

Abstract

This study is focused on one particular group of the halogenated molecules called polychlorinated biphenyls (PCBs) – synthetic, organic compounds derived from biphenyl with bound chlorine atoms. Depending on the position and number of the chlorine atoms, there are theoretically 209 individual PCB congeners. Although PCBs production was brought to a halt thirty years ago, recalcitrance to degradation makes them a major environmental pollutant at a global scale. Large amounts of PCBs were produced in several countries, and former Czechoslovakia belonged to the ten major world producers. Despite the PCB congener resistance to chemical modification, bacterial process of reductive dechlorination, named organohalide respiration (OHR), was shown to be efficient in the dechlorination of extensively chlorinated PCB congeners and a prerequisite step towards their subsequent complete mineralization by aerobic bacteria. In our study, reductive dechlorination of polychlorinated biphenyls (PCBs) was assessed using long term anaerobic microcosms. The microcosms were inoculated with highly contaminated with weathered Delor sediments, sampled from the efflux channel of the former PCB manufacturer Chemko Strazske. After one year of cultivation the chemical analysis showed a degradation of up to 36 % of the highly chlorinated congeners in favor of medium and low chlorinated ones. T-RFLP analysis of the bacterial communities demonstrated that diverse microbial consortia evolved from the sediment samples used for their inoculation. Analysis of the rRNA gene pools indicated the presence of numerous members of the phylum *Chloroflexi*, including “*Dehalococcoides*” sp. and “*Dehalococcoides*”-like group (DLG), as well as already known secondary fermenters.

Second study aimed at exploring degradation contributions by other taxa using sediment-free microcosms (SFMs) supplemented with the commercial PCB mixture Delor 103. Our results showed high rates of congener dehalogenation (up to 95.5 %) in the long term (692 days). The bacterial communities were represented by twelve major phyla dominated by *Chloroflexi*, *Proteobacteria*, and *Firmicutes*. In the first batch of SFMs, *Dehalococcoides mccartyi* strains CG4 and CBDB1 were considered as the main congener degraders. However, addition of 2-bromoethanesulfonate (BES) in a second batch of SFMs inhibited *Dehalococcoides* sp. From all retrieved partial 16S rRNA gene sequences from BES-treated microcosms only two sequences affiliated to genus *Dehalococcoides*, were detected contributing to a mere 0.02 % and 0.04 % of

the community (one sequence out of 5983 sequences from SFM 11 and one out of 2494 sequences from SFM13). The BES-treated SFMs showed different community structures, especially with contributions of organisms involved in syntrophic activities. Indirect evidence provided by both statistical and phylogenetic analysis validated the significant implication of a new cluster of actors, affiliated with family *Geobacteraceae* (phylum δ -*Proteobacteria*) in the dechlorination of PCBs. Members of this Family are known already for the degradation capacity of chlorinated solvents. This study provides first evidence about the possible implication of the new *Geobacteraceae* taxon in the PCB congener degradation.