

RESEARCH ARTICLE

Moderate size diversity of tree roots has largest effect on the carbon loss in tropical soils

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Abstract

1. Most studies focused on the above-ground diversity on leaf litter decomposition and soil respiration in tropical ecosystems, however, the mechanism understanding of root diversity on decomposition is still unclear.
2. We selected the fine-roots of 21 dominant tree species from a tropical rainforest in Xishuangbanna, China, then conducted a 360-day and well-replicated (21 replications) incubation decomposition experiment with a 0, 1, 3, 6, 9, 12, 15, 18 and 21 species gradient of root diversity. The fine-root mass loss, CO₂ release, and their potential drivers were analysed.
3. The results showed that as fine-root diversity increased, soil properties, microbial diversity and fungal biomass changed nonlinearly, leading to higher litter mass loss and soil CO₂ release in the moderate diversity with 9, 12 and 15 species mixtures. Non-additive effect analysis also indicated that synergistic effects were greater in these three mixtures than others on soil CO₂ release and litter mass loss. The indirect effects of soil properties and microbial communities were larger than the direct effect of fine-root diversity.
4. Our findings suggest that fine-root diversity has nonlinear relationships with litter decomposition and soil CO₂ release in tropical forests, thus highlighting the importance of plant diversity due to its role in the carbon cycle under global change scenario.

KEYWORDS

biodiversity, fine-root, litter mass loss, soil CO₂ release, tropical forest

1 | INTRODUCTION

Plant diversity is decreasing due to global climate change and human activity (Cao et al., 2022; Ohashi et al., 2019), with environmental pressures on plants expected to increase in future, biodiversity loss worsens (Lehner et al., 2019; Yang et al., 2019). Due to their large carbon (C) pools, tropical forests are particularly important to the global C budget (Barbier et al., 2020). Despite their

high biodiversity and large C storage capacity (Gibbs et al., 2010; Pan et al., 2011), tropical forests are one of the most threatened ecosystems in the world (Schulz et al., 2019). Litter decomposition in forests plays a critical role in the global C cycle, which transfers nutrients to the soil and represents an important source of CO₂ entering the atmosphere (Gessner et al., 2010). Root-derived C is sequestered in the soil more efficiently than leaf-derived C and is thus more consequential for the global C cycle (Craig et al., 2022).

Although many studies focused on the decomposition of above-ground litter, the effects of root diversity and root litter decomposition on soil C cycling have been frequently overlooked in forest ecosystems (Canessa et al., 2022). Therefore, a better understanding of root diversity and its effect on soil C cycling is imperative in tropical rainforests.

Because root-derived C forms a larger portion of the relatively stable soil C pool than C originating in above-ground litter, root decomposition is an important driver of terrestrial C flux (Kätterer et al., 2011). Root diameter influences the chemical and physical properties of root litter and, subsequently, litter quality (Silver & Miya, 2001). Root decomposition appears to be particularly sensitive to soil conditions such as moisture, oxygen concentration, pH and inorganic nutrient limitation (Garcia-Palacios et al., 2013; See et al., 2019). Mixed litter can alter decomposition by its effects on litter quality (i.e. mass ratio hypothesis) and litter trait dissimilarity (i.e. complementary use) (Canessa et al., 2022; Zhang et al., 2023), the fine-roots contain different elements and substances, and their chemical properties vary significantly (Gessner et al., 2010; Prieto et al., 2016). The effects of mixed root litter on decomposition rate and nutrient release have not been well-studied (Man et al., 2020; Yang et al., 2022). Fine-roots (diameter < 2 mm) have higher nutrient contents and are regarded as high turnover rate in terrestrial ecosystems (McCormack et al., 2015), in which the fine-roots of many plant species die within a year of their formation (Fogel, 1985). The turnover of fine-root biomass accounts for c. 14%–27% of net primary production globally (McCormack et al., 2015) and is estimated to contribute 33% of annual litter inputs in forests around the world (Freschet et al., 2010). Fine-root litter input can result in faster rates of decomposition, which in turn appear to activate microorganisms to stabilise soil organic matter (Cotrufo et al., 2013). Compared with fine-root growth and production, the fine-root decomposition processes and mechanisms need to be better understood due to their important role in C dynamics of the forest below-ground.

Microorganisms transfer nutrients between different litter types within mixtures, which can help optimise resource availability for decomposers, and these effects may be stronger for slowly decomposing litter types within a mixture (Liu et al., 2020; Man et al., 2020). For example, mixed litter has positive effects on decomposition, largely driven by increased microbial diversity (Liu et al., 2020). Microbial decomposition converts the C contained within the detritus into CO₂ and releases nutrients for plant growth (Heijboer et al., 2018). The mechanisms underlying the non-additive effects of diverse mixtures of leaf and root litter on decomposition are still disputed, because different diversity and experimental durations yielded inconsistent results, such as antagonism and synergism effects in forest ecosystems (Gripp et al., 2018; Lecerf et al., 2011; Leppert et al., 2017). For example, a previous study suggested that litter species composition drives this effect and that the chemistry of composite litter may be the predominant factor under specific environmental conditions (Handa et al., 2014). In addition, soil fungi play critical and unique roles

in terrestrial ecosystem processes, and fungi are better equipped to decompose complex litter (Tedersoo et al., 2014). Therefore, fungal communities were considered as the primary agents of decomposition (Glassman et al., 2018). However, there are knowledge gaps on how the relationship between fungi and fine-root diversity influences decomposition in tropical rainforests.

