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Biogeosciences Discussions

Interactive comment on "Modelling and quantifying the effect of heterogeneity in soil physical conditions on fungal growth" *by* R. Pajor et al.

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We are grateful to both referees for their favourable comments and useful suggestions for further improvements to the paper. We have taken the majority of the comments on board in the revised manuscript and we respond in detail to them below. Changes are highlighted in the revised manuscript.

Referee #1

Spatial scale: Referee one raises a highly relevant and challenging question related to the spatial scale of the samples and asks if we can relate such small samples to soil management. Currently there is no mathematical framework available that can

address scaling from pore to field. Developing such a framework is beyond the scope of the current paper, but we believe that the work described in this paper is relevant even at the small spatial scales that we used. As the modelling of fungal growth within a complex 3-D geometry is computationally challenging, the sample sizes that currently can be dealt with are restricted to those used in this study.

In response to the comment made by the referee, we have made two changes to the paper in the discussion section. Firstly, our statistical analysis confirmed that the difference in pore architecture between treatments was significantly different, but that the difference between small samples within the same treatment was not. This demonstrates that the smaller sample size is representative for the treatment and a meaningful volume to use for our simulations. We agree that this is likely to be specific for our reconstructed microcosms and that larger scale heterogeneity is expected for natural soils, which would require larger samples. The impact of tillage on microbial activity is more difficult to predict. Tillage operations will alter soil structure, but do not necessarily disrupt soil structure at the spatial scale at which microbes operate. We included a citation to a review paper by Young and Ritz which deals with the effect of tillage operations on microbial habitat and functioning. However, a quantitative extrapolation of our results to soil management is not appropriate and was not the objective of this study.

C distribution and soil structure: Soil structure and distribution of C in undisturbed soils are closely related, and separating the effects in experimental studies is complicated. Our main aim of the modelling study was to ask if the physical structure does have an impact on fungal growth. To make sure that growth would not be limited by C availability we did the majority of our simulations first at high C content. We subsequently repeated our simulations at a low C content to test if way fungi colonize soil pores was affected by C availability. We amended the aims of our work to clarify this.

Minor comments: - We have changed Fig. 6 so they have identical time scales; we retained the different scales for the biomass to make sure differences between soil physi-

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cal conditions within each graph are visible, but explicitly wrote in the figure legend that they are different for each C treatment. - The volumes of subsamples (128x128x128 voxels) do not overlap. They were cropped from each corner of 3D cube 300x300x300 voxels. No change made in the text. - We included a clarification of nearest neighbours which for our 3-D voxels only included the 6 direct neighbours. - Reference - year of publication corrected to 2004.

Referee #.2.

We have made all the corrections that were suggested, and provide more detailed response to some questions raised by this referee.

In paragraph 2: line 12 – by term parental materials we meant soil material of different origin, but on reflection we decided to delete this description in the revised paper.

The reference to visualization in paragraph 3 was deleted and the remaining suggestions were taken on board in the revision.

A more precise description of a soil sampling ring was included.

The final sentence of paragraph 3 was deleted and some sentences moved to the next paragraph to improve the structure of the paper as suggested by the referee.

A brief explanation of why other models might be less suited for spread through 3-D heterogeneous environments is included, and the aims of the paper are updated to include the work related to C-content, also following the comments made by referee #1.

The aim of the work does not directly relate to the work by Harris et al., but the same samples in which fungal spread was studied experimentally were used in this study. We are very confident that the different packing densities give different pore geometries; by definition, the porosity will reduce with increasing density. A detailed control over the pore geometry is obviously not possible in experimental systems, which is why the pore geometry was characterised with X-ray CT. The data obtained with X-ray CT agree with

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the expected changes in porosity, but in addition provide the detailed characterisation of the pore geometry that is required for our modelling study. No change to the paper was requested by the referee, and none was made.

Cubes 300x300x300 voxels were not cropped around fixed midpoint as the samples scanned were not uniform or regular. Cropping was done to reduce or avoid areas with artefacts and noise related to scanning procedure, and typically occurring near the edge of the sample. However subsamples (128x128x128 voxel size) were cropped in a consistent way using fixed midpoint of the 300 cubed samples.

We disagree with the referee that the method for the pore size distribution algorithm is not required. We think it is important to describe algorithms used to characterise soil physical properties, and we retained this description in the paper.

There was a cluster of connected pore space present in all samples. We agree that this is affected by resolution and sample size, but there were no samples where the largest cluster did not span the entire sample, which would have prevented invasive spread of fungi. None of the samples had a second cluster that spun over the entire sample, though we agree with the referee that for some specific soil structures this would have been possible. As we used a plane on one side of each sample to start the simulations, all connected pore space is automatically included in the simulations and available for fungal spread. There was no need to make changes to the manuscript.

The confusing sentence in paragraph 3.1 has been rephrased as suggested, and

Please also note the supplement to this comment:
http://www.biogeosciences-discuss.net/7/C3452/2010/bgd-7-C3452-2010-supplement.pdf

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