

Microbial Communities in Wild and Cultivated Vineyards: Insights into the Native Microbiota Relevant to Fermentation Processes

Maripaz Villanueva Llanes, María Hernández Fernández, José Luis Padilla Agudelo, Gustavo Cordero Bueso, María Carbú Espinosa de los Monteros, Jesús Manuel Cantoral

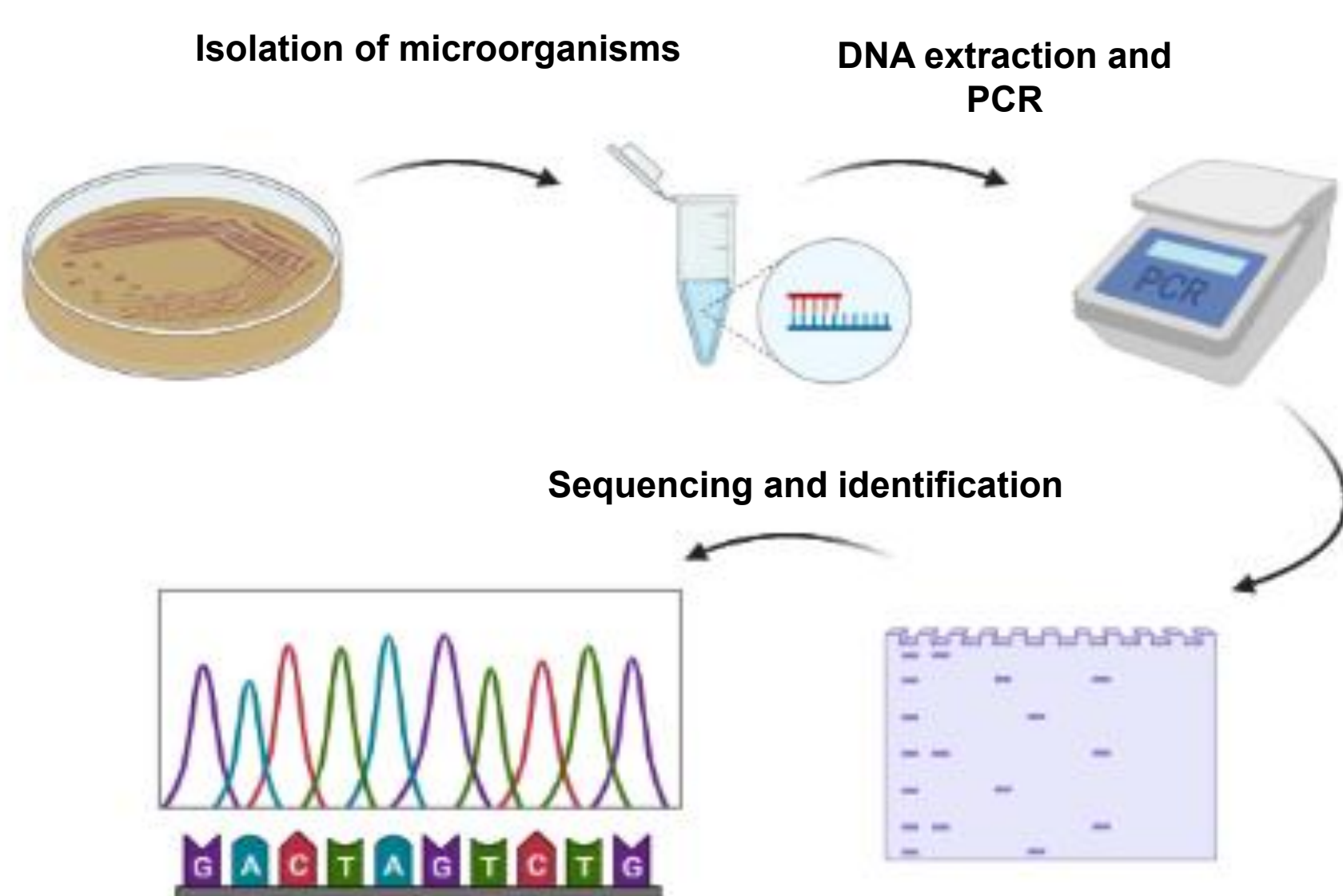
•Laboratory of Microbiology, Department of Biomedicine, Biotechnology and Public Health, University of Cádiz, 11510, Puerto Real, Cadiz, Spain
•mariapaz.villanueva@uca.es, maria.hernandez@uca.es, joseluis.padilla@uca.es, gustavo.cordero@uca.es, maria.carbu@uca.es, jesusmanuel.cantoral@uca.es

INTRODUCTION & AIM

Microbial communities associated with grapevines play a crucial role in fermentation, influencing both its dynamics and the sensory quality of wines. This “vineyard microbiome”, shaped by grapevine genotype, environment, and management practices, includes bacteria and fungi that contribute to wine complexity. While cultivated vineyards under conventional or organic systems are influenced by human intervention, wild populations of *Vitis vinifera* subsp. *sylvestris* represent unmanaged ecosystems that can serve as reservoirs of unique and underexplored microbial taxa.

The aim of this study was to characterize cultivable bacterial and fungal communities from three contrasting vineyard types—wild *V. vinifera* subsp. *sylvestris* and cultivated *V. vinifera* subsp. *vinifera* under organic and conventional management. By comparing microbial distributions across these environments, we sought to reveal the ecological and oenological relevance of vineyard-associated microorganisms and their potential role in spontaneous fermentation processes.

