**YOUNG RESEARCH TEAMS - PN-II-RU-TE-2012-3**

*“Retrieving new bacterial isolates for potential bioremediation*

*and biotechnological applications”*

**S u m m a r y 2 0 1 4**

In this period, 156 new bacterial strains were identified based on the comparative sequence analysis of the 16S ribosomal RNA gene. These strains shared 92-100% similarity values with the type strains of bacterial species with validly published names. Pure cultures of several potential new genera and species were obtained, mainly belonging to the bacterial phyla Proteobacteria and Bacteriodetes, which supported the efficiency of the applied non-conventional cultivation methods. Gellan gum proved to be a superior solidifying agent compared to agar, since higher ratio of new species were obtained comparing media having the same composition but containing different gelling agent. The detailed taxonomic characterization of selected new species candidates has been initiated, including a phylogenetic analysis based on the complete 16S rRNA gene and side-by-side physiological tests with type strains of closely related species. High-resolution next generation sequence analysis of bacterial communities confirmed the results of T-RFLP fingerprinting that was performed in the previous year. Furthermore, additional bacterial isolates were retrieved during the second sampling campaign, in which we used the enrichment culture technique to obtain potentially phenol-degrading bacteria. Strains were screened with 4 different primer sets targeting genes, which are involved in the degradation of aromatic compounds. In the case of positive reaction, sequence analysis was performed. These strains will be used for the phenol degradation experiments in the next period.