

## CHARACTERIZATION OF METAGENOMIC SEQUENCES FROM A BRAZILIAN PETROLEUM RESERVOIR WITH POTENTIAL FOR HYDROCARBON BIODEGRADATION

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### Abstract:

Alkanes are the major components of crude oil and the most abundant and available carbon and energy sources in reservoirs. Microorganisms are common inhabitants of these environments and may have effective biodegrading strategies, based on specialized enzyme systems and metabolic pathways, as a form to access hydrocarbons as carbon and energy sources. However, the current knowledge of the microbial diversity in petroleum reservoirs is still limited, mostly due to the difficulty in recovering the complex community present in such extreme environments. This limitation imposed by conventional culturing techniques can be circumvented by the metagenomic approach, which is based on culture-independent molecular methods that allow access to the metabolic potential of previously uncultured microorganisms. In a previous work, a metagenomic fosmid library derived from aerobic and anaerobic petroleum enrichments was screened for the ability to biodegrade hexadecane as sole carbon source. Five fosmid clones showed high biodegradation ability, confirmed by Gas Chromatography – Mass Spectroscopy (GC-MS) analysis [1]. The present work aimed at the identification and characterization of the metagenomic sequences responsible for the hydrocarbon biodegradation. Shotgun cloning approach was used to determine the whole insert sequence of one selected fosmid clone, FOS1A, which showed high biodegradation value (91%). Putative proteins were identified by comparison of deduced aminoacid sequences with protein databases (NCBI and EMBL), and included alcohol dehydrogenase (72% identity) and aldehyde dehydrogenase (69% identity), among others. According to literature, these enzymes are involved in alkane degradation system. This study may offer a more comprehensive view of the poorly understood biodegradation processes that take place in petroleum reservoir and may constitute a potential source for new biocatalysts of interest in biotechnological processes, such as bioremediation and microbial enhancement oil recovery (MEOR). **Financial support: FAPESP, PETROBRAS.** [1] Vasconcellos, S.P. et al. 2010. Screening for hydrocarbon biodegraders in a metagenomic clone library derived from Brazilian petroleum reservoirs. *Organic Geochemistry*. **41** (7): 675-681.

**Key words:** Biodegradation, Hydrocarbon, Metagenomic, Petroleum, Reservoir