Journal of Hazardous Materials, Volume 511, June 2026, Article number 142281
DOI: 10.1016/j.jhazmat.2026.142281

Supplementary Materials for

Carbon metabolic homogenization is linked to microbial competition and antimicrobial resistance in soils under forest-to-cropland conversion

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The final published version (version of record) is available online at DOI:10.1016/j.jhazmat.2026.142281. Please refer to any applicable publisher terms of use.

Supplementary Figures

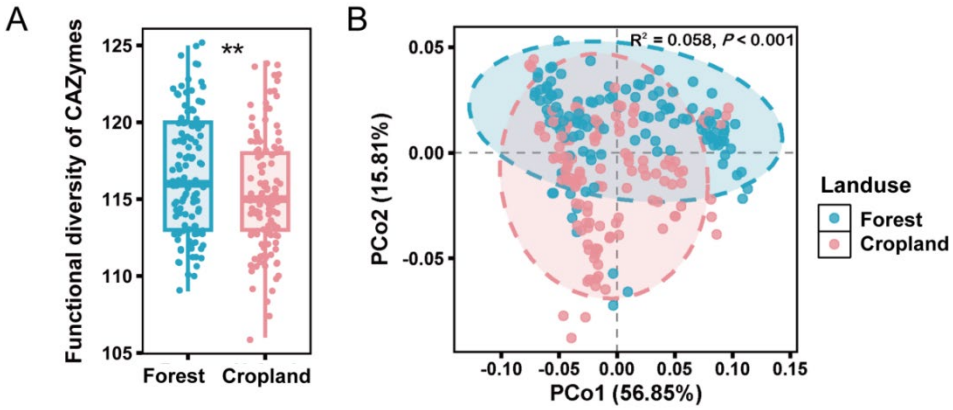


Fig. S1 Microbial CAZyme diversity (A) and structure (B) in forest and cropland soils. Asterisks indicate significant differences (paired t-test, $^{**}P < 0.01$). Principal coordinate analysis (PCoA) is based on Bray-Curtis dissimilarities, with structural differences tested using PERMANOVA.

