



SynCom mediated herbicide degradation activates microbial carbon metabolism in soils

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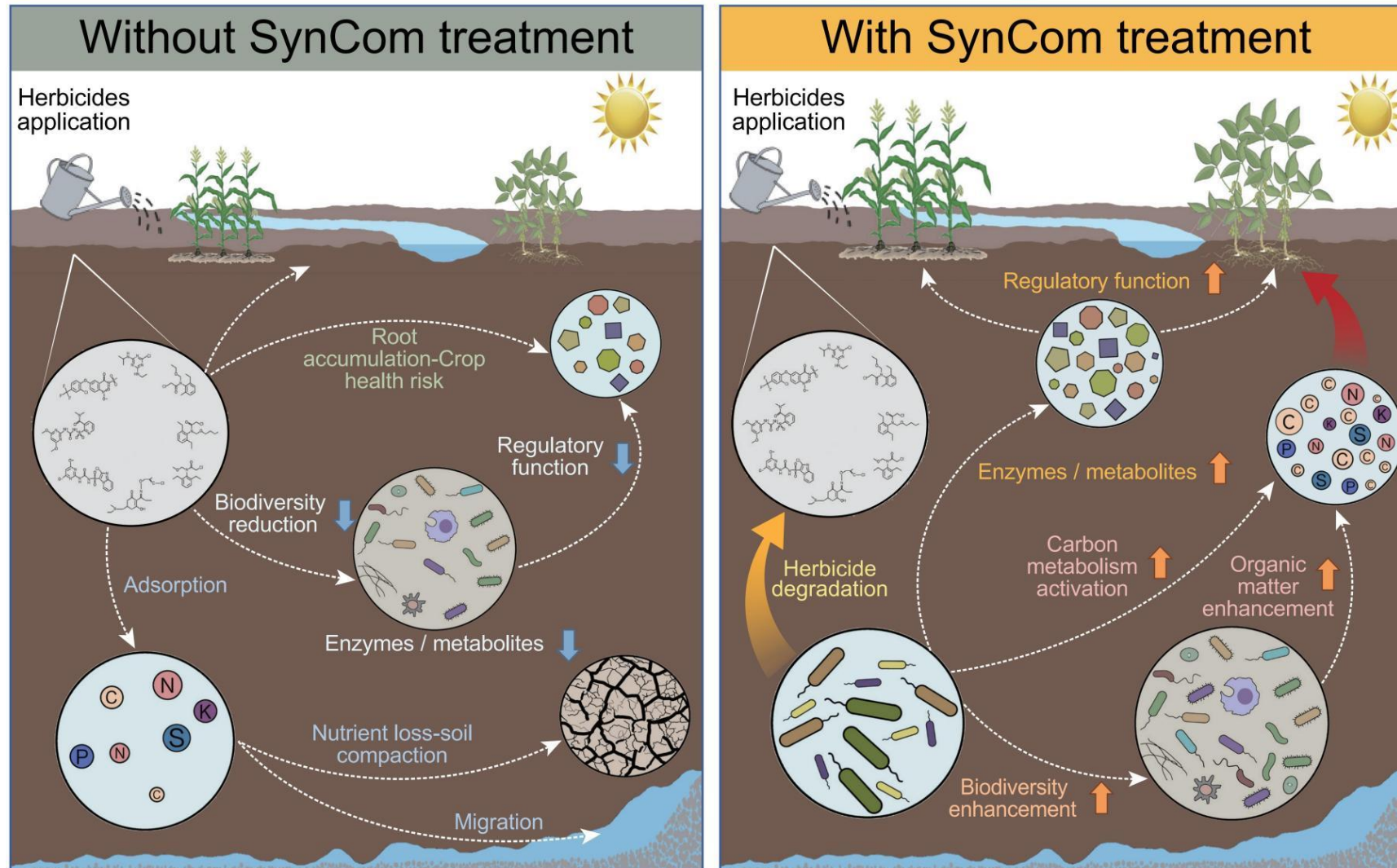


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Highlights



We provided an herbicide degradation and ecosystem regulation model of SynCom in soil. We demonstrated the effectiveness of SynCom “S1–S4” to remediate up to 8 herbicides, to increase soil biodiversity and carbon metabolism, and to enhance soil organic matter contents. This study provides novel insights into microbial remediation of herbicide-contaminated soils and thus offers a practical solution to sustainable food production.



