Rhizosphere microbiome dynamics associated with Esca disease in Barbera vineyards

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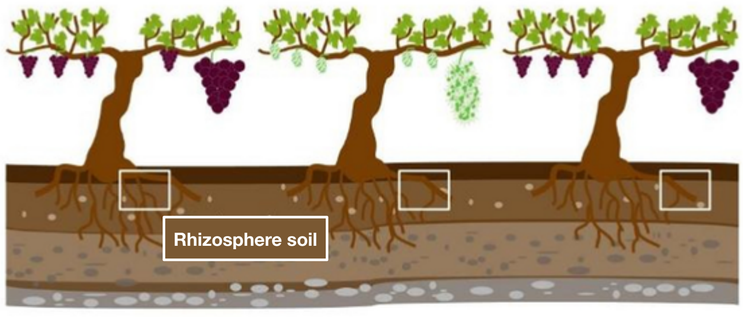
Introduction

For a sustainable viticulture, a deeper understanding of the soil-plant pathosystem is essential [1]. The rhizosphere microbiome is a critical component of vineyard health [2], yet its role in the context of Esca disease, one of the most destructive grapevine trunk diseases worldwide [3], remains largely unexplored. This knowledge gap limits our ability to develop reliable bio-indicators for soil health and innovative disease management solutions [4]. Therefore, this research investigated the rhizosphere microbiome dynamics in Barbera vineyards by comparing the taxonomic structure and metabolic potential of fungal and bacterial communities in soils with high (**HE**) and low (**LE**) Esca incidence.

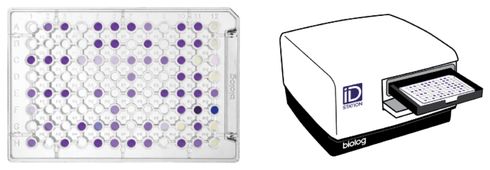
Materials and Methods

Experimental Design
- *Vitis vinifera* cv. Barbera Vineyards
- **HE** vs **LE**

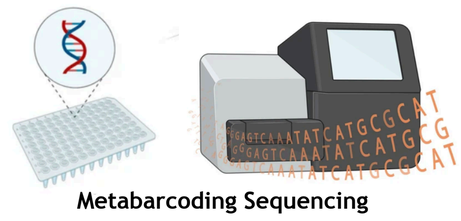
Rhizosphere Soil Samples



Functional Metabolic Profiling
- BIOLOG® EcoPlates™
- Carbon Source Utilization



BIOLOG® EcoPlates™



Metabarcoding Sequencing

Total Microbial DNA Extraction
- DNeasy PowerSoil Pro Kit (QIAGEN)

Amplicon Metabarcoding
- ITS2 region → Fungi
- 16S rRNA gene → Bacteria

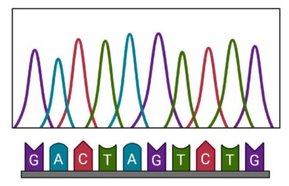
Bioinformatic Analysis (QIIME 2)
- Taxonomic assignment
- Community & Diversity profiling

Culture-Dependent Isolation
- Fungal Isolation (MEA/RBCA)
- Morpho-molecular Identification (ITS)

