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ARTICLE

Climate Ecology

Nonsignificant elevational trends of soil microbial respiration and temperature sensitivity in a subtropical forest

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Abstract

Soil carbon (C) cycling plays a critical role in regulating global C budget and atmospheric CO₂ concentrations. The ongoing global warming potentially accelerates soil C loss induced by microbial respiration (MR) and makes soil a large C source to the atmosphere. Quantifying the drivers of MR and its response to rising temperature (also called temperature sensitivity, Q_{10}) should be a high priority to improve the modeling and prediction of terrestrial C cycle under global warming. In this study, we applied a standardized soil sampling along nine gradients from 410 to 1080 m in a subtropical forest in southern China. All soil samples were incubated at varying temperature gradients (10–15–20–25–20–15°C) to measure MR and Q_{10} every day for three weeks. Then all the measured MR was adjusted by the field temperature of each elevation gradient. Our objectives were to examine the response of MR and Q_{10} to the environmental change induced by elevational gradients in the subtropical forest and then quantify their main drivers. We totally collected 54 abiotic and biotic factors relative to the MR and Q_{10} . Our results showed that the incubated MR increased from low to high elevation. However, a significant elevation trend of the adjusted MR was not examined after adjusting the field temperature of sampling sites, due to the trade-off between increasing soil C concentration and declining temperature as elevation increased. We further found that the elevational gradients did not cause significant change in Q_{10} . The variation in Q_{10} was negatively dominated by soil C quality, which declined nonlinearly along the elevation gradients. This study

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highlights the trade-off between environment and biotic factors in determining soil C decomposition along elevational gradients. The uncertainty of MR measurements caused by unifying incubated temperature should not be ignored in future model development.

KEYWORDS

elevational trend, soil carbon quality, soil microbial respiration, subtropical forest, temperature sensitivity

INTRODUCTION

Soil stores twice as much carbon (C) as the atmosphere (Jobbágy & Jackson, 2000; Lal, 2004; Scharlemann et al., 2014), and the decomposition of soil C induced by soil microbes (also called soil microbial respiration, MR) releases approximately 6–10 times more CO₂ into the atmosphere than the current levels of fossil fuel consumption every year (Boden et al., 2009; Friedlingstein et al., 2021). Thus, soil C cycling plays a key role in regulating the global C budget and atmospheric CO₂ concentrations (Bond-Lamberty et al., 2018; Friedlingstein et al., 2021; Liu et al., 2021). Moreover, many studies have confirmed that MR is critically sensitive to current climate change, especially rising temperatures (Bond-Lamberty & Thomson, 2010; Bradford et al., 2021; Davidson & Janssens, 2006). The ongoing global warming may potentially accelerate soil C loss (Friedlingstein et al., 2021; Gutiérrez-Girón et al., 2015) and thus make soil a large source of C to the atmosphere in the future (Bond-Lamberty et al., 2018; Bond-Lamberty & Thomson, 2010; Davidson & Janssens, 2006). Therefore, quantifying the variations and drivers of soil C loss would largely improve the modeling and prediction of the terrestrial C cycle under global warming (Gutiérrez-Girón et al., 2015; Zhou et al., 2009).

Elevational gradients are ideal for the study of the response of soil C cycling under climate warming (Kong et al., 2022). Different elevational gradients cause various climate levels, such as declining temperature and increasing precipitation as elevation increases (He et al., 2021; Kong et al., 2022). The altered environmental factors subsequently impact several biotic and abiotic factors that regulate soil C cycling. For example, high precipitation promotes plant growth and carbon input into soil, which enhances the respired substrates in the soil and favors MR. The influence of declining temperature has two sides: on the one hand, low temperature suppresses plant growth and microbial activity that suppresses MR; on the other hand, the suppressed MR contributes to more C storage in soil that supports MR (Conant et al., 2011; Kong et al., 2022; Longbottom et al., 2014). Therefore, how MR varies along the elevational gradients relies on the trade-off

between climate and respired substrate along elevation. Various studies have found that MR declined along elevational gradients (Garten & Hanson, 2006; Gutiérrez-Girón et al., 2015) because warmer soils in low elevation contribute to more active soil microorganisms and high decomposition rates (Gutiérrez-Girón et al., 2015). In contrast, Kong et al. (2022) suggest that elevation positively affects MR due to the high soil C concentration at high elevation that offsets the negative effect of low temperature. Overall, how soil C decomposition varies along elevational gradients is still inconclusive.

Laboratory incubation is a commonly used method to determine MR wherein multiple soil samples are incubated at the same time under the same temperature or temperature range (Ding et al., 2016; Li et al., 2020; Liu et al., 2017; Zhang et al., 2022). The unified incubation temperature might be too high for samples from cold sites and too low for warm sites (Li et al., 2020). However, setting a specific incubation temperature for each soil sample in the laboratory is critically challenging. Recently, researchers used an adjusted MR by the field temperature of each site based on the unified incubation temperature, which solved the problem that emerged from the difference between field temperature and incubated temperature (Li et al., 2020).

The value of temperature sensitivity (Q_{10}) of MR, the factor by which soil respiration increases by a 10°C increase in temperature (Lloyd & Taylor, 1994), also serves as a reference for how soil C responds to future warming (Davidson & Janssens, 2006; Gutiérrez-Girón et al., 2015). Until now, there has been no consistent elevational trend of Q_{10} along elevational gradients (Gutiérrez-Girón et al., 2015). Several studies suggested that high elevation increased Q_{10} due to the higher activity energy requirement of soil enzymes under low temperature (Gutiérrez-Girón et al., 2015; Kong et al., 2022; Okello et al., 2022; Zeng, Feng, Chen, et al., 2022), while others reported higher Q_{10} at lower elevations (Lipson, 2007), or no significantly elevational trend (Schindlbacher et al., 2010; Wang et al., 2016; Xu et al., 2014; Zuo et al., 2021). These contradicting results indicate that the current understanding of the elevational effect on Q_{10} has not been comprehensive enough.

