



## Composition of Soil Fungal and Bacterial Communities and their Relation with Soil Physicochemical Properties under different Agricultural managements in a Mediterranean Almond Orchard

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Soil microbiome is the most diverse ecosystem in the world and carries out some of the most important soil functions through nutrient cycling. Agroecosystem health and sustainability are strongly connected to understanding soil microbiome and its composition, yet unknown in many agricultural areas. In this study we compared in a rainfed almond orchard in Spain the long-term effect of intensive tillage (IT), reduced-tillage (RT) and reduced-tillage with alley cropping (RTAC) on soil fungal and bacterial communities and their interrelationship with soil physicochemical properties and almond yield. Fungi and bacteria population were characterized using next-generation sequencing technology. Soil organic C, total N and particulate organic C were significantly higher in RT and RTAC treatments compared to IT, with no significant differences concerning cation exchange capacity, ammonium or nitrates. RTAC showed the highest proportion of macro-aggregates (>250 µm). Richness and diversity indices showed no significant differences among treatments for fungal and bacterial communities. Within bacterial genera, we observed higher abundance of *Sphingomonas*, *Streptomyces*, *Blastococcus*, and *Nocardioides* in RT and RTAC treatments. Within fungi genera, *Mortierella*, *Coprinopsis* and *Chaetomium* showed higher abundance in IT. Multivariate analysis showed that soil fungal and bacterial communities were different depending on the treatment, mostly associated to changes in soil organic C. Deep identification of bacterial and fungal taxa may give light to the understanding of soil microbiome and functions in almond orchards, and brings the producers one step closer to make productive areas more sustainable related to soil C sequestration and fertility.