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BACTERIAL COMMUNITIES OF DRILLING MUD AND DEEP SURFACE SAMPLES OF VACA MUERTA RESERVOIR IN NEUQUEN, ARGENTINA

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Vaca Muerta oil reservoir in Neuquén, Argentina, is a high-temperature and high-pressure ecosystem located deep beneath the surface. Microbial communities in oil reservoirs often consist of sulfate-reducing, nitrate-reducing, and fermentative bacteria, and archaeal methanogens. The exploitation of these resources can alter the bacterial communities inhabiting deep sediments by introducing foreign microorganisms or nutrients. The aim of this work was to characterize the bacterial communities present in rock samples from two oil fields (approximately 2600 meters deep) and in the drilling mud used during drilling operations in the Vaca Muerta reservoir. DNA present in 15 cores, 106 cuttings and 28 drilling mud samples was extracted using an optimized protocol developed for these types of samples. The V3-V4 region of the 16S gene was amplified and sequenced using Illumina technology. Amplicon Sequence Variants (ASVs) were obtained using DADA2 and classified using Qiime2. The communities were analyzed using the phyloseq, microViz, microbiomeMarker and packages in Rstudio and PICRUST. Alpha diversity measures of rock samples were within the ranges described for deep surface bacterial communities. No significant correlation was found between alpha diversity indices and the depth of the samples. Drilling mud samples showed significantly higher diversity than the cutting samples from the oil field where it was used ($p < 0.05$). Bacterial communities found in mud were enriched in sequences belonging to the *Bacillaceae* family when compared to cuttings and core samples. Shared taxa found in core and cutting samples from oil fields A and B belonged mainly to Gammaproteobacteria, Actinobacteria, Bacilli, Bacteroidia, Alphaproteobacteria, Clostridia, Chlamydiae, Chloroflexia, Anaerolineae, Thermoleophilia, Oligoflexia, Planctomycetes, and unassigned Bacteria. Functional prediction showed that the bacterial communities of these oil fields are potentially composed of fermenters, nitrate-reducing bacteria and thiosulfate-reducing bacteria that employ the SOX

system. Bacteria that could aerobically degrade alkanes and aromatic compounds such as naphthalene, toluene, and phenol were found. The potential to anaerobically degrade benzoate was found less abundantly. The abundance of predicted pathways related to aromatic compound degradation, fermentation, anaerobic degradation of amino acids, methanogenic cofactors, and osmolyte biosynthesis were significantly different between rock samples and drilling mud. This study allowed the characterization of bacterial communities from the deep surface at two location sites. Although both oil fields had different metagenomic profiles, probably associated with different geochemical characteristics, shared taxa were found abundantly in both sites. Additionally, functional prediction analyses could be a baseline for future studies aimed at evaluating active metabolic pathways in these extreme environments.

Palabras clave: oil – cuttings – core - deep surface - bacteria