Beyond microbes: mapping *soil food web* biodiversity via lipid fingerprinting

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01 WHY THIS MATTERS

Soil life runs the **carbon cycle**, **crop yield**, and the **climate**. Yet the whole **soil food web** has never been profiled on a single platform.

~1,500 Gt	~95 %	~1/3
SOIL ORGANIC CARBON	GLOBAL FOOD PRODUCTION	OF SOILS DEGRADED

Soils hold **more carbon than atmosphere and vegetation combined**, feed nearly all of us, and are degrading fast.

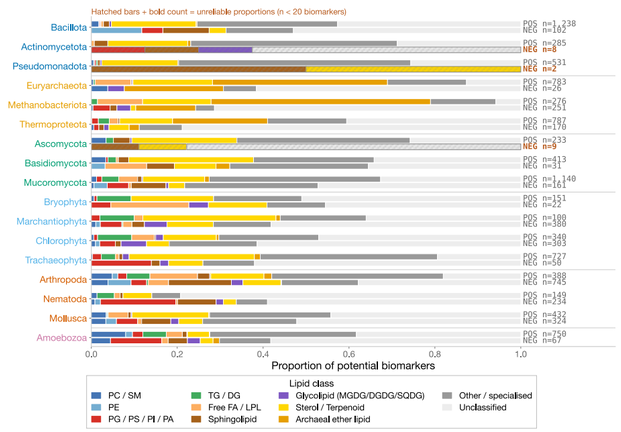
> EU **soil-monitoring laws, restoration targets, and carbon markets** are being defined *now* — and all need scalable biological indicators to function.

> Each kingdom currently needs its own toolkit — **sequencing** for microbes, **PLFA** for biomass, **microscopy and faunal extraction** for animals — and the resulting data don't combine.

02 WORKFLOW

01	**SOURCE**	112 species · axenic + non-axenic cultures · direct soil collections · 6 kingdoms · 17 phyla
02	**EXTRACT**	Total intact polar lipids · modified Bligh–Dyer
03	**MEASURE**	Dual-polarity UPLC–Orbitrap MS/MS
04	**ANNOTATE**	Feature finding + molecular networks (MZmine, GNPS2)
05	**BIOMARKERS**	Phylum-annotated atlas · 10,454 POS / 5,741 NEG features
06	**FINGERPRINT**	Bray–Curtis SIMPER → per-phylum fingerprints
07	**APPLY**	Source decomposition · ClimGrass long-term climate plots

03 BIOMARKERS PER PHYLUM



Each phylum carries a distinctive lipid-class mix. POS (top bar) and NEG (bottom) capture complementary chemistry.

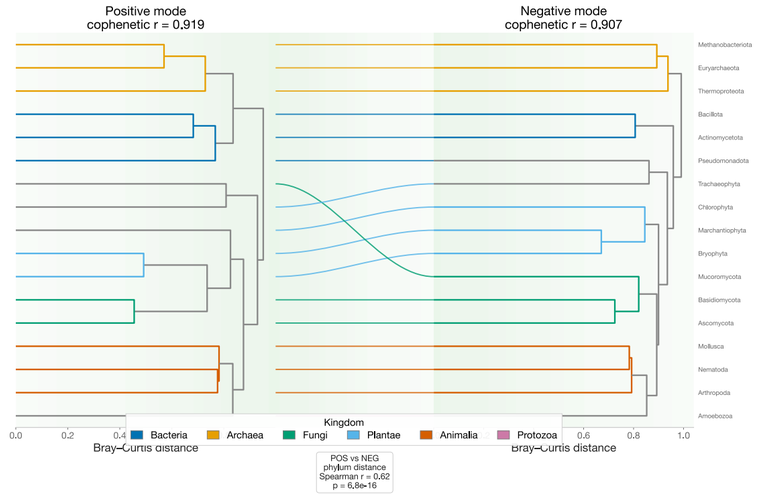
04 LIPIDOMES = PHYLOGENY

17 phyla · 6 kingdoms · unsupervised

UPGMA clustering of phylum-level lipidomes recovers known evolutionary relationships — **no taxonomic priors**.

