

Microbiome of a suppressive agricultural amended soil

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The application of organic amendments to the soil is a strategy that cause the improvement of avocado agricultural soils. This strategy is included in the integrated management of avocado white root rot, caused by the phytopathogenic fungus *Rosellinia necatrix* in the Mediterranean area. In this study, we evaluate the suppressive capacity of an agricultural soil amended with composted almond shells and the role of its microbiome. The application of composted almond shells as organic amendment increase the suppressive activity of field soil against the pathogen, and this suppressiveness can be associated to the microbiota present in amended soil. Soil suppressivity is reduced when soil was heat treated, and then recovered when the heat-treated soil was partially complemented with field soil. Accordingly, we characterized the microbial community of amended suppressive soil by sequencing the 16S rRNA gene and ITS regions. This analysis showed the microbiome structure of the suppressive amended soil. The comparison among this community with the microbial community of an unamended soil reveals subtle differences in the structure of the microbiome. Specifically found in amended soil, we observed a high relative abundance of different classes of bacteria as Gammaproteobacteria and Betaproteobacteria (Proteobacteria), Acidimicrobiia (Actinobacteria) and Solibacteres (Acidobacteria). Regarding fungal communities, we observed a high relative abundance of some classes as Dothideomycetes, Lecanoromycetes (Ascomycota) and Tremellomycetes (Basidiomycota). Furthermore, we performed a functional analysis of the suppressive microbiome to understand the potential activities involved in suppressiveness. The use of a comercial microarray (GeoChip) with more than 80000 different probes, showed the significant increase in amended soil of carbon cycle genes, specifically genes of degradation routes of different carbon sources, as well as the significant reduction of virulence, metal resistance or aromatic compounds degradation related genes. By this analysis, we observed unique detected genes belonging to microorngnisms involved in biological control as Gammaproteobacterias, Firmicutes or Dothideomycetes.

The role of these subtle changes as final responsible of the induced suppressiveness in agricultural amended soils is discussed.