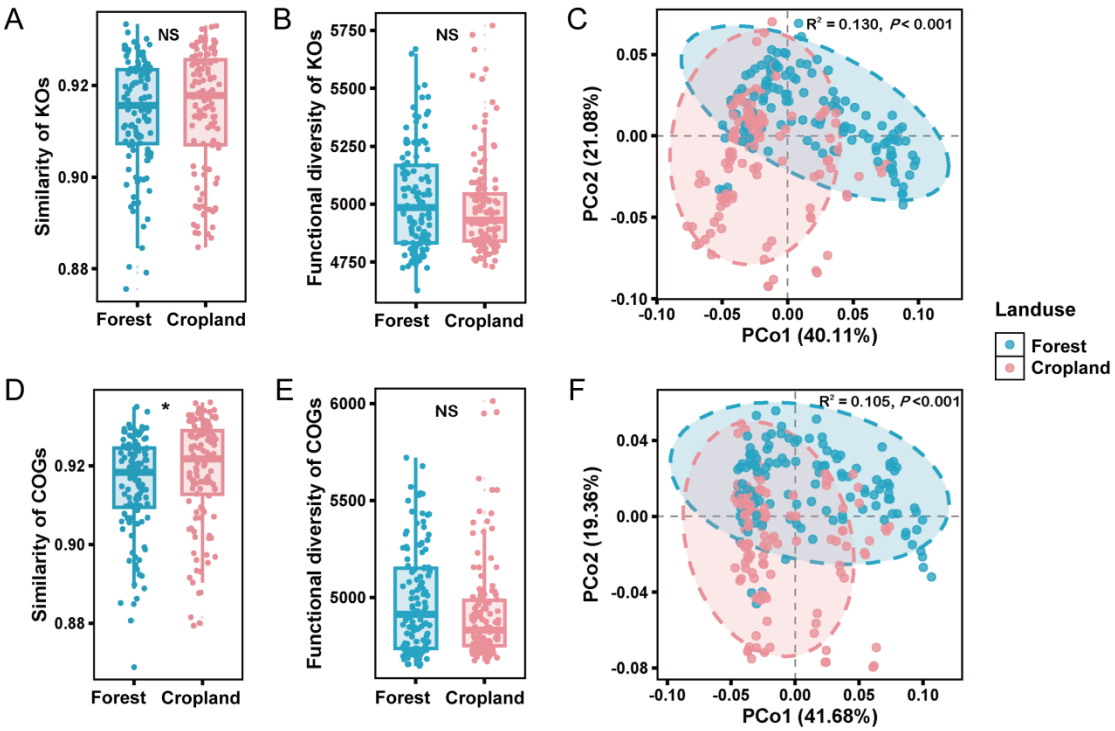


Fig. S2 Microbial functional similarity, diversity, and structure in forest and cropland soils. KO similarity **(A)**, diversity **(B)**, and structure **(C)** in forest and cropland soils. COG similarity **(D)**, diversity **(E)**, and structure **(F)** in forest and cropland soils. Asterisks indicate significant differences (paired t-test, $^{*}P < 0.05$), while "NS" denotes non-significant differences (paired t-test, $P > 0.05$). Principal coordinate analysis (PCoA) is based on Bray-Curtis dissimilarities, with structural differences tested using PERMANOVA.

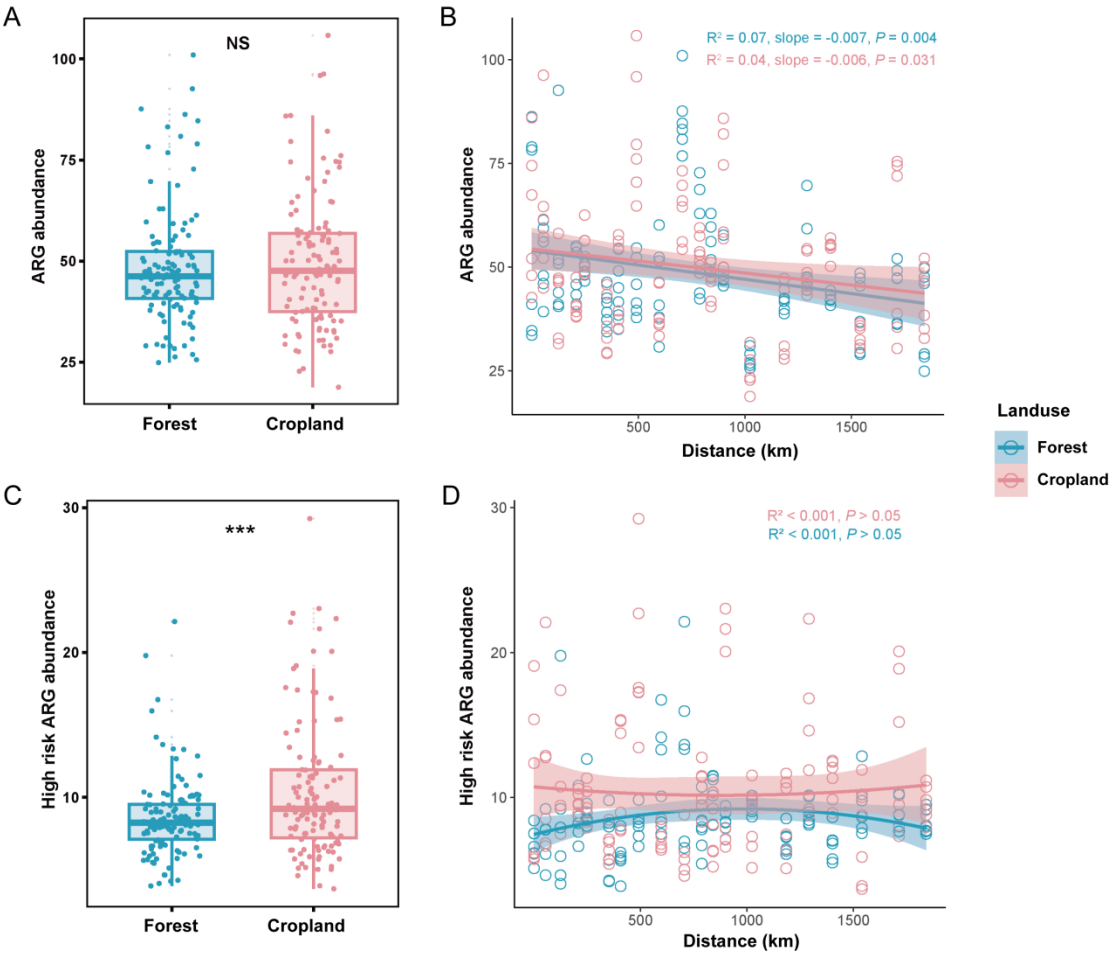


Fig. S3 ARG abundance and its correlation with sampling site distance. A ARG abundance in forest and cropland soils. **B** Correlation between ARG abundance and the distance from the first sampling site. **C** High-risk ARG abundance in forest and cropland soils. **D** Correlation between high-risk ARG abundance and the distance from the first sampling site. Asterisks indicate significant difference (paired t-test, $^{***}P < 0.001$), while "NS" denotes non-significant differences (paired t-test, $P > 0.05$). Distance: Cumulative sum of distances between sampling sites, from the first to the last.

