

Root-associated microbiome network connectivity and composition linked to disease resistance in strawberry plants

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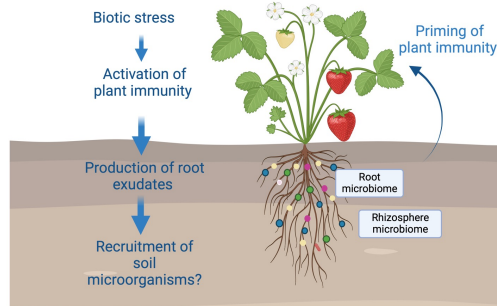
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Background

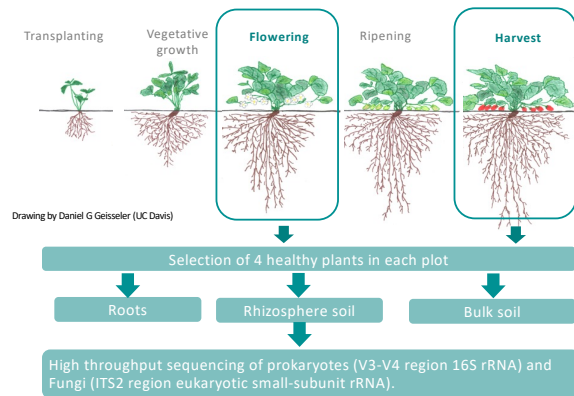
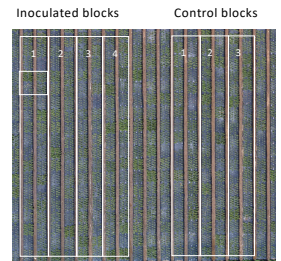
Plants are colonized by diverse and multi-kingdom microbial communities, collectively designated as the plant microbiome. Plant-microbiome interactions are essential for plant growth and overall health. Harnessing these interactions could be a path forward to expand sustainable agriculture. In strawberries, crop success is strongly impacted by soil-borne pathogens such as *Macrophomina phaseolina* which poses a serious threat to the industry. Recent research has identified commercial and experimental cultivars with various degrees of resistance to the pathogen. However, understanding of the mechanisms responsible for the resistance is still limited.



We hypothesized that the rhizosphere and the root microbiomes of resistant cultivars assemble distinct bacterial and fungal communities that foster microbial connectivity and mediate disease resistance.

Field experimental design

- One pathogen: *Macrophomina phaseolina*
- Three cultivars:
 - Manresa (resistant)
 - Marquis (resistant)
 - Sweet Ann (susceptible)
- 20 strawberry plants of the same cultivar per plot



1 Marked difference in alpha diversity between rhizosphere and roots, not between cultivars

Pathogen presence did not change soil, rhizosphere and root prokaryotic and fungal diversity

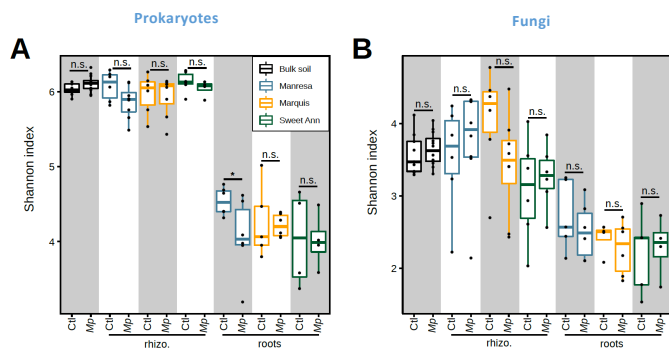


Figure 1. Box-plots depicting alpha-diversity (Shannon index) of the bacterial (A) and the fungal (B) communities associated with the bulk soil (black), root (blue) and rhizosphere (orange) of three strawberry cultivars. Overall, *M. phaseolina* does not have a significant impact on the diversity of bacterial and fungal communities associated to the bulk soil, the rhizosphere and roots of all tested strawberry cultivars. We note one exception of the root bacterial microbiome of Manresa that shows a decrease in diversity upon soil infestation by *M. phaseolina* (A, root, blue box-plots).

2 Differences in beta diversity between resistant and susceptible cultivars

Resistant cultivars assemble different root and rhizosphere microbiomes and respond to pathogen presence

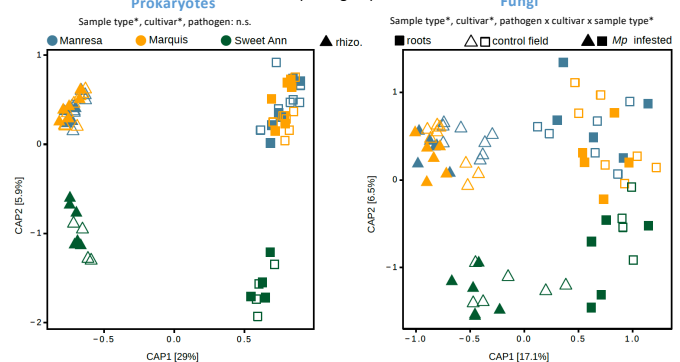


Figure 2. Constrained principal coordinates analysis of Bray-Curtis distances of bacterial and fungal communities associated to the rhizosphere (triangles) and root (squares) of the three strawberry cultivars, respectively. The rhizosphere and the root bacterial microbiomes of Sweet Ann were dissimilar from those of Manresa and Marquis. The rhizosphere fungal microbiome of Sweet Ann was different from Manresa and Marquis. Filled and unfilled shapes indicate *M. phaseolina* infested and control samples, respectively.

3 Differences in co-occurrence networks between susceptible and resistant cultivars

Sweet Ann showed lower connectivity, higher path length and higher modularity than Manresa and Marquis

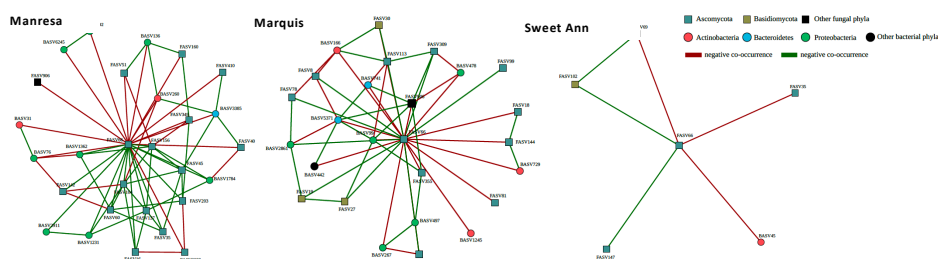


Figure 3. Microbial co-occurrence sub-networks of bacterial and fungal species that positively (green lines) or negatively (red lines) co-associate with *M. phaseolina* (FASV66) in Manresa, Marquis and Sweet Ann.

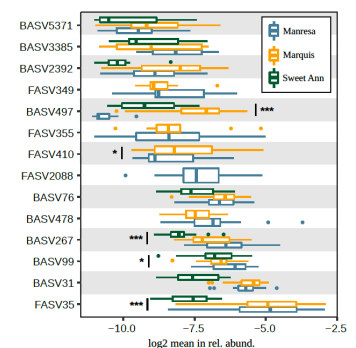


Figure 4. Log₂ mean in the relative abundance of bacterial and fungal ASVs that negatively co-associate with *M. phaseolina* in the sub-network of Manresa and/or Marquis. Significance within-group medians were tested using Kruskal-Wallis significance test and Conover's multiple comparisons tests.