

GENETIC DIVERSITY OF THE COMMUNITY OF RHIZOSPHERE MICROORGANISMS FROM MAIZE AND SORGHUM GENOTYPES GROWN UNDER FIELD CONDITIONS UNDER DIFFERENT SOURCES AND LEVELS OF PHOSPHORUS

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Chemical fertilizers have been instrumental in the intensification of agriculture. However, if applied in excess, they can contaminate the environment, and can significantly increase the production cost. Cereals receive almost half of the world's phosphate fertilizer applications. Therefore, plant's phosphorus (P) use efficiency should be increased, aiming a more sustainable agriculture. One alternative is to use less soluble P sources associated with genotypes that are more efficient. In addition, the symbiosis between arbuscular mycorrhizal (FMA) and/or P solubilizing bacteria and plants can contribute to increase the acquisition of this nutrient and promote the growth of cultivated plants. Thus, the objective of this study was to evaluate the genetic diversity of FMA and rhizosphere bacteria of maize and sorghum genotypes grown under different sources and levels of P. Four maize and four sorghum genotypes were grown under field conditions under three sources of P, completely soluble (triple superphosphate), partially soluble (reactive phosphate - Bayovar) and low soluble (rock phosphate - Itafós) and three P doses, 0, 50 and 100 kg P₂O₅ ha⁻¹. Samples of rhizospheric soil and non-rhizospheric soil (control) were collected during the flowering time, and they were analyzed by the T-RFLP technique (Restriction Fragment Length Polymorphism). Within each culture, no significant effect of genotype and phosphate source was observed in the microbial community. However, the P dose was significant in the microbial community structure, within each phosphate source, forming three distinct groups: I) non-rhizospheric soil; II) 0 kg ha⁻¹ and III) 50 and 100 kg ha⁻¹ for all maize and sorghum samples, both for FMA and bacteria. These results suggested that P availability is the predominant factor in bacterial and FMA communities' structures in the maize and sorghum rhizosphere from the evaluated genotypes, followed by P source. The greater understanding of

the microbial community modification in this scenario will occur through the identification of the taxa of each group and the analysis of their role in the environment.

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