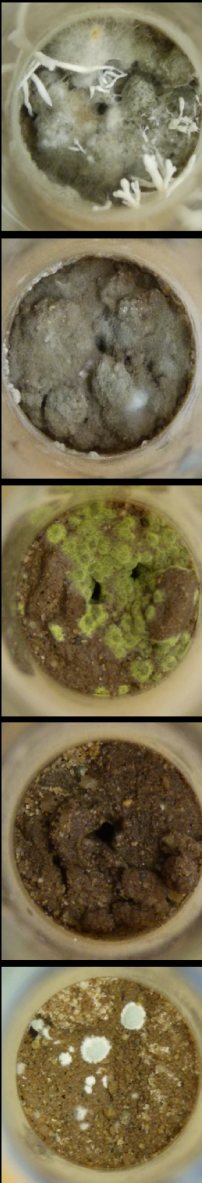


Microbial diversity drives carbon use efficiency in an artificial soil



Online 4-8
May 2020

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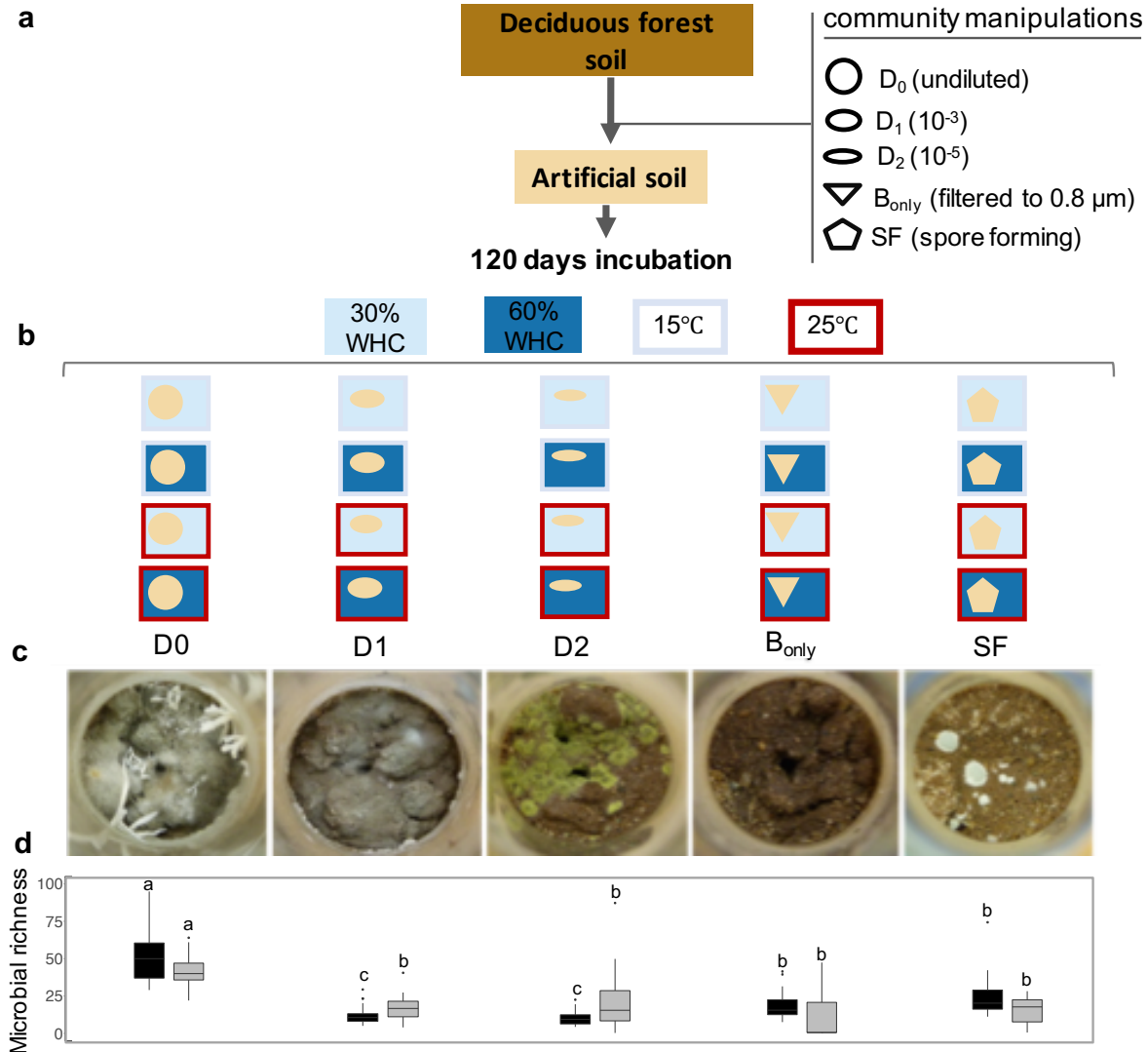
U.S. DEPARTMENT OF
ENERGY



Experimental design

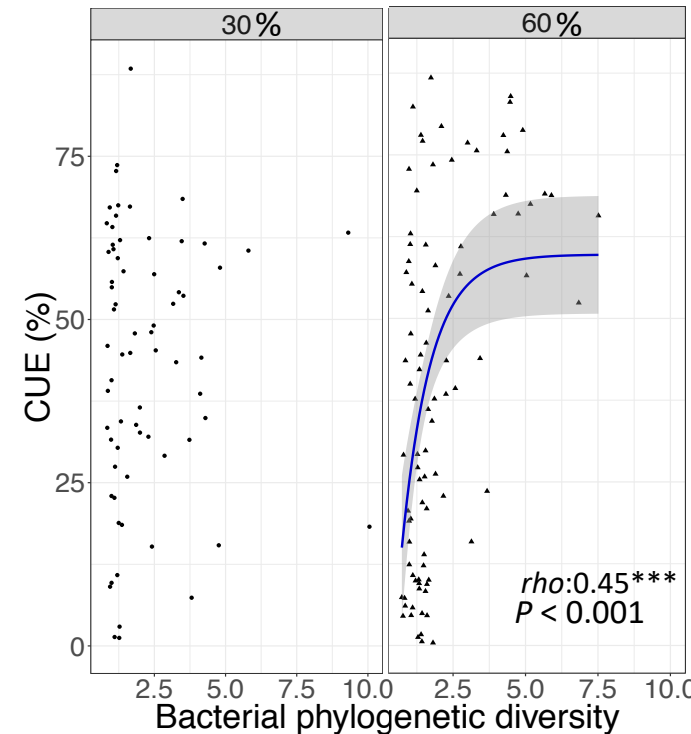
Manipulation of microbial communities to achieve different richness and community composition for bacteria and fungi between treatments in the model soil.

- The microbial diversity of a soil inoculum obtained from a temperate deciduous forest was manipulated by (1) sequential dilutions; (2) excluding fungi ("Bonly"); and (3) selecting for spore-forming microorganisms (SF)
- These inocula were added to a model soil incubated for 120 days under two moisture (30 and 60% water holding capacity) and two temperature (15 and 25°C) regimes.
- Images of model soils at the end of incubation.
- Average bacterial (black) and fungal (grey) richness (operational taxonomic units) for each diversity treatment.



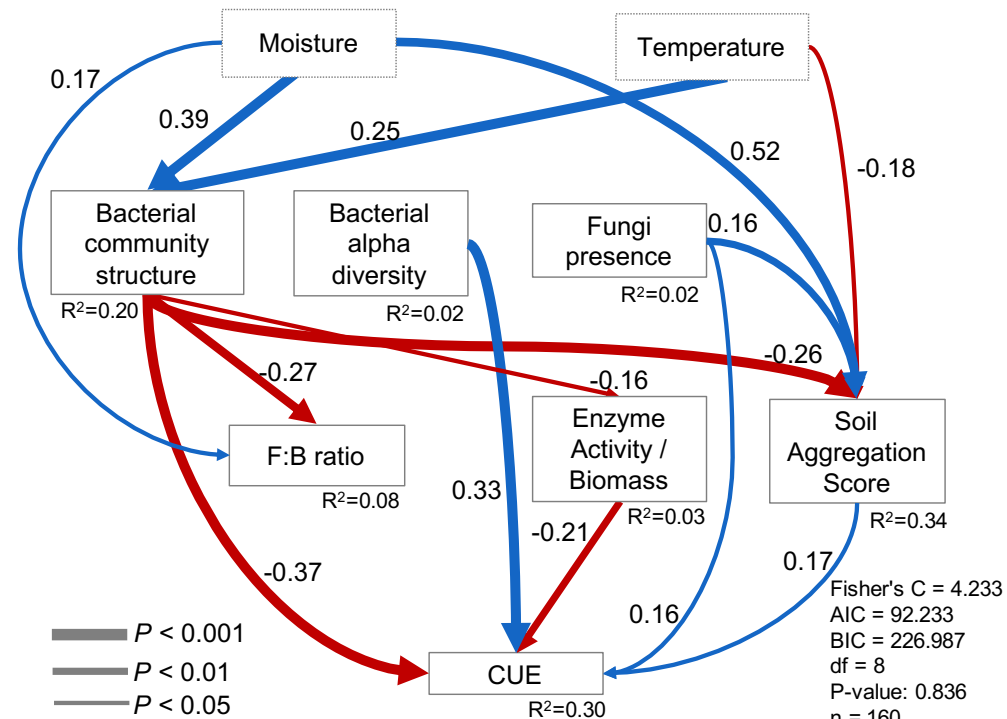
Domeignoz-Horta, *In review* Nat. Comm.

