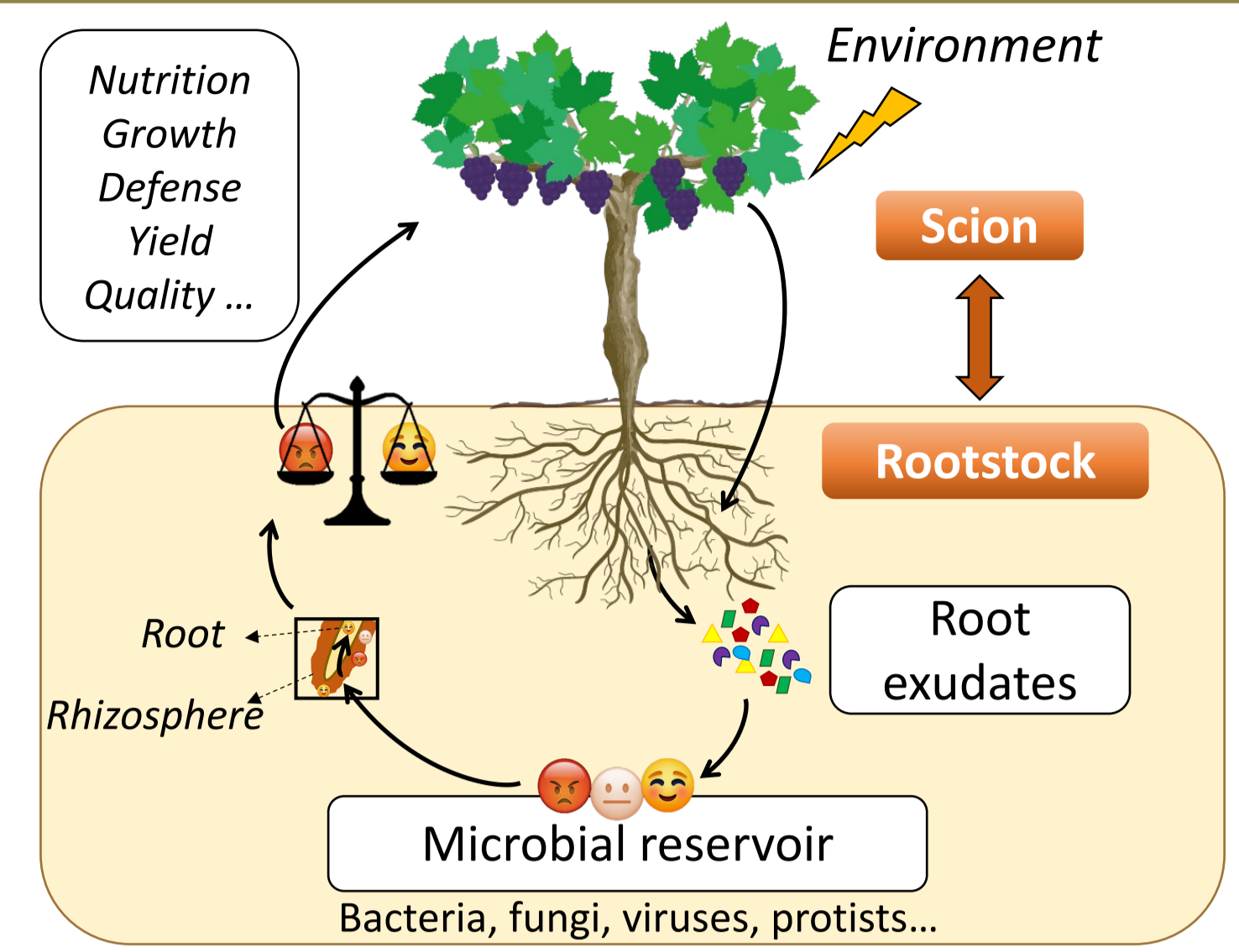


Vincent Lailheugue, Romain Darriaut, Ulysse Tuquoi, Tania Marzari, Joseph Tran, Elisa Marguerit and Virginie Lauvergeat
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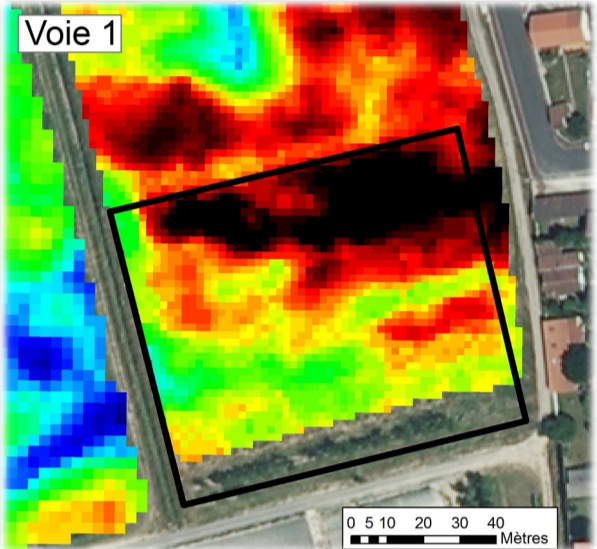
Grapevine interacts with soil microorganisms

Soil is a reservoir of microorganisms playing important roles in biogeochemical cycles and in interactions with plants in the rhizosphere (Darriaut et al., 2022). The rhizosphere is the volume of soil that sticks to the roots, which influences its biology and chemistry. The rhizosphere is the gateway of various microorganisms in the root endosphere. In both compartments, microbial communities impact the plant health. For example, arbuscular mycorrhizal fungi improve grapevine growth and tolerance to biotic and abiotic stresses (Trouvelot et al., 2015). Rhizodeposits (such as sugar, organic and amino acids, secondary metabolites, dead root cells ...) are released by the roots and influence the community of rhizospheric microorganisms. They act as signaling compounds or carbon sources for microbes. Root exudates composition depends on several factors including genotype. Recent studies showed that grapevine rootstock-scion combination regulates the bacterial and fungal microbiomes in the rhizosphere and the root endosphere (Marasco et al., 2022; Vink et al., 2021). The molecular mechanisms involved in this regulation are still misunderstood as well as the impact of microbiomes composition on grapevine health. The aim of this study is to understand the effects of rootstock and scion genotypes on rhizosphere and root endophyte microbiomes. Correlation between microbiomes composition and phenotypic data (plant vigor, berry yield and mineral nutrition) will be explored in order to better understand the relation between the microbiomes and plants physiology.



GreffAdapt plot:

- 3 blocks according to the soil resistivity
- Annual phenotypic analysis on plants & yield



10 rootstock-scion combinations were studied:

- * 6 rootstocks grafted with the same scion → Rootstock impact on the microbiomes
- * 5 scions grafted on the same rootstock → Rootstock impact on the microbiomes

One combination is common!

Experimental design

Sampling in May 2021



3 roots samples with rhizosphere on 2 blocks for each combination at a depth of 20-30 cm in sterile condition



Roots with rhizosphere



Rhizosphere

Sterilized roots

Quantitative PCR (bacteria, fungi & archaea)

Cultivable approach (bacteria & fungi)