To understand how fine-root diversity affects litter decomposition in tropical rainforests, we presented a year-long laboratory experiment to elucidate the effects of fine-root diversity on litter decomposition. Since litter decomposition has an important effect on soil C cycling (McGuire & Treseder, 2010), soil CO₂ release was measured to analyse how the soil C cycle responded to fine-root diversity. We hypothesised that: (1) The decomposition of mixed root litter has a non-additive effect such that moderate but not highest diversity has the strongest effect on fine-root litter mass loss during decomposition. Since the mixed litters with different physical and chemical properties lead to various nutrient inputs, which can affect soil microbial community structure and its function (Chen et al., 2017; Gessner et al., 2010); (2) The pattern of soil CO₂ release would be similar to the decomposition of fine-root litter, while soil microbial community regulates the processes. Because the substances that are difficult to decompose within mixed litters would inhibit microbial activities (Gessner et al., 2010; Prieto et al., 2016; Sun et al., 2018).

2 | MATERIALS AND METHODS

2.1 | Materials

Fine-root litters (FRL) were collected in October 2018 and surface soil (0–20 cm) was collected in October 2020 in a tropical rainforest in Xishuangbanna (101°34′26″–47″ E, 21°36′42″–58″ N), Yunnan Province, China. This study did not need permission for fieldwork. For fine-root collection, 21 dominant tree species belong to 12 families and 17 genera were selected (Table 1). Each species of fine-roots was obtained from 4 randomly selected trees to make them enough for experiment. FRL was air-dried and sterilised with humid heat (121°C, 30 min, two successive sterilization treatments). For soil collection, five sampling locations were randomly chosen. The humus was removed from the soil surface, sampled soil was mixed into a single composite sample, the residual roots and stones were manually removed, and the soil was passed through a 2 mm sieve.

2.2 | Experimental design

A well-replicate incubation experiment was established with 9 treatments with 21 replicates in each treatment. They were coded with root species 0 (CK), 1 (M1), 3 (M3), 6 (M6), 9 (M9), 12 (M12), 15 (M15), 18 (M18) and 21 (M21), respectively. Before we set the experiment, 21 kinds of fine-roots were labelled from No. 1 to

TABLE 1 Classification of 21 tropical tree species and their fine-root nutrient contents.

No.	Order	Family	Genus	Species	TC (g kg ⁻¹)	TN (g kg ⁻¹)	TP (g kg ⁻¹)
1	Ranales	Annonaceae	<i>Pseuduvaria</i>	<i>Pseuduvaria indochinensis</i>	335.12	14.10	0.25
2			<i>Alphonsea</i>	<i>Alphonsea monogyna</i>	434.71	7.55	0.14
3		Myristicaceae	<i>Knema</i>	<i>Knema furfuracea</i>	406.43	11.69	0.14
4			<i>Myristica</i>	<i>Myristica yunnanensis</i>	401.03	9.95	0.14
5		Lauraceae	<i>Litsea</i>	<i>Litsea dilleniifolia</i>	400.78	16.18	0.15
6				<i>Litsea verticillata</i>	358.83	5.76	0.05
7	Euphorbiales	Euphorbiaceae	<i>Cleidion</i>	<i>Cleidion brevipetiolatum</i>	353.44	14.68	0.19
8			<i>Trigonostemon</i>	<i>Trigonostemon thyrsoideus</i>	344.08	13.01	0.11
9			<i>Baccaurea</i>	<i>Baccaurea ramiflora</i>	373.64	7.19	0.14
10	Urticales	Moraceae	<i>Ficus</i>	<i>Ficus auriculata</i>	402.50	5.56	0.12
11				<i>Ficus langkokensis</i>	390.93	5.20	0.09
12				<i>Ficus oligodon</i>	352.11	5.95	0.13
13	Parietales	Guttiferae	<i>Garcinia</i>	<i>Garcinia cowa</i>	423.26	7.13	0.11
14				<i>Garcinia lancilimba</i>	440.04	5.54	0.08
15		Dipterocarpaceae	<i>Parashorea</i>	<i>Parashorea chinensis</i>	426.46	8.21	0.14
16	Rutales	Meliaceae	<i>Chisocheton</i>	<i>Chisocheton paniculatus</i>	417.91	8.99	0.04
17			<i>Dysoxylum</i>	<i>Dysoxylum binectariferum</i>	383.03	12.58	0.02
18	Ebenales	Ebenaceae	<i>Diospyros</i>	<i>Diospyros nigrocortex</i>	404.95	10.74	0.11
19	Fagales	Fagaceae	<i>Castanopsis</i>	<i>Castanopsis hystrix</i>	398.05	13.62	0.19
20	Sapindales	Icacinaceae	<i>Pittosporopsis</i>	<i>Pittosporopsis kerrii</i>	411.90	4.85	0.06
21	Malvales	Elaeocarpaceae	<i>Elaeocarpus</i>	<i>Elaeocarpus varunua</i>	368.62	7.25	0.18

Abbreviations: AM, arbuscular mycorrhiza; EM, ectotrophic mycorrhiza; TC, total carbon; TN, total nitrogen; TP, total phosphorus.

No. 21. To exclude the effects caused by the identity of species rather than diversity, we set 21 replicates and ensured that each species can be included in the incubation experiment in our study. With the treatment of 1 species fine-root (i.e. M1), we chose each species of fine-root for one repeat. With the treatments of 3, 6, 9, 12, 15 and 18 species fine-roots, we started with No. 1 to No. 3, No. 6, No. 9, No. 12, No. 15 and No. 18, respectively, then rotations started from No. 2. For example, the treatment of 3 species fine-roots (M3), for the first repeat we chose roots No. 1, No. 2 and No. 3; for the second repeat we use roots No. 2, No. 3 and No. 4; for the third repeat we use roots No. 3, No. 4 and No. 5, and so on. For each treatment with one or different species, the average weight of fine-roots was weighted for each repeat; that is, with the treatment 21 of species fine-roots, 0.1429 g for each species of fine-root was weighted and added 3 g to the bottle. Then, these 3 g of FRL were added to each 500 mL culture bottle with added 100 g of dry soil for each. The fine-roots were mixed with the soil. In total, there were 189 bottles in our study. Soil moisture in the bottle was held at 60% and sustained during experiment. In line with the dynamics of seasonal temperature in tropical Xishuangbanna, the bottles were incubated in the dark at 25°C, 21.5°C and 18°C for 120 days for each temperature. Soil CO₂ release was measured every month and residual FRL was recovered at the end of the experiment.