Main results



- CUE was positively related to diversity but only in the high moisture samples

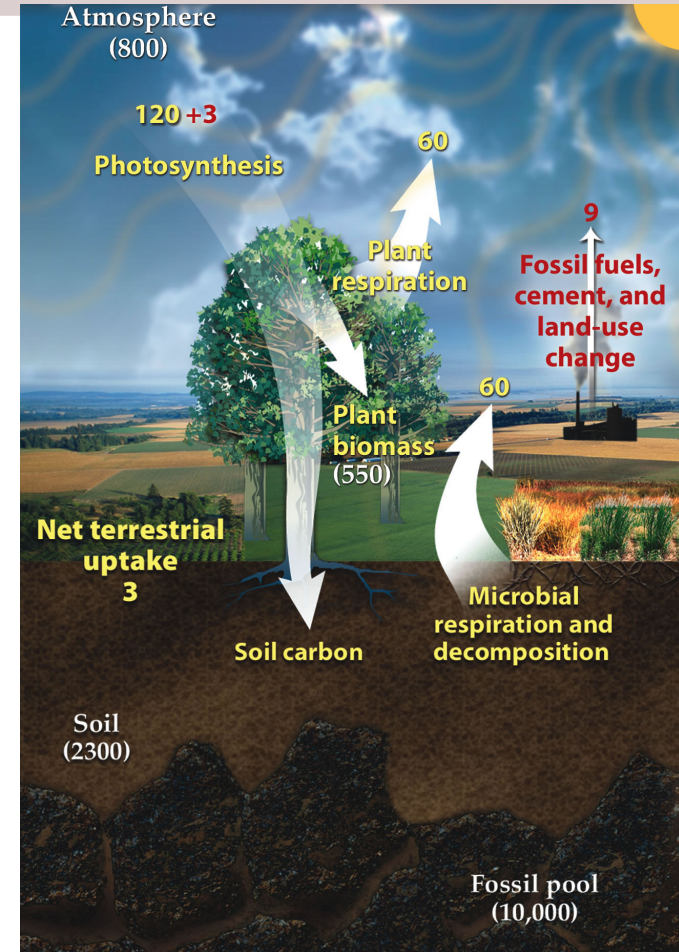
- Moisture and temperature indirectly affected CUE by impacting the microbial communities
- Direct drivers of CUE: bacterial community structure and diversity, fungal presence, enzyme activity and microbially driven soil aggregation



Soil Carbon Cycling

Contain up to 80% of terrestrial carbon pool

Microorganisms regulate soil carbon cycling



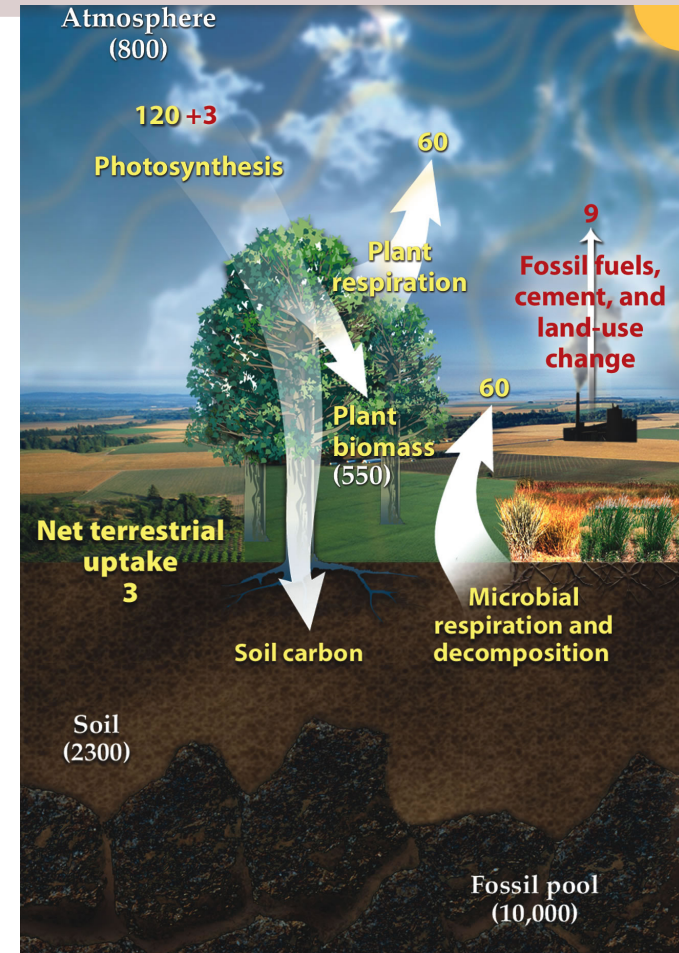
US DOE. *Climate Placemat: Energy-Climate Nexus*, US Dep. of Energy Office of Science.

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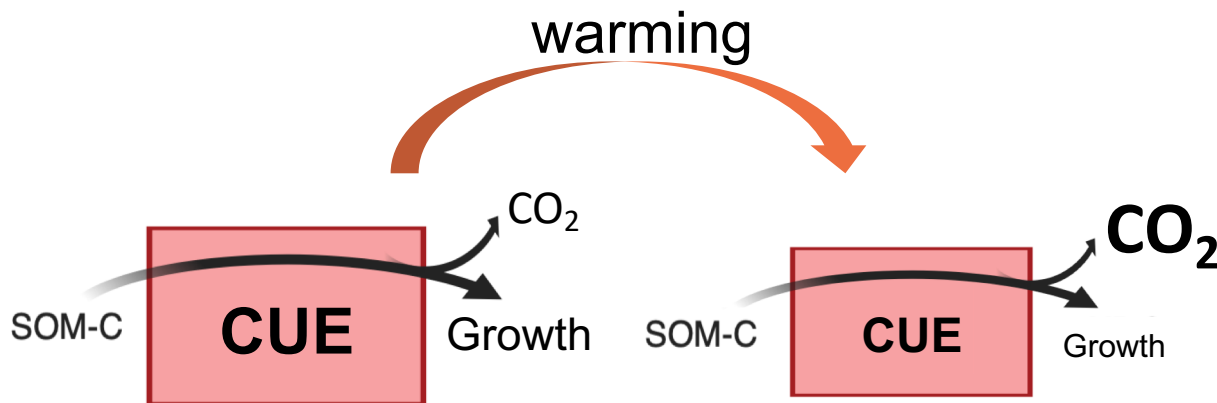
$$\text{CUE} = \frac{C_{\text{growth}}}{C_{\text{growth}} + \text{Respiration}} \times 100\%$$



US DOE. *Climate Placemat: Energy-Climate Nexus*, US Dep. of Energy Office of Science.

