

Ourry



Deciphering Brassica napus-microbiome associations in interaction with root herbivorous insect *Delia radicum*: a feedback loop in the rhizosphere

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Plants are known to be major biological hubs, which above- and belowground organs interact with either beneficial or detrimental macro- and microorganisms. Even though plant-microorganism interactions are better understood, tripartite interactions involving herbivorous insects remain more complex.

We studied the feedback loop of the tripartite interaction between soil microorganisms, oilseed rape (*Brassica napus*) and a specialist belowground herbivore, the cabbage root fly (*Delia radicum*). Our aims were i) to determine the effects of herbivory on the plant root chemistry and on the root and rhizosphere microbiota and ii) to assess in return the effects of selected soil microorganisms on the herbivore development. To tackle this question, we focused on the plant root primary and secondary metabolites and chemical elements, and analyzed both bacterial and fungal communities assemblages.

In this study, herbivory influenced the temporal dynamics of root metabolites by decreasing most metabolites but increasing trehalose, indolyl glucosinolate and sulfur contents. These changes modified the dynamics of root and rhizosphere microbial communities, such as enhancing the abundance of *γ-Proteobacteria* and *Firmicutes*. Among these bacterial phyla, four genera (*Bacillus*, *Paenibacillus*, *Pseudomonas*, and *Stenotrophomonas*) had a higher abundance following herbivory, which was associated to modifications of root chemical compounds. Also, plants associated to different levels of soil microbial diversity marginally influenced root metabolite profiles but contributed to a modification of the fly emergence rate.

Further research would help to identify the biological function of plant, microbiome and insect and the potential implications of microbiome in plant defenses.