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STIMULATION OF BACTERIAL CHLOROBIPHENYL METABOLISM THROUGH THE ADDITION OF PLANT SECONDARY METABOLITES

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Abstract

Interactions between plants and their rhizosphere bacteria are very important for an effective transformation of environmental contaminants which is the essence of rhizoremediation. It has been shown that the presence of a particular plants' root system highly influences soil microbial community structure. Among others, aromatic pollutant-degrading bacteria are fostered via root exudation, or root turnover. These processes provide plant secondary metabolites, which can promote microbial cometabolism of aromatic pollutants after they were released into soil.

The aim of the study was to investigate the influence of selected natural compounds (naringin, limonene, and caffeic acid) and natural materials rich in these compounds (grapefruit peel, lemon peel, and pears, respectively) on the diversity of chlorobiphenyl-metabolizing bacterial populations in long-term PCB-contaminated soil. We have integrated analytical methods of determining PCB degradation with DNA-stable isotope probing (SIP) as a direct method which links the metabolic process with its microbial originators. ¹³C-DNA, isolated after stable isotope probing, was used to generate 16S rRNA gene amplicons which were further processed by pyrosequencing. Our results show that plant secondary metabolites promote the activity of different chlorobiphenyl-metabolizing microbial populations in soil. Specifically, naringin and limonene in soil foster mainly populations of *Hydrogenophaga* spp., caffeic acid *Burkholderia* spp. Similarly, the degradation of individual PCB congeners was influenced by the addition of different plant compounds. Residual content of PCBs was the lowest after treating the soil with naringin. Similar trends were observed after the addition of plant materials, where naringin-rich grapefruit peel addition resulted in the most effective degradation. After the addition of caffeic acid, higher substituted congeners were more degraded compared to all other treatments.

Overall, the findings reveal that active utilization of chlorobiphenyls in soil bacteria is promoted by the presence of plant secondary metabolites. The results may therefore be beneficial to bioremediation (especially rhizoremediation) research in a way they permit predicting the behaviour of populations potentially involved in biodegradative processes.

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