Results

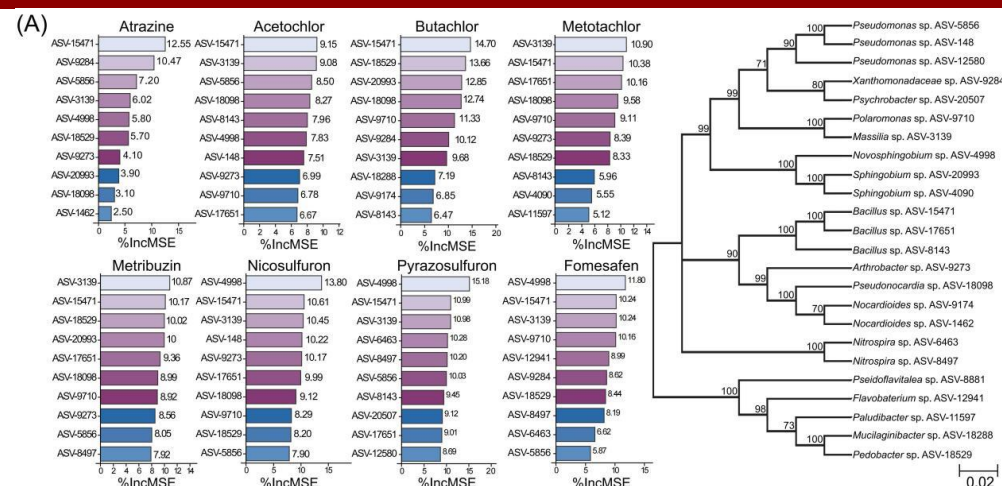
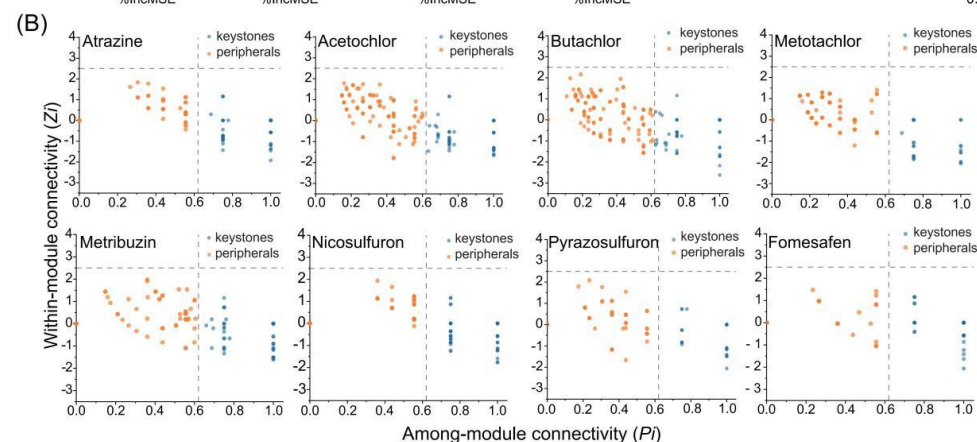
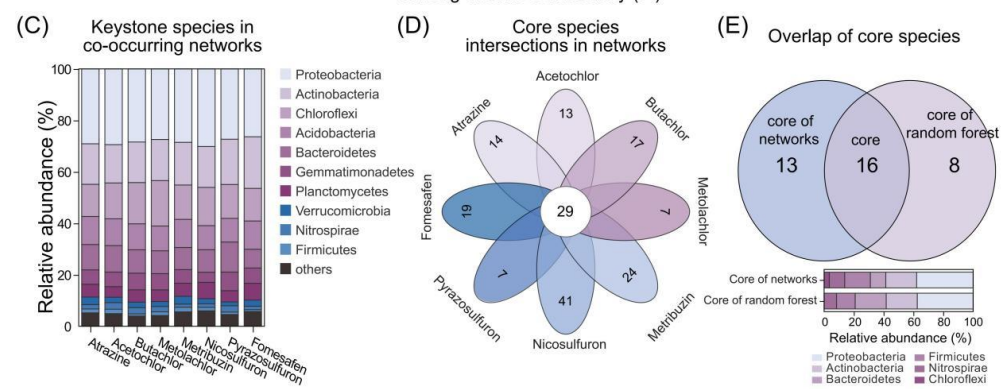


