TITLE: STUDY ON THE EFFECTS OF MINERAL PHOSPHATE FERTILIZERS ON SOIL BACTERIAL COMMUNITIES OF TROPICAL AGROECOSYSTEMS

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ABSTRACT:

Phosphate-solubilizing microorganisms (PSM) have been utilized as biofertilizer to improve the phosphorus (P) use efficiency by maize crop. This work aimed to investigate the bacterial community profiles of maize rhizosphere soil and bulk soil under different sources of phosphate fertilizers. The field experiment was conducted using a randomized block design with four replicates, with the treatments consisting of three P fertilizers applied to the soil at planting: triple superphosphate (TSP), Itafós rock phosphate (IRP), and Bayóvar reactive rock phosphate (BRRP), and a control treatment without P fertilization. Samples of non-rhizosphere and maize rhizosphere soils were collected at the flowering stage. Total DNA extracted from the soils was used as template for partial amplification of the 16S ribosomal gene using universal primers. The amplicons were sequenced on the Illumina Miseq platform and mapped against the database to infer the bacterial taxonomy. In relation to the OTUS (Operational Taxonomic Units) richness, the lowest and highest values were observed, respectively, in the non-rhizosphere soil fertilized with TSP and the control for the rhizosphere soil. The Chao1 index, which estimates the total number of species present in a community, corroborated the OTU results. The analysis using the weighted UniFrac metric showed that 66.83% of the total data variation could be explained by the three main coordinates, while using the unweighted UniFrac metric only 23.55% of the total data variation could be explained by the three main coordinates. In addition, it was observed two groups separating the microbial community from the rhizosphere and non-rhizosphere soils. These results suggest that both the relative richness and relative abundance of OTUS are similar in each one of the groups formed. Also, the individual analysis of each source of phosphate fertilization in non-rhizosphere soils using the UniFrac unweighted metric showed the formation of two groups between BRRP and IRP. In relation to the taxonomic affiliation, the phylum Proteobacteria was predominant in all rhizosphere and non-rhizosphere samples.

Keywords: metabarcoding, metagenomic, microbial community, ecology.