



Influence of rhizosphere, root and P soil on fungal and bacterial communities associated with maize genotypes with contrasting P use efficiency

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Maize (*Zea mays* L.) represents one of the main economic crops for food and energy in the world, and its associated microbial communities have been intensively investigated using different approaches. However, low-resolution profiling methods often make it difficult to understand the complicated microbial communities. Using Illumina MiSeq high-throughput sequencing, we analyzed the bacterial and fungal communities from washed roots (endosphere) and from the rhizosphere soil both originated from the same root sample of two maize genotypes with contrasting phosphorus (P) use efficiency cultivated in two different P soil concentrations. A total of 2,588,087 and 2,516,453 reads were identified from 16S-V4 (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 the 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 (85.7%) was the dominant phylum, followed by Basidiomycota (9.5%) and Glomeromycota (3.0%) in the rhizosphere and endosphere in both P conditions. Glomeromycota phylum (mycorrhizal fungi) was represented at 1% in the rhizosphere and at 5% in the endosphere, and was especially abundant in the low P soil. In general, we conclude that rather than maize genotypes, the overall patterns of soil microbial diversity was influenced by the rhizosphere and endosphere habitats followed by the soil P concentration.