



## **Relation between composition, microstructure and indigenous microbial activity is a key to potential bioremediation of the aged tar oil contaminated soil**

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Finding interlinkages between soil chemistry, microstructure and microbial communities in the contaminated soils is a fundamental requirement to assess their remediation strategy.

We studied composition, microstructure and microbial communities of an aged tar oil contaminated technosol on a former manufactured gas plant site in Germany. The soil contained several thousand of high molecular weight hydrocarbons (HC) which are deemed to be recalcitrant and toxic. High concentrations of heavy metals may also hinder HC biodegradation.

We found that content and composition of the tar oil varied both laterally and vertically. The most contaminated source layer (90-120 mg g<sup>-1</sup> total petroleum hydrocarbons, TPH) consisted of spherical macroaggregates (up to 1-2 cm) with isolated macropores inside, sometimes filled with siderite crystals (proved by SEM-EDX and FTIR-microscopy, supported by larger differences between total- and dithionite-extractable Fe values) to indicate anaerobic conditions. On the rim of the site, vegetation overgrew the source layer; plant residues accumulated as particulate organic matter (POM) on top of the source layer to form the soil with peat-like structure (15-28 mg g<sup>-1</sup> TPH). In the layer beneath the source layer (10-16 mg g<sup>-1</sup> TPH), we observed porous microstructure with disperse Fe-rich particles, especially along macropores and root channels (shown by SEM-EDX), presumably in the form of Fe(III) (hydr)oxides. This assumption is corroborated by FeTOT/FeDCB values and indicates aerobic conditions in this layer. Below the visually contaminated layers, some root channels and macropores were coated with HC fractions which were more oxidized than the tar oil in the source layer (shown by FTIR microscopy) and contained a lot of Fe (shown by SEM-EDX).

Contaminated layers revealed higher microbial biomass (based on cell counts with a luminescence microscopy and microbial C extraction) than the uncontaminated soil on the site. The preliminary CARD-FISH analysis showed that microbial community in the source layer was dominated by  $\alpha$ -,  $\beta$ - and  $\gamma$ -Proteobacteria; while the layers on top and below revealed high dominance of  $\alpha$ -Proteobacteria.

Catalase, dehydrogenase, lipase,  $\beta$ -glucosidase and acid phosphatase activities on top and at the bottom of the source layer were higher than in the other contaminated layers and the uncontaminated soil. This proves the presence of a highly active microbial community with various biogeochemical functions.

We conclude that natural attenuation of the toxic aged tar oil occurs in situ and that the microbial communities are well adapted to the tar oil with varying contents along the profile. The varying microstructure of the contaminated layers results in occurrence of different domains with oxic and anoxic conditions and specific microbial communities. Thus, we expect varying attenuation rates and degradation pathways, coupled with POM decomposition and oxidation and reduction of Fe. We hypothesize that in well aerated macropores and root channels below the source layer the attenuation is more pronounced.