Rhizosphere interface microbiome reassembly by arbuscular mycorrhizal fungi weakens cadmium migration dynamics

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Hong-Rui Wang, Xin-Ran Du, Zhuo-Yun Zhang, Fu-Juan Feng, Jia-Ming Zhang. 2023. Rhizosphere interface microbiome reassembly by arbuscular mycorrhizal fungi weakens cadmium migration dynamics. ***iMeta*** 2: 133.
https://doi.org/10.1002/imt2.133

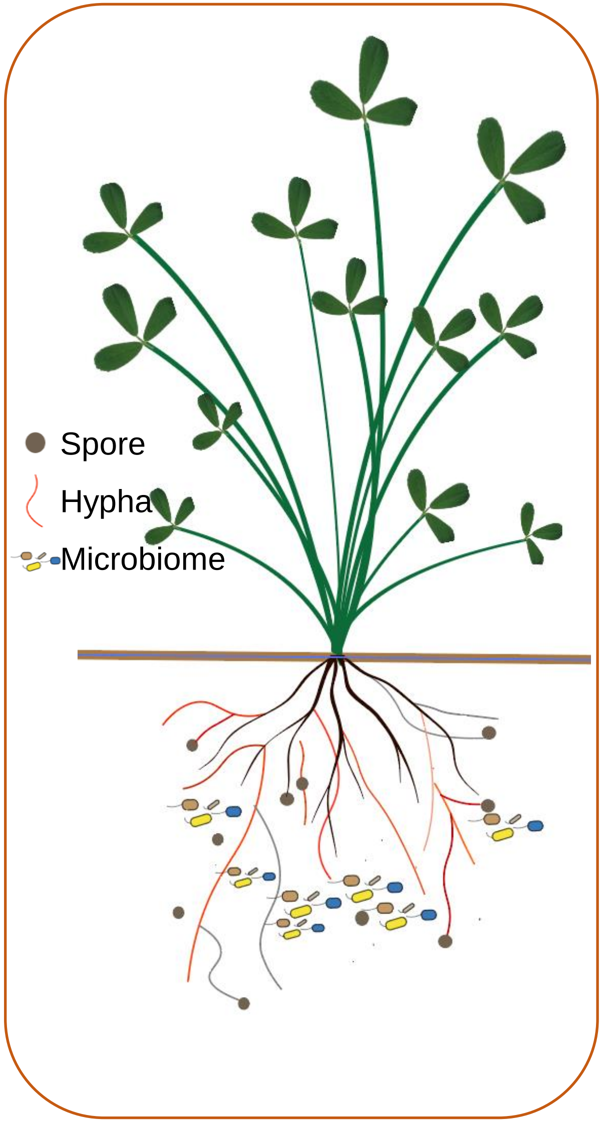
Introduction

- Improve photosynthesis
- Improve the activity of antioxidant enzymes
- Reduced absorption and transport
- Regulatory plant hormone
- Regulates ion transport channels

AMF enhance plant resistance

Interaction

Nonspecific	Specific
Physiological metabolism	Signal transduction
Metal migration and morphological transformation	Regulation of gene expression



