

Review of the manuscript egusphere-2025-2584

This is a valuable study investigating the effects of plant diversity on soil carbon accrual and biopore formation. The topic is novel and highly relevant to the journal's scope. The title is well-formulated, the experimental design is robust, and the dataset is comprehensive. However, there are a few minor issues, such as formatting errors, that should be addressed. Additionally, some methodological details in the Materials and Methods section need to be clarified or expanded. Overall, I believe the manuscript is suitable for publication after minor revisions.

Please review and feedback the general and specific comments as follows:

Specific remarks

Line 30: Please delete the extra space between *including* and *grasslands*.

Line 57: Please remove the extra space between *Root-originated* and *biopores*.

We apologize for the typographical errors, and have removed the extraneous spaces throughout the manuscript.

Lines 84–88: Could you clarify the rationale behind the assignment of treatment (CE) numbers? For instance, why is the bare system labeled as CE1, while the monoculture is labeled CE7?

- Treatment identifiers (CE1–CE12) were assigned by the Kellogg Biological Station. We selected only the treatments relevant to our objectives, which explains the non-sequential numbering. We have revised the manuscript for clarification as follows:

“The experiment consists of twelve plant systems representing a 12-point gradient of plant diversity (CE1-CE12), six of which were used in this study.” (Lines 83-84 in the revised manuscript)

Additional details for all treatments are available at: <https://lter.kbs.msu.edu/research/long-term-experiments/cellulosic-biofuels-experiment/> which is also provided in line 97 in the revised manuscript. Lastly, we provided the description of each plot with their treatments in each caption of related figures (Fig. 1-4).

Line 125: Please provide a citation to a published study that supports the biopore identification method used.

- We have provided a reference as follows:
“Detailed procedures for biopore segmentation are publicly available (https://github.com/Maik-Lu/Roots_and_Biopores) (Lucas et al., 2022).”

Line 129: Could you clarify what is meant by “distance average distance to biopore”? The phrasing is unclear.

- We apologize for the confusion. We have changed the term to “mean distance of soil matrix to biopores” throughout the manuscript. (Line 136, 204, 220, 262, 266, and Figure 4c and d in the revised manuscript)

Line 161: It would be helpful to include a brief summary sentence at the end of each paragraph or subsection to reinforce key points.

We have added a dedicated summary paragraph to each section in Discussion, as follows:
“These findings emphasize the currently underestimated importance of formation, abundance, and surface properties of biopores in affecting soil biochemical status, specifically, influencing plant-derived inputs and their potential protection within the soil matrix. This study suggests that this role might be particularly pronounced in ecosystems with high plant species diversity.” (Lines 269-272 in the revised manuscript)

“We see the need for further investigation into the role that individual members of grassland communities may play in stimulating soil pore structure development and soil C accumulation. Identifying keystone species enabling more efficient C accumulation can guide plant restoration and SOC accrual efforts.” (Lines 291-293 in the revised manuscript)

Line 181: Please format the R^2 correctly by placing the 2 as a superscript.

→ We have updated all instances to “ R^2 ” throughout the manuscript.

Line 255–256: This sentence is unclear—“accumulated for 12 years” appears abrupt and could be better integrated.

→ According to reviewer’s comment, we revised the sentence as follows:
“Biopores are root-formed channels that reflect root growth and senescence, as well as the resulting changes in the soil physicochemical properties including organic matter (Mueller et al., 2024).” (Lines 257-258 in the revised manuscript)

Lines 255–262: These sentences are more appropriate for the Introduction section and would fit better there.

→ We moved the mentioned sentences to Introduction part, and reorganized paragraph as follows:
“We surmise that information on biopores from μ CT scanning can be of particular relevance for assessing root impacts and root-soil interactions in perennial plant systems. Diverse plant communities exhibit complex root architectures due to interspecific interactions, leading to varying quantities and spatial distributions of root-derived carbon. Increased root-originated bioporosity may indicate diversified root growth paths in perennial systems, reflecting strengthened root-soil contacts in such system.” (Lines 75-79 in the revised manuscript)

L284 It would be reasonable to include a clear conclusion section at the end of the main text.

→ Following reviewer’s suggestion, we have provided Conclusion as follows:
“The 12-year grassland experiment demonstrates that SOC accumulation is governed by plant diversity, with the benefits of high plant diversity being, in part, exhibited via the development of root-derived biopores. Yet, certain species combinations may lead to biopore formation and SOC accumulation benefits disproportional to the actual level of the plant system diversity. Specifically, the two-species mixture of C4 switchgrass and C3 Canadian rye created the greatest bioporosity, shortest mean soil-to-pore distance and biopore surface area, thereby accelerating microbial processing and stabilization of root-derived carbon in the surrounding matrix. These findings highlight bioporosity as a more reliable proxy for SOC gains than plant species number alone, and point to specific “keystone” species combinations that disproportionately enhance soil structure and carbon sequestration. Identifying and deploying such functionally complementary plant species can offer a targeted pathway for optimizing grassland restoration and long-term SOC storage.” (Lines 295-304 in the revised manuscript)