

# Patterns of soil microbial biomass and diversity across Mediterranean agroecosystems in areas under desertification risk



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## INTRODUCTION

**Soil health** plays a central role in the EU biodiversity strategy for 2030. Degraded soils fail to promote the ecosystems services required for a productive agriculture, hamper ecological restoration and increase climate change effects and desertification. The **soil microbiota** is recognized as key player in both diversity and productivity of terrestrial ecosystems, and its correct management is the best **nature based solution** for sustainable agriculture. The drivers of belowground diversity are still largely unknown and is still unclear whether soil physico-chemical features are potential drivers of microbial diversity or are regulated by it. The **LIFE Project DESERT-ADAPT - Preparing desertification areas for increased climate change** - (<http://www.desert-adapt.it>), focuses on agricultural adaptation measures aimed at reverting ongoing desertification trends.



## AIM

Investigate the relationship between soil microbial biomass (SMB) and bacterial diversity with soil physical-chemical indicators across diverse types of land use in soils under high desertification risk in Italy, Spain and Portugal.

## METHODS

Top soil (0-10 cm) was sampled from 30 sites, situated in 10 municipalities, in Southern Portugal (Alentejo, PT), Central Spain (Extremadura, SP) and Southern Italy (Sicily, IT) with aridity index <0.65 (Fig. 1). The soil samples were subjected to Metagenomic DNA extraction. The total soil microbial biomass (SMB) is estimated as total extracted dsDNA; while soil bacterial diversity is obtained with Automated Ribosomal Intergenic Spacer Analysis (ARISA) and metagenomics 16S gene sequencing.

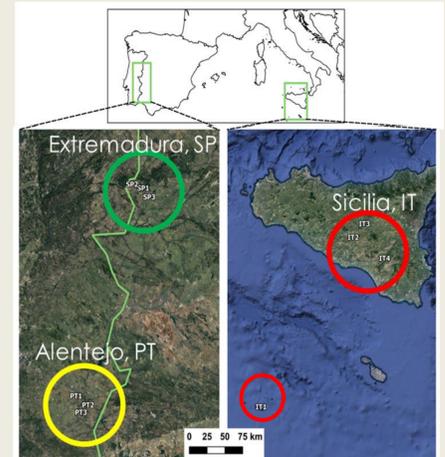


Fig. 1 Study area and soil sampling sites localized in Sicily (Italy - IT), Extremadura (Spain - SP) and Alentejo (Portugal PT)

## RESULTS

### Soil microbial biomass and bacterial diversity

The **total soil microbial biomass (SMB)** and **bacterial diversity** significantly varied across countries and land uses (Fig. 2). SMB was significantly higher in Extremadura (SP) with conifer forests presenting significantly higher values compared to other land uses (Fig. 2a). Richness was highest in Italian farm and in conifer soils (Fig. 2b), while Shannon index was higher in croplands; the lowest diversity was observed in shrublands (Fig. 2c). SMB was related to soil organic carbon (SOC) and total nitrogen (TN), while bacterial diversity resulted strongly related to pH but, surprisingly, not to SOC (Tab. 1). The beta-diversity was related to biogeography and main soil parameters: pH, SOC and CEC (Fig. 3).

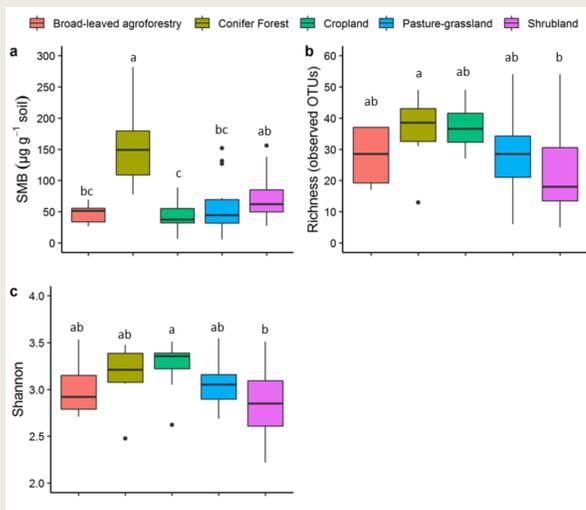


Fig. 2 Boxplots of SMB (a), and bacterial diversity, (b) richness, (c) Shannon index, across the five land uses in the farms of Italy, Spain and Portugal. SMB was estimated as total soil dsDNA, diversity indices were based on ARISA.

