TITLE: METATRANSCRIPTOMIC ANALYSIS OF GENES INVOLVED IN THE METABOLIC PATHWAY OF NITROGEN AND PHOSPHORUS OF AEROBIC ENRICHMENTS FROM A PETROLEUM RESERVOIR IN NORTHEAST BRAZIL

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Biodegradation in petroleum reservoirs may result in physicochemical changes in crude oil and natural gas properties, being responsible for the decrease of saturated hydrocarbons and yielding heavy oil with low economic value. However, there are some key factors that can affect the biodegradation process, including the deficiency of nutrients, such as nitrogen and phosphorus, essential for microbial growth. Scarce information is available about the genes involved in the metabolic pathway of nitrogen in microbial communities inhabiting oil reservoirs. The aim of this study was to evaluate the metatranscriptome involved in nitrogen and phosphorus uptake and assimilation in samples of an aerobic microbial enrichment from Brazilian oil reservoirs. After 10 and 20 days of incubation, community RNA was extracted from the oil microbial enrichments and sequenced using Illumina platform. The sequences were analyzed using MG-RAST, revealing the expression of genes directly involved in deprivation of nitrogen such as gltBD, encoding glutamate synthase, and glnA, encoding glutamine synthetase related to ammonia assimilation, and amtB, encoding the protein ammonium transporter, and other genes involved in deprivation of nitrogen. The sequences revealing the expression of genes that encode a high-affinity phosphate transport system (pst operon) and the genes of the pho regulon, which is a group of genes and operons that are induced in response to phosphate limitation. After 20 days, there was an increase in gene expression as gltBD, glnA and amtB involved in nitrogen metabolism, and the pstA and pstC related genes operon pst, phoB gene pho regulon and other genes phosphate metabolism. These genes were related to groups of hydrocarbon degrading bacteria such as genus Streptomyces and Azoarcus. The increase of transcripts related to nitrogen and phosphorus uptake and assimilation genes after 20 days suggest that the deficiency in both nutrients in the enrichment may affect the growth of degrading bacteria and consequently the process of biodegradation.

Keywords: Metatranscriptomic, Illumina platform, ammonia, assimilation, operon pst.

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