

Characterization of Archaeal Diversity in the Leachate of a Traditional Landfill by Determining Restriction Fragment Length Polymorphisms of 16S rRNA Genes

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Abstract: The diversity of Archaea community associated with the leachate of a traditional municipal solid waste landfill was examined by cultivation-independent analysis. Total-community genomic DNA was isolated from the leachate and archaeal 16S rRNA gene sequences (16S rDNA) were selectively amplified. The 16S rDNA amplicon was subcloned and further characterized by a restriction fragment length polymorphism analysis (RFLP, enzymes *Hha* I and *Hae* III). A total of 80 cloned 16S rDNA fragments were analyzed, and they were finally clustered into 29 different groups (RFLP patterns), with five most abundant groups accounting for 53% of all the 16S rDNA clones. The remaining 24 groups presented at low levels, of which a total of 16 groups were represented by a single clone. Our results demonstrated that RFLP analysis of PCR-amplified 16S rDNA is a powerful tool for assessing the diversity of microbial communities in complex anaerobic ecosystems.

Key words: traditional landfill; Archaea; 16S rRNA gene; RFLP

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本刊再度被评为“学术影响范围最广的前30名期刊”

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(本刊通讯员)