

EGU2020-18435

<https://doi.org/10.5194/egusphere-egu2020-18435>

EGU General Assembly 2020

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PAH natural attenuation in Mediterranean forest soils

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Polycyclic aromatic hydrocarbons (PAHs) are worldwide contaminants and, due to their long-range transport, they can accumulate far from the emission sources, in carbon-rich forest soils; thus new exploration in the indigenous microbial response to PAH exposure is important to deeper understanding of PAH natural degradation process. Since most of the studies are limited to aged PAH contaminated soils, we aimed to fill the gap in our knowledge on recent contamination.

In order to investigate indigenous microbial community involvement in soil PAH degradation, a mesocosm trial was established. Soils from two forest systems (holm oak and black pine) were spiked with 3 PAHs (phenanthrene, pyrene and benzo[a]pyrene) and incubated under controlled conditions (T: 22 °C, R.H.: 88%). Along 360 days, structural and functional changes in soil microbial community were monitored analyzing bacterial and fungal biomass (by phospholipid fatty acid and ergosterol content) and enzyme activities (hydrolase, laccase and peroxidase).

Both soil types indicated a capability of indigenous native microbial community to degrade almost completely PAHs yet after one year, with phenanthrene and pyrene faster degrading than benzo[a]pyrene, according to their molecular weight. In pine soil, the PAH degradation proceeds with a minor extent likely in relation to the sequestration of PAHs in soil richer in organic matter. In both forest soils fungi are mainly involved in the degradation of PAHs, as highlighted by the increase of both content of the fungal marker and enzyme activity mainly carried out by fungi, e.g. laccase in holm oak soil.

Regarding the community structure, PAH contamination influences the relative abundance of several soil microbial groups yet after 4 days from contamination, when the microbial community composition shifts towards Gram+ bacteria in holm oak soil, whereas in pine soil pyrene and phenanthrene stimulate fungi and actinomycetes. In the long-term, after one year from contamination, a variation in microbial community was more evident in the holm oak soil, with an increase of fungi in the treatment with benzo[a]pyrene, and an increase of Gram+ in the treatment with phenanthrene. All the enzymes activities, after some fluctuations in the early stages of incubation, decreased after one year. During the quick and strong PAH degradation, hydrolytic activity showed high and constant values, exhibiting a stability in the long-term after the contamination.

The obtained findings show the role of several microbial groups in PAH natural attenuation in different forest soils. Different PAH degradation rates between systems can be attributable to soil microbiome dominated by different populations in the two investigated forest soils. The use of indigenous microorganisms in bioremediation processes can reduce the risks associated with PAH contaminated soils, and a better understanding of the effects of PAH contaminants on soil

microbial community is very critical for understanding microbial activity during bioremediation. The findings highlight the importance of fungi in the potential recovery of a soil polluted by organic contaminants.