Figure 1 Screening of potential keystone species for herbicide degradation by random forest model and co-occurrence networks.

(A) The result of predicting the level of bacterial interpretation of herbicide residue by RF model, and a NJ tree based on 16S rRNA gene sequences showing the phylogenetic relationships of core ASVs.



(B) Screening of keystone species based on co-occurrence networks.



(C) Relative abundance of keystone species at the phylum-level in co-occurrence networks.

(D) Venn diagrams of keystone species in co-occurrence networks constructed with 8 herbicides.

(E) Venn diagrams and phylum-level relative abundances of keystone species in co-occurrence networks versus core species in random forests.



Results

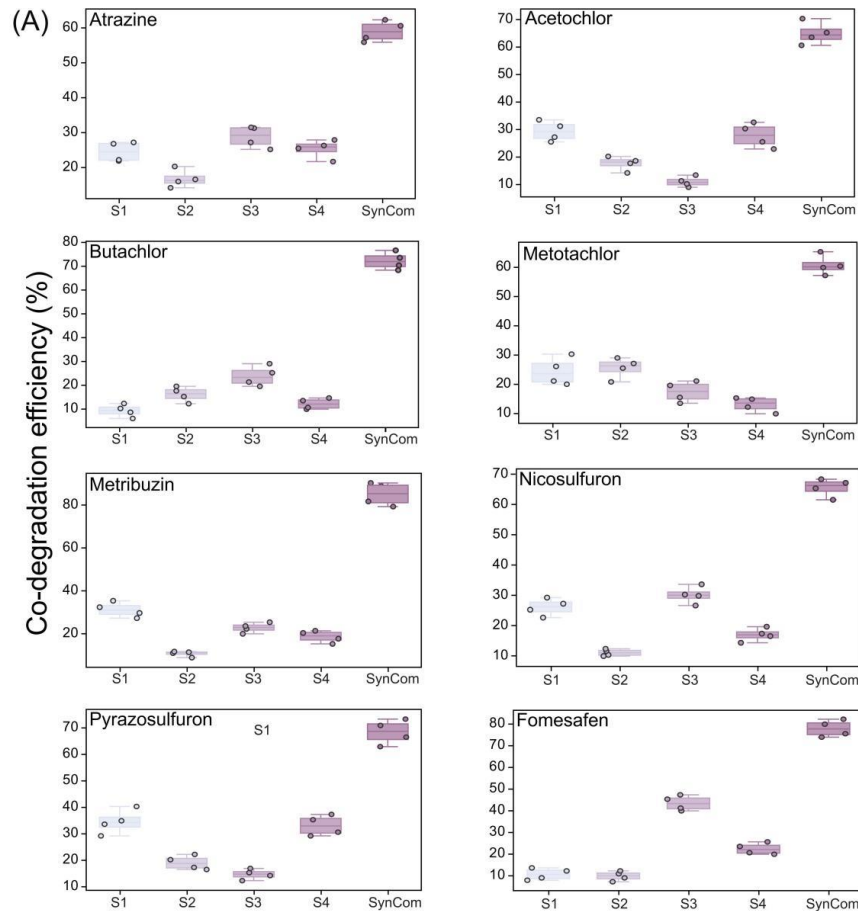
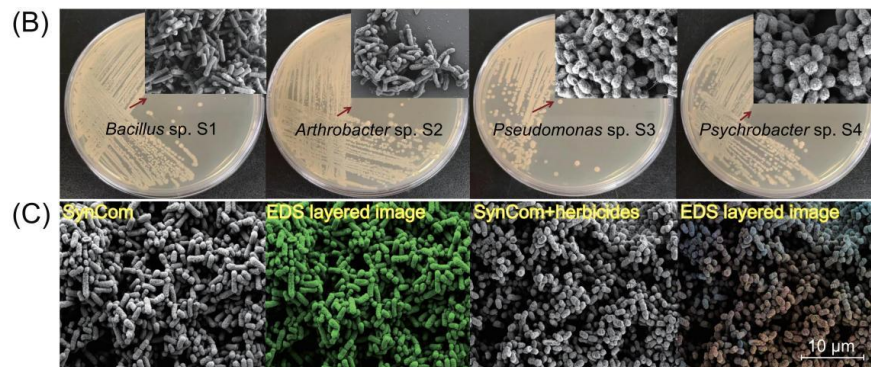