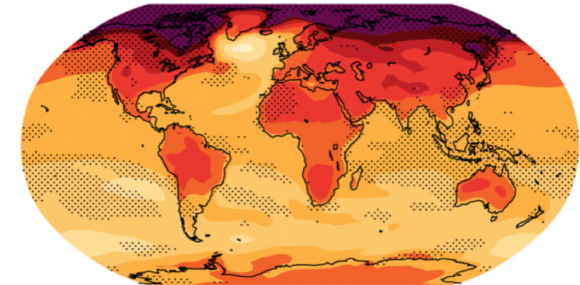
Climate drivers of CUE

How CUE respond to changes in climatic factors will determine the fate of Soil Organic Carbon (SOC)

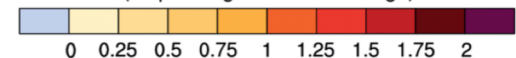


Temperature

CMIP5 : 2081-2100

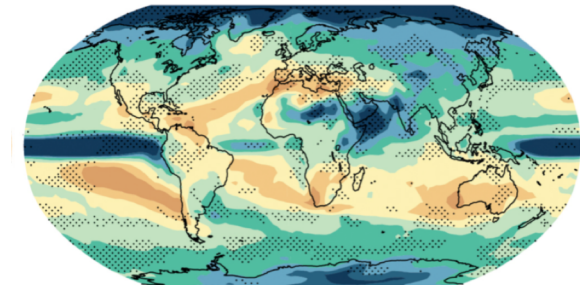


(°C per °C global mean change)

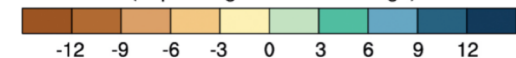


Moisture

CMIP5 : 2081-2100



(% per °C global mean change)

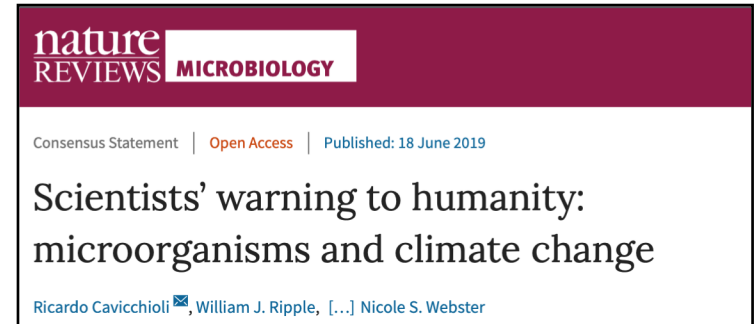


IPCC 2014

Microorganisms as drivers of CUE

Regulate soil carbon cycling

Important drivers but are also affected by global changes



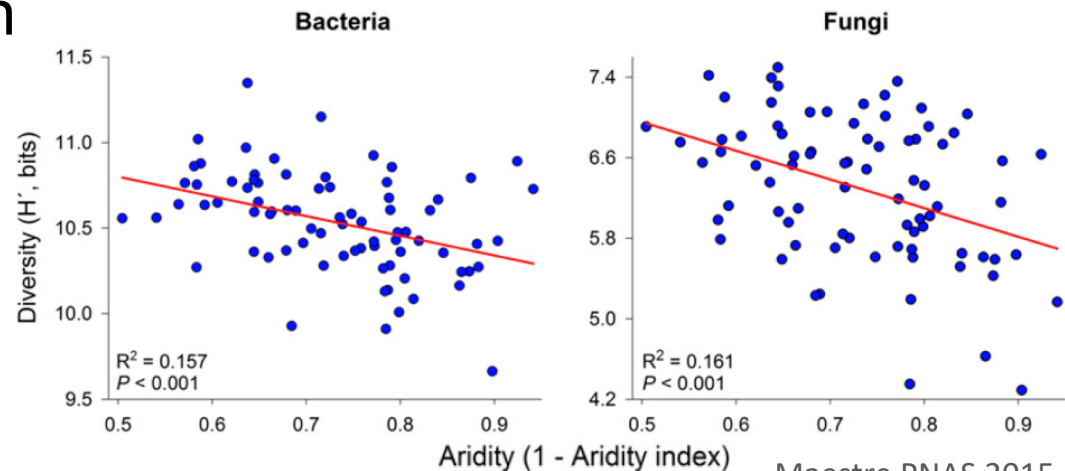
Microorganisms as drivers of CUE

Regulate soil carbon cycling

Important drivers but are also affected by global changes

Diversity loss and shifts in communities drive ecosystem changes

(Hooper Nat. Lett. 2011)



Maestre PNAS 2015

Microorganisms as drivers of CUE

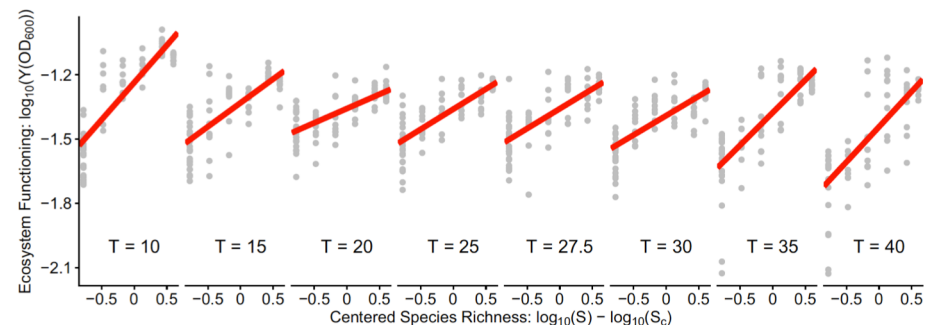
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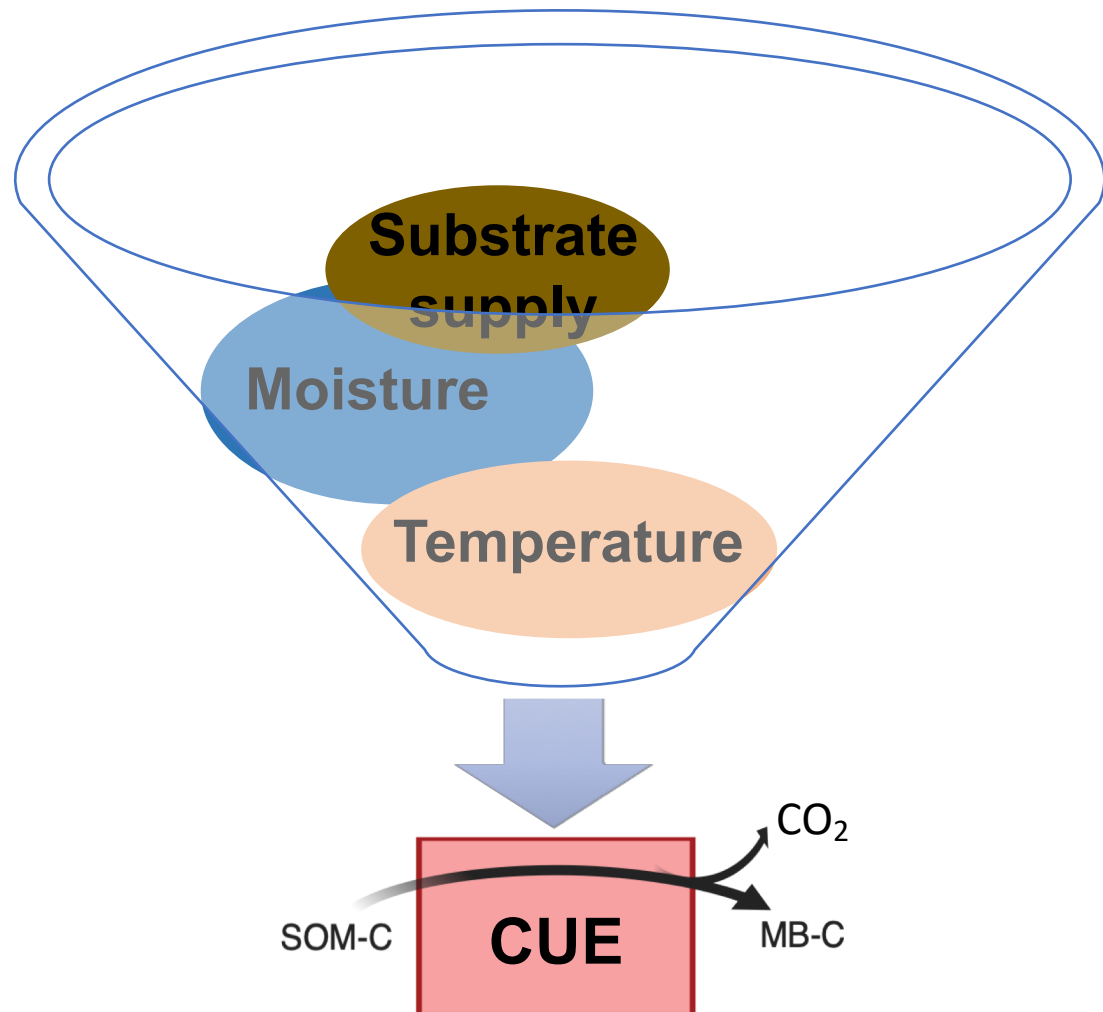
Temperature can modulate the diversity-ecosystem function relationship



