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MOLECULAR APPROACHES AND METAGENOMIC INVESTIGATIONS FOR OPTIMIZING CLEAN-UP OF PAH CONTAMINATED SITES (MAGICPAH)

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Abstract

MAGICPAH aims to explore, understand and exploit the catalytic activities of microbial communities involved in the degradation of persistent PAHs, where the main objectives are: (i) to generate a knowledge base of the microbial aerobic catabolome, (ii) to develop concepts to quantify *in situ* degradation of PAHs through stable isotope analyses, (iii) to identify key players and key reactions involved in anaerobic PAH metabolism, (iv) to achieve a detailed understanding on key processes for PAH metabolism in marine and composting environments, (v) to develop methods to predict the ultimate fate and the kinetics of aerobic degradation of PAH under different conditions of bioavailability, (vi) to isolate and sequence novel key players in PAH metabolism to understand the genomic basis of niche specificities, (vii) to investigate the potential synergistic links between environmental biotechnology and medical biotechnology, (viii) to integrate detailed catabolome and reactome information to reconstruct metabolic networks, (ix) to apply gathered information to improve the treatment performance of PAH contaminated sites.

In the presentation we will give an overview on a subset of recent results.

Extensive samplings were performed to obtain impacted materials and an Illumina-based barcoded deep sequencing strategy applied, allowing a detailed survey of community compositions and shifts. To obtain a reliable frame of reactions involved in PAH degradation, curated databases on key catabolic enzyme families were constructed, and used to design PCR primers and microarray probes to survey the spread and activity of respective genes in contaminated environments and to obtain a reliable annotation of genes observed in metagenomic and metatranscriptomic surveys. To be able to construct upgraded databases on anaerobic key steps, key steps of the anaerobic naphthalene degradation pathway were elucidated.

We also exploited the enormous biodiversity through the mining for novel activities from metagenomic libraries, where active clones were now fully sequenced.

To understand the distribution of aromatic degradation networks, (meta-) genomic and shotgun (meta-) proteomics were used to deduce previously unrecognized correlations between systems performance and phylogenetic, genomic and proteomic blueprints. As a step further in understanding community behaviour, mRNA sequencing has been successfully applied to obtain a metatranscriptomic overview of contaminated groundwater samples.

The genome of *Cycloclasticus zancoles* a key PAH degrader in marine environments was sequenced revealing a large repertoire of genetic determinants for the uptake of mineral nutrients that are limiting in marine environments and the strong biodegradation potential was evidenced by the exceptional multiplicity of key aromatic degradation genes.
