

## MOLECULAR CHARACTERIZATION OF MICROBIAL COMMUNITIES INVOLVED IN SHORT-CHAIN ALKANE METABOLISM IN SOIL SAMPLES

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### Abstract:

The contents of gaseous hydrocarbons in sub-surface soil and sediment occur in highly variable amounts and the origin and occurrence of such compounds on Earth surface are not entirely understood. The upper formations of oil reservoirs may produce gas leaking which is supposed to be indirectly detectable through soil bacterial populations capable of consuming it. The goal of the present work was to characterize microbial communities in two soil samples received from Petrobras, focusing on populations specialized in short-chain alkane metabolism which can represent a biotechnological tool for petroleum prospection. Sedimentary basin soil sample was named as "P soil" and the non-petroliferous soil sample as "Np soil". Three clone libraries were constructed for each sample, one 16S rRNA gene library for each of the Domains Bacteria and Archaea, and one for the catabolic gene coding for the soluble di-iron monooxygenase (SDIMO) enzyme alpha subunit. Microbial community of Np soil presented high occurrence of Firmicutes and Alphaproteobacteria groups and Methanosarcinales archaeal order. In P soil high abundance of the phylum Actinobacteria and Crenarchaeota group I.1b were observed. The analysis of the catabolic genes revealed the occurrence of two Operational Protein Families (OPF) in Np soil and five in P soil. Clones related to the Ethene monooxygenase group (EtnC) were detected only in the latter, which also presented higher values of OPF's richness and diversity. Hydrocarbon measures performed by gas chromatography showed higher levels of methane and lower levels of ethane and propane in the P soil sample. Results obtained demonstrated that clone libraries of functional genes offer a more appropriate technique to evaluate microbial populations related do light gas metabolism. According to rarefactions curves generated by the Dotur program, the sampling effort employed for the characterization of P soil was insufficient to recover the total diversity of catabolic genes present in the sample, indicating that this soil may house an even higher diversity of such genes, not fully explored in the current survey. The majority of catabolic genes obtained from the libraries correspond to potentially new genes not related to those found in known bacterial species. **Financial support: Petrobras, CAPES.**

**Key words:** Gene Libraries, Light Hydrocarbons, Microbial Communities, Soil, Soluble Monooxygenase Enzymes