2.3 | Sample measurements

Nutrient elements were measured in FRL and soil of 21 plants prior to the beginning of the experiment. After 360 days of incubation, a total of 189 soil samples were measured. A portion of the soil was used for the nutrient analysis, and the remainder was frozen at -80°C for fungal community and soil microbial phospholipid fatty acid (PLFA) analysis. All soil samples of ammonia nitrogen (NH₄⁺-N), nitrate nitrogen (NO₃⁻-N) and dissolved organic carbon (DOC) were extracted with 0.5 mol L⁻¹ K₂SO₄. Soil available phosphorus (AP) was extracted with 0.5 mol L⁻¹ NaHCO₃ solution (pH = 8.5), total nitrogen (TN) and total phosphorus (TP) were determined with sodium salicylate and molybdenum antimony methods, respectively. SOC and DOC were determined using a merged Vario TOC analyser (Vario TOC, Langensfeld, Germany); SOC was determined by dry combustion at 980°C in solid mode, and DOC was determined in liquid mode. The concentrations of TN, NH₄⁺-N, NO₃⁻-N, TP and AP were determined through auto discrete analyser (De Chem-Tech. GmbH, CleverChem380, Hamburg Germany). Soil C to N ratio (C:N) was calculated as the ratio of SOC to TN. Soil pH in water was measured using pH meter, and the soil-to-solution ratio (v/v) was 1:2.5.

Fresh soil was used to determine soil microbial PLFA and fungal community composition. Soil bacterial and fungal biomass was

characterised by PLFA analysis (Chen et al., 2022). The PLFAs were considered as bacterial indicators (i14:0, a15:0, i15:0, i16:0, a17:0, i17:0, 16:1 ω 7c, 16:1 ω 9c, cy17:0, 17:1 ω 8c, 18:1 ω 7c, 18:1 ω 9c and cy19:0) and fungal indicator (18:2 ω 6c). Fungal communities were profiled by sequencing amplicons targeting the fungal ITS sequence of the 18S rRNA gene using an Illumina MiSeq platform (San Diego, CA, USA). Fungal diversity was assessed using the Shannon, Simpson, Chao1 and Pielou-e indices. Pairwise mean Bray-Curtis dissimilarities were calculated using the 'vegan' package in R statistical software. We also defined and compared fungal functional guilds using the FUNGuild database. To collect gas samples, culture bottles were sealed and placed back in the incubator for 2 h. A syringe was used to collect and transfer gas to 12 mL exetainers and CO₂ concentration was measured using a gas chromatograph (GC-2014, Shimadzu, Japan).

2.4 | Calculations and statistical analysis

We used linear regression to examine generalised patterns of microbial variables (microbial biomass and fungal diversity) and soil properties along the root diversity for different FRL diversity and litter mass loss values. Based on the values obtained from single species litter, we calculated the expected values (*E*) of each soil CO₂ release rate and litter mass loss (Wardle et al., 1997):

$$E = \sum_{i=1}^S R_i / S, \quad (1)$$

where R_i is the soil response variable when only species i is included and S denotes the number of species in each litter mixture. For each FRL mixture, we determined the difference between observed values (O) and E via paired t -tests for non-additive effects in each response variable. For each response variable, a significant difference between O and E ($p < 0.05$) indicated a non-additive effect; otherwise, an additive effect was inferred. The direction and magnitude of non-additive effects (or litter mixture effects, LME) were calculated as the following equation:

$$\text{LME} = [(O - E) / E] \times 100\%, \quad (2)$$

wherein, positive values ($O - E$) indicate synergistic effects, and negative values ($O - E$) indicate antagonistic effects.

Soil CO₂ release rate was calculated as the following equation:

$$RR = M / V_m \times 460 (C_2 - C_1) \times 1 / 1000 \text{ m} \times P / P_0 \times T_0 / T, \quad (3)$$

where RR is CO₂ emission (mg (CO₂) g⁻¹ soil h⁻¹), M is the molar mass of CO₂ (44 g mol⁻¹), V_m is the molar volume of 22.4 (L mol⁻¹), 460 is the gas volume to be measured in the culture bottle (mL), C_1 is the concentration of the gas to be measured (ppm) in the container, C_2 is the concentration of the gas to be measured (ppm) in the container for every hour; m is the mass of dry soil used in the experiment (g), P is atmospheric pressure in Kunming, China, 80.735 kPa, P_0 is standard atmospheric pressure of 101.325 kPa, T_0 is absolute temperature under standard conditions of 273.15 K and T is the absolute experimental

temperature (273.15 + T (°C)) K. Litter mass loss was calculated as the following equation:

$$ML = (m_0 - m_1) / m_0 \times 100\%, \quad (4)$$

where m_0 is the initial FRL dry weight and m_1 is the dry weight of FRL at the end of the experimental period. Since addition of different litter species would change soil physico-chemical properties and microbial community structure, which would affect the rate of microbial respiration and litter decomposition (Hu et al., 2016). We used a piecewise structural equation model (SEM) to assess the effects of FRL diversity on the biomass, diversity, and composition of fungal communities via changes in soil abiotic variables (Lefcheck, 2016). The priori SEM was designed based on the fact that different litter addition to the soil would change the physical and chemical properties and microbial community structure of soil, which would change soil CO₂ release and litter decomposition (Hu et al., 2016; Man et al., 2020). Differences in soil properties, CO₂ release, microbial PLFAs, fungal alpha diversity and fungal trophic mode relative abundance were compared using ANOVA and least significant difference methods. All statistical analyses were performed with R version 3.6.3 (R Core Team, 2017).