METHOD

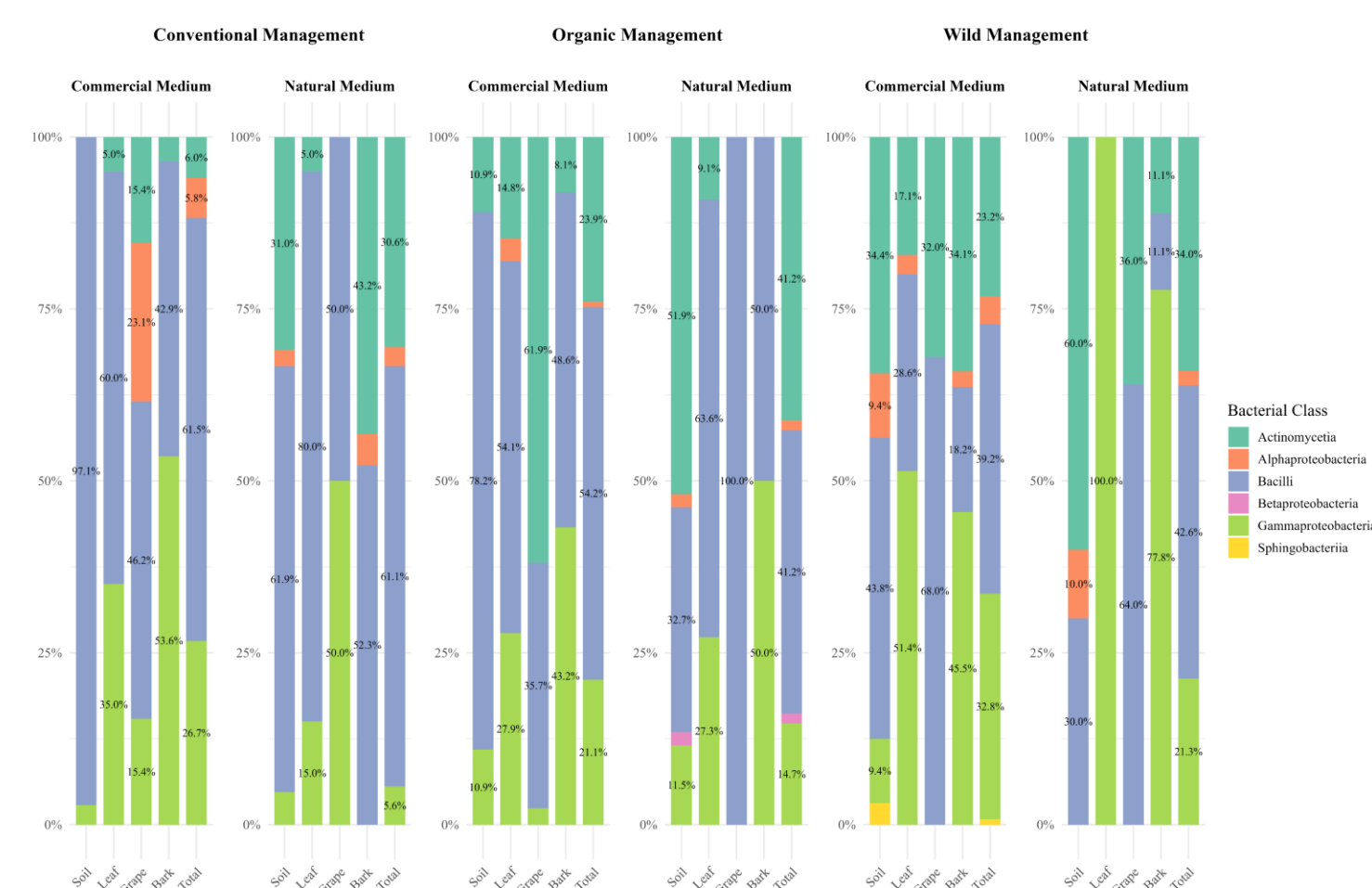


Samples were collected from wild and cultivated vineyards under organic and conventional management.

Microorganisms were isolated using both commercial media (TSB, PDB) and natural grapevine-based media, followed by DNA extraction and sequencing of 16S rDNA and ITS regions for taxonomic identification.

Community composition was compared across vineyard types to assess the influence of management and environment on microbial diversity.

RESULTS & DISCUSSION



In the case of bacteria, **Bacilli** dominated most samples, but community recovery strongly depended on the culture medium: commercial media favored **Gammaproteobacteria**, while natural media enhanced **Actinomycetia**, particularly in cultivated vineyards, and promoted **Gammaproteobacteria** in wild vines. **Betaproteobacteria** were only recovered from organic soils with natural media, and **Alphaproteobacteria**, though minor, appeared in conventional grapes and wild soils.



Regarding fungi, a similar pattern was observed: **Dothideomycetes** were generally dominant, while **Eurotiomycetes** were more abundant in commercial media. In contrast, natural media allowed the detection of **Xylonomycetes** and revealed a more balanced profile in wild grapevines, with a moderate presence of **Sordariomycetes**, highlighting the importance of natural media in promoting the growth of otherwise minor or overlooked microbial taxa.

CONCLUSION

Natural media proved more effective in capturing hidden microbial diversity, underscoring their value for exploring vineyard-associated microorganisms with ecological and oenological relevance.

FUTURE WORK / REFERENCES

Future work will focus on integrating culture-independent approaches, testing the functional roles of key isolates in fermentation and biocontrol, and exploring natural media as tools to recover rare vineyard-associated taxa.