Fungal biomass sorbent → Cd

Excretion → Cd

Rebuilding microbiome → Cd

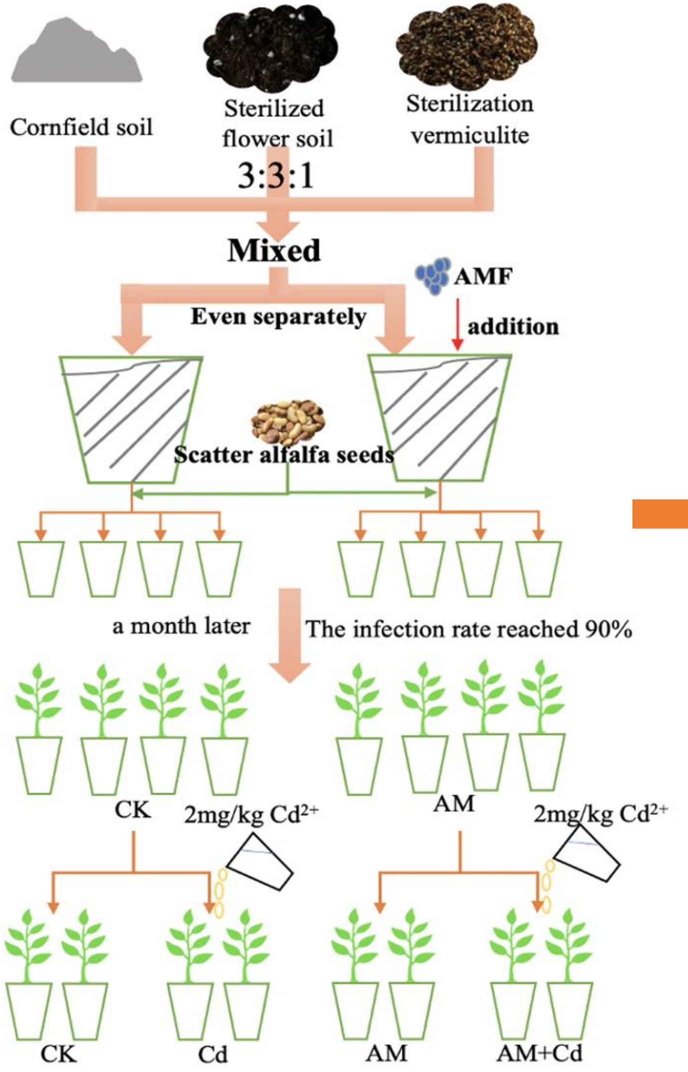
AMF → Cd migration

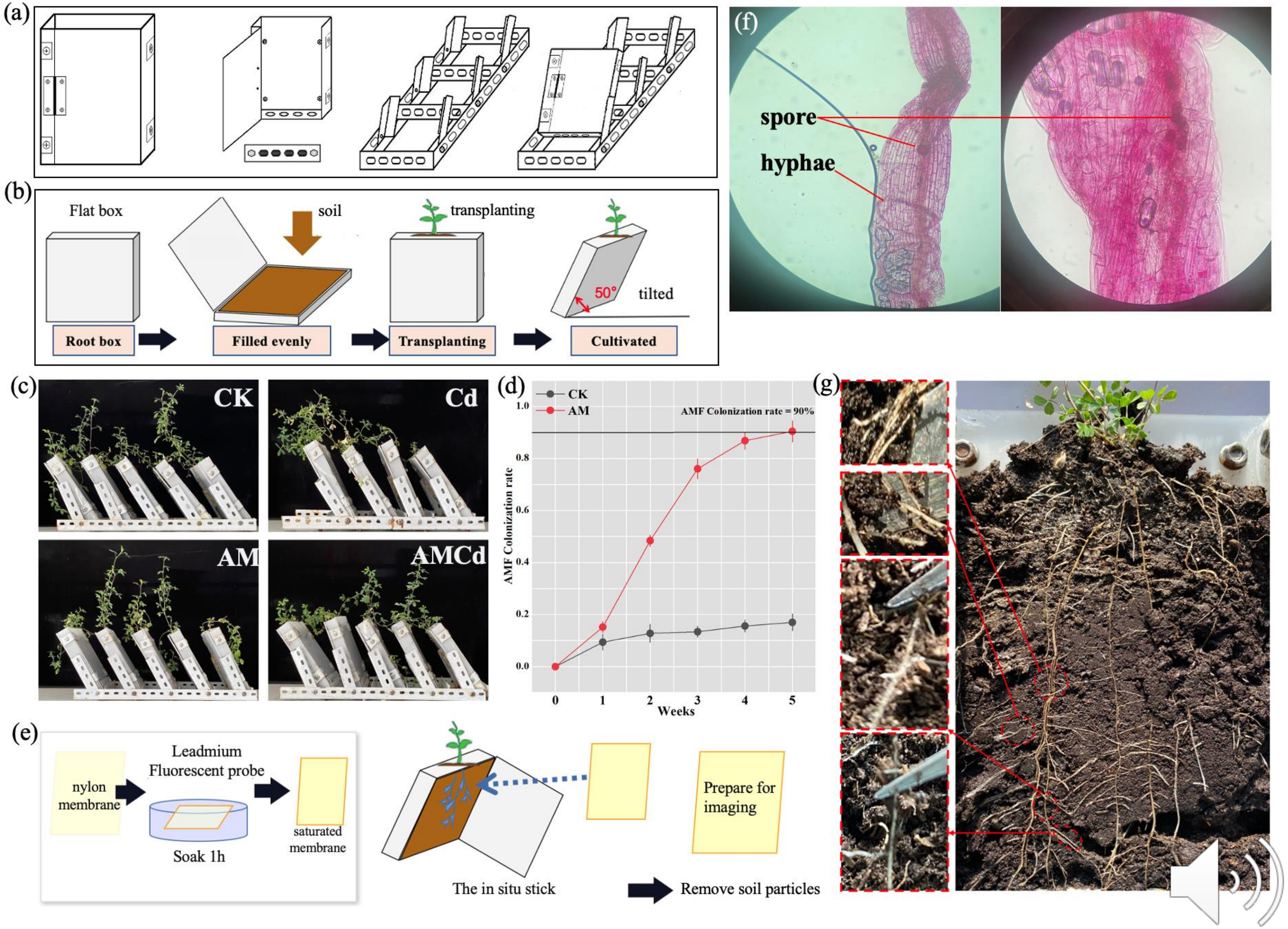
excretion

cadmium	soil	microbiome
Location Form Content	Eh pH SWC Enzymatic activity	Diversity Keystone species Ecological function Community building mechanism

