



## High variability of carbon stable isotope fractionation of chlorinated ethenes during microbial reductive dechlorination

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Chlorinated aliphatics are widespread groundwater contaminants and it is believed that reductive dechlorination is a key process resulting in depletion of these pollutants in anaerobic aquifers. To estimate biodegradation of chlorinated compounds, stable isotope fractionation analysis (SIFA) may be used but it requires an appropriate stable isotope fractionation factor ( $\alpha$ ). Dehalorespiring microorganisms dechlorinate tetrachloroethene (PCE) via the same pathway but may have different end products: trichloroethene (TCE), *cis*-dichloroethene (DCE), vinyl chloride (VC) or ethene. Since it is thought that the reaction proceeds via the same mechanism during reductive dechlorination, it was expected that carbon isotope fraction would be similar for the tested microorganisms. Previously we observed that fractionation of PCE by *Desulfitobacterium* sp. strain PCE-S was one order of magnitude higher than by *Sulfurospirillum* spp. A further investigation showed that fractionation of TCE was in the same range for both *Desulfitobacterium* sp. strain PCE-S and the *Sulfurospirillum* spp. Evaluation of fractionation by further representatives of major groups of known dehalorespirers showed that the fractionation was even more variable. *Desulfitobacterium* strain Viet1 had higher fractionation factor for PCE than strain PCE-S and the highest of all studied strains. On the other hand, PCE fractionation by *D. michiganensis* and *G. lovleyi* strain SZ was very low, close to the detection limit and similar to *Sulfurospirillum* spp. Fractionation of TCE was relatively low for *D. michiganensis* and *G. lovleyi* strain SZ, but in a similar range for all other organisms. Our results suggest a correlation of fractionation patterns for PCE and TCE to the phylogeny of the specific strains. The high variability of observed fractionation limits the use of SIFA for the assessment of chlorinated ethenes *in situ* but SIFA potentially can be applied

in combination with an investigation of the *in situ* microbial community.