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RESEARCH ARTICLE

Fungi rather than bacteria explain home-field advantage for decomposition of litter carbon fractions

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Abstract

1. The home-field advantage (HFA) hypothesis proposes that specific interactions between litter and microbial communities can accelerate litter mass loss in home habitats relative to away habitats. However, the role of HFA in regulating the decomposition of individual carbon (C) fractions with distinct chemical structures remain largely unexplored. In particular, it is unclear to what extent litter-layer microbial communities—shaped by interactions between litter and soil microbial communities—drive the fraction-specific manifestation of HFA during litter C decomposition.
2. A 480-day reciprocal litter transplant experiment was conducted across forest and cropland ecosystems. The effect of HFA on the loss of four C fractions (dissolved organic carbon, cellulose, hemicellulose and lignin) with varying chemical qualities, as well as the role of litter-layer microbial communities in this process, were assessed using four litter types: two forest litters (*Schima superba* and *Castanopsis fargesii*) and two cropland litters (*Zea mays* and *Eleusine indica*).
3. HFA significantly accelerated the loss of both total litter mass and individual C fractions, with particularly strong effects on the recalcitrant lignin fraction. Litter-layer microbial communities were the key drivers of HFA, as microbial community dissimilarity between home and away sites showed a significant negative correlation with HFA for lignin loss. Moreover, a higher abundance of specific fungal taxa at home sites accelerated C fraction decomposition, whereas specific bacterial taxa suppressed decomposition.
4. These findings suggest that HFA differentially affects the decomposition of individual C fractions, likely mediated by specific litter-layer microbial communities at home sites. Overall, this study underscore the critical role of recalcitrant C substrates and litter-layer fungal taxa in shaping HFA and advance understanding of the microbial processes underlying litter decomposition in terrestrial ecosystems.

Cheng-Kang Xia and Yong Lin contributed equally to this work.

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KEYWORDS
cropland, forest, home-field advantage, labile carbon, litter-layer microbial communities, recalcitrant carbon

1 | INTRODUCTION

Litter carbon (C) decomposition is a key process in the terrestrial C cycle and is crucial for maintaining soil fertility and regulating the global C balance (Berg & McClaugherty, 2020; Chapin et al., 2011; Sokol et al., 2019). Among the various factors influencing litter C decomposition, the home-field advantage (HFA) has emerged as an important ecological hypothesis for explaining the variability in decomposition rates (Veen et al., 2015; Wang et al., 2023). The HFA describes the tendency for litter to decompose at an accelerated rate at its home site than at an away site (Ayres et al., 2009; Palozzi & Lindo, 2018). This phenomenon is primarily driven by the functional adaptation and specialization of native microbial communities in the litter layer to their historical litter C substrates (Fanin et al., 2021; Wang et al., 2023; Zhu et al., 2024). However, most existing studies on HFA have primarily focused on overall litter mass loss (Austin et al., 2014; Zhang et al., 2024), with relatively limited attention to litter C dynamics, especially the decomposition of individual C fractions and the specific microbial mechanisms underlying their degradation.

The main C fractions in litter include dissolved organic carbon (DOC), cellulose, hemicellulose and lignin (Wu et al., 2023). Owing to differences in their chemical structure and stability, these fractions exhibit distinct decomposition characteristics and vary in their microbial dependence during breakdown (Wang et al., 2022). For instance, DOC, the most labile C fraction, is primarily leached or metabolized by nonspecific microorganisms. In contrast, cellulose and hemicellulose are mainly decomposed by generalist microorganisms, whereas lignin is degraded by a limited set of specialized microorganisms due to its complex and recalcitrant structure (Shipley & Tardif, 2021). HFA tends to be more pronounced during the decomposition of recalcitrant substrates because of their strong dependence on locally adapted microbial communities (Freschet et al., 2012; Lyu et al., 2019; Pugnaire et al., 2023). However, an alternative perspective—the functional breadth hypothesis—suggests that the persistence of recalcitrant substrates may select for microbial decomposers with broad functional capacities, enabling them to decompose both home and away litter efficiently, thereby reducing the magnitude of HFA (Fanin et al., 2016; Keiser et al., 2011). Accordingly, the extent of HFA among C fractions may vary with their chemical recalcitrance and the adaptive breadth of local microbial communities. Yet, whether decomposability, microbial dependence and microbial functional breadth consistently predict the HFA across individual litter C fractions remains unclear.

Existing studies on HFA have predominantly emphasized the role of soil microbial decomposers (Benito-Carnero et al., 2021; Li et al., 2020), whereas relatively fewer have examined the contribution of litter-layer microbial decomposers, which play a critical role in C decomposition of litter (Fanin et al., 2021; Kohl et al., 2021; Wang et al., 2025). Soil microbial communities typically exhibit greater adaptability and functional redundancy than litter-layer microbial communities (Roy et al., 2023). Although broad-spectrum microbial capabilities are beneficial for overall decomposition processes, they may weaken the substrate-specific microbial interactions that drive HFA (Keiser et al., 2014). Litter-layer microbial communities are stochastically assembled but shaped by selective pressure (Veen et al., 2019), resulting in high substrate specificity towards litter C. This specificity may enable them to exert a stronger influence than soil microbial communities in driving HFA for litter C loss. Considering the biochemical heterogeneity of litter C fractions, the contribution of litter-layer microbial communities to HFA may vary significantly across fractions, particularly between two major microbial groups: fungi and bacteria (Hanson et al., 2008). Fungi are generally more efficient at degrading complex and recalcitrant C sources, such as lignin, whereas bacteria generally favour more labile C sources (Cao et al., 2024; Deveau et al., 2018). Therefore, a more comprehensive understanding of how different litter-layer microbial groups influence the strength of HFA across various C fractions is essential for elucidate the ecological processes governing litter C decomposition and the mechanisms underlying HFA in terrestrial ecosystems.

