

DIVERSITY AND DISTRIBUTION OF BACTERIAL GENES RELATED TO ANAEROBIC DEGRADATION OF ALIPHATIC AND AROMATIC HYDROCARBONS IN ANTARCTIC SOILS

Sampaio, D.S.¹, Jurelevicius, D.A.¹, Alvarez, V.M.¹, Seldin, L.¹

¹Instituto de Microbiologia Paulo de Góes (Avenida Carlos Chagas filho, 373, Cidade Universitária - Ilha do Fundão, Rio de Janeiro, RJ).

The crude oil is a complex mixture consisting mainly of aliphatic and aromatic hydrocarbons. Because of its exploitation and use, the petrochemical industry deals constantly with the contamination of the environment with crude oil and/or crude oil derivatives. Different microorganisms are able to use petroleum hydrocarbons as carbon and energy sources. However, in soils with low diffusion of O₂, the anaerobic degradation of aliphatic and aromatic hydrocarbons by microorganisms is the main bioremediation process. Soils containing low diffusion of O₂ are frequently found in Antarctica. However, the presence and the distribution of anaerobic bacteria able to degrade petroleum hydrocarbons in Antarctic soil are still unknown. Therefore, the aim of this study was to evaluate the anaerobic aliphatic and aromatic hydrocarbon-degrading bacterial communities from soils sampled in King George Island, Antarctica. A total of 30 samples (representing 10 soils in triplicate) was collected during the summer of 2009, 2010 and 2011 in the vicinity of the Brazilian Comandante Ferraz Station. Anaerobic aliphatic and aromatic hydrocarbon-degrading bacterial communities were studied through the analysis of the genes coding for: (i) alkyl-succinate synthetase (AssA - related to anaerobic degradation of aliphatic hydrocarbons), (ii) benzyl succinate synthetase (BssA - anaerobic degradation of aromatic hydrocarbons) and (iii) 6 OCH-hydrolase (BamA - anaerobic degradation of aromatic hydrocarbons). The PCR results showed that genes coding for BamA could be detected in all soils analyzed, whereas genes coding for BssA and AssA were found only in non-contaminated soils. The BamA-based PCR-DGGE results showed the presence of complex anaerobic aromatic hydrocarbon-degrading bacterial communities in Antarctic soils. However, the results showed that the Total Petroleum Hydrocarbons (TPH) was the main factor influencing the distribution of these communities in the analyzed soils. Further, *bamA*-based clone libraries were set up and the sequenced DNA were compared with sequences previously deposited in the GenBank database using the BLASTx tool. The results showed the presence of BamA related to enzymes described in seven bacterial genera, including *Magnetospirillum*, *Sulfuritalea*, *Rhodovulum*, *Azoarcus*, *Sedimenticola*, *Rhodomicrobium* and *Rhodomicrobium*. The results obtained in this study may be useful to monitor the bioremediation of hydrocarbon-contaminated Antarctic soils.

Keywords: Petroleum. Hydrocarbons. Anaerobic.

Grants: CNPq, FAPERJ and CAPES