The blank area

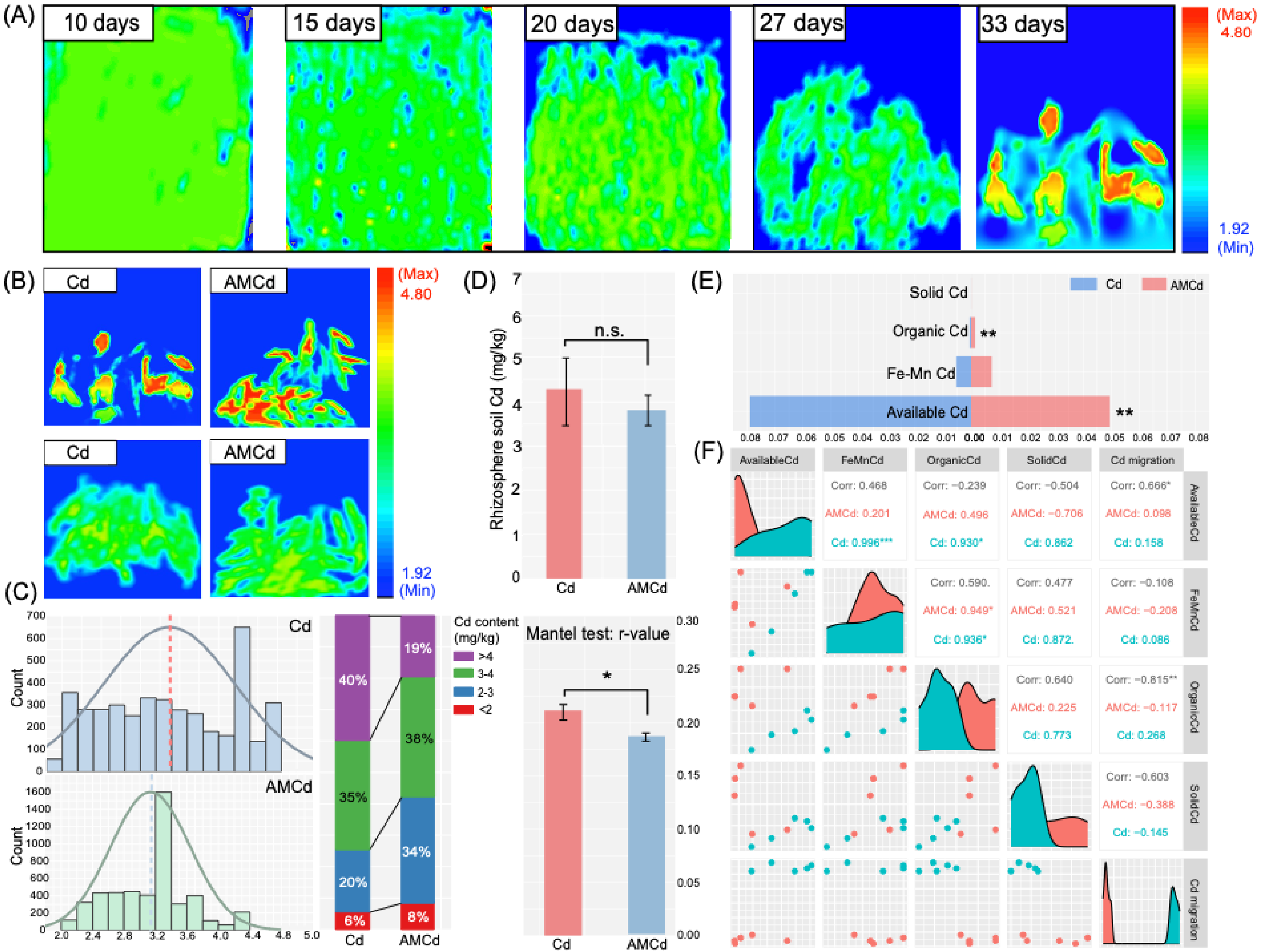
Materials and Methods





Results

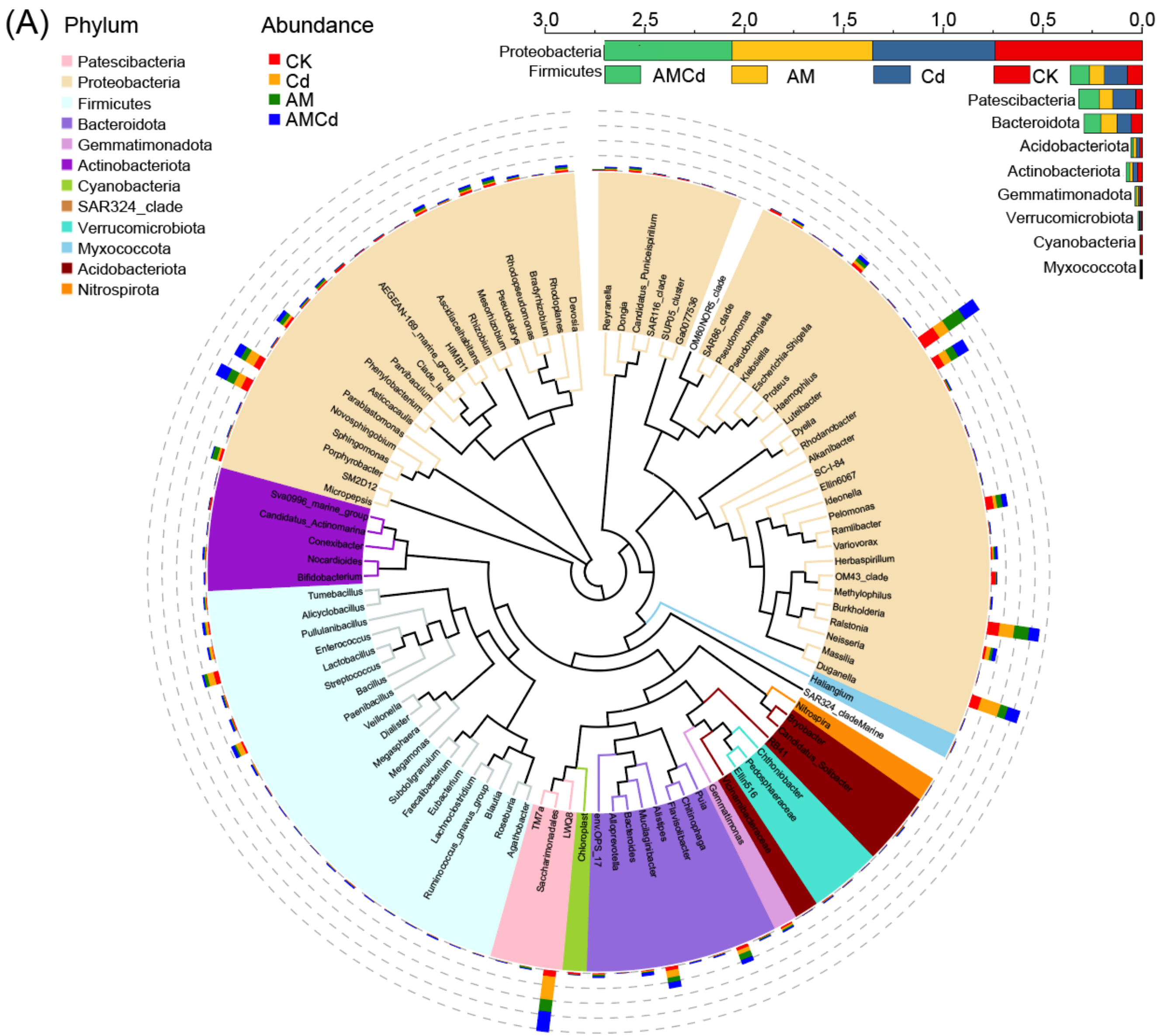
AMF drives the reduction of Cd migration in the rhizosphere

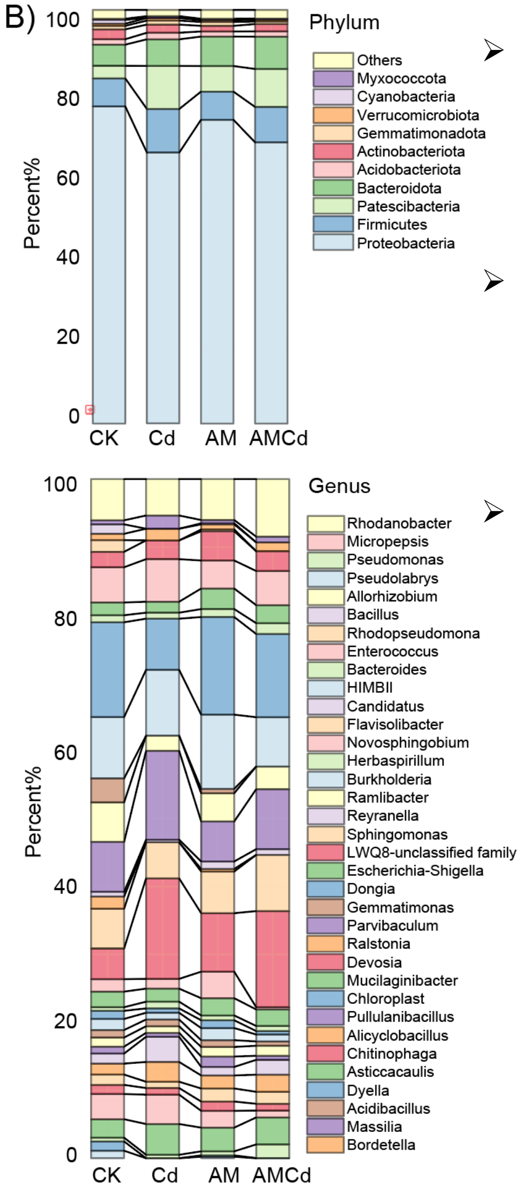


- Until day 27, Cd was distributed along the plant roots, and hot spots of Cd accumulation appeared on day 33.
- The hotspot percentage in the AMCd was lower than Cd exposed.
- Cd concentration in the AMCd lower than Cd exposure, but not significant.
- Available Cd change to organic-bound Cd is the reason that Cd hot spots dispersion.

