TITLE: FACTORS AFFECTING THE SOIL MICROBIAL COMMUNITY: VARIATION OF PH AND PLANTS SPECIES

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ABSTRACT

The soil is a highly complex and heterogeneous environment, being the reservoir of nutrients of different biogeochemical cycles, and harbouring the highest diversity of microorganisms on Earth. Many microorganisms found in the soil also live in association with plants, providing nutrients, producing growth promoting substances and protecting against pathogens. Thus, alterations of microbial groups in the soil can influence plant productivity. Several factors influence the microbial community, from which the most influential are the pH and the type of plant present in the environment. However, the studies that correlate alterations in these factors with microbial community were mostly obtained in established natural systems, being difficult to determine the relation of cause and effect between them. Better understanding of community structuring is an important step for future management of soil microorganisms. In order to quantify the degree of influence that changes in pH and vegetation coverage promote on the soil microbial community, a factorial experiment was established using different pH and plant species as factors. For the experiment the soil samples were submitted to the characterization of the fertility and determination of the initial pH (4,7). In order to correctly adjust the pH, a pilot experiment was set to obtain the dose (CaCO3) x response curve (pH) of the soil, that is, the amount of $CaCO_3$ at the doses needed to reach a certain pH range (4.7, 5.9, 6.9 and 8.0). Each pH was planted with two plant species (bean and maize). In total, 32 vessels were assembled. Preliminary results showed that 0, 0.6 , 3.4 and 10.9 $Mg.ha^{-1}$ of $CaCO_3$ was needed to correct the pH, obtaining the desired gradient of pH. After 3 months of planting, it was observed that both pH variation (p = 0.02) and plant species (p <0.01) influenced root biomass, with higher values in maize in ph 6.9. Rhizosphere samples were submitted fertility characterization and to DNA extraction followed by 16S rRNA sequencing to determine the microbiome of each sample. The correlation of the data will allow to evaluate the degree of influence of each factor, increasing the knowledge about the microbial ecology of the soil.

Keywords: soil microbiome modulators, soil, sequencing and bioinformatics