0.919 COPHENETIC R · POS

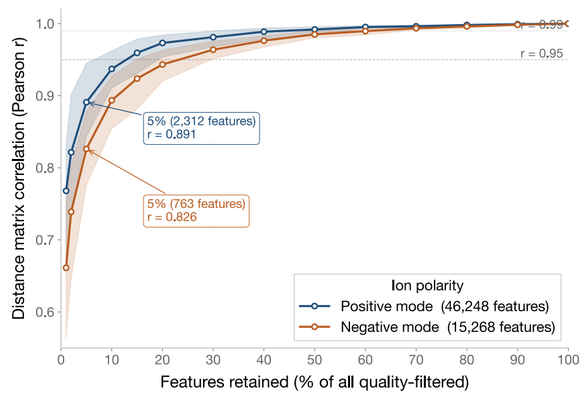
0.907 COPHENETIC R · NEG



POS (left) and NEG (right) cluster the 17 phyla on the same tree — independently.

05 DISTRIBUTED SIGNAL

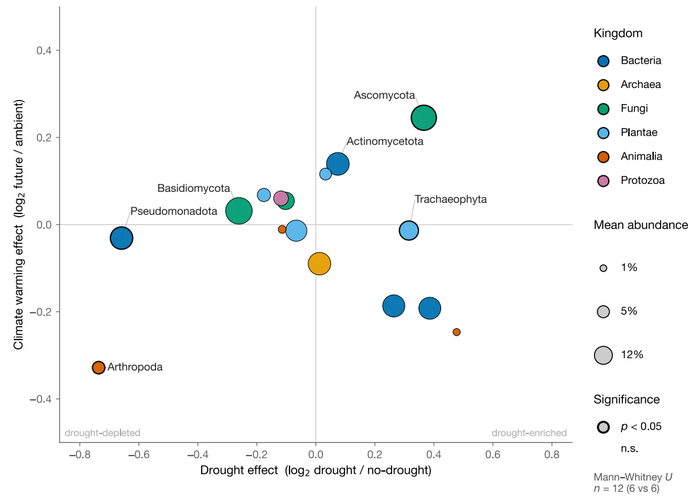
Robust to feature loss



Drop 95% of features at random — phylum distances still rank correctly. The signal lives across the whole lipidome, not in a few biomarkers.

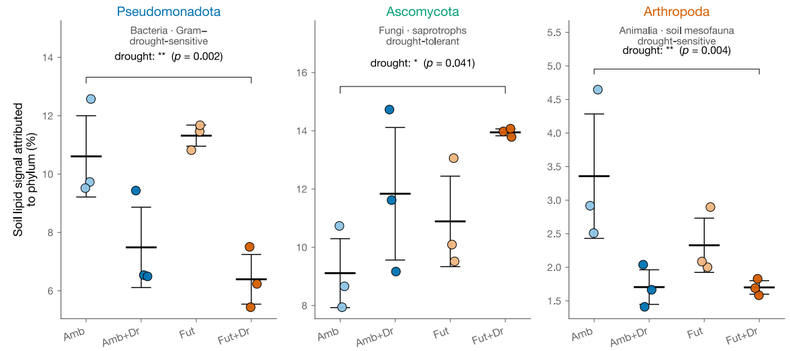
06 PHYLUM EFFECT MAP

Drought × warming · ClimGrass



From one lipid extract per plot, each phylum lands on its drought × warming response. Ringed = significant ($p < 0.05$); point size = abundance.

07 THREE DROUGHT SIGNATURES



*Three kingdoms, three drought stories in one experiment: **Pseudomonadota** ↓ p=0.002, **Ascomycota** ↑ p=0.041, **Arthropoda** ↓ p=0.004.*

08 TAKE-HOME MESSAGE

i.

One extract → six kingdoms

Bacteria, archaea, fungi, plants, soil fauna and protozoa from a single lipid extraction — no separate assays for microbes vs animals.

ii.

Common axes across the food web

Every organism profiled in the same lipid-feature space — drought responses of a bacterium and an arthropod sit on the same plot, in the same units.

iii.

Discovery without priors

The lipid pattern alone reveals community structure — useful where reference sequences or established markers are sparse or absent.

iv.

A reusable phylum atlas

~16,000 phylum-annotated biomarkers (POS + NEG) and per-phylum SIMPER fingerprints — apply either to your own soil samples.

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