Soil physicochemical properties, seasonality, plant niche and plant genotype affect bacterial and fungal communities in olive orchard soils

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Introduction

Why olive tree?

Landscape conservation

Millenary cultivation

Soil fixation

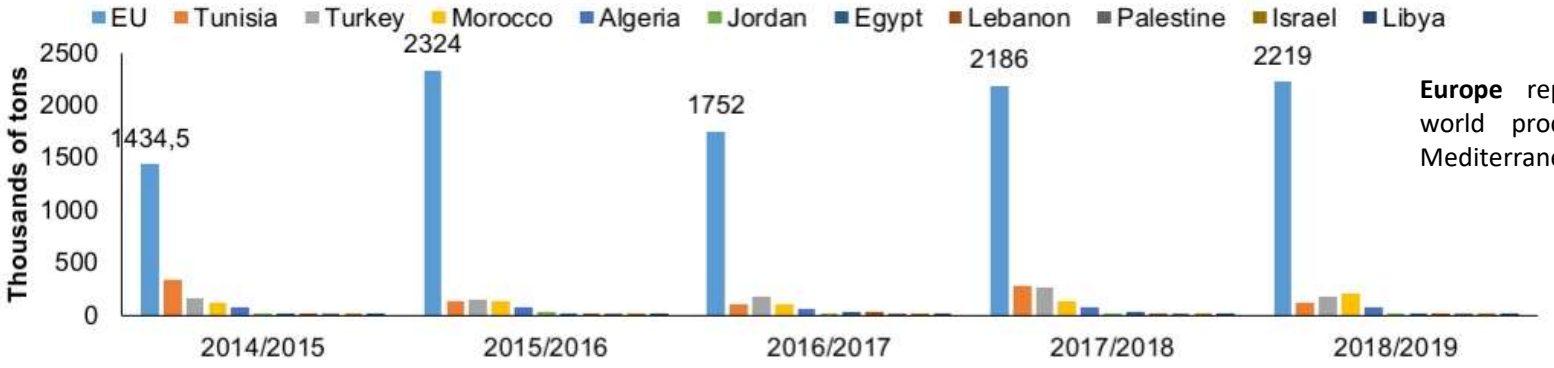
Ecology niche

Olive oil and table olive

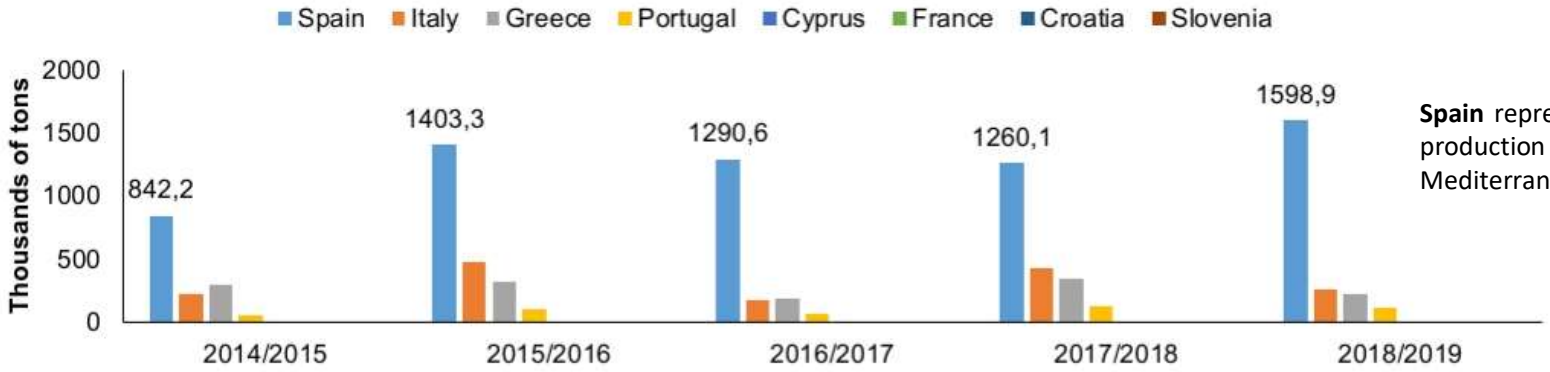
Landa et al. 2019, Gómez et al. 2016, Müller et al. 2015

Introduction

Olive oil production



Europe represents 70% of the world production and 75% of Mediterranean Basin production.