García PNAS 2018

Drivers of CUE

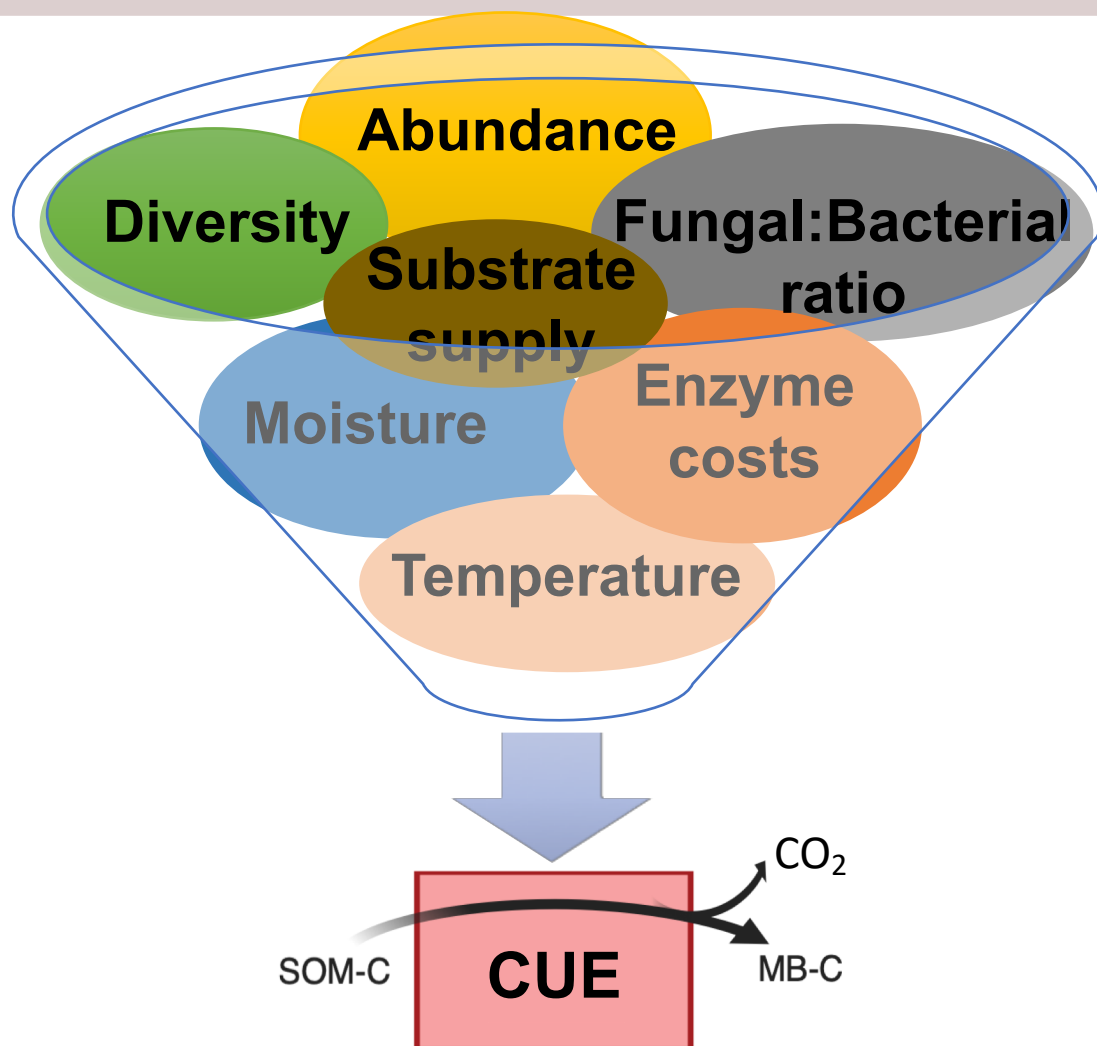
Direct (climate)



Drivers of CUE

Direct (climate)

Indirect (microbial communities)



Drivers of CUE

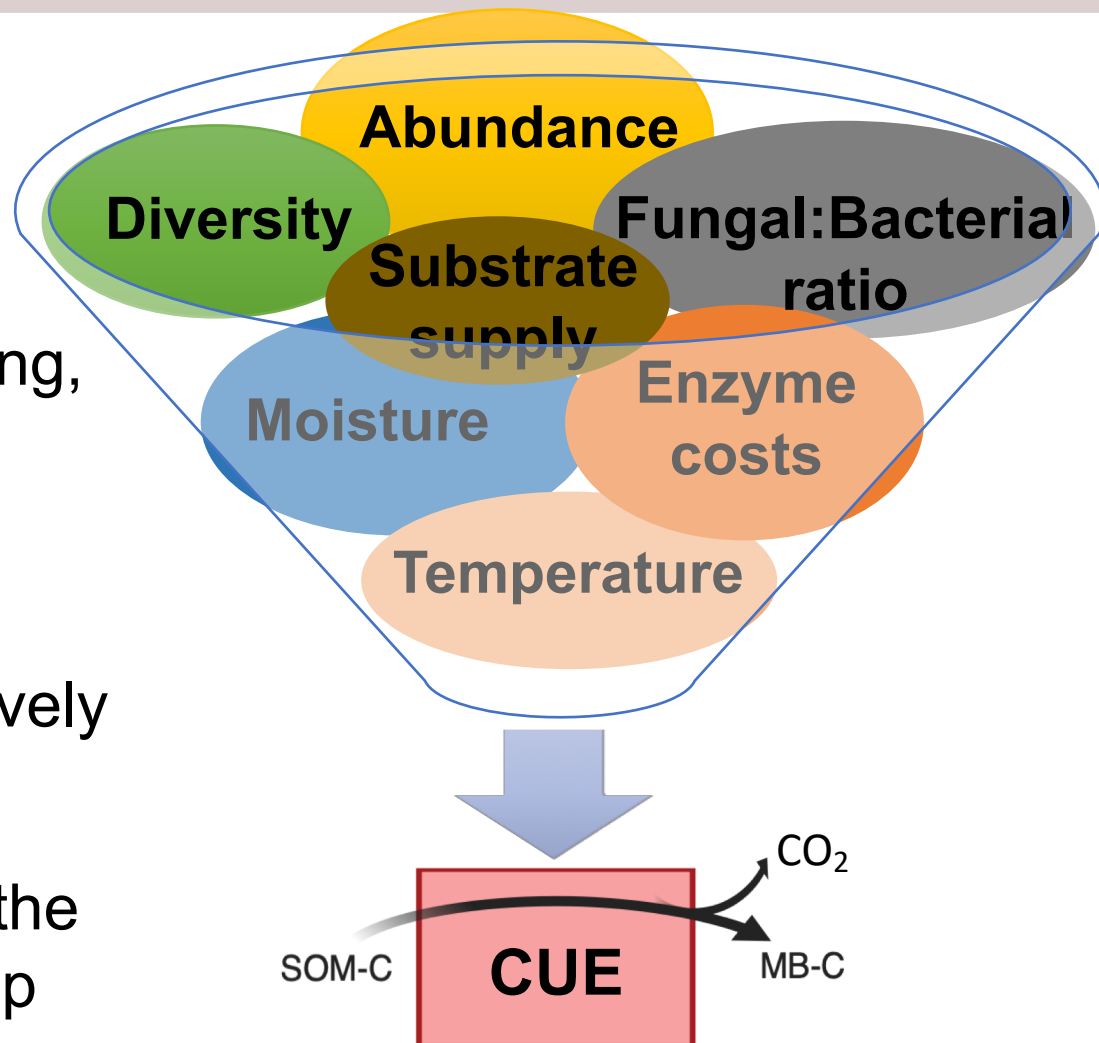
- Our aim:

Empirical evidence for the response of CUE to the combined effects of warming, drought and diversity loss

- Hypotheses:

