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Biogeosciences Discussions

Interactive comment on "Maize root and shoot litter quality controls short-term CO_2 and N_2O emissions and bacterial community structure of arable soil" *by* Pauline Sophie Rummel et al.

Anonymous Referee #1

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The manuscript submitted by Rummel and coworkers for publication in Biogeoscienes describes the role of litter quality for N2O as well as CO2 emissions as well as bacterial community structure. The authors used litter material from maize roots and shoots which were grown under different fertilization levels, applied the materials in a pot experiment to soil which was obtained from an agricultural field and measured for a period of 22 days gas fluxes as well as chemical parameters. At the end of the incubation period also bacterial community structure was analysed. As expected depending on the C:N ratio of the litter material and the availability of easily degradable materials gas emissions and N pools in soil changed, which was also reflected by shifts in bacterial community structure. The study is nicely performed and the data presented of interest,

although not totally new. The paper is nicely written and the figures are clear. Like always in such experiments, there is the issue of water content, which was fixed to 50 % max WHK, however other water contents would for sure change the results (mainly fluctuation water levels like observed in the field) and also the use of other soil types may induce different response patter. I think here the discussion must be adapted accordingly to make sure that this is showcase but not a general response. Furthermore there are several issues that need to be considered during revision 1. The description of the sequencing data is very poor. Neither basic data on reads quality rarefraction subsampling etc is given, nor analysis of core microbiomes (together with responders) were made. I guess this is somehow a missed change and the paper would much benefit from a better integration of the molecular data. Further the sequencing data needs to be submitted to a public database. Finally it is general accepted that all DNA extraction kits contain contaminating DNA. Thus a water extraction control would be essential to remove contaminating OTUs from the data. 2. I miss data on bacterial abundance microbial biomass C and N etc. This information is required and the one hand as soil microbes are an important storage device for N. On the other hand all molecular data is relative, thus to translate the data to absolute numbers biomass values are needed. 3. I am quite confused that only three replicates were used for molecular analysis, despite 4 replicates were used for each treatment. Further I wonder why only shoots from N2 were used and not shoots from N1 treatment. 4. The provided hypothesis is very generic and I guess it must be specified as it is quite obvious that the degree of label materials influences process rates in soil.

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