



Characterization of bacterial communities during a field biotreatment of PAHs contaminated soils

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This study aims at monitoring the evolution of bacterial diversity during a field biotreatment of a soil highly contaminated with PAHs (the concentration of 16 PAHs (US-EPA) was about 3 g.kg⁻¹ of dry soil) and to evidence specific bacteria, which may be used as bioindicators for monitoring a biotreatment process. In parallel, a laboratory experiment with the same polluted soil was realized.

The field treatment consisted of putting into place a swath on an industrial site located in the North of France.

Total and PAHs-degrading bacterial communities were evaluated by using direct DNA extraction, PCR amplification of 16S rRNA and denaturing gradient gel electrophoresis (DGGE). Bacterial population profiles were analysed in parallel to total and PAHs-degrading bacterial counts and 16 PAHs measurements.

Results showed that six months of biological treatment of this soil led to an important reduction of the 16 PAHs concentration, which related to mainly 2- and 3-ring PAHs, and to a lesser extent to 4-ring PAHs. The similar kinetic of PAHs-biodegradation was obtained by the laboratory experiment.

The bacterial community was characterized by a high diversity, with the persistence all over the biotreatment of a bacterial consortium represented by Gram-negative bacterial strains belonging mainly to the Gamma-proteobacteria group. This bacterial group seems to be a good bioindicator for evidencing a potential of biodegradation. Conversely, the bacterial community structure underwent significant change during the biological treatment. Other species appeared in the course of time and seems to be

specific of different steps of biodegradation. These results were corroborated by those obtained to the laboratory experiment.