Spain represents 48% of the world production and 51% of Mediterranean Basin production.

(IOC, www.internationaloliveoil.org/; FAOSTATS,http://www.fao.org/faostat/)

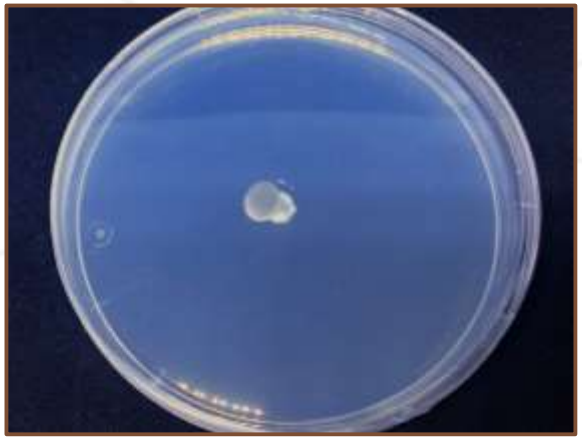
Introduction

Soil borne, xylem inhabiting pathogen

Verticillium dahliae → **Verticillium wilt**

Factors that influence the development of the disease:

- Plant age
- Soil humidity
- Soil and air temperature
- Crop management



Disease symptoms

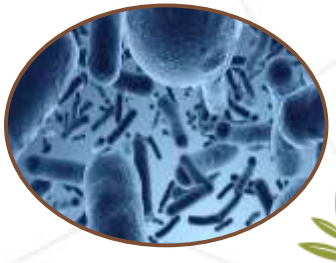
Jiménez-Díaz et al. 2011

Introduction

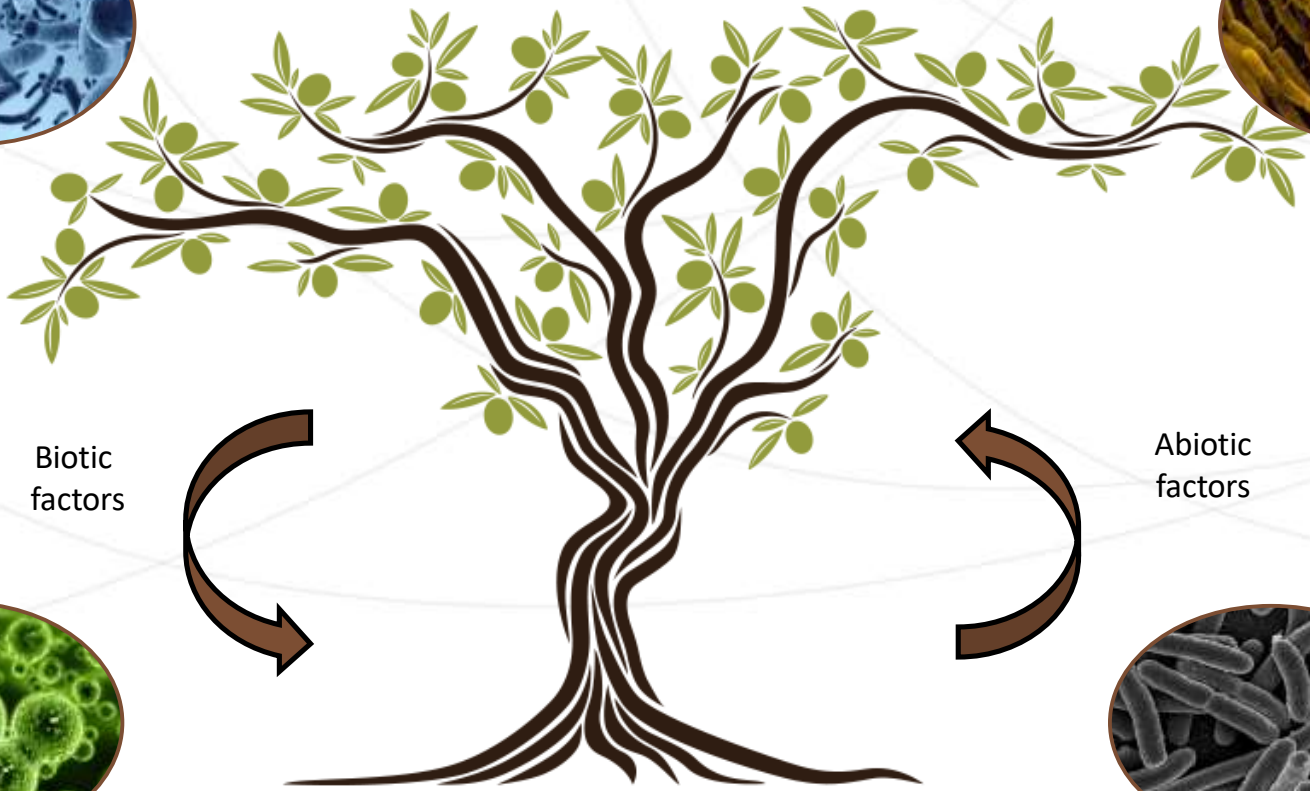
Olive microbiome

Berg et al. 2014; Turner et al. 2013

Introduction



Olive microbiome



Biotic factors

Abiotic factors

The olive xylelm microbiome can be used as a biocontrol strategy to mitigate or suppress the development of Verticillium wilt

Berg et al. 2014; Turner et al. 2013

Objective

To characterize the effect of soil physicochemical properties, seasonality, plant niche and plant genotype on the assemblages and shifts of the bacterial and fungal communities present in olive orchard soils located at Southern Spain

Methodology

Experimental design and sampling

'Cortijo Guadiana-Grupo Castillo de Canena'
(Úbeda, Jaén, Spain)

Picual

Arbequina

Frantoio

Selection of 4 trees per genotype.

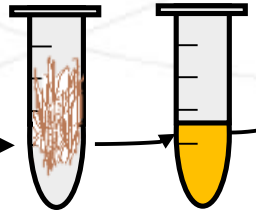
Autumn 2018 / Spring 2019

Samples of root, rhizosphere and soil.

Methodology

Next generation sequencing (NGS)

