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Interactive comment on "pH-based ecological coherence of active canonical methanotrophs in paddy soils" *by* Jun Zhao et al.

Anonymous Referee #2

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Zhao et al. investigated the active aerobic methanotrophs in six different paddy soils. They do find the key roles of pH in mediating the niche differentiation of aerobic methanotrophs. Methylocystis-affiliated type II methanotrophs were most active in soils with pH (5.44-6.10), while Methylobacter/Methylosarcina-affiliated type I methanotrophs were most active in soils with pH (7.02-8.02). In addition, no significant changes in 13C-labelled methanotrophic community compositions was detected with the fertilization of ammonium nitrate. The study is interesting and the manuscript is well written. The questions are appropriately introduced and explored and the results are well presented. Therefore, I would recommend the manuscript for publication. However, it should be noted these results were obtained from rice paddy soils. The consistency in other soils should be further studied. For example, deng et al. 2016

(Ref: Identification of active aerobic methanotrophs in plateau wetlands using DNA stable isotope probing) found that both Methylocystis and Methylobacter methanotrophs were dominated in methane consumption in Dangxiong peatland soils with a pH of 6.1. Therefore, the authors should consider more comprehensively when interpreting the results. In line 217, why did the authors cluster the pmoA genes at a nucleotide level of 93/ similarity. In fact, we usually define 93/ similarity at amino acid level and corresponding to methanotrophic species (Reference: Lüke C. and Frenzel P., 2011 Potential of pmoA Amplicon Pyrosequencing for Methanotroph Diversity Studies). If the authors want to cluster the pmoA sequences at a nucleotide level, Wen et al., updated the pmoA gene cutoff at nucleotide level to 86/ corresponding to 97/ similarity of 16S rRNA gene (Reference: Wen et al., 2016 Evaluation and update of cutoff values for methanotrophic pmoA gene sequences).

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