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Autotrophic Degradation of Perchlorate with ZVI

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Perchlorate (ClO_4^-) is a major contaminant of ground water and surface water. It is chemicallystable and persistent in water. Besides, its high solubility in water causes extensive contamination in watersheds. Although various technologies have been developed to remove perchlorate from water, biological reduction is the method of choice to convert perchlorate to unharmful products such as Cl^-, O_2, and H_2O. Conventional methods of perchlorate removal employ heterotrophic perchlorate-reducing bacteria (PRB). Employing heterotrophic PRB requires high cost due to continuous supply of C source and even causes clogging problem. To overcome the limitations, zero valent iron (ZVI) particles and autotrophic PRB were employed to remove perchlorate in this study. When activated sludge or digested sludge was inoculated in the reactors containing ZVI and perchlorate, autotrophic PRB in the inocula used H_2 produced by iron corrosion and catalyzed perchlorate reduction. Activated sludge showed better reduction activity than digested one while more biomass concentration of activated sludge showed higher ClO_4^--removal efficiency. SEM revealed biofilm formed on iron particles used for perchlorate removal. Microbial profiles of the inocula were different from those of bacterial cultures used in the autotrophic perchlorate removal, as revealed by DGGE analyses. Major bands of the autotrophic culture samples were phylogenetically related to the class *Clostridia*. Taken together, the results of this study suggest that autotrophic degradation of perchlorate with ZVI is a promising technology to remove perchlorate.

Key words: Autotroph, biodegradation, perchlorate, reduction, ZVI

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Isolation and Identification of Xylanase-Producing *Bacillus* sp. CS21 from Spent Mushroom Substrate

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A Gram-positive, endospore-forming, rod-shaped bacterium, designated CS21, was isolated from the spent mushroom substrate. The isolate produced a xylanase and mannanase. The strain was aerobic and motile by means of flagella. The strain grew optically at 30°C and pH 6.0. Chemotaxonomic data (G+C content: 45%, major fatty acids: anteiso-C13:0, C16:0, and iso-C14:0) supported the affiliation of the isolate to the genus *Bacillus*. Comparative 16S-rDNA sequence analysis showed that the isolate formed a distinct phylogenetic tree within the genus *Bacillus* and was most closely related to *Bacillus subtilis*. Based on phenotypic, chemotaxonomic characteristics and phylogenetic inference, this strain *Bacillus* sp. CS21 was assigned to the genus *Bacillus*.

Key words: Spent mushroom substrate, Xylanase, Mannanase, *Bacillus* sp.