Metagenomic analysis of the rhizosphere and endosphere microbiome associated with maize genotypes with contrasting P use efficiency

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Using Illumina MiSeq high-throughput sequencing, we analyzed the bacterial and fungal communities from rhizosphere and endosphere of three maize genotypes with contrasting phosphorus (P) use efficiency cultivated in two different P soil levels. A total of 2.588.087 and 2.516.453 reads were identified from 16S (bacteria) and ITS (fungi) rRNA gene regions, respectively, and all taxonomic classifications were assigned using the naïve Bayesian algorithm developed for the RDP Classifier. We observed higher Chao 1 richness and Shannon–Weaver diversity indices in the rhizosphere than inside roots, suggesting that endosphere has a specific microbial community. The predominant bacteria in rhizosphere were from the phyla Proteobacteria (63.9%), Actinobacteria (8.4%), and Bacteroidetes (6.7%), while the main phyla inside the roots were Proteobacteria (50.5%), Tenericutes (15.8%) and Bacteroides (13.4%). The soil P level also influenced the bacterial community distribution since members of *Burkholderia* and *Ralstonia* genera were enriched in the low P rhizosphere while *Pseudomonas* and *Leclercia* were predominant in the high P rhizosphere soils. Considering the fungal communities, Ascomycota was the dominant phylum, followed by Basidiomycota and Glomeromycota in the rhizosphere and endosphere in both P conditions. Glomeromycota (mycorrhizal fungi) was represented at 1% in the rhizosphere and at 5% in the endosphere, and it was especially abundant in the low P soil. In general, we conclude that rather than maize genotypes, the overall pattern of soil microbial diversity was influenced by the soil P concentration followed by the rhizosphere and endosphere habitats.

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