

# Investigation of the microbial community and associated element cycles involved in chlorobenzene biotransformation in a model wetland system

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Monochlorobenzene (MCB) is a frequently detected groundwater contaminant and represents the main pollutant in the anoxic aquifer of the field site in Bitterfeld, Germany. Thus far, information related to anaerobic biodegradation of MCB is very limited but it was observed that degradation was enhanced in planted compared to unplanted wetland systems or by the addition of e.g. Fe (III)-oxides. Therefore, to understand the biodegradation *in situ*, the fate of MCB was investigated in more detail in model wetland systems with or without plants and with or without amendment of iron oxides. Groundwater from the aquifer in Bitterfeld was used to inoculate and feed the systems. After an initial acclimatisation, decrease in MCB was observed in both planted wetlands, with a concurrent enrichment in <sup>13</sup>C, however not in systems without plants. Anoxic conditions were observed in the deeper zone but micro-oxic conditions in the upper zones of the planted wetlands. After stable degradation activity was observed a multiple-tracer test was performed in the planted systems using both uranine and bromine to investigate the flowpath as well as with <sup>13</sup>C<sub>6</sub>-labelled MCB to study the fate of the contaminant. After the tracer-pulse, the column was sacrificed and sediment material was further analysed. Proteomic analysis allowed to evaluate the overall as well specific microbial community incorporating MCB-derived-<sup>13</sup>C and compared to the overall community obtained by Illumina sequencing and functional gene-specific PCR. Communities with <sup>13</sup>C incorporation varied over depth and the presence of *bamA*, a gene encoding a conserved enzyme in the benzoyl-CoA-degradation pathway, supported the anaerobic degradation of MCB. Furthermore, advanced visualisation methods including nano-SIMS should allow to elucidate the responsible, MCB degrading, microbial community.