

**TITLE:** TAXONOMIC AND FUNCTIONAL DIVERSITY OF THE MICROBIOME OF ANTARCTIC SEDIMENTS RELATED TO THE BIODEGRADATION OF PETROLEUM HYDROCARBONS

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**ABSTRACT:**

Human activities in the Antarctic environment have increased in recent years, especially in the South Shetland Islands. The traffic of ships associated with activities such as fishing, supply of scientific facilities and increased tourism have caused the contamination of antarctic ecosystems with petroleum hydrocarbons. In addition to several adverse factors such as low temperatures and nutrient concentration, high ultraviolet radiation and desiccation, the antarctic microbiota deals with the presence of complex organic compounds. Due to exposure to these compounds, bacteria population able to degrade hydrocarbons have been selected, often using them as a carbon source. This project aims at evaluating the genetic potential of microbial communities of antarctic sediments for the degradation of petroleum hydrocarbons, performing a comparative analysis of the diversity of genes involved in the aerobic and anaerobic degradation of hydrocarbons under the influence of low temperatures at different sites of two Shetland South islands, subjected to different levels of anthropic impact: Deception and Livingston. For this, metagenome shotgun sequencing was carried out followed by subsequent bioinformatics analyses for assembly, prediction and annotation of hydrocarbon degradation genes and pathways using specific databases. Information derived from taxonomic annotation of metagenomic datasets allowed to select some of previously isolated bacteria from the Antarctic environment to evaluate the degradation ability if such bacteria at low temperatures. In preliminary screening tests with bacteria isolated from the Antarctic environment, some genera such as *Arthrobacter*, *Psychrobacter* and *Flavobacterium* showed potential for degradation of different hydrocarbon sources. In metagenomic analysis, we identified genes related to degradation of: toluene, xylene, styrene, ethylbenzene, naphthalene, polycyclic aromatic hydrocarbons and alkanes. We also observed that the diversity and abundance of degradation genes varies with temperature, so that lower temperatures indicate lower metabolic potential than higher temperatures. The results of this project will contribute to the understanding of the metabolic potential of these microbial communities for the recovery of impacted Antarctic environments and may provide support for the design of future bioremediation strategies.

**Keywords** Antarctic sediments, petroleum hydrocarbons, metagenomics, biodegradation.

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