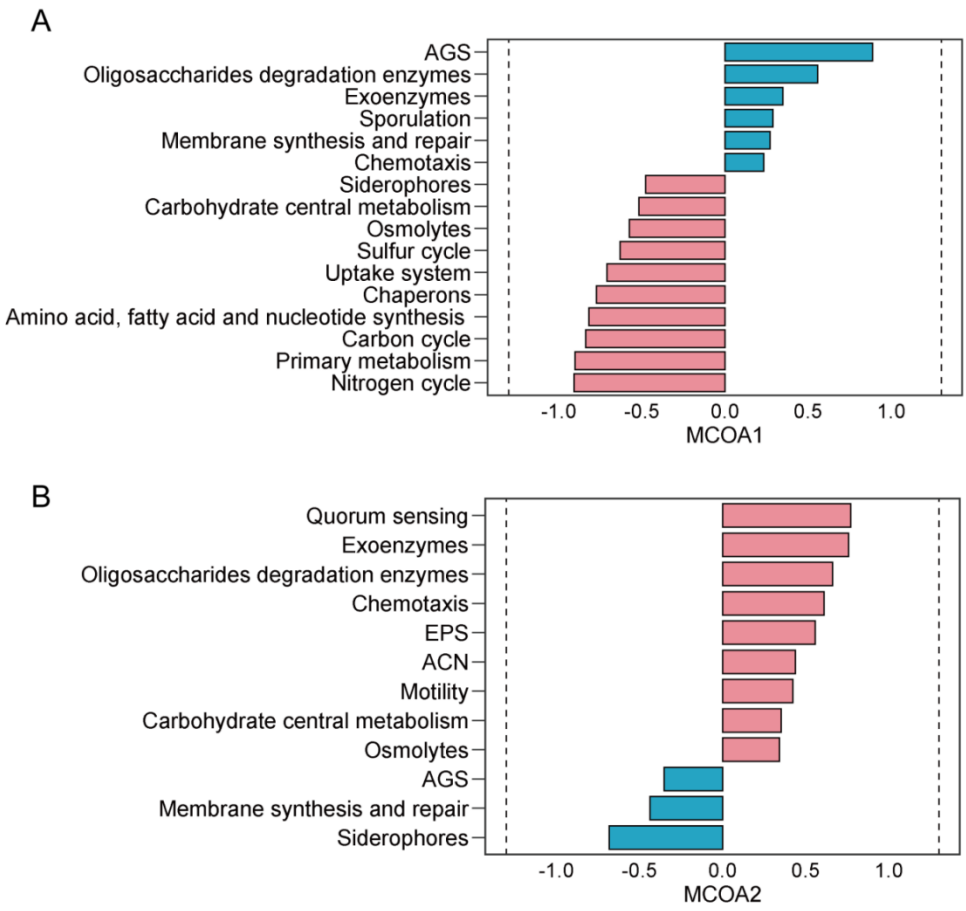


Fig. S4 Trait dimensions of soil prokaryotic metagenomes. Variable contributions to multicable co-inertia analysis (MCOA), summarizing information from four community aggregated traits (CAT) databases (life history traits, CAZy, eggNOG, and KEGG) along the common MCOA dimensions, MCOA1 **(A)** and MCOA2 **(B)**. Only the most significant variables ($P < 0.001$) correlated with each dimension are shown. Positive and negative bar values indicate the direction of the association between variables and MCOA dimensions. Blue bars represent traits more abundant in forests, while red bars indicate higher abundance in croplands.

