Agroecological characterization of abandoned alpine summer pastures: insights into vegetation, soil conditions, and microbial communities

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agritech National Research Center for Technology in Agriculture

iNEST Interconnected Nord-Est Innovation Ecosystem

Finanziato dall'Unione europea NextGenerationEU

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DAFNAE
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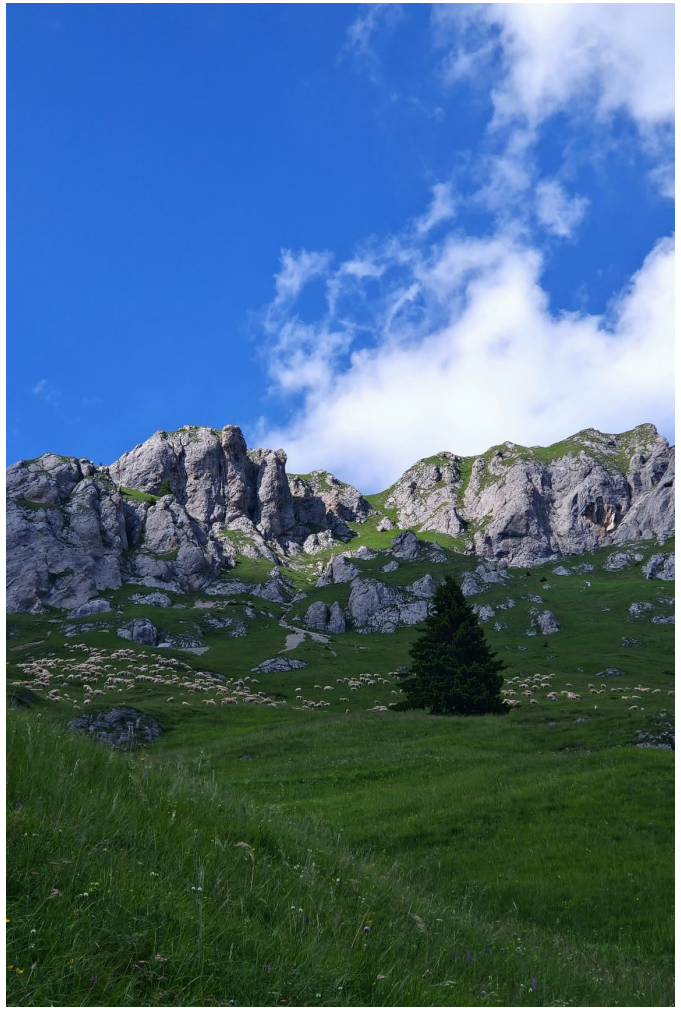
75° Annual Meeting of the European Federation of Animal Science (EAAP), Firenze, 1st of September – 5th of September 2024

Alpine pasture

High-altitude grasslands

Rich multifunctionality:

- Provisioning Ecosystem Services (feed supply for livestock)
- Biodiversity and Non-Provisioning Ecosystem Services



Aim

To characterize an abandoned alpine pasture

To define a control status (without grazing)

