

Bacterial diversity of activated sludge treating slaughterhouse wastewater ⁽¹⁾

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The objective of this study was to investigate the bacterial diversity of activated sludge with different sludge retention time (SRT) to treat slaughterhouse wastewater. The microbial DNA of activated sludge samples from those with SRTs of 7, 14, 21 and 28 days were extracted directly using a commercial kit and bead-beating protocol, respectively. The 16S ribosomal RNA genes of bacteria from 4 activated sludge samples were amplified with bacterial specific sets of primers by PCR. The amplicons were ligated into TA cloning vectors to construct 16S rRNA gene libraries for DNA sequencing and bacterial diversity analyses. A total of 312 almost full-length 16S rRNA gene clones from 4 activated sludge samples were obtained. The results indicated that the bacterial profiles comprising of *Acidobacteria*, *Actinobacteria*, *Bacteroidetes*, *Firmicutes*, *Gemmatimonadetes*, *Chloroflexi*, *Candidatus Saccharibacteria*, *Planctomycetes*, *Proteobacteria*, *Verrucomicrobia* and unclassified bacteria differed in SRT samples. The most of these communities belonged to *Proteobacteria* phylum (> 70%). In OTU analysis, the OTU percentage of 28-day SRT sample was the lowest (38.0%) which revealed that the bacterial profile tended towards simplicity and photosynthetic bacterium *Rhodobacter* was the majority. However, the COD removal rate under SRT28 test run was still as high as 96% and the concentration of microorganisms in effluent waster was very low as 8 mg VSS/L. The study is expected to apply for the treatment of lager scale wastewater from poultry slaughterhouse.

Key words: Activated sludge, Microorganism, Bacterial diversity.

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