

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

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Thank you for your review of our paper. We will adjust the language we use regarding our interpretation of our 16S rRNA results in the discussion as advised. Additionally, we will add in some text regarding our choice of 16S rRNA as follows:

16S rRNA was chosen as a molecular target for the total bacterial community size; although 16S rRNA gene copies vary from 1-15 copies per genome, its use has continued to be the ‘gold standard’ for microbial ecology (Case et al., 2007; Vos et al., 2012). Although an alternate target, such as *rpoB*, which is a single copy gene would be valuable if assessing phylogenetic diversity, there are no universal primers for it (Adékambi et al., 2009) as *rpoB* is not conserved enough to be of use as a univer-

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sal marker and only a subset of the microbial community can be targeted (Vos et al., 2012). Therefore in order to use *rpoB* as a target we would have had to design a suite of different primer sets to target several orders within the same bacterial phylum, which was not feasible for this paper, and would not have measured total bacterial abundance from our diverse environmental soil samples. Taking this into account, many studies have used 16S rRNA gene copy numbers as a proxy for the total bacterial community size; and some have found that the total estimated numbers of proteobacteria species was not significantly different if using *rpoB* or 16S rRNA markers (Vos et al., 2012). As this study has not assessed phylogenetic relationships of the microbial communities, 16S rRNA is an appropriate target for the relative comparison of the overall bacterial community size between environmental treatments/variables.

Adékambi, T., Drancourt, M., Raoult, D., 2009. The *rpoB* gene as a tool for clinical microbiologists. *Trends Microbiol.* 17, 37–45. doi:10.1016/j.tim.2008.09.008

Case, R.J., Boucher, Y., Dahllöf, I., Holmström, C., Doolittle, W.F., Kjelleberg, S., 2007. Use of 16S rRNA and *rpoB* genes as molecular markers for microbial ecology studies. *Appl. Environ. Microbiol.* 73, 278–88. doi:10.1128/AEM.01177-06

Vos, M., Quince, C., Pijl, A.S., Hollander, M. De, Kowalchuk, G.A., 2012. A Comparison of *rpoB* and 16S rRNA as Markers in Pyrosequencing Studies of Bacterial Diversity 7, 1–8. doi:10.1371/journal.pone.0030600

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