

**Ecology of
Soil Microorganisms**



Abstract Book

Ecology of Soil Microorganisms

Microbes as Important Drivers of Soil Processes

19.-23.6.2022, Prague, Czech Republic

POSTER 35 – Effects of agricultural management on the olive tree root microbiome

Wentzien NM(1), Fernández-González AJ(1), Villadas PJ(1), Valverde-Corredor A(2), Mercado-Blanco J(2), Fernández-López M(1).

(1) *Departamento de Microbiología del Suelo y Sistemas Simbióticos, Estación Experimental del Zaidín, Consejo Superior de Investigaciones Científicas, 18008, Granada, Spain, nuria.martin@eez.csic.es.*

(2) *Departamento de Protección de Cultivos, Instituto de Agricultura Sostenible, Consejo Superior de Investigaciones Científicas, Córdoba, Spain.*

The aim of this study was to figure out the influence of manure amendment on the radicular (rhizosphere and root endosphere) microbial communities from olive trees. For this purpose, two adjacent olive orchards with different soil managements were surveyed: i) traditional management (TM) and ii) with manure amendment (MA). TM orchard was subjected to common agriculture procedures (including herbicides, mechanical plough and pesticides treatments), while MA cultivar did not receive any herbicides treatment, but a manure amendment was applied to the soil. For each orchard, 12 replicates (trees) were considered for analysis, all of them belonging to Picual variety. From each replicate and microhabitat, both bacterial and fungal communities were studied with the use of amplicon sequencing (paired-end 2x300-bp [PE 300] with the Illumina MiSeq platform). Raw reads were processed following our own tutorial, recently published in GitHub (<https://nuriaww.github.io/micro4all/>) and also available as an R package (micro4all). This tutorial includes analysis for ASV inferring with DADA2, α and β -diversity (index calculation, graphical representation and statistical analysis), differential abundance analysis with ANCOM-BC and taxonomical profiling (plots and tables). Moreover, microbial ecological networks were also studied with MENAP online tool. Our results showed that a higher fungal diversity was found in MA rhizosphere. However, no statistically significant differences were found for bacterial community at rhizosphere level, neither for fungal or bacterial endosphere community. Interestingly, community structure (β -diversity) seemed to differ for both microhabitats (rhizosphere and root endosphere) and kingdoms (bacteria and fungi). Furthermore, network analysis showed that in both compartments TM microbial communities had closer interactions (i.e., a shorter geodesic distance) as well as a greater percentage of positive links. Regarding taxonomical profiles, it should be highlighted that endosphere microbial communities were dominated by bacterial phylum Actinobacteria and fungal phylum Ascomycota. In fact, bacterial genus Actinophytocola alone represented a 20.20% (MA) and an 18.40% (TM) of the sequences. Our previous studies also showed the importance of this genus, as it is highly abundant in the olive endosphere across different environments.

POSTER 36 - Date palm (*Phoenix dactylifera*) root and bulk soil fungal communities are distinct and altered by salinity of irrigation water (Sunil Mundra) - SEE BRIEF TALKS