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Effects of drought on the rhizosphere microbiome of a tolerant common bean cultivar

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The microbial community plays a fundamental role in plant adaptation to adverse environmental conditions. With the increasing frequency and intensity of abiotic stresses driven by climate change, sustainable and cost-effective mitigation strategies are urgently needed. In this study, the microbiome associated with the drought-tolerant common bean genotype SEA5 (*Phaseolus vulgaris* L.) was assessed under a hidric gradient (80%, 60%, 40%, and 20% of field capacity (fc) to investigate the progressive microbial responses to drought stress within the rhizosphere. Plants subjected to 40% and 20% field capacity exhibited the highest stress levels, as indicated by biochemical assays (H_2O_2 and MDA). Microbial community showed within each soil (bulk, rhizo) significant alpha diversty differences between more irrigated (60 and 80% fc) and less irrigated (20% 40% fc). A buffering effect on rhizospheric soil was evident through more differences between field capacities. Differential abundance analysis identified taxa that varied significantly across treatments, highlighting their potential roles in plant drought response. The latent functional potential of the soil microbiome was assessed using PICRUST2 and Tax4Fun2, indicating functional selection in the rizhospheric soil, with overrepresentation of pathways related to environmental sensing, whereas pathways associated with carbohydrate metabolism and biosynthetic processes were underrepresented. Overall, these results indicate that the plant rhizosphere under drought conditions modulates microbial community able to chemically feedback plant signals, as well as maintain a more stable microbial environment in relation to the bulk soil.

KEYWORDS: microbiome, drought, common bean, rhizosphere.

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