

The rate of lindane biodegradation in different constructed wetlands.

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In the last decades, the use of some types of pesticides was restricted or completely banned because of their adverse secondary effects to the environment and human health. The harmful effect of an insecticide γ -hexachlorocyclohexane (γ -HCH, lindane) on the environment and organisms is well known, and although field application was banned in 2010, contamination of soil and water is alarming. The aim of this two-year study was to compare removal of γ -HCH (Lindane) and its isomers in different constructed wetlands at a heavily contaminated site called Hajek.

Key words: Lindane, biodegradation, constructed wetlands, PCR, NGS.

Introduction

The gamma isomer of 1,2,3,4,5,6-hexachlorocyclohexane (γ -HCH), also known as lindane, is a cyclic, saturated and highly chlorinated pesticide. One of the serious environmental burdens in Czech Republic is connected with former production of lindane and technical HCH in the body of the dump of mine near the village Hájek (south-eastward from Ostrov in region of Karlovy Vary). Nowadays there are several constructed wetlands on site to minimise lindane contamination of environment.

Material and methods

Wetland A mimicked natural shallow-water wetland, wetland B was filled with organic substrate to support biodegradation, and on the inflow of wetland C, there were three permeable reactive barriers filled with iron sponges, wetland E filled with biochar (Fig.1).

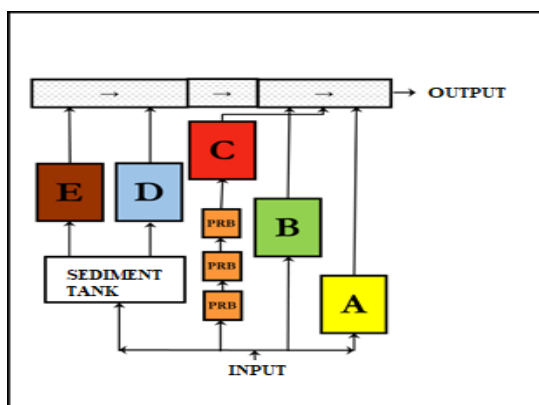


Fig. 1: Scheme of constructed wetland at the locality Hajek.

Specific genes were assessed for their potential in lindane biodegradation in all wetland biotops. The water and sediment samples were collected for DNA extraction and analysis by real-time quantitative PCR (qPCR) to determine total bacterial biomass, and presence of functional genes (LinA, LinB, LinB-RT, LinD). Based on the qPCR results, water and sediment samples from one part of the wetland system (A, B, C and E) were chosen to be analyzed by next-generation sequencing (NGS) to estimate the bacterial diversity.

Results and Discussion

The genes confirming the presence of enzymes involved in aerobic and anaerobic lindane biodegradation were detected in all of the samples. The NGS results indicated dynamic changes in bacterial community in 2017 and 2018, probably due to very dry season in the latter year. Sulfur and iron reducing bacteria dominated in the inflow and outflow of wetlands in 2017 (Fig. 2). In 2018, sediment samples from the B wetland, *Desulfovibrio* dominated. This species is known to be capable of lindane dechlorination. Microbial community in the outflow from B wetland in 2018 was more diverse comparing to previous year results (Fig. 3).

Interestingly, in C output mostly dominated *Gallionella* and *Sulfuricurvum* species, while in the sediment presence of this genera is minimal. But sediment samples turned out to be rich in *Acinetobacter*, *Comamonas*, *Flavobacterium*, and *Parapusillimonas*. Generally microbial diversity in inflow samples significantly higher comparing to

outflow samples from all wetlands regardless of the year.

Chemical analysis data of wetland in- and outflow indicate partial HCH elimination from the drain water. Wetland C is most effective in HCH removal.

