Collapse of soil microbial biodiversity after rapeseed-glucosinolate exposure

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Abstract

Land plants live in intricate communities with soil bacteria and fungi indispensable for plant survival and growth. Furthermore, plants are considered to be a major factor that affects communities of soil microbes. The plant-microbe interactions are largely governed by different allelochemicals. Here, we employed a combination of lipid-fingerprinting, enzyme activity assays and high-throughput DNA sequencing to uncover the dynamics of the microbial community structures in the soil after exposure to isothiocyanates, toxic glucosinolate catabolites with allelopathic properties produced by rapeseed and other Brassicaceae. We show that rapeseed-derived isothiocyanates drastically diminish diversity of bacteria and fungi. After isothiocyanate exposure, only few bacterial taxa of the Gammaproteobacteria (Acinetobacter, Thermomonas), Bacteriodetes (Flavobacterium) and Acidobacteria (Geothrix) proliferated while *Trichosporon* (Zygomycota) dominated the fungal soil community. The current findings provide evidence for the fundamental shift in soil microbial community structure after the introduction of rapeseed-derived isothiocyanates into the soil. Thus, plants of the Brassicaceae strongly modify the soil microbiota, leading to extreme losses within the microbial community structure and affecting the capacity to adapt to a changing environment. The community profiles revealed in this study are the basis for further investigations on specific microbial groups to understand their relevance to soil health. The present knowledge on microbial genetics, taxonomy and systematics and the largely unknown biochemical and physiological properties of many microbial organisms clearly limits the understanding of the true impact of glucosinolates on microbial diversity and community structure. Therefore, the relevance of these bacteria and fungi from soil can only be explained after conducting functional studies. Accordingly, future analyses will concentrate on the different strategies resulting in glucosinolate tolerance, by characterizing the microorganisms retrieved from glucosinolate treated soil during the present study.

Keywords: rapeseed, glucosinolates, soil microbial biodiversity, lipid, fingerprinting, high, throughput DNA sequencing

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