

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

Anonymous Referee #1

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This study combined DNA-based stable isotope probing (DNA-SIP) with high-throughput sequencing to identify the taxonomic identities of active methanotrophs in physiochemically contrasting soils from 6 different paddy fields across China. They found that pH is potentially the key driving force selecting for canonical gamma- (type I) and alpha- (type II) methanotrophs in rice paddy soils. It is of interest and innovate to check if the specific functional microbes like methanotrophs are selectively favoured under different pH conditions in natural wetland system. In general, the manuscript is well-written, the results are sound to me, and the discussion are profound. I only have several minor comments as follows: 1. Authors provide solid evidences proving the pH-based ecological coherence of active canonical methanotrophs in paddy soils, but no significant difference of CH₄ oxidation was observed between high-pH and low-pH

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soils. Why? Please added some discussions. 2. Each microcosm incubation was completed at different time and the longest might be 42 days. Is the microcosm still under oxic condition? Is there any indicators? 3. Subsection 2.8. Sequence data processing and deposition, where is the sequence data deposited? 4. One of the important things for SIP study is to compare the unlabelled and labelled treatments and then identify the labelled microbes. In this study, the control was set as microcosm under natural atmospheric condition. Why not with ^{12}C - CH_4 supplementation. Please discuss the possible effect in the discussion.

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