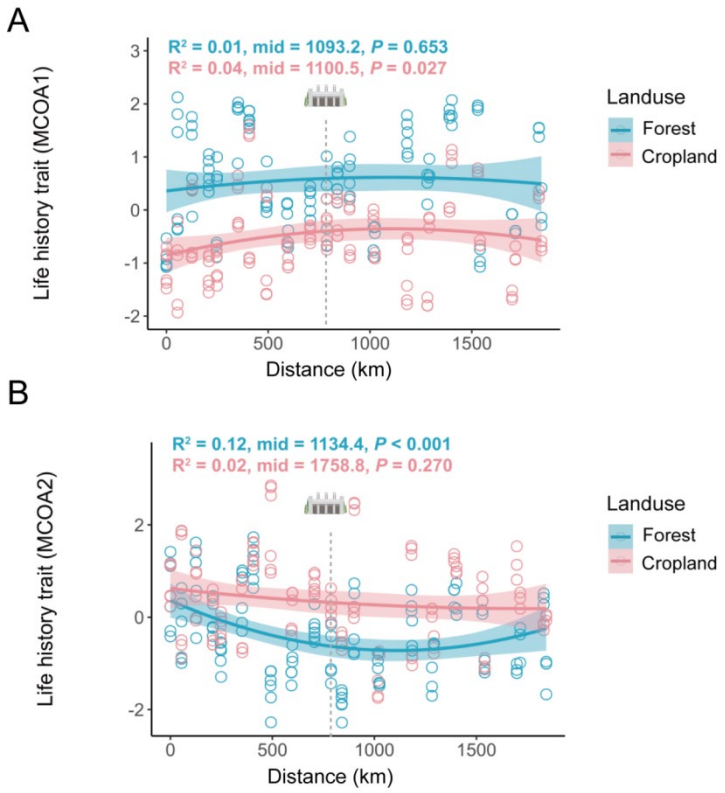


Fig. S5 Correlations between microbial life history traits and distance from the Yangtze River. A Correlation between life history trait (MCOA1) and the distance from the first sampling site. **B** Correlation between life history trait (MCOA2) and the distance from the first sampling site. Distance: Cumulative sum of distances between sampling sites, from the first to the last.

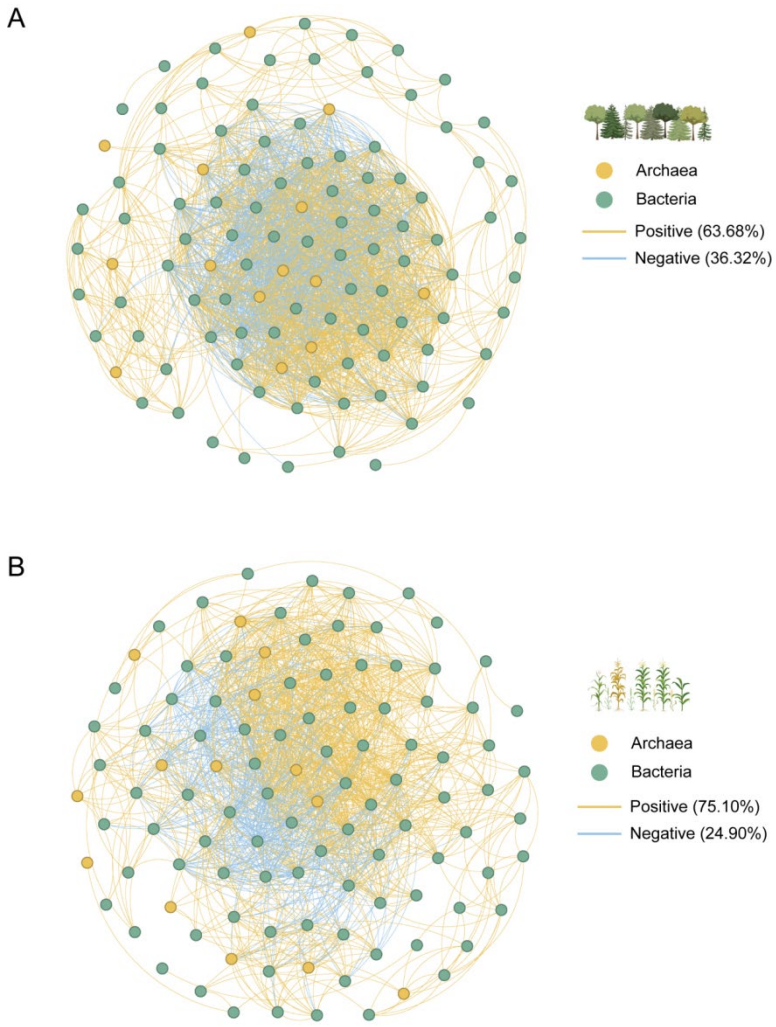


Fig. S6 The co-occurrence networks of forest (A) and cropland (B) soil microbes. Nodes are colored based on MAG species classification, with yellow representing archaeal MAGs and green representing bacterial MAGs. Positive interactions are shown as yellow lines, while negative interactions are depicted as blue lines.