Most previous studies exploring HFA for litter decomposition have focused on translocations within or between forest and grassland ecosystems (Van Den Brink et al., 2023; Veen et al., 2015; Yuan et al., 2019), whereas translocations across fundamentally different land-use types, such as between forest and cropland systems, remain limited. Given the increasing concerns regarding land-use transitions in subtropical regions, understanding the decomposition of litter C fractions is crucial for advancing knowledge of C cycling in agroforestry systems (Long et al., 2023). To address this gap, we carried out a reciprocal litter transplant experiment in subtropical regions to examine how HFA influences the decomposition of different C fractions and the underlying microbial mechanisms. To minimize confounding effects associated with decomposition period and litter quality, we selected two litter types with distinct qualities from forest and cropland ecosystems. We conducted a 480-day reciprocal litter transplant experiment. By tracking the decomposition dynamics of four C fractions with varying recalcitrance and analysing the composition of litter-layer microbial communities, we aimed to test the following hypotheses: (1) All C fractions exhibit an HFA during litter decomposition, with strength ranked as lignin > hemicellulose > cellulose > DOC. This is because the complex and recalcitrant structure of lignin requires highly specialized microbial activity, whereas DOC, as a labile fraction, is readily accessible to a broad range of microorganisms. (2) HFA for litter decomposition of different C fractions is primarily driven by litter-layer microbial communities, with fungi predominantly contributing to HFA for the loss of recalcitrant C fractions (e.g. lignin) and bacteria mainly contributing to HFA for the loss of labile C fractions (e.g. DOC).

2 | MATERIALS AND METHODS

2.1 | Study site

The study was conducted at two observation sites representing distinct ecosystems: an evergreen broadleaved forest (forest ecosystem) and a corn dryland (cropland ecosystem). Both sites are located within the Jiulianshan National Nature Reserve, Longnan City, Jiangxi Province, Southeast China (24°35′ N, 114°28′ E). The two sites differ in both micro- and macroclimatic conditions: the forest site (435 m elevation) has a mean annual temperature (MAT) of 16.4°C, mean annual precipitation (MAP) of 2155.6 mm and relative humidity of 80%, whereas the cropland site (203 m elevation) experiences a MAT of 18.5°C, MAP of 1617.9 mm and relative humidity of 68%. Four representative plots were established at each site, each separated by 50 m, for the experimental setup.

2.2 | Reciprocal litter transplant experiment

Two abundant and representative plant species were selected from each site. At the forest sites, leaves of *Schima superba* and *Castanopsis fargesii* were collected from freshly senesced leaf litter as forest litter samples. At the cropland site, the aboveground parts of *Zea mays* and *Eleusine indica* were collected from pest-free, naturally senescing plants as cropland litter samples. All litter samples were collected in August 2020. Forest litter was obtained using litter traps, while cropland litter was collected manually. Following collection, all litter samples were oven-dried at 65°C for 72 h. Then, 15.0 g of intact litter were sealed in litterbags (20 cm × 25 cm) with a 1 mm mesh size and tagged with plastic labels. The prepared litterbags were stored in a dry, low-temperature, sealed environment prior to field deployment. Litterbags from all species were reciprocally translocated between the forest and cropland sites in late September 2020. Additionally, 15.0 g of each litter type was used to determine initial litter quality.

To ensure consistent soil conditions across treatments, surface soil (0–10 cm) was collected from eight plots in both forest and cropland ecosystem after removing surface litter. The soils collected from each ecosystem were thoroughly homogenized and used as the soil substrate for the experiment. After soil removal, a nylon net (mesh size: 0.01 mm) was placed in the excavated area to prevent fine root intrusion, and a 2 m × 3 m plot was established using polyvinyl chloride (PVC) boards. Each plot was divided into four equally sized subplots with PVC partitions for different litter types (Figure 1). The homogenized soil was uniformly backfilled and levelled before placing the litterbags. Subsequently, litterbags were gently positioned flat on the soil surface in all subplots. To prevent animal disturbance, all plots were enclosed with poultry wire-mesh cages.

A total of 256 litterbags were deployed across two sites (forest and cropland), four replicate plots, four litter types (*S. superba*, *C. fargesii*, *E. indica* and *Z. mays*), two replicate litterbags and four collection times. After 120, 240, 360 and 480 days of decomposition, two replicate litterbags of each litter type were retrieved from every subplot. The litter was carefully removed from the litterbags. One litterbag was oven-dried at 65°C for 72 h for measurements of mass and C fraction loss, while the other was stored at −80°C for DNA extraction.

2.3 | Chemical analysis

Litter organic C was measured using the H_2SO_4-$K_2Cr_2O_7$ oxidation method (Cui et al., 2023). Litter DOC was determined using the leaching method (Soong et al., 2014) and analysed using a TOC analyser.

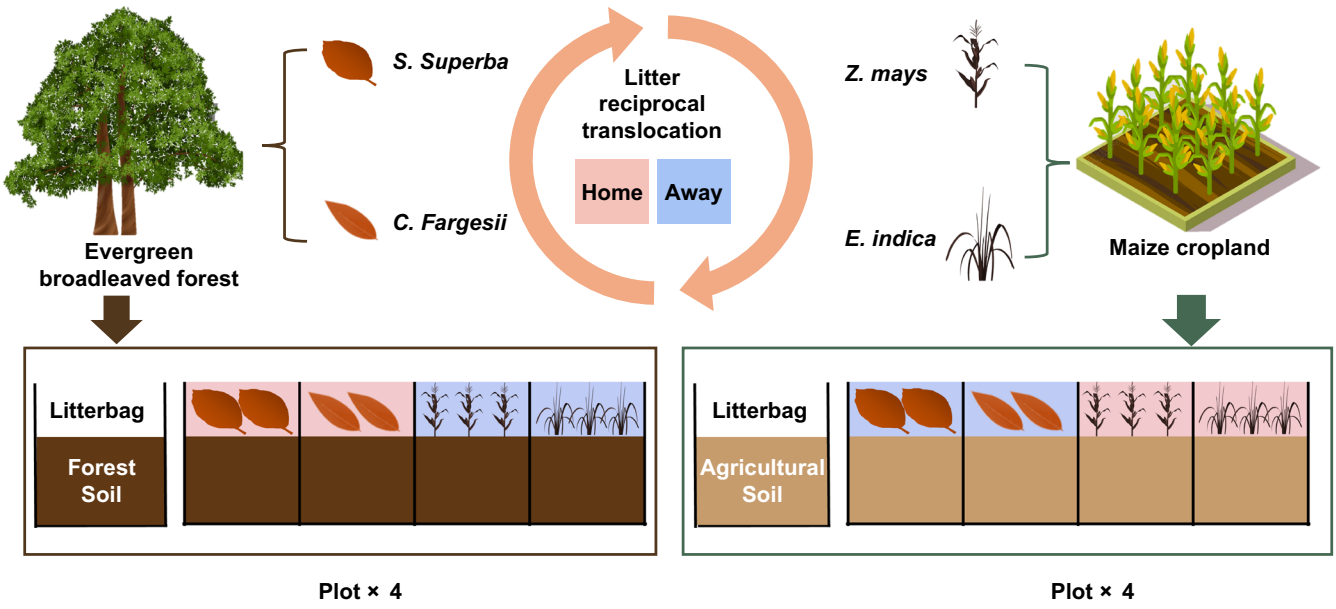


FIGURE 1 Experimental design of litter reciprocal transplant from evergreen broadleaved forest and maize cropland in subtropical China.

