

Response to reviewer's comments

Part 1: Response to General Comments (Webpage):

The paper describes the relationships among litter properties, soil organic carbon (SOC), carbon fractions, and genes encoding enzymes across three subtropical forest types. The abstract clearly summarizes the main findings of the study and provides a conclusion that is likely to capture readers' interest.

Response: We sincerely thank you for the positive evaluation of our manuscript. We are pleased that the abstract was considered clear and effective in summarizing the main findings and highlighting the significance of the study. We also appreciate your broader recognition of the relevance and overall presentation of our work.

The authors proposed three main objectives: (i) to assess how genes encoding carbohydrate-active enzymes (CAZymes) respond to different forest types; (ii) to identify relationships between CAZyme genes and soil and litter properties; and (iii) to determine how these factors are associated with SOC across forest types. To address these objectives, the authors measured a range of litter and soil properties, evaluated SOC and its carbon fractions, and characterized the abundance and diversity of genes encoding enzymes involved in carbon degradation through metagenomic sequencing and annotation against the CAZy database.

Response: We sincerely thank you for this clear and accurate summary of our research objectives and methodological framework. We appreciate your recognition that the combination of litter and soil measurements, SOC fraction analysis, and metagenomic characterization was appropriately aligned with the three objectives of the study. We are pleased that the overall study design and analytical approach were clearly conveyed in the manuscript.

The introduction effectively presents the key concepts needed to understand the study and clearly identifies relevant knowledge gaps. The information provided is clear, sufficient, and supported by up-to-date references. Moreover, the rationale for the study is well established and convincing, and the objectives and hypotheses are clearly stated.

Response: We appreciate your favorable comments on the Introduction. It is encouraging that the background, knowledge gaps, and study rationale were considered clear and sufficiently supported by recent literature, and that the objectives and hypotheses were viewed as well defined.

The methods and data analyses are generally appropriate for addressing the proposed objectives. However, additional methodological information is needed, particularly in the metagenomics section, to ensure that the study is sufficiently detailed and reproducible.

Response: We agree that additional methodological details were needed to improve reproducibility, particularly for the metagenomic workflow. We have therefore substantially expanded the Methods section to clarify the amount of soil used for DNA extraction and sample processing, DNA quantity and quality assessment, library preparation, paired-end sequencing configuration and sequencing depth, metagenome assembly strategy, software and database versions, ORF and protein prediction, taxonomic and functional annotation procedures, construction and use of the

non-redundant gene catalog, and gene abundance normalization. We have also clarified the relevant statistical procedures, including data normalization and the assumptions and variables considered in subsequent analyses. These revisions provide a more complete and reproducible description of the analytical workflow.

The results are clearly described, and the figures adequately represent the data collected during the study. I suggest using a different color palette in most figures, preferably one with greater contrast, to facilitate the differentiation of groups and improve the overall readability of the figures.

Response: Thank you for the positive comments on the presentation of the Results and figures. Following your suggestion, we have revised the color palettes of the relevant figures using higher-contrast colors to improve group differentiation and overall readability. We also adjusted the presentation of significance markers and other graphical elements where necessary to improve readability and consistency across the figures.

The discussion is concise, well structured, and provides insightful interpretations of the findings. Nevertheless, some of the interpretations and suggestions would benefit from additional supporting analyses or data. Finally, although the conclusion is well written, it could more explicitly address the findings associated with each of the objectives proposed at the beginning of the study.

Response: We thank you for the constructive assessment of the Discussion and Conclusion. In response to these comments, we carefully revised the Discussion to strengthen the connection between our interpretations and the corresponding results. Where appropriate, we added supplementary analyses and comparisons to provide additional support; where the available data were insufficient to support a specific interpretation, we revised, qualified, or removed the corresponding statements to avoid overinterpretation. We also clarified several sections concerning CAZyme-associated taxonomic information, database-related limitations, relationships between enzyme families and soil properties, and the interpretation of SOC fractions and stability. In addition, we reorganized several discussion paragraphs to improve the logical flow. Finally, the Conclusion was revised to more explicitly summarize the major findings in relation to the three objectives of the study and to remove statements that were not directly supported by the analyses.

Overall, although the methodological and analytical approaches used in this study are not particularly novel, the authors make good use of these approaches to address the proposed objectives and present their findings clearly. Furthermore, while differences in litter and soil properties, SOC, and carbon fractions among forest types are not a new concept, the inclusion of the enzymatic profile adds value to the study by providing further insight into soil carbon degradation and the potential roles of soil properties and carbon pools in this process.

