

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.

Anonymous Referee #2

Received and published: 27 February 2017

This manuscript uses an interesting design to explore the complex relationships between changes in precipitation regimens and soil N dynamics. The authors monitored changes in microbial functional genes, N-mineralization rates, and soil N₂O flux to understand how changes in precipitation regime, but not total precipitation amount, might affect soil biogeochemical cycles (i.e. N-cycle). Results indicated that 20% of total N-mineralization and nitrification rate were explained by microbial abundance (determined via fumigation) and soil moisture content, and that amoA abundance also helped to explain a significant portion of variation in measured N pools. Together, the results indicate that predicted changes in seasonal precipitation associated with

[Printer-friendly version](#)

[Discussion paper](#)



changing climate may result in increased NO₃⁻ leaching from soils and decreases in N₂O emissions.

Although the manuscript is scientifically sound and interesting, it should be heavily edited for proper grammar, spelling, and sentence structure.

Specific Comments: Line 35-37: the wording of this sentence is confusing, please clarify “main factor” (i.e. is it a statistical inference that is meant here?) Line 39: do the authors mean “both dry and wet seasons”? this sentence should be clarified. Line 43: what was “determined by changes in DOC and NH₄⁺”? please clarify this conclusion. Line 49: this sentence is missing a word, are the authors indicating that precipitation changes have been observed as increasingly severe, or that they are predicted to be increasingly severe. Line 54: how have changes in precipitation events have exceeded other climate change-related fluctuations? Line 57: seasonal redistribution of what metric? Line 123: reference for the SEM? Also, please introduce SEM and how/ if they have been previously used in a similar manner. Line 130: please clarify “easily” Line 135-145: please add a reference for these data, or indicate how the authors collected the data. Line 174: was this water also examined for microbial community structure and functional genes? Is it possible that this water acted as a source of microbial change? Line 231: why did the authors not also quantify bacterial and archaeal 16S rRNA genes? The assay would independently confirm results indicated by chlороform fumigation techniques, and may potentially help to shed light on the negative results associated with amoB gene quantification. Line 381: could the opposite also be true here? That alterations in DOC and N are due to changes in functional gene abundance? Line 398: reference? Line 424: is there a figure or table that would also demonstrate this statement? Line 433: please clarify this sentence, how are microorganism responsible for reducing microbial abundance? Line 444: are there other appropriate references available here? Figures 2-5 would benefit from the addition of panel indicators (i.e. “Fig1 A”) to help clarify to the reader exactly which data the authors are discussing in the MS. Fig 5: this is a nicely illustrated complex figure.

BGD

Interactive comment

[Printer-friendly version](#)

[Discussion paper](#)



Interactive
comment

[Printer-friendly version](#)

[Discussion paper](#)

