

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





Paula Brandão Miqueletto¹, Justo Camejo Ferreira², Eugenio Vaz dos Santos Neto² & Valéria Maia de Oliveira¹ ¹Microbial Resources Division, Research Center for Chemistry, Biology and Agriculture (CPQBA), UNICAMP, CP 6171, Campinas, SP, CEP:13081-970, Brazil; ²PETROBRAS P & D Cidade Universitária, Q-7, CEP:21949-900, Rio de Janeiro, RJ, Brazil. E-mail: pamique@gmail.com

INTRODUCTION

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 shortchain alkane metabolism which can represent a biotechnological tool for petroleum prospection.



MATERIAL AND METHODS







Statistical Analysis - Dotur

Sample Np Soil P Soil	ACE 760.063 391.464	Chao 465.5 331.867	Shannon 4.43455 4.49058	Bacteria
	Sample	ACE	Chao	Shannon
Archaea	Np Soil	30.9741	26 17	2.2046
	<u> </u>	16.000	17	2.00307

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

RESULTS

Short-chain Hydrocarbon Contents (Petrobras Research Center)

	Np Soil	P Soil
Methane	140.36	1152.14
Ethane	5.36	1.16
Propane	3.43	0.39

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. The majority of catabolic genes obtained from the libraries correspond to potentially new genes not related to those found in known bacterial species.



Clone C11 -----> OPFs IV & V — Clone E4 —— -Acireductone Dioxygenase [*Streptom yces* averm ###s](Q828K8) |

Phylogenetic Analysis