To further explore the biotic and abiotic mechanisms driving MR and Q_{10} along elevational gradients, we applied a standardized sampling method along nine elevational gradients from 410 to 1080 m in a subtropical forest in South China. These soil samples were incubated at varying temperatures in the laboratory to determine MR and Q_{10} . Our study aimed to examine the response of MR and Q_{10} to the environmental change induced by elevational gradients in the subtropical forest and quantify their key drivers. We hypothesized that (1) high elevation reduces MR due to the low temperature and microbial activity but enhances Q_{10} due to the increased activity energy requirement of soil enzymes and (2) the varied MR and Q_{10} along elevation would be largely explained by soil properties, plant community structure, and environmental change induced by elevational gradients.

MATERIALS AND METHODS

Site description

This study was conducted in Chebaling National Nature Reserve in the Guangdong Province of southern China (114°09′–114°16′ E, 24°40′–24°46′ N), with elevation ranging from 330 to 1256 m. The climate is a typical subtropical monsoon, with mean annual temperature (MAT) and mean annual precipitation (MAP) of 19.6°C and 1468 mm, respectively (He et al., 2021). The vegetation is well-preserved subtropical evergreen broad-leaved forests, dominated by *Schima superba*, *Machilus chinensis*, and *Eurya nitida*. According to the USDA soil classification system, soils are classified in the ultisol order and the adult suborder (He et al., 2021).

Field sampling

The field samplings were conducted along elevational gradients from 410 to 1080 m, including nine permanent plots (40 × 40 m). All plots were located on the south side to reduce the influence of aspect (He et al., 2021). In each plot, all tree individuals with dbh above 1 cm were surveyed for species, location, and dbh.

The field soil sampling was conducted in October 2018. First, we randomly selected five 10 × 10 m subplots in each plot. Second, five litter samples were randomly collected in five 1 × 1 m squares and mixed as one sample in each subplot. After that, five soil cores (3.5 cm in diameter and 20 cm in depth) in each subplot were collected and mixed as one sample. This resulted in 45 soil samples from the elevational gradients (9 gradients × 5 soil samples for each gradient) in total. All soil samples

were sieved by a 2-mm mesh to remove the stone. Visible roots were collected as the root samples and the rest of soil were collected as soil samples. The living roots were separated into coarse and fine roots (diameter <2 mm) according to the root diameter (Zhang et al., 2022). Litter, fine-root, and coarse-root samples were oven-dried at 65°C for 48 h to obtain their dry mass. Soil water-holding capacity (WHC) was measured using the ring knife method (Zhang et al., 2022).

Soil and plant physicochemical properties

C and N concentrations of litter and fine-root samples were determined using CHNOS Elementar Analyzer (Vario EL III, Elementar, Hanau, Germany), and P concentration was determined using an ultraviolet spectrophotometer (UV-2550, Shimadzu, Kyoto, Japan).

Soil samples were separated into four parts. One was air-dried to determine soil physicochemical properties. Soil C and N were also determined by CHNOS Elementar Analyzer. Soil available N was determined using a continuous flow analyzer (San++, Skalar, Breda, the Netherlands), and soil P and available P were determined using an ultraviolet spectrophotometer: we digested these samples using 98% concentrated sulfuric acid and 60% HClO₄ volume ratio of 10:1 at 390°C for 3 h. After digestion, soil total P concentration of these samples was determined using the molybdate colorimetry method using a UV-Vis spectrometer (UV1800, Shimadzu, Japan). Soil pH was determined using a glass electrode in a suspension of 25 mL distilled water and 10 g of dried soil of each sample by a pH meter (FE20-FiveEasy). Soil texture, as reflected by the mass percentages of sand, silt, and clay, was determined using the hydrometer method (Ashworth et al., 2001; Jiang et al., 2020). The second part was freeze-dried to measure the phospholipid fatty acids (PLFAs) to represent the microbial community structure, including community total PLFAs and the components of bacteria, gram-positive bacteria, gram-negative bacteria, actinomycetes, and fungi (Frostegård & Bååth, 1996). The fatty acids i14:0, i15:0, a15:0, i16:0, a17:0, and i17:0 were selected to represent gram-positive bacteria; 16:1ω7, cy17:0, 18:1ω7, and cy19:0 were selected to represent gram-negative bacteria; 16:1ω5c was selected to represent arbuscular mycorrhizae fungi; and 16:1ω5, 18:2ω6c, and 18:1ω9c were selected to represent other fungi (Zelles, 1999). The ratios between these components represent the composition of microbial community (Zhang et al., 2022). The third part was stored at 4°C and used to measure soil microbial biomass C, N, and P, using chloroform fumigation extraction technique (Li et al., 2018; Vance et al., 1987), which was measured as the difference in the

soil organic C and N content of 24-h fumigated soil and unfumigated soil at an extraction efficiency of 0.45, determined by a TOC analyzer (Multi N/C 3100, Jena, Germany). The fourth part was incubated in the laboratory at various temperatures to determine MR and its temperature sensitivity (Q_{10}).

Soil incubation and measurements

The incubation and measurement of MR and Q_{10} were conducted using a 32-channel MR automatic measurement system in the laboratory. For details about this measurement system, see Zhang et al. (2022).