MEA

RBCA

DNA Extraction

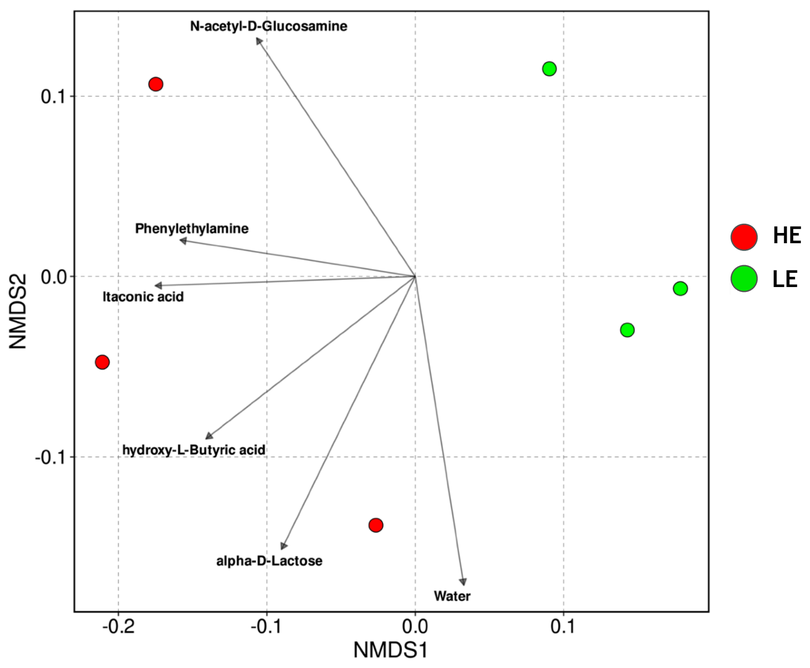


ITS Sequencing

Taxonomic assignment

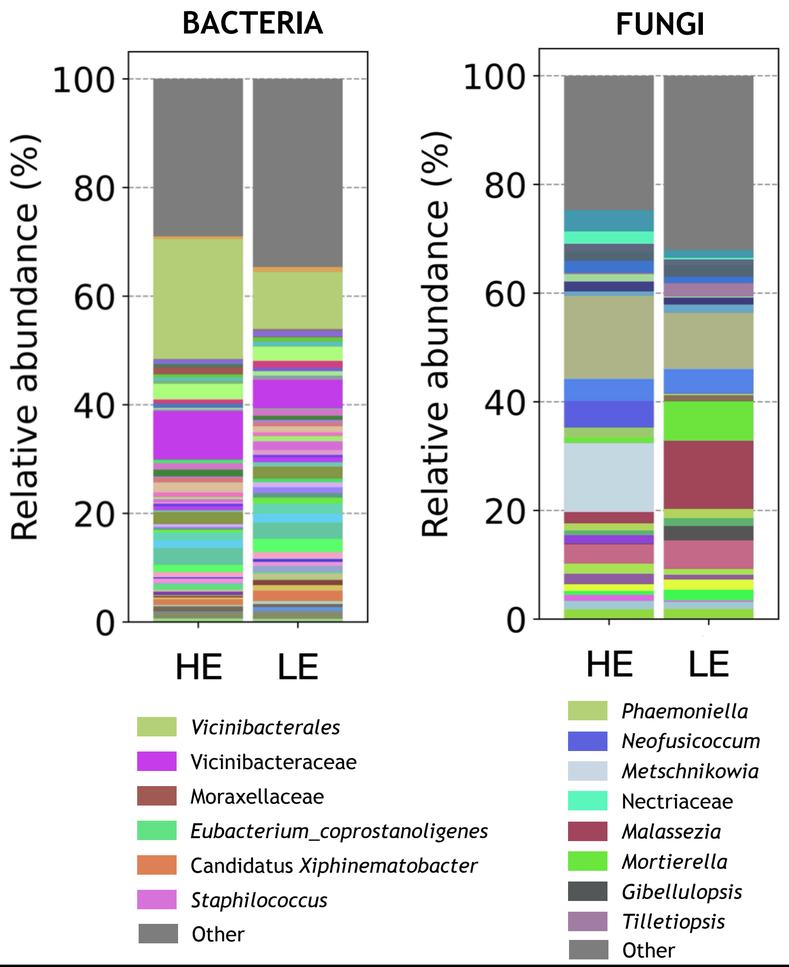
Results

Distinct Soil Metabolic Profiles

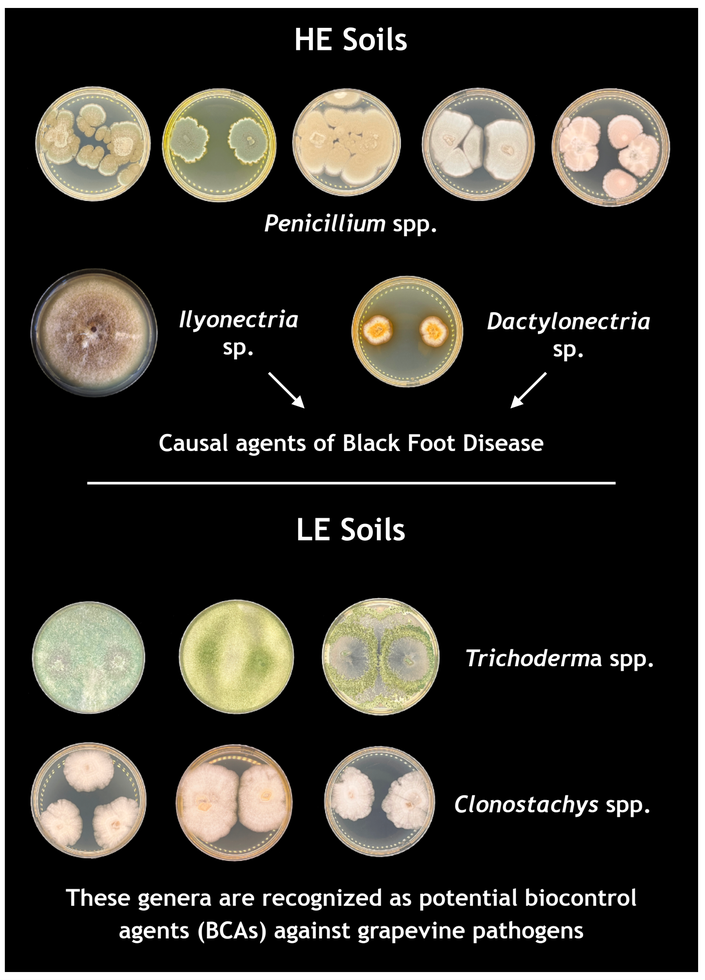


The metabolic profiles were significantly different, with **HE** soils showing a preferential utilization of substrates like **Phenylethylamine, Itaconic acid** and **hydroxy-L-Butyric acid**, suggesting a specific functional signature for the microbial communities in diseased vineyards.

Microbial Community Composition



Culturable Fungi



Conclusions

- **LE** and **HE** vineyards host **distinct microbial** and **metabolic profiles.**
- **LE** soils are enriched with a **beneficial microbiome** (e.g., *Mortierella*, *Trichoderma*), driving **disease-suppressive functions.**
- The rhizosphere microbiome provides powerful **bioindicators** for developing **targeted** and **sustainable management strategies.**

References

1. Zarraonaindia, I., Owens, S. M., Weisenhorn, P., West, K., Hampton-Marcell, J., Lax, S., Bokulich, N. A., Mills, D. A., Martin, G., Taghavi, S., van der Lelie, D., & Gilbert, J. A. (2015). The soil microbiome influences grapevine-associated microbiota. mBio, 6(2), e02527-14.
2. Berendsen, R. L., Pieterse, C. M., & Bakker, P. A. (2012). The rhizosphere microbiome and plant health. Trends in plant science, 17(8), 478-486.
3. Gramaje, D., Úrbez-Torres, J. R., & Sosnowski, M. R. (2018). Managing Grapevine Trunk Diseases With Respect to Etiology and Epidemiology: Current Strategies and Future Prospects. Plant disease, 102(1), 12-39. https://doi.org/10.1094/PDIS-04-17-0512-FE
4. Bettenfeld, P., Cadena I Canals, J., Jacquens, L., Fernandez, O., Fontaine, F., van Schaik, E., Courty, P. E., & Trouvelot, S. (2022). The microbiota of the grapevine holobiont: A key component of plant health. Journal of advanced research, 40, 1-15.

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