

**Título: Combined high throughput methods to analyse microcosms community and catabolic gene structure under continuous long term pollutant stress**

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**Resumo:**

Volatile organic compounds and hazardous air pollutants are important environmental contaminants. Among these are benzene and the structurally related toluene, ethylbenzene and xylenes, collectively known as BTEX. They are frequently discharged into soil and groundwater as a result of leakage through underground storage tanks and pipelines, improper waste disposal practices, inadvertent spills and leaching from landfills posing massive environmental threats. Among all remediation technologies, biological processes are economical, energy-efficient and environmentally sound approaches. Some microorganisms are able to use aromatic compounds, such as BTEX, as their carbon source. Enzymatic reactions involved in BTEX degradation have been described and in detailed study in bacterial isolates, pointing out the relevance from single cell studies. However monoculture of bacteria does not describe the in vivo community dynamics thus a detailed understanding of the functioning and interactions within microbial communities is essential. Thus, using contaminated soil, from different origins (Czech Republic - CZE, Brazil - BRA and Switzerland - SUI), benzene and BTEX microcosms experiments were set. Applying high throughput methods (Next Generation Sequencing - Illumina Platform and DNA-Microarray), the structure of microbial communities was characterized and catabolic genes were identified. The different bacterial community structure of the three different soil revealed that contaminated soil subjected to long term remediation are more stable, as in the case of CZE microcosms. Other than, both BRA and SUI fresh contaminated soils, showed a clearly bacterial community succession. In addition, was possible to link shifts in the microbial communities with shifts in the catabolic genes, which might be involved in the catabolism of benzene and BTEX and selected under respective pollutant stress.

**Palavras chave:** Microarray, NGS, microbiome, pollutant

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