

EVALUATION OF MICROBIAL DIVERSITY IN SLUDGE OF REFINERY WASTEWATER BY DGGE AND RAPD

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Polycyclic aromatic hydrocarbons (PAHs) are widely distributed and relocated in the environment as a result of the incomplete combustion of organic matter. Many PAHs and their epoxides are highly toxic, mutagenic and/or carcinogenic to microorganisms as well as to higher systems including humans. Xenobiotic-degrading organisms have tremendous potential for bioremediation since they could be effective and efficient in removing these recalcitrant compounds. Three microorganisms were isolated directly from an effluent oil refinery which has been subjected to a microbiological treatment. The microorganisms were isolated by growth in the same aqueous system enriched on naphthalene, phenantrene or anthracene as the carbon source. One colony of each organism was identified by amplification of rDNA 16S followed by sequencing in MegaBace system. One of them was identified as *Pseudomonas aeruginosa* whereas the other two, as *Pseudomonas sp.* The identities of *Pseudomonas* isolates were analyzed by an additional discriminating typing polymorphisms technique (RAPD) using two 10-mer primers of arbitrary sequences, OPA-13 and OPD-13 (Operon Technologies). A similarity from 40,0% to 51,4% between the three isolates showed that they belong to distinct strains. Variability in bacterial population profiles from the activated sludge with different composition is being evaluated by PCR-DGGE (Denaturing Gradient Gel Electrophoresis). Support: CENPES/PETROBRÁS, FAPERJ, CAPES, FUJB.