

FROM SOIL MICROBIOME TO GRAPEVINE ROOT TRANSCRIPTOME: AN INTEGRATIVE STUDY OF PLANT-MICROBE INTERACTIONS

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The study of plant-microbe interactions has gained significant attention in recent years, particularly in the context of sustainable agriculture and climate change adaptation. Understanding the complex interplay between plants, soil, and their associated microbiomes is key to harnessing the potential of these relationships for improved crop production and environmental sustainability. In this context, *Vitis vinifera* presents an excellent model system to investigate the interaction of the soil microbial community with plant responses. Grapevine is not only a globally important economic crop, but also displays an intriguing relationship with soil microbial community, displaying a wide range of interactions with beneficial and detrimental microorganisms, making it an ideal candidate to study plant-soil-microbiome relationships. Here we present a focus on the root transcriptome-soil microbiome interaction in the context of the research project "Intevine", an interdisciplinary work with the aim of shedding light on the intricate relationships between soil, grapevines, and the soil microbiome.

To investigate this relationship, one-year-old grapevines were grown in individual pots in an experimental tunnel, with three sources of

variability considered: soil type, soil sterilization, and roots heat treatment. The plants were grown in three different soil types with distinct chemo-physical properties and organic matter content: sand, peat, and a peat-manure mixture. Soil sterilization and root heat treatment were employed to evaluate the impact of pre-existing microbial populations. After one year, leaf, root, bulk soil, and rhizosphere soil samples were collected. We adopted a multiomics approach, including leaf ionomics, multispectral imaging, rhizosphere metagenomics (16s and ITS), root transcriptomics, and soil chemistry. A comprehensive bioinformatics analysis was conducted using advanced tools to classify reads and integrate data.

Our initial findings revealed several associations between the root transcriptome and the rhizosphere microbiome. Using weighted gene correlation network analysis, we identified clusters of highly correlated genes that showed significant correlations with the bacterial relative abundance at the phylum, genus, and species levels. These results suggest a mutual impact between the plant and the microbiome. We are further investigating these correlations to highlight microorganisms and genes of agricultural interest.

Our observations have highlighted that the rhizosphere microbiome composition and root transcriptomic data are influenced by the soil type and are correlated with the leaf ionomics and soil chemistry analysis. Building on these findings, we plan to perform an integrated analysis to explore whether the combination of microbiome and transcriptome data can be linked to other analyses, such as leaf ionomics and multispectral imaging, which may provide insights into the plant's health status.