Litter cellulose, hemicellulose and lignin contents were measured using the method of Van Soest et al. (1991). Total nitrogen (TN) and phosphorus (TP) were measured after H_2SO_4-H_2O_2 digestion (Parkinson & Allen, 1975) and analysed using a full-automatic continuous flowing analyser (Westco Scientific, Danbury, Connecticut, USA).

2.4 | Microbial community analysis

DNA was isolated from litter samples with the Mag-Bind Soil DNA Kit following the manufacturer's instructions. DNA concentration and purity were measured with a NanoDrop NC2000 spectrophotometer and verified by agarose gel electrophoresis.

The bacterial 16S rRNA gene (V3–V4 region) was amplified using primers 806R and 338F. The fungal ITS region was amplified using primers ITS1R and ITS1F. Primers containing unique 7-bp barcodes were used for multiplex PCR. Amplifications were carried out with FastPfu polymerase under standard conditions (98°C, 5 min; 25 cycles of 98°C for 30 s, 53°C for 30 s and 72°C for 45 s; final extension at 72°C for 5 min). Amplicons were cleaned, quantified, pooled at equal concentrations and sequenced (2×250 bp) on the Illumina NovaSeq 6000 platform.

Sequences data were processed in QIIME2. Reads were demultiplexed, trimmed and denoised with Cutadapt and DADA2 plugin (Callahan et al., 2016). Non-singleton ASVs were aligned using MAFFT (Katoh, 2002) and used to construct phylogenies via fasttree2 (Price et al., 2009). Taxonomy was assigned using a naive Bayes classifier (classify-sklearn) (Bokulich et al., 2018) trained on SILVA v132 (bacteria) and UNITE v8.0 (fungi) databases (Kõljalg et al., 2013).

2.5 | HFA for litter total mass and four carbon fractions

The percentage of litter mass loss was calculated as

$$\text{Mass loss}\,(\%) = \frac{M_0 - M_t}{M_0} \times 100$$

where M_0 is the initial litter mass, and M_t is the litter mass remaining at sampling time t.

The percentage of litter C fraction loss was calculated as

$$\text{C loss}\,(\%) = \frac{C_0M_0 - C_tM_t}{C_0M_0} \times 100$$

where C_0 is the C fraction concentration of the initial litter, and C_t is the C fractions concentration of the litter at sampling time t.

To minimize the environmental influence during the decomposition period, the HFA index (HFAI) was calculated following the method of Ayres et al. (2009). This approach, which integrates data from four reciprocal combinations of forest and cropland litter decomposition at their respective home and away sites, minimizes the confounding effects of environmental variation between sites, enabling a more accurate evaluation of the HFA. The relative litter mass and C fraction loss within each habitat were calculated as:

$$\text{ARMLa} = \frac{\text{Aa}}{\text{Aa} + \text{Ba}}$$

where 'ARMLa' represents the relative loss of litter mass and C fraction from species A at habitat a, 'Aa' and 'Ba' represent the percent mass and C fraction loss of species A and B decomposing in habitat a, respectively.

The HFAI was calculated as:

$$\text{HFAI}\,(\%) = \left(\frac{\text{ARMLa} + \text{BRMLb}}{\text{ARMLb} + \text{BRMLa}} - 1\right) \times 100$$

where 'HFAI' represents the net difference in litter mass and C fraction loss between home and away habitats, calculated across both species (A and B) in the reciprocal transplant. This method typically requires a reciprocal transplant involving two litter types; however, we selected four litter types (two per habitat). Therefore, we calculated the HFAI of the following four litter combinations: *S. superba–Z. mays* (S–Z), *S. superba–E. indica* (S–E), *C. fargesii–Z. mays* (C–Z) and *C. fargesii–E. indica* (C–E). The relative differences in litter quality between these reciprocal transplants varied among combinations. This helped to minimize the confounding effects associated with the impact of differences in litter quality between home and away sites.

2.6 | Replication statement

Scale of inference	Scale at which the factor of interest is applied	Number of replicates at the appropriate scale
Site type	Site origin	4 home, 4 away
Plant	Litter types	2 forest, 2 cropland

2.7 | Statistical analysis

All statistical analyses were performed in R (v4.2.3). Normality and homogeneity of variance were assessed using the Shapiro–Wilk and Levene's tests. PCA was applied to visualize the variation in initial litter traits among the four litter types. Differences in litter traits were tested using one-way PERMANOVA. A one-way ANOVA with LSD was used to compare litter traits among the four litter types, as well as in the HFAI for total litter mass, and the four carbon fractions at each sampling day. Repeated-measures ANOVA, followed by Holm-corrected pairwise comparisons was used to evaluate differences in HFAI among the four C fractions across all sampling days. A one-sample *t*-test was performed to assess whether the HFAI differed significantly from zero. Unpaired *t*-tests were performed to compare mass loss, C fraction loss and α-diversity between home and away sites for each sampling day. NMDS based on Bray–Curtis dissimilarity matrices was used to visualize variations in bacterial and

fungal communities. A two-way PERMANOVA tested the effects of litter type and treatment (home vs. away) on microbial community structure. Linear mixed-effects models were used to assess the relationships between HFAIs (response variables) and the Bray–Curtis dissimilarity indices for microbial communities (fixed effects), with litter combinations included as random effects. Microbiome-wide association analysis was used to identify differentially abundant microbial ASVs between home and away litter-layer samples. These were defined as specific fungal and bacterial taxa for each litter type. The relative abundances of ASVs were expressed as $\log_2$ fold changes, with an adjusted p-value <0.001. Generalized linear mixed models with a beta distribution and logit link function were constructed to examine the relationships between litter C fraction loss and specific microbial communities. The relative abundances of these microbial communities were used as a fixed effect, while sampling day was treated as a random effect. Likelihood ratio tests was used to evaluate the significance of fixed effects.

