

Interactive comment on “Soil nitrogen transformation responses to seasonal precipitation changes are regulated by changes in functional microbial abundance in a subtropical forest” by Jie Chen et al.

Jie Chen et al.

shenweij@scbg.ac.cn

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General Comment:

The manuscript bg-2017-3 reported soil N transformation rates in relation to soil properties and microbial functional gene abundance in a rainfall-manipulation experiment in a subtropical forest. The authors showed that the rainfall manipulation (dry-season reduction and wet-season addition) increased NO₃⁻ leaching and had a minor effect on N₂O emission, which can be linked to changes in soil properties and specific microbial functional genes (by SEM). This topic is very relevant to Biogeosciences, and the

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results are robust based on solid data (monitoring of soil properties, in situ N transformation rate measurements, and microbial functional gene measurements). I have few suggestions for the authors to consider in revision. Response: We thank the referee for his/her valuable comments. All the questions and suggestions provided by the reviewer are really helpful for the improvements of our manuscript. We acknowledged the reviewers for their constructive comments in the Acknowledgement section. The revised manuscript is attached as a Supplement to the point-by-point response to reviewers comments. All the changes have been marked in the revised version.

Specific Comments:

Comment #1: To be more accurate, DOC is EOC (extractable organic carbon). Response: Agreed. DOC has been changed to EOC throughout the manuscript.

Comment #2: The writing should be improved for clarity and readability. In some sections, it is wordy and not easy to follow the logic. Response: The writing has been carefully revised in the new version. The long sentences have been rewritten with short and clear sentences. Some sections (e.g., descriptions on N₂O measurement methods) have been largely shortened (see lines 286-311).

Comment #3: Microbial functional gene abundance has limited power in explaining the N transformation rates: a) many genes are involved in a process, and b) a gene is there does not mean it is expressed or “functioning”. This needs to be mentioned. Response: Many thanks for the constructive comment. These points have been mentioned in the section where the contributions of functional gene abundance to N transformation rates are discussed (see lines 522-529).

Comment #4: L397-402: Why select these 8 plots for the experiment? The initial differences in stand characteristics between treatments should be minimized for such an experiment. Response: These 8 plots were assigned randomly to minimize the spatial variation of soil properties. Actually, we compared the stand characteristics (i.e., species composition, tree height, tree number, DBH and crown width) between the

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precipitation manipulation plots and the control plots prior to the experiment, and found no significant differences in these characteristics. The information of stand characteristics of the two plots have been described in the manuscript (see lines 174-180).

Comment #5: Figure 1 and 5: why soil pH was not included in the SEM? Was it measured? Response: We only measured the soil pH before and after our experiments, and there were no changes in soil pH caused by the treatments either in the dry or wet season. Thus, we assumed that soil pH was not an important factor in driving the changes of functional gene abundance and N transformation rates in our treatments. Therefore, soil pH was not involved in the SEM analysis. The general information of soil pH has been added in the results section (see lines 378-383).

Comment #6: Figure 2: Why rainfall addition in the wet season did not lead to expected increase in soil water content, in both years? Also, MBC was not significantly affected by the rainfall treatment even in the dry season, which is unexpected. Do you have continuous measurement of soil moisture (by TDR or Decagon sensors) in these 8 plots? Response: No, we did not monitor soil moisture continuously during the experiment. That is probably one reason why adding water actually did not rise soil moisture: our manual sampling of soils usually lagged 1 week behind the date of water addition; we therefore missed capturing the moisture changes caused by the water addition. There may be other reasons for the result of lower soil water content in water addition plots. The larger trees in the precipitation addition treatment plots (height: 10.2 ± 5.0 m, DBH: 10.7 ± 6.3 cm) may have greater transpiration rate than the trees in control plot (height: 7.7 ± 3.5 m, DBH: 9.5 ± 5.2 cm) in summer, which might have caused greater soil water loss in the water addition plots compared to the control plots. We have tried to minimize the stand variation by selecting the plots with similar vegetation features before the experiment, but it was difficult to find 8 plots with the same stand characteristics in field. Secondly, more than 55 mm water was added each time in the wet season which might result in flood-irrigation in the precipitation manipulation plots. As suggested by previous studies, flood-irrigation could break the

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soil pores and lead to soil structural decline (Barber et al., 2001; Murray and Grant, 2007), which may affect the water retention capacity, as soil water retention capacity is related to pore-size and pore-distribution (Loll and Moldrup, 2000). More discussions have been added to address such concerns (see lines 445-458). We expected that MBC would decrease under the precipitation reduction treatment. But actually MBC was not significantly changed by the 67% of precipitation reduction during the dry season. This result is also confirmed by the unaffected total microbial phospholipid acids (PLFAs) as reported in Zhao et al. (2017). We argue that the main reason was that soil moisture reduction (10-21%) was not as severe as we expected – it only decreased by 10-21% in responding to a 67% precipitation exclusion. Such a moderate reduction of soil moisture might have not reached the point at which microbial growth and other activities can be limited. Although the total microbial biomass was not changed, but the composition of the microbial community was altered, which have been reported in Zhao et al. (2017). Barber, S.A., Katupitiya, A., and Hickey, M.: Effects of long-term sub-surface drip irrigation on soil structure, Proceedings of the 10th Australian Agronomy Conference, Hobart 2001. Loll, P., and Moldrup, P.: Soil characterization and polluted soil assessment, Aalborg University, 2000. Murray, R.S., and Grant, C.D.: The impact of irrigation on soil structure, The national program for sustainable irrigation (Land & Water Australia), Braddon, 2007. Zhao, Q., Jian, S., Nunan, N., Maestre, F. T., Teder-soo, L., He, J., Wei, H., Tan, X., and Shen, W.: Altered precipitation seasonality impacts the dominant fungal but rare bacterial taxa in subtropical forest soils. *Biol. Fertil. Soils*, 53, 231-245, doi: 10.1007/s00374-016-1171-z, 2017.

Comment #7: Table S2: stand characteristics (species composition, stem density, tree height, basal area, etc.) should be included. Response: The information of vegetation characteristics for the precipitation manipulated plots and control plots has been added in the manuscript (see lines 174-180).

Please also note the supplement to this comment:

<http://www.biogeosciences-discuss.net/bg-2017-3/bg-2017-3-AC3-supplement.pdf>

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