

Food System Microbiomes 2024 International Conference

Session: MICROBIOMES MITIGATING BIOTIC AND ABIOTIC STRESS

Title: Unveiling the Microbial Players: Metagenomic Insights into Olive Varieties' Response to Drought

Authors: *Visca A.*^{1,*}, *Bevivino A.*¹, *Clagnan E.*¹, *Costanzo M.*¹, *Di Gregorio L.*¹, *Baldoni L.*², *Perrotta G.*¹

¹ENEA, Italian National Agency for New Technologies, Energy and Sustainable Economic Development, Department for Sustainability, Rome, Italy

²Institute of Biosciences and Bioresources, Italian National Research Council, 06128 Perugia, Italy

*presenting author: andrea.visca@enea.it

The worldwide rise in water scarcity poses a significant challenge to maintaining crop productivity. Insufficient water leads to the deterioration of the photosynthetic machinery, disruptions in crucial metabolic pathways, heightened production of free radicals, and a weakening of plant root architecture. Drought stands out as a primary stressor directly impacting the osmotic balance of plant cells. In the context of the BIOMEnext Project, the implementation of innovative, composite and eco-friendly farming systems, in order to enhance the resilience of Mediterranean fruit farming to climate change, has been evaluated. In particular, metagenomic analyses, characterization of the core rhizosphere and endophytes microbiomes and their predicted functions on four olive variety (*Arbequina*, *Chemlal*, *Koroneiki* and *Shengeh*) growth on wet and dry condition in a one-year field experiment was performed. The DNA from both root endophytes and soil rhizosphere was extracted and sequenced using the Oxford Nanopore technology, producing long reads of the gene *16S rRNA*. The long reads made it possible to identify the microbial composition at specie level using the Emu tool. Moreover, a novel tool has been developed to perform the functional annotation using PICRUST2 with long reads. Interestingly, up to 2752 different microbial species were found in rhizosphere and root endophyte samples. The most abundant ones were *Vicinamibacter silvestris*, *Microbunus phosphovorus* and *Microvirga tunisiensis*, which are known to be typical root nodule symbiotic bacteria of subtropical savannah soils, able to accumulate polyphosphate. These findings lay the groundwork for addressing the issue of drought in arid and semi-arid regions, utilizing natural solutions such as selected microbial consortia enriched with indigenous strains capable of tolerating extreme drought conditions and still providing benefits to plants.

Acknowledgments. This project has received funding from the European Union (project BIOMEnext) under the Grant Agreement no. 101102316.