Bacterial adaptive response to changing herbicide discharge rates in the streambed sediments impacted by a landfill

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Introduction
Phenox acid herbicides related to plant growth hormone are ground water contaminants originating not only from agricultural practice, but also from landfill leachate.

Old landfills are major sources of multiple ground water contaminants entering surface water by ground water discharge. We previously determined that the mineralization potential of phenox acid herbicides at field-relevant concentrations depends on the herbicide mass discharge and initial abundance of tfdA gene classes (Batıoğu-Pazarbaş, et al., 2012).

In our current study, the effect of landfill leachate-contaminated ground water on bacterial diversity of ground water-surface water transition zones was studied at much higher concentration (120 mg kg\(^{-1}\)) and compared with field-relevant concentration scenario.

Methods
Map showing the sampling locations of the Risky Landfill and the ground water discharge zones

Streamed sediments were sampled from around the seepage meters installed in three discharge zones of the Risky stream impacted differently by leachate from the nearby Risky landfill.

We previously determined that SM1-streamed sediment received the highest mass discharge of phenoxy acid herbicide residues followed by SM2 and SM1 (Batıoğu-Pazarbaş, et al., 2012).

The landfill leachate entering the sediments contains phenoxy acid herbicides besides other typical landfill leachate compounds (Batıoğu-Pazarbaş, et al., 2012).

The sediment samples were transferred to microcosms and used for quantification of mineralization potential.

The sediment samples were collected before, during and after mineralization of field-relevant and higher concentrations and stored at -20°C for molecular analysis (multiplex qPCR, T-RFLP and pyrosequencing).

Hypothesis
The understanding of landfill impact on streamed sediments due to ground water discharge is highly important to secure stream water quality. At our sampling site, the streamed sediment has been receiving herbicide mixtures at variable discharge rates for years.

We therefore hypothesize that this long-term in situ phenoxy acid herbicide exposure influences the bacterial community composition and tfdA gene diversity.

Results
Mineralization curves of (A) benzoic acid, (B) 2,4-D, (C) MCPA, (D) MCPP and (E) 2,4-DP in the streamed sediments of three discharge zones at 120 mg kg\(^{-1}\) concentration

The initial abundance of 16S rRNA, total tfdA, tfdA class I and class III genes before mineralization and the changes in gene abundance in the stationary phases of mineralization at 120 mg kg\(^{-1}\) concentration

Error bars represent standard errors of the mean for sediment triplicates, some error bars are smaller than the symbol size.

Conclusions
The most rapid mineralization of phenoxy acid herbicides in SM3 and slower mineralizations in SM2 and SM1 were observed depending on the landfill impact on discharge zones.

The highest increase in tfdA gene classes as bacterial response was mostly observed in SM3 receiving the highest-herbicide-contaminated ground water discharge. However, in SM2 and SM1, higher abundance of tfdA gene classes for each discharge zone was observed where the shorter time needed to achieve 10% mineralization of 2,4-D and 2,4-DP than those of MCP and MCPP indicating the higher affinity of degraders to 2,4-D and 2,4-DP.

Principal component analyses of both relative abundance of T-RF patterns and quantitative beta diversity of bacterial communities based on the pyrosequencing data disclosed similar clustering according to discharge zone.

Our study demonstrates that specific bacterial communities proliferate in streamed sediments in response to changing discharge rates of landfill-phenoxy acids.

Our results also indicate that bacterial responses of streamed sediment in each discharge zone differentiated after mineralization at field-relevant and higher concentrations despite of their similar clustering depending on the discharge zone.

Specifically, members of Betaproteobacteria (Comamonadaceae) increased in pyrrotag read abundance with mineralization in sediments from the first discharge zone, while reads affiliated to Acidobacteria GpII were enriched in sediments from the third discharge zone after mineralization at field-relevant concentration.

Under high herbicide concentrations, the relative abundance of Alphaproteobacteria (Sphingomonadaceae) enriched after incubation in sediments from the first discharge zone.

In the second discharge zone, pyrrotag related to Betaproteobacteria (Comamonadaceae) and certain Flavobacteria increased in abundance at low herbicide concentration, while Flavobacteria were enriched, to a lesser extent, at high concentration.

These comprehensive findings based on integrated genomic-metagenomic approach are highly important to provide microbial ecological indicators to perform more accurate and advanced human health and ecological risk assessments and to protect stream water quality.

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Reference