Microbial diversity is positively related to CUE

Climatic factors modulate the diversity x CUE relationship



Methods

Sterile
C-free soil

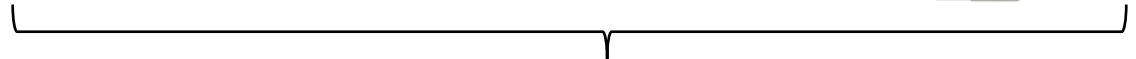
Clay



Silt



Sand

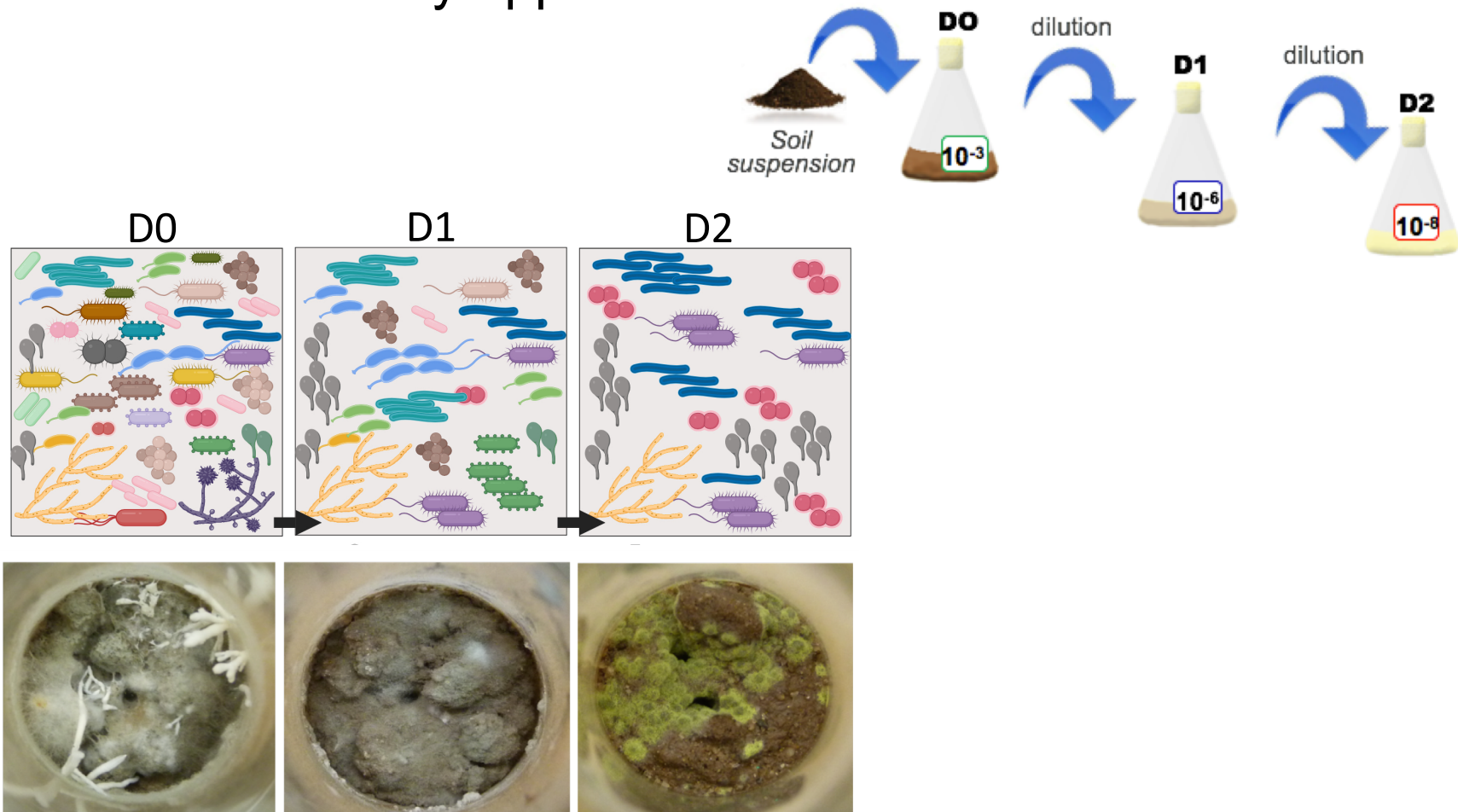


Artificial soil



Methods

Removal diversity approach



Methods

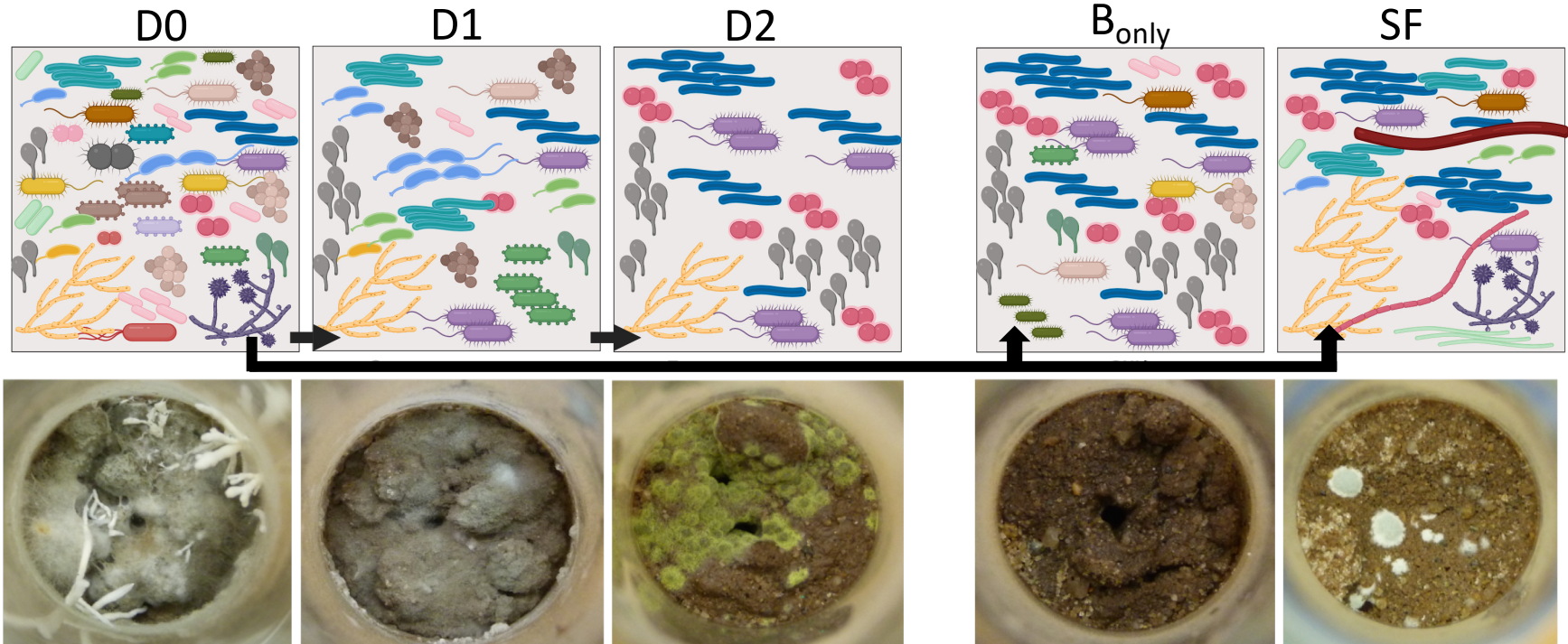
Removal diversity approach

Bacteria only (B_{only})

Spore forming (SF)

Filter to
0.8 μm

Heat and
Phenol



Assays

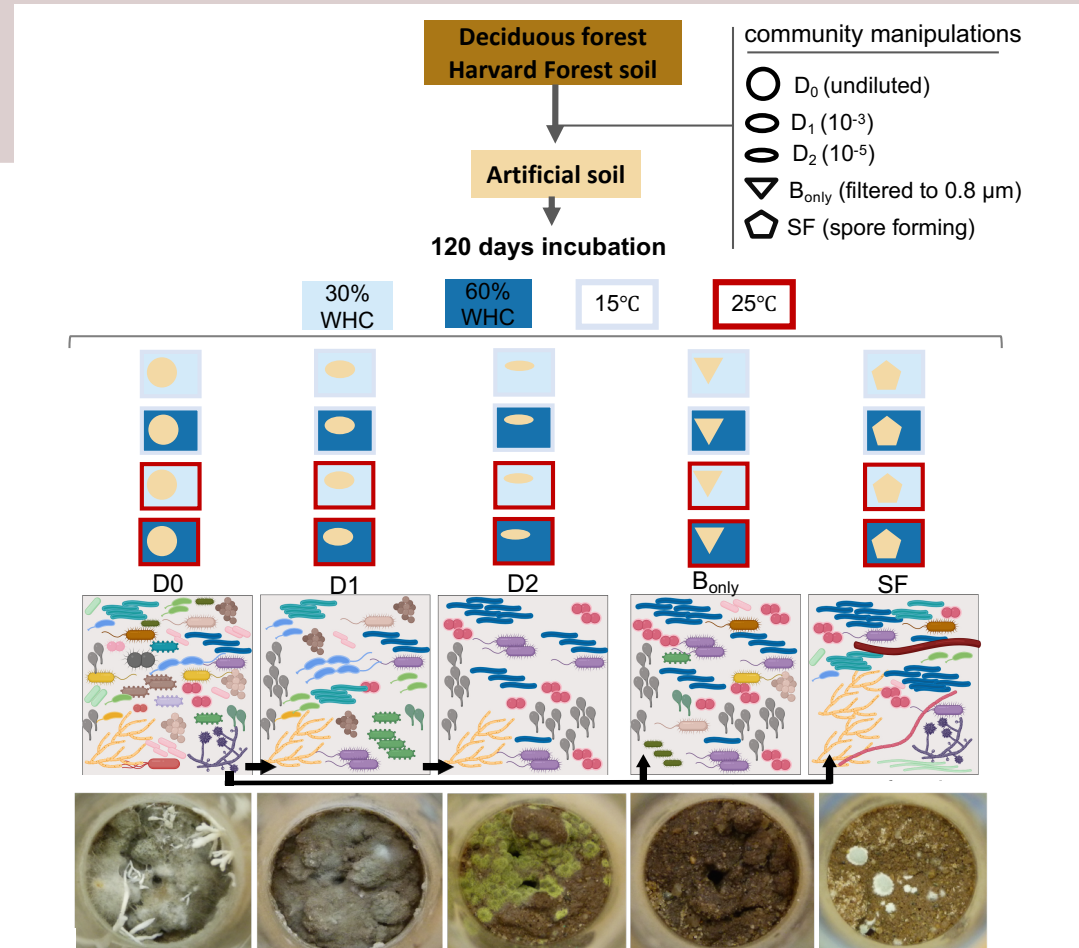
CUE (^{18}O -H₂O method)