Results

Changes in rhizosphere soil bacteria community

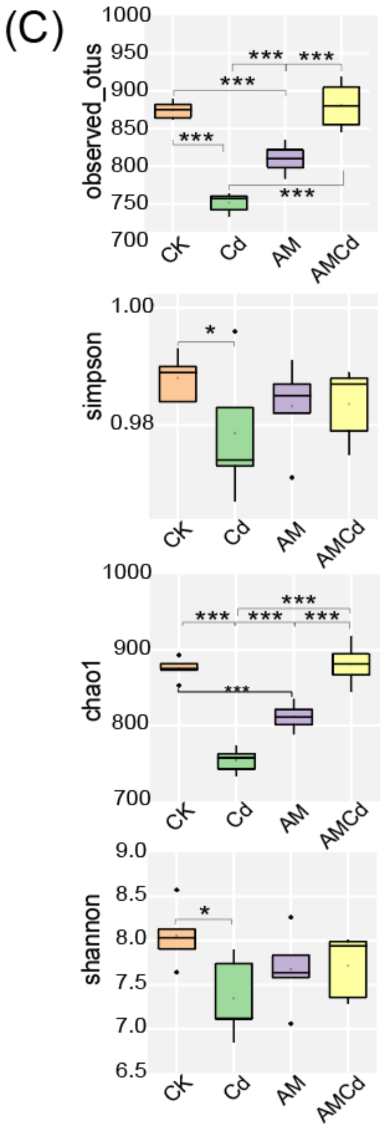


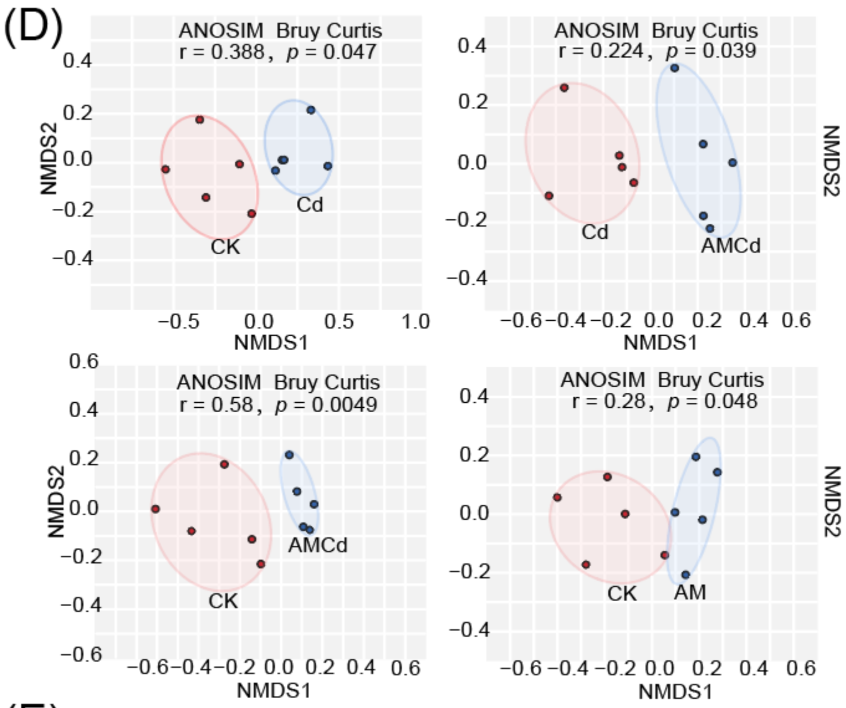


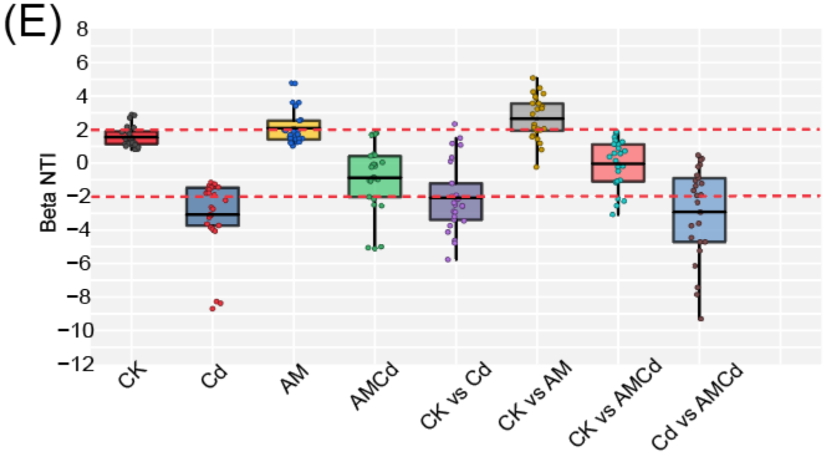
- ➢ *Proteobacteria* was the largest, followed by *Firmicutes*, *Patescibacteria*, *Bacteroidetes*, *Actinobacteriota* and *Acidobacteriota*.
- ➢ *Proteobacteria* and *Actinobacteriota* decreased significantly after Cd exposure compared to CK.
- ➢ In the AMCd treatment, *Dyella* and *Sphingomonas* showed significant increase compared to Cd. Notably, *Sphingomonas* exhibited higher levels than in CK, while *Dyella* did not show a significant difference from CK.