Figure 2 Morphological characteristics and functional annotations at the genomic level of strains S1, S2, S3, and S4.

(A) Co-degradation efficiencies of functional strains and SynCom on 8 co-herbicides.

(B) Colony morphology and SEM of functional strains.

(C) SEM electron micrographs and EDS layered image of SynCom with or without the addition of herbicides.





Results

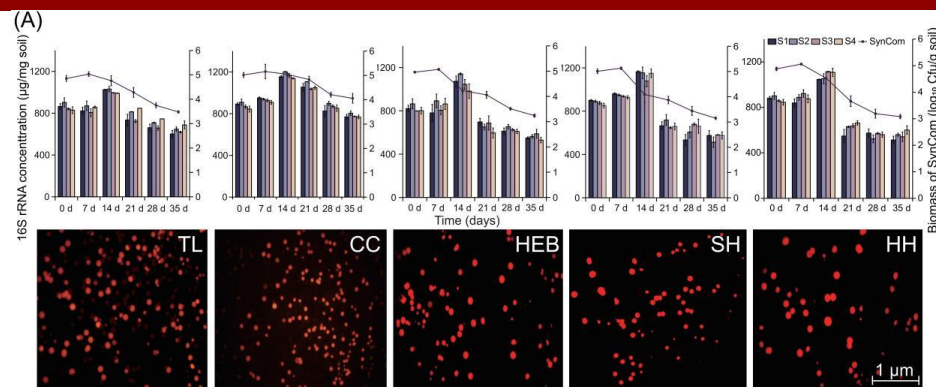
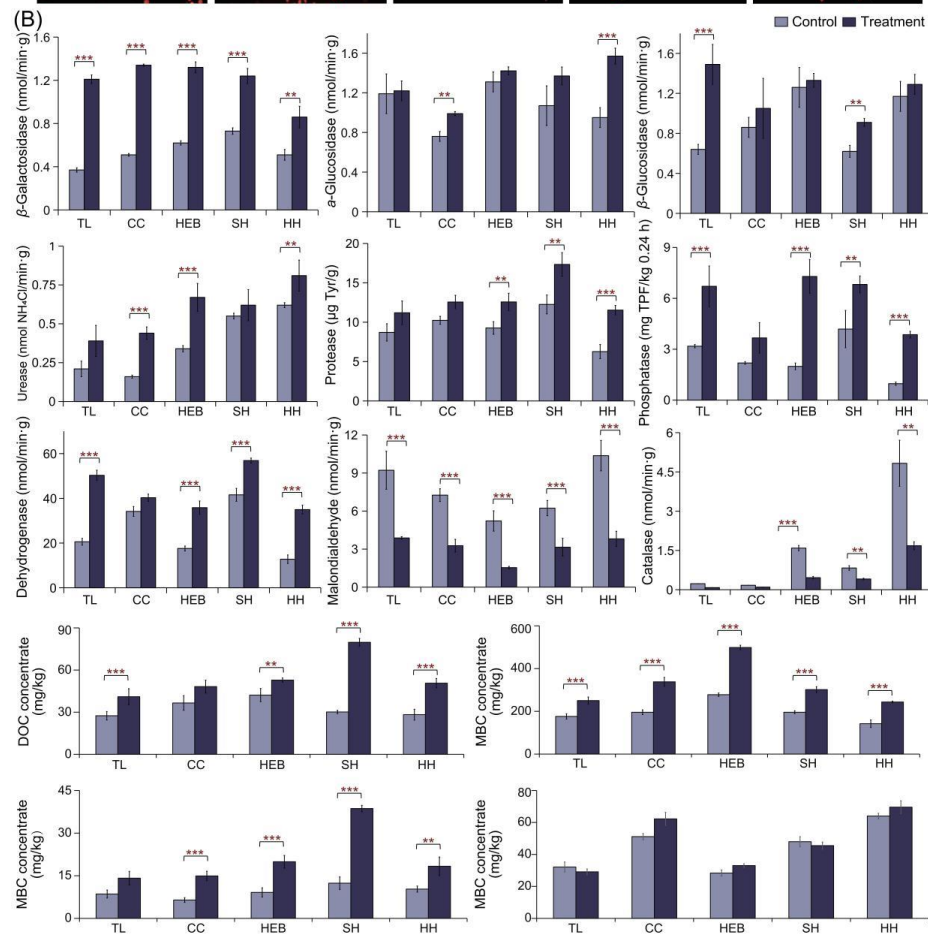