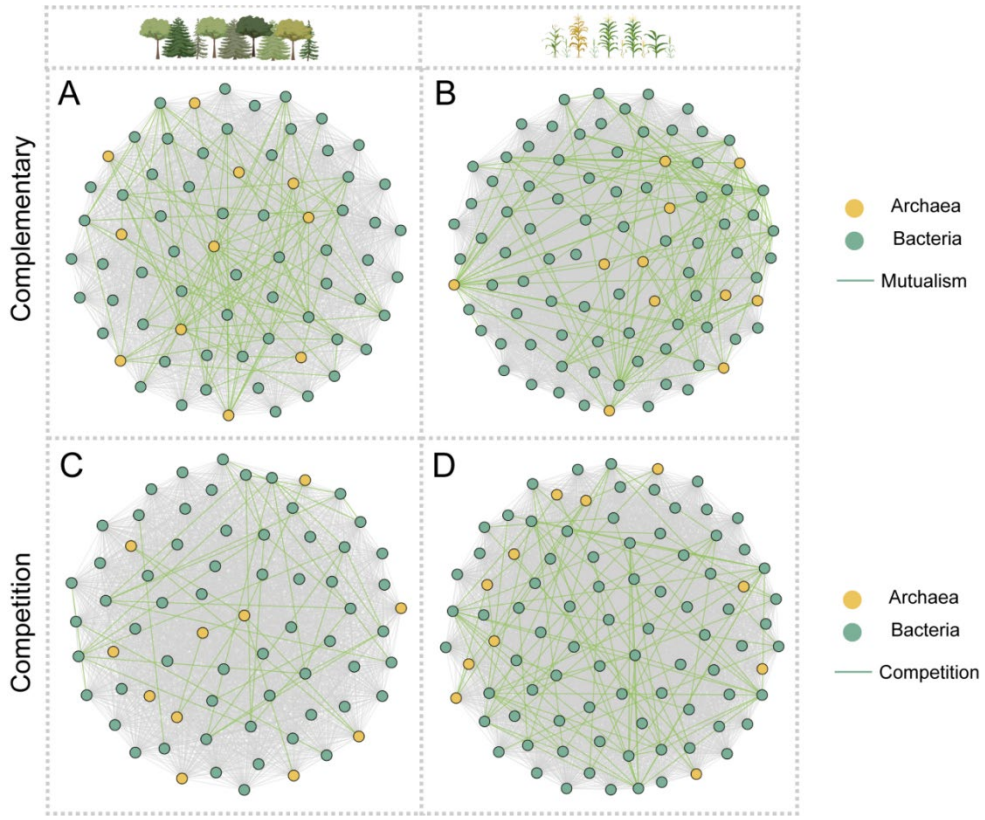


Fig. S7 Pairwise $MI_{complementarity}$ and $MI_{competition}$ values showing the distributions of mutualism and competition interactions. A,B Distributions of mutualistic interactions based on pairwise $MI_{complementarity}$ in forest and cropland soils, shown separately. **C,D** Distributions of competition interactions based on pairwise $MI_{competiton}$ in forest and cropland soils, shown separately. Nodes are color-coded by MAG species classification: yellow for archaeal MAGs and green for bacterial MAGs.