Vegetation types

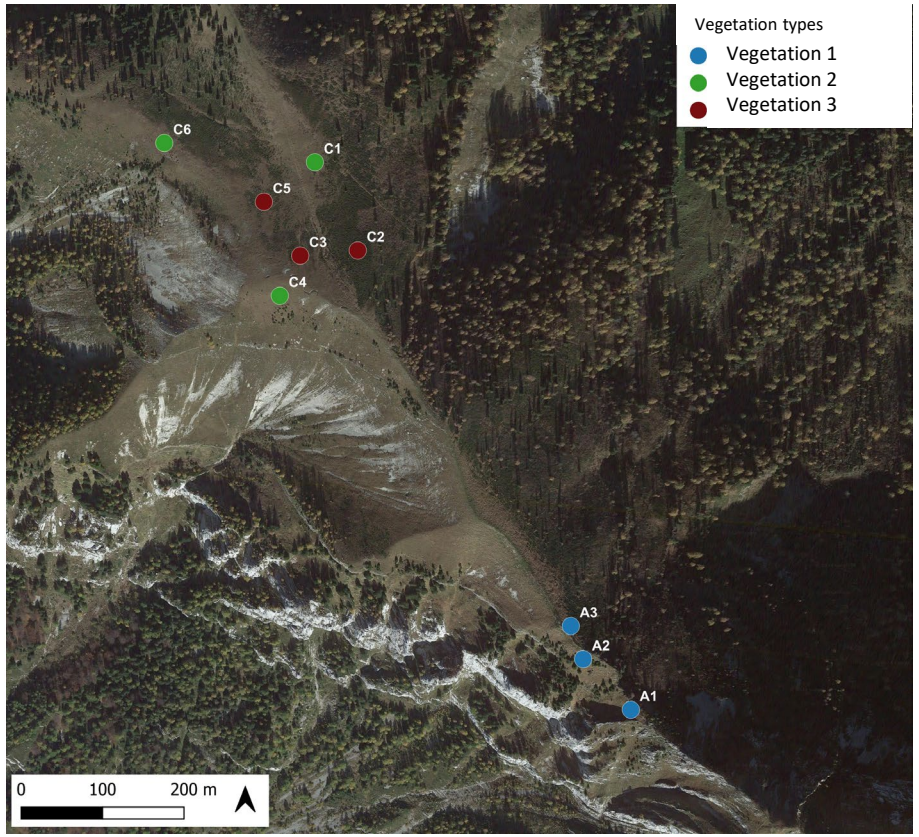
Pedological conditions

Soil microbial communities

Taxonomical diversity

Functional diversity

Study area



Monte Coppolo – Alpine pasture:

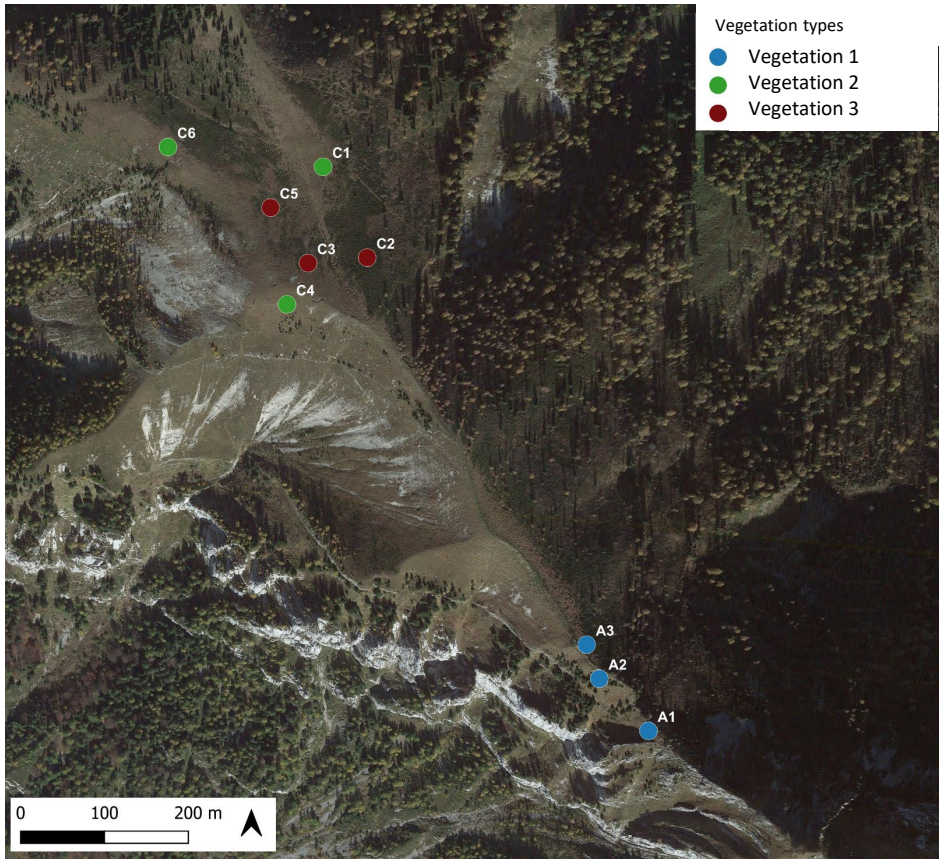
- North-Eastern Alps (Dolomites)
- Nature 2000 site
- Grazed by sheep until 2018
- Slope range: 5 – 37°
- Altitude: 1800 – 2050 m.asl