First, 40-g samples of dry soil were put into 250-mL bottles for incubation and adjusted to 60% WHC to maximize soil microbial activity before incubation (Zhou et al., 2014). Then all incubation bottles were immediately placed in an artificial weather box. One week of preincubation was performed before four weeks of the measurement program. Preincubation and measurement temperature were carried out under the artificial weather box, which was set by the same temperature cycle every day, that is, 10–15–20–25–20–15–10°C. All soil samples were maintained with 60% WHC by weekly weighing and adding distilled water to compensate for water loss (Wang et al., 2018). Each temperature lasted 240 min, in which the former 80 min was equilibration time and the latter 160 min was for measurement. Each measurement lasted 150 s, with the 60th–140th s data for determining the soil C decomposition rate. The rates of soil C decomposition at different temperatures were used to calculate the daily accumulated MR and Q_{10} following Equation (1) (Lloyd & Taylor, 1994).

$$MR = ae^{bT}, \quad (1)$$

where MR is the soil C decomposition rate at a specific incubated temperature, T is the incubated temperature, a represents the base respiration at $T = 0^\circ\text{C}$ for each soil sample (MR_0), and b is the parameter of the exponential equation and was used to calculate Q_{10} value, following Equation (2):

$$Q_{10} = e^{10b}. \quad (2)$$

MR at each specific field temperature was calculated as follows:

$$MR_{MAT} = ae^{bT_{MAT}}, \quad (3)$$

where MR_{MAT} is MR at the specific field MAT at each plot, and T_{MAT} is the field MAT at each plot.

For the four-week incubation, we calculated the accumulated MR, such as $AccMR$ for the incubated respiration, $AccMR_0$ for the base respiration at $T = 0^\circ\text{C}$, and $AccMR_{MAT}$ for the adjusted respiration. $AccMR_0$ was further normalized by soil C concentration ($AccMR_0_{perSC}$) to represent the decomposability and quality of soil C substrate (Creamer et al., 2014; Ding et al., 2016).

Statistical analysis

MAT and MAP of each plot were extracted from the global climate layers of WorldClim (1 km² spatial resolution; <http://www.worldclim.org/>) of relevant latitude and longitude, using the extract function in the “raster” R package (version 2.6.7), and the aspect was obtained by analyzing the digital elevation model data using the “raster” R package (He et al., 2021; Hijmans, 2020). Based on the plant community composition including the species and dbh of each tree in the plot, aboveground biomass (AGB) was calculated using a pantropical model (Chave et al., 2014) in the “BIOMASS” R package (version 2.1.1) (Réjou-Méchain et al., 2017).

We collected in total 54 abiotic and biotic factors relative to the $AccMR_{MAT}$ and Q_{10} . Regression analyses were used to examine the elevational trends of all response variables. The 54 factors were then classified into eight groups: topography (elevation, and aspect) and climate (MAT and MAP), soil environment (WHC and pH), soil texture (bulk density, sand content, silt content, and clay content), plant community structure (AGB, species richness, Shannon diversity index [H'], and Simpson index), plant carbon input (litter C, N, P concentration and C:N ratio [litter CNR], C:P ratio [litter CPR], N:P ratio [litter NPR], fine-root biomass, fine-root C, N, P concentration and C:N ratio [root CNR], C:P ratio [root CPR], N:P ratio [root NPR]), soil organic matter (soil C, N, P, C:N ratio [soil CNR], C:P ratio [soil CPR] and N:P ratio [soil NPR], soil available N and P), soil microbial biomass (soil microbial biomass C, N, P, C:N ratio [microbial CNR], C:P ratio [microbial CPR] and N:P ratio [microbial NPR]), soil microbial community structure (total PLFA, and its components of bacteria, gram-positive bacteria, gram-negative bacteria, actinomycetes, fungi, gram positive:negative bacteria ratio [GNR], actinomycetes:bacteria ratio [ABR], actinomycetes:fungi ratio [AFR], and fungi:bacteria ratio [FBR]).

We performed all subsets regression analyses for each group of factors to select the best model with the lowest Bayesian information criterion (BIC) in predicting $AccMR_{MAT}$ and Q_{10} , respectively (Appendix S1: Tables S1 and S2). If the difference in BIC was <2 units

(Burnham & Anderson, 2002), we chose the model with the highest adjusted R^2 . Using such criteria, 14 and 12 variables were finally selected for AccMR_MAT and Q_{10} , respectively. Then, structural equation modeling (SEM) was performed to explain the elevational variation of AccMR_MAT and Q_{10} using these selected variables. Nonsignificant paths and variables were dropped to simplify the initial SEM and improve the model fit. The indirect effect of each predictor was calculated by multiplying the standardized direct effects of a given predictor on AccMR_MAT or Q_{10} via mediator in one route, and the total effect was summed from the multiple indirect effects and direct effect of the given predictor (Lefcheck, 2016). All the analyses were conducted in R 3.3.4, with packages corrplot (Wei & Simko, 2013), leaps, and piecewiseSEM (Lefcheck, 2016).

RESULTS

During the four weeks of incubation, daily MR rates at the incubation temperature (MR), adjusted MR at the field MAT (MR_MAT), base respiration at 0°C (MR_0), and their normalizations by soil C concentration were all declining over time in each elevational gradient. Meanwhile, there was no significant temporal trend of Q_{10} over the four weeks (Appendix S1: Figures S1 and S2).