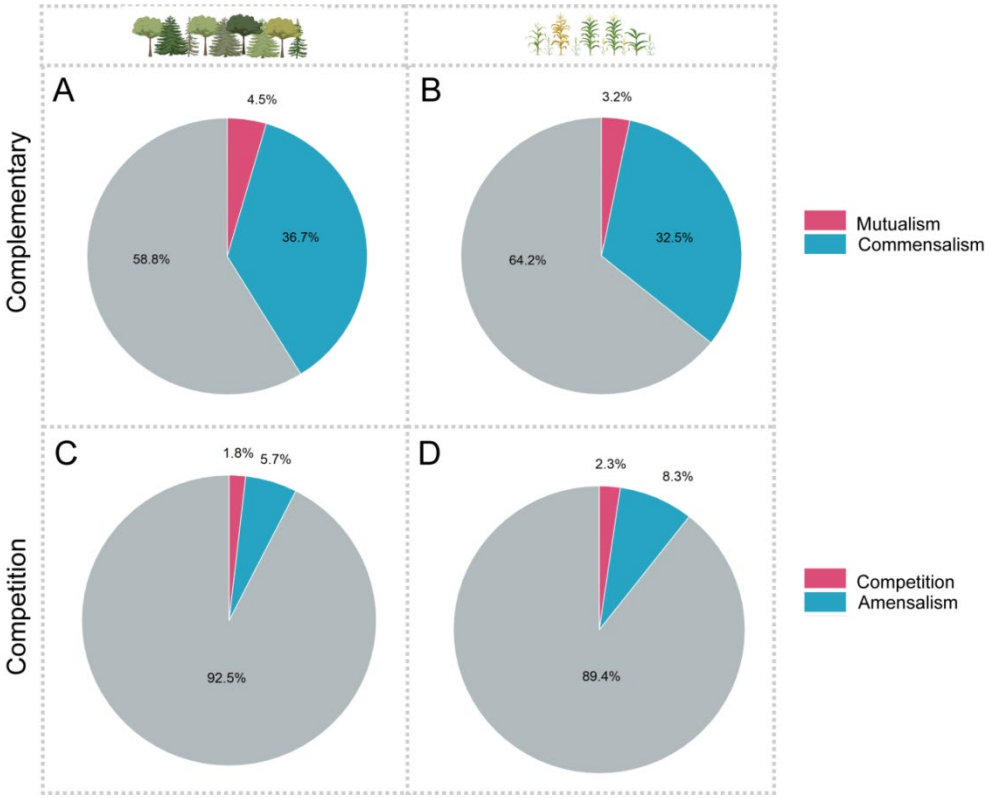


Fig. S8 Proportions of symbiotic and competition interactions based on $MI_{complementarity}$ and $MI_{competition}$ values. A,B Proportions of symbiotic and competitive interactions in forest soils. **C,D** Proportions of symbiotic and competitive interactions in cropland soils.

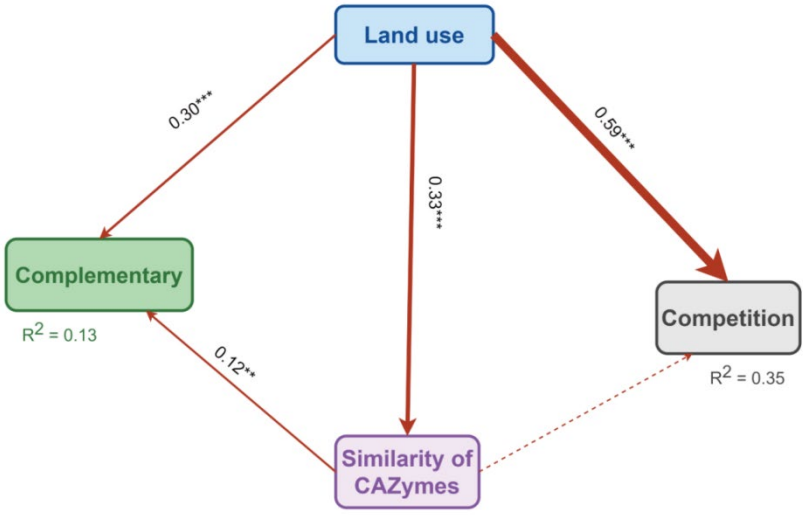


Fig. S9 Structural equation model (SEM) showing the relationships among land use, microbial metabolism, and CAZyme similarity. Red solid arrows indicate significantly positive relationships ($P < 0.05$), while dashed lines represent non-significant relationships. Numbers near the pathway arrows indicate the standardized path coefficients.

