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CONTAMINANT REMOVAL AND CHANGES IN BACTERIAL COMMUNITIES DURING "IN SITU" BIOSTIMULATION AND BIOAUGMENTATION FIELD STUDIES USING ANTARCTIC SOILS CHRONICALLY CONTAMINATED WITH DIESEL FUELS

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Because their low temperatures and other harsh environmental conditions, bioremediation processes are strongly limited in Antarctica. In this work we analysed how biodegradation of hydrocarbons presents in chronically contaminated Antarctic soils is affected by biostimulation (with N and P) and bioaugmentation (with two Antarctic hydrocarbon-degrading bacterial consortia). A 48 d-length "in situ" assay was carried out in 1m^2 plots with diesel polluted soil at Jubany station, Antarctica. The following systems were performed: community control (CC), biostimulation (AB), biostimulation and bioaugmentation with two different bacterial consortia (M10 and J13 systems). Heterotrophic and hydrocarbon-degrading aerobic bacterial counts, total hydrocarbon content (FT-IR / GC-MS) were determined. Bacterial communities were characterised by T-RFLP analysis of PCR amplified 16S rDNA at three different time followed by cluster analysis of the electrophoretic patterns. Highest degradation levels were observed in AB system (69.60%) but showing no significant differences compared with M10 or J13 (62.61% and 58.01% respectively). Bacterial communities in all plots were similar at the beginning of the experiment. There were rapid changes (within three weeks) in the structure of communities in all treated plots, which were highly similar (82%) irrespective of the treatment applied. Under the assayed conditions, consortia M10 and J13 were not detected as established components of the community in bioaugmented plots. The treatments caused an increase in the equitability (J') of the communities; although no major variations in Shannon diversity (H') was observed. Results showed that autochthonous bacterial flora of chronically polluted Antarctic soils is effective to reduce hydrocarbon concentration in "in situ" bioremediation processes. At the used inoculum levels, consortia M10 and J13 were not more effective that the natural microflora. Molecular results suggest that under the assayed conditions these bacterial consortia were not able to colonize the contaminated soils.