Four-week accumulated MR at incubated temperature (AccMR) and base respiration at 0°C (AccMR_0) increased as elevation increased, while the adjusted accumulated MR at the field MAT (AccMR_MAT) and Q_{10} did not vary significantly along the elevation gradients. The normalized AccMR_MAT and AccMR_0 by soil C

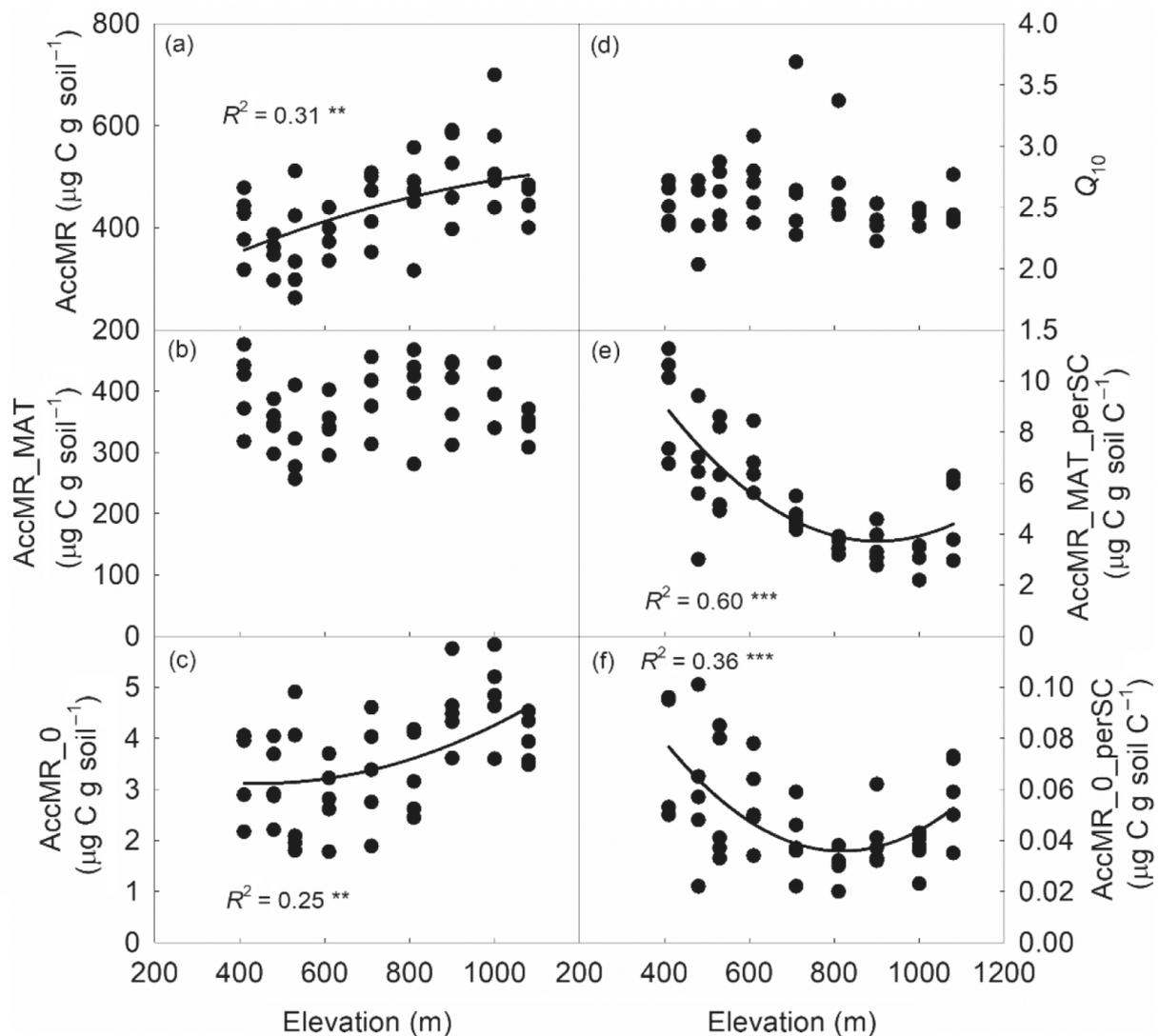


FIGURE 1 Elevational variation of accumulated MR (AccMR (a), AccMR_MAT (b), and AccMR_0 (c)), temperature sensitivity (Q_{10} , d), and the normalized AccMR_MAT and AccMR_0 by soil C concentration (AccMR_MAT_perSC (e) and AccMR_0_perSC (f)) from 410 to 1080 m. AccMR, accumulated microbial respiration; AccMR_0, the base AccMR at $T = 0^{\circ}\text{C}$; AccMR_MAT, the adjusted AccMR by MAT.

concentration (AccMR_MAT_perSC and AccMR_0_perSC) both decreased nonlinearly as elevation increased (Figure 1; Appendix S1: Figures S3–S6).

In the selected model for each group of factors (Appendix S1: Figures S7–S12), AccMR_MAT was positively affected by pH and WHC in the soil environment factors, root P concentration and root NPR in the carbon input factors, and soil available N and NPR in soil organic matter factors. AccMR_MAT was negatively affected by Actinomyces in soil microbial factors. In total, soil organic matter explained the largest elevational variation of AccMR_MAT (0.24), followed by

soil environment (0.13) and soil microbial community (0.10; Figure 2a). In the SEM analysis, 71% variation of AccMR_MAT was explained by the selected 14 biotic and abiotic factors (Figure 3a). The majority of this explanation was directly contributed by the positive effects of soil pH, AccMR_0_perSC, and WHC, with standardized total effects of 0.63, 0.54, and 0.51, respectively (Figure 4a). MAT, aspect, and MAP also positively affected AccMR_MAT, with standardized total effects of 0.27, 0.10, and 0.09, respectively. Elevational gradients caused a significant negative effect on AccMR_MAT, with a standardized total effect of -0.16 (Figure 4a).

