

1 **Bacterial contribution to nitrogen processing in the atmosphere**

2 by F. Mathonat et al.

3 **Author response to comments by Referees**

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5 We sincerely thank the editor and the two reviewers for their constructive comments, which have significantly
6 improved the quality of the final manuscript.

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8 Report Referee #2

9 I comment the authors for their thorough revisions and for their transparency in addressing the technical errors
10 previously identified. The manuscript is significantly stronger, and the focus on the "nitrogen processing" and
11 "bio-assimilation" narrative is much better supported by the data.
12 Before the manuscript is accepted for publication, I ask the authors to address the following minor but important
13 points:

14 Thank you for your positive assessment of our work and for your constructive comments, which helped elaborating
15 an improved version of the manuscript. Please find our point-by-point responses below.

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18 - Section 4.2.4 and abstract: The global estimate of 18×10^6 kg N₂ per year is calculated assuming that 15% of all
19 atmospheric Pseudomonadota are diazotrophs. As discussed in our previous exchange, this 15% value was derived
20 from a targeted screening of 34 strains pre-selected for their likelihood of carrying nifH. Applying this percentage
21 to the entire phylum for a global estimate is an overstatement.
22 It is therefore should be stated as a "theoretical upper-bound estimate" in both abstract and Discussion and that the
23 15% refers to the screened candidate isolates, not the broader atmospheric community.

24 Thank you for your comment. We have added in Section 4.2.4 that this represents a theoretical upper-bound
25 estimate.

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28 - Conclusion: One of the most interesting findings in the Meta-T data is that several N-related functions showed
29 higher RNA:DNA ratios in clear air than in clouds. This may challenges the paradigm that liquid water in clouds
30 is the primary driver of activity. Thus, authors should ensure the Conclusion Section reflects this nuance, noting
31 that while functional resilience is maintained across both conditions, transcriptional activity for many N-processing
32 genes was notably higher in clear atmosphere samples.

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34 Thank you for your comment. We have included an additional sentence in the conclusion stating that metagenomic
35 and metatranscriptomic data indicate that microbial activity associated with the nitrogen cycle is maintained across
36 atmospheric conditions (cloud or clear atmosphere).

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38 - There is a different between the track-changed file and the updated manuscript file. Some changes are not seen
39 in the later. for example, the updated statistical analysis section, presented in the track-changed version is not
40 seen in the updated manuscript file. please check this and all other changes made.

41

42 Thank you for highlighting this issue. We have reviewed and updated the submitted version of the manuscript
43 accordingly.