

Effects of Dissolved Oxygen and Nitrogen Source on Bioremediation Capacity and Microbial Community Structure

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ABSTRACT

The objectives of the research are to investigate the bioremediation capability in an MTBE- and BTEX-contaminated bioreactor, and to evaluate substrate removal efficiencies under biostimulation and bioaugmentation conditions. In addition, a relationship between removal efficiencies and concentrations of nitrogen source and oxygen will be determined by using response surface analysis. Exploring microbial community changes under various environmental conditions (concentrations of nitrogen source and oxygen) by using SSCP profiles of PCR-amplified 16S rDNA genes and linking the changes with simultaneously diminishing substrate concentration in the microcosms are the goals of this research. Results of the research show that: (1) the removals for MTBE and BTEX decrease in the order of ethylbenzene, p-xylene, toluene, benzene, and MTBE; (2) additional 10 – 30 % removals for both MTBE and BTEX were observed via. biostimulation and bioaugmentation, thereby indicating the significant contributions of nitrogen source, oxygen and the substrates-degrading pure cultures; (3) the Benzene removal increased to 63.8 % via. biostimulation with the concentrations of nitrogen source and oxygen at 65 mg/L and 15.6 mg/L, respectively. The MTBE and BTEX removals increased to 62 % via. biostimulation with the concentrations of nitrogen source and oxygen at 61 mg/L and 15 mg/L, respectively. The MTBE removal increased to 46 % via. biostimulation and bioaugmentation with the concentrations of nitrogen source and oxygen at 63 mg/L and 14 mg/L, respectively. The MTBE and BTEX removals increased to 73.8 % via. biostimulation and bioaugmentation with the concentrations of nitrogen source and oxygen at 60 mg/L and 15 mg/L, respectively. Dissolved oxygen plays more significant role while compared to nitrogen source from the response surface analysis; (4) the microbial consortium were divided into different groups, by examining the increasing rates for MTBE and BTEX removal efficiencies; and (5) Bands-6 and -11 are the dominant species in degrading MTBE and BTEX, by comparing population profiles with SSCP pure culture patterns.

Keywords : 16S rDNA, Bioremediation, Bioaugmentation, Biostimulation, Methyl tert-butyl ether, Microbial community structure, Molecular profiling, Response surface analysis

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