Sample treatment



DNA extraction

16S and ITS libraries

Sequencing

illumina

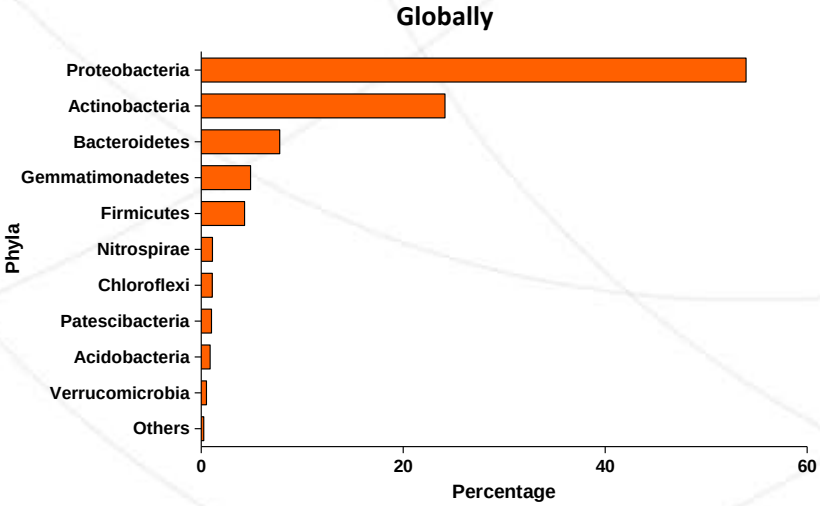
Bioinformatic ans statistical analysis

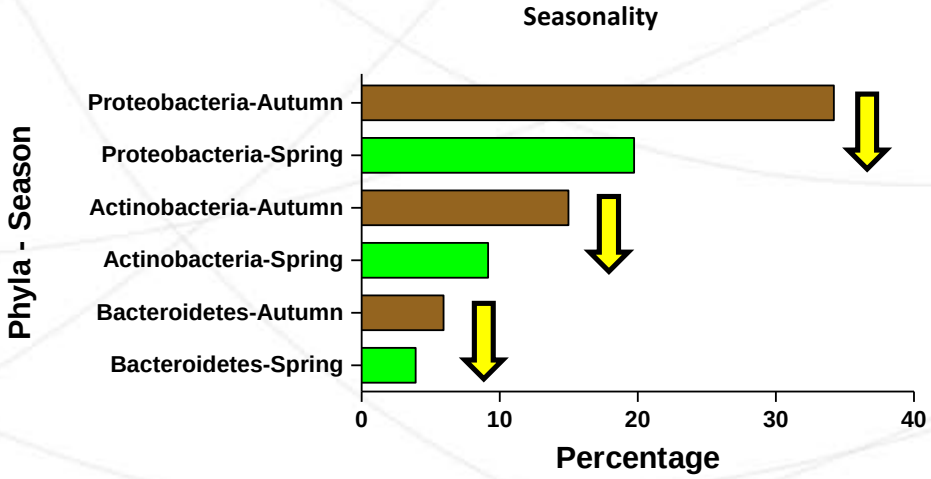
Linux

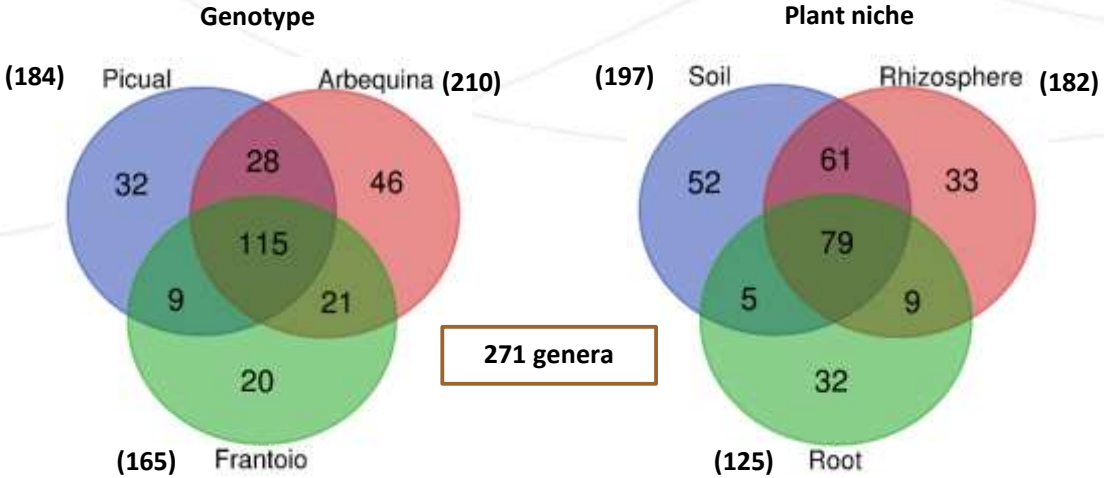
qiime2

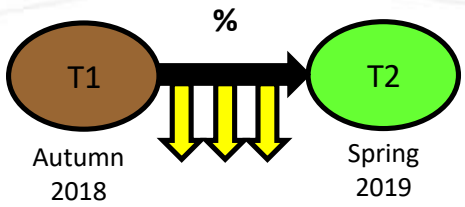
R

