

**Title: ANALYSIS OF THE IMPACT OF NITRATE INJECTION OVER BACTERIAL COMMUNITY PRESENT IN WELLS FROM OFFSHORE PLATFORMS LOCATED ON THE COAST OF RIO DE JANEIRO**

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**Abstract:**

The continuous injection of seawater supplemented with nitrate has been considered a promising technology in controlling sulfate-reducing bacteria (SRB) and the production of hydrogen sulfide (H<sub>2</sub>S) in secondary oil recovery systems. This technique is an alternative to the use of chemical biocides (toxic substances that may lead to microbial resistance) and has been studied because of its ability to increase the redox potential in the oil reservoir, leading to a biocompetitive exclusion between bacterial groups. This process occurs by selective manipulation of the microbial community of the reservoir, through the use of nitrate to stimulate the metabolism of nitrate-reducing bacteria (NRB) and / or nitrate-reducing and oxidizing sulfur bacteria (OS-NRB) instead of the SRB metabolism. However, the nitrate injection efficiency in the treatment of SRB is still controversial and few studies have been done assessing their application directly in oil production line. Thus, the aim of this study is to evaluate the response of the total bacterial community and SRB present in two oil wells located in Bacia de Campos (Rio de Janeiro) to the addition of nitrate during secondary oil production. To achieve this goal, 66 samples including injection water (IW) produced water (PW) and produced water containing oil (PWO), were collected from two producing oil wells. Each water sample (250 ml) was filtered in a Millipore membrane (0,45 µm-pore) that was subsequently subjected to DNA extraction. Then, the DNA isolated from water samples were used to study the total bacterial community through *rrs* gene amplification using PCR, followed by denaturing gradient gel electrophoresis (DGGE). Amplicons from *rrs* gene were obtained for 47 samples. Through the analysis of the DGGE profiles it was observed that the nitrate injection into the P48 platform well did not directly influence the total bacterial community over time. On the other hand, the nitrate injection in the platform P43 well resulted in total bacterial community changes. To study the SRB community, two functional genes involved in sulfate reduction metabolism were amplified, *apsA* (coding adenosine-5'-phosphosulfate reductase enzyme) and *dsrA* (coding the sulfite reductase enzyme). In this case, amplification products were obtained only for PW samples, being 17 samples for *apsA* gene and 13 samples for *dsrA* gene.

**Key words:** denaturing gradient gel electrophoresis, nitrate reducing bacteria, sulfate reducing bacteria.

**Support:** CNPq, Petrobras.