Response: We thank you for this thoughtful overall assessment. We particularly appreciate the recognition that integrating CAZyme-based enzymatic profiles with litter properties, soil characteristics, SOC, and carbon fractions adds functional insight beyond conventional comparisons among forest types. This integration is a central contribution of our study, as it allows the observed differences in soil carbon pools to be considered together with microbial carbon-degradation potential and its associations with litter and soil conditions. In the revised manuscript, we have further clarified this contribution and strengthened the interpretation of the

links among CAZyme genes, environmental properties, and SOC fractions.

Additional comments and minor corrections are included in the attached file.

Response: Thank you for providing the additional comments and minor corrections in the attached file. We have carefully addressed each of these comments point by point and made the corresponding revisions throughout the manuscript. Detailed responses and corresponding manuscript changes are provided below.

Part 2: Response to Specific Comments (Attachment):

L108 Study area and Sample collection: Please indicate when the samples were collected (year, month, season, etc.)

Response: Thank you for pointing this out. We have added the sampling time to the “Study area and Sample collection” section. Specifically, soil sampling was conducted in December 2024, and this information has now been included in the revised manuscript.

L122: For how long was the soil air-dried?

Response: Thank you for this comment. We have clarified the air-drying procedure in the revised Methods. Specifically, the soil subsamples used for pH and EC measurements were air-dried at room temperature until completely dry.

L132: Did you use the soil stored at 4°C or the air-dried soil for this part?

Response: We have clarified this point in the revised Methods. Soil stored at 4 °C was used for the determination of ammonium nitrogen ($\text{NH}_4^+\text{-N}$), nitrate nitrogen ($\text{NO}_3^-\text{-N}$), microbial biomass carbon (MBC), and microbial biomass nitrogen (MBN), whereas air-dried soil was used for the determination of soil pH and electrical conductivity (EC). In addition, undisturbed soil cores used for the determination of soil physical properties were stored at 4 °C until analysis.

L149: How much soil did you use? Did you follow the manufacturer's instructions as given, or were there any modifications or preprocessing of the sample? Did you evaluate the quality and/or quantity of the extracted DNA?

Response: We have expanded the description of DNA extraction and quality assessment. DNA was extracted from 0.5 g of soil from each sample using the FastDNA® Spin Kit according to the manufacturer's instructions without modification. DNA concentration and purity were quantified using a TBS-380 fluorometer and a NanoDrop 2000 spectrophotometer, respectively, and DNA integrity was assessed by 1% agarose gel electrophoresis. These details have now been added to the revised Methods.

L149-150: Was this a pair-end sequencing? What type of library did you use? What was the coverage of the sequencing? Was the sequencing carried out for you or in a core facility?

Response: These sequencing details have now been specified. Sequencing libraries were prepared using the NEBNext® Ultra™ DNA Library Prep Kit for Illumina, and metagenomic sequencing was performed on the Illumina NovaSeq 6000 platform using 2 × 150 bp paired-end sequencing.

Approximately 10 Gb of raw sequencing data per sample were generated. Library preparation, sequencing, and bioinformatic processing were performed by Shanghai Personal Biotechnology Co., Ltd. (Shanghai, China).

L149-170: What version of each software was used?

Response: We agree that the software versions are important for reproducibility. We have therefore added the versions of the software used throughout the metagenomic workflow, including fastp v0.23.2, MEGAHIT v1.1.2, Prodigal v2.6.3, MMseqs2 v13.45111, Minimap2 v2.24-r1122, featureCounts v2.0.3, and DIAMOND BLASTP v2.0.15.

L152: Is this a typo: ontained?

Response: Yes, this was a typographical error. “ontained” has been corrected to “contained” in the revised manuscript.

L153: Optimized, how? Maybe you mean the filtered sequences?

Response: We agree that the term “optimized sequences” was unclear. It has been replaced with the more accurate term “quality-filtered reads”, referring to reads retained after adapter removal and quality filtering with fastp. The corresponding quality-filtering criteria are also explicitly provided in the revised Methods.

L153-154: Did you assemble a unique metagenome using all the samples? Was it a separate one for each soil type or for each sample?

Response: We have clarified the assembly strategy in the revised Methods. The quality-filtered reads from each sample were initially assembled independently using MEGAHIT v1.1.2. Reads that remained unmapped after the initial sample-wise assembly were subsequently pooled and reassembled to recover additional contigs. Thus, the initial assemblies were performed separately for individual samples rather than by forest type or by directly combining all samples into a single assembly.

