

MICROBIOLOGICAL AND CHEMICAL ANALYSIS OF OIL DEGRADATION IN TWO GREEK MARINE ECOSYSTEMS

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Abstract

The structure of the bacterial community prior and after crude oil contamination in two different marine ecosystems, a chronically exposed to petroleum pollution and a low polluted, was investigated using experimental microcosms. Seawater samples for 16S rRNA gene diversity and chemical analysis were taken at critical time points. More than 30% of the phylotypes retrieved from contaminated microcosms showed highest similarity to members of the Alteromonadaceae family. Chemical analysis revealed that biodegradation of n-alkanes and low MW unsubstituted PAHs was almost complete whereas higher MW- PAH were degraded to a much lower extent.

Keywords : Bacteria, Chemical Analysis, Petroleum.

Introduction

Hydrocarbonoclastic bacteria (HCBs) usually exist in very low abundance in marine environments but oil-pollution may stimulate their growth and cause changes in the bacterial community structure of the contaminated area [1]. Prior studies have shown extended oil-pollution in some coastal areas of Attiki (Saronikos Gulf) [2]. The aim of this study was to describe and compare the structure of the bacterial community prior and after oil contamination in two different marine ecosystems: the chronically exposed to petroleum pollution Elefsina Bay (Saronikos Gulf, Greece) and the low polluted Anavyssos Bay (Saronikos Gulf, Greece). Material and Methods Four 100-l microcosms were used. One microcosm from each site served as a control (uncontaminated) whereas a second was contaminated with a reference mixture of different crude oil. Seawater samples were taken when bacterial abundance was highest for the determination of the community structure and chemical analysis of the degrading oil. Mixed community DNA was extracted and used as template in PCR amplifications with 16S rRNA specific primers. PCR products were cloned, sequenced and the sequences were used as templates in database (GenBank) searches to identify the closest relatives. Phylogenetic analysis was performed according to standard procedures.

Results and Discussion

The majority of the sequences retrieved from both contaminated and uncontaminated samples showed a higher homology to members within the phyla of alpha- and gamma- Proteobacteria and Bacteroides/Flavobacteria. Phylotypes exhibiting higher similarity to members of the Rhodobacteraceae family and *Flavobacterium* genus, both positively associated with hydrocarbon degradation [3], appeared more frequently in samples originating from Elefsina Bay; the latter may reflect its chronic oil polluted state. In contrast, the uncontaminated microcosm of Anavyssos Bay contained the most abundant bacterium on the planet, *Pelagibacter ubique*. More than 30% of the phylotypes retrieved from contaminated microcosms showed highest similarity to members of the Alteromonadaceae family. Although this group has not been as yet strongly associated with oil degradation, members of it have been reported as "non-professional" HCBs [4]. The most significant biodegradation was observed for n-alkanes (n-C₁₄-n-C₃₅) and low MW unsubstituted PAHs, as these compounds were almost completely removed in both microcosms. Higher MW- PAH were degraded to a much lower extent and only in Elefsina microcosm, while in all cases significantly lower biodegradation of substituted compounds was obtained in comparison with the parent ones. This is an expected event since the substitutes obstruct bacterial attack. The rate of oil degradation in the contaminated Elefsina microcosm appeared to be greater than that of Anavyssos Bay.

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