PLANT GENOTYPE, SOIL AND CLIMATE AS DRIVERS OF THE OLIVE MICROBIOME COMPOSITION

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INTRODUCTION

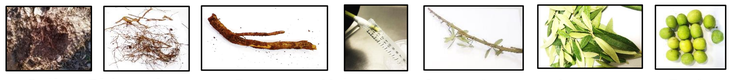
Unravelling the function and structure of microbial communities prevailing in soils and the endosphere of plants is essential to understand plant life cycle. Soil microorganisms play essential roles through the transformation of organic matter and mineral solubilisation and are also key determinants for supporting plant growth and health, since they act as a natural defense against soilborne plant pathogens. Understanding of the plant microbiome (microbial epiphytes and endophytes) is becoming of relevant importance for promoting plant health as it could include microbes that may protect against plant pathogens sharing same niches.

MATERIAL AND METHODS

Study area and collection samples

In this study, we sampled during Autumn 2018 and Spring 2019 the soil, rhizosphere, roots, xylem sap, stem tissues, leaf and fruits from three olive cultivars (Picual, Arbequina and Frantoio). Olive trees, originally propagated from same mother plants and hypothetically sharing same microbiome within each plant genotype, were transplanted in three field plots located in Baena, Antequera and Úbeda, in Andalusia, Southern Spain. The three locations differ in physicochemical soil characteristics and climate.

Plant niches sampled



Soil Rhizosphere Roots Xylem sap Stem tissues Leaves Fruits

DNA extraction, PCR library and bioinformatics

Fungal populations were analyzed using the Illumina MiSeq platform to determine the structure and diversity of olive microbial communities, and to estimate the principles governing their assemblages and dynamics (plant genotype, plant niche, soil physicochemical properties, climate or seasonality).

ACKNOWLEDGMENTS

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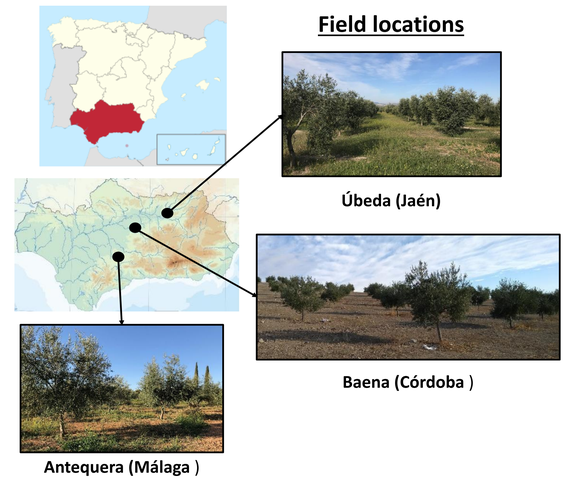
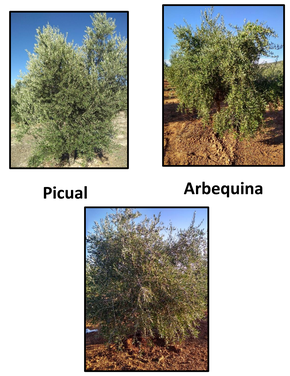
Andalusía (South of Spain)