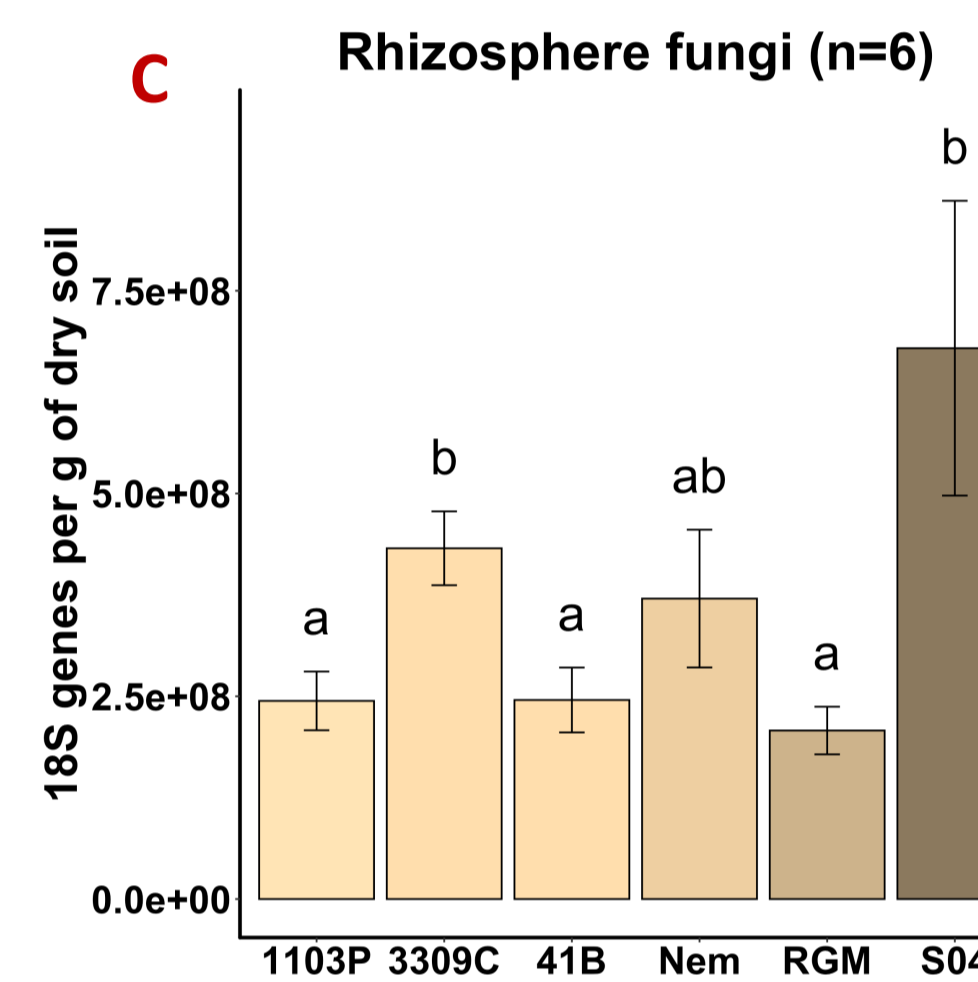
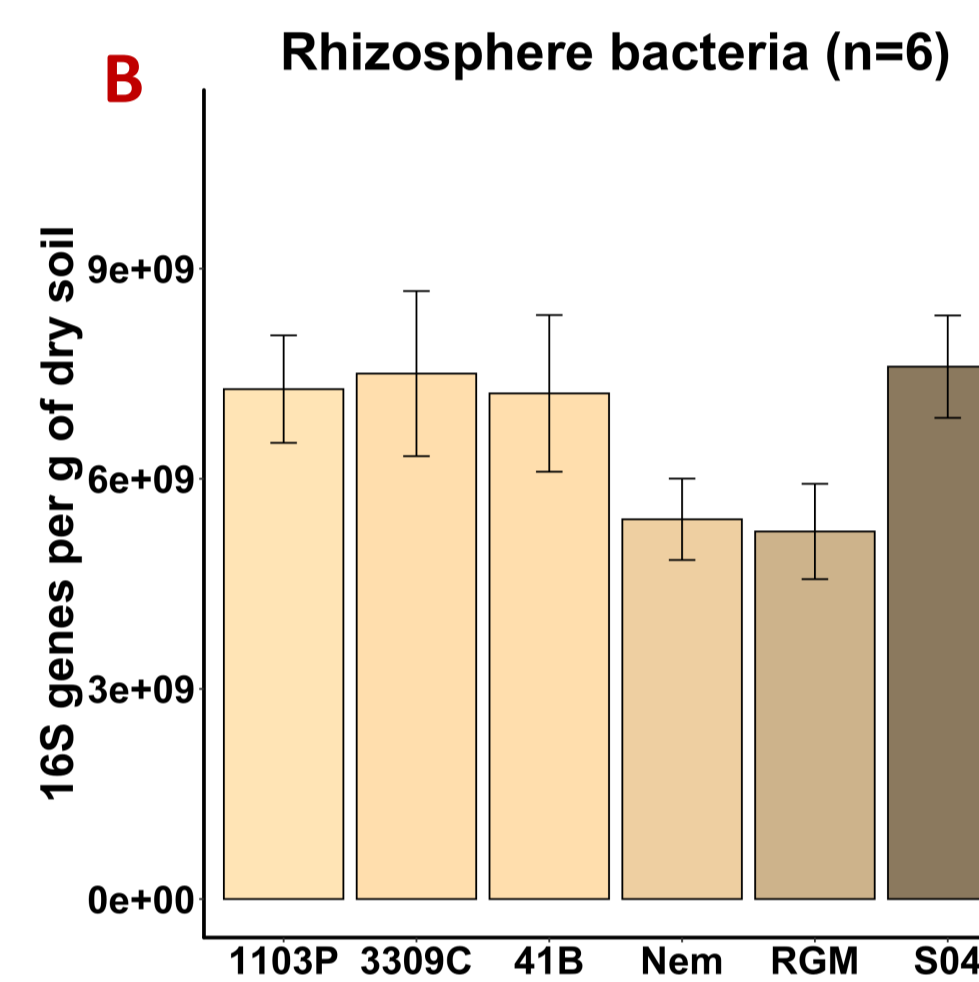
Targeted metagenomics:
- Bacteria: 16S rRNA gene
- Fungi: ITS region
- Arbuscular mycorrhizal fungi: 28S rRNA gene

