As the response to reviewer was sent before the actual update of the article, the changes do not always correspond 1-to-1 to what was initially written. We therefore send an update of the letter, with, where relevant, new text in green.

The old text is in blue.

Reviewer 1:

> We sincerely appreciate Reviewer 1’s remarks, which have significantly helped us improve the quality of our article. Our responses can be found below.

1. General comments:

The study by Giraud et al. (2025) presents a novel modelling framework that enables to simulate plant growth and related C and water flow within the plant, in interaction with a soil model simulating the interactions between C inputs from roots and soil microbial dynamics. Using this new and exciting framework, the authors have investigated in silico the effect of drought on soil C dynamics in the rhizosphere of a young hypothetical cereal plant, taking into account the effect of dry spells on root C inputs and on their dynamics in the soil. Considering this impressive piece of work, authors have already done a good job in synthetizing the main features of the coupled models and of their simulation outputs, although the manuscript remains quite dense and demanding for a reader not familiar with the original models.

> We will reorganise the article, add explanatory graphics and shorten the plant-related sections to make the work clearer to the readers, using the recommendation of reviewer 1. We explain our intended adaptations in response to the detailed reviewer’s comments below.

Besides the detailed comments below, here are my main remarks:

1. The present work is built on two main models described in Giraud et al. (2023) and Sircan et al. (2025), which have been further improved and coupled here. Given that both previous articles have already tackled some of the issues described here (e.g. effects of water stress on plant growth and exudation, C dynamics in the rhizosphere), I would recommend the authors to try to focus more on the benefit of the coupling when describing the simulation results or discussing them, i.e. to focus on the effect of drought on root-derived C and their effects on SOC dynamics in the rhizosphere, while reducing the length of other, less important parts of the manuscript.

> We will shorten the results and discussion section with respect to the plant part. However, in line with some of the detailed comments of the reviewer, we will keep details on the description of the plant processes to point out relevant differences to the previous paper. In the discussion, as recommended as well by reviewer 2, section 4.3 will be expanded.
>
> Part of the results and discussion linked to the plant model were moved to appendix K3 ‘Plant processes’. Moreover, section 4.3 of the discussion was subdivided in sections (to underline the different points made) and expanded.

2. Only few details are given in the main manuscript regarding the soil model, although some are indicated in Appendix. I think it is especially important to mention in

the Material & Methods which soil processes have been taken into account or not in the model (not necessarily the equations), and how soil water content and soil temperature may affect microbial activity, so that the reader is able to better interpret the simulation results. In particular, I understood that the dynamics of the bulk soil organic matter is not represented, but only the dynamics of dissolved C. In this regard, the discussion on rhizospheric priming effect is interesting, but may be limited if all the “native” soil organic matter is not included in the model but only its labile part.

We have added figures 1, 2, and 3 for this purpose, but we will update these figures to clearly list the processes that are represented. We will underline how water content may affect the microbial activity in more detail, as the link between water and microbes is one of the main advancements of the soil model. Currently, the effect of the soil temperature is not implemented.

The discussion in section 4.3 about the priming effect will be expanded to include this additional limitation of the represented carbon.

The captions of Fig. 2 and .3 were adapted to list directly the soil processes considered and their effects on microbial activities. Moreover, lines 81-90 and 118-124 were updated to describe more clearly the carbon pool represented and their characteristics. The decision of representing the non-microbial soil carbon as two pools is also described in more details at lines 88-90 and discussed at lines 603-606 and 672-687. This discussion now takes up the limitations of our approach to conclude on priming of “native” soil organic matter.

3. The study focuses on the effect of drought, but here and there a change in temperature is mentioned during the drought period, without information about this in the Material & Method. If temperature changed over time or among the scenarios, this should be clearly stated; if not, this should also appear explicitly in the M&M.

In the current version of the model, the temperature affects only the plant processes and not the soils (as shown in Figure 3). We will add a table to show the weather conditions during the baseline and drought conditions.

Table 1 was added to give a better overview of the changed environmental parameters during the dry spells. The fact that the temperature affects the plant but not the microbes is stated was added at lines 124-125.

4. I keep struggling to understand the link between macroscale voxels and microscale domains of root segments or outside root segments… As it seems to be an important feature of this work and could be inspirational for other similar modelling frameworks, I would recommend authors to illustrate this a bit more clearly in Fig. 1, using realistic volume dimensions and showing which volumes/segments are included within which types of voxels.

We will update figure 1 for a better illustration of the coupling framework.

Figures 1 and 2 (image and caption) were updated to describe more clearly the link between the scales.

