Rhizosphere microbiome engineering and root exudate metabolites have the potential to enhance the bioremediation of petroleum hydrocarbons

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Nature-based solutions for historically polluted sites remediation include the enhancement of the degradative potential selected in the soil microbiome over time. Biostimulation of degradative microorganisms can be achieved by adding specific compounds directly to the soil or it can be mediated by plants, that act synergistically with the soil microbiome in rhizoremediation approaches, often prompted by the addition of selected microorganisms.

Here, sunflower was employed alone or supplemented by degradative strains to optimize petroleum hydrocarbon (PHC) remediation of an industrial polluted soil. The dynamics of the rhizosphere microbiome and the abundance of PHC catabolic genes were monitored on the soil metagenome by metataxonomic and qPCR analyses, while the efficacy of microbial inoculation in boosting PHC removal was chemically assessed. Moreover, leveraging untargeted metabolomics data, the role of specific root exudate metabolites as possible biostimulants of PHC degradation was evaluated *in vitro* providing them to the microbial cells detached from the target soil.

In soil, we observed that sunflower recruited a rhizosphere community diverse from that evolving over time in unplanted microcosms. Moreover, bioaugmentation with degrading strains further steered the structure of the overall rhizosphere microbiome, increasing the abundance of catabolic genes and the removal of PCHs compared to non-inoculated plants. *In vitro*, soil-detached microbiome showed improved PHC degradation when supplemented by the tested metabolites, suggesting that these plant-derived molecules trigger degradation pathways of the native bacterial populations naturally selected in the historical contaminated soil.

Our findings demonstrate that the understanding of ecological interactions in the rhizosphere, mediated by invading degrading strains and by plant via root exudation is essential for optimizing the design of rhizoremediation interventions.

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