

## Roots and rhizosphere microbiota diversity is influenced by rootstock and scion genotypes: can this be linked to the development of the grafted plant?

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### Abstract

Soil is a reservoir of microorganisms playing important roles in biogeochemical cycles and interacting with plants whether in the rhizosphere or in the root endosphere. Through rhizodeposition, plants regulate their associated microbiome composition depending on the environment and plant factors, including genotypes. Since the phylloxera crisis, *Vitis vinifera* cultivars are mainly grafted onto American *Vitis* hybrids. Rootstocks play a pivotal role in the grapevine development, as the interface between the scion and the soil. Our work was carried out in the GreffAdapt plot, a unique experimental vineyard, including 55 rootstocks grafted with five different scions. Roots and rhizospheres from ten scion x rootstock combinations were collected in May 2021. Rhizosphere bacteria and fungi were quantified using cultivable approaches and qPCR. The communities of bacteria, fungi, and arbuscular mycorrhizal fungi in the rhizosphere and the roots were analyzed by Illumina sequencing of 16S rRNA gene, ITS and 28S rRNA gene, respectively. Our results highlight that both rootstock and scion genotypes influence the community structure in the rhizosphere and root compartments. The metabarcoding approach shows dissimilarities among bacterial and fungal communities depending on the rootstock or the scion genotype, suggesting that the two partners influence the microbial composition of the rhizosphere and the roots, as well as the putative functions of the microbiome (inferred using Picrust2 and FUNGuild). Finally, the roles of the microbiome in plant development and adaptation will be discussed by correlating its composition with plant phenotypic traits, as well as nutrient content of petioles and roots.

**Keywords:** grapevine, root system, metabarcoding, PICRUST2, FUNGuild