Given the number of variables investigated, crossing three scenarios of drought with three sets of soil parameters makes it quite challenging to get a clear picture of the main results in the end. An idea to clarify things for the reader could be to formulate some hypotheses about the effects of drought on root-derived C inputs to the soil and their dynamics in the rhizosphere, and to use the simulation results to validate or invalidate them.

We will add compact hypotheses to the introduction, to help guide the discussion section. For instance:

1. Droughts will lead to a lower microbial activity in the rhizosphere and to a lower release of plant carbon
2. Consequently, we will observe a slower soil carbon dynamic, which can lead to both an increase or decrease of soil carbon storage.

We added hypotheses, which are slightly different from the ones given above (see lines 60-62): "We evaluated three hypotheses: (1) dry spells will lead to a lower release of plant carbon and thus to (2) lower microbial growth in the rhizosphere, and (3) these changes in soil carbon input and loss can lead to both an increase or decrease in short-term soil carbon storage."
The results are discussed according to the hypotheses in lines 61-63.

2. Detailed comments:

Title: "carbon stabilization by plant" is a bit confusing. Also, authors have only investigated the dynamics of root-derived C (not aerial residues). Maybe something more neutral: In silico analysis of carbon and water dynamics in the rhizosphere under drought conditions?

We thank the reviewer for this suggestion, we will change our title to the one proposed by the reviewer.

The title was changed as proposed

Abstract:

L8 (and throughout the text): I am not familiar with the use of "biokinetic" in this context; I would suggest only using "kinetic"

We will update the term.

L11-13: The reader may also wonder whether the drought experienced in the soil affected soil microbial activity, independently on the indirect effect of drought on C input by roots

We will evaluate the results in the bulk soil, far away from the roots. The drought had however a limited effect on the microbial activity as we do not represent the effect of temperature on the microbial activity and we only had a small decrease in water content far away from the roots.

Presentation of the results in the bulk soil were added to appendix M1 and help support the discussion about the different scales at lines 565-566.

Introduction:

L18: “and as an intra- and inter-domain signalling carrier” is not very clear to me, please explain/rephrase

> We will update the sentence to: “and as a variable connecting domains and processes […]”.
>
> The whole section was removed, following the comment of reviewer 2 about streamlining the introduction.

L37: “Plants can also exert direct feedback effects on themselves (e.g., aboveground-belowground feedback)” : this could be rephrased and simplified

> We will rephrase to: “Plant also have inner feedback loops, such as aboveground-belowground interactions, which affect their fitness”.
>
> The whole section was removed, following the comment of reviewer 2 about streamlining the introduction.

L41: What about nutrient concentration gradients in the rhizosphere?

> We will rephrase to: “Plant-soil exchanges lead to the creation of the rhizosphere, an area of soil around the root with characteristics distinctive from the bulk soil, such as rhizodeposition, microbial communities, soil structure, water and nutrient content”.
>
> The whole section was removed, following the comment of reviewer 2 about streamlining the introduction.

L76-79: This study extends the work of Giraud et al (2023) that focused on water and C flow within the plant. It would therefore be useful to state a bit more explicitly that this new study focuses on the root-derived C dynamics in the rhizosphere, taking into account the previous modelling framework of Giraud et al. for integrating the retroaction between water flows and C inputs in the rhizosphere, and coupling it to another model of rhizospheric soil C dynamics. Also, stating here at the end of the Introduction some hypotheses linked to water spells that will be verified with this new modeling framework would help the reader to focus a bit more on the originality of this work.

> We will change lines 76-79 to:
> “This study aimed to set up and implement a fully integrated plant-soil-microbiome model that accounts for root-microbiome interactions via the release of C and uptake of water from the rhizosphere by the roots. We present an extended version of the FSPM CPlantBox […]. The two models were coupled using an updated version of the multiscale setup of Mai et al. (2019) to obtain higher accuracy and stability. The framework was used to conduct an in-depth analysis of the root-derived C dynamics in the rhizosphere under drought conditions against baseline scenarios”.
> For the hypotheses, see the “general comments” section.

Lines 76-79 were removed but we added the sentence 'The resulting framework was used to conduct an in-depth analysis of the root-derived C dynamics in the rhizosphere under drought conditions against baseline scenarios' at line 60. The earlier introduction focuses also more on the rhizosphere. The hypotheses were added in the following sentences.

M&M:

L100: Meunier et al. (2017). Rephrase "and the coupled the stomatal".

We will rephrase to "CPlantBox simulates the plant water flow using the analytical solution of Meunier et al., (2017), and the resulting stomatal regulation."

This change is now at lines 76-77.

L123-124: This could be mentioned earlier on in the Introduction.

We will add this simplified description of the coupling in the introduction at line 88.