		Estimate	SE	t	p
<b>SMB</b>	Intercept	-19.156	28.005	-0.68	0.496
	SOC	0.572	0.177	3.23	<b>0.002</b>
	pH	7.013	4.089	1.72	0.091
	TN	10.012	3.974	2.52	<b>0.014</b>
	CEC	-0.889	0.798	-1.11	0.270
<b>Richness</b>	Intercept	-3.368	6.723	-0.50	0.618
	SOC	0.099	0.042	2.33	0.023
	pH	4.676	0.982	4.76	<b>&lt; 0.001</b>
	TN	-2.249	0.954	-2.36	0.021
	CEC	0.334	0.192	1.74	0.086
<b>Shannon</b>	Intercept	2.498	0.240	10.393	<b>&lt; 0.001</b>
	SOC	0.002	0.001	1.648	0.105
	pH	0.091	0.035	2.612	<b>0.011</b>
	TN	-0.068	0.034	-2.022	0.048
	CEC	0.005	0.007	0.712	0.480

Tab 1. Summary of the regression testing the effects of SOC, pH, N and CEC on soil microbial biomass (SMB), richness and diversity (Shannon index) calculated on ARISA profiles.

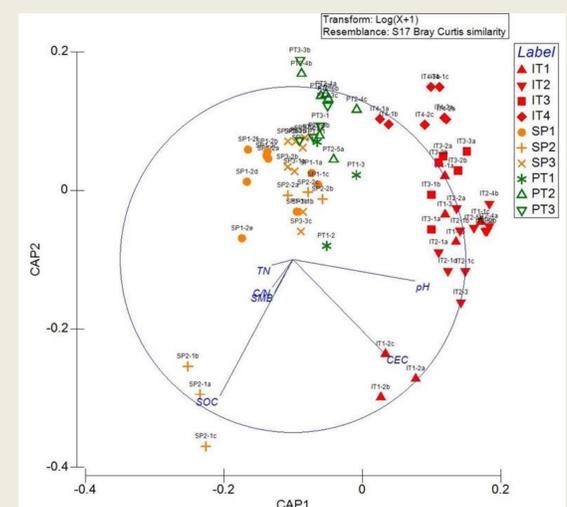


Fig. 3. Canonical Analysis of Principal Coordinates (CAP) calculated on the ARISA profiles of soil samples of the ten farms located in Sicily (Italy), Extremadura (Spain) and Alentejo (Portugal) and the relative main chemical physical soil variables.

### The soil microbiota

All soils contained the main typical soil bacterial phyla. Actinobacteria, Proteobacteria, Bacteroidetes, Acidobacteria, Chloroflexi, Firmicutes, and Verrucomicrobia were detected in all countries with relative abundance variable across sites and land uses (Fig. 4, Fig. 5).

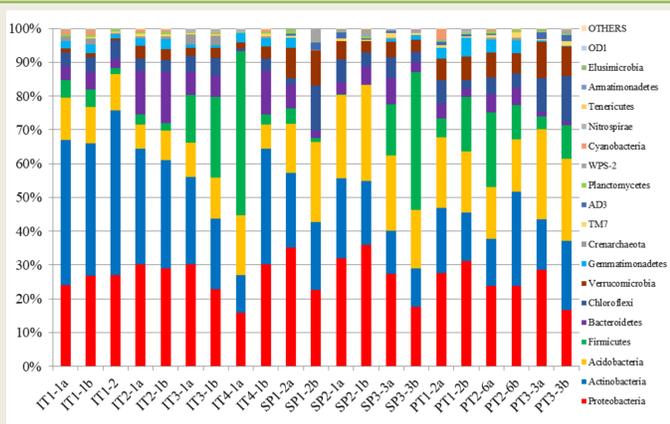


Fig. 4 Relative abundance of soil bacterial and archaeal phyla in the semi-arid soils of Southern Europe. Others includes phyla < 0.1%.

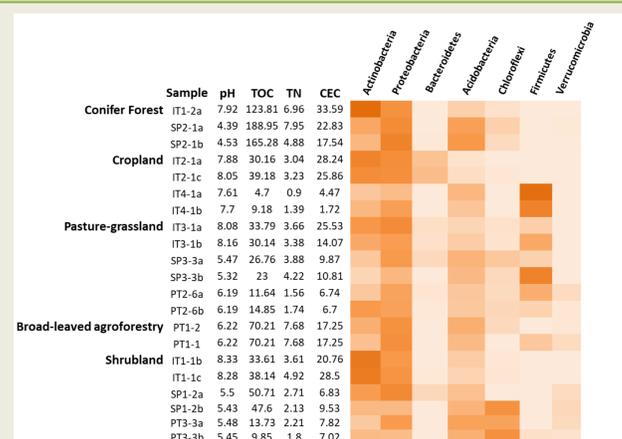


Fig. 5 Heat map based on the relative abundance of the most abundant phyla across all land-use related to soil edaphic variables.

## CONCLUSIONS

- Desertification seems not to influence bacterial diversity, but it could affect its functionality, by acting on the composition of the communities.
- The impact of desertification and soil degradation on the soil microbiota, could be fundamentally different from that detected on plants and animals.
- Microbial biomass rather than microbial diversity is the soil biological index most appropriate to indicate the negative effect of desertification on soil biology.
- The correct management of the soil microbiota is a promising nature-based approach to improve agricultural productivity and sustainability.