Environmental Engineering and Management Journal *March 2012, Vol.11, No. 3, Supplement, S32*
http://omicron.ch.tuiasi.ro/EEMJ/

"Gheorghe Asachi" Technical University of Iasi, Romania

P45

IDENTIFIACATION OF CULTIVABLE AND NON-CULTIVABLE RHIZOSPHERE BACTERIA FROM LONG TERM CONTIMANTED SOIL BY PCBs WITH USING MOLECULAR GENETIC

Petr Stursa, Petra Prouzova, Tomas Macek, Martina Mackova

Department of Biochemistry and Microbiology, Faculty of Food and Biochemical Technology, ICT Prague, Technicka 3, 166 28 Prague 6, CZ

Abstract

A number of persistent substances got to the environment due to human activity during the 20 century. Toxicity for the humans has been detected in many of these substances. Polychlorinated biphenyls (PCBs) belong among such substances. PCBs can be removed from the environment only via physical-chemistry methods, which are very complicated and expensive. Therefore, the attention is focused on use of phytoremediation and bioremediation in the degradation of PCBs. In our experiment plants of tobacco, black nightshade and horseradish were grown in long-term PCB contaminated soil and we focused on description of microbial diversity in the rhizosphere of these plants. Diversity was measured using the analysis of 16S rRNA gene and by MALDI-TOF MS and the results were compared (cultivable microorganisms). In the second part of the experiment, we focused on characterizing non-cultivable micro-organisms using methods of Stable Isotope Probing (SIP) and terminal-restriction fragment length polymorphisms (T-RFLP). To identify non-cultivable strains T-RFLP was done with heavy DNA fractions. Genomic libraries were created, containing a part of 16S rRNA to identify the individual peaks of the spectra. These genomic libraries were sequenced and obtained sequences represented different bacterial species contained in heavy DNA. Sequences thus obtained were assigned to individual peaks from T-RFLP profile using In Silico digestion. From the results obtained using SIP it is clear that the vast majority of bacterial species obtained from heavy DNA is completely different from bacteria which we identified by 16S rRNA analysis and MALDI-TOF MS. Dominant representative cultivable species is *Rhodococcus* and dominant representative non-cultivable species are bacterial genera *Hydrogenophaga* or *Methylophillus*.

Acknowledgements

The work has been supported by projects 525/09/1058, ME 09024, FP7-KBBE-2010-4/265946