

TITLE: METATRANSCRIPTOMIC ANALYSIS OF GENES INVOLVED IN RESISTANCE AND TRANSPORT OF HEAVY METALS IN PETROLEUM NORTHEAST RESERVOIR SAMPLES.

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The biodegradation process can alter the physicochemical properties of the oil present in the petroleum reservoirs, reducing its quality and economic values. Some factors may alter this process, such as the presence of heavy metals, as it hinders the development of the microbial community that degrades hydrocarbons. Heavy metals are micronutrients usually essential to life in small amounts; however, in higher concentrations they can be maleficent. These harmful effects occur in the oil wells because they have concentrations around 8% of heavy metals, such as Fe, Cd and Zn which are liberated extensively in the environment, due to the burning of oil and derivatives. Some microorganisms, naturally present in the reservoirs, have the capacity of resistance, tolerance and regulation of the accumulation of heavy metals, avoiding or minimizing their toxicity. This study aimed to analyze and evaluate the expression of genes involved in the resistance and transport of heavy metals in samples from a microbial aerobic enrichment of Brazilian oil reservoirs after 10 and 20 days of incubation. The RNA was extracted and sequenced using the Illumina platform and the sequences were deposited in the MG-RAST database. The results demonstrated that after 20 days of incubation there was an increase in the expression of *znuA*, *znuB* and *znuC* genes, involved in zinc resistance, *czcABC* genes, which mediate resistance to Co^{2+} , Zn^{2+} and Cd^{2+} , and *copA* gene, involved in copper homeostasis. The results of the present work provide significant information on the microbial response of hydrocarbon degrading bacteria in the presence of heavy metals from aerobic assay in the presence of petroleum, allowing future research on the factors that interfere in the biodegradation process to better understand this system.

Keywords: Heavy metals, Metatranscriptomic, Illumina, Petroleum

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