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研究论文

对降解喹啉的厌氧生物反应器中重要功能菌群的鉴定

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摘要 通过把微生物区系组成的分子水平的动态变化情况与微生物群落的整体功能变化相关联，鉴定重要的功能类群是微生物分子生态学研究的一个重要的策略。应用分子生物学的方法，对一个实验室规模的用于降解喹啉的厌氧反应器生物膜样品的微生物区系组成变化进行解析，找出可能的主要功能菌。通过DGGE对反应器的种子污泥和运行稳定的厌氧生物膜反应器的微生物区系组成进行了对比分析，并对主要的优势条带进行了分子鉴定。同时对以上两个样品构建16S rDNA克隆文库，通过统计学分析对克隆文库的有效性进行验证，并对文库进行测序分析。DGGE条带及克隆文库的序列分析均表明，在驯化过程中，Gamma *Proteobacteria* 亚纲与*Desulfobacter postgatei*种的微生物显著增加，这种动态变化表明这些细菌可能是在厌氧条件下对喹啉的降解起关键作用的微生物。

关键词 生物膜；厌氧反应器；DGGE；16S rDNA克隆文库
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Identification of functionally important microorganisms in a lab-scale anaerobic biofilm reactor for quinoline-degradation

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Abstract Microbial community structure in a lab-scale quinoline-degrading anaerobic biofilm reactor was dissected in comparison with the seeding sludge to identify the functionally important members. Samples were collected from the biofilm when the reactor reached the stable quinoline and COD removal efficiency. Total DNA was extracted from the samples. 16S rDNA v3 region was amplified and DGGE analysis was performed. The dominant bands were excised and the nucleotide sequences of the rRNA genes were determined. At the same time, a near-full length 16S rDNA library was constructed. Nucleotide sequences of 100 randomly selected clones were determined and identified by nearest neighbor analysis. Comparison analysis with the seeding sludge indicated a significant increase of the Gamma Proteobacteria and Desulfobacter postgatei during the acclimation period in the reactor, this suggested that these microorganisms may be functionally important for quinoline-degradation under anaerobic conditions.

Key words biofilm _ anaerobic reactor _ DGGE _ 16S rDNA clone library

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