Figure 3 Effects of SynCom on herbicides degradation, enzyme activities regulation, and nutrients promotion in soils.

(A) The ability of SynCom colonization in the soil.



(B) The soil enzyme activities of control and treatment groups at 14 days (average maximum degradation slope), and the concentration of DOC, MBC, DON, and AP in soil after 35 days.

Results

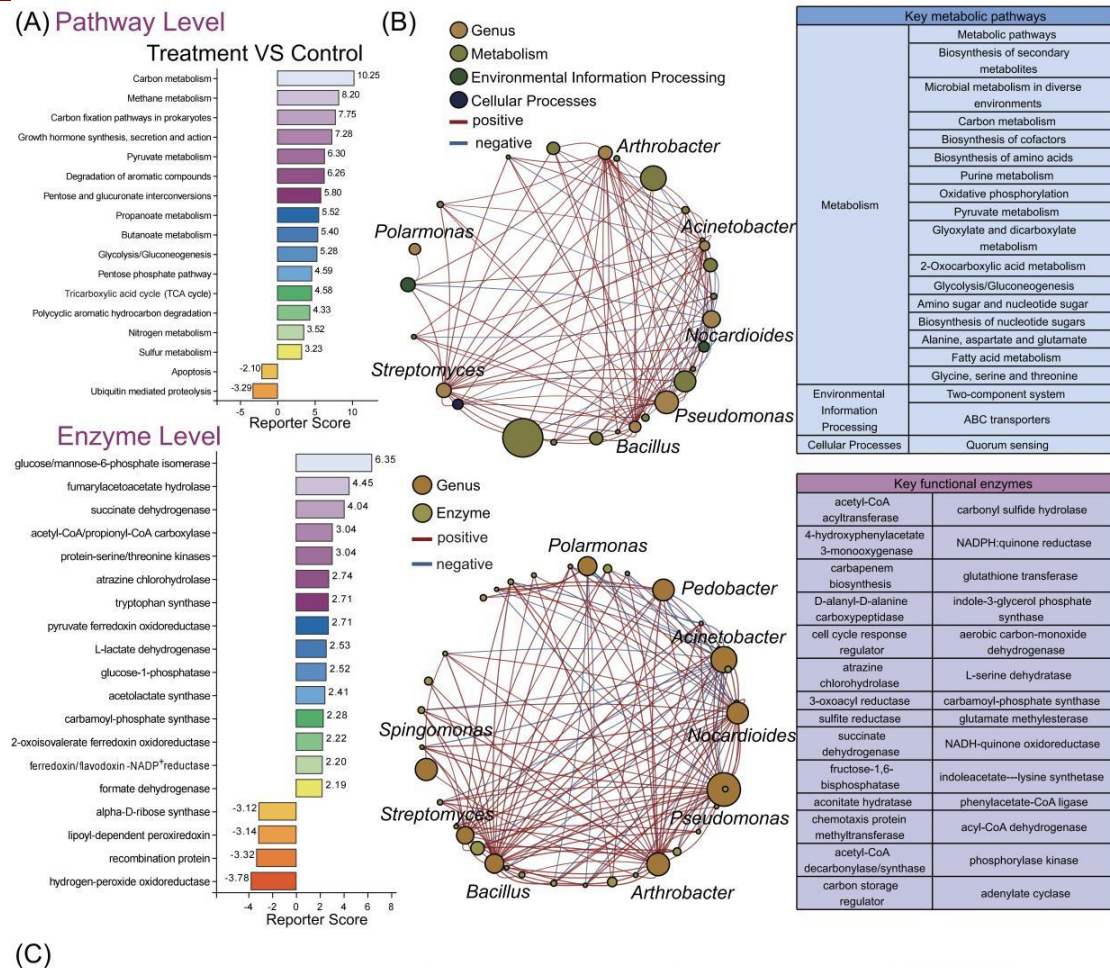


Figure 4 Effect of SynCom on soil metabolic functions at the KEGG pathways and enzyme levels.

(A) KEGG pathways and key functional enzymes that were significantly different from the control in the treatment group.

(B) Correlation networks between species and functions in the treatment group.

(C) Effect of incorporation of SynCom on major pathways of soil carbon metabolism compared to control. The red lines indicate a significant up-regulation of the function in this step.