L159: Did you get the translated proteins from Prodigal or did you use an additional tool?

Response: The translated protein sequences were generated directly using Prodigal v2.6.3, and no additional translation tool was used. We have clarified this by stating that open reading frames were “predicted and translated into protein sequences using Prodigal v2.6.3 in metagenomic mode”.

L160: Which version of the NR database did you use?

Response: The database information has now been added. Taxonomic annotation was performed against the NCBI non-redundant (NR) protein database downloaded on 12 November 2022.

L160: Did you use Diamond for the taxonomical classification of the homologous protein or also to annotate additional proteins besides the CAZymes? Please specify.

Response: We have revised this section to distinguish the taxonomic and CAZyme annotation procedures more clearly. Taxonomic annotation of representative protein sequences was performed against the NCBI NR protein database using the taxonomy module of MMseqs2

v13.45111 with a lowest common ancestor (LCA)-based assignment strategy. In contrast, DIAMOND BLASTP v2.0.15 was used for functional annotation against the CAZy database to identify CAZyme-related genes. These two annotation procedures are now described separately in the revised Methods.

L163: Did you use the gene catalog for the annotation, or did you annotate every sample? Did you use any tool for annotation, such as dbCAN? What version of the CAZyme database did you use?

Response: We have clarified the annotation workflow. Rather than annotating each sample independently, representative protein sequences from the non-redundant gene catalogue were used for taxonomic and functional annotation. CAZyme annotation was performed by aligning these representative protein sequences against the CAZy database downloaded on 29 July 2021 using DIAMOND BLASTP v2.0.15. Thus, dbCAN was not used in this analysis. These details have been added to the revised Methods.

L168: Did you use any program to normalize the counts? Was the normalization used just for the CAZyme abundance comparison, or did you also use the normalized counts in other parts of the analysis?

Response: We have expanded the description of gene abundance quantification and normalization. High-quality reads from each sample were mapped to the non-redundant gene catalogue using Minimap2 v2.24-r1122, and mapped read counts were quantified using featureCounts v2.0.3. Gene abundances were then normalized as transcripts per million (TPM) based on mapped read counts and gene lengths. The TPM-normalized gene abundances were used for all subsequent gene-abundance-related analyses, rather than only for CAZyme abundance comparisons.

L172: Did you evaluate whether the data were normally distributed before using a parametric test? If yes, what test did you use?

Response: We agree that the assumptions underlying the parametric analyses should be explicitly stated. Before conducting one-way ANOVA, data normality was assessed using the Shapiro–Wilk test, and homogeneity of variances was evaluated using Levene’s test. We have added this information to the Statistical analyses section of the revised manuscript.

L174-176: Was this analysis performed with the normalized genes?

Response: Yes. The Shannon diversity analysis was performed using TPM-normalized gene abundances. As clarified in Section 2.4, TPM-normalized gene abundances were used for all subsequent gene-abundance-related analyses, including the diversity analysis. We have revised the Methods accordingly to make the normalization procedure and its application explicit.

L178-179: Did you also include other variables in the PERMANOVA analysis?

Response: No additional environmental variables were included in the PERMANOVA model. Forest type was the sole explanatory factor, because the purpose of this analysis was specifically to test whether CAZyme-encoding gene profiles differed among the three forest types. We have clarified this in the revised Methods.

L196: What do you mean by “lower mass”? In which figure is the mass depicted?

Response: We appreciate the reviewer's query. The phrase "lower mass" was inaccurate and did not refer to litter mass or accumulation. We intended to describe the relatively low litter quality associated with a high carbon-to-nitrogen ratio and lignin content. To avoid confusion and to report the measured traits more directly, we have removed "lower mass" and revised the sentence to state that broadleaf litter had the highest natural water content and carbon-to-nitrogen ratio, while its lignin content was significantly higher than that in bamboo litter but did not differ significantly from that in coniferous litter.

L206: It would be convenient for this and the other figures to use a more contrasting gradient of colors or a different palette.

Response: We have revised the color schemes of the relevant figures using a more contrasting palette to improve visual distinction among groups and overall readability. Similar adjustments were also made to the other figures where appropriate.

L211: The figures described in this section do not match the right figure (Figure 2).