16S - Taxonomic affiliation

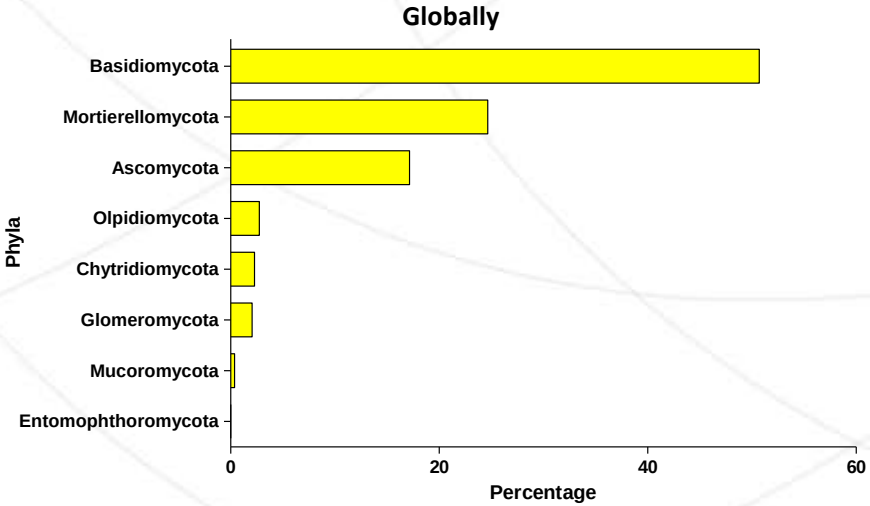


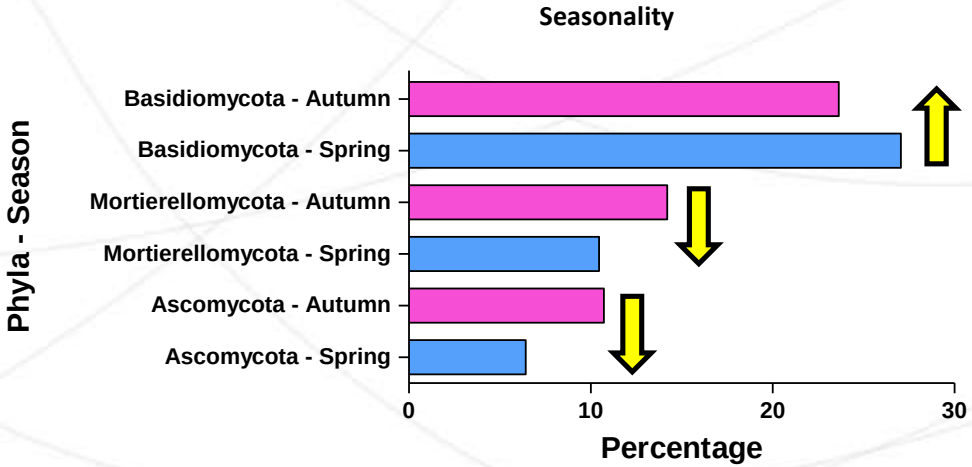


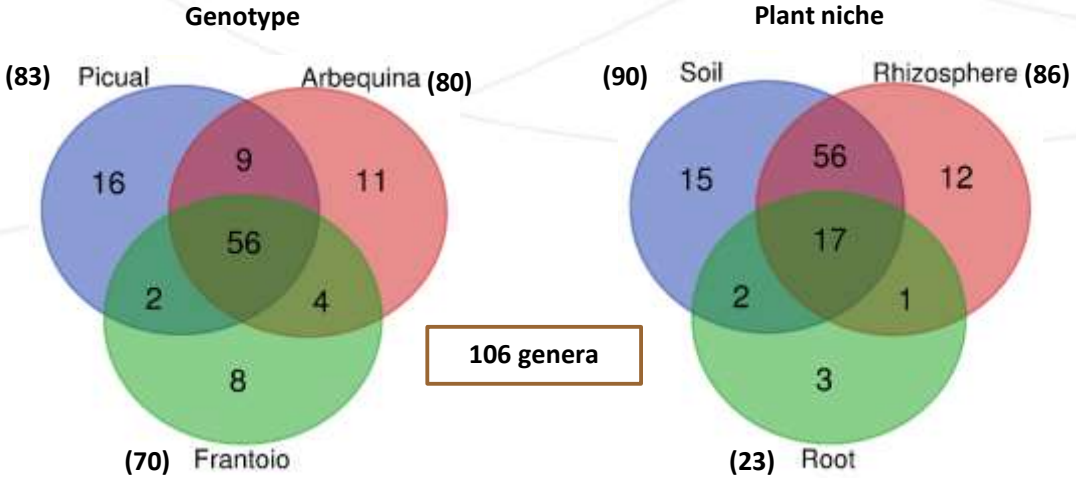


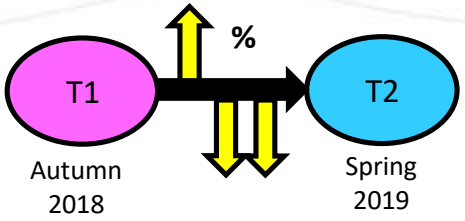


ITS - Taxonomic affiliation









Soil Physicochemical Properties

Soil quality parameters measured:

