

Interactive comment on “Environment Gradient related Dissimilatory Nitrate Reduction to Ammonium in Huangmao Sea Estuary: Rates and Community Diversity” by Ran Jiang et al.

Ran Jiang et al.

458750084@qq.com

Received and published: 1 April 2019

C1: The English of the paper needs an overhaul. Most of the sentences are wrong, unclear, lacking logic, or misleading. Some references cited in the main text are missing in the list.

R1: The English of the paper has been carefully checked and some paragraphs have been completely rewritten. The missing references have been added in the list.

C2: The methods were not described clearly. Many key details are missing. For example, the one-year observations were not stated; the biogeochemical parameters

[Printer-friendly version](#)

[Discussion paper](#)



Interactive
comment

(temperature, salinity, nutrient concentrations, etc.) measurements are missing; the procedure of the high-throughput sequencing of the *nrfA* gene is incomplete: : :

R2: In the revised manuscript, the description of the methods has been rewritten.

C3: The method on time-series incubations with supplemental ^{15}N -NO₃⁻ to examine potential rates of DNRA needs to clarify the cross-feeding effect since heterotrophic bacteria can uptake ^{15}N -NO₃⁻ and release ^{15}N -NH₄⁺ to the experiment system.

R3: We take most denitrifying and DNRA bacteria can grow heterotrophically while some grow autotrophically. In the revised manuscript, the clarification for the method on time-series incubations with supplemental ^{15}N -NO₃⁻ to examine potential rates of DNRA has been provided.

C4: There is no statistical analysis in this manuscript. All statements and conclusions on the control of environmental parameters on communities are not supported by any specific analysis or statistical test.

R4: The statistical analysis has been provided in the revised manuscript, to support the statements and conclusions addressed in this work.

C5: The whole paragraph of “2.4 Rate calculations” (Page 4, Line 22-30) was plagiarized from the literature. Also, some statements in the Introduction section (Page 2, Line 17- 22) were from the literature directly.

R5: These sentences have been revised.

C6: Very few discussion was made in the Results and discussion section. And the descriptions are not logical and distracted!

R6: More discussion has been provided in the “Results and discussion section”. We paid more attention to present them logically.

C7: The authors did NOT analyze RNA but used “transcripts” to describe the gene copy abundances throughout the manuscript.

[Printer-friendly version](#)

[Discussion paper](#)



Interactive
comment

R7: The mistake has been corrected.

C8: All figures were unclear. There are Chinese characters in Figure 2. The phylogenetic tree is too rough.

R8: These figures are revised. The mistake in Fig. 2 has been corrected. The figures mentioned by the reviewer have been modified to improve their quality. Fig 3,5 have been remake by Arcgis soft. Fig 7 was still difficulty to show the minor number of bacteria. The phylogenetic tree have recalculate the similarity rate and delete some unrelated strain fragments.

Please also note the supplement to this comment:

<https://www.biogeosciences-discuss.net/bg-2019-31/bg-2019-31-AC5-supplement.pdf>

Interactive comment on Biogeosciences Discuss., <https://doi.org/10.5194/bg-2019-31>, 2019.

[Printer-friendly version](#)

[Discussion paper](#)