Diversity of Bacteria and Fungi (MiSeq)

Abundance of Bacteria and Fungi (RT-qPCR)

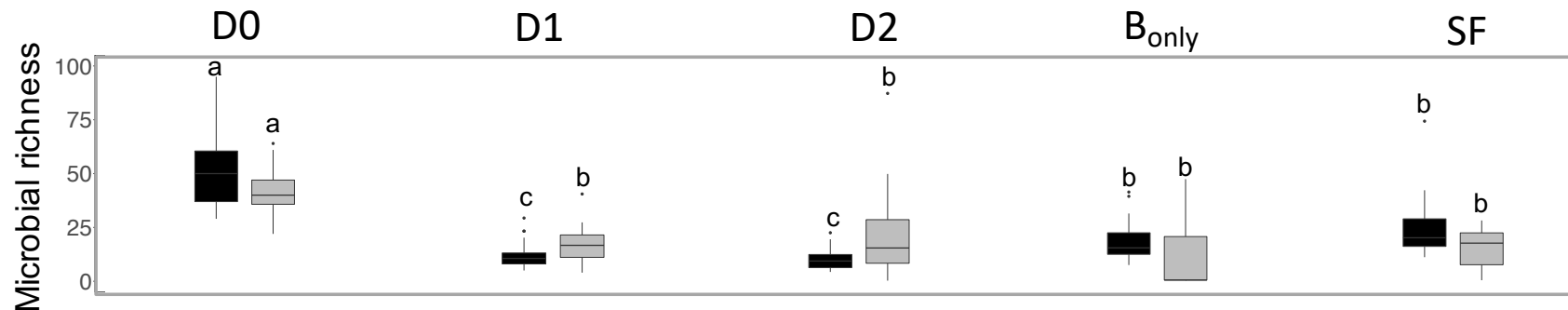
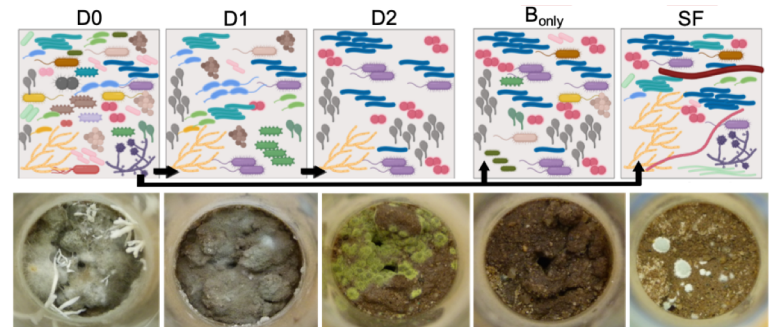
Extracellular enzyme activity (Betaglucosidase)

Soil aggregation (water stable aggregate formation)



Successful diversity manipulations

Diversity manipulations affected microbial richness



black: bacteria

grey: fungi

Drivers of microbial communities

Alpha diversity: diversity treatments

Community structure: diversity treatments and moisture and temperature factors

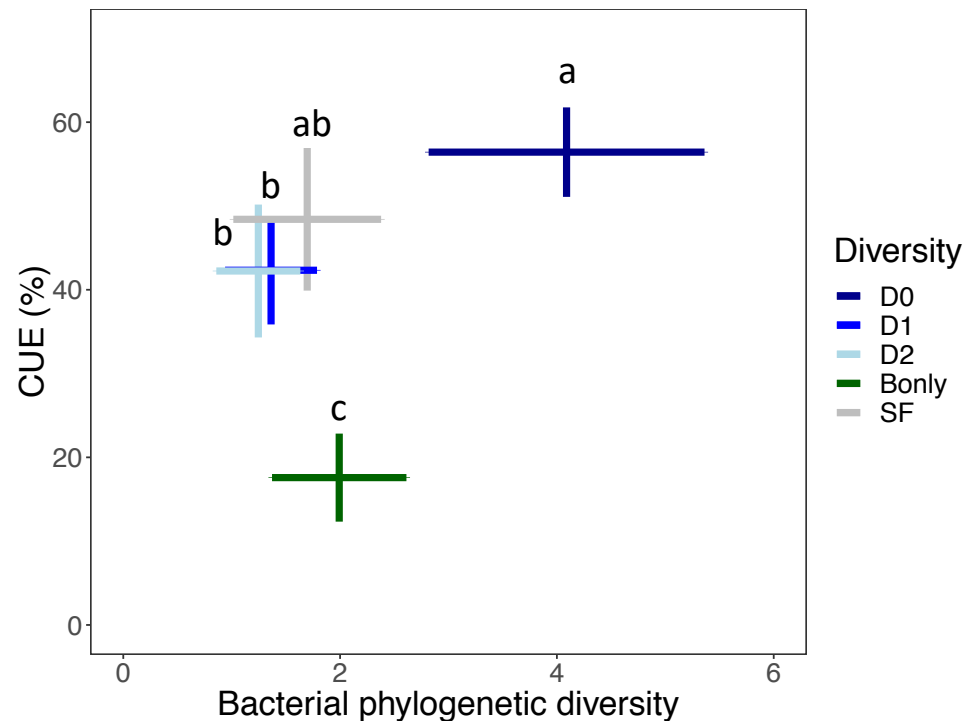
Percentage of explained variance:

Treatments	Bacterial alpha diversity (PD)	Fungal alpha diversity (shannon)	Bacterial community structure	Fungal community structure
Diversity	49.81***	33.37***	29.74***	21.81***
Moisture	0.04	0.11	10.57***	2.92***
Temperature	0.39	0.05	2.80***	1.52*
Diversity:Moisture	1.73	2.68	5.96***	1.91
Diversity:Temperature	2.46*	2.27	2.78*	1.86
Moisture:Temperature	1.61*	1.12	0.53	0.24
Diversity:Moisture:Temperature	1.88	0.95	1.41	1.11
Residuals	42.08	59.44	46.22	68.62

Higher CUE in the more diverse treatment

Overall the results support the hypothesis of more diverse treatments with high CUE

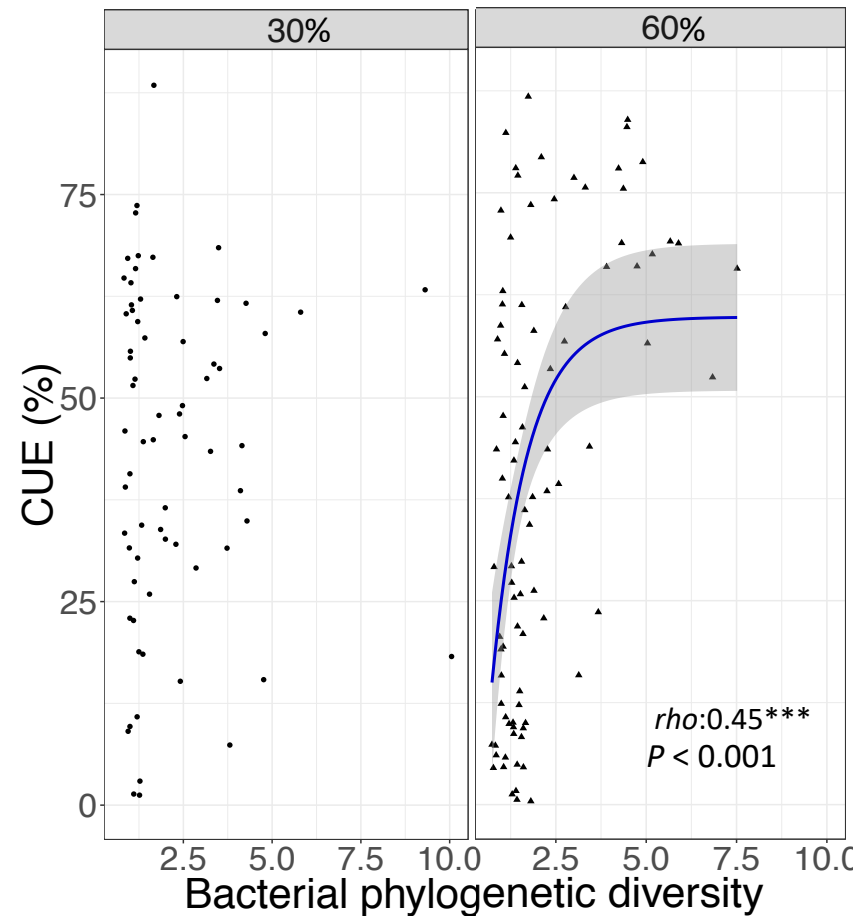
B_{only} treatment have the lowest CUE, suggesting that fungi presence was important to maintain high CUE