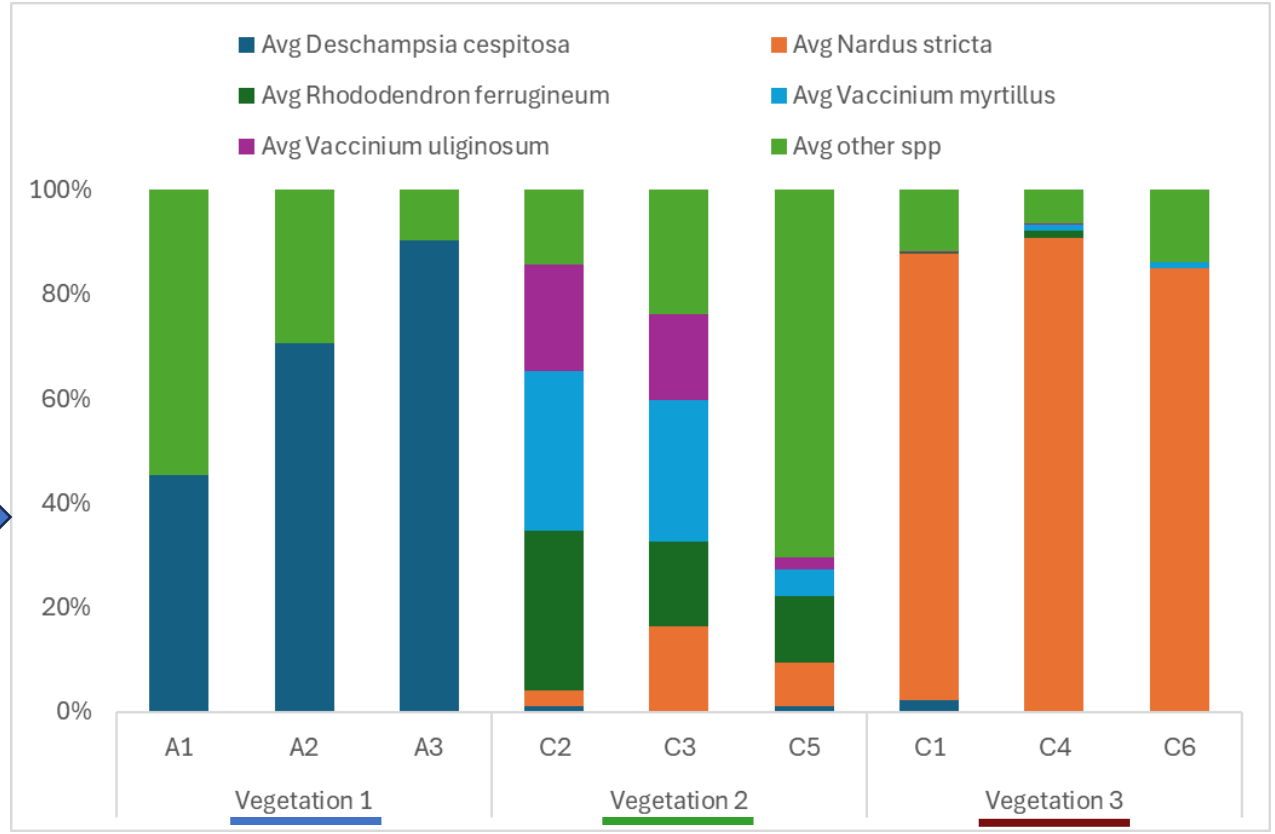
Restoration of grazing in 2023 (project “Habitat preciso”)

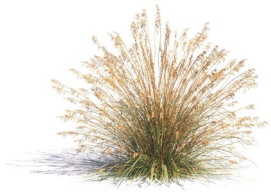
Sampling design:

- 9 sites
- 5 random replicates for each site (topsoil bulks)
- Braun-Blanquet method (vegetation)