3 | RESULTS

3.1 | Initial litter traits

The PCA ordination effectively separated the four litter types along the first two PCA axes (PERMANOVA, $p<0.001$; Figure S1). These axes reflected chemical traits recognized to impact litter decomposition rates, including C fractions (e.g. DOC, cellulose, hemicellulose and lignin), nutrients (e.g. N, P, etc.) and stoichiometric ratios (e.g. C:N, lignin:N, etc.). Litter chemistry varied significantly among the four litter types (Table 1), particularly between the forest and cropland litters. Forest litters were positioned at the low-quality end of the PCA axes and were more recalcitrant than the cropland litters (Figure S1). Moreover, chemical traits also differed between litter types within the same ecosystem. For instance, *S. superba* had significantly higher N and P concentration than *C. fargesii*, while *E. indica* exhibited higher lignin concentration than *Z. mays* (Table 1).

3.2 | Losses of litter total mass and four carbon fractions and their respective HFAI

The mass loss of forest litters (*S. superba* and *C. fargesii*) was significantly higher at home sites than at away sites across all sampling days (Figure 2A). However, cropland litters did not exhibit a significantly higher mass loss at the home sites, except for *E. indica*. Across all sampling days, the HFAI for mass loss was significantly higher than zero, indicating a significant positive HFA effect on litter mass loss (Figure 2B).

The loss of litter C fractions also differed significantly between home and away sites, with distinct patterns among the individual C fractions (Figure S2). For DOC, forest litters decomposed significantly faster at home sites, whereas cropland litters decomposed faster at away sites. For lignin, forest and cropland litters, except *Z. mays*, decomposed significantly faster at home sites than at away sites. The HFAI for all C fractions was significantly higher than zero (Figure 2C). Furthermore, there were significant differences in HFAI among the different C fractions. Across the four sampling days, the average HFAIs were 4.65% for DOC loss, 12.90% for cellulose loss, 17.84% for hemicellulose loss and 96.49% for lignin loss.

3.3 | Microbial community composition, diversity

The composition and diversity of the litter-layer microbial communities differed markedly between home and away sites (Figure 3; Figures S3–S6). At the phylum level, bacterial communities showed the largest differences in the relative abundance of *Proteobacteria*, *Actinobacteriota*, *Acidobacteriota* and *Firmicutes* (Figure S3), whereas the fungal communities showed the greatest differences in *Ascomycota*

TABLE 1 Initial litter traits (mean ± standard error, $N=4$) of litters from forest and cropland ecosystems in the reciprocal litter transplant experiment.

	Evergreen broadleaved forest		Maize cropland	
Litter traits	***Schima superba***	***Castanopsis fargesii***	***Eleusine indica***	***Zea mays***
Organic C (mg g^{-1})	494.47 ± 22.12^{a}	468.36 ± 17.9^{a}	424.98 ± 22.85^{b}	380.61 ± 4.07^{c}
DOC (mg g^{-1})	46.89 ± 1.63^{c}	55.96 ± 1.45^{b}	73.21 ± 2.39^{a}	35.64 ± 1.47^{d}
Cellulose (mg g^{-1})	158.77 ± 5.21^{c}	165.09 ± 8.11^{c}	226.48 ± 10.03^{b}	287.71 ± 5.95^{a}
Hemicellulose (mg g^{-1})	144.11 ± 3.98^{c}	120.94 ± 3^{d}	206.83 ± 9.27^{b}	227.23 ± 8.25^{a}
Lignin (mg g^{-1})	252.27 ± 6.99^{a}	249.66 ± 10.92^{a}	212.02 ± 10.63^{b}	175.8 ± 7.47^{c}
N (mg g^{-1})	5.93 ± 0.22^{c}	9.00 ± 0.88^{b}	12.25 ± 1.00^{a}	13.31 ± 0.98^{a}
P (mg g^{-1})	0.16 ± 0.00^{d}	0.33 ± 0.09^{c}	2.79 ± 0.07^{a}	2.67 ± 0.02^{b}
C/N	83.32 ± 0.95^{a}	52.27 ± 3.49^{b}	34.78 ± 1.62^{c}	28.7 ± 1.75^{d}
C/P	3098.61 ± 73.93^{a}	1498.31 ± 385.72^{b}	152.46 ± 4.73^{c}	142.72 ± 0.50^{c}
Lignin/N	42.53 ± 0.85^{a}	27.85 ± 1.57^{b}	17.35 ± 0.58^{c}	13.24 ± 0.5^{d}
Lignin/P	1581.28 ± 4.9^{a}	797.44 ± 197.58^{b}	76.08 ± 2.66^{c}	65.91 ± 2.29^{c}

Note: DOC represents dissolved organic carbon. Different lowercase letters indicate significant differences among four litter types ($p<0.05$).