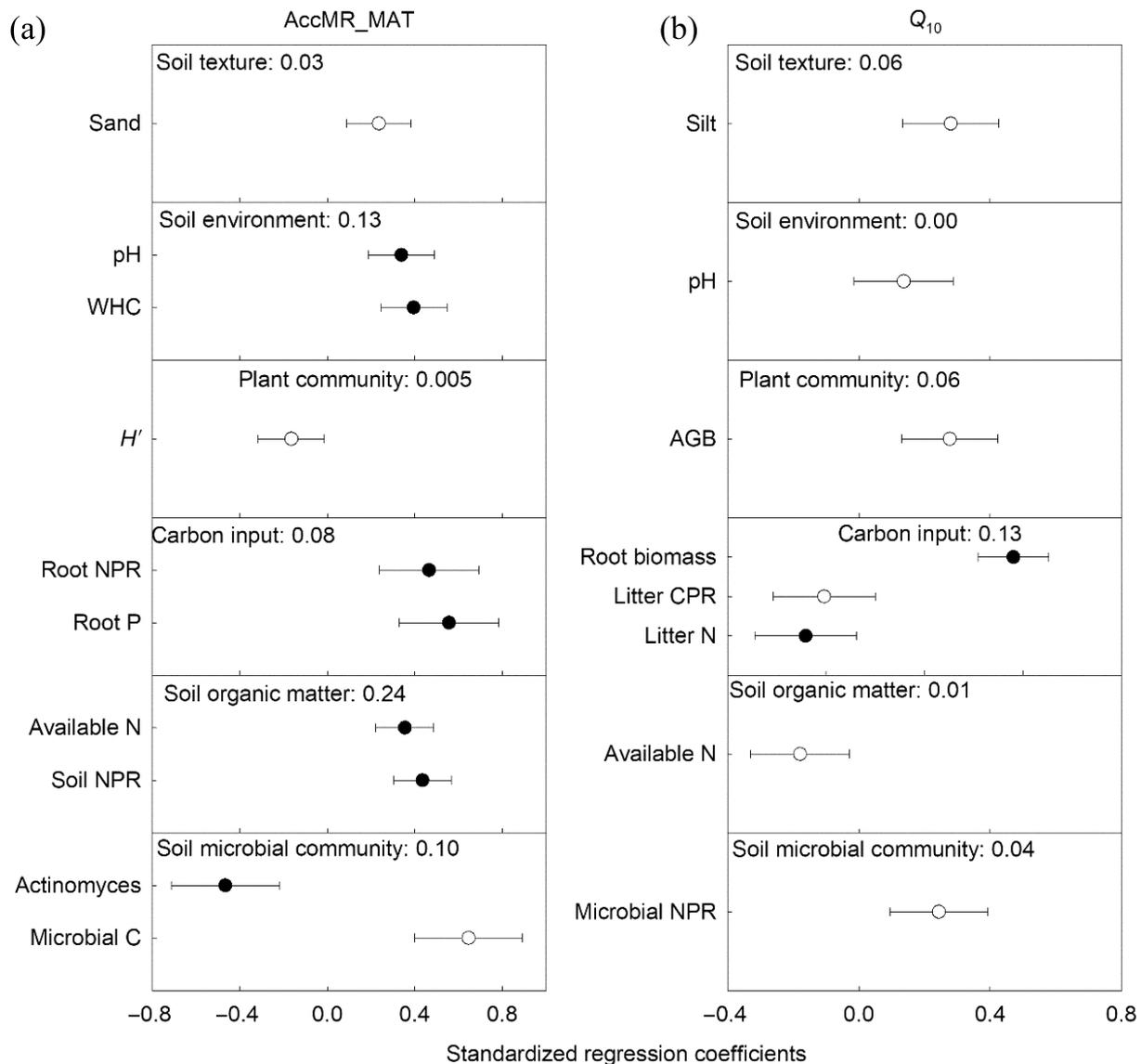


FIGURE 2 Standardized regression coefficients for the explanatory effects included in the selected AccMR_MAT (a) and temperature sensitivity (Q_{10} , b) models in each group of factors. Model R^2 is reported in each subpanel (factors of soil texture, soil environment, soil texture, plant community, carbon input, soil organic matter, and soil microbial community) for the selected model. Solid circles and open circles indicate a significant ($p < 0.05$) and nonsignificant ($p \geq 0.05$) effect on AccMR_MAT or Q_{10} , respectively, and lines indicate SEs. AccMR, accumulated microbial respiration; AccMR_MAT, the adjusted AccMR by MAT; AGB, aboveground biomass; CPR, C:P ratio; NPR, N:P ratio; WHC, water-holding capacity.

