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Interactive comment on "Competitive interactions between methane- and ammonia-oxidizing bacteria modulate carbon and nitrogen cycling in paddy soil" *by* Y. Zheng et al.

Anonymous Referee #4

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In their study, Zheng and co-workers investigated the competition between methane and ammonia oxidizers in paddy soil microcosms. Soil slurries were incubated with 13-C labelled CH4, 13-C urea, and 13-C-CH4 and 13-C-urea. Soils were incubated for 5 and 19 days. Methane oxidation and nitrification rates were determined and the microbial community was analyzed by qPCR and amplicon sequencing targeting the 16S rRNA and the marker genes pmoA/amoA. The authors could show a strong stimulation of methane oxidation by urea addition and on the other side, a decrease of nitrification rates by methane addition. Within the methane oxidizing community, type Ia methanotrophs were highly enriched under the tested conditions and also labelled. Within the ammonia oxidizers, Nitrosospira was most abundant; however, Nitrosomonas domi-

nated the labelled fraction. Ammonia oxidizing archaea do not seem to play a role in this system. Furthermore, the authors describe the labelling of 16S rRNA genes affiliated to known methanol degraders, indicating the close food web between methanotrophs and methylotrophs that feed on methanol.

This is an interesting topic and the authors used an appropriate experimental approach to address this question. Nevertheless, the documentation of results and discussion is in my opinion not always concise and the manuscript contains too many figures and tables. This experiment contains a large dataset and not every aspect has to be discussed. However, what is missing in my opinion is the overall result of the 16S rRNA pyrosequencing (Archaea and bacteria). Of course it has not to be discussed in detail, but it should be shown to follow the authors' argumentations and the selection of specific subsets.

Specific comments: In my opinion, not all phylogenetic trees have to be shown. Information on abundance and labelling could be combined in single trees. Furthermore, if shown at all, trees in figure 4b and S7b should be mirrored. A presentation like this only makes sense in direct comparison of 16S and functional genes as in figure S3 and S4. Figure S8 is not important here. Side 3911 Lines 13-27: There are already genomes of methanotrophs published. The authors should check this. As far as I remember, sequenced type Ia methanotrophs have a single copy of the rRNA operon as well as the pmoA (excluding the very different isoenzyme).

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