3 | RESULTS

3.1 | Effects of FRL diversity on the decomposition and soil CO₂ release

The mass loss of FRL was nonlinearly correlated with FRL diversity (Figure 1a). Treatment M9 had the maximum and treatment M3 had the minimum of FRL mass losses (Table S1). There was a nonlinear correlation between soil CO₂ release and FRL diversity (Figure 1; Figure S1). With increasing FRL diversity, CO₂ release first increased and then decreased, and M9, M12 and M15 had the highest rates of CO₂ release (Figure 1b). There was a positive relationship between soil CO₂ release rate and FRL mass loss ($p = 0.012$) (Figure 1c). In addition, soil CO₂ release rate was positively correlated with soil C:N ratio ($p = 0.035$, Figure 1d), negatively correlated with soil N:P ratio ($p = 0.016$, Figure 1e), but uncorrelated with soil C:P ratio (Figure 1f). Three-way ANOVAs showed that FRL diversity, incubation time, incubation temperature and their interactions had significant effects on soil CO₂ release rate (Table S2).

3.2 | Effects of FRL diversity on soil properties

The FRL diversity had different effects on soil properties (Figure 2; Figure S2; Table S3). With increasing FRL diversity, SOC and NH₄⁺-N concentrations increased (Figure 2a,d), DOC and NO₃⁻-N concentrations and soil C:N ratio first decreased and then increased (Figure 2b,e,i), but TN, AP and pH responded oppositely (Figure 2c,g,h). The mass loss of FRL was positively correlated with SOC, TN, DOC, NH₄⁺-N and NO₃⁻-N and negatively correlated with AP, pH and C:N, but not significantly correlated with TP (Figure S3). Three-way ANOVAs showed

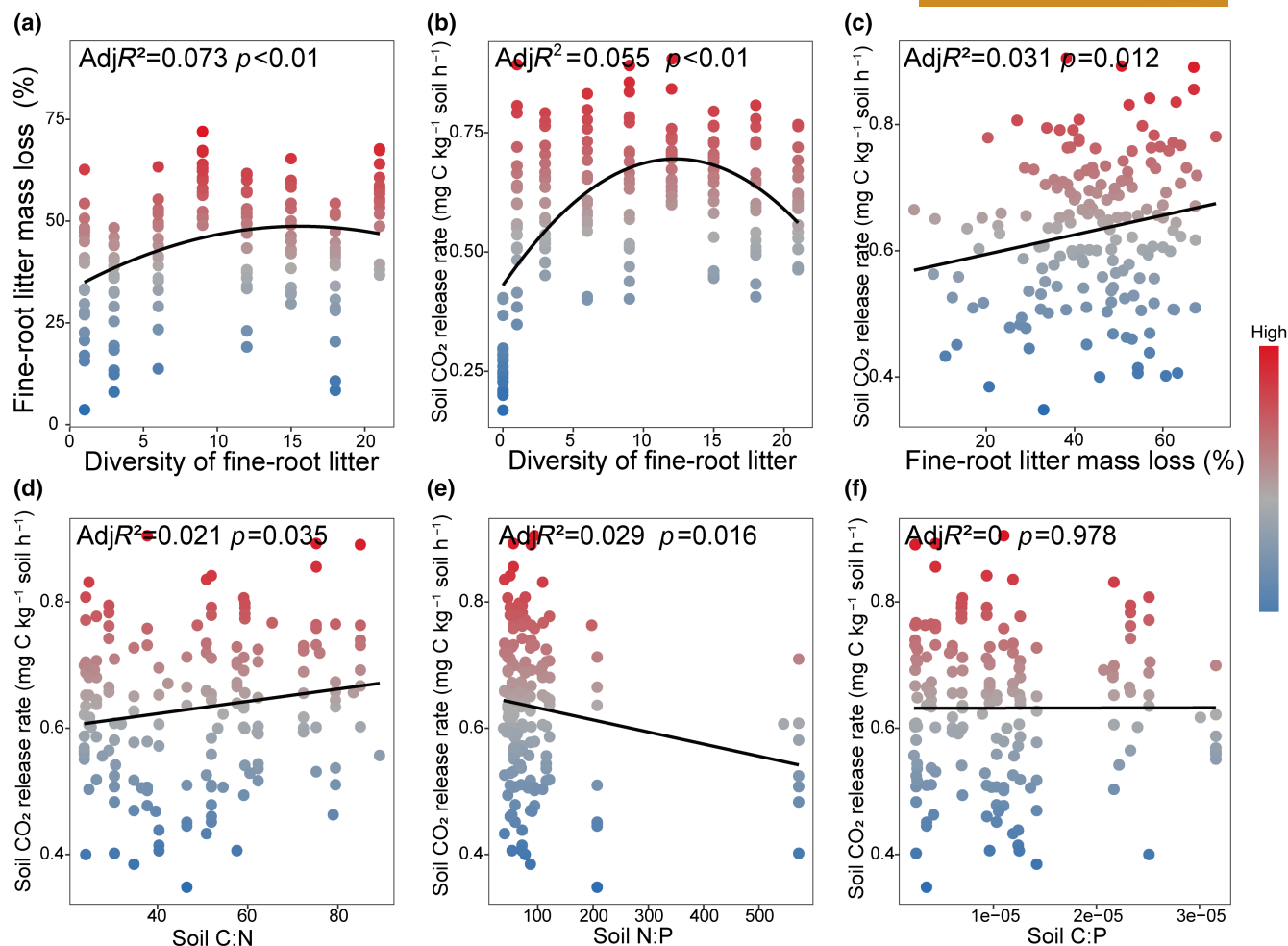


FIGURE 1 The relationships between fine-root litter diversity, mass loss and soil CO₂ release (a–c) and the effect of soil stoichiometry on soil CO₂ release rate (d–f).

that the added C, N and P content of FRL affected soil properties and microorganisms, and soil CO₂ release and FRL mass loss are mainly affected by the added C content of FRL (Table S3).