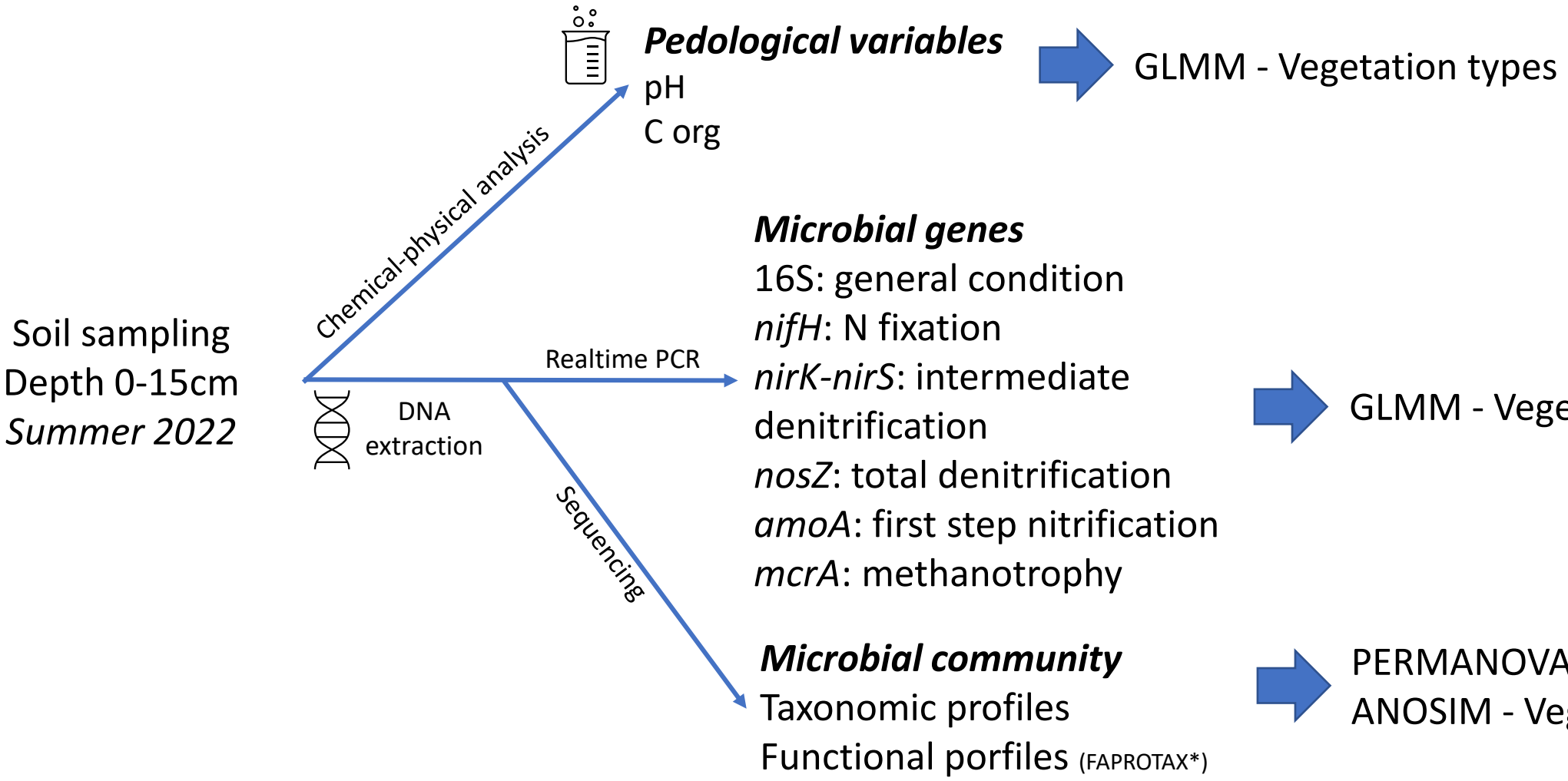
Vegetation types





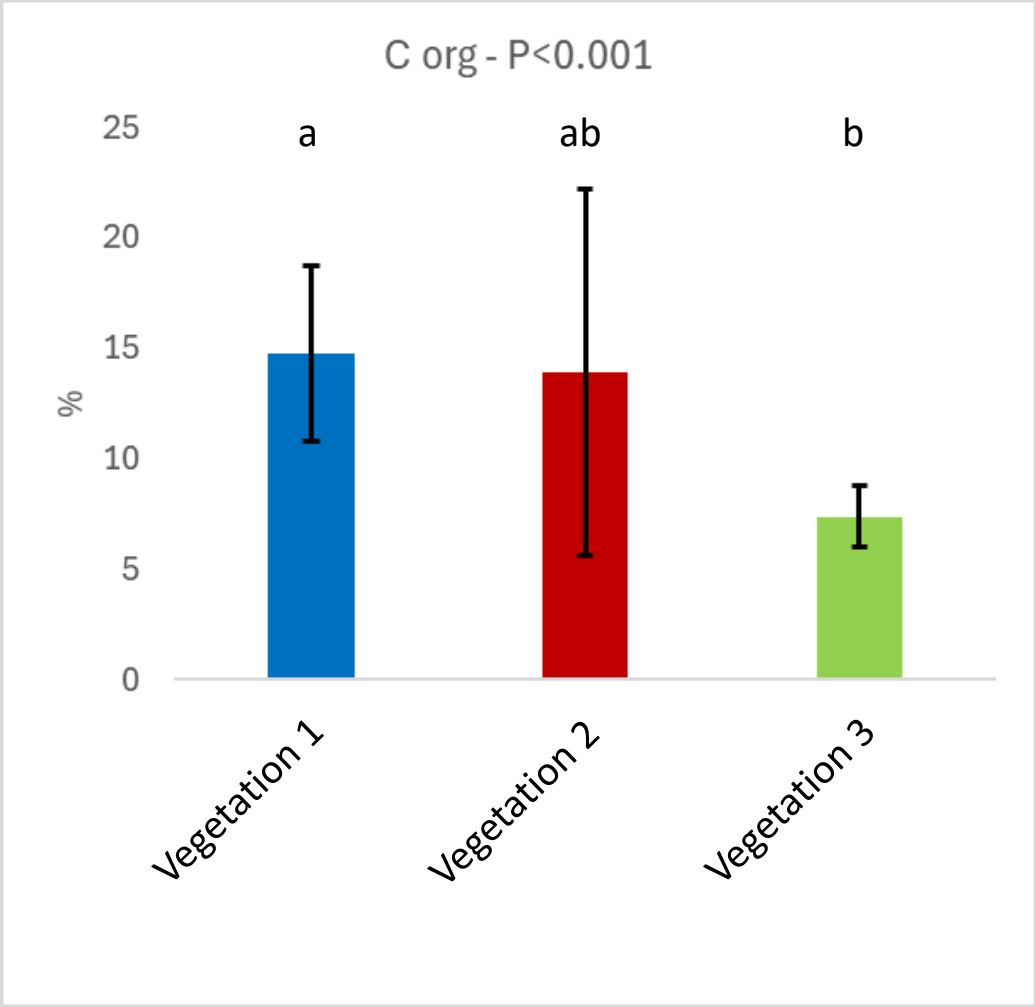


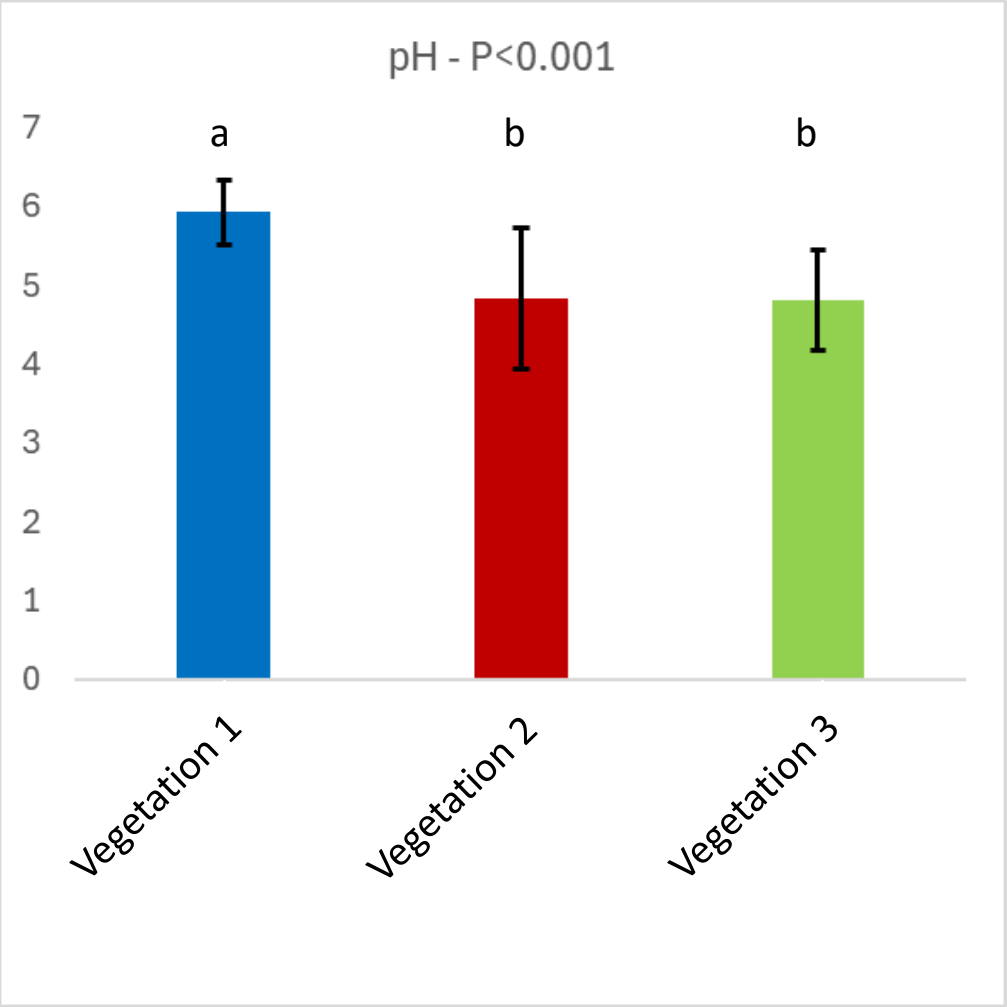
Sampling Design - Data Framework



*FAPROTAX (Louca, S., Parfrey, L.W., Doebeli, M. (2016) - Decoupling function and taxonomy in the global ocean microbiome. Science 353:1272-1277)

Pedological conditions





Gene abundances

	log 16S *General condition*
Vegetation 1	
Vegetation 2	*
Vegetation 3	

EQUAL HIGH LOW VERY LOW

Gene abundances

	log 16S *General condition*	log *nifH* *N fixation*
Vegetation 1		
Vegetation 2	*	
Vegetation 3		