Measurement of macro-/micro-elements

Effect of the rootstock genotype on the quantity of bacteria and fungi in the rhizosphere

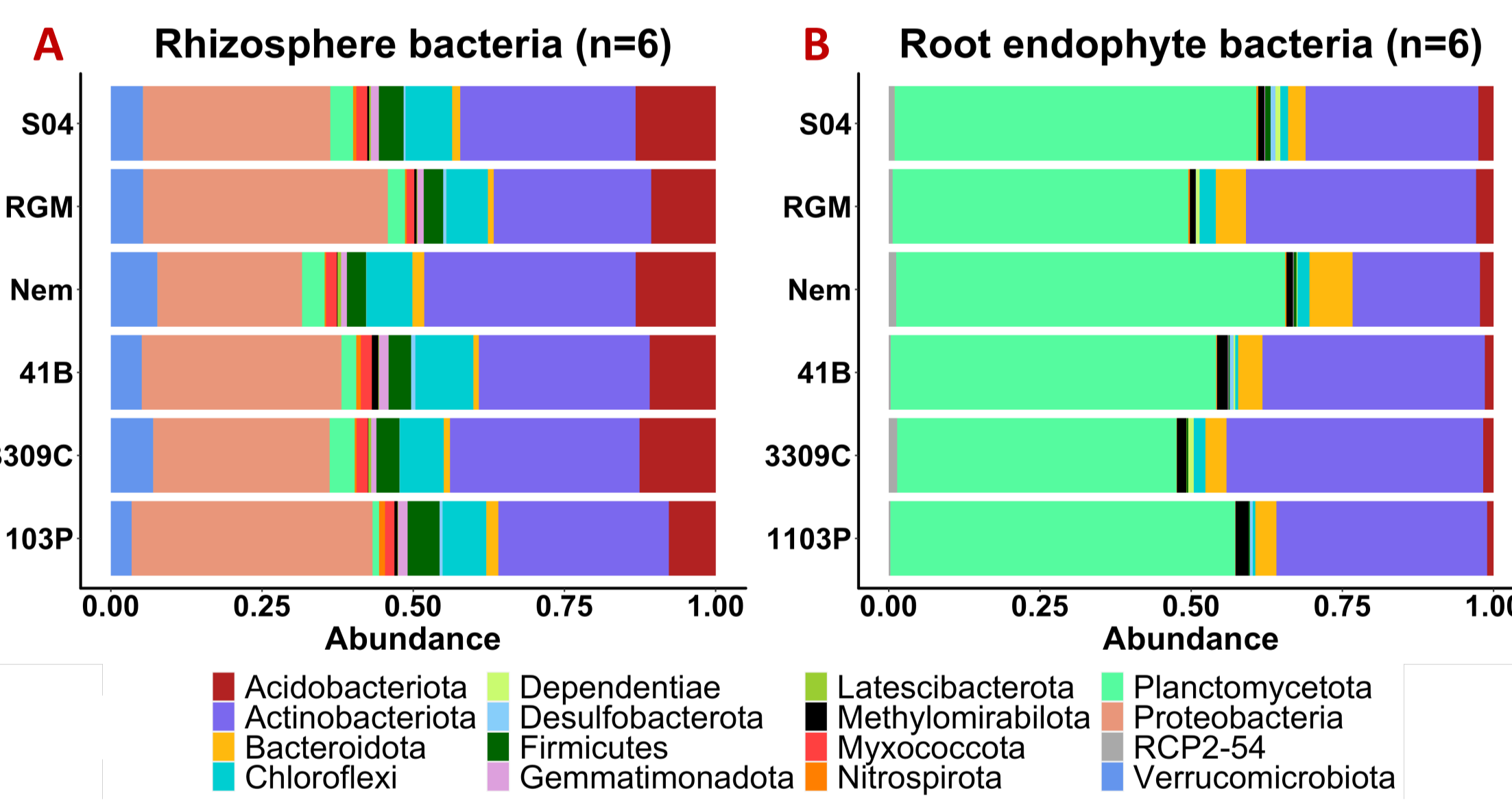
Fig.1: Rootstock effect on total bacteria and fungi measured by the cultivable and the qPCR approaches (A). n=3 individual plants. Results obtained by qPCR for the bacteria (B) and the fungi (C). Data are presented as means ±SE, n=6 individual plants. Letters indicate significant differences between genotypes as determined by Pairwise Wilcoxon Rank Sum Tests.

