

TITLE: IDENTIFICATION AND CHARACTERIZATION OF GENES AND METABOLIC PATHWAYS INVOLVED IN HYDROCARBONS DEGRADATION FROM AMAZONIAN BASIN METAGENOMIC DATA

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ABSTRACT

The petroleum industry is growing in the past few years due to its use in the humanity daily basics, as a result, the exploration of this commodity becomes more frequently. However the oil recovery process, refining and transport is able to accidents that can result in its spill in environment. The coastal areas at Brazilian territory, in which has its majority exploration located at *offshore* platforms, have their economy based in its environment; in particular, the amazonian basin that has extractivism as important part of economy. In addition to its recalcitrant and toxic features, the petroleum is also known as a potential carcinogenic substance, therefore petroleum spills will lead to economic losses and social consequences. Bioremediation is currently the best choice for these situations, thus knowing the microbial communities of these locations that will be affected by petroleum in the condition of oil spill and their potential for degradation of said substance is one of the first acts for strategic remediation. In this work, samples were obtained from the coastal area at the north of Pará State during the low tidal at the points located in a mangrove area (sediment sample) and beach area (sea water sample). Both samples were submitted to their total DNA extraction, sequenced with Ion Torrent PGM platform and to metagenomic analysis platforms, MG-RAST and EBI metagenomics. In addition, another pipeline has been chosen, combining the Diamond script and MEGAN CE. The reads obtained throughout the pipelines were be annotated by KAAS and their metabolic abundance were estimated by MetaPath script. The coding genes directly involved in petroleum degradation, such as *alkB* and *PAH-RHD α* , will have their sequences extracted and clustered. Taxonomic results shows that Proteobacteria is the most abundant phylum in both samples – 31% of total reads in mangrove's sample and 40% reads in sea water's sample – as for more specific taxons the Gamma- and Alphaproteobacteria had similar abundance in both sites; said phylum is frequently mentioned in the literature begin related to the biodegradation of oil contaminated sites or samples. The 16S rRNA reads were as well identified as part of Oceanospirillales order, *Pseudomonas* and *Acinetobacter* genus, also know by its presence and petroleum biodegradation potential. The Amazonian basin's microbial composition, in accordance with literature knowledge, has meaningful probability potential for petroleum bioremediation.

Keywords: amazonian basin, metagenome, petroleum, bioremediation, bioinformatics

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