A short overview of the coupling was added at line 56-58.

L126-137 and Fig. 1 & 2: After reading this several times, I am still not sure that I really understood the spatial scheme. There are macroscale soil voxels that may or not contain microscale root segments. However, both appear with the same size on Fig. 1. The terms macroscale and microscale are perhaps misleading? And what is then the perirhizal zone described as microscale in Fig. 2: one full voxel containing at least one root segment? Perhaps this could be clarified in Fig. 1, e.g. if showing a spatial description of the 3D root segments and the voxelization around it with realistic dimensions, and explaining where materials are actually exchanged and where specific reactions may - or not - take place.

We thank the reviewer for the precise description of what is unclear in the figure. We will update it to illustrate the coupling approach in more detail. Among other changes, we will make our graphic more similar to Figure 1 of Mai et al (2019) to point out the exchange of information.

We will aim to make the graphics self-explanatory in response to the reviewer's questions: in our setup, all soil voxels are of same size, whether or not they contain a root. The perirhizal zone is described as microscale because the logarithmic scaling of the cells allows us to have very small cells around the root surface. We have therefore a much higher resolution than on the macroscale.

To avoid confusion, we will rename the macroscale model as "3D soil model" and the microscale models as the "1D soil models".

The two figures were updated and the terms 'macro' and 'micro' soil were changed to 3D and 1D soil.

L175: I don't understand what $\Omega\backslash\partial\Omega$ means

$\Omega\backslash\partial\Omega$ means that the equation is valid for the whole domain except for its boundaries. We will add an explanation at first occurrence.

An explanation was added at line 163.

L219: For simplicity

> We will rephrase to 'For simplicity, the implementation of Eq. (6) for the 3D soil and 1D soil are given respectively in appendices B1 and B2.'
>
> The changed sentence is at line 256.

L225: It would be useful to remind to the reader what ξ is, even if it was introduced a few equations ago

> We will explain the meaning of that variable below equation (12) as well.
>
> The explanation was added at line 214.

L329-332: If a new calibration was introduced to better reproduce expected trends, this should be emphasized more in the discussion, e.g. if authors choose to discuss the validity of hypotheses from their simulation results.

> We will expand the discussion around L645. The calibration allowed us to have the starch storage as the regulatory variables, then exudation, while growth and maintenance were maintained.
>
> The explanation was added at lines 554-557.

L347: Again, an illustration of all these different scales in Fig. 1 would really help the reader to understand more quickly how these scales are interconnected

> We will add an illustration of those scales in Fig. 1.
>
> Figure J1 was added to illustrate the scales.

L373: I don't think that oligotrophic and copiotrophic have been defined anywhere. For a reader not familiar with soil microbial ecology, it would be useful to define these terms, and explain what are the expected behavior of these two microbial pools.

> We will add an explanation of the oligotrophs and copiotrophs in the description of the TraiRhizo model (section 2.1.1).
>
> Information was added at lines 83-86.

L380: It would be worth adding to which class these tresholds correspond to Poeplau and Don, i.e. 0.65 (threshold between degraded soils and moderate soil quality), 0.83 (moderate/good soil quality) and 1.16 (good/very good soil quality). It would also be important to state that the pedotransfer function used here was developed for German soils. One may also wonder whether this study from Poeplau and Don at field scale across Germany is really relevant to identify hotspots of C in the rhizosphere, this could lead to additional comments in the Discussion.

> We will add the interpretations of the classes and underline that they are used to exemplify the hotspot analysis. Indeed, these thresholds were developed for a

different scale. Therefore, they might not be relevant for our smaller scale model. For this reason, we did not consider it in the original manuscript.

Information about the soil classes was added at lines 355-359. We have also added a statement on the limited qualitative interpretation in lines 678-680.

Results:

L405: “an increasing concentration” compared to what or according to what?

We will rephrase to: ‘The simulation highlights a concentration of dissolved low molecular […] that increase with time in response to root exudation in the upper part of the root system, near its centre’.

The new sentence is at line 385-387.

L408-432: For brevity, I would remove this part. If these simulations results have already been presented and explained in Giraud et al. (2023), shouldn’t the focus be here rather on the exudation and mucilage secretion in response to drought, starting at L433?

Because of the re-calibration of the plant model, the results are different to the ones obtained in Giraud et al. (2023). Consequently, we found it important to explain these new results, as mentioned by the reviewer about lines L645-647. We will add this remark at the beginning of the section.

The section 3.2 was consequently shortened to remove the sections which were already the focus of Giraud (2023): water potential and carbon usage for growth and maintenance.

