

MA-0428

Effect of phosphorus fertilization on bacterial microbiome in microsites *Zea mays* rhizosphere and endosphere

VL Santos¹, UC Silva¹, JD Medeiros², SC Orellana², CA Oliveira³, EA Gomes³¹ Universidade Federal de Minas Gerais, Brazil.² René Rachou Research Center, Brazil.³ Embrapa Milho e Sorgo, Brazil

The microbial communities along of the endosphere and rhizosphere differ in their composition, activity and abundance according to diverse biotic and abiotic factors, such as root exudates, plant genotype, type of soil and agronomic practices like phosphate fertilization. In this study we analyzed the effect of the P fertilization on microbial composition in microsites of the rhizosphere and endosphere of 30F35YH hybrid *Zea mays* fertilized with synthetic phosphate (superphosphate) or Araxá natural rock phosphate (added in 100 Kg P₂O₅ ha⁻¹). Total DNA was obtained from 60 days old corn plants, and V3 and V4 regions of the 16S rDNA gene were sequenced on the MiSeq platform. The results revealed that the species richness varied between the different fertilizer sources, but did not vary significantly by region of the sampled plant, suggesting a strong influence of nutritional stress in the number of OTUS in these microsites. In general, treatment without phosphate showed the lowest OTUS number, followed by treatment with phosphate Araxá and conventional fertilizer. It was observed the predominance of the Proteobacteria in all treatments, although the relative frequency of the phylum varied with the P source applied to the soil. The relative abundance of the Proteobacteria corresponded to 66% on the rhizosphere and 59 % on the endosphere of plants grown in low P. In Araxá phosphate added treatment, the values corresponded to 58% in the rhizosphere and 53% in endosphere, whereas on conventional fertilizer treatment, Proteobacteria corresponded to 42%. Within of the phylum proteobacteria, there is a higher frequency of Gamaproteobacteria, followed by Betaproteobacteria, Alphaproteobacteria and Deltaproteobacteria. Furthermore, it was found that in treatment with addition of Araxá phosphate was observed enrichment of the subphylum Betaproteobacteria (22%) compared to the samples without P (14%) and with superphosphate (10%). Between Betaproteobacteria, Burkholderiales corresponded to the 25.3%, with predominance of Oxalobacteriaceae family and genus *Burkholderia* that have species able to secrete organic acids, considered as the main mechanism of solubilization of the Araxá phosphate. Principal Coordinate Analysis shows that samples clustered by source and concentration of P applied in the soil. It was observed a greater distance between the P added group compared to the others, indicating that the low concentration of P (4 mg/kg P₂O₅) led to a change in the profile of the bacterial community. In addition, can be inferred that this condition has potential for search of bacteria promoting plant growth under phosphate stress. Finally, the productivity of plants grown with Araxá phosphate (lower solubility P source) was similar to cultivated with conventional phosphate (high solubility P source), suggesting that this natural rock phosphate is a promising P source, besides the lower cost and environmental benefits. Financial Support: Fapemig, Capes, CNPq.