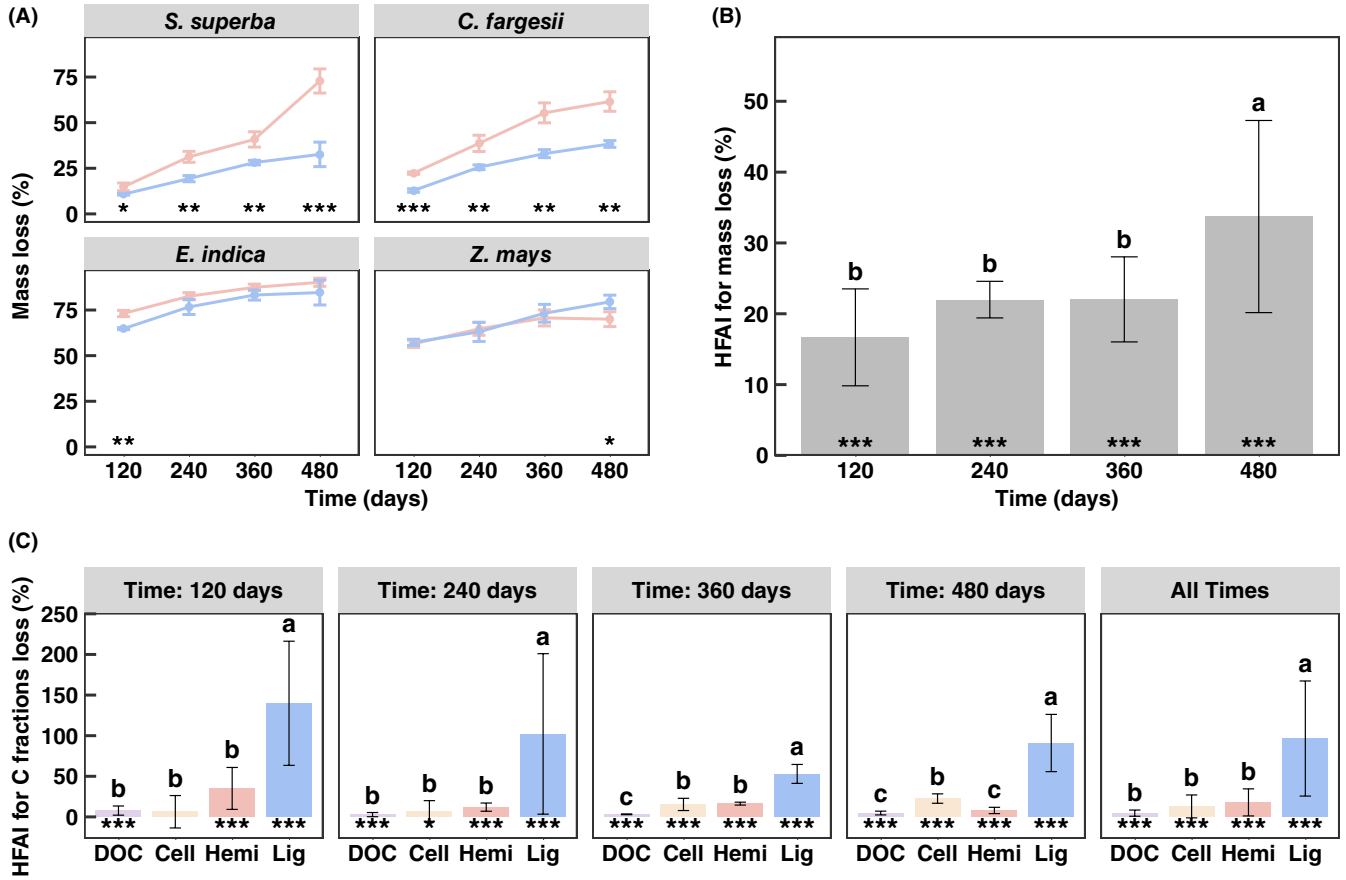


FIGURE 2 Losses of litter total mass and four C fractions and their respective home-field advantage indexes (HFAI) across four sampling days. DOC represents dissolved organic carbon. Cell represents hemicellulose, Hemi represents hemicellulose, and Lig represents Lignin. Data are expressed as means ± standard error (A: $N=4$; B, C: $N=16$). Stars in (A) indicate estimates significantly different between home and away sites within each of the four sampling days (*$p<0.05$, **$p<0.01$, ***$p<0.001$). Stars in (B, C) indicate estimates significantly different from zero at the corresponding significance levels. Different letters denote significant differences at $p<0.05$.

and *Basidiomycota* (Figure S4). Moreover, microbiome-wide association analysis revealed that these taxa were also the dominant microbes, specifically enriched at home versus away sites (Figures S7 and S8). NMDS showed distinct separation patterns for both bacterial and fungal communities composition (Figure 3; Stress = 0.115 and 0.145, respectively). PERMANOVA further demonstrated that treatment (home vs. away), litter type and their interaction all exerted significant effects on microbial communities throughout the decomposition process (Tables S1 and S2).

3.4 | Relationship between microbial community and HFAI

Linear mixed-effects models revealed significant correlations between the microbial community dissimilarity index and HFAI for both mass loss and individual C fractions (Figure S9; Figure 4). However, the strength and direction of these correlations varied among C fractions (Figure 4). Specifically, the microbial community dissimilarity index was significantly negatively correlated with the HFA for DOC (bacteria and fungi $p<0.001$), hemicellulose (bacteria and fungi $p<0.001$) and lignin (bacteria and fungi $p<0.001$), but positively correlated with the HFAI for cellulose (bacteria and fungi $p<0.05$).

GLMMs showed significant relationships between the relative abundance of specific microbial ASVs and both mass loss and C fractions loss (Figure S10; Figure 5). The relative abundance of specific bacterial ASVs were significantly negatively correlated with all C fraction losses. The relative abundance of specific fungal ASVs showed significant positive relationships with all C fraction losses.

4 | DISCUSSION

4.1 | HFA for litter decomposition of carbon fractions

We found that HFA significantly influenced both litter mass loss and the decomposition of all litter C fractions, whether labile or recalcitrant. This finding aligns with previous studies showing that HFA plays a key role in litter C decomposition across various ecosystems, including coniferous forests, shrublands and meadows (Perez et al., 2013; Wang et al., 2023; Yuan et al., 2019). The results indicate

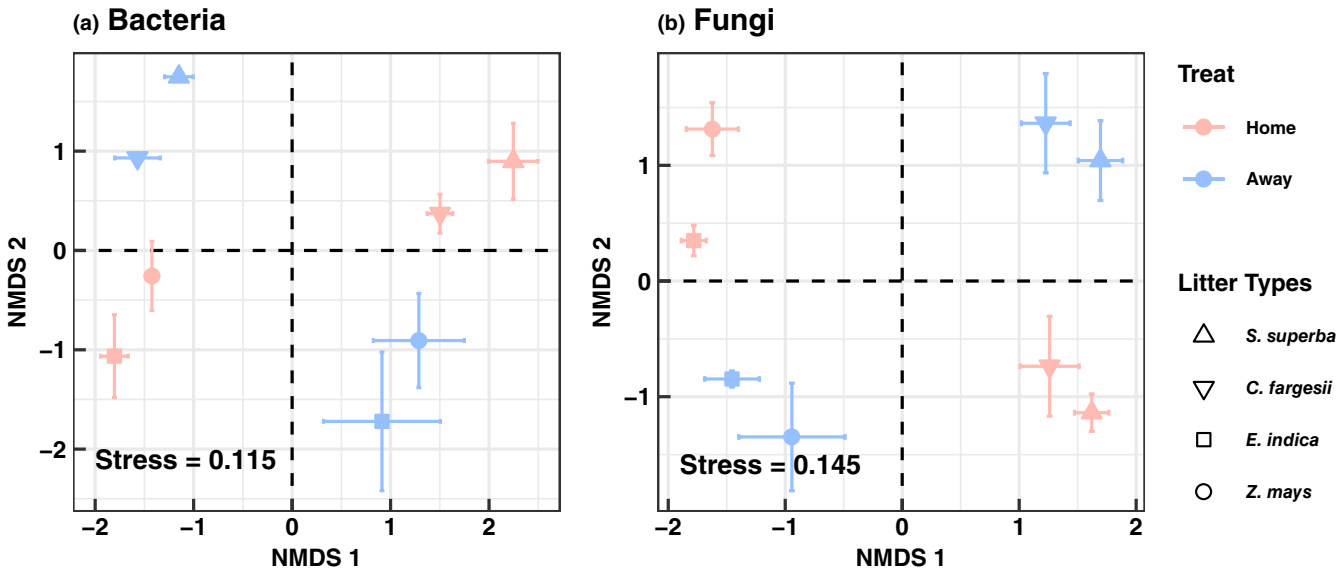


FIGURE 3 NMDS of bacterial (a) and fungal (b) communities based on Bray–Curtis dissimilarity matrices across four sampling days. The colour indicates the home and away sites, and the shapes indicate the different litter types. The centroids and error bars indicate the degree of separation and variability among groups across sampling days ($N = 16$).

