

## **Studies on xenobiotic degradation potential of soil and rhizosphere microbial communities from heavily polluted aquifers in Czech Republic**

Bioremediation of polluted environments has become one of the fast evolving and cost-saving technologies, employing the natural potential of soil microorganisms to degrade organic pollutants. Development of molecular biology techniques enables monitoring of microbial communities and their dynamics *in situ*. This work is dealing with analysis of soil DNA and bacterial isolates from polluted aquifers with purpose to acquire information about the activity, diversity and dynamic changes of soil bacterial communities related with the processes leading to degradation and decreasing of the pollutant concentration. Former military localities in Czech Republic belong to the most contaminated with petroleum hydrocarbons sites in Eastern Europe. Contaminated soil from the Čáslav military airbase was used in the study. Molecular genetics techniques were applied for bacterial community characterization and complemented with microbiological methods. Denatured gradient gel electrophoresis (DGGE) was applied after amplification of variable regions of 16S ribosomal gene for monitoring of the bacterial diversity in soil or for distinguishing between many isolates with degrading capabilities. Bacteria with different DGGE fingerprints were further taxonomically identified by sequencing of the 16S ribosomal genes. PCR with primers targeting key genes in aromatic hydrocarbon degradation - encoding for enzymes with *meta*-cleavage activity to catechol, was giving information for the fraction of isolates able to degrade the toxic mono-aromatic compounds.

Mesocosm systems were developed and the changes in soil microbial community profile and cultivable bacterial number, in correlation with depletion of the pollutant during bioaugmentation, phytoremediation and natural biodegradation, was studied. Tn7-*lux* system for bioluminescence-chromosomal tagging of gram-negative bacteria was used in this work, as well. The main purpose was monitoring the fate of bacterial degraders, isolated from the locality and used in the in the mesocosm experiments.

**Keywords:** BTEX, biodegradation, phytoremediation, mesocosm, soil DNA, DGGE, catabolic genes, Tn7-*lux* system

**Klíčová slova:** BTEX, biodegradace, fytoremediace, mesokosmy, půdní DNA, DGGE, katabolické geny, Tn7-*lux* systém