

Analyses of Bacterial community in wastewater by DGGE and cloning methods

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Abstract

The bacterial community of wastewater from an industrial complex in Dae-gu was investigated and compared using a molecular approach combining fingerprinting by DGGE (denaturing gradient gel electrophoresis) with the screening of 16S rDNA clone libraries by DGGE and sequencing. DGGE is attractive technique, as it separate same length dsDNA according to sequence variation typical 16S rDNA genes. The diversity and similarity of bacterial community in wastewater was analyzed by GC341f and 536r primer sets for amplification of V3 region of 16S rDNA. We also investigated the changing of bacterial community by heavy-metal(Cd, Cu, Pb) containing media and the metal removing efficiency of bacterial community. Analytical grade of metal salts were used and each metal solutions were sterilized with 0.45 um filter. Nearly complete 16S rDNA was amplified and sequenced and there were slight changes in bacterial diversity between different metal containing media.

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