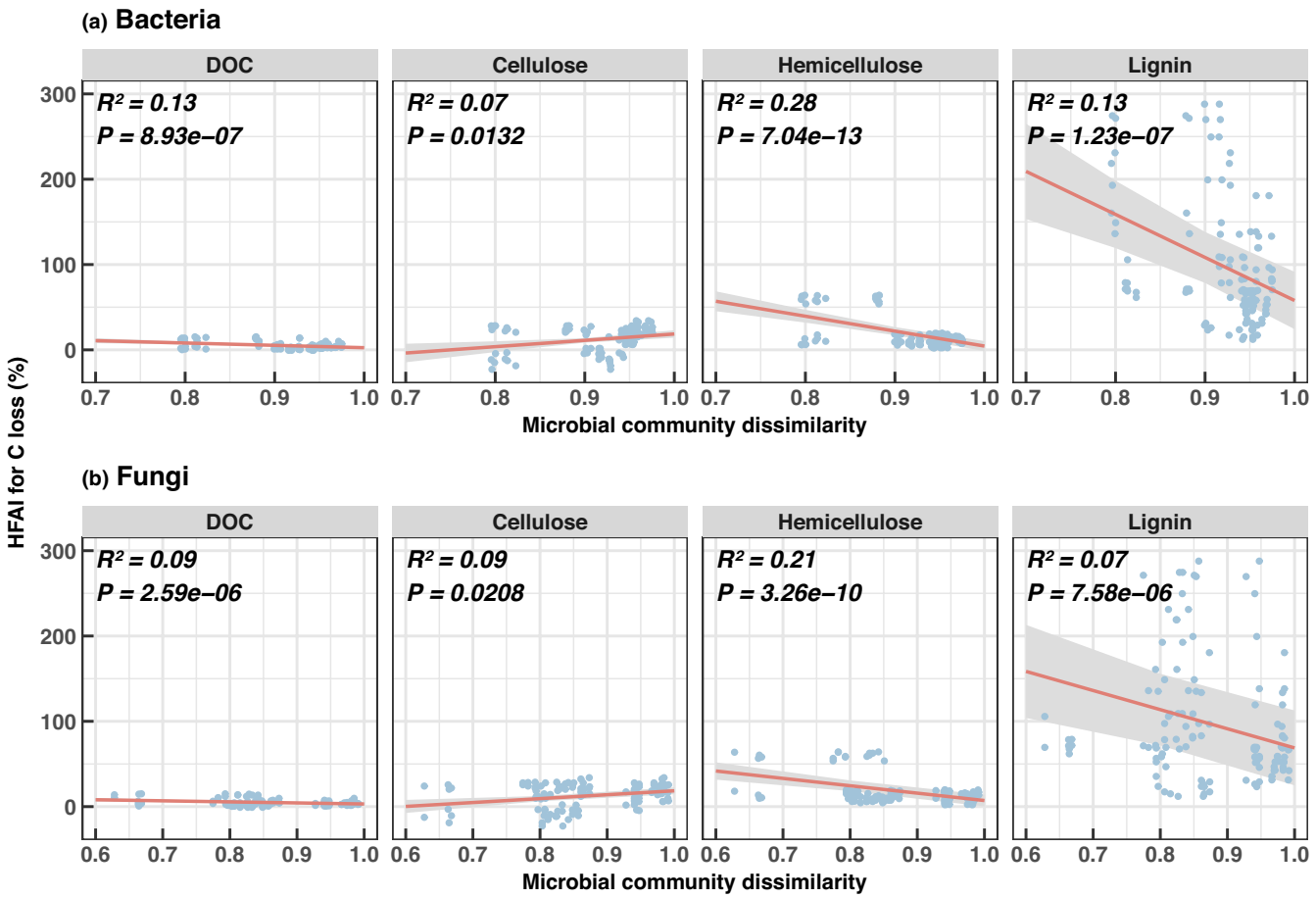


FIGURE 4 Relationships between HFAI for the loss of four C fractions and bacterial (a) and fungal (b) community dissimilarity. DOC represents dissolved organic carbon.

