Reply #2 to reviewer

Dear Dr. Schwab and Dr. Hilton,

Please find bellow a point-by-point reply to the comments of reviewer Dr. Schwab.

"Dear Dr. Hilton and authors,

I appreciate the authors' efforts in addressing my initial comments, but there are still some crucial recommendations for enhancing scientific transparency and reproducibility that were overlooked. The comments below pertain to the tracked changes manuscript."

Thank you for your valuable input on this paper. Regarding the major concern about employing the Monte Carlo Model to delineate the contributions of different end members, I have incorporated your suggestion to use the MixSIAR package in the R environment. After conducting multiple validation calculations, I observed that this model yields results differing from previous reports. However, this discrepancy does not detract from the paper's main argument. On the contrary, the higher proportion of OC_{lps} (organic carbon in loess-paleosol sequences) reaffirms our hypothesis that intensified erosion of deep loess-paleosol sequences is a significant contributor to fluvial particulate organic carbon (POC) in the Huanghe River. The manuscript has been revised in the following key areas:

1. Model: Implementation of the MixSIAR model, accompanied by diagnostic runs.
2. Figures: Updates to Figures 1, 3, 6, 7, and 8. Enhancements to the captions of Figures 3 and 5, including illustrations to denote that scatter size corresponds to collection depth.
3. Supplementary Material: Inclusion of Table S1 detailing particle size parameters and addition of Figure S7, which illustrates the geometric surface area in the carbon isotope mixing space."

"Lines 204 to 217:
1. The geometric surface area (GSA) is not reported. I recommend using the calc_area algorithm from the MixSIAR R-package (Brett, 2014; Stock et al., 2018) to compute GSA and test if the end-member composition is distinct for all end-members. The GSA value should be included in the manuscript.
2. Please specify which convergence diagnostic tests were employed for estimating model convergence (Geweke, Gelman-Rubin, or Heidelberg-Welch).
3. Report the chain length and the number of chains used in the analysis.
4. The burn-in of 1000 appears to be relatively small for an unmixing model; typically, it would be in the range from 100,000 to 1,000,000.
5. In Table 2, the average values for the endmembers should be accompanied by the number of samples used to calculate the mean d13C and D14C for each. Report the amount of samples used for calculating d13C and D14C."

Thank you for your comments. We have now implemented the MixSIAR model, with detailed information provided in Section 3.3.
GSA: We used the calc_area algorithm to get the GSA which is 7.13 SD^2 (provide in the caption of Figure. S7), the end-members are distinct.Model: "Prior information is assumed to be

uninformative. We computed the posterior distribution of the Bayesian formulation using the MCMC method, facilitated by the MixSIAR package (Moore & Semmens, 2008; Stock & Semmens, 2016), all computations were performed in the R environment (http://www.r-project.org/). To ensure reliable simulation, the model was run with chain length of 300,000 by 3 chains, using a burn-in of 200,000 steps, and a data thinning of 100 for each sample." Diagnostics: "Further model diagnostics was performed using Gelman-Rubin and Geweke test, both diagnostics validated the robustness and convergency of the model."

"To adhere to APA statistical guidelines for scientific work, it is essential to cite results properly. Each mean should be reported with either a standard deviation (SD) or standard error (SE) or a similar metric. Indicate with the first usage of the mean and error statistic whether it is (M ± SD) or (M ± SE). M, SD, and SE are accepted APA abbreviations. This essential information should not be excluded for the reader's clarity, and I highly recommend including the sample size (n) for each average.
• Line 241: Missing SD and n, and lack of proper description.
• Lines 259-260: Missing n.
• Line 264: Missing n.
• Line 266: Missing n.
• Line 270: Missing n, and missing SD and n for the D14C value.
• Line 272: Missing SD and n.
• Lines 274-275: Missing SD.
• Line 307: Missing n.
• Lines 615-617 and following: Missing SDs and ns."

Thank you for your thorough review. We have incorporated the suggested information. To enhance clarity and avoid redundancy, we explicitly state at the outset that our results and analysis rely on 10 samples collected from the cross section. We indicate in the result section that we always report M±SD (when necessary) in the manuscript.

"Line 247: All used data should be made accessible to the reader. Please add the D10 and D90 values to Table 1, especially as this data is not deposited into a database. Reporting values in a figure is insufficient."

We added Table S1 in the supplementary material to report these values.

"Line 310 and following, including figures: Use two or three decimal places and report exact values for all p-values greater than .001. For p-values smaller than .001, report them as p < .001 (APA)."

We adopted your suggestion, using 0.001 as the threshold.

"Figure 1: Spelling error - "Guaging station" instead of "gauging station" within the map. Figure 3 and 5: Add a legend for sample depth. Does the small dot represent surface or deep water?"

The spelling error in Figure 1 is corrected. For Figure 3 and 5, we added "The size of each circle indicates the water depth at the corresponding SPM, with smaller circles representing shallower depths and larger circles indicating deeper waters" in the caption.

Thank you for your attention to these matters.
Best regards,

Dr. Yutian KE, on behalf of all co-authors