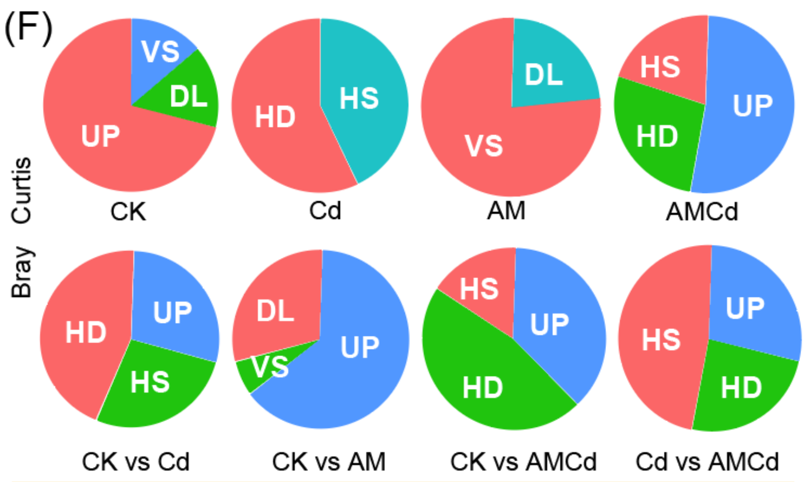
Results

Changes in rhizosphere soil bacteria community







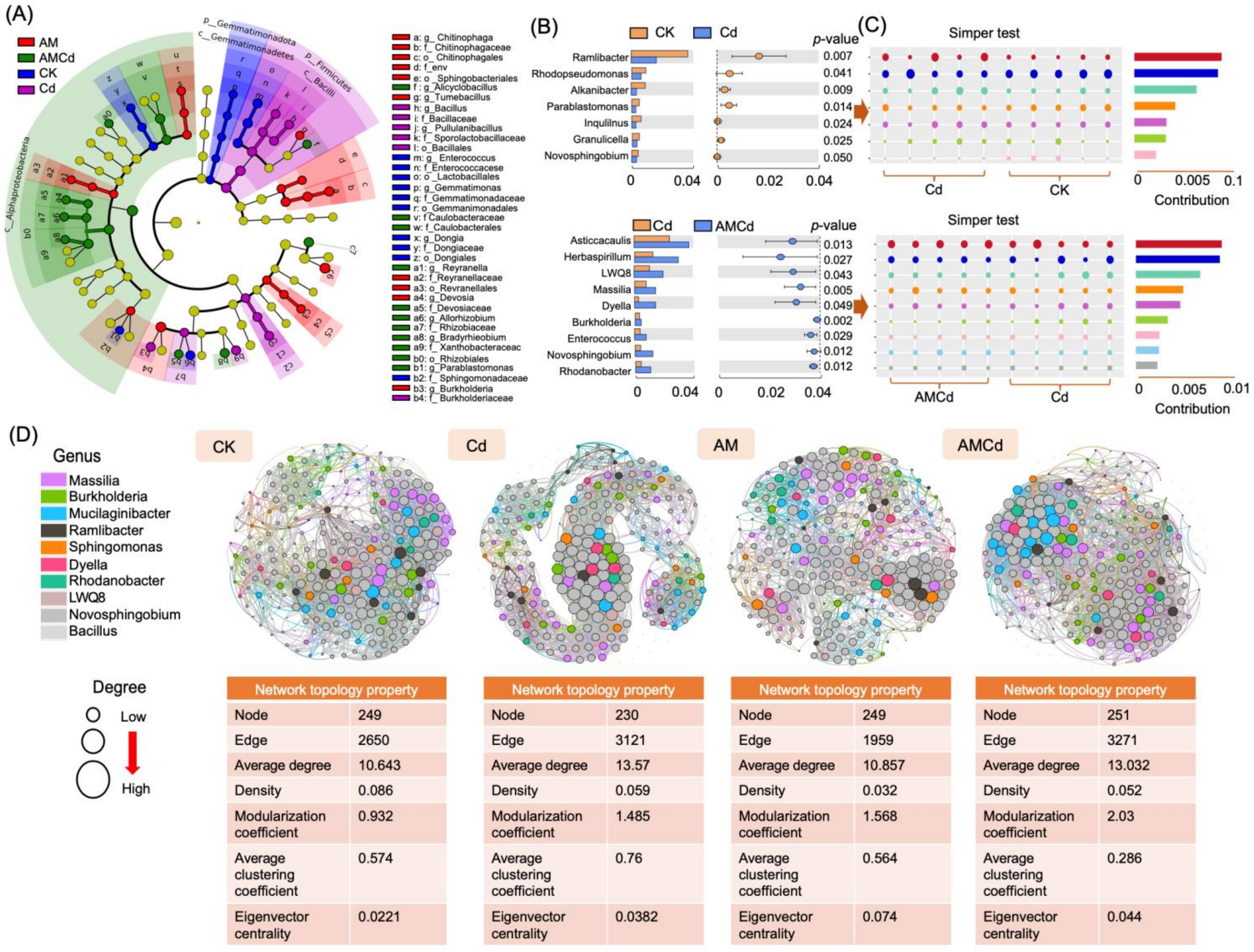


UP: Undominated processes	VS: Variable selection
DL: Dispersal limitation	HS: Homogeneous selection
HD: Homogenizing dispersal	

- AM treatment and Cd exposure resulted in variations in the bacterial community.
- CK and AMCd treatments were random processes, Cd and AM treatments were deterministic.
- Both Cd and AM were primary factors in the assembly of bacterial communities, favoring deterministic processes. However, Cd was associated with homogeneous selection, while AM was linked to variable selection.

Results

Bacterial biomarker and keystone



Network topology property	
Node	249
Edge	2650
Average degree	10.643
Density	0.086
Modularization coefficient	0.932
Average clustering coefficient	0.574
Eigenvector centrality	0.0221

Network topology property	
Node	230
Edge	3121
Average degree	13.57
Density	0.059
Modularization coefficient	1.485
Average clustering coefficient	0.76
Eigenvector centrality	0.0382

Network topology property	
Node	249
Edge	1959
Average degree	10.857
Density	0.032
Modularization coefficient	1.568
Average clustering coefficient	0.564
Eigenvector centrality	0.074

Network topology property	
Node	251
Edge	3271
Average degree	13.032
Density	0.052
Modularization coefficient	2.03
Average clustering coefficient	0.286
Eigenvector centrality	0.044

Paired t-test

- Significantly different in CK vs. Cd were *Ramlibacter* and *Rhodopseudomonas.*
- In Cd vs. AMCd were *Asticcacaulis* and *Bacteroides*

