

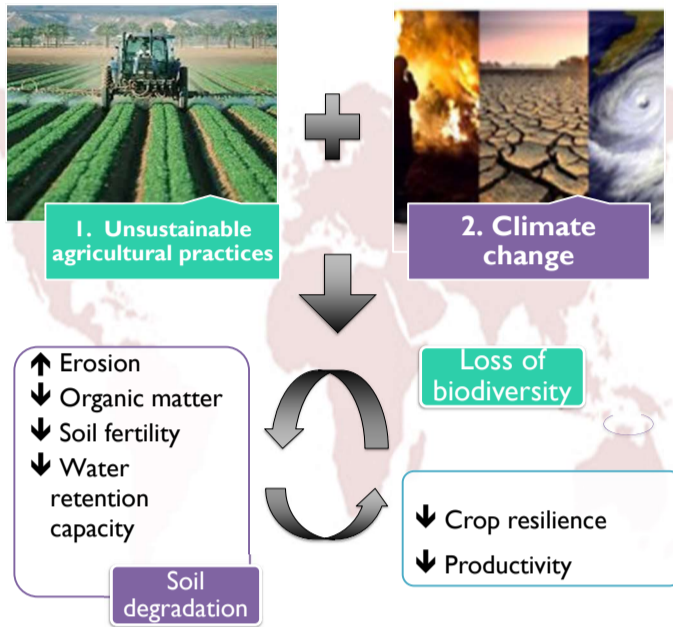
Sustainable solutions for Mediterranean agroecosystems through enhanced soil microbial diversity



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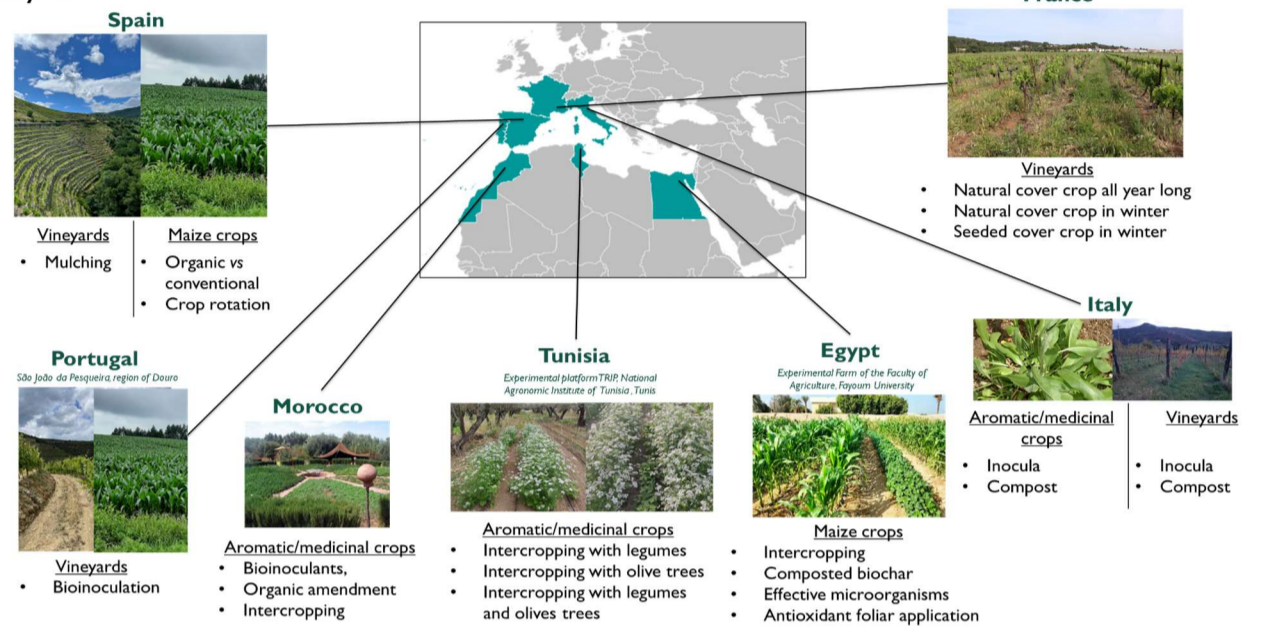
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INTRODUCTION:

