Biogeosciences Discuss., 11, C1561–C1563, 2014
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Biogeosciences
Discussions
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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 #3

Received and published: 11 May 2014

In this study the authors investigated the abundance and community composition of ammonia oxidizing archaea and bacteria in meadow soils of northwestern China alpine environments. Five meadow soils were investigated which differed in the composition of the meadow vegetation. The authors found that AOA outnumbered AOB at all sites with one exception, and that the different meadow types influenced the community composition of AOA and AOB. Here, vegetation cover was the most important explanatory variable. The topic is of general interest to readers interested in distribution patterns of ammonia oxidizers in different environments. However, in this merely descriptive inventory of AOA and AOB abundance and community composition, the biogeochemical relevance of the observed community patterns in terms of nitrification

activity remains unclear. Nitrification rates were not measured, and the soil chemical data are not discussed in this context. Consequently, the contribution to our current knowledge in this field is very limited. With the objectives stated at the end of the introduction, the authors follow an experimental design that has been used in numerous studies before. They should place their study more clearly in the context of previous research. The sentence that "More studies about the relative contributions of AOA and AOB to ammonia oxidation are necessary" (p. 5125, l. 25-26) is very general, and the aspect of ammonia oxidation activity is not addressed in this study. The authors should point out more clearly what their expectations or hypotheses were regarding potential effects of meadow types on ammonia oxidizers. Besides, the interpretation of data needs revision. As one can see from Fig. 2b, the gene copy numbers of amoA are rather low compared to other studies and differences between meadow types are not large. Here, the authors should compare the observed gene abundances to published data from other soils, and they should discuss the observed differences among sites in the context of the error range of the qPCR method. Similarly, I wonder if 50 sequences per clone library are enough to reliably calculate relative fractions of individual phylotypes and to use these data for multivariate statistics. What was the coverage of the clone libraries? Was it the same for all the samples to allow the comparison among samples? Finally, large parts of the discussion consist of a summary of literature findings, however, the link to the results obtained in this study is not always clear (e. g., p. 5132, l. 1-19, p. 5133, l. 18-26). Here, a thorough revision of the discussion is needed to place the authors' findings more clearly in the context of other studies. Especially the observed relationship between AOP community composition and vegetation type and coverage is poorly discussed. What could be the mechanisms by which vegetation has an influence on the community composition and abundance of AOA and AOB? Why should especially vegetation cover play a role in these relationships?

Specific comments: p. 5126, l. 24: Please indicate from which depth soil samples were taken. p. 5128, l. 2: Should the annealing temperature for this primer set not be 53°C instead of 63°C? Please check. p. 5128, l. 15: Why did the authors use a cutoff

of 0.03 for OTU assignment? Please explain. p. 5128, l. 25: Please provide the name of the software used for tree calculation. p. 5129, l. 16: What does "a high NH4+" mean? Please provide numbers. p. 5129, l. 18: Please provide gene copy numbers in the text. What was the estimated relative fraction of AOA and AOB within the total community? Would this yield the same overall picture of differences among sites? p. 5130, l. 4-10: Please provide a reference for the nomenclature of AOA phylogeny. p. 5131, l. 3-8: Why did the authors not include NH4+ in the RDA analysis? p. 5132, l. 23-25: What is the basis of defining a new AOA group? What was the sequence distance to other groups? p. 5132, l. 25: What is so special about the study region? Please explain. p. 5133, l. 17-18: A similar sentence already appears in the results section (p. 5130, l. 26-27). This conclusion is too general, please be more precise. Fig. 3: What is the difference between the two graphs shown in this figure? Fig. 4 and 5: More reference sequences from other studies and cultured species should be included in the tree calculation.

Interactive comment on Biogeosciences Discuss., 11, 5123, 2014.