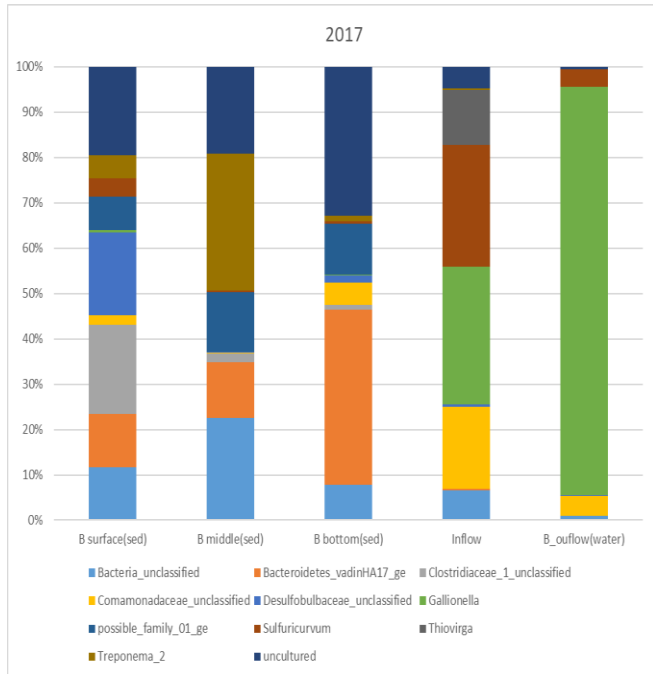


Fig. 2: Relative representation of microorganisms at family level (abundance > 5%) in the wetland B inflow and outflow and sediment samples in 2017.

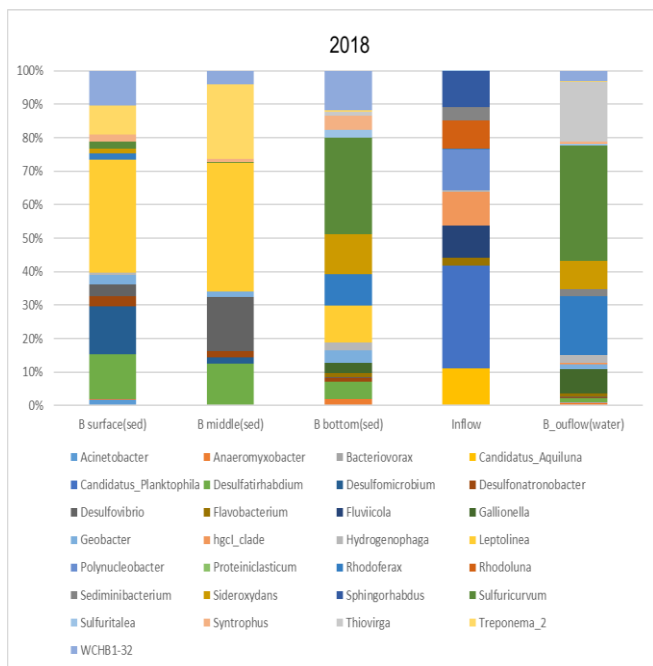


Fig. 3: Relative representation of microorganisms at family level (abundance > 5%) in the wetland B inflow and outflow and sediment samples in 2018.

Conclusion

Different bacterial diversity was found in sediments and water. Bacterial groups and enzymes involved in biogeochemical cycles of sulphur and iron were identified in large quantities. Detection of specific biomass capable of HCH biodegradation prevails in water samples than in sediments. Which allows us to draw conclusion that the conditions in water for lindane-degrading bacteria are much more favorable in comparison with the conditions in sediments.

Acknowledgments

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Reference

- [1] SAEZ, JULIANA MARIA & ALVAREZ, ANALIA & S. FUENTES, M & AMOROSO, MARÍA & BENIMELI, CLAUDIA. (2017). An Overview on Microbial Degradation of Lindane. Available from: doi: 10.1007/978-3-319-45156-5_9.
- [2] GEUEKE, B. , GARG, N. , GHOSH, S. , FLEISCHMANN, T. , HOLLIGER, C. , LAL, R. AND KOHLER, H. E. (2013), Metabolomics of HCH transformation. Environ Microbiol, 15: 1040-1049. Available from: doi: 10.1111/1462-2920.12009
- [3] LAL R, PANDEY G, SHARMA P, KUMARI K, MALHOTRA S, PANDEY R *et al* (2010). The biochemistry of microbial degradation of hexachlorocyclohexane (HCH) and prospects for bioremediation. *Microbiol Mol Biol Rev* 74: 58–80. Available from: doi: 10.1128/MMBR.00029-09