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Biogeosciences Discussions

Interactive comment on "An approach to the investigation of CO_2 uptake by soil microorganisms" *by* K. M. Hart et al.

Anonymous Referee #1

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bg-2011-332 An approach to the investigation of CO2 uptake by soil microorganisms K.M. Hart et al

The authors describe an experimental system to study CO2 exchange between soil and air under constant CO2 concentrations. Unfortunately, the manuscript is not up to standards and shows major issues concerning the experimental design, the data treatment, presentation and interpretation. And the manuscript has been poorly written. I will only address several main issues.

A major problem with the experimental system is that it shows a major CO2 leak to the atmosphere. The authors used a provisional procedure to correct the fluxes for this leak. However, the data seem not to be very reliable. For instance, in the initial incubations there is a very large variation in CO2 fluxes between replicas (by a factor

of 50 to 60, page 9251 line 16), which is incomprehensible given the extensive mixing and sieving of the soil. The explanation offered is at best vague (pages 9251/2).

Most of the measurements were done with the addition of 20 mM thiosulfate and it is shown that this leads to a large CO2 uptake in the soil probably due to the activity of chemoautotrophic sulfur oxidizing bacteria. This is not really surprising given the high concentration of thiosulfate used which is an excellent substrate for these microbes, but it is certainly not field relevant. So, I do not understand why the authors conclude that chemoautotrophic microbes are important in soil CO2 sequestration.

A 13C-CO2 labeling experiment was done to show incorporation of CO2 by microbial biomass trough 13C fatty acid analysis. Labeling was indeed detected in many fatty acids. However, I believe that most of the FA identifications are incorrect. The GC-IRMS chromatogram of the soil FA is rather typical (fig 10), but many of the identified FA are uncommon. 12Me15:0 should probably be a15:0 and the unidentified peak preceding it is i15:0; a16:0 doesn't exist in detectable amounts and should be i16:0; and finally all double bond positions in de mono-unsaturated FA are wrong (16:1w9 is 16:1w7 etc). It is unclear to me what happened given the extensive mass spectrometry done to identify the FA.

Also, there seems to be no relation between the peak heights of the GA the GC-IRMS chromatogram in fig 10 and the FA concentrations as given in table 4.

Many of the tables and figures are not really informative. The paper should also be rewritten and substantially shortened as there is very little synthesis.

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