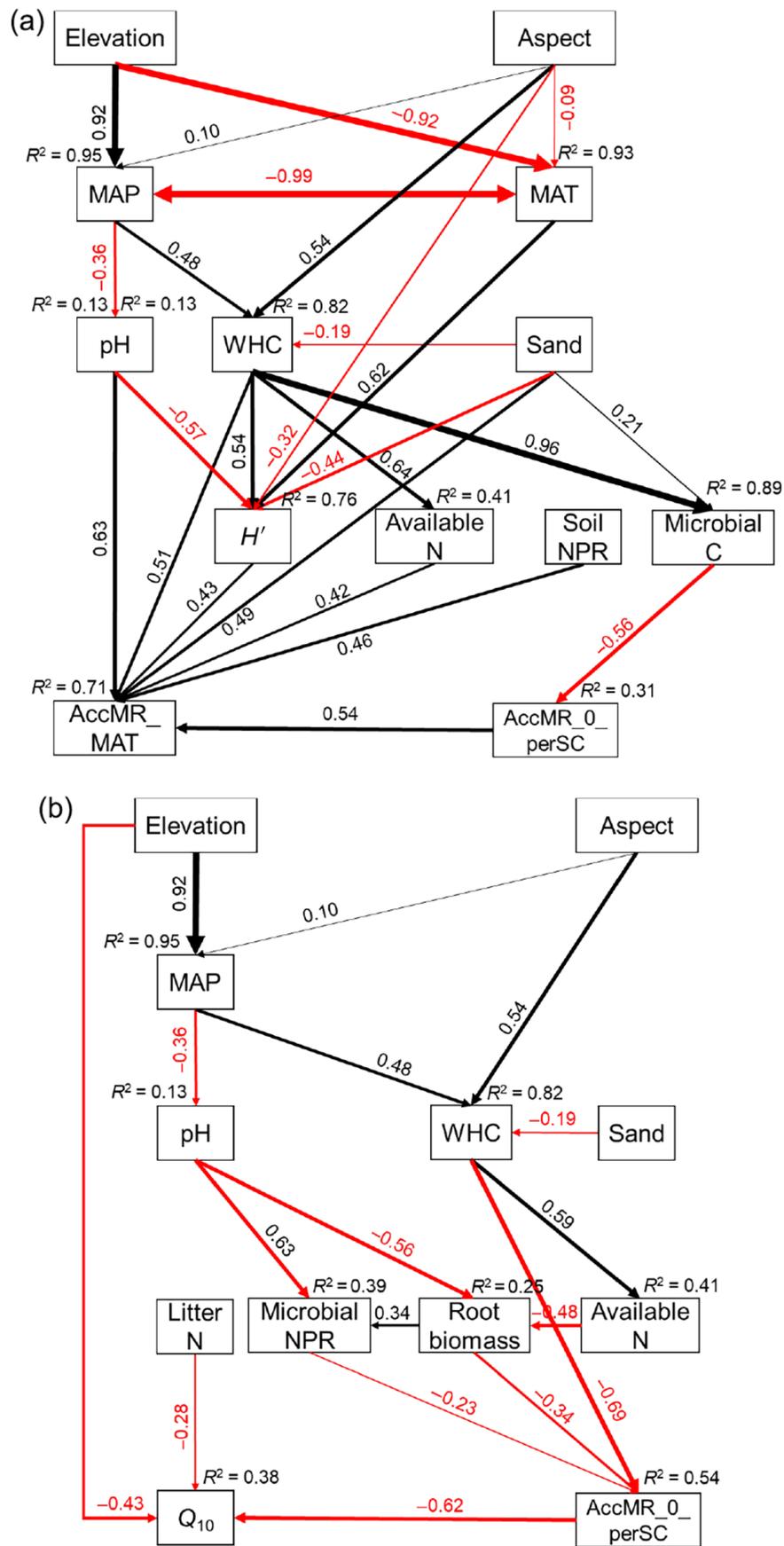


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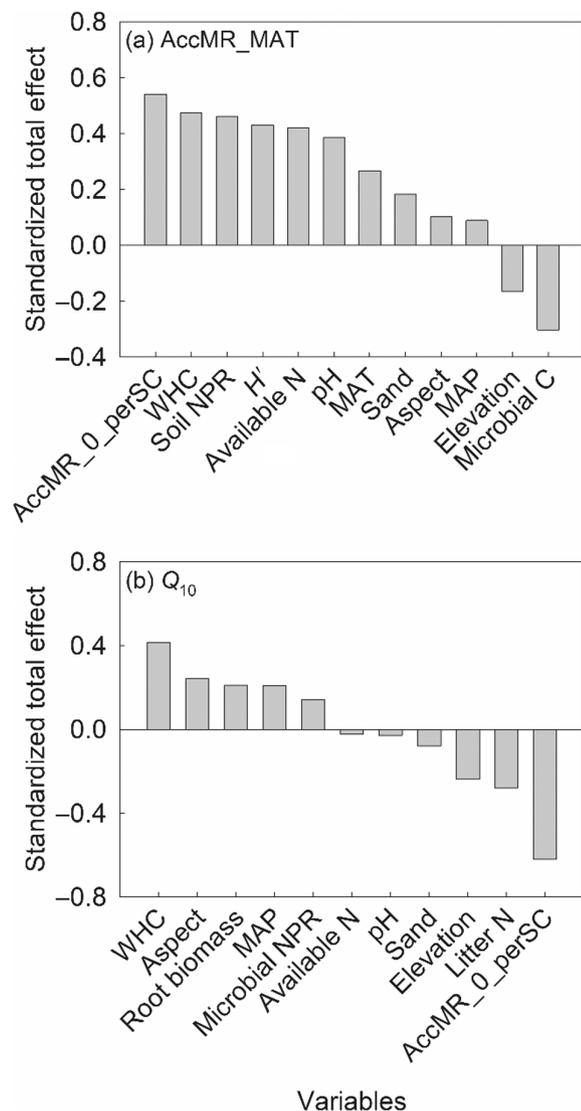


FIGURE 4 Standardized total effects derived from the SEMs for the abiotic and biotic factors in impacting AccMR_MAT (a) and temperature sensitivity (Q_{10} , b). AccMR, accumulated microbial respiration; AccMR₀, the base AccMR at $T = 0^{\circ}\text{C}$; AccMR_{0_perSC}, the AccMR₀ after normalized by soil C concentration; AccMR_MAT, the adjusted AccMR by MAT; MAP, mean annual precipitation; MAT, mean annual temperature; NPR, N:P ratio; WHC, water-holding capacity.

