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Discussions

Interactive comment on "Distribution of ammonia oxidizers in relation to vegetation characteristics in the Qilian Mountains, northwestern China" *by* X. S. Tai et al.

Anonymous Referee #1

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Tai et al describe the distribution of ammonia oxidizers along the alpine meadow soils in northern China. They determined the amount of ammonia oxidizers' amoA genes and their diversity. The aim of the study was to find out the distribution patterns of ammonia oxidizers along the Qilian Mountains. Some of their results were interesting. However, this MS had some limitations which should be addressed.

Specific concerns about the manuscript: 1. Although the quality of English is generally satisfactory, the paper would require language editing to correct non-standard phrases. For example, in page 5125, alpine meadow covered, the " covered" should be as covering. In page 5129, the sentence " Nutrient poor soils are usually indicated by ....dissolved N poor." need to be polished. 2. Materials and methods; from Fig.1

we know the sampling sites cover a large area, but why the size the sampling site was not described in this MS? Moreover, how the author made sure three quadrats could represent the different types of alpine meadow? As we all know, the spatial variability is huge for plant or soil in a mountain area. And which level of soil was taken for this study? 3. Materials and methods; only fifty clones of each library were picked up for sequencing. Is it enough to represent the diversity? Had the author done the rarefaction curves analysis ? Moreover, they might have sequenced 1500 clones for AOA and AOB according to the author's description. However, only 175 sequences of amoA genes were deposited in genbank. In my opinion, all sequenced clones should be submitted to genbank. 4. Materials and methods; nitrification rate is an important indicator for ammonia oxidizing enzyme activity. However, the data was not present in this MS. 5.Results; in page 5130, line 4~10, "Group I.1a. . . . ..", the long sentence was not suitable in here or to be concised. Fig. 4. and Fig. 5 were bad at presentation. The phylogenetic trees of amoA in supplemental materials were better. But both of them should be added the access number information in the phylogenetic trees. 6. For Q-PCR analysis of amoA genes, the author had listed the standard curve of amoA gene Q-PCR and their R2, efficiency. However, from the supplemental materials and Fig. 2, we know the copy numbers of bacterial and archaeal were very low. So I am not sure these data really represent the AOA and AOB populations. Sometimes even the negative control could be detected a signal as high as the data present in this study. Please attach the Q-PCR and their melting curve graphs in the supplemental materials. 7. Discussion; in this part, the author always stayed in a descriptive model, and didn't convincingly explain the distribution pattern of AOB and AOA in five different alpine meadow.

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