Analysis of microbial diversity in heavy metal contaminted soil using culture-independent methods

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In this study, the microbial diversity in six samples of soil collected from a mine was analyzed using culture-independent methods. The culture-independent methods applied in this study were DGGE (Denaturing Gradient Gel Electrophoresis) and random cloning, and because there are extremely low concentration of DNA in contaminated soil with heavy metals, bacterial 16S rDNA region was amplified by PCR using primers of 9f (5'-GAGTTTGATCCTGGCTCAG-3'), 341fGC (5'-CGCCCGCCGCGCGCGGCGGGCGGGGCGGGGGCACGGGGGGCCTACGGGAGGCAGCAG-3'), 536r (5'-GTATTACCGCGGCTGCTG-3') and 1512r (5'-ACGGCTACCTTGTTACGACTT-3') for these experiments. The DGGE profiles for each sample were different, and the major bands were excised and then, eluted to water to get DNA from each band. The DNA from the major bands were sequenced and identified. In the DGGE result, almost microorganisms in the soil samples were uncultured strains. In order to identify the microbial diversity in heavy metal contaminated soil samples more exactly, random cloning experiments will be conducted.