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Characterization of Soil Microbial Communities from Vineyard under a Spectrum of Drought Pressures in Sensitive Area of Mediterranean Region

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Abstract : Global warming, with rapid and sudden changes in meteorological conditions, is one of the major constraints to ensuring agricultural and crop resilience in the Mediterranean regions. Several strategies are being adopted to reduce the pressure of drought stress on grapevines at regional and local scales: improvements in the irrigation systems, adoption of interline cover crops, and adaptation of pruning techniques. However, still, more can be achieved if also microbial compartments associated with plants are considered in crop management. It is known that the microbial community change according to several factors such as latitude, plant variety, age, rootstock, soil composition and agricultural management system. Considering the increasing pressure of the biotic and abiotic stresses, it is of utmost necessity to also evaluate the effects of drought on the microbiome associated with the grapevine, which is a commercially important crop worldwide. In this study, we characterize the diversity and the structure of the microbial community under three long-term irrigation levels (100% ETc, 50% ETc and rain-fed) in a drought-tolerant grapevine cultivar present worldwide, Syrah. To avoid the limitations of culture-dependent methods, amplicon sequencing with target primers for bacteria and fungi was applied to the same soil samples. The use of the DNeasy PowerSoil (Qiagen) extraction kit required further optimization with the use of lytic enzymes and heating steps to improve DNA yield and quality systematically across biological treatments. Target regions (16S rRNA and ITS genes) of our samples are being sequenced with Illumina technology. With bioinformatic pipelines, it will be possible to obtain a characterization of the bacterial and fungal diversity, structure and composition. Further, the microbial communities will be assessed for their functional activity, which remains an important metric considering the strong inter-kingdom interactions existing between plants and their associated microbiome. The results of this study will lay the basis for biotechnological applications: in combination with the establishment of a bacterial library, it will be possible to explore the possibility of testing synthetic microbial communities to support plant resistance to water scarcity.

Keywords : microbiome, metabarcoding, soil, vinegrape, syrah, global warming, crop sustainability
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