Response: We appreciate the reviewer for identifying this inconsistency. The figure citations in this section were incorrect; the results described here correspond to Figure 2 rather than Figure 1. We have corrected all figure references in this section accordingly.

L218-219: At the beginning of the paragraph, you're talking about the increment in percentages, but here you are talking about rates. Maybe it would be better to keep the same units.

Response: We agree that using consistent units improves the clarity of the comparisons. We have therefore converted the fold differences for DOC and MBC to percentage increases, consistent with the presentation of SOC and MAOC at the beginning of the paragraph. The corresponding sentence has been revised accordingly.

L248-250: It would be clearer to describe only Figure 4 in this paragraph (without introducing Figures S2 and S3 at the beginning of the paragraph) and use the next paragraph to include Figures S2 and S3.

Response: We agree that separating the descriptions of the main and supplementary figures improves clarity. We have therefore removed the reference to Figs. S2–S3 from the beginning of this paragraph and revised the paragraph to focus exclusively on the results shown in Fig. 4. The detailed differences in specific CAZyme gene families shown in Figs. S2–S3 are now described in the following paragraph.

L258: The selection of colors in this plot does not allow to differentiate between enzymes. I suggest using a different color palette with better contrast.

Response: The color palette of this figure has been revised to provide greater contrast among the different enzyme families, thereby improving their visual distinction and the overall readability of the figure.

L266-267: How is this a decreasing trend if it is higher in coniferous?

Response: We agree that the term "decreasing trend" was inaccurate because the abundances of AA3 and AA4 did not decrease monotonically across the three forest types. We have therefore

revised the sentence to describe the actual pattern, with the highest abundances observed in coniferous forests and the lowest in bamboo forests. We also revised the subsequent description of GH16 and GH20 to avoid implying a monotonic trend and to more accurately state that these genes encode enzymes involved in fungal-derived chitin degradation.

Figure S3 and S4: Although this is just a supplementary figure, it would be easier to distinguish the significant differences if the lines with the asterisks were closer to the bars. The same for Figure S4. Consider using a more contrasting color palette. This would benefit the visualization of the results.

Response: We have revised Figs. S3 and S4 accordingly. The significance lines and asterisks have been repositioned closer to the corresponding bars to facilitate identification of pairwise differences, and a more contrasting color palette has been applied to improve the visual distinction among forest types and the overall readability of the figures.

L274-283: Figure S4 is mentioned here more times than Figure 5. Maybe it would be more reasonable to have Figure S4 in the main manuscript instead of Figure 5. It is also better suited to what you want to describe.

Response: We agree with the reviewer that the original Fig. S4 is more directly aligned with the results described in this section, particularly the statistical comparisons of bacterial phyla among forest types. We have therefore moved the original Fig. S4 to the main manuscript as the revised Fig. 5. Conversely, the original Fig. 5, which provides an integrated overview of the taxonomic composition associated with CAZyme-encoding genes, has been moved to the Supplementary Information as Fig. S4. The corresponding figure citations and captions have been updated throughout the manuscript.

L284-285: Maybe something to include in the discussion.

Response: We agree that this statement is more appropriate for the Discussion than the Results. We have therefore removed it from the Results section and incorporated the relevant interpretation into the Discussion.

L303: Microbial metabolic activity? Perhaps it would be better to call it a metabolic profile, since you are not measuring the metabolic activity.

Response: We agree with your comment that “microbial metabolic activity” was not an appropriate term because metabolic activity was not directly measured in this study. We have therefore replaced it with “microbial metabolic profile” in the figure caption and revised the corresponding wording where necessary.

L309-310: Although the soil physical and chemical properties were combined, the total variation should sum 100%, and this is not the case.

Response: We appreciate your comment. We re-examined the variation partitioning results and found that the apparent discrepancy was caused by a negative shared fraction that was not displayed in the original Fig. 6d. For genes encoding enzymes involved in bacteria-derived carbon decomposition, litter properties independently explained 40.95% of the variation, soil physicochemical properties independently explained 31.48%, the shared fraction between these

two predictor groups was -18.35%, and the residual fraction was 45.92%. Thus, these fractions sum to 100%. Negative shared fractions can occur in adjusted R^2 -based variation partitioning because the shared component is derived by subtraction among adjusted fractions, particularly when predictor groups are correlated or overlapping. Such negative values should not be interpreted as negative ecological effects. We have now included the -18.35% shared fraction in the revised Fig. 6d and added the corresponding values to the Results.