Moisture affect the CUE x Diversity relationship

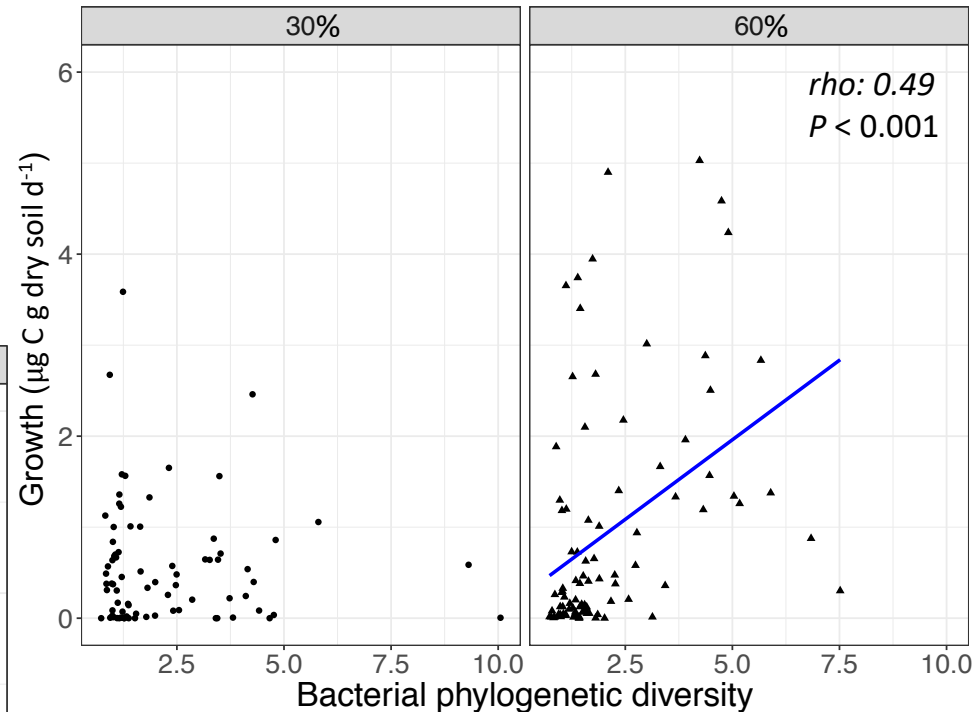
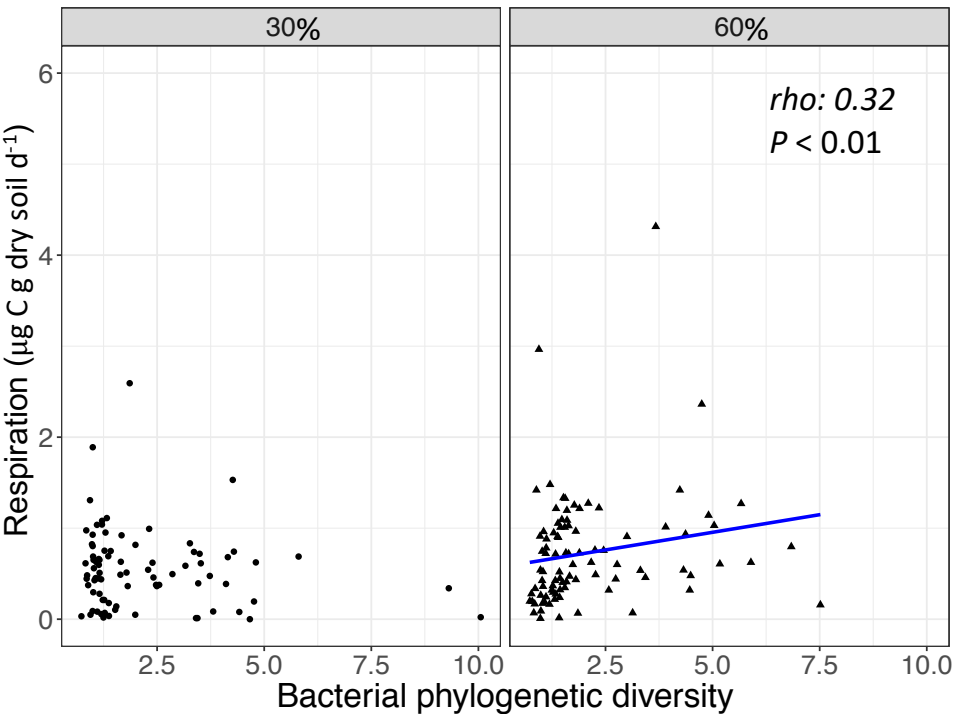
Diversity x CUE relationship:
positive relationship controlled
by moisture

- 1) Dry soils: organisms might be in isolation
- 2) Wet soils: allowed synergistic interaction between microorganisms (e.g. sharing amino-acids) (Washina, 2016)



CUE as a compilation of growth and respiration

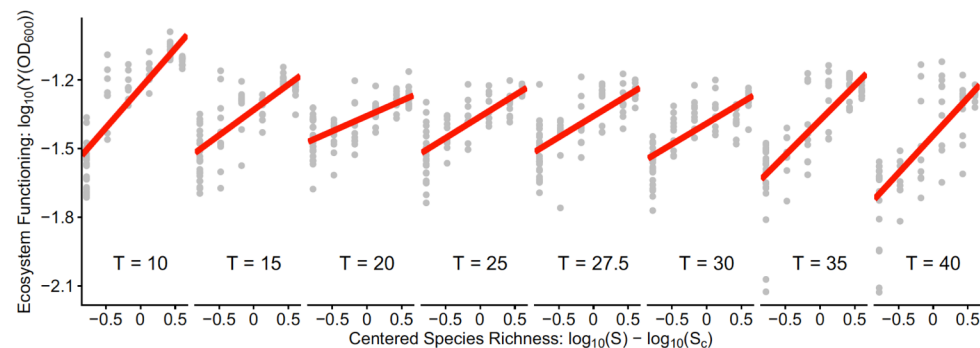
Growth increases faster with phylogenetic diversity than respiration



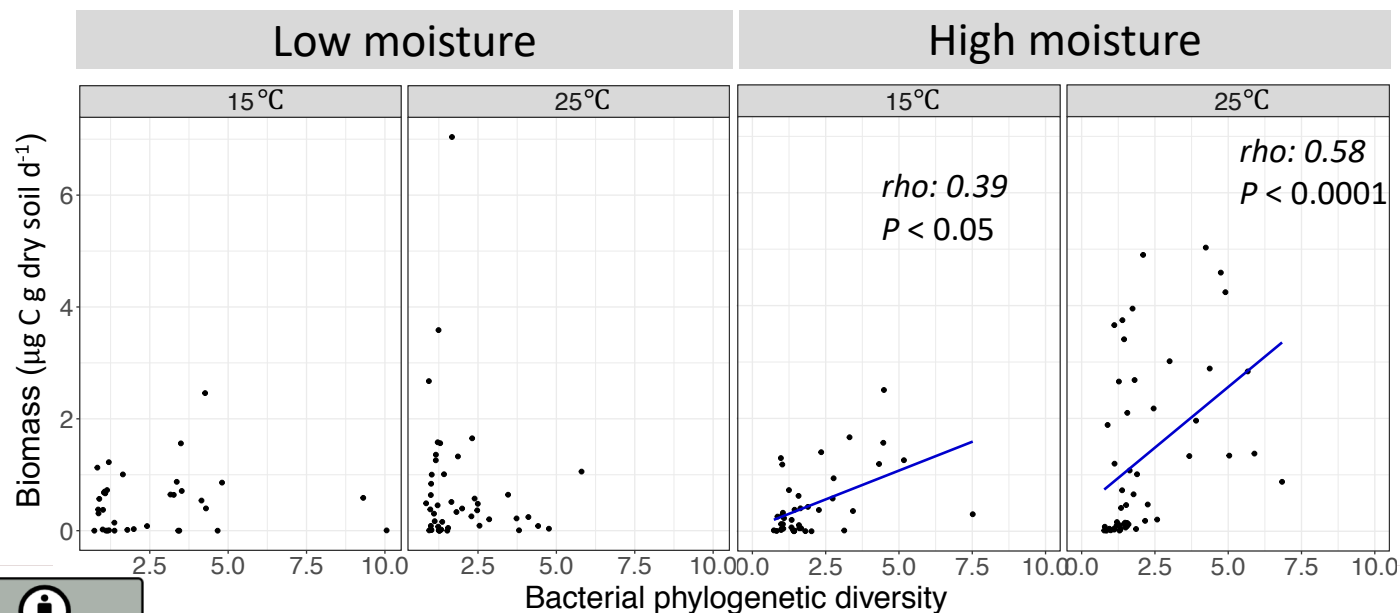
Moisture x Temperature affect on CUE

Temperature affect on CUE was constrained by moisture

Stronger relationship between biomass production and diversity in wet and 25°C.