Results

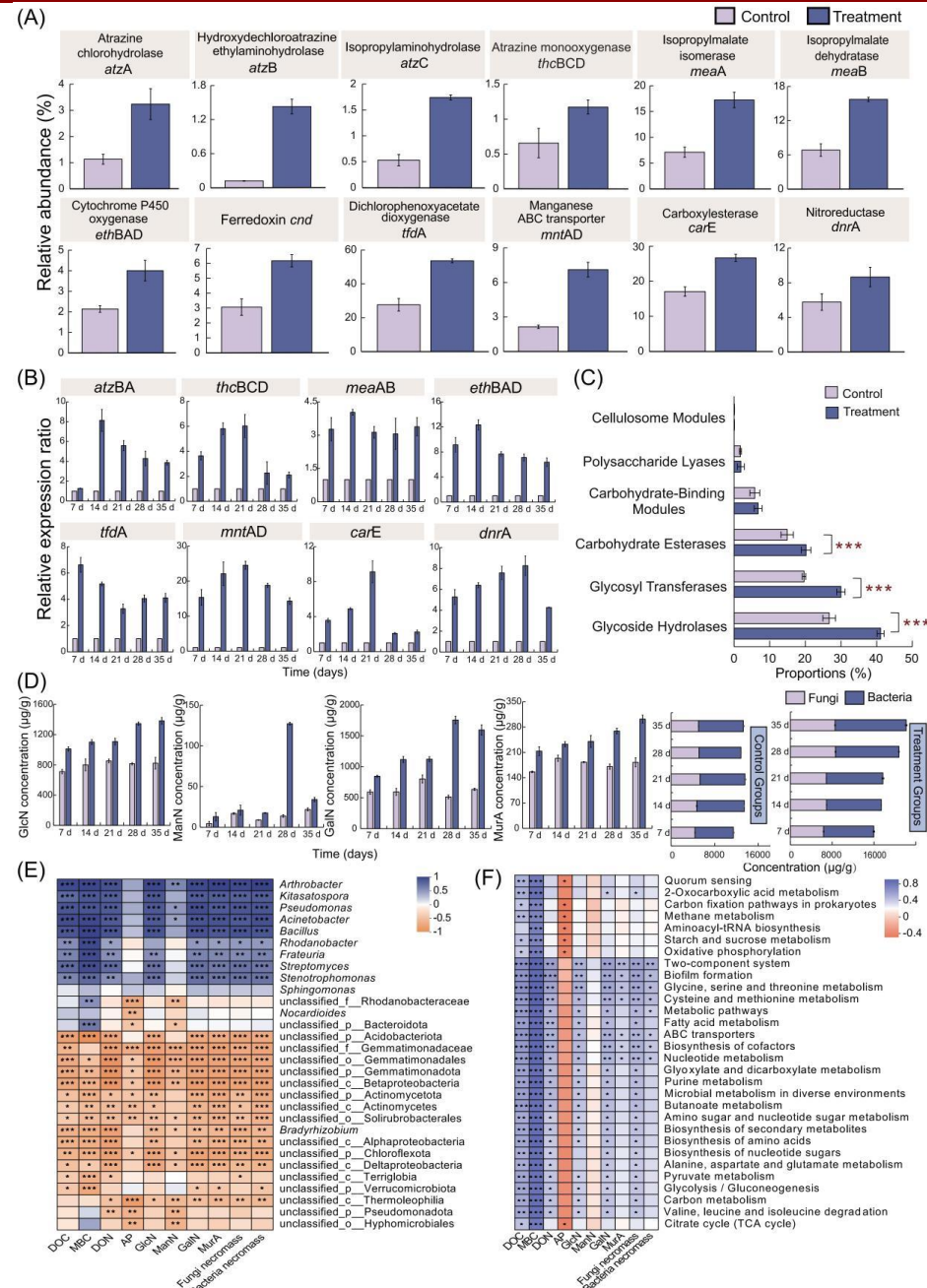


Figure 5 Effects of SynCom on herbicides degradation and microbial carbon pool function in soil.

(A) Metagenomic annotation of expression levels of key enzymes for herbicide degradation.

(B) Expression levels of herbicide degrading functional protein in soil by qRT-PCR.

(C) Metagenomic annotation of the relative abundance of carbohydrate-active enzymes (CAZy).

(D) The concentration of amino sugars and microbial necromass C in soil during the degradation processes.

(E) Heatmap of Spearman correlation of soil active fractions and microbial residues with soil species composition.

(F) Heatmap of Spearman correlation of soil active fractions and microbial residues with metabolic function levels.