L318-319: What was the interactive effect of the bacteria-derived carbon?

Response: We have clarified this point in the revised manuscript. In variation partitioning analysis, the overlap between predictor groups represents a shared fraction rather than an interaction effect. For genes encoding enzymes involved in bacteria-derived carbon decomposition, the shared fraction between litter properties and soil physicochemical properties was -18.35%. As explained above, this negative value can arise in adjusted R^2 -based variation partitioning and should not be interpreted as a negative ecological interaction. The value is now explicitly shown in the revised Fig. 6d and described in the Results.

L322-323: Water content is twice. Maybe you mean the carbon-nitrogen ratio.

Response: We appreciate your careful observation. The two “water content” terms refer to different variables rather than a duplicated label. Specifically, one represents litter natural water content, whereas the other represents soil gravimetric water content. To avoid confusion, we have revised the corresponding text to explicitly distinguish these two variables.

Figure 7a: What does the size of the square represent?

Response: We appreciate your question. In Fig. 7a, the size of each square represents the absolute magnitude of Pearson’s correlation coefficient, with larger squares indicating stronger correlations. We have now clarified this information in the revised figure caption. We also specified that color indicates the direction and magnitude of the correlation, with red representing positive correlations and blue representing negative correlations.

L342-346: Either the diversity of the enzymes and the carbon fractions is different between forest types, so why not try a separate analysis for each of them if that is also part of your third aim? A correlation test is also possible here.

Response: We agree that the relationships observed across all samples may partly reflect differences among forest types. We therefore retained Fig. 7c to show the overall relationships across the full dataset, while additionally conducting Spearman correlation analyses separately for broadleaf, coniferous, and bamboo forests. These forest-type-specific analyses showed that the associations were not consistent across forest types, with significant correlations occurring mainly in coniferous forests. The additional results are now presented in Supplementary Fig. S5, and the description of Fig. 7c has been revised to clarify that it represents relationships across all samples.

L351-354: To talk about community structure, you would need to consider the phylogeny of the full community after the metagenome assembly, and that was not what you did. What you presented is just the taxonomy associated with the homology of the annotated CAZyme, which, as you mentioned in the results, represents only 18.83% of all genes in the metagenome.

Response: We agree with your comment. Our taxonomic analysis was based on the taxonomic assignments associated with CAZyme-encoding genes, rather than on a phylogenetic analysis of the entire metagenomic community. Because these genes accounted for only 18.83% of all genes in the metagenome, referring to the observed patterns as changes in “microbial community structure” was too broad. We have therefore revised this section to describe the results as CAZyme-associated taxonomic composition and explicitly clarified that these taxonomic patterns should not be interpreted as changes in the structure of the whole microbial community.

L357-359: This can also be influenced by the database. Many of them (including CAZyme and the NCBI NR database) are more enriched with bacterial genomes than fungal genomes.

Response: We appreciate this important point. We agree that the apparent predominance of bacterial taxa in the CAZyme-associated taxonomic assignments may partly reflect the greater representation of bacterial than fungal sequences in reference databases such as CAZy and NCBI NR. We have therefore revised the Discussion to explicitly acknowledge this potential database bias and to interpret the bacterial predominance more cautiously. Specifically, we now note that the relatively low proportion of fungal assignments may partly result from unequal database representation rather than necessarily reflecting a correspondingly minor fungal contribution to carbon decomposition.

L366-368: Could this be related to the amount of biomass available for degradation?

Response: We agree that the amount of biomass available for degradation may also contribute to the observed CAZyme gene diversity pattern. We have therefore revised this section to acknowledge that, in addition to differences in substrate chemistry, variation in the relative amount of plant- and microbial-derived biomass available for degradation may also influence CAZyme gene diversity. This interpretation is now supported by relevant literature (Cuartero et al., 2025).

L377-379: That is an interesting insight.

Response: We appreciate your positive comment. We are pleased that you found this interpretation insightful. We have retained this discussion in the revised manuscript.

L385-386: This suggestion would be better supported by the results that contrast soil properties with enzyme abundances for each family, as you did for the plant-derived, fungi-derived, and bacteria-derived classification.

Response: We agree that this interpretation would be better supported by directly examining the relationships between environmental properties and the abundances of individual CAZyme classes. We therefore conducted additional Spearman correlation analyses between litter and soil physicochemical properties and the abundances of the six CAZyme classes (PLs, AAs, CBMs, CEs, GHs, and GTs). The results, now presented in Fig. S1b, showed distinct environmental associations among CAZyme classes. We have also added these results to the Results section and revised the Discussion accordingly to more directly link the contrasting CAZyme profiles among forest types with their observed associations with litter and soil properties.

