

Natural Attenuation of Organochlorine Compounds in Low- Permeability Aquifers: Chemical and Isotopic Evidence of Back-Diffusion and Biodegradation

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The persistence of organochlorine compounds (OCCs) in low-permeability aquifers poses significant challenges for groundwater remediation, in part due to a back-diffusion effect, taking place at the aquifer/aquitard interface [1]. This study investigates the influence of back-diffusion on natural attenuation processes of 1,2-dichloropropane (1,2-DCP) and tetrachloroethylene (PCE) in an aquifer contaminated with OCCs, in the Jura region, France. While 1,2-DCP and PCE degradation pathways are relatively admitted [2], reductive dechlorination genes (RDases) responsible for 1,2-DCP dechlorination in aquifer systems are less known. The study utilizes a multidisciplinary approach, combining compound-specific isotopic analysis (CSIA), analytical chemistry and molecular microbiology. Laboratory batch experiments were conducted to study biodegradation kinetics under aquifer-like conditions (anaerobic conditions), using microbial communities from two different contaminated aquifers. Two-dimensional (2D) flow tank experiments were employed to mimic back-diffusion scenarios, demonstrating that contaminants stored in low-permeability zones can re-enter the aquifer, prolonging contamination and affecting biodegradation kinetics. A combined CSIA of carbon and chlorine isotopes was used to characterize biodegradation and evaluate specific reaction pathways involved [1]. The evolution of contaminant concentration and the production of metabolites were monitored using gas chromatography – mass spectrometry (GC-MS). The changes in major ions (anions, cations) were measured using ion chromatography. The physicochemical conditions (pH, conductivity, redox potential) were monitored. The microorganisms and functional genes involved in the biodegradation of organochlorine compounds were analyzed for a comprehensive understanding of the involved processes. A reduction in PCE and 1,2-DCP concentrations in both batch and 2D tank setups are expected, with specific isotopic fractionation patterns. Microbial community analyses will identify key, such as *Dehalococcoides* and *Dehalogenimonas*, which exhibit specific genetic markers linked to reductive dehalogenation pathways. This research aims to advance our understanding of

back-diffusion and biodegradation in complex hydrogeological systems, offering practical insights for improving modelling tools and remediation strategies.

References

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