With increasing FRL diversity, soil total PLFAs first decreased and then increased, while fungal PLFAs and beta diversity exhibited the opposite trend (Figure 3a,b,f). FRL diversity had no significant effect on bacterial PLFAs or on the ratio of F:B (Figure 3c,d), but it was negatively correlated with fungal alpha diversity (Figure 3e). In M21, bacterial and fungal PLFAs increased significantly, as did PLFAs for Gram (–) and Gram (+) bacteria (Figure S4B–E). FRL mass loss was not correlated with fungal or bacterial PLFAs, the ratio of F:B, or fungal alpha diversity, but it was negatively correlated with fungal beta diversity (Figures S5 and S6). Soil fungal community composition was mainly affected by TN and pH, followed by AP, SOC, DOC, NO₃[–]-N and NH₄⁺-N. TP was the only variable that did not have a significant effect on fungal community composition (Figure S3A). Moderate size diversity resulted in higher Chao1, Simpson, Shannon and Pielou-e indices of soil fungi (Figure S7). Bray-Curtis dissimilarities of soil fungi were significantly correlated with TN and pH (Figure S3B). The increased FRL diversity enhanced the relative abundance of Ascomycota and decreased the relative abundance of

Basidiomycota at the phylum level (Figures S8 and S9). Increased FRL diversity had no significant effect on saprotrophic fungi, but reduced Pathotroph-Saprotroph-Symbiotroph and Pathotroph-Symbiotroph fungi (Table S4; Figures S8–S10).

3.3 | Linking FRL mixed decomposition with soil properties

The FRL diversity had a synergistic effect on soil CO₂ release and FRL mass loss. M12 had the largest mixture effect on CO₂ release, while M21 had the smallest effect. The mixture effect values of M12 and M15 were significantly higher than M3 (Figure 4a). The mixture effect value of M9 was the largest, while M3 and M18 had the smallest FRL mass loss. The mixture effect values of M21 and M12 were significantly different from other treatments (Figure 4b).

Piecewise SEM shows that the change in soil properties significantly affected soil CO₂ release and soil microorganisms, and soil microorganism PLFAs significantly affected soil CO₂ release (Figure 5a). The direct effect of FRL diversity on soil CO₂ release was lower than the indirect effects of soil properties, soil microbial PLFAs and soil