Q_{10} was positively affected by fine-root biomass in carbon input factors and negatively affected by litter N concentration in carbon input factors. In total, carbon

input factors explained the largest elevational variation of Q_{10} (0.13; Figure 2b). In the SEM analysis, variation in Q_{10} was explained by the direct negative effects from AccMR_{0_perSC}, elevation, and litter N concentration, with standardized total effects of -0.62 , -0.43 , and -0.28 , respectively (Figure 3b). These factors explained a total of 38% of the variation of Q_{10} (Figure 3b). The results also showed that WHC, aspect, fine-root biomass, MAP, and microbial NPR had indirect positive effects on Q_{10} through MR_{0_perSC} (Figure 4b).

DISCUSSION

Elevational variation and drivers of soil MR

In this study, the incubated AccMR increased along with the elevation (Figure 1a). This phenomenon is similar to that observed in other incubation studies (Kong et al., 2022) but opposite to the field measurements that soil respiration declines from low to high elevation (Garten & Hanson, 2006; Gutiérrez-Girón et al., 2015). In the laboratory measurement, because all soil samples were incubated at the same temperature, the exhibited high AccMR of the soil samples obtained from high elevation was largely due to their high soil C concentration and microbial biomass C (Appendix S1: Figures S10 and S11). However, the field temperature declined from low to high elevation (Appendix S1: Figure S7). After being adjusted by the field MAT, no significant elevational trend of AccMR_MAT was examined because the low MAT of sampled high elevation limited microbial activity and offset the positive effect of high soil organic carbon concentration (Figure 5). However, most previous incubation studies used a unified temperature (or temperature range), ignoring where the soil was sampled. The unified incubation temperature was relatively high for cold-site samples and potentially overestimated their soil C release, and relatively low for the warm-site samples and potentially underestimated their soil C release (Li et al., 2020; Zhang et al., 2022). Future incubation experiments should pay more attention to this uncertainty using different incubating temperatures or at least adjusting the C

FIGURE 3 Structural equation modeling analyses to examine the overall effect on AccMR_MAT (a) and Q_{10} (b). The model fits the data well (AccMR_MAT: Fisher's $C = 172.98$, $p = 0.00$, $df = 94$, Akaike information criterion (AIC) = 256.98, Bayesian information criterion (BIC) = 332.86, $N = 45$; Q_{10} : Fisher's $C = 170.27$, $p = 0.00$, $df = 86$, AIC = 236.27, BIC = 295.89, $N = 45$). Solid arrows indicate significant ($p < 0.05$) positive (black) or negative (red) relationships. Values associated with the arrows represent standardized path coefficients. Widths of significant paths are scaled by standardized path coefficients. AccMR, accumulated microbial respiration; AccMR₀, the base AccMR at $T = 0^{\circ}\text{C}$; AccMR_{0_perSC}, the AccMR₀ after normalized by soil C concentration; AccMR_MAT, the adjusted AccMR by MAT; MAP, mean annual precipitation; MAT, mean annual temperature; NPR, N:P ratio; WHC, water-holding capacity.