SIMPER analysis

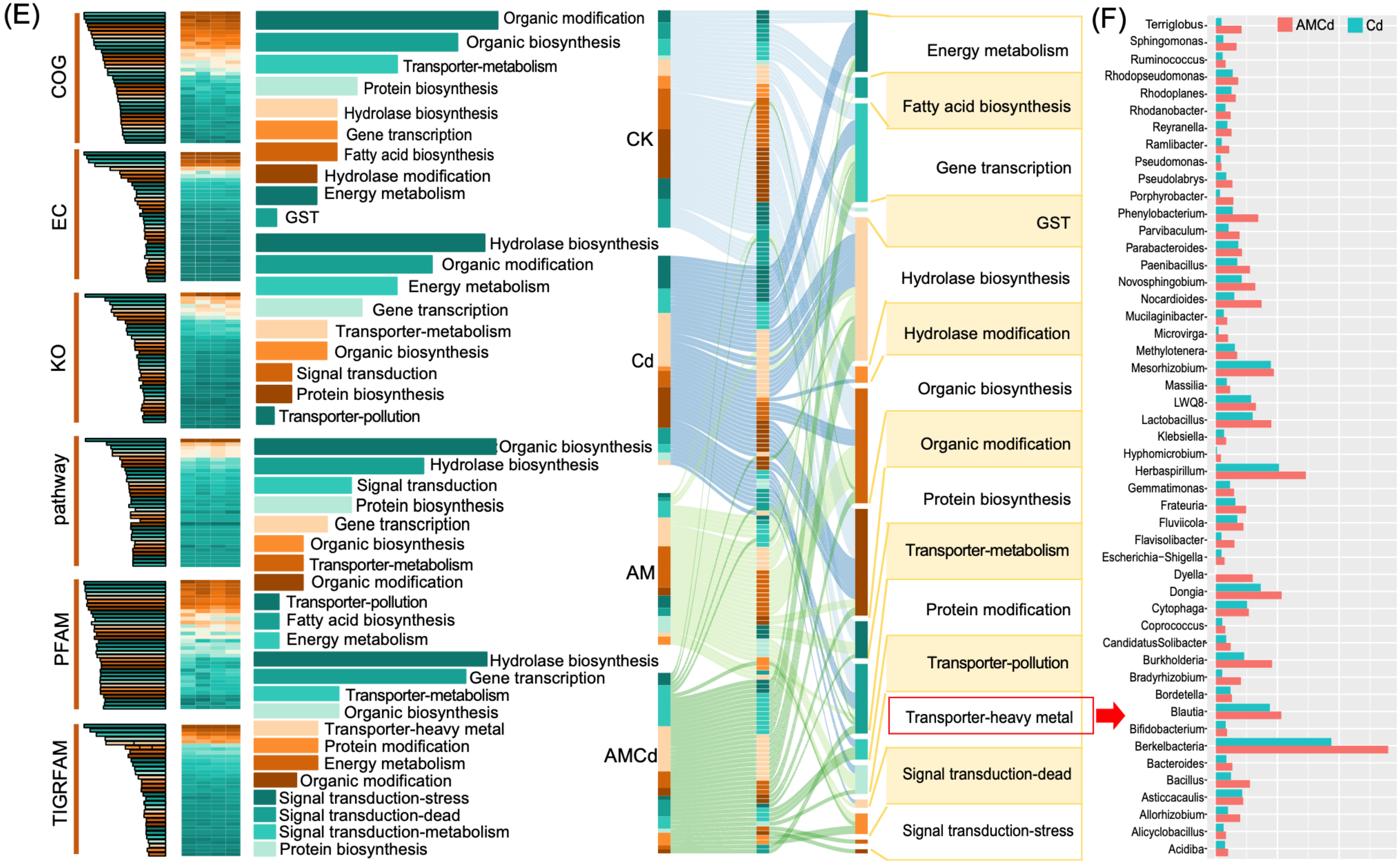
- Top five contributors of CK vs. Cd and Cd vs. AMCd were *LWQ8*, *Massilia*, *Dyella*, *Burkholderia*, and *Enterococcus.*

Keystone

- The keystone of CK was *Asticcacaulis*, *Methylobacterium*, *Sphingomonas*, et al. (nine genera).
- Cd exposure was *Rhodanobacter*, *Dyella*, and *Burkholderia*, et al.
- AMCd was *Parvibaculum*, *Massilia*, and *Alistipes*, among others(eight genera),and some keystones overlapped with CK (*LWQ8*, *Ramlibacter*) and Cd (*Massilia*).
- AMF and Cd can affect bacterial communities by rec ting preferred keystones.

Results

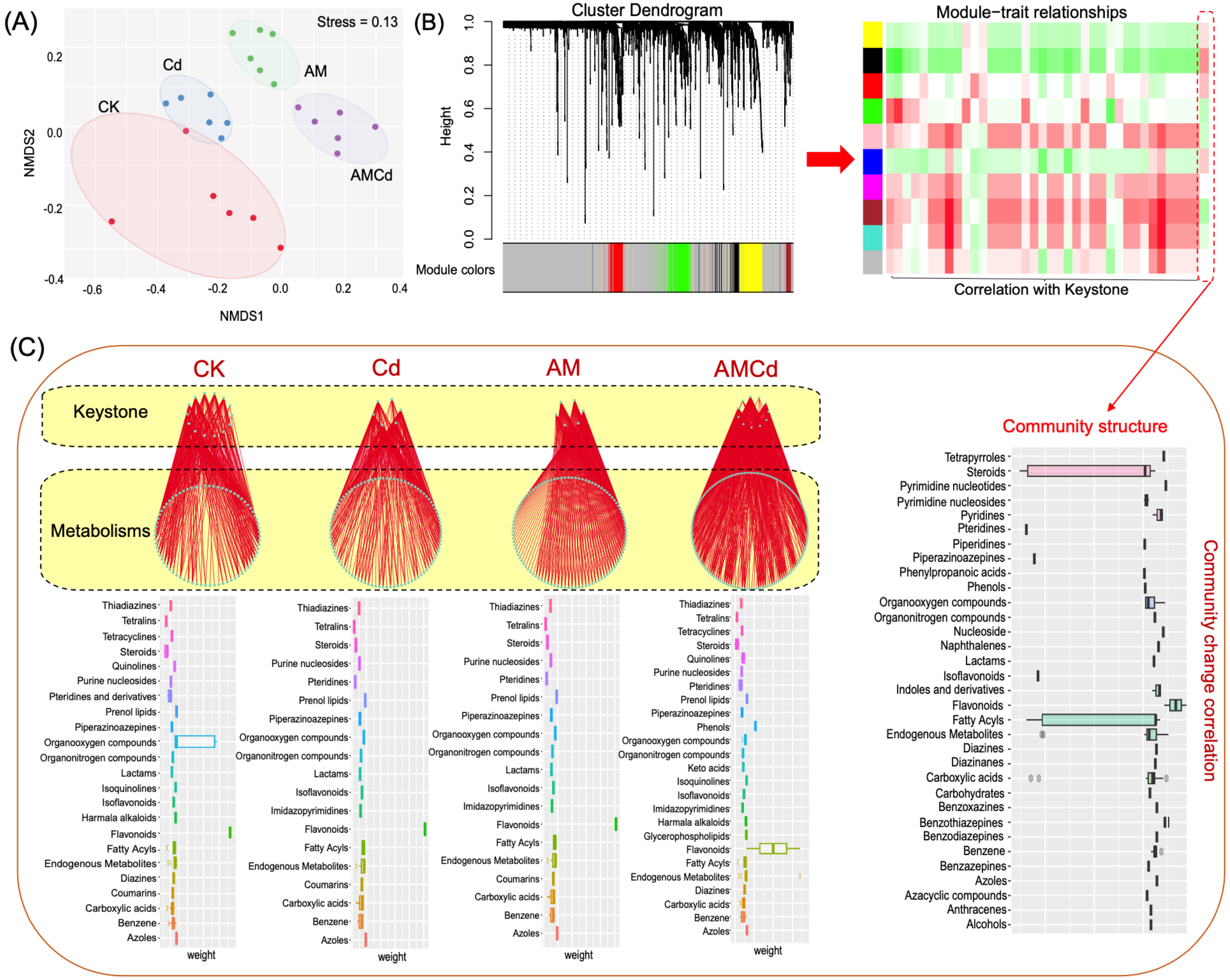
AMF recruits bacteria capable of passivating heavy metals



