

Bioinformatic pipelines are determinant in the analysis of microbial communities from different ecological niches in cultivated olive trees

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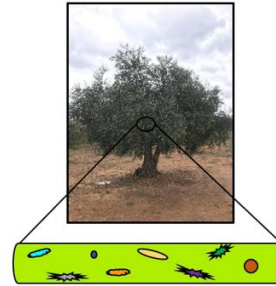
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Olive tree is one of the most important crop in the Mediterranean Basin. However, nowadays its viability is seriously threatened by plant pathogens such as *Verticillium dahliae* and *Xylella fastidiosa* which colonize the xylem vascular bundles and ultimately can cause the death of the olive tree.

Recent studies indicate that plant-associated microbial communities play an important role in controlling vascular wilt diseases and could form the basis of sustainable biocontrol strategies for crop production.

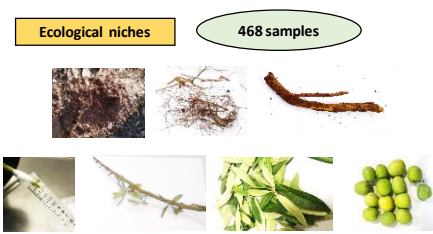
NGS approaches with advances in bioinformatics and statistical analyses represent valuable tools for characterizing the diversity of these plant-colonizing microorganisms



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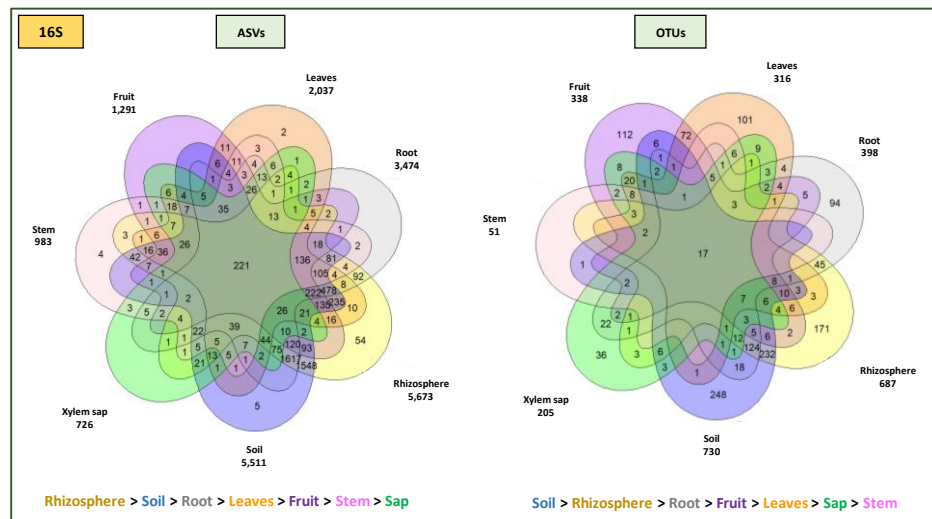
In this work, we deciphered the bacterial and fungal microbial communities from different olive ecological niches (soil, rhizosphere, root, xylem sap, stem, leaf and fruits) using distinct bioinformatics pipelines based on the identification of operational taxonomic units (OTUs) or amplicon sequence variants (ASVs).



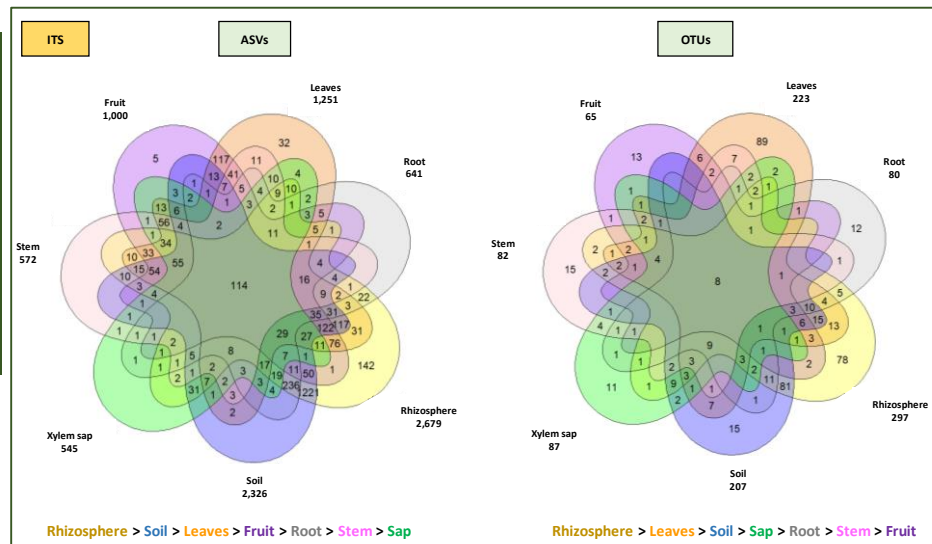
Ecological niches

468 samples

Sequence analysis reported a greater number of taxa using ASV-based pipeline (5.891 for bacteria and 3.055 for fungi) in contrast to the OTU-based pipeline (1.269 and 553, for bacteria and fungi, respectively). Interestingly, for the xylem, we estimated 726 ASV for bacteria and 545 ASV for fungi; whereas a much lower of OTUs was determined (i.e. 205 and 87, for bacteria and fungi, respectively).



Our results showed that bioinformatic pipelines may affect significantly the characterization of the plant-associated microbiome and highlight the importance of standardizing the computational methods for downstream analysis of NGS data, especially when searching for potential microbial taxa associated to suppression of vascular plant pathogens.



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