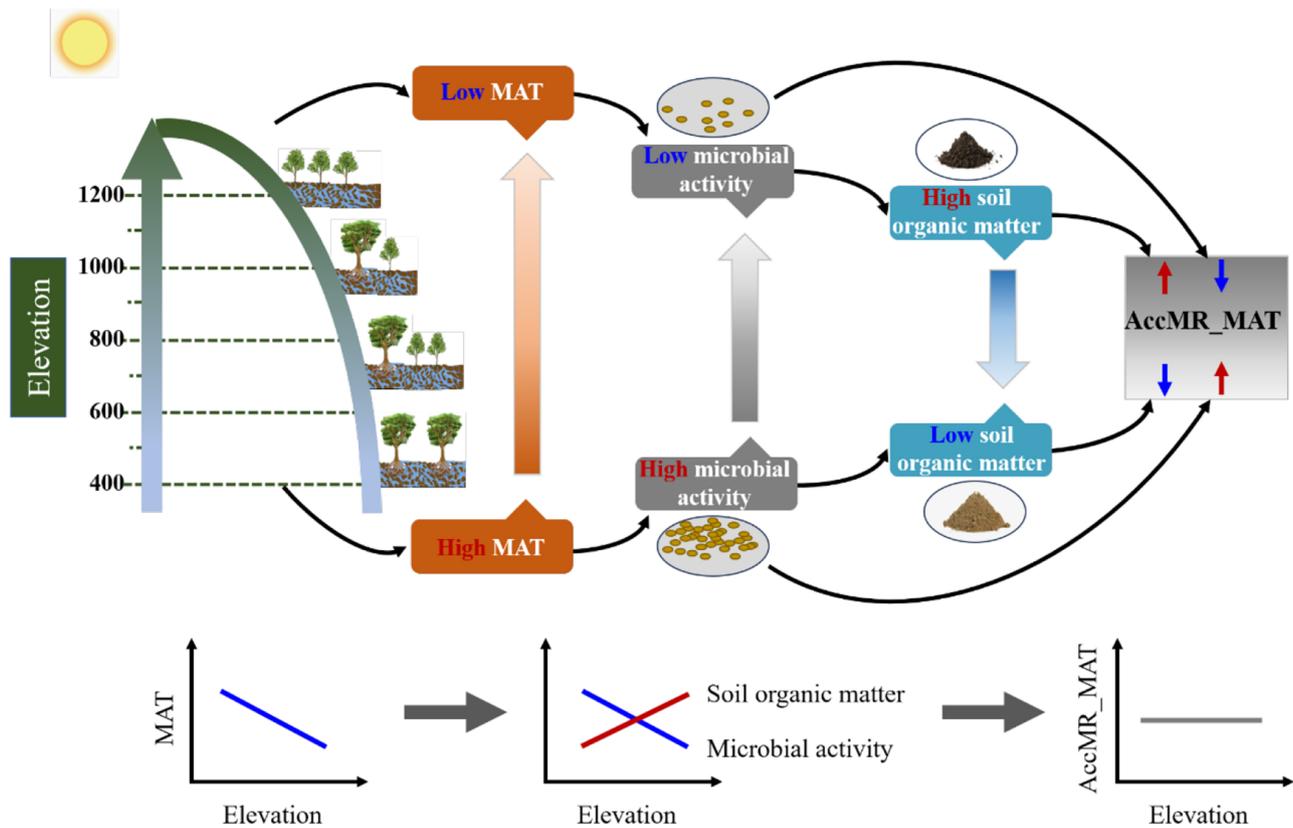


FIGURE 5 A conceptual diagram illustrating the mechanism of elevational effect on the adjusted accumulated microbial respiration by the mean annual temperature (AccMR_MAT) using the trade-off of mean annual temperature (MAT) and soil organic matter.

release by the natural temperature gradients of each sampling site (Li et al., 2020).

In this study, the variation in AccMR_MAT was predominantly influenced by soil environments (pH and WHC) and soil C quality (AccMR_0_perSC), followed by soil microbial biomass C, MAT, aspect, and MAP. Previous studies have shown that soil microenvironments (Ding et al., 2016; Li et al., 2020; Zhang et al., 2022) and initial quality of soil C (Guo et al., 2022) played critical roles in regulating MR, which was consistent with our results. However, our results differed from studies that suggested the critical role of soil microbes in determining soil C decomposition (Colman & Schimel, 2013). A possible explanation is that soil microbe is highly collinear with soil pH and WHC, the influence of soil microbe was implied in the effects of soil pH and WHC. These results suggest that soil environment and soil C quality are much more important in determining soil C decomposition.

Elevational variation and drivers of temperature sensitivity of MR

We found that Q_{10} did not significantly vary along with elevation (Figure 1d). Similar results were also observed in

a recent global meta-analysis (Li et al., 2022) and several observation studies (Schindlbacher et al., 2010; Xu et al., 2014; Zuo et al., 2021), suggesting that microbial response to temperature is similar among different elevational gradients. Such results do not support the microbial thermal adaption that Q_{10} declined from low- to high-temperature sites (or from high to low elevation) (Bradford et al., 2019). Moreover, our SEM analysis revealed no significant direct and indirect effects of MAT on Q_{10} , suggesting no significant influence of elevation and temperature on Q_{10} in the elevational gradients. As many studies predicted that climate warming is faster at high than that at low elevation (Pepin et al., 2015), the unified Q_{10} means that future climate warming will cause more C loss at high elevation. Meanwhile, other studies report different elevational trends of Q_{10} : Q_{10} increased (Gutiérrez-Girón et al., 2015; Kong et al., 2022; Okello et al., 2022; Zeng, Feng, Chen, et al., 2022; Zeng, Feng, Yu, et al., 2022) or decreased (Lipson, 2007) along with elevation, suggesting that the elevational trend of Q_{10} still need more studies to confirm.

In this study, the unchanged Q_{10} along with elevation might be due to the trade-off between the direct negative effect from elevation and its indirect positive effect (Figure 3b). All these indirect influences were via the

pathway of AccMR_0_perSC, showing that high elevation indirectly enhanced Q_{10} by reducing AccMR_0_perSC. Low AccMR_0_perSC indicated low soil C quality, contributing to high Q_{10} . Similar results were also observed in previous studies (Ding et al., 2016). These findings support an earlier carbon quality–temperature hypothesis: that Q_{10} of low-quality soil C contributes to greater Q_{10} than the high-quality soil C (Bradford et al., 2021; Fierer et al., 2006; Liu et al., 2017; Wang et al., 2018).

In summary, elevational variation of soil MR and its temperature sensitivity in a subtropical forest in South China were assessed using laboratory incubation experiment. We found that incubated AccMR increased from low to high elevation. However, a significant elevational trend of AccMR_MAT was not detected after adjusting the field temperature due to the trade-off between increasing soil organic matter and declining field temperature. We also found that Q_{10} did not vary significantly along the subtropical forest elevational gradients. The variation in Q_{10} was negatively dominated by soil C quality (AccMR_0_perSC). These findings have an important implication: the large uncertainty in soil incubation experiments caused by uniform incubation temperature should be addressed in future studies and model development, for example, using different incubation temperatures or adjusting based on the field temperature of the sampling site.

AUTHOR CONTRIBUTIONS

Bingwei Zhang contributed to conceptualization, methodology, visualization, investigation, software, formal analysis, and participated in writing the original draft as well as in writing, reviewing, and editing. Yun Jiang was involved in visualization, investigation, and contributed to the original draft. Xianjin He conducted field investigations. Youshi Wang contributed to visualization and formal analysis. Jiawei Li participated in formal analysis. Xueli Huang also contributed to formal analysis. Zufeishu conducted field investigations. Buhang Li conducted field investigations. Chengjin Chu contributed to conceptualization and methodology.

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CONFLICT OF INTEREST STATEMENT

The authors declare no conflicts of interest.

DATA AVAILABILITY STATEMENT

Data (Jiang, 2024) are available from Zenodo: <https://doi.org/10.5281/zenodo.10633597>.

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SUPPORTING INFORMATION

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

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