Test	Cultivable		qPCR	
	Bacteria	Fungi	Bacteria	Fungi
Rootstock (R)	ns	ns	ns	**
Block (B)	ns	ns	ns	ns
R x B	ns	ns	ns	ns

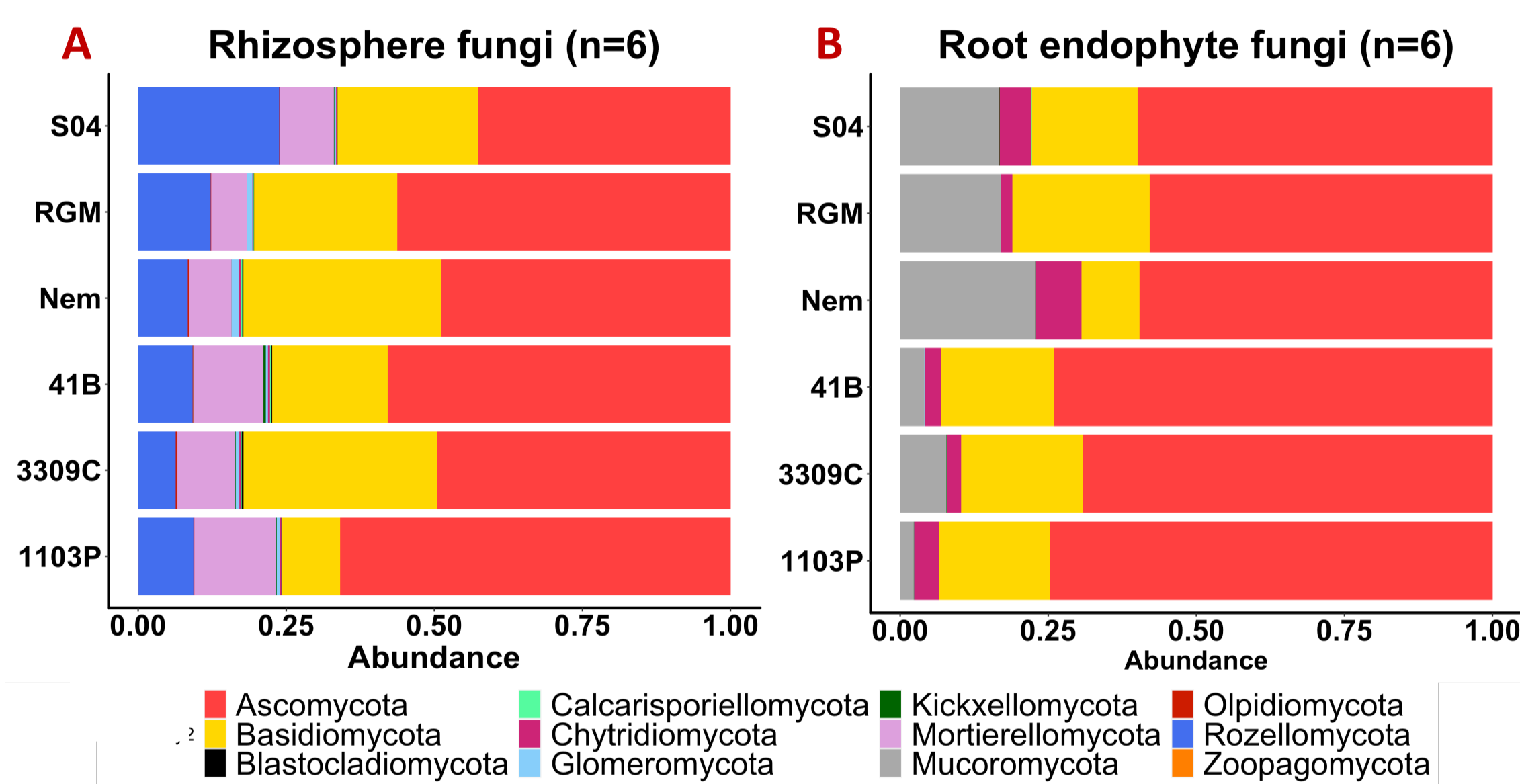


- * No effect of the rootstock on the amount of rhizospheric bacteria & fungi with the cultivable approach
- * Effect of the rootstock on the amount of fungi with the qPCR approach
- * S04 has the highest level of fungi in the rhizosphere

Effect of the rootstock on the proportion of bacterial and fungal phyla in the rhizosphere and the root endosphere



- * Rhizosphere: domination of proteobacteria & actinobacteriota, followed by acidobacteriota & chloroflexi
- * Roots: domination of planctomycetota, followed by actinobacteriota & bacteroidota
- * Proportion of bacterial phyla in both microbiomes differs between rootstock



- * Rhizosphere: domination of ascomycota, followed by basidiomycota, rozellomycota & mortierellomycota
- * Roots: domination of ascomycota, followed by basidiomycota, mucoromycota & chytridiomycota
- * Proportion of fungal phyla in both microbiomes differs between rootstock