L449-450: Shouldn’t this sentence be mentioned earlier in the paragraph, before showing the actual results for each soil parametrization?

We will move the sentence ‘We found an effect of the biokinetic parameterisation on exudation and mucilage release.’ to line 434: ‘Both the plant water balance and the kinetic parametrisation affected the exudation rate and mucilage release’.

The sentence was merged with the one at line 394: “The plant water balance affected the exudation and mucilage release rate much more strongly than the kinetic parameterisation of the soil microbes.”

L456-458: I am not sure this is a very important simulation result to emphasize, given that the variation of this maximum exudation rate per cm2 among the scenarios is quite small.

We will replace the description of the maximum exudation rate per scenario and give only the overall maximum, to be compared against experimental results in the discussion.

The updated sentence is at line 416-418: “The highest exudation rate per unit of root surface for a single segment across all simulations was obtained at 11 day 5hrs with baseline and lateDry (0.153 mmol C cm−2 d)”

L464-465: I don’t understand. If there are fewer roots, why is there a higher maximum C concentration?

> We will rephrase to: ‘That second peak is especially strong for earlyDry and lateDry due to lower root growth, i.e., We had root tips in that area of soil over a longer period, leading to higher concentrations’.
>
> The corresponding explanation was put in the discussion section (following the recommendation of reviewer 2), at lines 612-615: “The C concentration peaks observed for earlyDry and lateDry at deeper depth were due to lower root growth: The root tips remained in that area of soil over a longer period, leading to higher concentrations. Stronger plant growth under baseline resulted in perirhizal zones and rhizodeposition at lower depths such that the C accumulation at the root tips was much less pronounced compared to the dry spell scenarios”.

Fig. 8: I would suggest to increase the size of the figures and to add a title to each sub-graph with the name of the variable detailed in the caption

> We will increase the figure size and separate it in several figures if needed, as well as adding the caption.

L492: I still struggle to understand the meaning of a variable perirhizal truncated volume among the treatements... Please try to better explain why it is important and which biological or physical information it actually brings.

> Using the truncated values enabled to compare the concentration of the different C pools across the 1D models (by giving them the same outer radius).The complementary cumulative volume distribution allowed us to observe the concentration profiles across the perirhizal zones. We could thus underline that we obtained results at this smaller scale that differed from those in section 3.3. We will put this section (as well as section 2.4.3 and the description of the truncated 1D models) in the appendices to clarify and shorten the article. The difference between the scales can still be observed by using the sections 3.3 and 3.7.
>
> The information related to the truncated perirhizal zone was moved to appendix L.

L499 and after: Please give the full meaning of each concentration when used in the main test, and not only its symbol, as reading and understanding this part is quite challenging…

> We will replace all the symbols of concentration with the full names.

L519: “the negative effects of the low soil θ on microbial activation” - but this relationship was not introduced in the Material & Method. It’s really necessary to better explain how the SOC model works and how it depends on soil water content and soil temperature.

> We will update figures 1-3 to better illustrate the different interactions. The effect of water potential on the microbial community was relegated to the appendices (like all soil reactions) to put the main focus of the article on the interactions between the models.
>
> The explanation was added at lines 119-125.

L531: “the relative volumes of the SOC hotspots” - I continue to be lost…

> We will add an explanation on the meaning and relevance of the volume-normalised hotspot volume, using the work of Landl et al (2021) at the end of section 2.4.5 .
>
> The explanation was added at lines 372-374.

Discussion:

L616-617: “the virtual plant’s starch pool can be interpreted as representing both actual starch reserves and newly synthesised wall material”. I am not sure that I fully understand the conceptual difference between biosynthetic growth and expansion. Is the second type of growth independent on C? I thought that root growth was explicitly included here in the C balance. If so, why would a part of the root growth be included in another term with starch?

> Biosynthetic growth corresponds to the creation of new cell wall, and depends on the direct supply of carbon (Hillty, 2021, Verbanˇciˇc et al., 2018). The expansion growth corresponds to the dilatation of those walls, driven by the cell’s turgor pressure. Therefore, expansion growth depends on the supply of C but does not need to be concurrent to C supply. For this simulation, the virtual plant’s starch pool, which varied according to the C supply, can be interpreted as representing both actual starch reserves and newly synthesised wall material, thereby enabling expansion growth to occur at night.
>
> However, as this section will be strongly shortened, we will give a simpler description of the outputs of the plant models, compared against those of Giraud et al. (2023).
>
> The whole section related to plant growth was moved to the appendix K3.

L645-647: Now I understand why authors developed the description of such results at L408-432. The present statement could therefore be made earlier, at L408.

> See our response to the comment of L408.

L679: a ratio of dormant oligotrophs and what other variable?

