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Drought Stress Orchestrates Functional Gene Dynamics in the Common Bean Rhizosphere Microbiome

Ana Vitória Reina da Silva^{1*}, Thierry Alexandre Pellegrinetti¹, Izadora de Cássia Mesquita Cunha¹, Caroline Sayuri Nishisaka¹, Francisco Dini-Andreote², Rodrigo Mendes³, Siu Mui Tsai¹, Lucas William Mendes¹

¹ Cell and Molecular Biology Laboratory, Center for Nuclear Energy in Agriculture (CENA), University of São Paulo (USP), Piracicaba, SP 13416-000, Brazil.

² Department of Plant Science & Huck Institutes of the Life Sciences, The Pennsylvania State University, University Park, PA, USA.

³ Laboratory of Environmental Microbiology, Embrapa Environment, Jaguariuna 18020-000, Brazil.

*Corresponding author: anareina@usp.br

Drought stress threatens global food security, highlighting the need for resilient crops. Harnessing rhizosphere microorganisms can improve plant performance in harsh conditions. Here, we investigated the rhizosphere microbiomes of drought-tolerant (BAT477, SEA5) and susceptible (IAC Milênio, IAC-Carioca 80SH) common bean cultivars (*Phaseolus vulgaris* L.) under contrasting water regimes in mesocosm experiments to assess microbiome functional modulation under drought. Analysis of rhizosphere microbial functional diversity revealed that drought-tolerant cultivars exhibited greater water management, enrichment of beneficial microbial functions, including genes linked to drought tolerance. Notably, drought stress triggered differential abundance in 1.864 microbial genes, highlighting a robust functional shift. Specifically, drought-tolerant cultivars showed an enrichment of genes related to osmotic response, photosynthetic efficiency, oxidative stress mitigation, and osmoprotectant production, whereas susceptible cultivars relied more on genes associated with DNA repair and antioxidant defense, indicating a reactive rather than proactive stress response. Additionally, the rhizosphere microbiomes of drought-tolerant cultivars were enriched in functions related to biofilm formation and dormancy survival. These findings underscore the potential of plant-microbiome interactions in adapting to water stress, suggesting that microbiome selection could be a promising strategy for developing drought-resilient crops and advancing sustainable agricultural practices.

KEYWORDS : Abiotic stress, Metagenomics, Plant-microbe interaction, Water stress

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