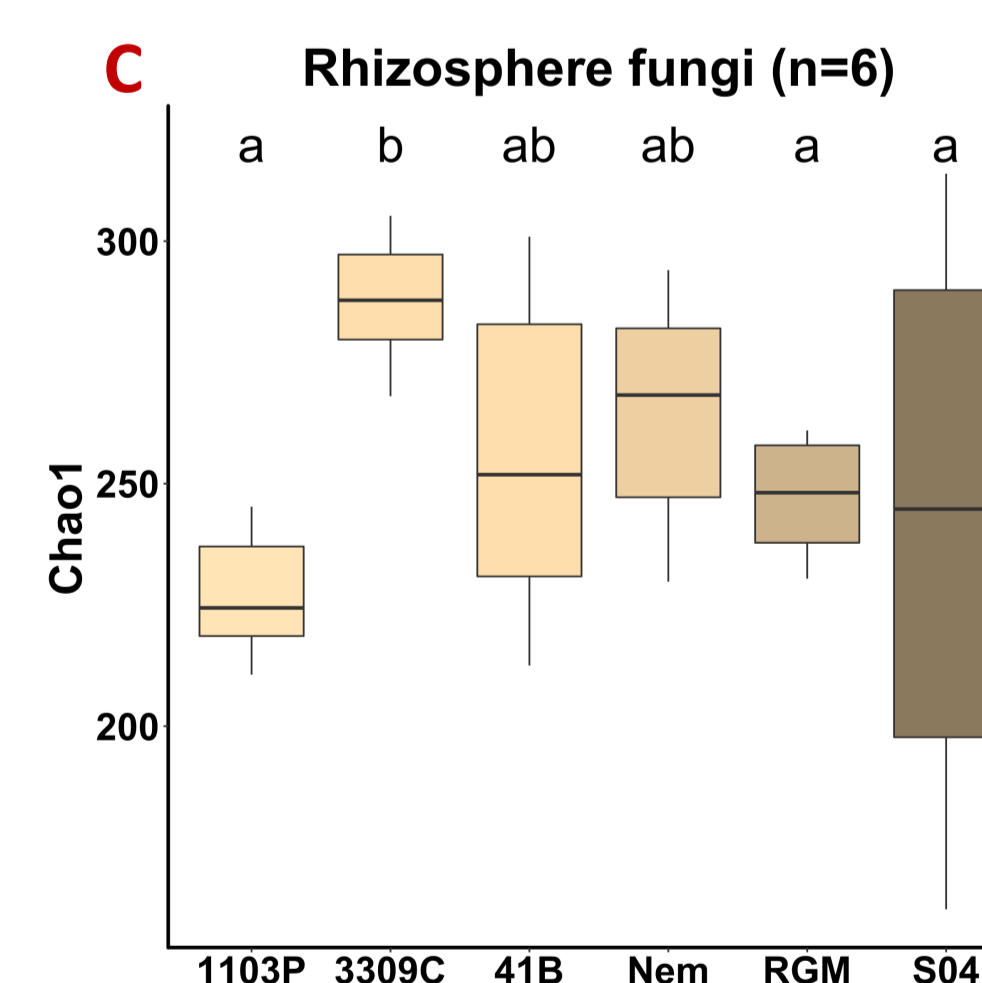
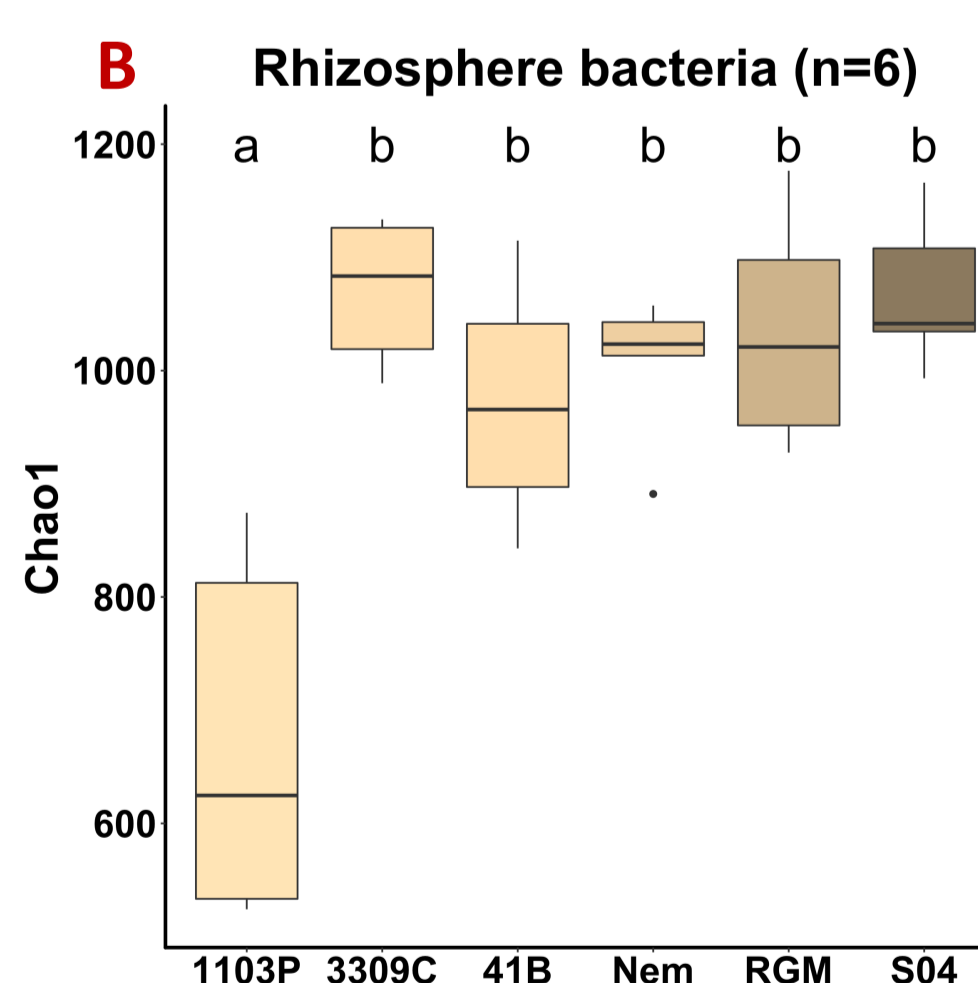
Effect of the rootstock genotype on the α-diversity of bacteria and fungi in the rhizosphere and the root endosphere

