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KINETICS OF REDUCTIVE DECHLORINATION OF CHLORINATED ETHENES: DYNAMICS, ABUNDANCE AND ACTIVITY OF DECHLORINATING POPULATIONS

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Abstract

Three microbial cultures were enriched on PCE (hereafter named RM3), TCE (B2), or cis-DCE (B3) (as electron acceptors) and lactate (as electron donor). All cultures, which were found to completely transform the chlorinated contaminants to ethene, were kinetically characterised and analysed to define the dynamics and activity of dechlorinating microbial populations. Specific biodegradation rates were estimated by means of conventional biomass parameter (i.e. VSS, volatile suspended solids) and by cell numbers of dechlorinating population specifically discriminated and quantified by biomolecular tools.
Kinetic batch experiments, carried out after a pseudo-steady state performance had been established, revealed that the observed dechlorination rates followed the order RM3 (PCE-enriched)>B2 (TCE-enriched)>B3 (cis-DCE-enriched).
Dechlorinating bacteria were quantified by combining *in situ* hybridization techniques and PCR-based approaches. Fluorescence in situ hybridization (FISH and CARD-FISH) allowed the cell numbers estimation of active and not active i) dechlorinating bacteria involved in the partial degradation of PCE or TCE to cis-DCE (*Desulfitobacterium* spp., *Dehalobacter* spp., spp., *Geobacter* spp., *Sulfurospirillum* spp.) as well as ii) "*Dehalococcoides"* spp. known to be able to completely dechlorinate such compounds to harmless ethene. Gene expression profile of reductive dehalogenase genes (tceA, bvcA, vcrA) were also estimated and correlated to kinetic performances and dechlorinating bacteria abundances. The potential for field application of the outputs of this study will be discussed.