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A+0SA污泥减量工艺的微生态特性

Microecology of an anoxic+oxic-settling-anaerobic sludge reduction process

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中文摘要:

采用16S rDNA序列与PCR-DGGE (polymerase chain reaction-denaturing gradient gel electrophoresis) 分析技术相结合的方法,研究了A+OSA (the anoxic+oxic-settling-ana erobic)污泥减量工艺在不同工况下的减量效果及其微生态特性。结果显示,在自然条件下,A+0SA工艺可有效减少剩余污泥27%左右。分子生物研究表明,解耦联池的插入可以明显改变系 统微生物的群落结构,且随着解耦联池水力停留时间的延长,系统中部分微生物被"淘洗",微生物丰富度和多样性指数均有所降低。相似性分析表明,参照系统和A+0SA工艺分属于2个不 同的集群,但在A+0SA工艺内部各反应池样品间具有较高的相似性,且各反应池在HRT为5.16 h和7.14 h时,表现为显著相似。通过上述研究可为该工艺优化及调控提供理论指导。

英文摘要:

The microbial community structure and biodiversity in an anoxic+oxic-settling-anaerobic (A+OSA) process were studied by polymerase chain reaction (PCR)denaturing gradient gel electrophoresis (DGGE) based on 16S rDNA sequence. The activated sludge samples were collected from different reaction tanks under operation conditions, and the minimization of excess sludge production of the A+OSA process was investigated. The experimental results demonstrated that the A+OSA process can reduce excess sludge by 27%. The DGGE profiles showed that the microbial communities were affected by the insertion of the uncoupling tank. Moreover, the richness index and the Shannon's index of diversity decreased with increasing the hydraulic retention time (HRT) in the uncoupling tank. The similarity analysis revealed that the samples from the reference belonged to one cluster and the samples from the A+OSA process belonged to the other. Additionally, the bacterial communities found in samples from the A+OSA operated under different conditions were statistically similar amongst themselves, especially for the samples at the HRT of 5.16 h and 7.14 h. This study will provide scientific guidance for process optimization and application.

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