SOIL Discuss.,
doi:10.5194/soil-2016-34-RC1, 2016

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 #1

Received and published: 29 July 2016

The manuscript represents a good contribution to scientific progress within the scope of SOIL; it include a multidisciplinary approach and also this is good. The results are well discussed in a balanced way and conclusions are presented in a clear and cocise way; the English is appropriate. The approach and applied methods are valid even if I have some doubts about the choice of the gene used in qPCR, because of the reason I explain below.

The authors aim was to compare the effects of LUC from corn-soybean to PG biomass production on the relative abundances of total (16S rRNA gene target) and denitrifier (nirS and nosZ gene 94 targets) soil bacterial communities.

But, from literature (Case et al., 2007 Appl. Env. Microbiol. 278–288; Větrovsky

Printer-friendly version

Discussion paper

and Baldrian, 2013 PLoSONE 8(2): e57923. doi:10.1371/journal.pone.0057923) we know that the 16S rRNA gene copy numbers per genome vary from 1 up to 15 or more copies. This limits the interpretation of 16S rRNA-derived results, specially for a quantitative interpretation of the soil bacterial community. The use of a single-copy in this case would be more appropriate and could allow for a more accurate measurement of microbial community.

Thus, I suggest to the author to add some more reasons about the choice of 16SrRNA gene for bacterial quantitative purposes.

Interactive comment on SOIL Discuss., doi:10.5194/soil-2016-34, 2016.