> We will update the sentence to ‘a high ratio of dormant-to-total oligotrophs’.

L707: “and organic C-dependent soil hydraulic parameters” - I guess that the benefit of having simulated specifically mucilage secretion in this study would be linked to this s feedback on plant water uptake. Maybe it is worth explaining this?

> We will add a longer discussion on the effect of organic C on the soil hydraulic parameters as part of an outlook on the future development of the model. The effect of organic C on soil hydraulic parameters will indeed be added to the setup in a following study.
>
> Further explanations were added at lines 638-641.

L709-719: I find this paragraph very interesting. However I am surprised that authors do not link this heterotrophic respiration by soil microorganisms to root respiration simulated during the dry spells, as the modelling framework enables to do this, which is rather unique. Looking at how the ratio between the two sources of CO2 evolves over time and how the resulting total basal respiration evolves over drought may reveal interesting features.

We thank the reviewer for pointing to this very relevant link. We will add a figure of the proportional respiration dynamics and include this interesting aspect in section 3.5 and in the discussion after line 719.

Figure 10 was updated (see subpanel d) and the discussion in section 4.2.7 was updated.

L735-736: "The lateDry scenario led to the lowest plant growth but to a higher SOC hotspot volume, indicating a more resource-efficient root system exudation." Why would an increase in the number of rhizospheric hotspots be considered more resource efficient? Do authors suggest that SOC hotpsots are associated to a better feedback for the plant (e.g. in terms of water or nutrient uptake)? Please explain.

Following our usage of the SOC classes of Poeplau and Don (2023), higher SOC concentrations are linked to healthier soil. However, as their classes were created for a higher scale, we will be more careful in describing the possible effects of these larger SOC hotspot volumes.

The limitation of our setup to evaluate the hotspot was added at lines 686-687.

L870-871: This definition of microbial pools is really needed in the main text.

We will add a description in section 2.1.1.

The description was added at lines 83-86.

3. Typos

L23: A comma is missing after "exudation)"

L289: Remove bracket

L540: cycling

L564: "can cause a the"

L598: for further optimizing

We thank the reviewer for taking the time to point out the spelling errors. These typos will be corrected and the text carefully checked for other errors.

Reviewer 2:

We thank the reviewer for these in-depth comments, they raise important points and are an important help in improving the article.

This work presents a technically ambitious and novel coupling of a three-dimensional functional–structural plant model (CPlantBox) with a microbial-explicit soil model (TraiRhizo) implemented in DuMux. The work addresses an important frontier—dynamically linking plant architecture, rhizosphere processes and microbial functioning to jointly simulate carbon and water fluxes across scales—and the overall concept and coding effort are impressive. The authors produce a rich set of scenario simulations that suggest compelling interactions between the timing of dry spells and microbial trait syndromes that can drive either net carbon retention or accelerated mineralization in the short term. The coupling and the multi-scale analysis framework are valuable contributions for modelling communities interested in rhizosphere processes and plant–soil feedbacks. To be honest, at 76 pages this is the most extensive review I've undertaken — it required a careful, time-consuming read to assess the modelling choices and their implications.

While the modelling effort is significant and presents useful, hypothesis-generating insights, the manuscript sometimes over-asserts ecological conclusions that the simulation scope and temporal extent cannot robustly support. Statements implying durable soil carbon "stabilisation" are particularly strong and risk overstating the results. The manuscript should consistently use language that reflects the model's temporal and mechanistic limits (e.g., "short-term net C balance shifts," "suggested potential for transient C accumulation," or "conditions that promote reduced short-term mineralization"), and explicitly frame the findings as model-derived hypotheses that require empirical validation over longer timeframes. Recasting conclusions in this way will preserve the impact of the study while avoiding claims that require organo-mineral interaction processes or multi-decadal validation that the current simulations do not include. My detailed comments and suggestions are described below.

> We will adapt the language and recast conclusions as recommended. We explain our intended adaptations in response to the detailed reviewer's comments below.

Abstract

Soil carbon stabilization is a long-term process involving complex organo-mineral interactions. Your model, as described, likely simulates microbial turnover and short-term respiration. To claim "stabilization" is a strong overstatement that must be tempered. The conclusions must be carefully rewritten to reflect exactly what the model outputs: namely, **net C flux** (input vs. respiratory output) and **short-term C storage** in microbial biomass or slow pools. The model may suggest a potential for stabilization, but it cannot conclusively prove it without validation against long-term experimental data.

