

Exploring the effect of plant variety and developmental stage on the composition and diversity of the olive tree microbiome

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INTRODUCTION

Plant - associated microbial communities are key determinants of plant health and productivity, which may aid in nutrient availability and uptake, enhanced tolerance to abiotic and biotic stress, and increased biodiversity. Olive (*Olea europaea* L.) represents a hallmark crop of the Mediterranean basin, accounting for 95 % of the cultivated olive area worldwide. Although several studies investigated the microbiome of olive trees, we lack a holistic view of its microbiome in the different plant compartments, its seasonal patterns along the growing season and the occurrence of a core microbiome. In this work, we determined the prokaryotic, fungal and arbuscular mycorrhizal fungal (AMF) microbiome in below- (rhizosphere soil, roots) and above-ground (phyllosphere and carposphere) plant parts of two selected Greek olive varieties in five developmental stages along a full fruit-bearing season, using amplicon sequencing.

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METHODOLOGY

To address this aim, we followed two sampling strategies: (i) to determine whether the above- and below-ground plant compartments support distinct microbial (bacteria, fungi, arbuscular mycorrhizal fungi - AMF) communities and (ii) to address whether the microbiome of the different plant compartments exhibits different seasonal patterns along the olive tree fruit-bearing period season. In both cases, the samples (rhizosphere soil, roots, leaves and fruits) were derived from two emblematic Greek varieties cultivated at two experimental fields located in Crete ('Koroneiki') and Thessaloniki ('Chondrolia Chalkidikis'). Samples were collected at five selected developmental stages along the growing season. The microbiome diversity was determined by amplicon sequencing of the 16S rRNA gene (bacteria), ITS2 region (fungi) via Illumina HiSeq 2x250 bp paired-end analysis and of the

small ribosomal subunit (AMF) via Illumina Miseq 2x300 bp paired-end analysis. Results will be presented and discussed at the conference.

RESULTS

Our analysis verified that the above- (phyllosphere, carposphere) and below-ground (soil, roots) plant parts supported distinct microbial communities. In both varieties the rhizosphere and the above-ground plant microbiome were prone to seasonal changes related to the plant developmental stage, in contrast to a seasonally stable root microbiome. We noted that olive roots exhibited an AMF-specific (not relevant for bacteria and fungi) filtering effect onto the rhizosphere AMF communities of the two olive varieties, leading to the assemblage of homogenous intraradical AMF communities.

DISCUSSION

Olive trees supported a distinct above- and below-ground shared microbiome, which encompass bacteria and fungi with functional attributes that might contribute to olive tree tolerance to abiotic and biotic stress.