit, is one of the attractive aspects of the AGS technology since it greatly reduces the plant footprint. Pharmaceuticals are often present in influent wastewaters; therefore knowledge on their effect on the AGS microbial community and on the biological processes is crucial for the implementation of the AGS technology.All subsequent paragraphs are indented and justified.

Material and Methods

AGS-SBR was set-up and operated during 86 days as described elsewhere (Amorim et al., 2014). From day 29 to 57 the synthetic wastewater was amended with a mixture of pharmaceuticals from different therapeutic classes. Chemical oxygen demand (COD) was determined according to Standard Methods (APHA, 1998). Concentrations of ammonium (NH_4^+), nitrite (NO_2^-), nitrite (NO_3^-) and phosphate (PO_4^{3-}) were measured using the Photometric test kits (Spectroquant®, Merck). The biomass was sampled on different operational days and genomic DNA was extracted. PCR-Denaturing gradient gel electrophoresis (DGGE) of bacterial 16S rRNA gene was performed according to Amorim et al., 2014. DNA pyrosequencing on a 454 Genome Sequencer FLX platform combined with bioinformatic analysis was also performed.

Results and Conclusions

The load of pharmaceuticals into the AGS-SBR affected the biological processes such as C, N and P-removal (Fig. 1.1a,b). The COD removal efficiencies during the anaerobic phase slightly decreased but, the maximum COD content at the effluent was below the emission limit value (council directive 91/271/EEC). The P-removal was also consistent over the operational time. Nevertheless, from the day 28 onwards, the bulk liquid phosphate content after the anaerobic feeding period dropped, indicating that polyphosphate accumulating organisms' activity was affected. The load of pharmaceuticals also affected N-removal. An increase of the ammonium concentration at the effluent was observed indicating that probably ammonia oxidizing bacteria were inhibited but recovered after stopping the feeding. Nitrite oxidizing bacteria activity was only partially resumed at the end of the monitoring.

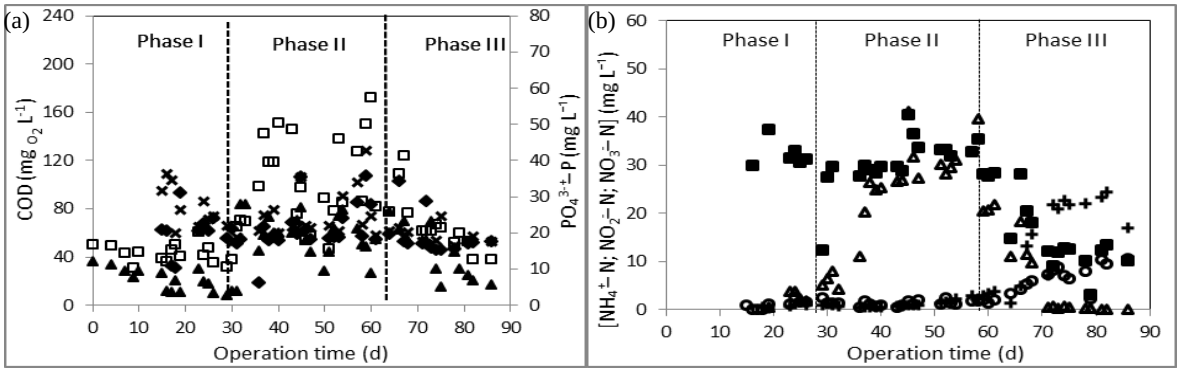

Figure 1.1 COD, P (a) and N (b) removal along AGS-SBR operation. The concentration of COD (□), PO_4^{3-}-P (x) and NH_4^+ -N (■) in reactor liquid after anaerobic feeding and COD (▲), PO_4^{3-}-P (♦), NH_4^+ -N (Δ), NO_2^--N (+) and NO_3^--N (○) effluent are shown.

The DGGE profiling revealed structural differences along bioreactor operation, probably related with the adaptation to the pharmaceuticals. Nevertheless, a greatly diverse bacterial population was observed, with some bands present along all bioreactor operation. The Shannon's diversity index (H) and the Equitability indexes (E) were similar over the operational period. Pyrosequencing analysis indicated that the top abundant phyla within the AGS microbial community were Bacteroidetes, Proteobacteria and Actinobacteria. However, the proportion of each phylum changed over time.

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