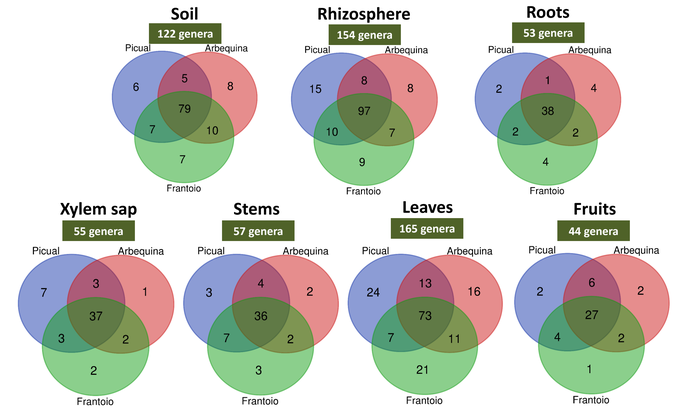
RESULTS

Olive plant genotypes

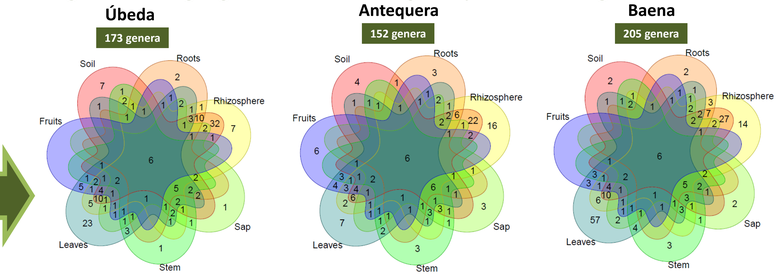


Leaves showed the highest fungal diverity (165), followed by rhizosphere (154), soil (122), stems (57), xylem sap (55), roots (53) and fruits (44). The rhizosphere displayed the greatest number of fungal genera shared (core microbiome: 97) among the olive genotypes (Picual, Arbequina and Frantoio) while fruits displayed the lowest (core microbiome: 27). Baena displayed the highest diversity of fungal genera (205), followed by Úbeda (173) and Antequera (152). Considering all samples collected in Úbeda, Baena and Antequera, six genera (*Alternaria*, *Aureobasidium*, *Filobasidium*, *Malassezia*, *Mycosphaerella* and *Vishniacozyma*) formed the core fungal microbiome of olive trees.

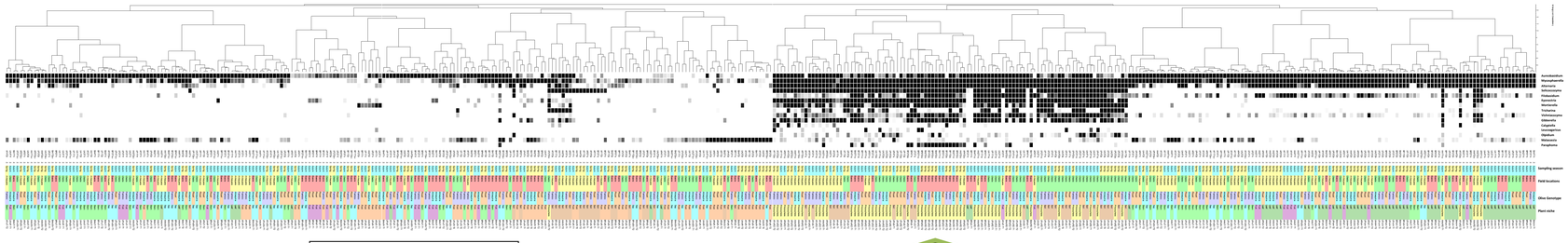
Venn diagram of unique and shared fungal genera among olive genotypes according to the plant niche



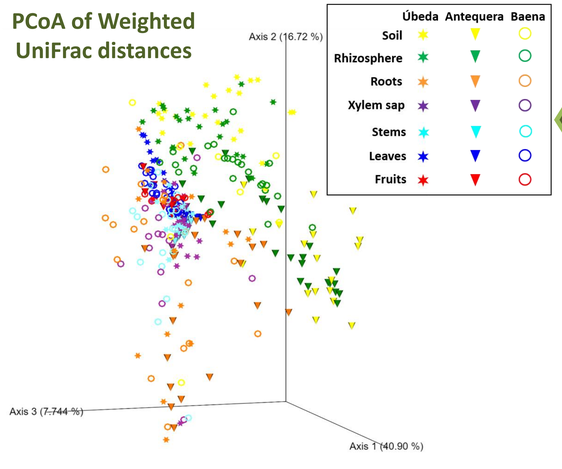
Venn diagram of fungal genera of collecting samples according to field locations



Heatmap hierarchical clustering using Ward algorithm and Bray-Curtis distance



PCoA of Weighted UniFrac distances



Principal coordinate analysis of weighted UniFrac distances and cluster analysis indicated that main differences among fungal communities (measured as phylogenetic distances) were due to the olive plat niche [especially differentiating the below-ground (soil, rhizosphere, roots) from aboveground (xylem sap, stem tissues, leaves and fruits) samples] followed by the environment where the plants grow (field locations) with minor effect of olive cultivar or season (Autumn vs Spring).

CONCLUSIONS

Our results suggest that main differences in fungal communities on olive crops are mainly due to the plant niche and soil physicochemical and environmental conditions and depend to a lesser extent on plant genotype or season. This basic information can contribute to generate new knowledge that may contribute to control olive diseases or increase plant health by manipulating, inoculating or selecting highly-specific microbiomes, better adapted to specific genotypes of olive, or with the greatest potential to survive under different climatic conditions.