OPERATION AND MICROBIOLOGICAL CHARACTERIZATION OF A BIOFITER TREATING WASTEWATER PRODUCED IN SURFACTANT-ENHNACED SOIL WASHING

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Introduction. Surfactant enhanced soil washing technique shows high removal of hydrophobic compounds such as TPH. However, large amounts of wastewater are produced. Consequently, the wastewater must be treated (1).Several technologies for treating these wastewaters have been reported in literature (2). One technology that attracts greater attention is biofiltration (3), in which the contaminants are removed due to the degradation abilities of the microbial communities developed in the biofilm (4).To identify the microorganisms involved in the biological process (such in biofiltration systems) the molecular biolology-based technologies are the most suitable ones(5).

In this work, a biofiltration system was evaluated in the treating of surfactant-enhanced soil washing wastewater. DGGE technique was employed to characterize the microorganism's diversity in the biofilter.

Methods. The treatment of the wastewater was performed in a biofilter with 50 cm length and 12 cm of diameter (working volume of 4.5L). Three sample ports were located along the reactor height to take samples of the packaging material. Liquid samples were measured in both inlet and outlet ports. During the wastewater treatment 3 fluxes (0.28, 0.4 and 0.63 L/h), 2 initial COD concentrations (300 and 480 mg/kg) and 3 surfactant concentrations of 0.5, 0.75 and 1% of Surfopon 30) were evaluated. DNA extraction with a PowerSoil DNA Isolation Kit (MO BIO) the PCR (Polymerase Chain Reaction) was conducted. The 16S rRNA gene was amplified using universal bacterial primers reported in reference (6), amplifying the three hypervariable regions (V3-V5).The PCR-amplified DNA products were separated by DGGE.

Results. The higher COD removal was obtained at a flux of 0.4L/h. For same COD initial concentrations, the highest removal efficiencies were obtained for the minimum flux. For fluxes of 0.28 and 0.40L/h, when increasing initial COD concentrations, the COD removals increased, except for 0.63L/h. The lower removal percentages obtained were with a flux of 0.63L/h. Regarding the oil and grease values, a similar behavior was noticed; the higher percentage was at a flux of 0.28 L/h (99.09%). Finally, the maximum surfactant removal was 99.68% for a 0.28 L/h flux.

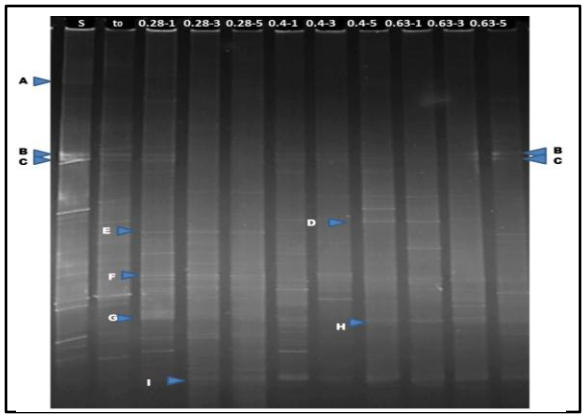

Fig.1 DGGE patterns of amplified 16S rDNA fragments from the packing material. The lanes are labeled as S (soil), t0 (initial time of operation), 0.28, 0.40 and 0.63 correspond to the different fluxes and the suffixes 1, 3 and 5 correspond to different levels in the biofilter. All correspond to an initial COD concentration of 480 mg/L and 0.5% of SP30.

In Fig. 1, several DGGE profiles are presented. The DNA sample of the soil (S) 16 main bands (OTUs) were detected. In comparison with the initial time (t0), the number of bands was significantly reduced. 5 bands disappear including band A. This result was expected since the adaptation of the microorganism to the waste automotive oil as an only carbon source.

Conclusions. The highest COD removal of 72% was obtained at a flux of 0.28L/h. The removal efficiencies were higher at lower fluxes. DGGE technology proved to be suitable technique to characterize the microorganism diversity present in the biofilm. The removal efficiencies were higher at lower fluxes values.

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