- Signal transduction, programmed apoptosis signals, heavy metal transport, and metabolite transport were increased （AMCd vs. Cd).
- The microbial increase in the AMCd treatment with the heavy metal transport (pollutant removal) function was selected.
- Forty-nine genera showed significant increases in abundance.
- The above bacteria could phagocytose, adsorb, or embed heavy metals; they were named HM (Heavy Metal)-removers.

Results

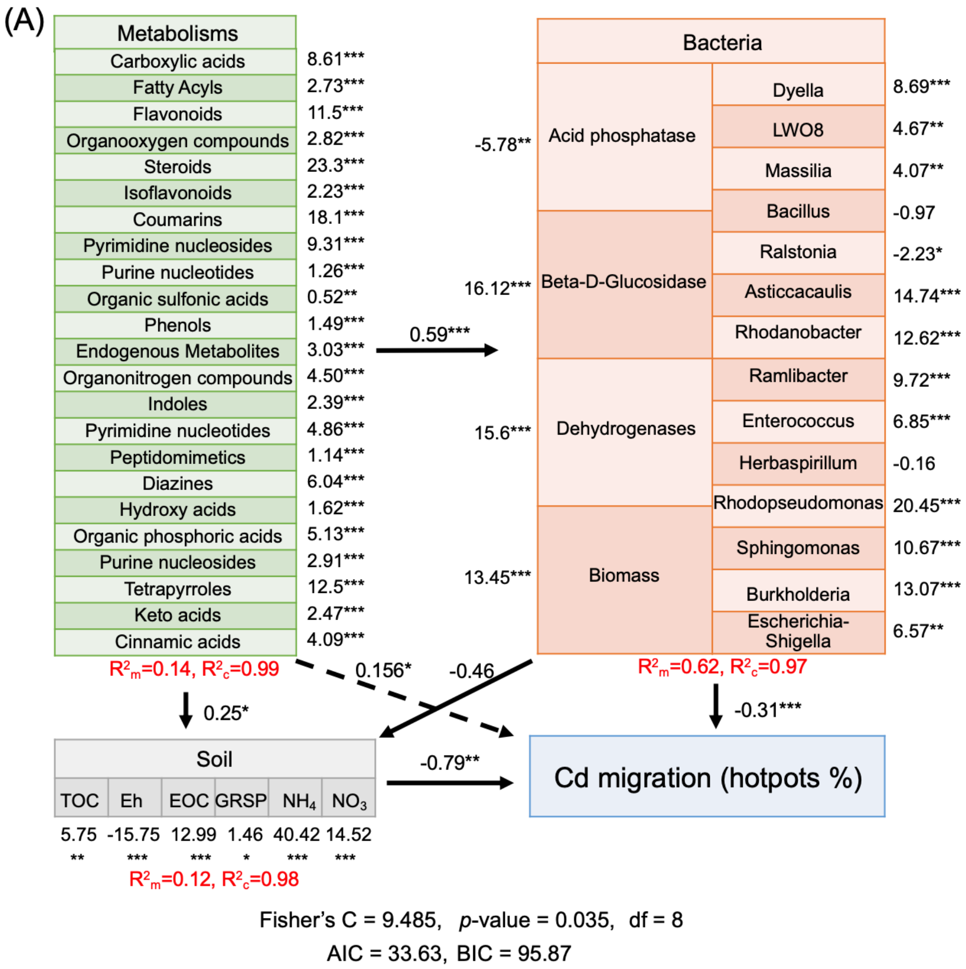
Rhizosphere microbiome associate with metabolism

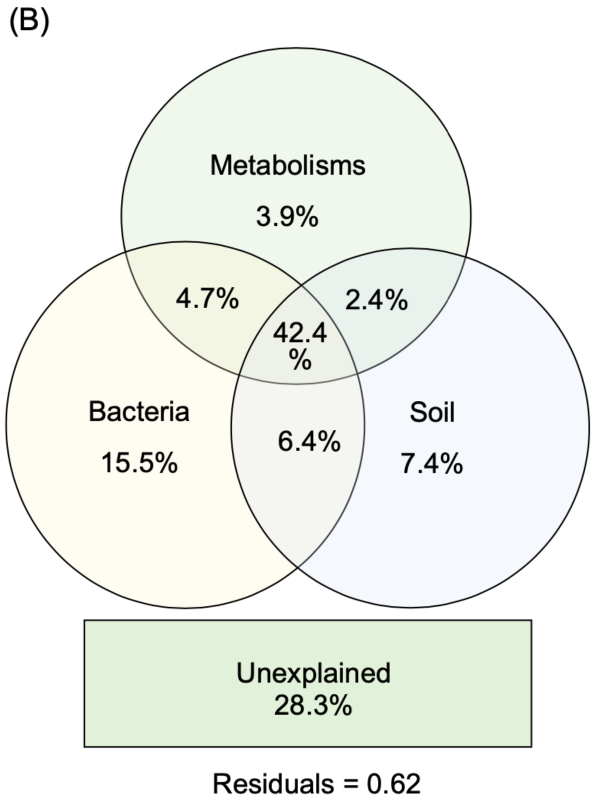


- ➢ Flavonoid metabolites were considered the key hubs affecting community change.
- ➢ AMF changed the bacterial community by increasing the flavonoid content.

