

Inoculation effect of phosphate-solubilizing bacteria on microbiota of maize rhizosphere cultivated with different phosphate fertilization conditions

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The use of bioinoculants for sustainable agriculture has grown in many regions worldwide. BiomaPhos[®] is a bioinoculant composed of two P-solubilizing *Bacillus* strains (CNPMS B2084 and CNPMS B119). Our aim was to evaluate the effect of inoculation with BiomaPhos[®] and phosphate fertilization on microbial communities of maize rhizosphere. Field experiments were carried out at Embrapa Milho e Sorgo Experimental Station in Brazil, in the 2019/2020 and 2020/2021 seasons. The maize genotype DKB390 was inoculated with and without BiomaPhos[®] and submitted to three P-fertilizer treatments: without P-fertilizer addition (P0); Rock phosphate (RockP) or triple superphosphate (TSP) at a rate of 120 kg of P₂O₅ ha⁻¹. Genetic diversity was assessed during flowering time by T-RFLP and taxonomic groups identified using the MiCA3 software. In the 2019/2020 harvest, no significant differences were observed in bacterial or fungal diversity among treatments. In 2020/2021, there were significant differences in both bacterial and fungal communities between inoculated and non-inoculated samples from RockP and bacterial communities from P0. The most abundant bacterial families in the first and second seasons were *Streptomyetaceae* (34.6% and 40.4%), *Micrococcaceae* (15.14% and 12.0%) and *Methylobacteriaceae* (10.9% and 13.7%), respectively. Furthermore, there was a significant increase in the abundance of the families *Rhizobiaceae*, *Sphingomonadaceae* and *Brucellaceae* and a significant reduction in the relative abundance of the families *Clostridiaceae*, *Geobacteraceae*, *Micrococcaceae* and *Pseudomonadaceae* in the second season. The most abundant fungal families in the first and second seasons were *Saccharomycetaceae* (38.2% and 49.8%) and *Tremellaceae* (23.1% and 40.7%), respectively, with significant increase in abundance of both families and the reduction of the families *Davidiellaceae*, *Phaeosphaeriaceae* and *Trichocomaceae* in the second season. The results indicated that the microbial communities' structure of maize cultivated under P0 and RockP were different between non-inoculated and inoculated treatments in the second season.