García PNAS 2018

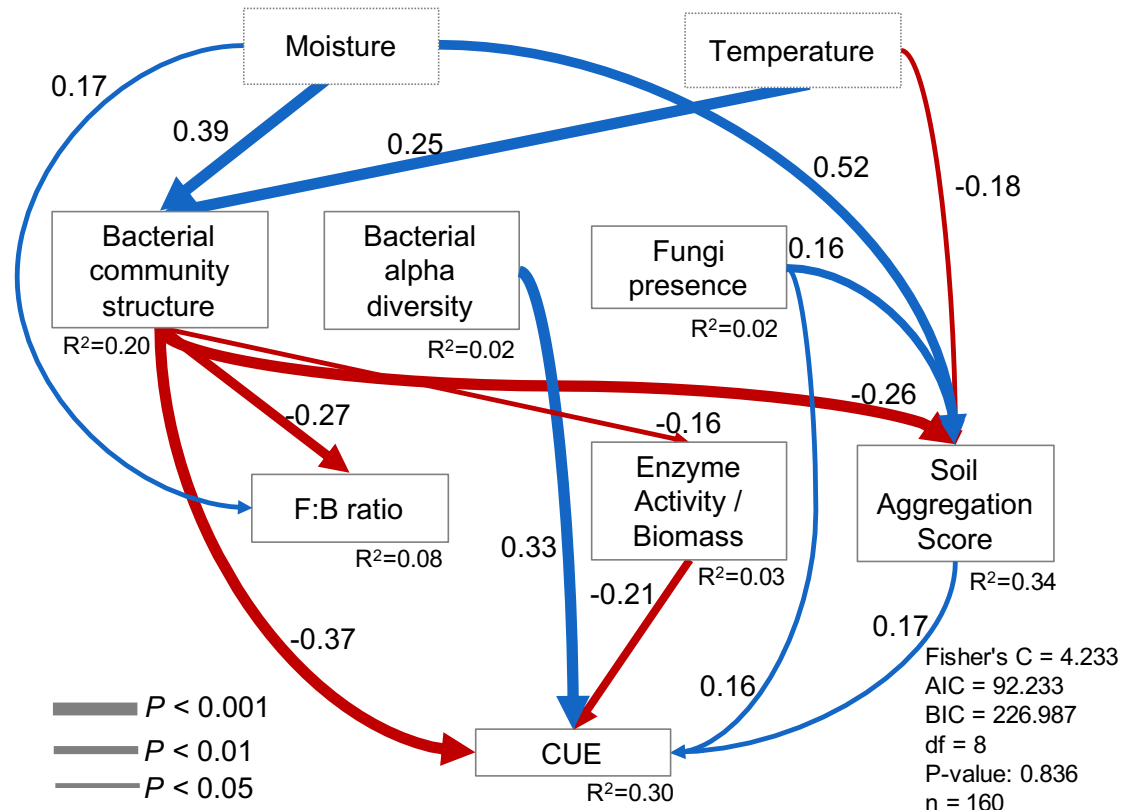


Indirect and direct drivers of CUE

• Structural Equation Modeling (SEM):

Moisture and temperature indirectly affected CUE by impacting the microbial communities

Direct drivers of CUE: bacterial community structure and diversity, fungal presence, enzyme activity and microbially driven soil aggregation



Take home message

- Moisture and temperature: drive indirectly CUE by impacting the microbial communities. It was the microorganisms that directly affected CUE
- The positive relationship between CUE and diversity was controlled by moisture
- Our results suggests that drier soils diminished the synergistic effect between diversity and CUE

Questions?

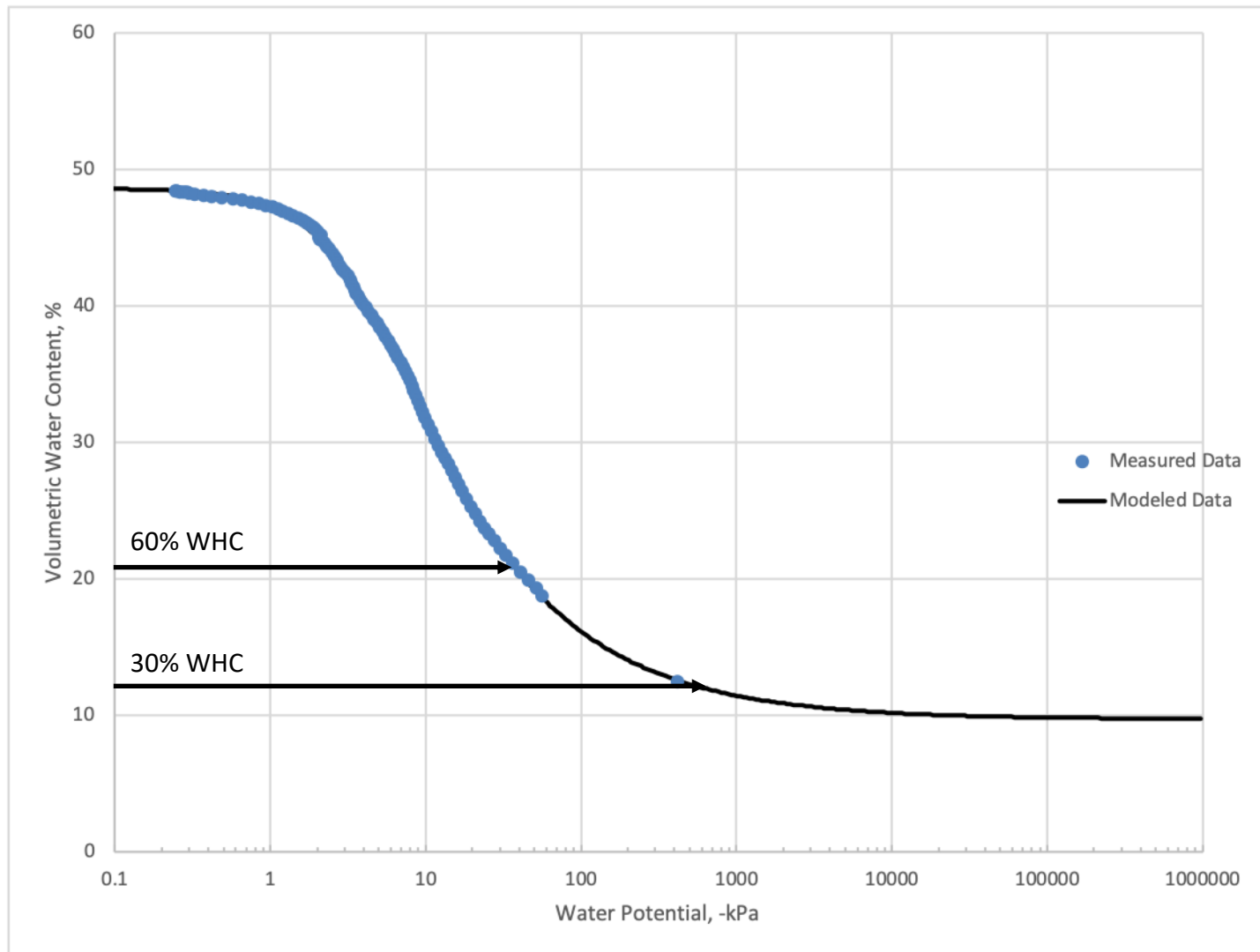


Fig S13. Water retention curve. Blue points indicate water potential measured by the HYPROP method and the black line is a fitted model to the data based on the van Genuchten model.