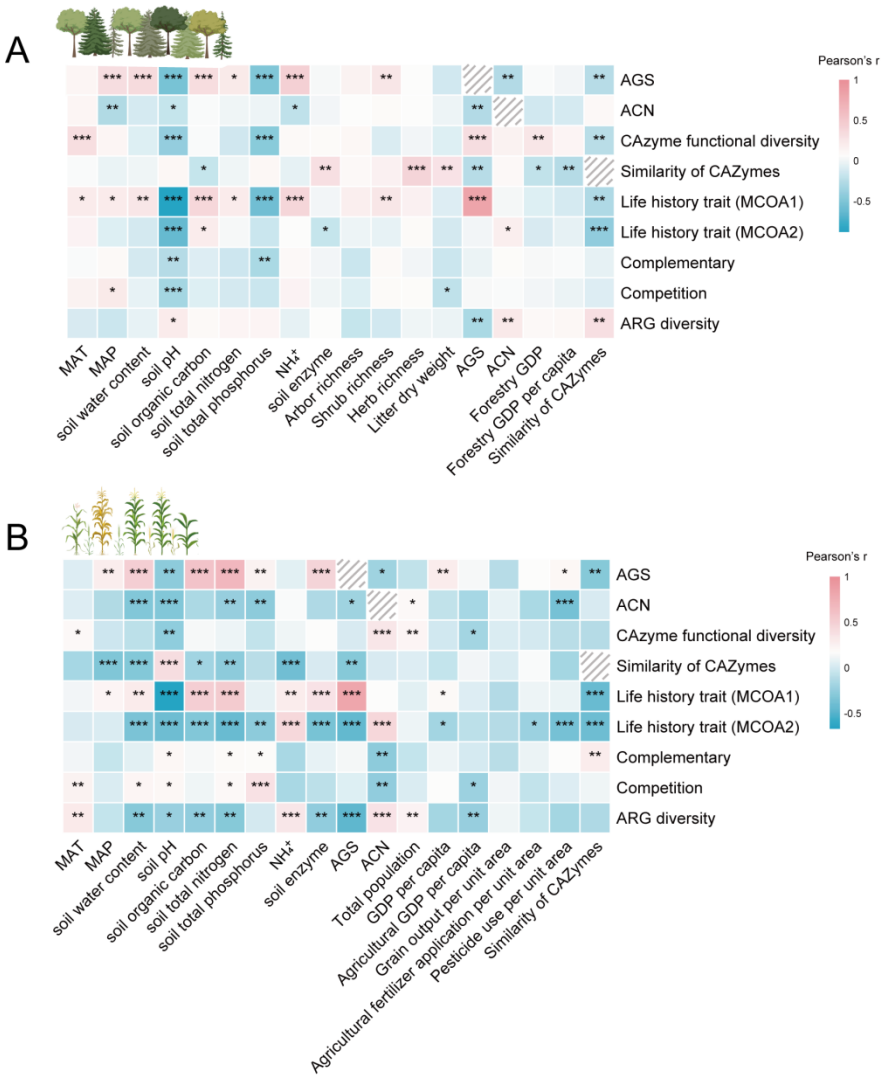


Fig. S10 Correlations between soil functions and environmental drivers. A Heatmap of Spearman correlations between climatic factors, soil factors, plant factors, soil functions, and ARG diversity in forest soils. **B** Heatmap of Spearman correlations between climatic factors, soil factors, socioeconomic factors, soil functions, and ARG diversity in cropland soils. AGS: Average microbial genome size. ACN: Average 16S rRNA gene copy number.

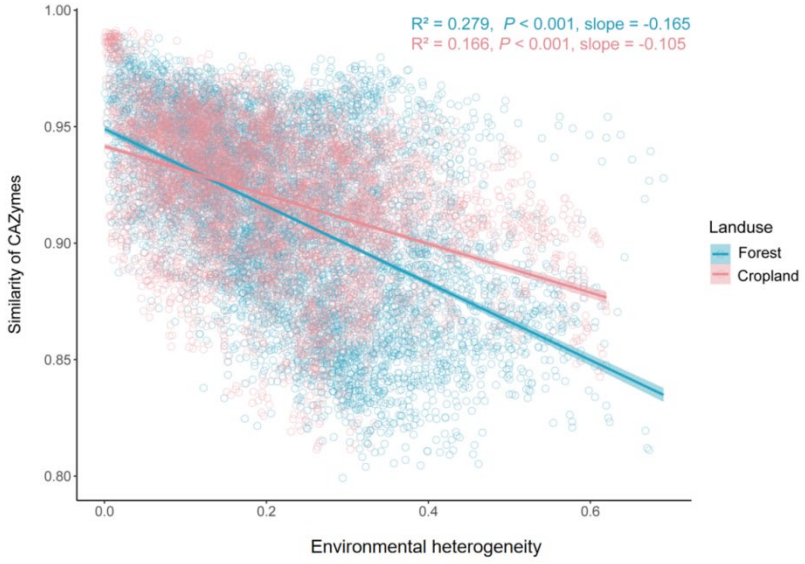
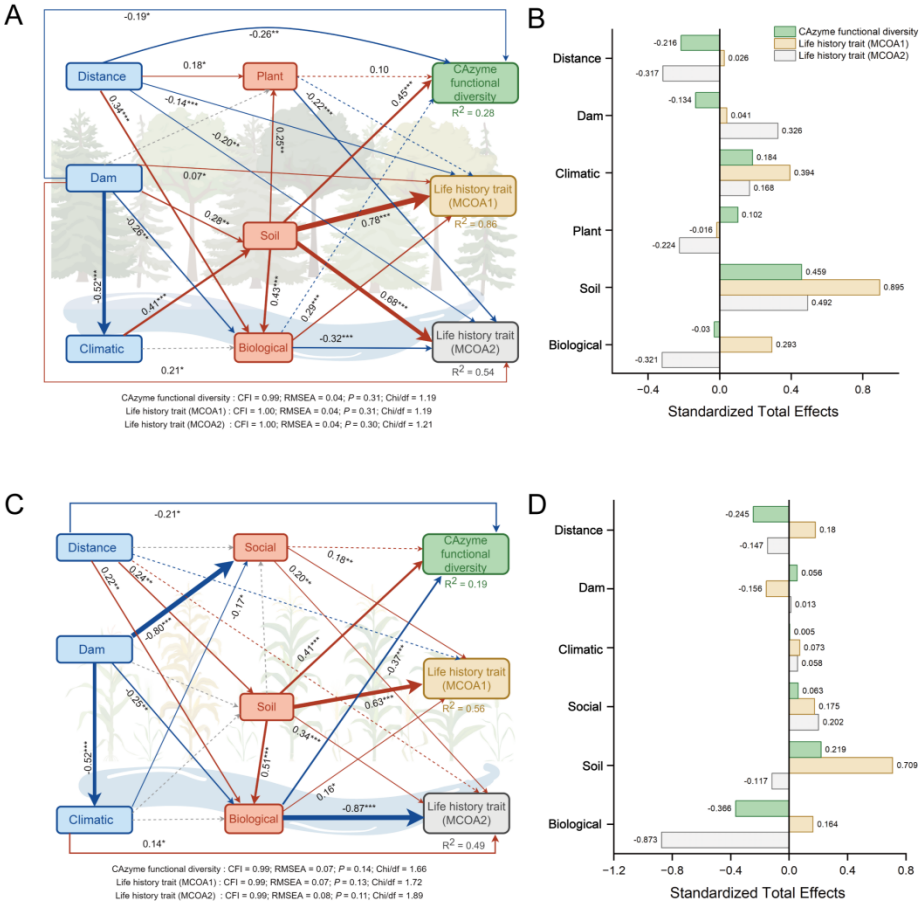


