
Does rhizospheric microbiome contribute to common bean tolerance to drought and tropospheric ozone ?

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Résumé

Plant can shape their rhizospheric microorganism communities via the quality and quantity of its root exudates, creating niches with carbon-rich resources used by microorganisms for their metabolisms. Plant useful nutrients are then release gradually in the rhizosphere. Furthermore, some of recruited microbes are beneficial for plants and help them to be more tolerant to abiotic stresses, such as drought and tropospheric ozone. Those plant and soil properties interactions are known as Plant-Soil-Feedbacks. Drought and elevated tropospheric ozone episodes are expected to be more frequent and severe in the near future. Both are threats to crop yield and food security through their negative impacts on plant carbon and nitrogen metabolisms, affecting the Plant-Soil-Feedback.

Common bean (*Phaseolus vulgaris*), a member of the *Fabaceae* family, is one of the most widely cultivated crop in the world. Its nutritional composition, in particular its high protein content, makes this crop an interesting source of protein for human consumption. In addition, its ability to fix atmospheric nitrogen through bacterial symbiosis contributes to sustainable cropping systems. However, common bean is sensitive to abiotic stresses.

In experiments conducted in 2023 and 2024, two common bean genotypes (R123 and S156) differing in their sensitivity to ozone, were grown on a natural soil and subjected to controlled drought, elevated ozone or the combination of both stresses, during the seed filling stage. We wondered if the physiological and yield discrepancies between the genotypes were related to their N use efficiency and/or to the structures of their respective rhizospheric microbial communities.

Physiological parameters, such as gas exchanges, chlorophyll content, stomatal conductance, chlorophyll fluorescence, were measured during the plants life cycle. N recycling processes in plant were studied using the stable isotope ¹⁵N labelling method and by studying foliar proteolysis. Moreover, rhizospheric and bulk soil samples were collected separately and metabarcoding analysis was carried out on the 16S rRNA gene of the DNA extracts.

R123 and S156 developed contrasting physiological strategies, which led to various impacts on yield parameters but not differently under drought. Furthermore, rhizospheric microbial communities of the two genotypes were very similar. The diversity and structure of rhizospheric microbial communities differ from those of bulk soils microbial communities.

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Drought induced modifications in the diversity and structuration of the rhizospheric communities but not in bulk soils. Further analysis will be carried out on the N cycle genes to figure out whether the structural modifications of microbial communities correspond to functional changes in soil N cycle.

Mots-Clés: ozone, drought, common bean, N use efficiency, rhizospheric microbial communities