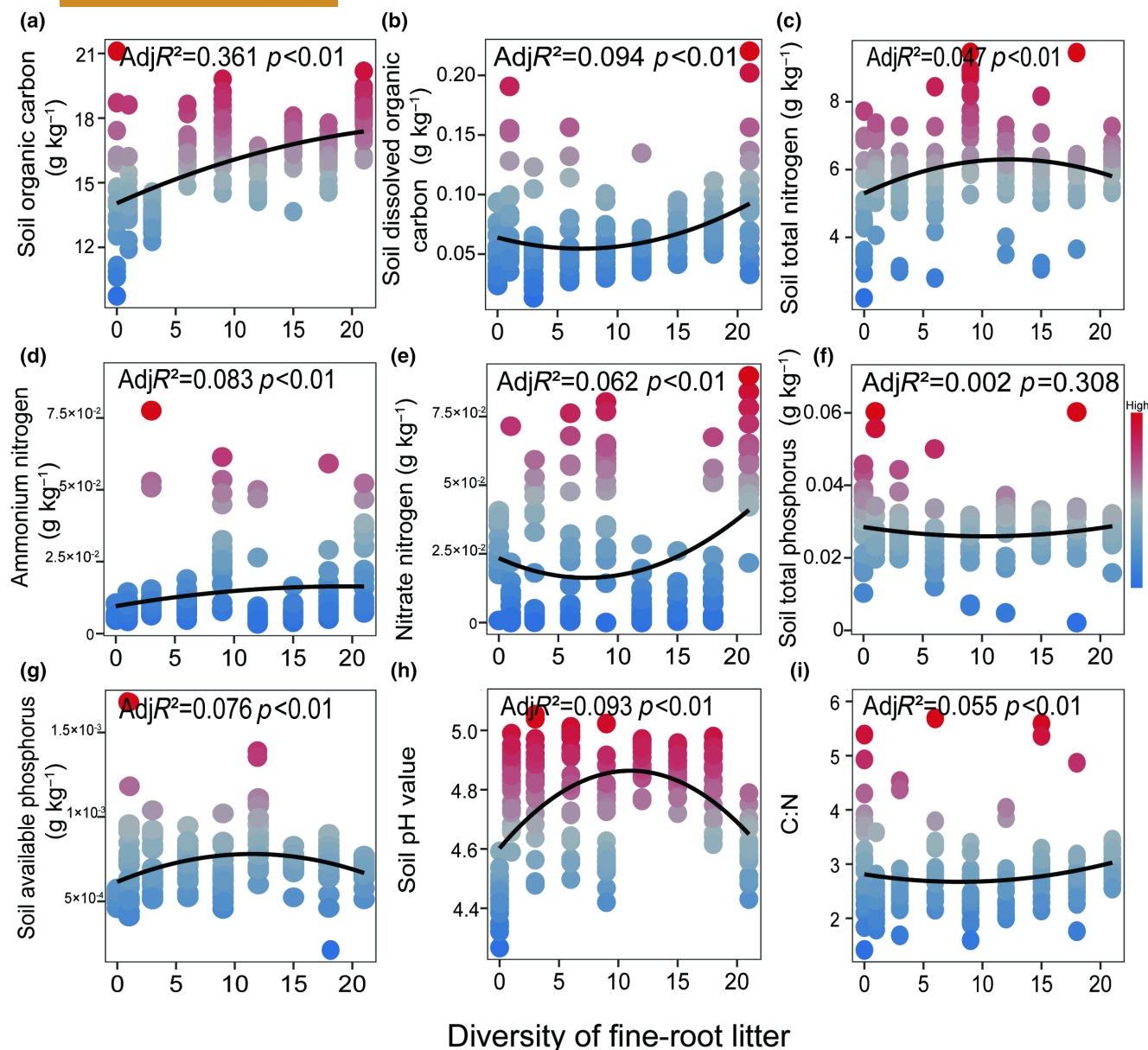


FIGURE 2 Effects of fine root litter diversity on soil properties, i.e. soil organic carbon (a), dissolved organic carbon (b), total nitrogen (c), ammonium nitrogen (d), nitrate nitrogen (e), soil total phosphorus (f), soil available phosphorus (g), soil pH (h) and carbon to nitrogen ratio (i).

fungi (Figure 5b). Both soil properties and soil microbial PLFAs significantly affected FRL mass loss (Figure 5c). The relationship between FRL mass loss and FRL diversity was determined by the indirect effects of soil properties, soil microbial PLFAs and soil fungi (Figure 5d).

4 | DISCUSSION

4.1 | Effects of fine-root diversity on litter mass loss

We investigated decomposition along a fine-root diversity gradient and found that litter mass loss showed a non-additive effect and moderate fine-root diversity had a greater positive effect on litter

mass loss (Figures 1 and 5). The mixture effects of decomposition with M9 and M12 were larger than other treatments, which was consistent with our first hypothesis. The first explanation would be that the different litter inputs changed soil nutrients (Chen et al., 2017; Gessner et al., 2010), the trade-off effect on soil nutrients would regulate decomposition. Since soil nutrients can strongly affect litter decomposition through various pathways (Wan et al., 2022; Wu et al., 2019). The evidence was that SOC, TN, NH_4^+-N and NO_3^--N were positively correlated with litter mass loss, while soil TP, AP and pH negatively correlated with litter mass loss in our study. The greatest loss of litter mass with moderate fine-root diversity implied the largest synergistic effect. The combination of different litter species can alter the process of decomposition via multiple non-exclusive mechanisms, leading to either an acceleration or deceleration in

FIGURE 3 Effects of fine root litter diversity on soil microorganisms, i.e. total PLFAs (a), fungal PLFAs (b), bacterial PLFAs (c), fungi to bacteria ratio (d), fungal alpha diversity (e) and fungal beta diversity (f).

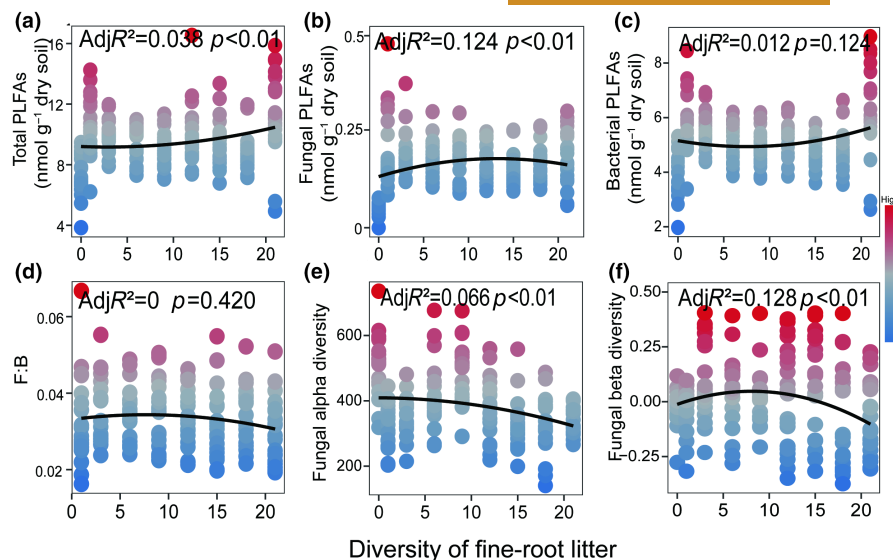
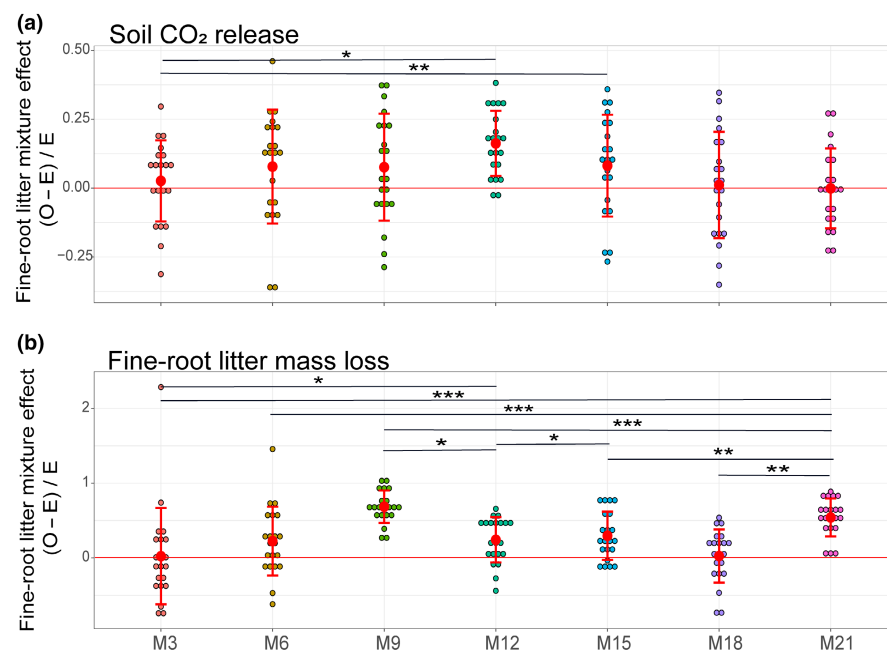


