***Epsilonproteobacteria* as dominant acetate utilizers in a sulfate-reducing microbial community mineralizing benzene unveiled by pulsed 13C2-labeled acetate protein-SIP**

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Benzene and alkylated aromatic compounds are amongst the most persistent contaminants in our environment. The aerobic degradation proceeds fast and is well understood whereas the anaerobic degradation is not fully explored yet. Many cultures that are able to degrade these substances anaerobically are of syntrophic nature. Thus, they rely deeply on the relationships between their key players. The mixed anaerobic culture investigated originates from a column system that is percolated with benzene contaminated groundwater from the grounds of a former hydrogenation plant in Zeitz, Saxony-Anhalt [1]. Protein stable isotope probing (Protein-SIP) is a well-established method to unveil elemental fluxes in mixed microbial communities [2]. This is achieved with time-resolved metabolic labeling of the cultures with e.g. 13C, 15N or 36S and subsequent analysis of the resulting proteomes with high resolution mass spectrometry. Studies using 13C-Protein-SIP showed that the benzene-degrading, sulfate-reducing microbial community, originating from the aquifer columns described above, can be divided into three metabolic groups by their isotopic incorporation characteristics: Firstly, benzene degraders which are related to the *Clostridiales* genus *Pelotomaculum*. Secondly, organisms affiliated to *Deltaproteobacteria* which thrive on fermentation products of group 1, CO2 fixation and sulfate reduction and thirdly, putative scavengers belonging to the *Bacteroidetes*/*Chlorobi* group [3]. Additionally, acetate is suspected to be a central intermediate of the culture [4]. Pulsed 13C-acetate Protein-SIP did not only approve the previously determined groups, but also revealed a complex secondary metabolism featuring the epsilonproteobacterial *Campylobacterales*, the deltaproteobacterial *Syntrophobacterales* as well as the *Archaeoglobales* with primary 13C incorporation derived from labeled acetate. However, the fastest and highest 13C-incorporation was affiliated to the *Campylobacterales* suggesting a dominant role in the acetate utilization within this community. Secondary 13C-incorporation of presumably CO2, derived from acetate oxidation, was shown for the fermenting *Clostridiales* and the deltaproteobacterial *Desulfobacterales*. In general, pure cultures in artificial systems are investigated to reveal *in situ* degradation capability. In this study, a prevalent microbial consortium that is able to degrade benzene *in situ* was analyzed in order to understand the underlying pathways of degradation.

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