Exploring host-bacteriome interactions in the sunflower/Verticillium pathosystem

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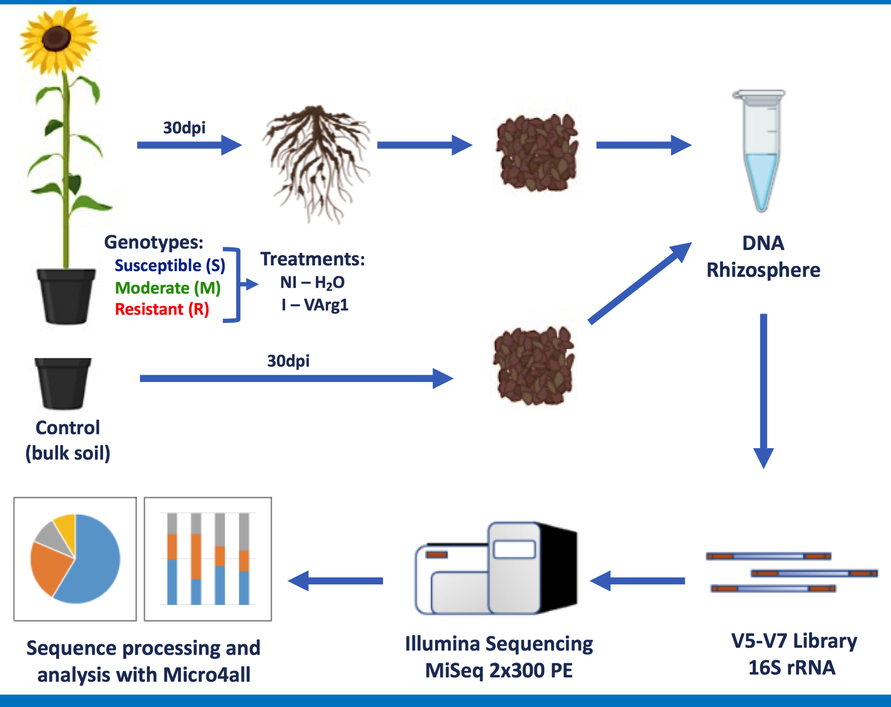
INTRODUCTION

Sunflower Verticillium wilt and leaf mottle (SVW), caused by the fungus *Verticillium dahliae* Kleb., has been the most extensive disease of sunflowers in Argentina, Canada, and the United States. Furthermore, it is becoming a major constraint to sunflower production in temperate European countries due to increasing incidence in France, Italy, Spain, and countries around the Black Sea. Plants infected by fungal pathogens actively recruit microbes in their root tissues to protect themselves. It is widely accepted that the plant´s microbiome plays a critical role in its health and that the hosts actively shape their rhizosphere microbiome to prevent or suppress disease development.

This work aims to study the influence of the genotype of three sunflower inbred lines (ILs), which differ in their resistance to SVW, on the composition and structure of the bacterial community in the rhizosphere in the presence of *V. dhaliae*.

MATERIAL & METHODS



RESULTS AND DISCUSSION

- No significant differences were found in alpha diversity indices.
- Beta diversity was explained to a greater extent by the phenotype of the ILs (PERMANOVA, R2 = 0.40, P = 0.045 and R2 = 0.33, P = 0.014 for the NI and I rhizosphere, respectively) than by inoculation with *V. dhaliae* (P > 0.05)(**Fig. 1A y B**).
- The predominant phyla comprised Proteobacteria, Bacteroidetes y Acidobacteria.
- *Rhodanobacter, Chujaibacter, Flavitalea, Lysobacter, Devosia, Bryobacter, Dokdonella y Bradyrhizobium*, were the most abundant genera.

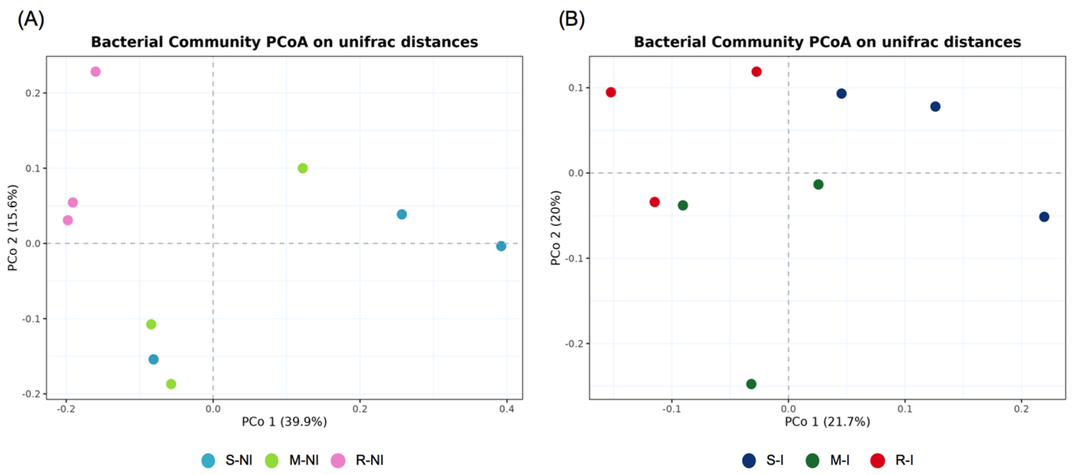


Fig. 1. Principal Coordinates Analysis (PCoA) based on unifrac distances of the rhizosphere communities from the sunflower cultivars non-inoculated (NI) **(A)** and inoculated (I) **(B)** with *V. dahliae*. S: susceptible; M: moderate; R: resistant.

