生物陶粒与生物活性炭上微生物群落结构的PCR-SSCP技术解析

摘要点击 102 全文点击 82 投稿时间：2006/5/31 最后修改时间：2006/7/17

中文关键词 生物陶粒 生物活性炭 微生物群落 群落结构 单链构象多态性

英文关键词 bio-ceramics biological activated carbon microbial community community structure single-strand-conformation-polymorphism (SSCP)

作者	单位
刘小琳	清华大学环境科学与工程系，北京100084
刘文君	清华大学环境科学与工程系，北京100084

中文摘要

采用PCR-SSCP(单链构象多态性)技术,以16S rRNA基因的V4-V5区为靶对象,分析用于饮用水处理的生物陶粒和生物活性炭上的微生物群落结构.对生物陶粒和生物活性炭上的微生物分别进行超声波洗脱、R2A和LB平板培养后提取基因组DNA.结果表明，除生物活性炭超声波洗脱不能提取到DNA外，其他处理均能提取到大小在10 kb以上的基因组DNA，但所提取的量有较大差异.以提取的DNA为模板分别进行PCR，均能扩增到408 bp的基因片段.这些片段经λ核酸外切酶消化处理后进行SSCP电泳.结果显示，超声波洗脱、R2A和LB培养对试验结果影响不明显.生物陶粒的微生物基因扩增片段SSCP图谱相同，且只出现1条带.测序后与基因组数据库对比,结果显示其与uncultured *Pseudomonas* sp. clone FTL201 16S rDNA （GenBank登录号AF509293.1）片段同源性为92%.生物活性炭的微生物基因扩增片段SSCP图谱也相同，但有2条带.测序对比的结果表明， 这2个基因片段与*Bacillus* sp. JH19 16S rDNA （GenBank 登录号DQ232748.1）片段和*Bacterium* VA-S-11 16S rDNA （GenBank登录号AY395279.1）片段的同源性分别为100%和99%.

英文摘要

Analyses of microbial community structure in bio-ceramics (BC) and biological activated carbon (BAC), which widely used in drinking water treatment were performed by polymerase-chain\|reaction-single-strand-conformation-polymorphism (PCR-SSCP) targeted eubacterial 16S ribosomal RNA gene. Microorganisms on bio-ceramics and biological activated carbon were detached by ultrasonic, culturing on R2A and LB agar, respectively, followed by genome DNA extracting. Results show that larger than 10 kb genome DNA could be extracted from all the samples except the BAC samples processed by ultrasonic. However, quantities of the extracted DNA were different. 408 bp gene fragments were observed after PCR using the extracted genome DNA as templates. These gene fragments were digested with lambda exonuclease followed by SSCP electrophoresis. Same SSCP profiles were observed between ultrasonic eluting, R2A and LB agar culturing. The identity of the segment from bio-ceramics with uncultured *Pseudomonas* sp. Clone FTL201 16S rDNA (GenBank, AF509293.1) fragment was 92%, and identities of the two segments from BAC with *Bacillus* sp. JH19 16S rDNA (GenBank , DQ232748.1) fragment and *Bacterium* VA-S-11 16S rDNA （GenBank, AY395279.1）fragment were 100% and 99%, respectively.