Effect of Bioinoculants and Biochar on Grapevine-Associated Soil Microbial Communities

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Aims and Scope

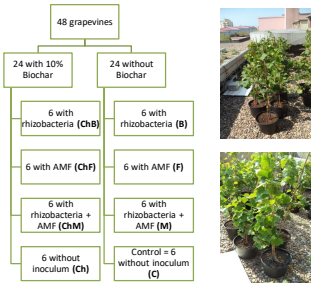
- Agricultural productivity is under serious threat due to climate change, soil degradation and water scarcity. This is worsened by poor agricultural management practices, such as the overuse of chemical fertilizers, overgrazing, and monoculture farming.
- Greener farming practices like the combined use of soil microorganisms, namely plant growth-promoting bacteria (PGPB) and arbuscular mycorrhizal fungi (AMF), together with soil amendments (*e.g.* biochar) can improve essential soil functions and soil microbial biodiversity.
- Changing the current farming practices towards greener ones with minimal use of chemical inputs is vital to increase crop productivity and resilience to different abiotic stresses.

This work aimed to assess the effect of microbial inoculants and biochar on the structural diversity of fungal and bacterial communities colonizing the rhizosphere of grapevines planted in a new vineyard in the North of Portugal.

Experimental Design

Field trial

Grapevines were first grown in pots with and without 10% of biochar and were inoculated with the rhizobacteria *Pseudomonas fluorescens* S3X and/or the AMF *Rhizophagus irregularis* as follows:



1 year later: Transplantation

After 1 year, grapevines were reinoculated and transplanted to the field trial established at Quinta do Azevedo, Barcelos.

2 years later

Rhizospheric soil samples were collected for microbial diversity analysis

Microbial diversity analysis

For each treatment, total DNA was extracted from grapevines' rhizospheric soil (3 replicates). Both 16S rRNA gene and ITS2 region were sequenced using Illumina technology. Sequences were processed using QIIME to obtain an OTU abundance table that was further analyzed using R software.

Results

Bacterial communities

- The treatments had no significant influence in the bacterial community alpha-diversity indexes.

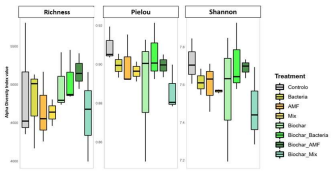


Fig 1. Box-plots for the alpha-diversity indexes of the bacterial community data.

Results

Bacterial communities (cont.)

- Most abundant Phyla: Proteobacteria, Actinobacteria, Planctomycetes, Bacteroidetes.

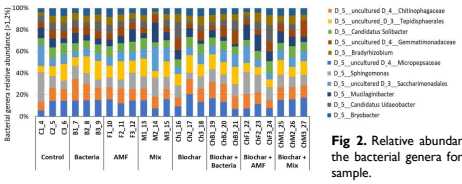


Fig 2. Relative abundance of the bacterial genera for each sample.

- Both types of inocula (rhizobacteria and AMF) affected the structure of the rhizosphere bacterial community in grapevines amended with 10% Biochar.

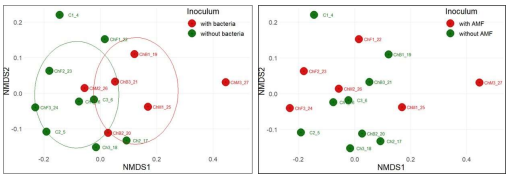


Fig 3. NMDS analysis of the bacterial community composition for soil samples amended with biochar. Bray-Curtis distance was used and a stress value = 0.146 was obtained.

Fungal communities

- In the presence of the AMF inocula, rhizospheric fungal communities were less diverse, and the distribution of fungal groups was less equitable.
- In treatments with Biochar, the diversity of rhizospheric fungal communities was lower when inoculated with both types of inocula (rhizobacteria and AMF).

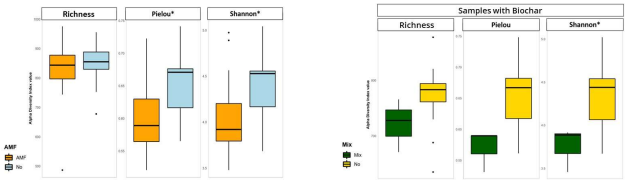


Fig 4. Box-plots for the alpha-diversity indexes of the fungal community data. The * indicates the existence of significant differences between groups for the marked index, with $p<0,05$.

- Most abundant phyla: Ascomycota e Basidiomycota

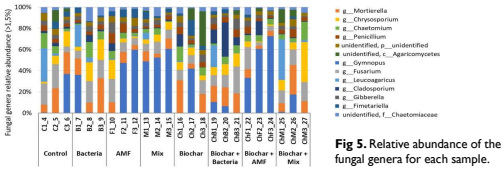


Fig 5. Relative abundance of the fungal genera for each sample.

- AMF inocula influenced the structure of the grapevines' rhizosphere fungal communities.

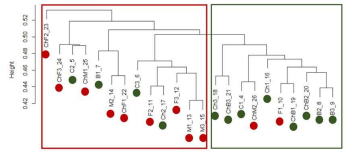


Fig 6. Cluster dendrogram obtained from Bray-Curtis distance matrix of the fungal community abundance data. Dots in red represent samples inoculated with AMF and green dots represent samples non-inoculated with AMF. Squares separate the clusters in which most of the samples were inoculated with/without AMF.

Conclusions

- Grapevine rhizosphere-associated microbial communities showed high genera diversity.
- In general, the applied microbial inocula and/or the supplementation with biochar influenced the structure and diversity of the microbial communities colonizing the rhizosphere of grapevines grown under field conditions.

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