

The former military air-base Hradcany is among the most contaminated with organic pollutants localities in Czech Republic. Main cleanup strategy in the area is the bioremediation taking advantage on the natural potential of the autochthonous soil microorganisms to evolve catabolic pathways for in situ degradation of the pollutant.

The diversity and abundance of the pathways, as well as the specificity and activity of the encoded enzymes are priority biotic factors determining the bioremediation efficiency. Main task of this work was to analyze the bacterial diversity in jet fuel contaminated soils based on key catabolic genes encoding the Rieske non-haem iron dioxygenases of the toluene/ biphenyl oxygenase branch. High molecular soil DNA was extracted and the sequences encoding catabolic genes were selectively enriched by hybridization to biotinylated oligonucleotides on magnetic microbeads with covalently bound streptavidin. Fragments of the genes for the  $\alpha$ -subunits of Rieske non-haem iron oxygenases were amplified and analyzed by restriction analysis, cloning and sequencing. Their evolutionary histories were inferred using the Neighbour-Joining and the maximum likelihood methods. The catabolic genes diversity in the actively bioremediated and highly polluted soil HRB was compared with the diversity in the soil HRB-M sampled from mesocosms which simulated phytoremediation. At least 98% of the analyzed sequences in HRB soil were affiliated with genes belonging to the toluene subgroup and similar to those encoding TodC1 of *Thauera* sp. strain DNT-1. In the plant containing mesocosm soil additional fraction of phylogenetically diverse sequences was observed, comprising 26% of all clones and representing the large subunit of biphenyl dioxygenase genes in polychlorinated biphenyl degrading bacteria. Thus, during the six month development of the microcosm microbial community in presence of willow trees changes inside the toluene/biphenyl family of Rieske non-haem iron dioxygenases were taking place. The increased abundance of biphenyl dioxygenase genes could be ascribed to the influence of willow rhizosphere metabolism and rhizosphere associated bacteria on the overall soil microbial activity.

(In Czech)