> In the abstract and throughout the paper we will remove the word stabilization and use those two terms. We will also update the title of the article, following the recommendation of reviewer 1.
>
> In the abstract, we will update the sentences:
> - '[..] to include an implicit time-stepping.' To '[..] to include an implicit time-stepping. This allowed for an increase in the accuracy and stability of the model outputs.'
> - 'we observed a lasting stabilisation of soil C with less reactive communities.' to 'we observed an increase in the C storage of soil C with less reactive communities.'

Define what you mean by “earlier” versus “later” dry spells using absolute timing or plant phenological stages (e.g., days after sowing or leaf-stage) and by how much. Are these linked to specific phenological stages? What are the specific "soil biokinetic parametrisations"? Briefly state the difference between "reactive" and "less reactive" communities (e.g., differences in maximum growth rates or substrate use efficiencies).

> We will add the start dates of the ‘earlier’ and ‘later’ dry spell and summarize in the abstract key parameters that differ between the three microbial parameter sets (growth rate, affinity to solutes, and yield).
>
> An explanation of earlier vs later was added at lines 10-11. The explanation of a reactive microbial community was added at line 12.

Introduction

The introduction convincingly argues that coupled water–C dynamics at the soil–plant–atmosphere continuum are important under climate change, and it highlights the rhizosphere and microbes as key players. However, the justification for this specific modelling effort (why extend CPlantBox with TraiRhizo, why in DuMux, and why the chosen coupling is required now) is not tightly argued: the reader is told the model is useful, but not why existing tools cannot already answer the questions posed.

The introduction begins with very broad, textbook-level concepts (e.g., "water is a resource," "C is a building block") and takes too long to narrow its focus. The necessity of **your** work—integrating a **specific** microbial-explicit soil model (TraiRhizo) into a **specific** FSPM (CPlantBox) to address a **specific** gap—is buried and needs to be the central thread from the outset. The justification is currently implicit. For instance, the authors list several gaps (few models consider both water and C; many rhizosphere models ignore microbes; many FSPMs don’t simulate soil C), but they do not synthesize these into a single crisp gap statement that maps to the paper’s aim. The gap therefore reads as a set of related deficiencies rather than a targeted problem the paper will solve.

> We will shorten the first section, to go quickly into the main limitations of current models and how our new coupling addresses them. The precise description of the soil and plant processes were meant to justify the processes implemented in the model, but this can be done more succinctly.

The text mentions updates (implicit time-stepping, updated multiscale coupling) but does not explain why these matter (stability? computational efficiency? ability to run larger/longer scenarios?). State concrete advantages and differences from prior CPlantBox couplings and from existing tools (e.g., TraiRhizo, SpatC).

> We will update the text to underline the effect of these temporal scales: The implicit time-stepping and updated multiscale coupling lead to higher stability and accuracy in cases where we use CPlantBox to simulate plant and soil interactions.

The necessity of **your specific approach** (coupling CPlantBox with TraiRhizo) is not sufficiently justified. Why is this particular combination of models the best solution to the problem you've identified? A brief comparative sentence on the strengths of each model and the synergy of their coupling would be very effective.

We will add a direct explanation of how the two models can address current limitations listed in the introduction.

The two models were developed in parallel to respond to key gaps in existing models (simulations of soil and plant water and C, and of soil microbes) and to complement each other (similar levels of precision in the number of pools represented, complementary inputs and outputs).

The first general section was shortened and the definition of the current gap was re-worked (lines 39-44).

The justification for using CPlantBox was added at lines 49-51, for the soil model at lines 52-57. The justification for the update of the solving method (e.g., time stepping) is given at lines 58-59.

Methods

The work described is highly sophisticated and represents a significant computational effort to integrate complex, multi-scale processes. The ambition to dynamically couple a 3D FSPM with a 1D microbial-explicit soil model is commendable.

Section 2.4.5: The definitions of the four different scales for analysis are innovative and thoughtful. The need to add a large, constant SOC_slow pool post-simulation because the model outputs were "almost always in the lowest SOC class" and "significantly below" measured values suggests a potential issue with the model's initial conditions or its fundamental ability to represent realistic background C levels. Adding SOCslow = SOCtheoric − SOCsimulated_init effectively injects an artificial, immobile C pool to match literature SOC. This is pragmatic, but it changes the meaning of “hotspot” thresholds and may bias hotspot fraction metrics. The assumptions and potential consequences must be clearly discussed and sensitivity tested. This requires a strong justification.

The effect of adding this pool will be discussed in more depth in the discussion section, as well as the limit of our calibration method. A sensitivity analysis and more precise calibration will be conducted for a following publication on the coupled model. The need to add this additional carbon pool was partly caused by the usage of the pre-set TraiRhizo parameter sets and process constraints.