Results

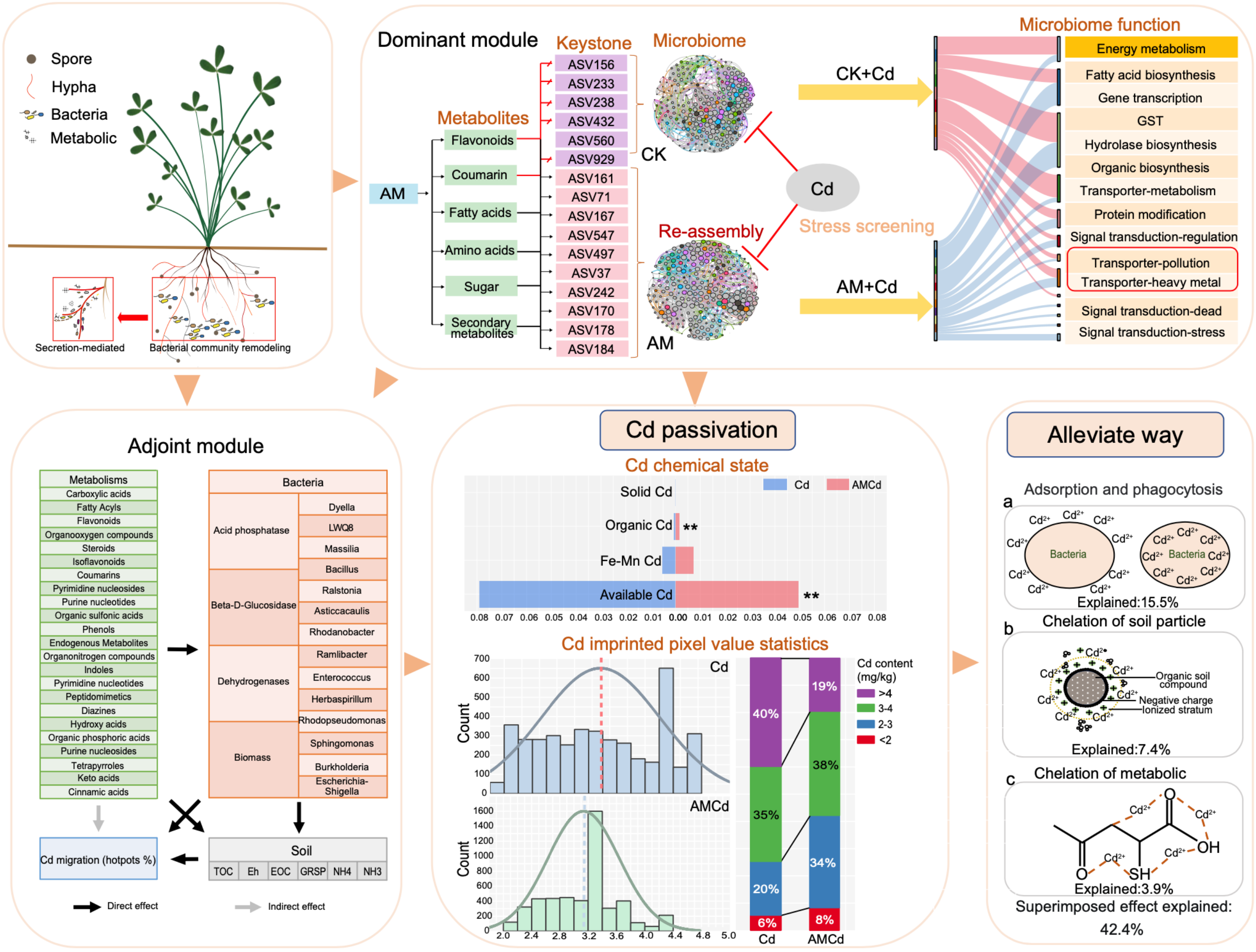
AMF passivates rhizosphere Cd based on the regulation of metabolic-microbial-soil





- ➢ Cd migration capacity was reduced in three ways, 'metabolite-microbe-soil-Cd', and 'metabolite-soil-Cd', two indirect actions, and 'metabolite-Cd' direct action mode.
- ➢ Complementary VPA found that the combined effect of the three could reduce the maximum explanation rate of Cd migration (42.4%).
- ➢ The microbial population was the largest (15.5%).
- ➢ Total explanation rate of microbes reached 72%.
- ➢ Microbial remodelling played an important role in reducing Cd migration.

Summary



- ➢ Controlled metabolism activities in alfalfa roots are critical for beneficial interactions with the rhizosphere microbiota.
- ➢ AMF specifically assembles bacteria of the taxon heavy metal resistant microbiome in the rhizosphere, and this in turn decreased Cd migration.
- ➢ A full understanding of the causal relationships between the rhizosphere microbiota, host metabolism regulation and soil factors.
- ➢ Based on our results, the flavones increased by AMF at alfalfa rhizosphere might recruit HM-remover bacteria.

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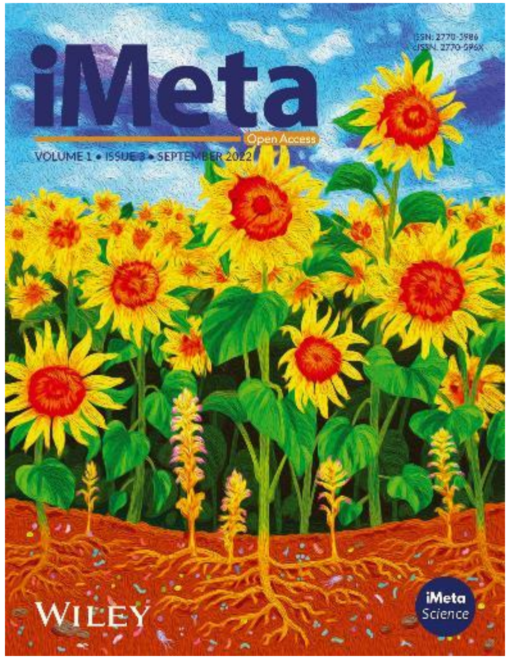

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