

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

Manuel Anguita-Maeso¹, Luis F. Arias-Giraldo¹, Juan A. Navas-Cortés¹, Alexandre de Menezes², Blanca B. Landa¹

¹ Institute for Sustainable Agriculture, Spanish National Research Council, Córdoba, Spain

² Ryan Institute, School of Natural Sciences, National University of Ireland, Galway, Ireland

Olive tree is one of the most important crops 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 indicated 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 which will lead to a better understanding of their interactions. 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). 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). Rhizosphere was the plant niche with the highest number of ASV for bacteria (5.662), whereas soil was the niche showing highest number when using the OTU pipeline (730). Interestingly, for the xylem, we estimated 689 and 2647 ASV for bacteria and fungi, respectively; whereas a much lower of OTUs was determined (i.e., 205 and 101, 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.

Study supported by Projects XF-ACTORS 727987 (EU-H2020), AGL2016-75606-R (MICINN Spain and FEDER-EU) and COST Action CA16107 EuroXanth.