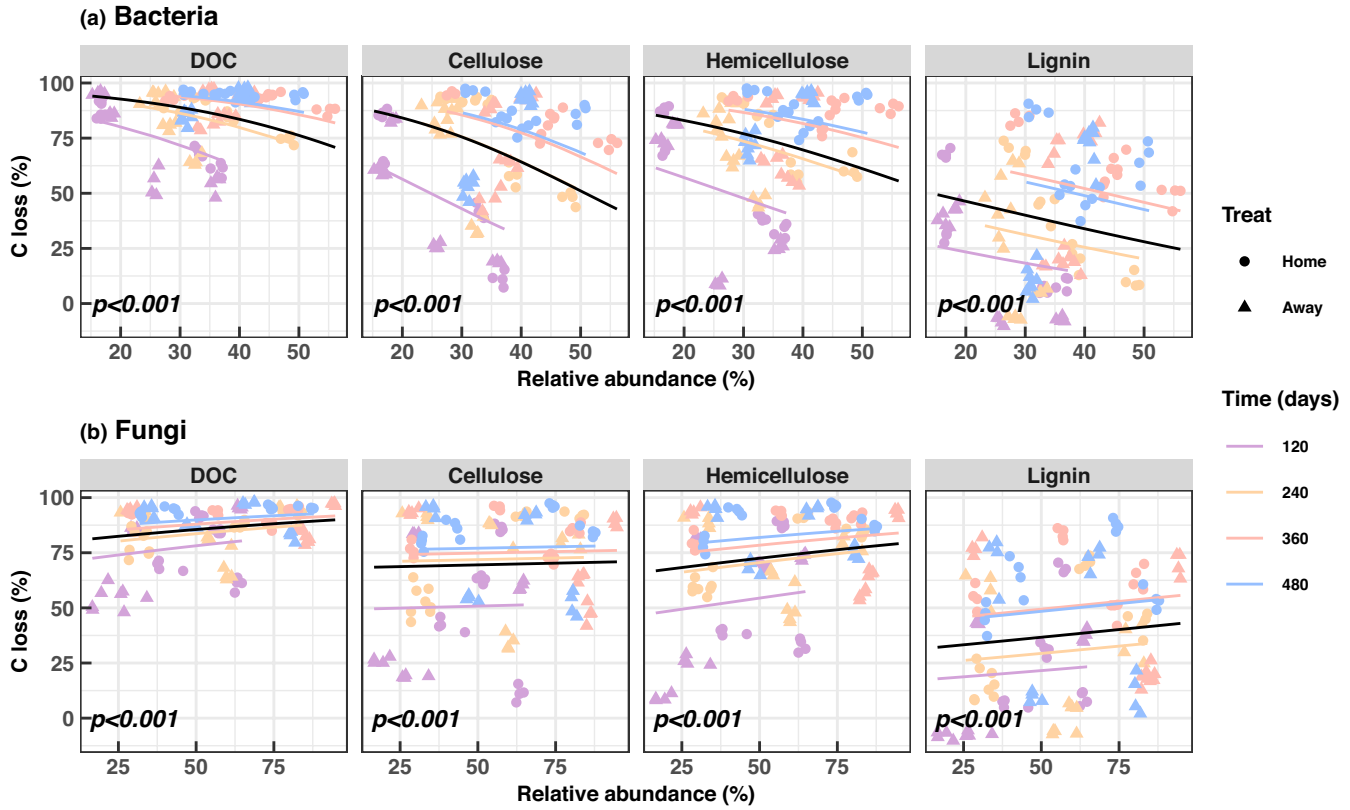


FIGURE 5 Relationships between the loss of four C fractions and relative abundance of specific bacterial and fungal taxa. Solid black lines depict significant relationships across sampling days obtained from generalized linear mixed models (GLMMs). Coloured lines show the relationship among each sampling day obtained from GLMMs. DOC represent dissolved organic carbon.

that HFA is not merely a consequence of general microbial adaptation to the whole litter but also reflects the specific adaptation of microbial communities to distinct litter C fractions. However, although HFA accelerated litter C decomposition, decomposition does not always proceed faster at home than at away sites, as inherent ecosystem properties may exert stronger influence. For instance, cropland litter C fractions decomposed faster at away than at home sites. Analogous to sports, victory is not always determined by HFA; superior capacity can be more decisive. In this study, the forest environment represents the 'greater athletic ability', attributable to several interacting factors. First, compared with cropland, forests typically have higher humidity and temperature, which enhance the metabolic activity of decomposer microbial communities and accelerate C breakdown (Coûteaux et al., 1995). Second, differences in microbial nutrient limitation between ecosystems lead to varying degrees of microbial growth constraint, thereby causing differences in decomposition rates. Forest soils with long-term organic matter accumulation maintain more stable nutrient cycling and provide a balanced and continuous nutrient supply for microorganisms (Li et al., 2023). In contrast, prolonged cultivation and harvesting in croplands disrupt nutrient cycling and decrease its efficiency, constraining microbial growth (Hu et al., 2025). Finally, differences in the functional potential of microbial decomposers are also important contributors to decomposition differences (Fanin et al., 2016; Osburn et al., 2022). Forest soils with long-term exposure to complex and recalcitrant litter select for more diverse microbial communities with stronger decomposition capacities. Conversely, cropland soils tend to harbour microbial communities with lower diversity and narrower functional ranges, particularly with weaker capacities to degrade complex organic matter, resulting in overall slower decomposition rates.

Consistent with our first hypothesis, HFA was stronger for lignin loss than for DOC loss. This difference is likely attributable to the distinct decomposition characteristics of these C fractions arising from their intrinsic chemical properties (Kögel-Knabner, 2002). Owing to their relatively simple molecular structures, labile C substrates such as DOC are widely metabolized by diverse heterotrophic microorganisms (Marschner & Kalbitz, 2003). This lead to limited variation in microbial utilization across sites, resulting in a weaker HFA expression. In contrast, recalcitrant C substrates due to their highly complex molecular architecture, require specialized enzymatic systems and microbial taxa, such as white-rot fungi and certain actinomycetes, for effective degradation (Janusz et al., 2017). The distribution and activity of these specialized microorganisms are strongly shaped by environmental conditions, substrate origin and long-term evolutionary adaptation to native environments, leading to a stronger expression of HFA. Overall, these findings highlight the necessity of integrating C fraction-specific HFA processes into terrestrial C cycling models to improve the predictive accuracy of ecosystem C fluxes.

4.2 | HFA and litter-layer microbial community

The relationship between HFA for the loss of the four C fractions and microbial community dissimilarity exhibited diverse patterns, including both significantly positive and negative correlations. In contrast, the abundance of specific bacterial taxa showed consistent directional correlations across the decomposition of multiple C fractions, a pattern mirrored by fungal taxa. These results suggest that the litter-layer microbial community drives the HFA for C decomposition through specific microbial activities specialized for certain C fractions at home sites rather than through broad shifts in overall community composition. The negative relationship observed for recalcitrant C may indicate dependence on a narrow set of specialized microbial taxa rather than on the broader microbial community (Pugnaire et al., 2023). This result supports the specific microbial community hypothesis (Shigyo et al., 2024), which posits that the identity of specific microbial groups is critical to HFA. Li et al. (2020) reported that HFA driven by bacteria and fungi may be attributed to specific microbial taxa, such as *Xanthomonadales* and *Cutaneotrichosporon*. Similarly, Veen et al. (2019) found that overall differences in fungal community composition between home and away sites were not significantly related to HFA, except for specific fungal taxa such as *Sordariomycetes*, which showed significant positive correlations with HFA. Moreover, we found that microbial community dissimilarity between home and away sites was closely linked to HFA for mass loss. Several other studies have reported similar findings (Veen et al., 2019; Yuan et al., 2024), further highlighting the pivotal role of litter-layer microbial communities in mediating HFA.

