



Response of microbial activities and diversity to PAHs contamination at coal tar contaminated land

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Coal tar is one of the most hazardous and concerned organic pollutants and the main hazards are polycyclic aromatic hydrocarbons (PAHs). The indigenous microorganisms in soils are capable to degrade PAHs, with essential roles in biochemical process for PAHs natural attenuation. This study investigated 48 soil samples (from 8 depths of 6 boreholes) in Beijing coking and chemistry plant (China) and revealed the correlation between PAHs contamination, soil enzyme activities and microbial community structure, by 16S rRNA denaturing gradient gel electrophoresis (DGGE). At the site, the key contaminants were identified as naphthalene, acenaphthylene, acenaphthene, fluorene, phenanthrene and anthracene, and the total PAHs concentration ranged from 0.1 to 923.9 mg/kg dry soil. The total PAHs contamination level was positively correlated ($p < 0.05$) with the bacteria count (0.9×10^7 - 14.2×10^7 CFU/mL), catalase activities (0.554-6.230 mL 0.02 M $\text{KMnO}_4/\text{g}\cdot\text{h}$) and dehydrogenase activities (1.9-30.4 TF $\mu\text{g}/\text{g}\cdot\text{h}$ soil), showing the significant response of microbial population and degrading functions to the organic contamination in soils. The PAHs contamination stimulated the PAHs degrading microbes and promoted their biochemical roles in situ. The positive relationship between bacteria count and dehydrogenase activities ($p < 0.05$) suggested the dominancy of PAHs degrading bacteria in the microbial community. More interestingly, the microbial community deterioration was uncovered via the decline of microbial biodiversity (richness from 16S rRNA DGGE) against total PAHs concentration ($p < 0.05$). Our research described the spatial profiles of PAHs contamination and soil microbial functions at the PAHs heavily contaminated sites, offering deeper understanding on the roles of indigenous microbial community in natural attenuation process.