Adaptation and resilence of microbial periphyton to pharmaceuticals and associated changes in community diversity and structure: an in situ translocation experiment.

Hélène Rogue*[1], Stephane Pesce[1], Chloé Bonnineau[2], Cécile Chardon[3], Amandine Daval[1], Bernard Motte[1], Rimet Frédéric[3], Christophe Rosy[1], Bernadette Volat[1], Cecile Miege[1], and Emilie Lyautey[3]

[1]INRAE, UR RiverLy, Villeurbanne – INRAE – France
[2]UR EABX – INRAE – France
[3]INRAE, UMR CARRTEL – INRAE – France

Abstract

The worldwide contamination of rivers by pharmaceuticals can affect microbial periphytic communities. One major challenge for *in situ* assessment of the ecotoxicological effects of pharmaceuticals (or other chemicals) on these communities is establishing the causal link between contamination and microbial responses. The present study aims at (i) assessing if chronic exposure to pharmaceuticals can cause an increase in the tolerance of periphyton to these substances ('pollution induced community tolerance', PICT) and (ii) studying the adaptation and resilience dynamics in relation with changes in community diversity and structure according to exposure levels.

We carried out an *in situ* translocation study in a small river (Tillet River, Savoie, France), considering an upstream (reference) and a downstream (contaminated) sites. After a 4-week growth period, the periphyton was moved, or not, from one site to the other, to simulate during 6 weeks a restoration (down- to upstream) or deterioration (up- to downstream) of the chemical water quality. Water contamination was monitored using polar organic chemical integrative samplers (POCIS), and the periphyton tolerance was assessed using a PICT approach. Acute toxicity tests on photosynthesis were performed on periphyton sampled every 2 weeks, using 2 pharmaceuticals tested individually (the beta blocker atenolol and the non-steroidal anti-inflammatory drug diclofenac) Community structure and diversity were assessed using metabarcoding approaches on 16S rRNA (bacteria and cyanobacteria) and *rbcL* (diatoms) genes.

Our results confirmed the increase in pharmaceutical concentrations from up- to downstream. The tolerance of phototrophic communities to atenolol and diclofenac was higher downstream than upstream. Following translocation, tolerance levels increased in communities transferred downstream, and decreased in communities transferred upstream, suggesting adaptation and resilience processes, respectively. Both metabarcoding approaches revealed a higher diversity in downstream communities as well as differences in community structures between the two sampling sites. Furthermore, both the diversity and structure of the communities changed substantially when they were moved from one site to the other,

*Speaker

suggesting that changes in tolerance can be related to changes in community diversity and structure. Among others, this work demonstrates the relevance of the PICT approach for *in situ* diagnosis oh the impact of pharmaceuticals on periphyton.

Keywords: biofilms, microbial ecotoxicology, PICT (pollution induced community tolerance), POCIS (polar organic chemical integrative sampler), rivers, metabarcoding