

MSc Research Project

Characterization of the microbial populations enrolled in the antimicrobial degradation in wastewater treatment plants

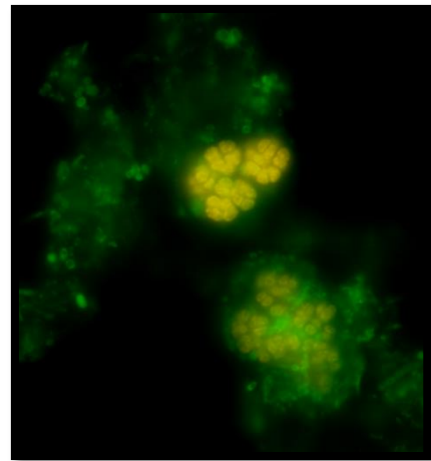
Laboratory: Microbiology

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Project Summary

Antimicrobials are widely used in pharmaceuticals and cleaning products. Removal of antimicrobials in wastewater treatment plants (WWTP) is often inefficient since they are not designed for the removal of such micropollutants present in sub-inhibitory concentrations (μgL^{-1} to ngL^{-1})¹. When released in the environment, they promote the undesirable selection of resistant microorganisms, besides having toxic effects on the surrounding biota^{2,3}. Antimicrobials are therefore an emerging group of environmental contaminants, and its elimination is a topic of utmost importance.



The performance of activated sludge to eliminate antimicrobials from wastewater is fairly documented concerning its capacity of adsorption and its bioremoval as well as the operational conditions that favors such procedures⁴⁻⁶. Nevertheless, while removal of antimicrobials in biological treatment processes has been assessed, little is known about the microorganisms within WWTP biomass that are responsible for their degradation. The studies only cover a few compounds⁷⁻⁸, and to the best of our knowledge, most of the microorganisms capable of mineralizing the antimicrobials are yet to be characterized.

The aim of this work is to analyze the microbial populations responsible for the biodegradation of a set of antimicrobials and to study the impact of the operational conditions on such populations.

Tasks description

1. Biomass samples will be obtained throughout time from a microbial culture subject to the antimicrobial pressure and a control one. Degradation of the antimicrobial and generation and degradation of metabolites will be followed throughout time.
2. Characterization of the microbial population that is actively involved in the degradation of each of the studied antimicrobials
 - a. Extraction of the total microbial DNA
 - b. Microbial structure analysis based on the 16SrDNA gene, using next generation sequencing.
3. Quantification of the abundance of such microbial populations throughout time by quantitative fluorescence *in situ* hybridization (qFISH)
4. Writing of Master thesis

References

- 1) Kümmerer, K. (2009) Antibiotics in the aquatic environment - a review - part I. *Chemosphere* 75(4):417-34
- 2) Martínez, J.L. (2009) Environmental pollution by antibiotics and by antibiotic resistance determinants. *Environmental Pollution* 157(11):2893-902.
- 3) Tatarazako, N., Ishibashi, H., Teshima, K., Kishi, K., Arizono, K. (2004) Effects of triclosan on various aquatic organisms. *Environmental sciences: an international journal of environmental physiology and toxicology* 11(2):133-40
- 4) Dorival-García, N., Zafra-Gómez, A., Navalón, A., González-López, J., Hontoria, E., Vílchez, J.L. (2013) Removal and degradation characteristics of quinolone antibiotics in laboratory-scale activated sludge reactors under aerobic, nitrifying and anoxic conditions. *Journal of Environmental Management* 120:75-83
- 5) Li, W., Shi, Y., Gao, L., Liu, J., Cai, Y. (2013) Occurrence and removal of antibiotics in a municipal wastewater reclamation plant in Beijing, China. *Chemosphere* 92(4):435-44.
- 6) Roh, H., Subramanya, N., Zhao, F., Yu, C.P., Sandt, J., Chu, K.H. (2009) Biodegradation potential of wastewater micropollutants by ammonia-oxidizing bacteria. *Chemosphere* 77(8):1084-9.
- 7) Lee do G, Zhao F, Rezenom YH, Russell DH, Chu KH. (2012) Biodegradation of triclosan by a wastewater microorganism. *Water Res.* 46(13):4226-34
- 8) Lolas, I.B., Chen, X., Bester, K., Nielsen, J.L. (2012) Identification of triclosan-degrading bacteria using stable isotope probing, fluorescence *in situ* hybridization and microautoradiography. *Microbiology* 158(Pt 11):2796-804