EQUAL HIGH LOW VERY LOW

Gene abundances

	log 16S *General condition*	log *nifH* *N fixation*	log *nirK* *Intermediate denitrification*	log *nirS* *Intermediate denitrification*
Vegetation 1				
Vegetation 2	*		**	**
Vegetation 3				*

EQUAL HIGH LOW VERY LOW

Gene abundances

	log 16S *General condition*	log *nifH* *N fixation*	log *nirK* *Intermediate denitrification*	log *nirS* *Intermediate denitrification*	log *nosZ* *Total denitrification*
Vegetation 1					
Vegetation 2	*		**	**	**
Vegetation 3				*	***

EQUAL HIGH LOW VERY LOW

Gene abundances

	log 16S *General condition*	log *nifH* *N fixation*	log *nirK* *Intermediate denitrification*	log *nirS* *Intermediate denitrification*	log *nosZ* *Total denitrification*	presence *amoAa* *First step nitrification*	presence *amoAb* *First step nitrification*
Vegetation 1							
Vegetation 2	*		**	**	**	**	*
Vegetation 3				*	***	*	*

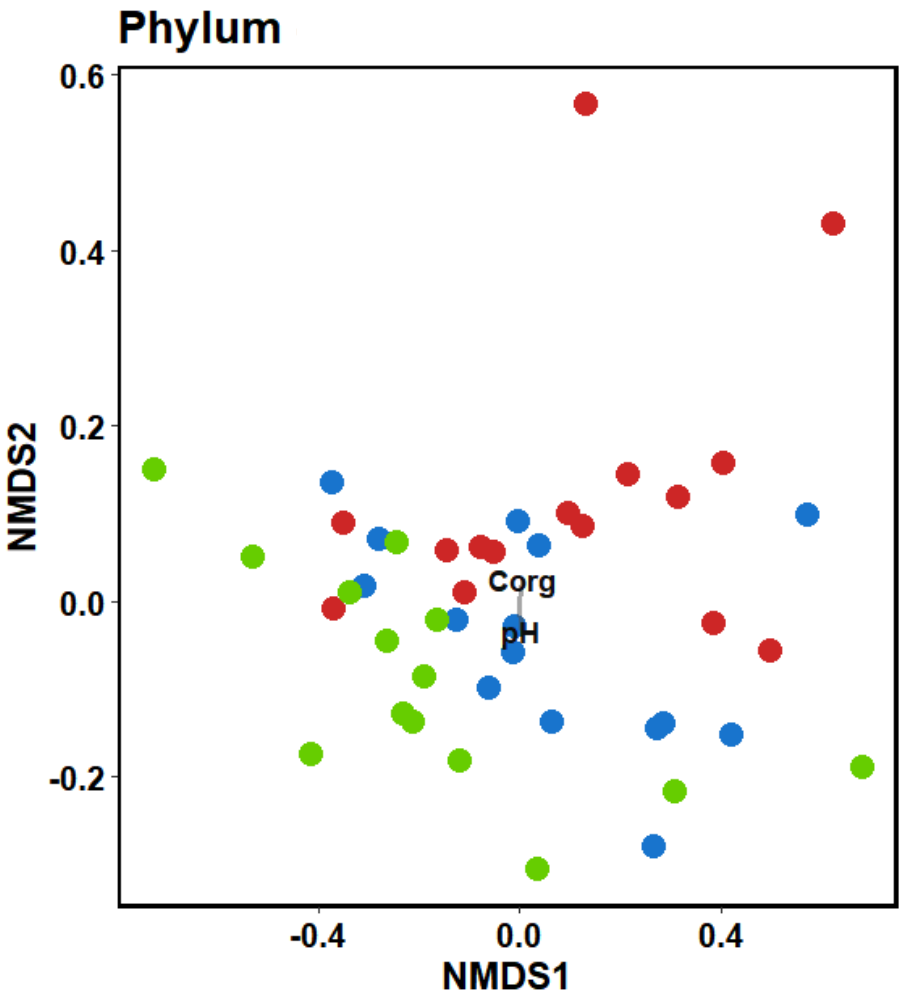
EQUAL HIGH LOW VERY LOW

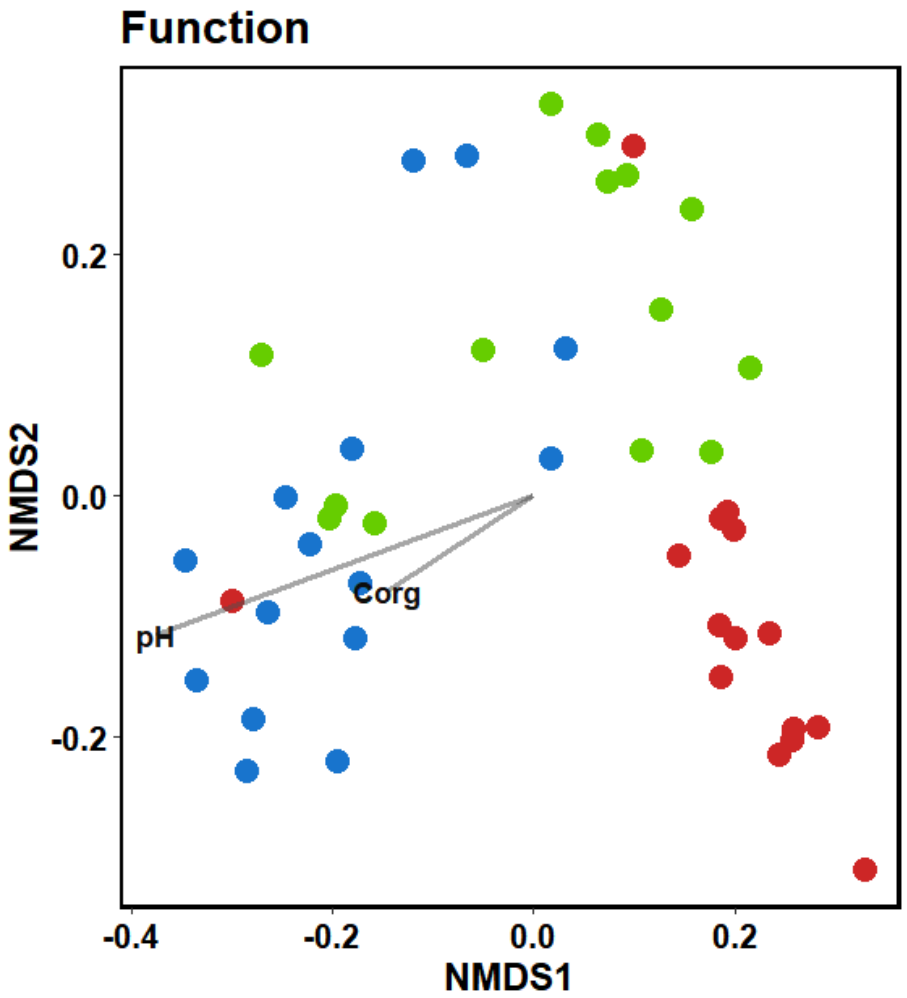
Gene abundances

	log 16S *General condition*	log *nifH* *N fixation*	log *nirK* *Intermediate denitrification*	log *nirS* *Intermediate denitrification*	log *nosZ* *Total denitrification*	presence *amoAa* *First step nitrification*	presence *amoAb* *First step nitrification*	presence *mcrA* *Methanotrophy*
Vegetation 1								
Vegetation 2	*		**	**	**	**	*	**
Vegetation 3				*	***	*	*	***

