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Abstract

Determination of a Bacterial Consortium in a Reductive Dehalogenation Process.

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Abstract: The microorganisms identified in the sludge belong to the following genera: *Desulfovibrio*, *Desulfomicrobium*, *Clostridium*, *Desulfitobacterium*, *Dehalobacter* and *Sulfospirillum*. All these genera of microorganisms identified in the sludge have been related to sulfate reducing conditions. *Desulfovibrio*, *Desulfomicrobium*, *Desulfitobacterium* and *Clostridium* and biodegradation of chlorinated compounds, specifically by dehalorespiration which is the case for *Sulfospirillum*, *Desulfitobacterium* and *Dehalobacter* although some strains of sulfate reducers such as *Desulfitobacterium hafniense* have also been related to biodegradation of chlorinated compounds under methanogenic conditions. *Sulfospirillum multivorans* and *Sulfospirillum halorespirans* are known for their capability of using TCE or tetrachloroethylene (PCE) as terminal electron acceptors. On the other hand *Desulfitobacterium* and *Dehalobacter* have also been studied in their capability of using a chlorinated solvent (PCE) as terminal electron acceptor. The identification of *Desulfotomaculum* and *Desulfomicrobium* in syntrophy with the other bacteria, for example, the known fermenting bacteria belonging to the genus *Clostridium*. *D. acetoxidans* and carbon source by *Desulfomicrobium* which is a mesophilic microorganism that uses hydrogen as electron donor and acetate as carbon source during sulfate reduction. The overall conclusions of this work is the consortium could be efficient on both, sulfate and TCE biodegradation.

Keywords: dehalorespiration, dechlorination, bioremediation

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