P28[♥]*@*tinoco morais

Inoculation effect of phosphate-solubilizing bacteria on the microbiota of maize cultivated under different phosphate fertilization conditions

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Plant Growth Promoting Bacteria (PGPB) are frequently utilized in agricultural settings as bioinoculants due to their positive impact on plant growth. BiomaPhos® stands out as the first Brazilian commercial bioinoculant, featuring a consortium of two P-solubilizing Bacillus strains (CNPMS B2084 and CNPMS B119). Our objective was to assess the influence of BiomaPhos® inoculation and phosphate fertilization on the microbial communities within the maize rhizosphere. Field experiments were conducted at the Embrapa Maize and Sorghum Experimental Station in Sete Lagoas, Minas Gerais, Brazil, using clayey soil (Oxisol) during the 2019/2020 and 2020/2021 seasons. The maize genotype DKB390 underwent inoculation with and without BiomaPhos® and was subjected to three P-fertilizer treatments: no Pfertilizer addition (P0), Rock phosphate (RockP), or triple superphosphate (TSP) at a rate of 120 kg of P2O5 ha-1. Genetic diversity was evaluated during flowering time through T-RFLP, and taxonomic groups were identified using MiCA3 software. In the 2019/2020 harvest, no significant differences in bacterial diversity were observed among treatments. However, in 2020/2021, notable distinctions in bacterial communities emerged between the rhizosphere soil of inoculated and non-inoculated maize crops cultivated with 120 kg.ha-1 of TSP and P0. The predominant bacterial families in the first and second seasons were Streptomycetaceae (34.6% and 40.4%), Micrococcaceae (15.14% and 12.0%), and Methylobacteriaceae (10.9% and 13.7%), respectively. Additionally, there was a noteworthy increase in the abundance of the Rhizobiaceae, Sphingnomonadaceae, and Brucellaceae families, coupled with a significant reduction in the relative abundance of Clostridiaceae, Geobacteraceae, Micrococcaceae, and Pseudomonadaceae in the second season. The comprehension the impact of inoculation should be further investigated. Further exploration is needed to understand the implications of inoculation.

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Insights into genomic regions associated with resistance and susceptibility to Gibberella ear rot

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Phytopathogenic fungi are some of the most damaging plant pathogens. In maize, ears can be colonized and infected with the fungus *Fusarium graminearum*, the causal agent of Gibberella ear rot (GER). Infected grain contains mycotoxins that causes severe health risks to humans and livestock when consumed. Host resistance is an important management strategy for GER. In 2021 and 2022 we screened a diverse panel of maize lines (n= 318) for resistance and identified markers associated with GER resistance and toxin accumulation. We then selected and screened near-isogenic lines based on our findings and the literature regarding GER resistance. The selected near-isogenic lines are either in a B73 background with introgressions from teosinte (n= 25) or Oh43 (n= 72), or in an H100 background with introgressions from NC344 (n= 202). We evaluated these lines for resistance to GER in 2023 in Urbana, IL. In the B73 × Oh43, B73 × teosinte, and NC344 × H100 populations most lines were moderately resistant with a slight skew towards susceptibility. We identified multiple lines that were significantly different ($\alpha = 0.05$) from their recurrent parent based on a Dunnett's post hoc test. A total of 6 and 3 lines were significantly more susceptible than B73 in the B73 × Oh43 and B73 × teosinte populations, respectively. In the NC344 × H100 population, 14 lines were significantly more resistant than NC344. We then identified regions associated with susceptibility and resistance. We plan to evaluate the selected near-isogenic lines again in 2024 to validate our findings. We believe that these lines will be useful for exploring the mechanisms underlying susceptibility to GER.

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