



Regulation of pesticide degradation in the detritusphere

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The detritusphere is a microbial hot spot of C turnover and degradation of pesticides in soils. We aimed at an improved understanding of the regulation mechanisms, which are responsible for stimulated degradation of the herbicide MCPA (2-Methyl-4-chlorophenoxyacetic acid) in response to increased C availability in the detritusphere. We combined a microcosm experiment with biogeochemical modeling and linked genetic information on abundances of total bacteria, fungi and specific pesticide degraders in soil to the coupled biogeochemical dynamics of C and MCPA.

As a result of diffusive and convective C transport from litter into the adjacent soil we found increased dissolved organic C (DOC) in soil up to a 6 mm distance to litter (detritusphere). In the detritusphere, we observed increased microbial C and accelerated MCPA degradation. These dynamics were accurately reproduced by the model. Whereas the observed increase of bacteria and pesticide degrader populations in the detritusphere was simulated satisfactorily, the model could not reproduce the steep increase of fungi indicated by the fungal marker gene. Our simulations suggest that bacterial MCPA degraders mostly benefited from high-quality DOC, whereas fungal activity and growth were specifically stimulated by low-quality DOC. According to the simulations, MCPA was predominantly degraded via fungal co-metabolism.

Our study demonstrates that biogeochemical processes in soil hotspots are regulated by the interaction of transport processes and microbial dynamics. It further reveals that mathematical modelling is as powerful tool to gain comprehensive insight into the microbial regulation of matter cycling in soil. Genetic information has a high potential to parameterize and evaluate complex mechanistic models, but model approaches must be improved based on extended information on gene dynamics at the cellular level.