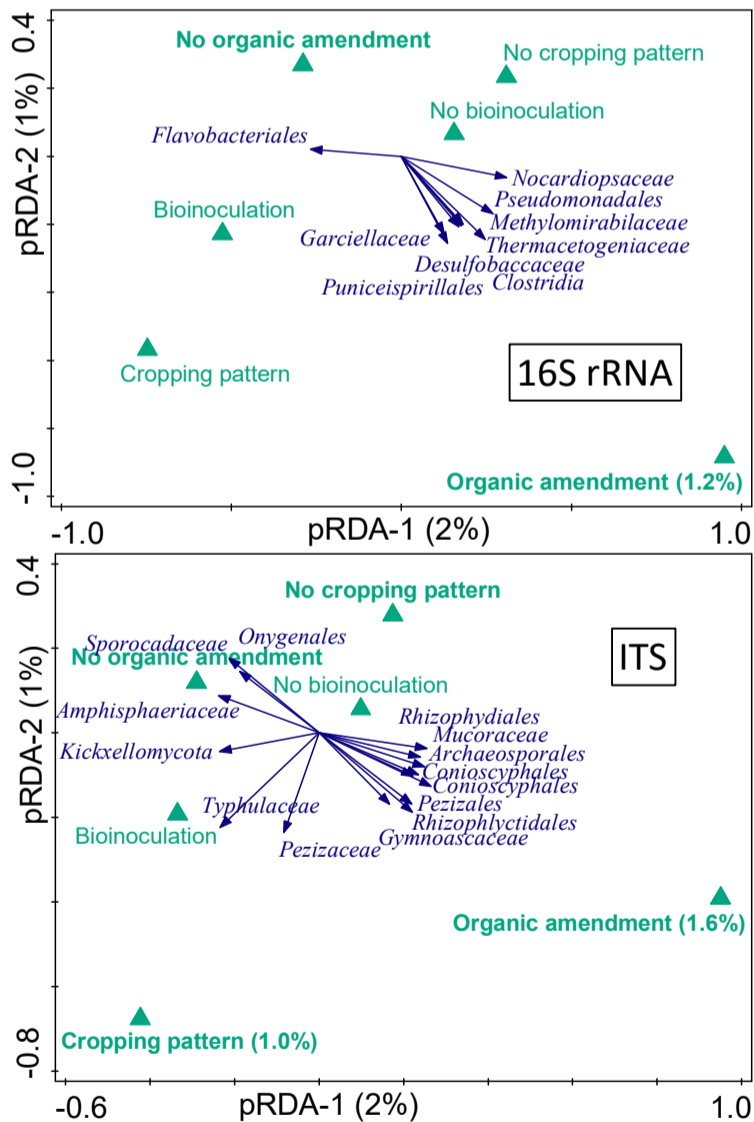


MATERIALS AND METHODS:

Case studies of sustainable practices that were sampled for 16S rRNA and ITS metabarcoding analysis.

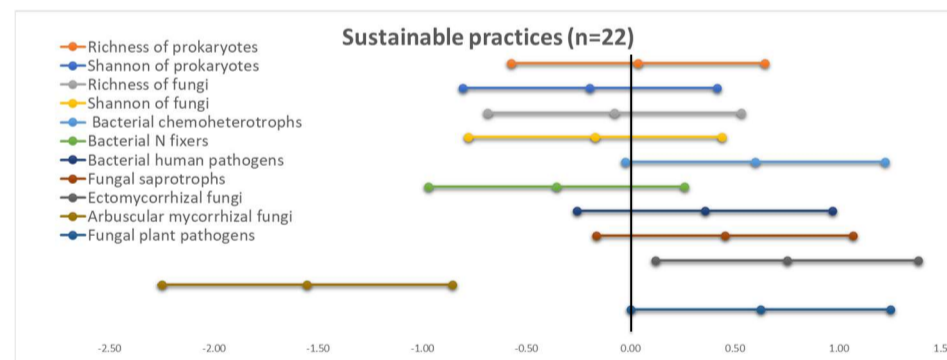


RESULTS:



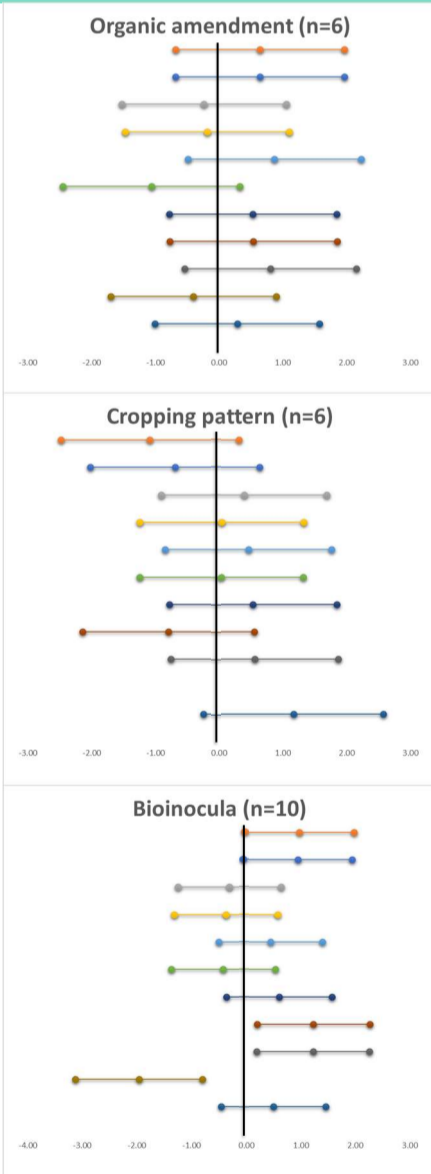
Partial redundancy analyses performed on taxa at the family level as response variables, sustainable treatments as explanatory variables (significant ones appear in bold), and crop and site as covariables (left):

- ✓ The sustainable practices applied explained a very low % of the variation in the composition of prokaryotes and fungi.
- ✓ Organic amendment applications were significant for prokaryotic and fungal composition, while establishing diversified cropping patterns was significant for fungal composition.



Hedges' g and 95% Confidence Intervals of some structural and functional metrics for all sustainable practices (above) and those corresponding to organic amendments, cropping patterns and bioinocula (right):

- ✓ Organic amendments mainly increased bacterial chemoheterotrophs and ectomycorrhizal fungi, while N fixers were reduced.
- ✓ Cropping patterns increased fungal pathogens and reduced prokaryotic richness.
- ✓ Bioinoculations increased richness and Shannon of prokaryotes, fungal saprotrophs and ectomycorrhiza. Arbuscular mycorrhiza were reduced.



CONCLUSIONS:

- ❖ The alterations in the microbiome induced by certain agricultural management practices could have implications for the provision of soil ecosystem services.
- ❖ Recognizing these consequences is crucial for developing climate-smart, resource-efficient, and stress-resilient agroecosystems.



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