Geophysical Research Abstracts,
Vol. 11, EGU2009-2456, 2009
EGU General Assembly 2009

Diversity of alkane degrading bacteria associated with plants in a petroleum oil-contaminated environment and expression of alkane monooxygenase (alkB) genes

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Among twenty-six different plant species, Italian ryegrass (Lolium multiflorum var. Taurus), Birdsfoot trefoil (Lotus corniculatus var. Leo), and the combination of both plants performed well in a petroleum oil contaminated soil. Hydrocarbon degrading bacteria were isolated from the rhizosphere, root interior and shoot interior and subjected to the analysis of 16S rRNA, the 16S and 23S rRNA intergenic spacer region and alkane hydroxylase genes. Higher numbers of culturable, degrading bacteria were associated with Italian ryegrass, which were also characterized by a higher diversity, particularly in the plant interior. Only half of the isolated bacteria hosted known alkane hydroxylase genes (alkB and cytochrome P153-like). Our results indicated that alkB genes have spread through horizontal gene transfer, particularly in the Italian ryegrass rhizosphere, and suggested mobility of catabolic genes between Gram-negative and Gram-positive bacteria. We furthermore studied the colonization behaviour of selected hydrocarbon-degrading strains (comprising an endopyhte and a rhizosphere strain) as well as the expression of their alkane monooxygenase genes in association with Italian ryegrass. Results showed that the endophyte strain better colonized the plant, particularly the plant interior, and also showed higher expression of alkB genes suggesting a more efficient degradation of the pollutant. Furthermore, plants inoculated with the endophyte were better able to grow in the presence of diesel. The rhizosphere strain colonized primarily the rhizosphere and showed low alkB gene expression in the plant interior.