Contrary to our second hypothesis, a significant negative relationship was detected between the abundance of specific bacterial taxa and the loss of C fractions, suggesting that the presence of specific bacteria may suppressed the decomposition of litter C at home sites. This suppression may be attributed to niche pre-emption by specific bacterial taxa in the litter (Lin et al., 2020). At home sites, specific bacterial taxa rapidly colonize litter surfaces, occupying available resources such as space, energy and nutrients, thereby inhibiting the subsequent establishment of functional decomposers (Wang & Kuzyakov, 2024). These bacteria preferentially utilize labile C sources that are broadly accessible to other microorganisms. Consequently, rapid consumption of nonspecific substrates, coupled with niche pre-emption, may lead to competitive exclusion and ultimately suppress the decomposition of C fractions at home sites.

Unlike bacteria, specific fungal taxa exhibited a distinct functional pattern. We found that an increase in the abundance of specific fungal taxa significantly accelerated the decomposition of C fractions in home-site litter. This effect was particularly pronounced for recalcitrant C, aligning with the established role of fungi as primary decomposers of such substrates (Hanson et al., 2008). For labile C, fungi may not directly metabolize these substrates but instead degrade physical barriers such as lignin (Ren et al., 2024), thereby indirectly facilitating access to other C pools. Furthermore, high functional redundancy within fungal communities enables multiple fungal taxa to cooperatively decompose a broad spectrum of C substrates (McGuire et al., 2010). Overall, these findings indicate that specific fungal taxa are involved in driving the HFA for litter C decomposition.

The contrasting roles of litter-layer bacteria and fungi in regulating HFA for C decomposition have important implications for ecosystem C source-sink dynamics. As primary decomposers of labile C, bacteria exhibit non-site-specific utilization patterns, playing a critical role in short-term C turnover. In contrast, fungi, which are the main decomposers of recalcitrant C, show preferential utilization at home sites, thereby accelerating the transformation of plant-derived C into microbial and soil C pools. These findings are crucial for advancing our understanding of microbial regulatory mechanisms in terrestrial C cycling.

5 | CONCLUSION

Based on a reciprocal litter transplant experiment, we investigated how HFA influences the decomposition of litter C fractions and the

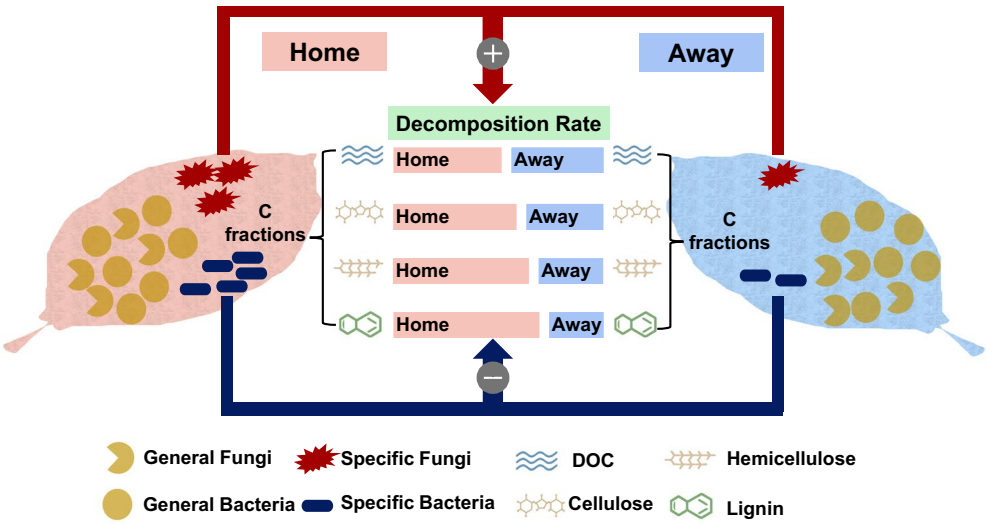


FIGURE 6 Conceptual framework illustrating how litter-layer microbial communities mediate the home-field advantage for the decomposition of carbon fractions with varying chemical recalcitrance.

role of microbial communities in this process. The results revealed significant variation in the effect of HFA across C fractions of differing qualities, with recalcitrant fractions being more strongly affected. This pattern is closely associated with the abundance of litter-layer microorganisms. Specifically, specific fungal taxa promoted the decomposition of home-site litter C, whereas specific bacterial taxa suppressed it (Figure 6). Overall, this study provides new insights into the microbial mechanisms regulating HFA for litter decomposition and highlights the crucial roles of recalcitrant substances and litter-layer microbial communities in this process.

AUTHOR CONTRIBUTIONS

Cheng-Kang Xia, Yong Lin and Fu-Sheng Chen planned the ideas, designed methodology and led the writing of the manuscript; Cheng-Kang Xia, Yong Lin, Baitong Hu and Yi Hu performed the experiments. Xuan Wu and Ying-Jie Liu analysed the data and drew the graphics. Chao Liang, Fangchao Wang, Shengnan Wang and Junjie Huang contributed substantially to revisions. All authors contributed critically to the drafts and gave final approval for publication.

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CONFLICT OF INTEREST STATEMENT

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

DATA AVAILABILITY STATEMENT

Data deposited in the Dryad Digital Repository: https://doi.org/10.5061/dryad.8pk0p2p1w (Xia et al., 2025).

STATEMENT ON INCLUSION

Our study includes scientists based in the country where the study was carried out. We recognize that more could have been done to engage global scientists with our research as our project developed and to embed our research within the national context and research priorities. We are planning to address these caveats in future research.

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SUPPORTING INFORMATION

Additional supporting information can be found online in the Supporting Information section at the end of this article.

Figure S1. PCA of initial litter traits.

Figure S2. Losses of litter four carbon fractions across four sampling days.

Figure S3. Relative abundances of dominant bacterial taxa (phyla) in litter layer.

Figure S4. Relative abundances of dominant fungal taxa (phyla) in litter layer.

Figure S5. Bacterial community α-diversity in litter layer.

Figure S6. Fungal community α-diversity in litter layer.

Figure S7. Relative abundances of specific bacterial taxa (phyla) in litter layer.

Figure S8. Relative abundances of specific fungal taxa (phyla) in litter layer.

Figure S9. Relationships between HFAI for mass loss and microbial community dissimilarity.

Table S1. PERMANOVA analysis of litter-layer bacterial community β-diversity.

Table S2. PERMANOVA analysis of litter-layer fungi community β-diversity.

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