- Several taxa increased their relative abundance in the rhizosphere associated with LEs concerning bulk soil (**Fig. 2A**).
- The presence of *V. dhaliae* modifies the composition of the rhizosphere bacterial communities in the different ILs (**Fig. 2B**).
- Significant increases were observed in bacteria previously described as antagonists of different soil pathogens, including *V. dhaliae,* in the rhizosphere of NI vs I ILs (**Fig. 2C, D y E**).

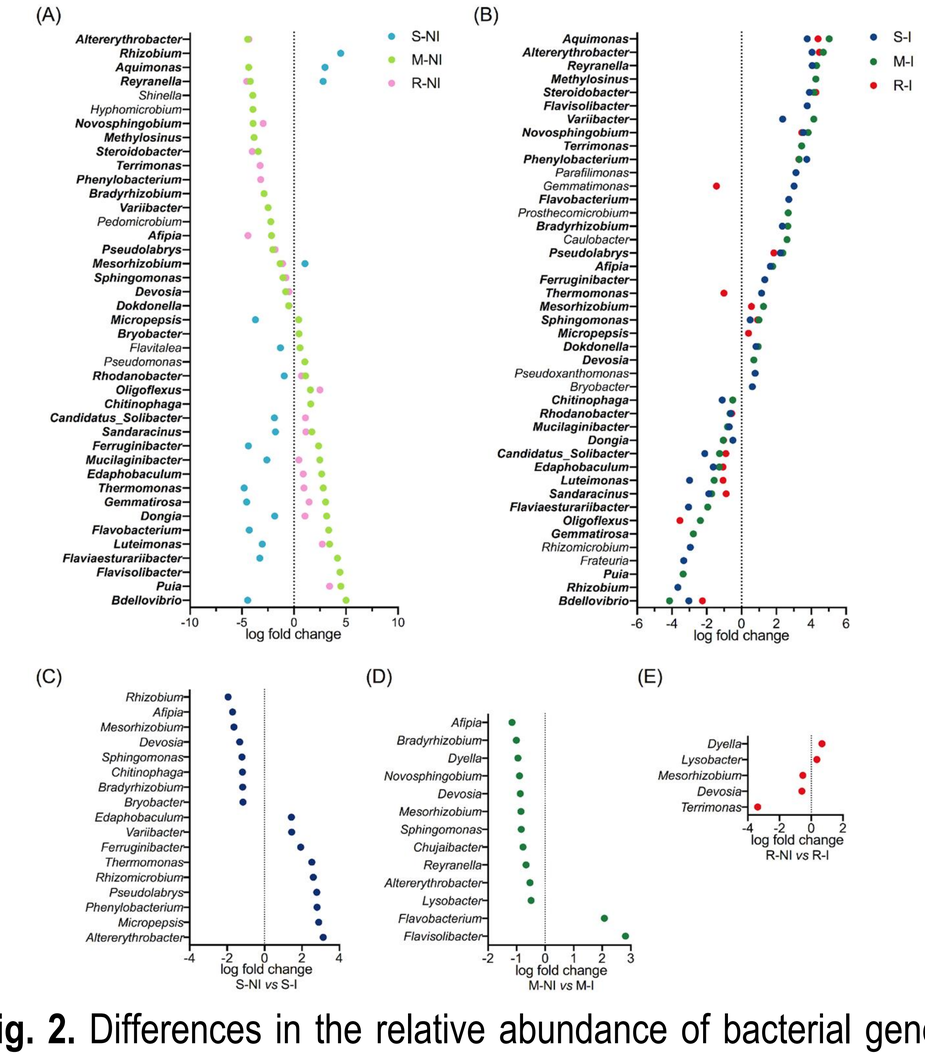


Fig. 2. Differences in the relative abundance of bacterial genera based on Analysis of Compositions of Microbiomes with Bias Correction. Bulk soil vs NI **(A)** and I **(B)** rhizosphere. S-NI vs S-I rhizosphere **(C)**, M-NI vs N-I rhizosphere **(D)** and, R-NI vs R-I rhizosphere **(E)**. The genera represented shown statistically significant differences (P < 0.05). Genera in bold letters are shared in (A) and (B). S: susceptible; M: moderate; R: resistant; NI: non-inoculated; I: inoculated.

These findings suggest that the microbial basis of resistance varies by host and that genotype-specific resistance factors play a role in recruiting beneficial bacteria that antagonize *V. dahliae.* Harnessing sunflower-associated rhizosphere bacteriomes for disease control offers a valuable alternative for developing innovative strategies that integrate microbiomes into plant breeding and sustainable crop protection.

FUNDINGS

This work was supported by projects funding by Instituto Nacional de Tecnología Agropecuaria (2023-PD-L01-I089, 2023-PD-L01-I087) and Fundación René Barón.