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MICROBIAL POPULATIONS DURING BIOREMEDIATION OF PAHs IN WOOD SLEEPERS TREATED WITH CREOSOTE OIL

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Abstract

Polycyclic aromatic hydrocarbons (PAHs) and their toxic degradation products represent a serious risk for the environment. One way of the risk reduction is application of bioremediation methods. Composting has recently been shown to be efficient for remediation of materials contaminated with PAHs (e.g. sleepers, soil). The process relies on the action of microorganisms able to degrade organic materials. Substrate (agricultural-waste mixture of optimum nutrient ratio or grass from experimental field of Institute of Microbiology) was mixed with woodchips made from sleepers treated with creosote oil and then composted in a special aerated composter. The composts were sampled several times at different thermal phases and after maturation. The scale of PAH degradation was analyzed by GC-MS. The results revealed a significant PAH reduction (up to 97%) of original contamination. The impact of different composting substrates on microbial populations during the degradation process and biodiversity was analyzed with PLFA. In addition, we extracted the metagenomic DNA and analyzed further bacterial and fungal diversity using DGGE and 454 pyrosequencing. DGGE analysis of rDNA was performed using primers gc984f and 1378r (bacteria) and gcITS1f and ITS2r (fungi). Amplicon pyrosequencing was performed using tagged bacterial (eub530f and eub1100r) and fungal (ITS1 and ITS4) primers targeting rDNA genes. Amplicons were pooled and sequenced on Roche GS Junior Titanium Platform. Our results support previous expectations based on PLFA quantification and show dramatic changes during different phases of composting process. The results indicate a high importance of fungal species that show increasing activity in the later phases of the composting process.

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