Identifying Dominant Anaerobic Microorganisms for Degradation of Benzene

Authors : Jian Peng, Wenhui Xiong, Zheng Lu

Abstract : An optimal recipe of amendment (nutrients and electron acceptors) was developed and dominant indigenous benzene-degrading microorganisms were characterized in this study. Lessons were learnt from the development of the optimal amendment recipe: (1) salinity and substantial initial concentration of benzene were detrimental for benzene biodegradation; (2) large dose of amendments can shorten the lag time for benzene biodegradation occurrence; (3) toluene was an essential co-substance for promoting benzene degradation activity. The stable isotope probing study identified incorporation 13C from 13C-benzene into microorganisms, which can be considered as a direct evidence of the occurrence of benzene biodegradation. The dominant mechanism for benzene removal was identified by quantitative polymerase chain reaction analysis to be nitrate reduction. Microbial analyses (denaturing gradient gel electrophoresis and 16S ribosomal RNA) demonstrated that members of genus Dokdonella spp., Pusillimonas spp., and Advenella spp. were predominant within the microbial community and involved in the anaerobic benzene bioremediation.

Keywords : benzene, enhanced anaerobic bioremediation, stable isotope probing, biosep biotrap

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