FIGURE 4 Mixture effects on the soil CO₂ release (a) and decomposition of fine root litter (b). O: observed values, E: expected values. M3: 3 kinds of fine-root litter, M6: 6 kinds of fine-root litter, M9: 9 kinds of fine-root litter, M12: 12 kinds of fine-root litter, M15: 15 kinds of fine-root litter, M18: 18 kinds of fine-root litter, M21: 21 kinds of fine-root litter. Values are means $\pm$ SE. Asterisks indicate significant deviations from zero (Student's t tests; * <0.05, ** <0.01, *** <0.001).



the mass loss of litter mixtures or individual components (Gessner et al., 2010).

Second, soil microbial community would be another important driver affecting decomposition (Gessner et al., 2010; Lecerf et al., 2011; Sheng et al., 2019). We found that fine-root diversity was significantly correlated with both microbial biomass and fungal diversity and moderate fine-root litter diversity led to the maximum fungal diversity (Figure 3; Figure S4). Recent work found that the transition from mono- to mixed-species plant litter could increase decomposition by 34.7% in forest ecosystems (Mori et al., 2020), which supported our findings. Our study indicated that moderate fine-root diversity can create positive feedback between mass loss and fungal activity, and may explain why the highest diversity was not associated with the highest litter mass loss. Since high diversity with various identities can also increase substances that are difficult to decompose and inhibit microbial

activities (Man et al., 2020; Prieto et al., 2016, 2017). Previous work has shown that higher diversity in forested systems will lead to antagonistic effects and decrease litter decomposition (Silver & Miya, 2001), supporting our findings. Furthermore, we found that fine-root diversity had no significant effect on the trophic mode of saprotrophic fungi, but increased their relative abundance. For example, M9 treatment increased the abundance of fungi belonging to the Sordariales order, which can stimulate the decomposition of organic matter (Zhou et al., 2021).

4.2 | Effects of fine-root litter diversity on soil CO₂ release

Our finding indicated that fine-root addition promoted soil CO₂ release, and moderate fine-root diversity was associated with higher

