



## **Sediment Biobarriers for Chlorinated Aliphatic Hydrocarbons in Groundwater Reaching Surface Water**

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We studied the intrinsic capacity of eutrophic river sediment microbial communities to degrade Chlorinated Aliphatic Hydrocarbons (CAHs) passing the sediment zone. An area of the Belgian river Zenne at Vilvoorde which drains groundwater polluted with CAHs was selected for this study. CAH groundwater concentrations were measured at multiple locations directly upstream from the river using both existing monitoring wells and Geoprobe direct-push sampling techniques. Results indicated that vinyl chloride (VC), *cis*-1,2-dichloroethene (*cis*-DCE) and 1,1 dichloroethane (1,1-DCA) are the major groundwater pollutants discharging into the river and that their presence is depending on the specific site location. A 50 m long test area in the river, where the highest concentrations of VC, *cis*-DCE and 1,1-DCA were detected in the inflowing groundwater was selected for further research. In this area the CAH influx zone in the Zenne riverbed was determined by sampling both the river sediment using a piston sampler and the interstitial water of the sediment using a specific pore-water probe. The CAH concentrations found in the sediment and the interstitial water indicated that the groundwater discharge spatial distribution is very heterogeneous, mostly depending on local sediment permeability. At some locations in the riverbed full dechlorination was observed while VC and *cis*-DCE reach the surface water and seem to discharge into the river at spots with a high velocity groundwater influx. Hy-

drogen and oxygen isotopic analysis of the groundwater, surface water and sediment pore water confirmed the spatial heterogeneity of the groundwater influx zones.

The structure and the catabolic potential of the microbial community present in the transition zone between groundwater and surface water was further analysed using anaerobic microcosm tests and molecular biological techniques. Anaerobic microcosm tests showed a rapid microbial dehalogenation of both VC and *cis*-DCE to non-toxic ethene in the sediment. Chloroethene degrading *Desulfuromonas* and *Dehalococcoides* species were present in high numbers in the sediment as shown by quantification of their 16S rRNA genes by real-time PCR. Furthermore, chloroethene dehalogenase genes of *Dehalobacter restrictus*, *Sulfurospirillum multivorans*, *Desulfitobacterium* and *Dehalococcoides* species were detected in the river sediment by PCR analysis. The *vcrA* and *bvcA* genes, which code for the VC reductive dehalogenases of respectively *Dehalococcoides* sp. strain VS and BAV1 indicate that these two *Dehalococcoides* species were both present. These two *Dehalococcoides* species can grow on VC and *cis*-DCE as a sole energy source and are probably responsible for the observed degradation of these groundwater pollutants in the microcosms. Vertical distributions of Eubacteria, iron-reducing bacteria, sulfate-reducing bacteria and methanogenic bacteria in the polluted sediment were investigated by Denaturing Gradient Gel Electrophoresis (DGGE) of respectively amplified 16S rRNA, *dsr* (dissimilatory sulfite reductase) or *mcr* (methyl coenzyme-M reductase) gene fragments. Our results indicate that the interface between groundwater and surface water harbors a unique microbial community structure that is capable of degrading CAHs in groundwater before they reach the surface water. In this way, the sediments act as a natural biobarrier for groundwater pollutants passing through the interface, hereby reducing the risk of surface water contamination.