L406-411: I'm not entirely sure if I understand the message of this paragraph correctly. At the beginning, you talk about distinguishing carbon sources when evaluating microbial functionality,

but the conclusion concerns forest type, with little clarification in between. I think you need to reword it a little bit.

Response: We agree that the original paragraph did not clearly connect the discussion of carbon-source-specific responses with the subsequent interpretation of forest-type effects. To avoid this abrupt transition, we removed the original concluding paragraph and revised the end of Section 4.2 to focus directly on the environmental associations supported by our analyses. The revised text now concludes that the relative importance of litter inputs and soil conditions in explaining variation in microbial carbon-degradation potential varies with carbon source.

L427-434: That is an interesting conclusion.

Response: We appreciate your positive comment. We are pleased that you found this interpretation interesting, and we have retained this discussion in the revised manuscript.

L439-445: How is this connected with the fact that your POC:MAOC is almost 1 in broadleaf, being the lowest one among all the forest types?

Response: We agree that the low POC:MAOC ratio in broadleaf soils provides important additional context for interpreting their relatively high POC content. We have therefore retained the original discussion regarding the association between POC and carbon-degrading genes, while adding consideration of the POC:MAOC ratio. Specifically, broadleaf soils had the lowest POC:MAOC ratio among the three forest types, with a value close to 1, indicating that their relatively high POC content co-occurred with a similarly large MAOC pool. We have revised the paragraph accordingly to clarify that high POC accumulation in broadleaf soils does not necessarily imply low SOC stabilization and should be interpreted together with the relative contribution of MAOC.

L450-454: This is a pretty interesting summary of your results. However, it doesn't reflect what you were explaining at the beginning of the paragraph. You should either consider including this in a different paragraph (like the next one) or reframe to specify that it includes all the results and not just the ones that you mention at the beginning of the paragraph, which is what this "together" is referring to.

Response: We agree that the original phrase "Together, these results" was ambiguous because it appeared to refer only to the DOC and MBC results described immediately before it, although the sentence was intended as a broader synthesis. We have therefore restructured this paragraph and removed the original general summary. The revised text now discusses the association of MBC with bacteria-derived carbon degradation across all samples and then incorporates the newly added forest-type-specific analysis, showing that the relationships between carbon-degradation-related genes and SOC pools varied among forest types, with significant within-forest correlations concentrated in coniferous soils (Fig. S5). This revision provides a clearer progression from the results discussed at the beginning of the paragraph to their forest-type-specific patterns.

L456-465: How is the soil stability defined? You find a high MAOC in broadleaf and low in bamboo, but the POC:MAOC is pretty low in broadleaf as well.

Response: We appreciate your question. In this study, SOC stability was defined as the

MAOC:SOC ratio, as already stated in the original manuscript in Line 95. Accordingly, a higher MAOC:SOC ratio indicates a greater relative contribution of mineral-associated organic carbon to the SOC pool and thus greater SOC stability. Broadleaf soils had the highest MAOC:SOC ratio, while also showing the lowest POC:MAOC ratio among the three forest types. These two patterns are consistent, because a lower POC:MAOC ratio likewise indicates a greater relative contribution of MAOC compared with POC. To avoid ambiguity, we have revised “MAOC ratio” to “MAOC:SOC ratio” in the Discussion.

L483-486: How is this a conclusion of your study when you never evaluated this possibility?

Response: We agree with your comment. Our study compared existing broadleaf, coniferous, and bamboo forests and did not directly evaluate forest conversion or bamboo expansion. Therefore, the original statement regarding conversion from coniferous to broadleaf forests and expansion of bamboo forests into coniferous forests was not supported by our study design. We have removed this statement and revised the conclusion to focus on the observed differences among forest types in microbial carbon-degradation potential, SOC stability, and their relationships with litter and soil properties.

L488: Since vegetation composition was never mentioned or evaluated in this study, you should probably call it forest type.

Response: We agree. Vegetation composition was not directly evaluated in this study, and “forest type” is therefore the more appropriate term. We have replaced “vegetation composition” with “forest type” in the revised conclusion and adjusted the sentence accordingly.

Once again, we sincerely thank you for the careful evaluation of our manuscript and for the valuable time and effort devoted to the review process.