EQUAL HIGH LOW VERY LOW

Microbial communities





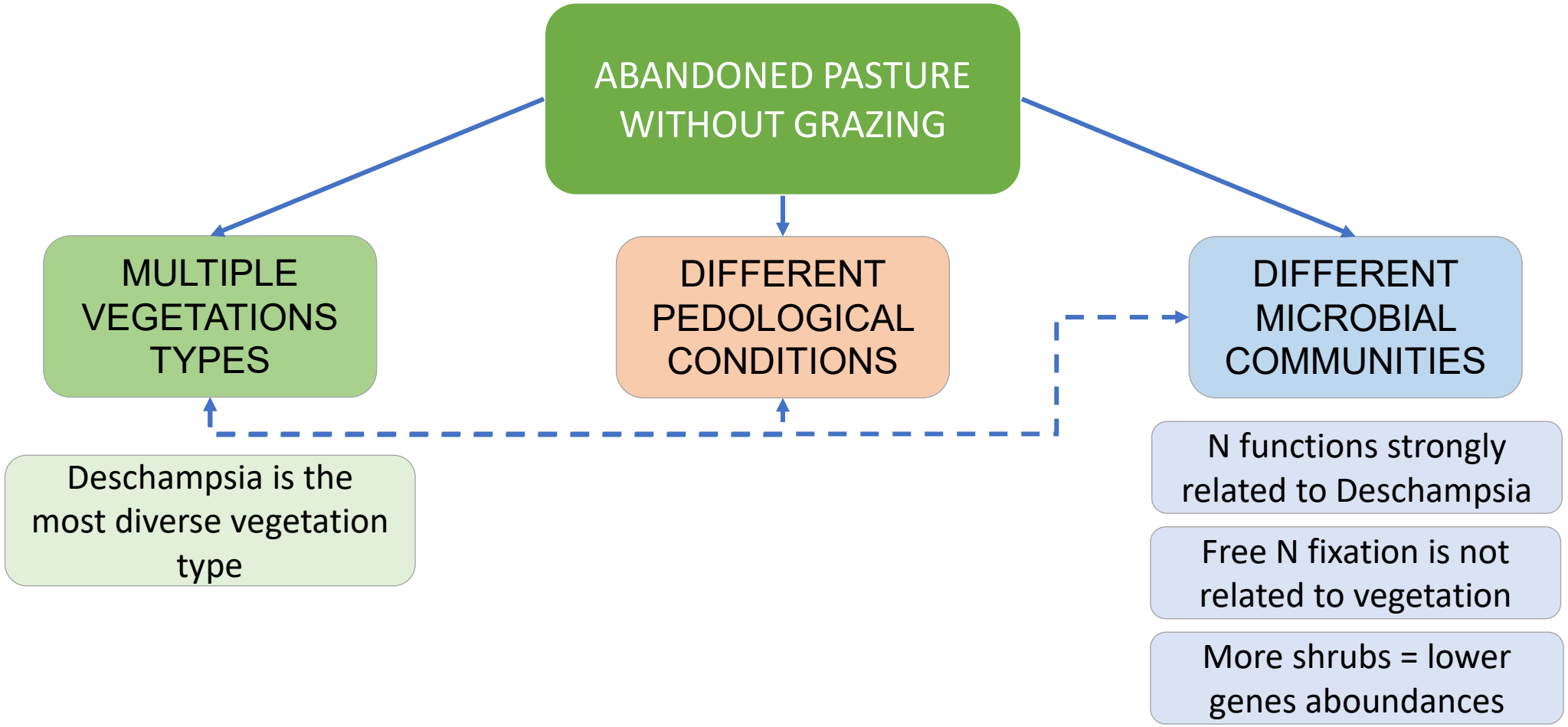
Functional profiles are more clustered by vegetation types than taxonomic profiles

Vegetation types

- **Vegetation 1**
- **Vegetation 2**
- **Vegetation 3**

pH is the most important driver for both taxonomic and functional profiles

Conclusions



Next step

2023 - 2024 → Restoration of grazing sheep:

- SOIL SAMPLING
- GPS TRACKING > INTENSITY USE OF PASTURE
- EXCLUSION CAGES (impact of grazing on vegetation)
- GHG FLUXES' MONITORING

Work in progress…

GPS TRACKING + SOIL ANALYSIS→ SERVICE/DISSERVICE OF PASTURE

AIM: IMPROVE SUSTAINABLE USE AND MULTIFUNCTIONALITY OF HIGHLAND PASTURES

THANK YOU

for your attention!

The study was carried out within the Agritech National Research Center and received funding from the European Union Next-GenerationEU (PIANO NAZIONALE DI RIPRESA E RESILIENZA (PNRR) – MISSIONE 4 COMPONENTE 2, INVESTIMENTO 1.4 – D.D. 1032 17/06/2022, CN00000022). In particular this contribution is related to the Spoke 7 "Integrated models for the development of marginal areas to promote multifunctional production systems enhancing agro-ecological and socio-economic sustainability" Task 7.1.2.: "Strategies for development of the agricultural and forestry systems, plant and animal biodiversity enhancement also at landscape level in marginal areas".

This study was carried out within the PNRR research activities of the consortium iNEST (Interconnected North-Est Innovation Ecosystem) funded by the European Union Next-GenerationEU (Piano Nazionale di Ripresa e Resilienza (PNRR) – Missione 4 Componente 2, Investimento 1.5 – D.D. 1058 23/06/2022, ECS 00000043).

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Microbial communities

Vegetation 1 - functions associated

Function	Function group	stat	p	
aliphatic non methane hydrocarbon degradation	Organic compound degradation	0.442	0.006	**
aromatic compound degradation		0.574	0.001	***
aromatic hydrocarbon degradation		0.442	0.006	**
aerobic ammonia oxidation	N cycle	0.573	0.001	***
denitrification		0.494	0.002	**
nitrate denitrification		0.494	0.002	**
nitrate reduction		0.576	0.001	***
nitrate respiration		0.498	0.002	**
nitrification		0.574	0.001	***
nitrite denitrification		0.494	0.002	**
nitrite respiration		0.494	0.002	**
nitrogen fixation		0.401	0.012	*
nitrogen respiration		0.498	0.002	**
ureolysis		0.347	0.033	*

Microbial communities