

[ENV06]

**Molecular biological analysis of hydrocarbon degraders from oily waste polluted sites**

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Naphthalene was identified as a major component in petroleum hydrocarbon and its derivatives. A few bacteria have been identified capable of degrading naphthalene using special degradation enzymes within the naphthalene degradation pathway. Naphthalene degradation pathway consists of *nah*ABCDEF and *nahR* genes. In this study, DNA sequences of naphthalene degradative gene were obtained from GenBank database. From the gene sequences, multiple alignments were performed to obtain conserved sequences. Phylogenetic tree based on the alignment of amino acid sequences were constructed. PCR primers were designed based on the conserved gene sequences. The designed PCR primers were used in amplification of selected naphthalene degradation genes. Amplifications were performed on DNA extracted from laboratory strains as well as from environmental samples. Positive results with expected DNA fragment size were obtained for PCR primer sets. Positive result was also obtained for environmental samples, which can be the first indicator to the presence of naphthalene degradative bacteria.