Fig. S11 Correlation between CAZyme similarity and environmental heterogeneity. Environmental heterogeneity is assessed using Principal Coordinate Analysis (PCoA) on mean annual temperature and precipitation, soil moisture, pH, soil organic carbon, total nitrogen and phosphorus, and NH_4^+-N). Euclidean distances between points are calculated based on their PCo1 and PCo2 coordinates to quantify heterogeneity.



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104 **Fig. S12 Environmental drivers of soil functions following forest-to-cropland**
105 **conversion at the watershed scale. A** Structural equation model (SEM) depicting
106 relationships among environmental factors, CAZyme diversity, and life history traits
107 (MCOA1 and MCOA2) in forest soils. **B** Standardized total effects on CAZyme
108 diversity and life history traits from the SEM in panel **A**. **C** SEM depicting relationships
109 among environmental factors, CAZyme diversity, and life history traits in cropland soils.
110 **D** Standardized total effects on CAZyme diversity and life history traits from the SEM
111 in panel **C**.

Supplementary Tables

Table S1. Co-occurrence network properties in forest and cropland soils.

Properties	Forest	Cropland
RMThreshold	0.67	
Total nodes	107	107
Total links	1988	1446
Average degree (avgK)	37.159	27.028
Average clustering coefficient (avgCC)	0.813	0.733
Average path distance (GD)	1.946	2.3
Density	0.351	0.255
Modularity	0.154	0.239

Table S2. Metabolic complementarity network properties in forest and cropland soils.

Properties	Forest	Cropland
RMThreshold	0.229	
Synergitic nodes	70	90
Synergitic links	995	1433
Average degree (avgK)	28.429	31.844
Average clustering coefficient (avgCC)	0.541	0.523
Average path distance (GD)	1.588	1.642
Density	0.412	0.358
Modularity	0.07	0.067

Table S3. Metabolic competition network properties in forest and cropland soils.

Properties	Forest	Cropland
RMThreshold	0.672	
Synergitic nodes	58	79
Synergitic links	181	424
Average degree (avgK)	6.241	10.734
Average clustering coefficient (avgCC)	0.651	0.692
Average path distance (GD)	2.996	2.354
Density	0.109	0.138
Modularity	0.467	0.315



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Zhang, Shaoyang; Zhang, Tianlun; Du, Shuai; Yang, Zhugen; Liu, Shengen ...

2026-06-15
Elsevier
https://doi.org/10.1016/j.jhazmat.2026.142281
Zhang S, Zhang T, Du S, et al., (2026) Carbon metabolic homogenization is linked to microbial competition and antimicrobial resistance in soils under forest-to-cropland conversion. Journal of Hazardous Materials, Volume 511, June 2026, Article number 142281

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