Geophysical Research Abstracts, Vol. 8, 00247, 2006 SRef-ID: 1607-7962/gra/EGU06-A-00247 © European Geosciences Union 2006



## Identification of novel PCE-dehalorespiring microorganisms in anoxic river sediment by RNA-based stable isotope probing

S. Kittelmann, M.W. Friedrich

Max Planck Institute for Terrestrial Microbiology, Germany (michael.friedrich@staff.uni-marburg.de / Phone: +49-6421-178830)

Perchloroethene (PCE), a persistent environmental contaminant, can be reductively dechlorinated by anaerobically dehalorespiring bacteria. However, the diversity of dehalorespirers and their environmental distribution is largely unexplored. Here, we identified novel PCE-dehalorespirers by stable isotope probing (SIP), a technique that allows to directly link structure and function of uncultivated microbial populations. River sediment was incubated with PCE at low aqueous concentration (20  $\mu$ M) at 15°C and dehalogenation activity (40 nmol *cis*-dichloroethene ml<sup>-1</sup> day<sup>-1</sup>) was detected after 8 weeks. The microbial community was probed with <sup>13</sup>C-labelled acetate (0.5 mM) as electron donor and carbon source for 4 days. After RNA extraction, "heavy" and "light" rRNA were separated by isopycnic centrifugation, and Bacteriarelated populations in gradient fractions were characterised by terminal restriction fragment length polymorphism analysis. In heavy gradient fractions of the microcosm with PCE, we detected a prominent 505-bp terminal restriction fragment (T-RF) and a few minor T-RFs, whereas in the control without PCE, bacterial rRNA was restricted to light fractions, and the prominent T-RFs found in the PCE-dechlorinating microcosm were of minor importance. Apparently, label was incorporated more effectively in PCE-respiring microcosms, which suggests the detection of dehalorespiring,  $^{13}$ C-acetate-assimilating populations. In clone libraries of the heavy fractions, a novel clone cluster distantly related to the PCE-dehalorespiring Dehalococcoides ethenogenes str. 195 (92-94% sequence identity) was predominant. Other abundant clones grouped with  $\beta$ -proteobacterial perchlorate-respiring *Dechloromonas* and *Dechloro*soma spp., and the  $\delta$ -proteobacterial *Desulfobacterium* and *Geobacter* spp.. We postulate that these populations are directly or indirectly involved in PCE dehalorespiration.