pH, CE, OM, CaCO3, NO3, P, Ca, Mg, Na, K, Fe, Mn, Zn, Cu, C, N, S

Olive genotype

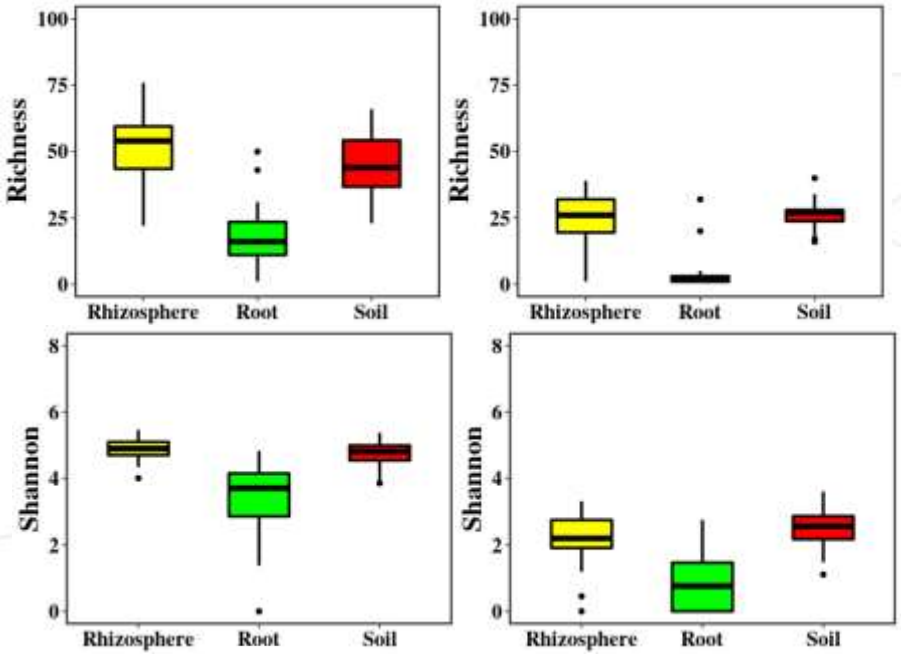
Season of sampling		Picual					Frantoio	
		OM	pH	NO_3	Mg	Na	Ca	Cu
Autumn 2018	T1	10,62	7,51	176,01	521,21	662,67	5140,01	9,38
ANOVA ✡		↓	↑	↓	↓	↓	↑	↓
Spring 2019	T2	8,30	7,71	115,58	432,62	498,67	5413,56	8,28