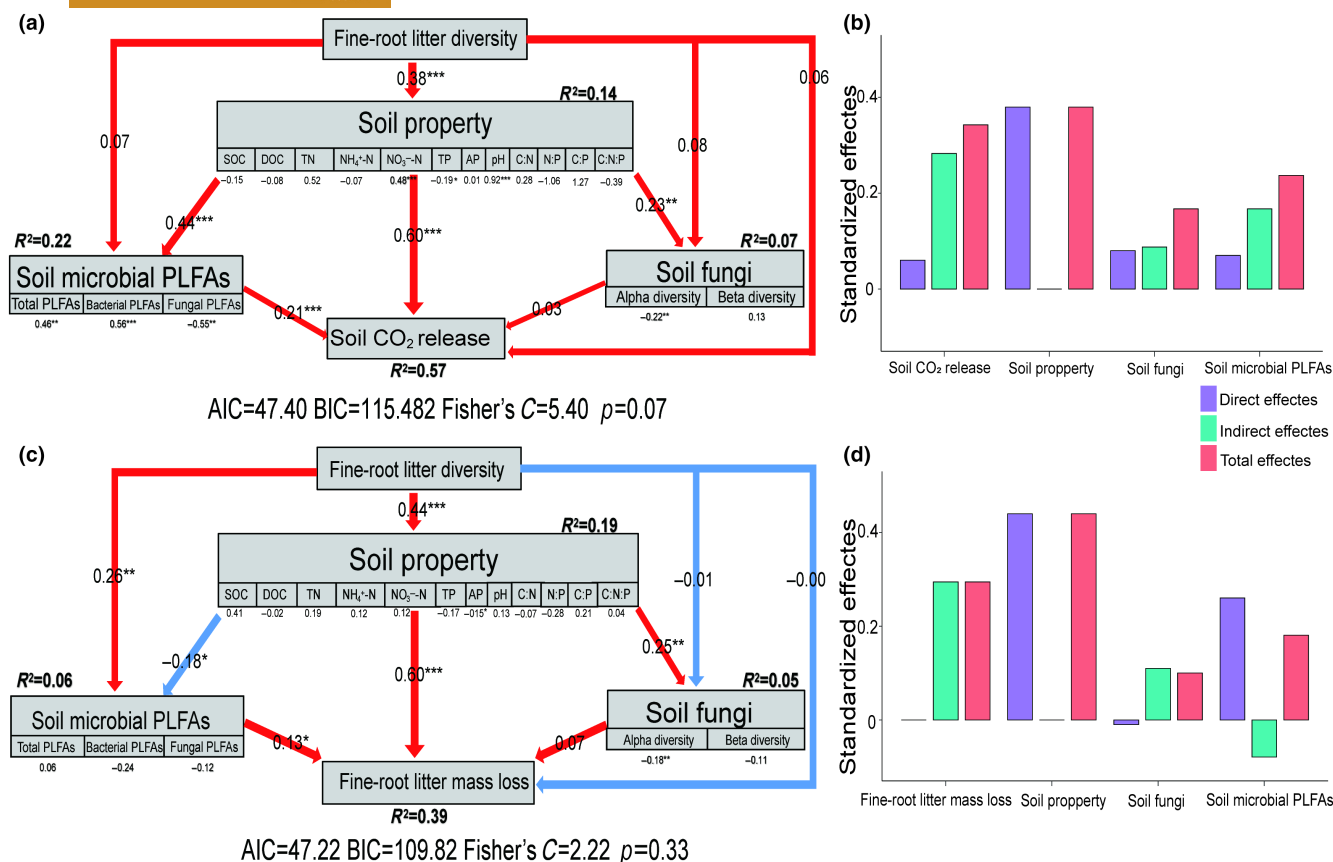


FIGURE 5 Structural equation model (SEM) of the effects of fine root litter diversity on soil CO₂ release (a, b) and fine root litter mass loss (c, d). AP, available phosphorus; C:N, ratio of SOC to TN; C:N:P, ratio of SOC, TN and TP; C:P, ratio of SOC to TP; DOC, soil dissolved organic carbon; N:P, ratio of TN to TP; NH₄⁺-N, ammonia nitrogen; NO₃⁻-N, nitrate nitrogen; SOC, soil organic carbon; TN, soil total nitrogen; TP, total phosphorus.

soil CO₂ release (Figures 1 and 5). Consistent with the second hypothesis, the release of soil CO₂ mirrored the decomposition process, the highest decomposition at moderate diversity of can promote the release of soil CO₂ in this study. Furthermore, the whole effect of mixed fine-root litter on CO₂ release was a synergistic effect, probably because the leaching and transfer of nutrients and inhibitory compounds between litter species can result in synergistic effect with litter mixtures (Handa et al., 2014). A recent study suggested that high species diversity of root litter reduces the cumulative release of soil CO₂ (Man et al., 2020), which partially supported our findings that highest diversity had not highest CO₂ release. The marginal antagonistic effect on cumulative soil CO₂ release in mixtures was likely the result of differences in the species composition of root litter. For example, litter with high C:N ratio or high lignin, tannin or polyphenol contents increased antagonism, influencing cumulative soil CO₂ (Gessner et al., 2010).

Moderate fine-root diversity had the highest soil CO₂ release, implying that litter decomposition and associated nutrient release can provide substrates for microbes (Liu et al., 2019; Tan et al., 2021). Because moderate fine-root diversity increased microbial activities and leads to accelerated organic C mineralization through the priming effect (Heijboer et al., 2018), thus enhanced soil CO₂ release in the tropical rainforest. As mentioned above, M9 treatment was

associated with a relatively high abundance of saprophytic fungi. Higher microbial biomass and activities have an obvious relationship with soil respiration (Wu et al., 2017). A previous experiment also found that litter removal reduced the diversity of fungi, especially saprotrophic fungi, thus reduced soil respiration (Zhou et al., 2021). Taking into account the nonlinear dynamics in our incubation experiment, the effect of fine-root diversity on soil C cycling should be given adequate attention in those forests with high plant diversity in future.

5 | CONCLUSIONS

Our one-year-long incubation experiment showed that there was a strong correlation between fine-root diversity and litter mass loss and soil CO₂ release, with moderate diversity of fine-root (i.e. 9, 12 and 15 species mixtures) having the greater effects. The potential mechanisms would be that different root diversity resulted in different releases of nutrients and changed soil microbial biomass and fungal community composition such as higher relative abundance of saprophytic fungi in moderate fine-root diversity. Changes in soil physico-chemical properties and microbial community composition directly and indirectly affected litter mass loss and soil CO₂ release,

and the effects of soil properties on both litter mass loss and soil CO₂ release were higher than those of microorganisms. In summary, our findings suggest that fine-root diversity has nonlinear relationships with litter decomposition and soil CO₂ release in tropical forests, thus, the appropriate plant diversity must be sustained under global change scenario.

AUTHOR CONTRIBUTIONS

Jianping Wu and Deyun Chen designed the experiment and wrote the manuscript. Deyun Chen, Shangwen Xia, Sicheng Li, Shuting Zhang, Hong Chen and Xiaoyue Ding conducted the fieldwork and laboratory work. Jianping Wu and Deyun Chen took part in statistical analysis. All authors have read and agreed to the published version of the manuscript.

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CONFLICT OF INTEREST STATEMENT

All authors declare that there is no conflict of interest.

DATA AVAILABILITY STATEMENT

The data that support the findings of this study are available in Zenodo (<https://doi.org/10.5281/zenodo.7825769>).

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SUPPORTING INFORMATION

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

Table S1: Experimental design and fine-root litter mass loss ($\pm$ SE).

Table S2: Fine-root litter diversity (Diversity), culture time (Time) and culture temperature (Temperature) were used for three-way ANOVA.

Table S3: Added C, Added N and Added P were used for three-way ANOVA.

Table S4: Biomarkers obtained from LEfSe analysis of the treatments.

Figure S1: The diversity of fine-root litter and different stages effects on soil CO₂ release rate.

Figure S2: The diversity of fine-root litter effects on soil properties.

Figure S3: Redundancy analysis of soil properties and microorganisms and correlation analysis of soil properties.

Figure S4: The diversity of fine-root litter effects on PLFAs of soil microorganisms.

Figure S5: Effects of fine-root litter moss loss on soil properties.

Figure S6: Effect of fine-root litter mass loss on soil microorganisms.

Figure S7: The diversity of fine-root litter effects on soil fungal alpha diversity.

Figure S8: The diversity of fine-root litter effects on relative abundance of soil fungi.

Figure S9: The diversity of fine-root litter effects on relative abundance of soil fungal trophic mode.

Figure S10: Cladogram of soil fungal in revegetation types via LEfSe method identifies the significantly different abundant taxa.

Data S1: Replication statement.

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