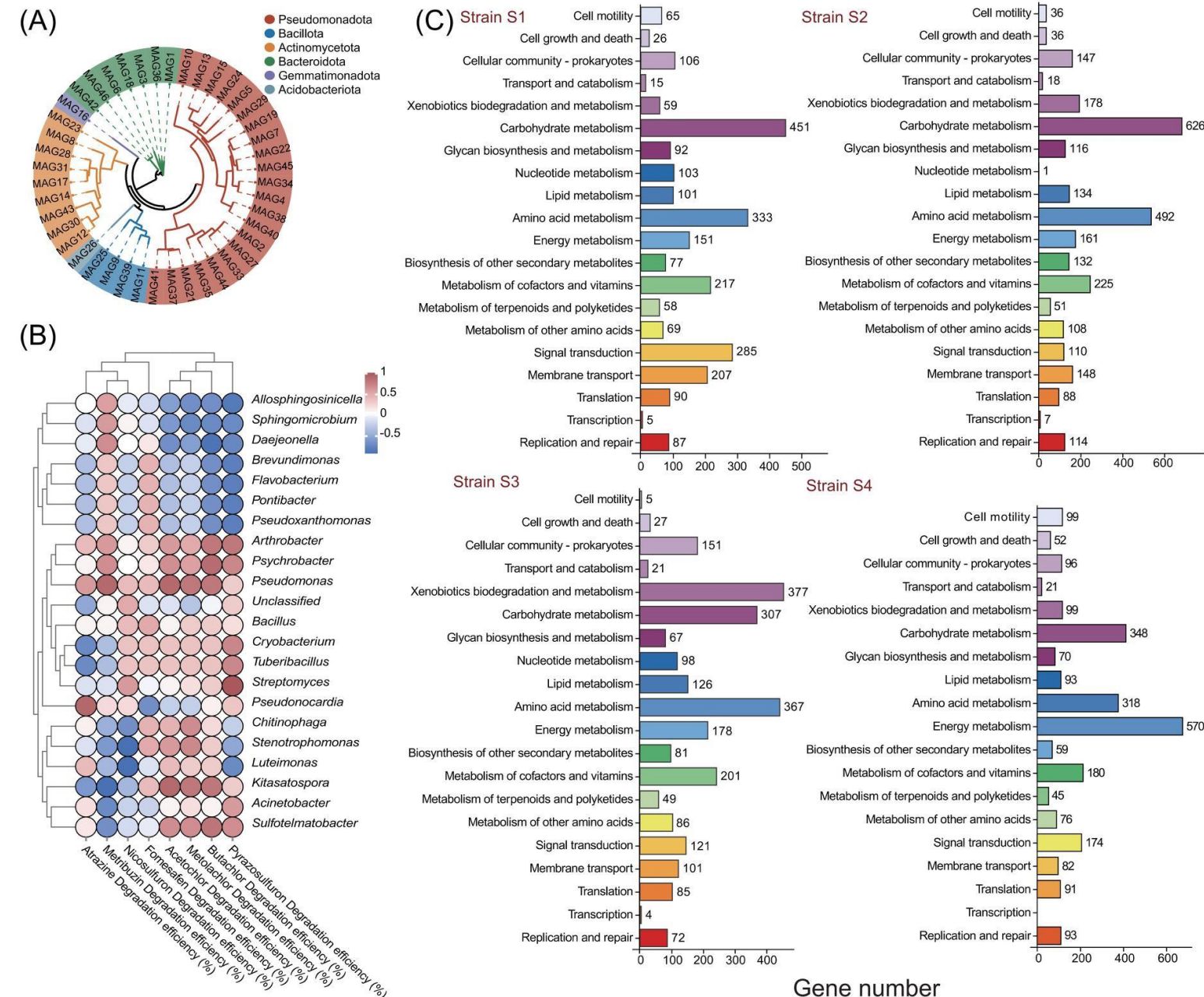
Results

Figure 6 Metabolic functions of key MAGs.

(A) Evolution tree of 45 MAGs at the phylum level.

(B) Spearman correlation analyses of MAGs at the genus level with herbicide degradation efficiencies in treatment groups.

(C) Functional annotation of KEGG metabolism of 4 key MAGs (Strain S1–S4).





Summary

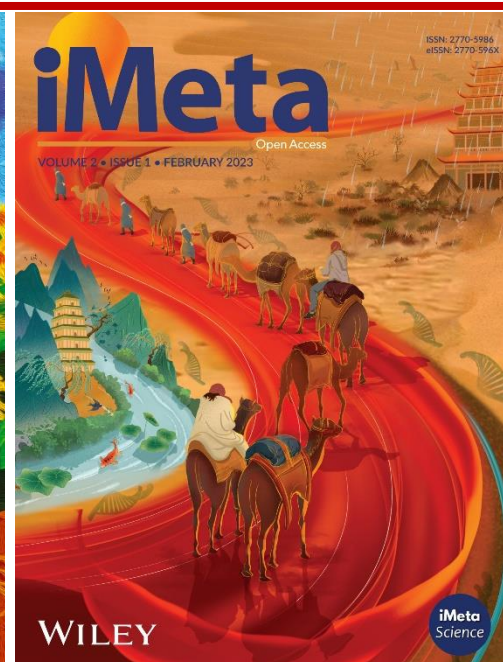
- 16 keystone species were screened after overlapping random forest model and co-occurrence networks.
- A four-membered SynCom degraded multiple herbicides, stabilized colonization, and altered soil enzyme activity.
- Application of SynCom promoted an accumulation of CAZy and microbial necromass-associated carbon.
- SynCom increased microbial carbon metabolism such as TCA cycle, pyruvate metabolism, and glycolysis in soil.
- SynCom members occupied different ecological niches and “divided the labor”.

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