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饮用水深度处理活性炭池中微生物群落分布研究

摘要点击 577 全文点击 161 投稿时间: 2010/6/2 最后修改时间: 2010/8/30

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中文关键词 [活性炭](#) [16S rDNA](#) [分子克隆文库](#) [微生物种群](#) [致病菌](#)

英文关键词 [activated carbon](#) [16S rDNA](#) [clone library](#) [bacteria community structure](#) [pathogenic bacteria](#)

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中文摘要

采集2种炭龄饮用水深度处理活性炭池表面生物膜,提取微生物总DNA,构建细菌16S rDNA克隆文库,并通过16S rDNA序列的系统发育分析,对样品中的细菌种群多样性以及群落结构进行了研究.结果表明,5 a炭龄炭样克隆文库中阳性克隆的16S rDNA序列分属11个细菌类群,分别为 α -Proteobacteria(26.5%), β -Proteobacteria(16.3%), δ -Proteobacteria(16.3%),Planctomycetes(12.2%),Gemmatimonadetes(6.1%),Acidobacteria(4.1%),Nitrospira(2.0%), γ -Proteobacteria(2.0%),Bacteroidetes(2.0%),Actinobacteria(2.0%),Unclassified Bacteria(10.2%).1.5 a炭龄炭样克隆文库中阳性克隆的16S rDNA序列分属10个细菌类群,分别为 α -Proteobacteria(21.6%),Planctomycetes(10.8%),Bacteroidetes(10.8%), β -Proteobacteria(9.0%),Acidobacteria(9.0%),Nitrospira(7.2%), δ -Proteobacteria(7.2%),Unclassified Proteobacteria(5.4%),Gemmatimonadetes(3.6%),Unclassified Bacteria(14.4%).可以看出,2种炭龄活性炭表面的微生物种群均十分丰富,变形菌门细菌在2个克隆文库中均居较大比例,优势种群为 α -Proteobacteria纲和 β -Proteobacteria纲.在炭龄5 a的活性炭表面, δ -Proteobacteria纲所占比例较高,硝化螺旋菌门(Nitrospira)所占比例较低,而炭龄1.5 a的活性炭上的情况恰好相反.在2个炭样中共发现了阿菲波菌属(*Afiplia*)和金黄杆菌属(*Chryseobacterium*)这2种潜在致病菌,可能对饮用水生物安全性带来一定风险.

英文摘要

Two granular activated carbon (GAC) samples with 1.5 a and 5 a age were collected, Bacterial genome DNA was extracted for the 16S rDNA gene amplification, and then a bacterial 16S rDNA gene clone library was constructed. After the phylogenetic analysis of 16S rDNA sequences, bacterial diversity and community structure of two activated carbon biofilm sample were studied. The results showed the bacteria in GAC with 5 a age could be divided into 11 groups, which were as follows α -Proteobacteria(26.5%), β -Proteobacteria(16.3%), δ -Proteobacteria(16.3%), Planctomycetes(12.2%), Gemmatimonadetes(6.1%), Acidobacteria(4.1%), Nitrospira(2.0%), γ -Proteobacteria(2.0%), Bacteroidetes(2.0%), Actinobacteria(2.0%), Unclassified Bacteria(10.2%). The bacteria in GAC with 1.5 a age could be divided into 10 groups, which were as follows α -Proteobacteria(21.6%), Planctomycetes(10.8%), Bacteroidetes(10.8%), β -Proteobacteria(9.0%), Acidobacteria(9.0%), Nitrospira(7.2%), δ -Proteobacteria(7.2%), Unclassified Proteobacteria(5.4%), Gemmatimonadetes(3.6%), Unclassified Bacteria(14.4%). The results revealed a variety of bacterial divisions on the studied GAC biofilm. Proteobacteria had the highest share in the two total clones, and α - and β -Proteobacteria were on a dominant position. A relatively high proportion of δ -Proteobacteria was observed in the biofilm of GAC with 5 a age, and Nitrospira was in a minor proportion. However, a totally converse condition appeared in GAC with 1.5 a age. Two pathogenic bacteria, *Afiplia* and *Chryseobacterium*, were detected in analyzed GACs, which implies a potential microbial risk in water supply.

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