

## ***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.**

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Dear Tina Treude,

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

Thanks a million for your suggestions and the reviewers’ comments! They are really helpful to improve our manuscript. I discussed with all the other authors and tried our best to revise the manuscript very carefully. Now the revised parts were in blue colored text. Here, we would like to address the detailed changes.

Comments to the Author 1. Gene symbols, e.g. "nifH", should be italicized throughout the text. Thanks! We italicized it.

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2. Spelling of scientific names should be checked carefully. E.g. it should be "Pseudomonas" instead of "Peseudomonas". Thanks for catching my typo! I'll be more careful.

3. P.5019, lines 6-8: a reference should be given to the primer set used here. The reference is provided now.

4. It is strange and cumbersome to devise a new section with only one single sentence. So section 2.3 in the M&M should be combined with section 2.4, and section 2.10 combined with section 2.6. The same also holds for section 2.8. We make changes as being suggested.

5. P.5019, line 17: as there are many varieties of the "heat shock method", a reference should be given here for clarification. We added the reference.

6. It should be "GenBank" instead of "Gen Bank" throughout the whole text. We changed it.

7. P.5020, lines 7-8: More details about the phylogenetic analysis should be given here. E.g. What's the model of nucleotide substitution chosen? How many bootstrapping replicates are performed? The tree was created based on a comparison of the nifH gene sequences of clone libraries from shrub and meadow soils and their closest phylogenetic relatives by using the neighbor-joining method and 1000 bootstrapping replicates were performed.

8. P.5021, line 10: the unabbreviated term is no longer required here as it's not the 1st time it's being abbreviated. Thanks for your kind reminder! It was changed.

9. The conclusion is too long, with so many raw data/results repeated. A more concise conclusion, preferably with insights into future directions, is expected. Thanks for the suggestion. We will rewrite the conclusion in revised ms.

10. Figures 4 & 5: Additional details should be given in the legend. E.g. What do the numbers at the modes represent? Also, coloring the figure according to e.g. the type of

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Proteobacteria, should facilitate the readability of the figures. Thanks. We changed it as suggestion. The numbers on the tree indicate the percentage of bootstrap sampling derived from 1000 replications.

Thanks again for your suggestions and referees' comments! I hope that the responses answer the Reviewers' comments, and that he and his colleague feel these are reflected in the revised manuscript. I look forward to hearing your decision soon.

Yours sincerely, Xi Sheng Tai

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

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