Interaction between glyphosate and dissolved phosphorus on bacterial and eukaryotic communities from river biofilms

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Context

Glycosphate is
the most used pesticide worldwide and is
transformed in AMPA (main metabolite).

Both compounds contaminate river ecosystems
Phosphorous × Glycosphate concentration gradient
Glycosphate-degrading microorganisms?

Objectives

✓ to determine the interaction effect of glycosphate and dissolved phosphorus on the structure and composition of bacterial and eukaryotic communities in biofilms
✓ to identity taxa potentially involved in glycosphate degradation by biofilms

Materials & methods

Biofilms communities

In situ colonization (2 weeks)
Artière river (France)

Exposed to glycosphate in river water (microcosms, 27-day experiment)

Analyses

✓ Illumina MiSeq sequencing on bacterial and eukaryotic communities in biofilms

Results

Species diversity responses

<table>
<thead>
<tr>
<th>Shannon’s diversity index (H’)</th>
<th>LowP</th>
<th>LowG</th>
<th>HighP</th>
<th>HighG</th>
</tr>
</thead>
<tbody>
<tr>
<td>LowG</td>
<td>5.88 (± 0.14)</td>
<td>5.92 (± 0.14)</td>
<td>5.77 (± 0.14)</td>
<td>5.66 (± 0.14)</td>
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LowP: Low phosphorous; LowG: Low glyphosphate; HighP: High phosphorous; HighG: High glyphosphate

Potential glycosphate-degrading phyla

Bacteria

Eukaryotes

Phylogenetic analysis on glycosphate-degrading bacteria

Five of the most abundant Bacterial phyla (Bacteroidetes, Chloroflexi, Cyanobacteria, Planctomycyes and Proteobacteria) contain ASVs abundance highly negatively correlated with glycosphate (Spearmann’s rank coefficient < -0.71).

Only three Eukaryotic phyla (Chlorophyta, Cryptophyta and Ochrophyta) contain ASVs abundance highly negatively correlated with glycosphate (0.84 < Spearmann’s rank coefficient < -0.69).

Conclusions

✓ While eukaryotic communities showed strong diversity plasticity when exposed to low glycosphate concentrations, shifts in bacterial communities’ structure were specifically observed during glycosphate dissipation.
✓ Biofilms capable to use glycosphate as P source were characterized by increases in the relative abundance of certain Bacteroidetes, Chloroflexi, Cyanobacteria, Planctomycyes and α-Proteobacteria members.

It has to be noted that our approach can rule out certain ASVs participating in the degradation of glycosphate but present in low ASV abundance when glycosphate is depleted.