The decision of representing the non-microbial soil carbon as two pools is described in more details at lines 88-90 and discussed at lines 603-606 and 672-687.

Section 3.2 Why were the two one-week dry spells chosen at days 11–18 and 18–25 after sowing? Are these phenologically relevant for the virtual plant? Provide biological/ecological justification.

The selected days were chosen to have similar simulation scenarios to the one in Giraud et. al. (2023). These days were selected as they are within the vegetative stage of the plant: CPlantBox does not yet simulate production of flowers, fruits or seeds. The selected time spans correspond in our simulation to the seedling growth and tillering stages.

An explanation of the selection of the dry spell span is given at lines 303-306.

The phrase "warmer and drier atmospheric conditions were simulated" is too vague. Precisely which driving variables were changed (e.g., VPD, radiation, temperature) and by how much?

We will add a table providing changes in the environmental variables during the baseline conditions and the dry spells.

Table 1 was added to describe the change in environmental variables during the dry spells.

Results

The results presented are complex and stem from a highly sophisticated modelling effort. The multi-faceted analysis across different scales (plant, bulk soil, perirhizaltrunc, microscale) is a particular strength, providing a comprehensive view of the system's behaviour. However, the results are presented as absolute truths from the model without any acknowledgment of uncertainty or variability. Phrases like "we observed," "we found," and "led to" are used throughout, but the reader has no way of knowing: Are the differences between scenarios (e.g., earlyDry vs. lateDry) and parameter sets statistically significant or just numerically different? For instance, line 431-432 is is a key finding but is stated without any statistical test to back up the word "significant."

The connection between root architecture and C concentration peaks is well-described. However, the comparison between scenarios and parameter sets is again purely descriptive. A quantitative measure of the difference would be much more impactful.

Many statements are given as percentages or qualitative (“strong increase”, “higher”, “lowest”) but without absolute units or baseline magnitudes. The authors could replace qualitative descriptions with quantitative percentages, effect sizes, or other measures where possible.

The reviewer raises a very good point. In the results section, we had wished to focus more on relative differences rather than absolute values, because of the limits of our calibration method, but it remains indeed necessary to offer a more precise description of the results. We will update this section, using values and statistical analysis to justify the causal effects described.

We added mean and standard deviation values throughout the results section.

Strictly report what the model output is in the results section. Move all speculative explanations for why a pattern occurs (e.g., competition, rhizosphere overlap) to the Discussion section.

We will move any interpretation of results to the discussion section.

Several sections were taken out of the results: effect of the root system growth rate (now at line 609), description of microbial competition and rhizosphere overlap.

Section 3.4, line 497: The claim that copiotrophs reach 580 µmol/cm³ is alarming high — show where and how large volumes have these concentrations (absolute volume in cm³) to contextualise (i.e., are hotspots tiny or spatially extensive?).

> A single truncated rhizosphere reached this value, which corresponds to 0.028651 cm³. This high concentration is also linked to the fact that our model does not include the movement of microbes, a limitation mentioned in the discussion. We will underline the high values obtained in our discussion.
>
> The information regarding the volume of the concentration peak was added at line 1200.

Discussion

The section 4.2 is overly long and reads more like an extended results section or a review of plant physiology. While comparing model outputs to literature is valid, the level of detail on biosynthetic growth, osmotic adjustment, and specific exudation rates from various papers is excessive and distracts from the paper's central focus on **soil-plant-microbe feedbacks**. This entire section should be drastically condensed. The key point—that the model qualitatively captured known dynamics despite its simplifications—can be made in a few paragraphs.

> The discussion of this section will be condensed (especially the comparison with the literature and the discussion of the different elements of growth). We will discuss the changes compared with the results of Giraud et al (2023) and focus on the ‘key point’ of this section.
>
> Part of the discussion on plant processes was put in appendix K3.

The introduction implicitly promised insights into how dry spell timing and microbial reactivity interact. While this is addressed in 4.3, the discussion does not explicitly return to frame the findings around the initial objectives. A strong discussion should begin by stating how the results have addressed the original knowledge gap. Additionally, Section 4.3 contains the most valuable discussion points but is buried. The insights about scale-dependency, microbial "starving-survival lifestyle," intra-microbial competition, and the rhizosphere priming effect are excellent and should form the core of the discussion.

> More emphasis will be put on section 4.3, and parts of the current results section will be integrated. We will more directly reference the objectives given in the introduction, and use the new hypotheses added in the introduction section, following the recommendation of reviewer 1.
>
> The former section 4.3 (now section 4.2) of the discussion was subdivided in sections (to underline the different points made) and expanded.

