

Interactive comment on “Soil Denitrifier Community Size Changes with Land Use Change to Perennial Bioenergy Cropping Systems” by K. A. Thompson et al.

Anonymous Referee #3

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The manuscript is based on the detection of nirS and nosK gene copies that could be useful to stimate the relative functional community variation, in the attendance with the title” Soil Denitrifier Community Size Changes with Land Use Change to Perennial 1 Bioenergy Cropping Systems.

However, as a consequence of the research approach there are some limitations to the scientific relevance of the manuscript. First, the adopted DNA soil extraction method do not permit to discriminate between relic DNA pool and the intracellular poll, without considering the PMA approach to discriminate by qPCR between relic and living cells due to contradictory results on its effciency on soil environment. Second, it is no possible to discriminate between the different nitrification/denitrification pathway and

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the related microbial community. Third, It is also not possible to discriminate which of the detected species is active in the gene function without mRNA detection. Fourth, it is no possible to discriminate between the potential activity and the real activity of the nirS and nosK bacterial species. Finally result impossible to obtain extremely interesting data by coupling these data with those related to soil N₂O/N₂ emission.

The present contribution for the above reported consideration represent a fair study of the topic but with the suggested revision, previously sent, could be published.

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