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Biogeosciences
Discussions

Interactive comment on "High diversity of nitrogen-fixing bacteria in upper reaches of Heihe River, Northwestern China" *by* X. S. Tai et al.

X. S. Tai et al.

leafturnred@163.com

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Dear M. K. Cheung: Thank you very much for your helpful suggestions. We will deal with them seriously in revised paper according to your comments. For the question 7 and 10, our reply is as follows: Phylogenetic dendrogram based on a comparison of the nifH sequences of clone libraries from shrub and meadow soils and some of their closest phylogenetic relatives. The tree was created using the neighbor-joining method. The numbers on the tree indicate the percentage of bootstrap sampling derived from 1000 replications. The tree is based on nucleotides. A total of 64 nifH clones of the unique RFLP patterns were sequenced and used for tree calculation. The representatives which most closely related to the nifH sequences in GenBank database were obtained by BLAST, coupled with the nucleotides of sequenced clones, the alignment

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was done with ClustalX (version 1.8). In case any questions arise, please contact me! Best wishes for you! Sincerely yours, X. S. Tai

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Interactive comment on Biogeosciences Discuss., 10, 5015, 2013.

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