Several sentences imply general ecological truths (e.g., “the model showed… making a 3D evaluation relevant”), while the work actually shows model-based scenarios for a single soil/site/plant parameterisation set. Rephrase to emphasize that findings are model-derived insights that suggest hypotheses for empirical testing.

> We will make our wording more careful throughout the discussion and conclusion sections.

A description of the limitations was added in section 4.2.9. A more careful phrasing was used in the other part of the discussion—e.g, “For our setup” (line 563), “Although our results depend strongly on modeling choices” (line 581).

The authors added an immobile SOC_slow pool to align simulated and literature SOC. This affects hotspot classification and interpretation. Discuss explicitly (a) how SOC_slow modifies hotspot thresholds and (b) whether the “stabilisation” conclusions hold without SOC_slow.

We will discuss the meaning and effect of the SOC_slow in more detail. Taking the advice from both reviewers 1 and 2 into account we shift the focus from carbon stabilisation to more general plant-soil interactions. Moreover, in the discussion part we will highlight the comparison between the scenarios, which makes the resulting bias caused by the SOC_slow less important for our conclusions.

The decision of representing the non-microbial soil carbon as two pools is discussed at lines 603-606 and 672-687. Conclusive statements on carbon stabilisation were removed from the text.

Some paragraphs are long and mix methods/results/discussion. Keep the Discussion focused on interpretation, implications, limitations, and future work; move implementation details back to Methods or an Appendix.

We will reorganise the results and discussion section to make sure that there are no overlaps between methods, results and discussion.

Some sections were removed from the discussion section. Namely, the text about the resolution of the 1D models, the description of the plant growth processes, the section about the exudation rate values. The discussion was subdivided in smaller sections to increase readability. The long discussion about the

Conclusion

The conclusion provides a brief and accurate summary of the work performed and correctly identifies the core findings. However, for a paper of this complexity and ambition, the conclusion is **significantly underdeveloped** and fails to adequately synthesize the study's full contributions, limitations, and broader implications. It reads more like an abstract than a conclusion. It should answer the "so what?" question. What is the broader significance of finding that C vs. water limitation in microbes dictates the soil C outcome? How does this advance the field of plant-soil modelling or inform future experimental work?

We thank the reviewer for this important and very helpful remark. We will replace the conclusion with the one given below, which aims to cover the points mentioned by Reviewer 2:

“In this paper, we presented the equations and implementation of a coupled model representing carbon and water flow in the soil-rhizosphere-plant continuum, influenced by atmospheric conditions through plant transpiration and photosynthesis. This framework accounts for the effects of water content variation on carbon flow and microbial activity. The multiscale implementation enables precise evaluation of fluxes and reactions at the soil-plant interface and can capture feedback across domains and scales. Despite the simplified representation of plant and microbial processes and limited calibration, the model reproduces trends reported in the literature, such as the “starving-survival” lifestyle of some microbial communities.

We found that the effect of water scarcity on soil carbon turnover is an emergent property arising from microscale feedbacks between plants, microbes, and local environmental conditions. The varied impacts of water stress highlight the strong influence of local soil and plant characteristics in determining whether carbon or water limitation dominates turnover. By representing multiple sources of plant and microbial stress, the model provides a mechanistic explanation for variability in plant and soil carbon allocation under combined stresses.

The model yields a wide range of variables (e.g., short-term carbon storage) across the soil-rhizosphere-plant continuum that can be used to assess the performance of plant phenotypes and management measures under dynamic conditions. By computing the resulting soil and plant conditions and identifying the key processes driving ecosystem responses, this model can both provide parameters for larger-scale models and inform the design of simplified models that focus on the most influential processes. Moreover, this work lays the foundation for a more comprehensive model of the plant-soil interaction cycle, including nutrient exchanges, which are essential to accurately represent the feedback of soil on plant processes. Finally, this model is uniquely adapted to re-create the experimental observations of isotopic carbon allocation in the plant and soil.”

The mention of experimental setup at the end of the conclusion is a reference to the work of Shultes et al. (2025, doi: 10.1038/s41467-025-62550-y), which will also be added in the discussion.

1. Typos

Fix small typos and duplicate words:

“to to the soil” -> “to the soil”;

“unterstanding” -> “understanding”;

“ans pore scales” -> “and pore scales”.

Line 399: “FSPM model of Giraud et al. (2023))” double parenthesis.

Line 433: respectivelly -> respectively.

Please check multiple typos and grammar issues:

“Expending” -> “Expanding”;

“compaired” -> “compared”;

“diurnal cylcing” -> “diurnal cycling”;

“hostpot” -> “hotspot”.

> Thank you for taking the time to point out the spelling errors. These typos will be corrected and the text carefully checked for other errors.