Data of elements and ions in mg/Kg
Data of OM in %

Alpha diversity indices

Plant niche

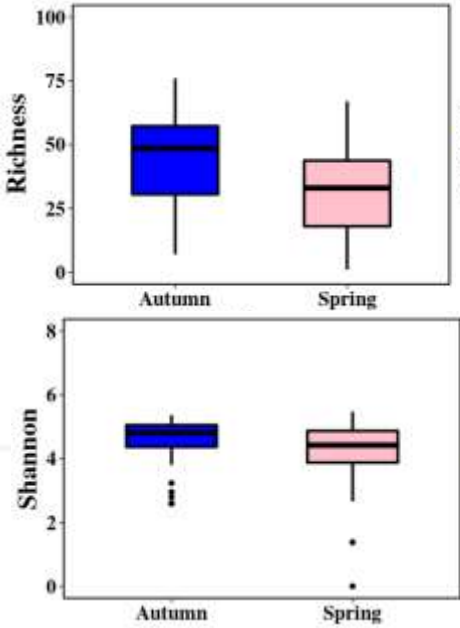
Bacteria – 16S



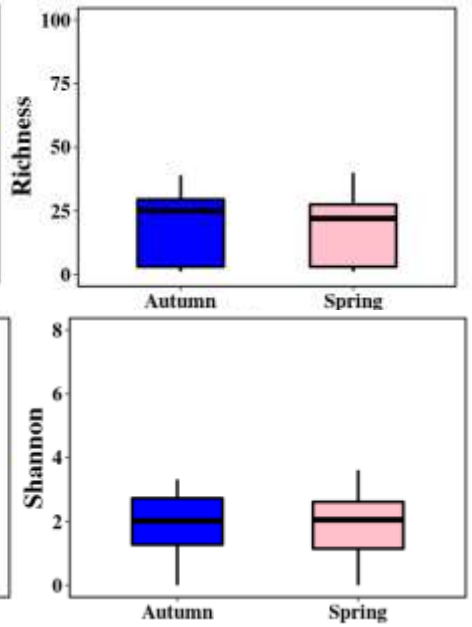
Fungi – ITS

Season

Bacteria – 16S

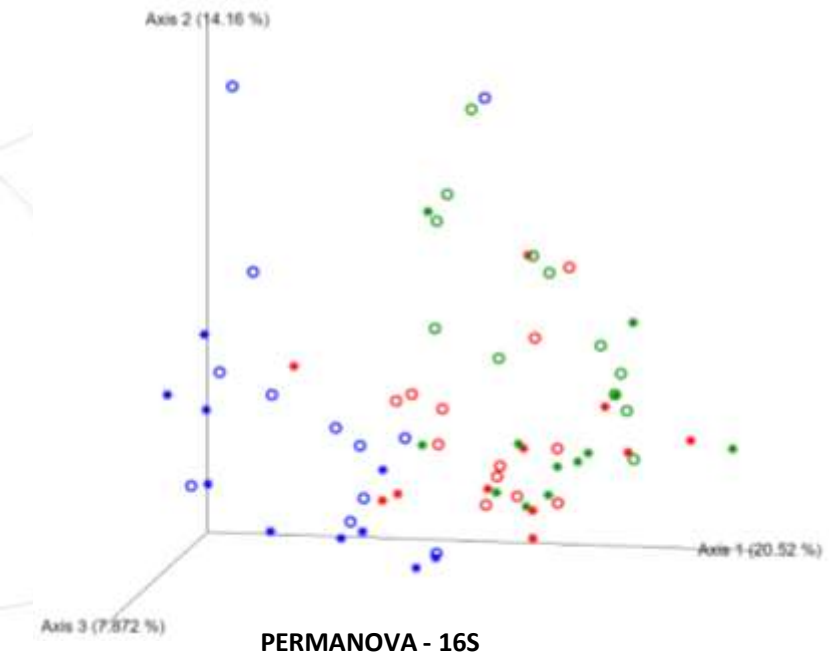


Fungi – ITS

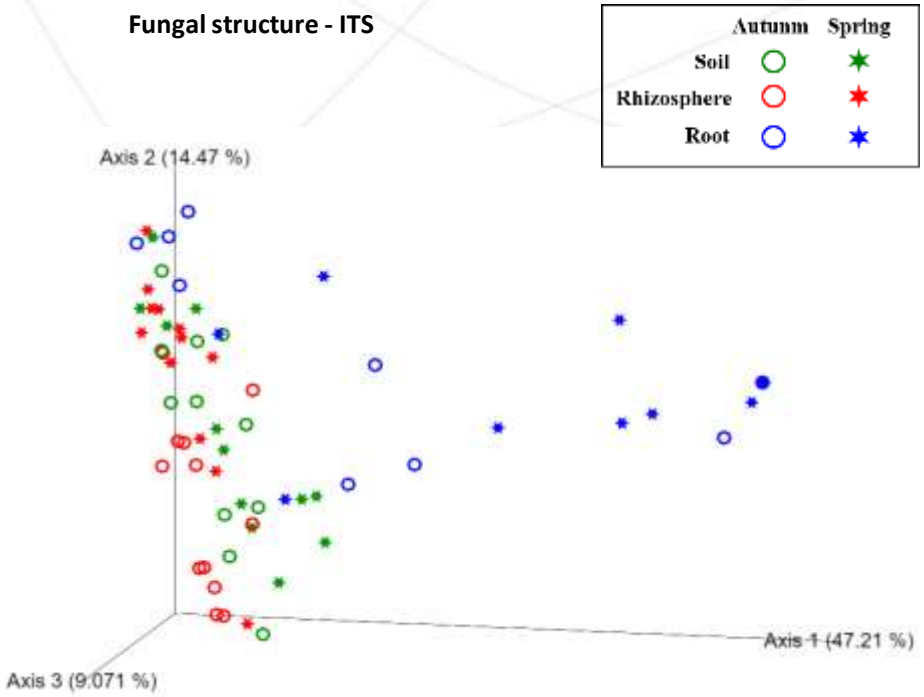


Principal coordinate analysis of weighted UniFrac distances

Bacterial structure – 16S



Fungal structure - ITS



PERMANOVA - 16S

Olive plant niche (*pseudo-F*=7.83; *P* < 0.001)	✓
Season of sampling (*pseudo-F*=2.48; P < 0.01)	✓
Olive genotype (*pseudo-F=1.04; P < 0.41*)	✗

PERMANOVA - ITS

Olive plant niche (*pseudo-F*=15.29; *P* < 0.001)	✓
Season of sampling (*pseudo-F*=1.59; P < 0.17)	✗
Olive genotype (*pseudo-F=0.81; P < 0.59*)	✗

Conclusions

1. Bacterial communities showed higher values of alpha diversity as compared to fungal communities in soil, rhizosphere and roots of olive trees.

2. Microbial communities varied mainly according to the plant niche, with the olive rhizosphere showing the greatest diversity of taxa, followed by soil under the influenced of roots, with the lower diversity being found in roots

3. Fungal communities were less affected to environmental changes due to seasonality while bacterial populations resulted significantly affected.

4. Plant host genotype had a minor effect in the microbiome composition, although each olive genotype presented differential microbial communities, which were also influenced by soil physicochemical properties.

Take home message

Plant niche and seasonality strongly affected the diversity and abundance distribution of microbial communities while olive genotype showed a relative minor role as driver of microbiome composition.

Thanks!

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