Chao1: Number of observed species (richness) + number of unobserved one (estimated)

Fig.4: Rootstock effect on the α-diversity of bacteria and fungi (A). n=3 individual plants. Comparison of Chao1 index for bacteria (B) and fungi (C) in the rhizosphere between rootstock genotype. Data are presented as means ±SE, n=6 individual plants. Letters indicate significant differences between genotypes as determined by Pairwise Wilcoxon Rank Sum Tests.

Test	Bacteria		Fungi	
	Rhizosphere	Roots	Rhizosphere	Roots
Rootstock (R)	***	ns	*	ns
Block (B)	ns	ns	ns	ns
R x B	***	*	ns	ns

- * Roots: no effect of the rootstock on the α-diversity of bacteria & fungi
- * Rhizosphere: effect of the rootstock on the α-diversity of bacteria & fungi



- * 1103P has the lowest α-diversity of bacteria in the rhizosphere
- * 3309C has a higher α-diversity of fungi than 1103P, RGM & S04

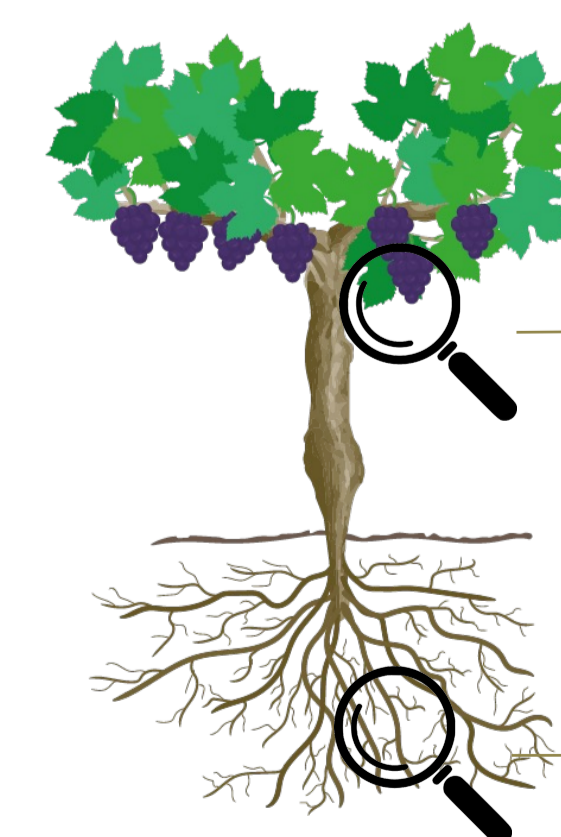
Effects of rootstock genotype on the rhizosphere and root endophyte microbiomes:

- Impact on the quantity of rhizospheric fungi but not on bacteria
- Impact on the proportion of bacterial and fungal phyla in both microbiomes
- Impact on α-diversity of bacteria and fungi in the rhizosphere but not in the roots

Conclusion and future directions

What is the contribution of the scion genotype ?

What is the influence of grapevine combination on the AMF?



Phenotypic analysis (vigor and yield) & Content of micro-/macro-elements

Microbiomes analyses

Data integration: Impacts of the microbiomes on plant health?

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